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The International Treaty ON PLANT GENETIC RESOURCES FOR FOOD AND AGRICULTURE

BOOSTING THE BIG DATA OF PLANT WITH DIGITAL IDENTIFIERS

Editors:
Muhamad Sabran | Puji Lestari | Dani Satyawan
Toto Hadiarto | Mastur | Rerenstradika Tizar Terryana

IAARD PRESS
AGRO INOVASI

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PREFACE

Significant research findings have been achieved in the area of information technologies concerning the utilization of plant genetic resources (PGR). Many progresses of big data produced from biological computation, omics and relevant management of the PGR have been reported. Despite the numerous contributions, there still exists a lack of representative information of the resulted big data of PGR along with digital object identifiers (DOI).

This book contains several articles with various topics. Some articles have been presented at the conference on "Boosting Big Data of Plants with Digital Identifiers" held in Bali, Indonesia, June 11-13, 2019, and some others are purposively written for this book. The main articles are on the use of DOI as permanent unique identifier on PGR; however, some papers presented at the conference also include papers on Intellectual Property Rights (IPR) related to PGR and gene bank management. To give the reader a broad overview on the big data of plant, two articles on the fourth agriculture revolution and Global Information System (GLIS) on PGR are introduced in chapter 1. Chapter 2 reviewed the rights, conservation and use of PGR.

The purpose of this book and the conference is to introduce to the scientific community, in particular agricultural scientist, the use of DOI as permanent unique identifier for plant genetic resources for food and agriculture (PGRFA); since agricultural scientist is one of the primary beneficiaries of the use of DOI on PGRFA. The assignation of DOI on PGR will trigger

improvement in crops information system and facilitate the appropriate and quality-controlled sharing of information of the PGRFA data. The adoption of unique identifier will further empower genomic and phenomic researches, functional gene discovery and increase the efficiency and effectivity of plant breeding program, which, ultimately increase the capacity to adapt to the climate change and food security.

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Bogor, April 2020

Editors

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PROLOGUE
BOOSTING BIG DATA OF PLANTS WITH DIGITAL IDENTIFIER

The extensive application of information technology in all supply chain activities will change the way of doing business. Those changes break the existing path and start a new era in industry, i.e. 4.0 industrial eras or the Fourth Industrial Revolution. Agriculture, as an industry, also enters this new era. By agriculture we means the process of harvesting solar energy through plant and transform it into product such as seeds, fruits, fibres or other products which might be developed further by animals. Millions of plant species found on earth and within plant species are a huge variation of genotypes or in many cases of group genotypes with similar phenotypic expression often called as cultivars, if it has been domesticated. This huge variation of plants will create big volume of data if they should be recorded and arrive in increasing velocity which often called as big data.

In the era of big data, one of the significant challenges scientists and researchers face, as they work to improve performance and productivity, is the need to access information about germplasm quickly and efficiently. Some of the big steps forward that many sectors have taken recently rest on the application of standards to produce, store and share data. Such approaches facilitate collaborative research and scale up the value of datasets and the related products.

While scientists and researchers are all interested in securing funding for research and access to new genetic material with desired traits for plant breeding, equally important is the related information. They want to benefit from automatic aggregation of related dataset across institutions and projects worldwide with a minimum effort. For years, they have been seeking better linkages between research datasets and scientific publications, and have been anticipating new data discovery functions and analysis tools to simplify their work.

The quality of big data of plant genetic resources for food and agriculture (PGRFA), play very important roles in agriculture research collaborations and communications. The International PGRFA community has tried to agree on common approach to facilitate the establishment of automated meaning links through the adoption of Permanent Unique Identifiers for improved identification of PGRFA. The reasons are the difficulty of collaboration on conservation, research and breeding without a common standard for identification, and the difficulty of finding information associated with the material. Following broad consultation, Digital Object Identifier (DOI) was selected as the most appropriate, web-resolvable digital identifier.

The International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) has established a Global Information System (GLIS) to facilitate linkage between existing systems and including the gene bank community, genomics community, plant breeders and journal editors. The broad definition of PGRFA encompasses not only accessions conserved in gene banks and PGRFA conserved in situ, but also breeding lines, research materials, and protected modern varieties. This allow for registration of DOIs applicable to all types of PGRFA. In addition, GLIS will not replace existing systems or duplicate their functionality but provide new services needed by the user

community and missing from existing systems. It is hoped that DOIs will become the global standard for public identification of PGRFA and will facilitate the effective crop improvement

Crop improvement is the main goal of plant genetic resources management. New techniques of crops improvement has emerged in this decade. These techniques, substantially differs from the conventional one, may result in more predictable and shorter period crop improvement. The key of the new techniques are the underlying molecular mechanisms, product based approach, precision breeding and potential application of synthetic biology, genome editing and gene drives. In addition to these new techniques, sequencing genomes of plant genetic resources (PGRs) increases faster breeding and complements with phenotypic characters. These new techniques as well as the old ones should be supported by the availability of PGR materials. Therefore proper management of gene bank including exchanges of genetic materials is necessary, however this exchanges of materials should recognize the sovereign rights of countries with regards to PGR or genetic resources in generals. These rights have been regulated by the Nagoya Protocol of the Convention of Biological Diversity and the Multilateral System of access and Benefit sharing of the ITPGRFA.

Muhamad Sabran and Puji Lestari

CHAPTER 1.
THE FOURTH INDUSTRIAL REVOLUTION AND GLOBAL INFORMATION SYSTEM ON PLANT GENETIC RESOURCES FOR FOOD AND AGRICULTURE

End hunger, achieve food security and improved nutrition, and promote sustainable agriculture are the second goal of the Sustainable Development Goals (SDGs). Agricultural productivity is also targeted to double and ensure sustainable food production systems and implement resilient agricultural practices in 2030 and beyond. The increase of productivity and production is also intended to help maintain the ecosystems, strengthen our capacity for adaptation to climate change, extreme weather, drought, flooding and other disasters, in addition to progressive improvement of land and soil quality. By 2020, the second goal has also set a very important target to maintain the genetic diversity of seeds, cultivated plants and varieties through soundly managed and diversified seed and plant banks at the national, regional and international levels. The Fourth Industrial Revolution (4IR) is defined as the crosscutting impact of information and communication technologies, especially Artificial Intelligence (AI), Internet of Things (IoT, and Cyber-Physical Systems (CPS). The concept of 4IR affects the agriculture sector and introduces significant changes in the way of

agricultural production systems in more efficient performance in the upcoming years. This revolution is supported by the development of systems that transfer the ubiquitous advantages of the latest technologies towards crop production systems, as well as agriculture sector in general.

Crops are cultivated or domesticated plants. Approximately seven million crop accessions are being conserved in genebank collections worldwide. This resource represents one of the greatest, largely untapped, opportunities for accelerating yield gains and overcoming emerging crop productivity bottlenecks. However to access this wealth of diversity will require the characterization of this material via the application of state-of-the-art genomic, phenomic and molecular technologies, and the release of the subsequent data via an online, open-access portal. Using the emerging deluge of omics data along with mathematical models and systems biology approaches, we can now study this diversity to reveal the many ways in which nature has solved these problems, and how humans have shaped the genomes of crop plants through domestication and breeding. This information will provide unprecedented insights into the intricate and finely tuned genetic networks that enable plants to respond to subtle or catastrophic perturbations in the environment. The International Treaty on Plant Genetic Resources for Food and Agriculture has developed the Global Information System to facilitate exchanges of information among the PGRFA community on non-confidential information on PGRFA, including their associated genomic and other omics data.

THE FOURTH INDUSTRIAL REVOLUTION AND EMBRACING THE LATEST TECHNOLOGIES TO SUPPORT CROP PRODUCTION SYSTEMS AND SUSTAINABLE AGRICULTURE

Haryono Suparno

INTRODUCTION

FAO's vision is of a 'world free from hunger and malnutrition, where food and agriculture contribute to improving the living standards of all, especially the poorest, in an economically, socially and environmentally sustainable manner', to help its Member Countries realize that shared vision – individually at the national level and collectively at the regional and global levels. In line with the FAO's vision, the second of the 17 Sustainable Development Goals (SDG's) is End Hunger that is to achieve food security and improved nutrition and promote sustainable agriculture. Agricultural productivity is also targeted to be doubles and ensure sustainable food production systems and implement resilient agricultural practices in 2030; and beyond. The increase of productivity and production is also intended to help maintain ecosystems,

strengthen capacity for adaptation to climate change, extreme weather, drought, flooding and other disasters and that progressively improve land and soil quality. By 2020, the second goal has also a very important target to maintain the genetic diversity of seeds, cultivated plants and farmed including through soundly managed and diversified seed and plant banks at the national, regional and international levels, and promote access to and fair and equitable sharing of benefits arising from the utilization of genetic resources and associated traditional knowledge, as internationally agreed. There is potentiality that the latest technologies contribute significantly to create efficient agriculture production and optimize bio-resources to achieve the second target of SDGs. There are many approaches, methods, or latest technologies in fourth industrial revolution (4IR) to support in achieving the second target of SDGs.

Having learnt that the world entering bio-based economy era and the 4IR era, both can be understood as driving circumstances, especially how we optimize bio-resources by using recent trends of technologies to support the target of SDGs. Biodiversity of the world should be utilized to feed the world, the raw materials of industry, as well as energy for people in the world. The 4IR, IR 4.0, or Industry 4.0, is defined as the crosscutting impact of information and communication technologies, especially Artificial Intelligence (AI), Internet of Things (IoT), and Cyber Physical Systems (CPS), and other latest technology such as Big Data, Gene Sequencing, Cloud Computing, Blockchain. The main purpose is to revolutionize the industry that will allow greater flexibility in production needs, efficient allocation of resources and integration of processes, as well as integration of the components such as machinery, software, and people; and in the real time interactions. The concept of Industry 4.0 is a reality that will affect the agriculture sector and significant changes in the

way of agricultural production and trade during the upcoming years, in more efficient ways. This revolution is supported by the development of systems that transfer the latest and recent trends of technologies towards agricultural production systems; the core of the revolution is the interaction of digital systems with agricultural-physical production systems.

Agriculture in the Fourth Industrial Revolution

From the 4IR recent surveys, Industry 4.0 is an extensive vision with clear contexts and reference architectures, principally categorized by the bridging of physical industrial resources and digital technologies in so-called cyber-physical systems. The basic techniques of Industry 4.0 which consists of big data, additive manufacturing, automation, intelligent robots, internet of things, cyber security, and cloud computing. Industry 4.0 is embracing the intelligent manufacturing where typical resources are transformed into intelligent objects so that they are able in sensing, act and behave within a smart environment through different pillars of Industry 4.0. The combination of embedded production system technologies with intelligent production processes in Industry 4.0 to overlay the new technological era that will principally renovate industry to business models with value chains and production value chains. Intelligent manufacturing used the key technologies such as the IoT, CPS, cloud computing, big data analytics (BDA) and information and communications technology (ICT).

Development of Industry 4.0 is often including the digitization or full-scale automation. Industry 4.0 is a model shifted to decentralized smart manufacturing and production from centralized system. Industry 4.0 refers to the automation of manufacturing and the creation of a smart factory. The works

reviews the different aspects in industry 4.0 encompasses developments in previously split and disconnected fields such as AI and robotics, nanotechnology, 3D printing, genomics and biotechnology. The impact of Industry 4.0 on various aspects like global value chains, education, health, environment, labour markets and many economic and social is to be expected.

Agriculture 4.0 has been drawn from the term "Industry 4.0" and refers to increased integration of IT and communications technology with agricultural production where the past, present and future perspective are explained using smart, networked systems combining various different types of data from multiple sources promises to increase productivity and efficiency. The transparency arises in supply chain management. Agriculture 4.0 is benefits to agriculture as well as the environment in which downstream economic activities reaches to end customer. The model for the future is a fully automated and autonomous agriculture.

The fourth industrial revolution, however, is not only about smart and connected machines and systems. Its scope is much wider. Occurring simultaneously are waves of further breakthroughs in areas ranging from gene sequencing to nanotechnology, from renewables to quantum computing. It is the fusion of these technologies and their interaction across the physical, digital and biological domains that make the fourth industrial revolution fundamentally different from previous revolutions. Agriculture development must take advantages of utilizing the recent trends of technology to support crop production systems as well as supply chain of agriculture commodities in general covering all of main strategic crops in the countries. Innovations in the biological realm – and genetics in particular – are nothing less than breath-taking. In recent years, considerable progress has been achieved in reducing the cost and

increasing the ease of genetic sequencing, and lately, in activating or editing genes. Synthetic biology is the next step. It will provide us with the ability to customize organisms by writing DNA. Setting aside the profound ethical issues this raises, these advances will not only have a profound and immediate impact on medicine but also on agriculture and the production of biofuels.

The Fourth Agricultural Revolution or Agriculture 4.0 is believed already on its way, and that the agricultural industry is about to be disrupted and transformed into a high-tech industry. There are numerous innovators spearheading attempts to tap into the growth opportunities embedded in improving yield efficiency, increasing supply chain efficiency, and decreasing complexity along farming's value chain. Although conventional investors or companies are only slowly getting involved, large agrochemical incumbents are already investing heavily in agricultural technology. In terms of the agricultural ecosystem, there is increased evidence of innovators active in seven major innovation areas (Deloitte Monitor 2016, modified):

1. Rerouting value chain: numerous players are attempting to leapfrog value chain steps via direct-to-consumer delivery, meal kits, food e-commerce and the like to reduce supply chain inefficiency
2. Crop efficiency technology: examples are start-ups and cross-industry innovators that offer drones, robots, big data sharing platforms as well as irrigation, soil, and crop technologies to increase effective yield
3. Bio-chemical and bio-energy: pursuing the reduction of the ecological footprint, innovators are developing biologically-produced agrochemicals, bio-materials and bio-energy

4. Food technology and artificial meat: companies are developing plant-based meat and eggs to harness "sustainable protein" to counter the notion of eight kilograms of grain to produce one kilogram meat
5. Contained and vertical farming: newcomer innovations showing potential are smart greenhouses and contained farming
6. Nano-based products: companies are producing nano fertilizer, nano coating for seeds, nano pesticide, nano pharmaceutical, and a number of nano-based materials
7. Big data and gene discovery: company are using bioinformatics and gene sequencing to find a specific character of crops to increase productivity

In the developing countries, the fourth agricultural revolution (4AR) give two options, adapting or transforming agricultural sector, agricultural business models, agricultural innovation platforms into digital systems together with the utilization of latest and recent trends of technologies. Meanwhile the 4AR is particularly noticeable in countries such as USA, Israel, Netherland, China, India, South Korea, and Taiwan which in general innovative in their implementations.

The Drivers of Agriculture in the Fourth Industrial Revolution

Although 4AR is regarded as being driven by extreme automation and connectivity, it is increasingly evident that disruption does not stem solely from technology, but it is also influenced by other circumstances such as globalization, demographic shifts, and macroeconomics trends and beyond. Therefore, it would be insufficient to examine the drivers of 4AR

only from technology point of view. Human behaviors and communications in certain societies are very complex systems, with many different types of circumstances and environmental conditions, so that using partial point of views are not suitable to measure and understand the entire phenomenon. To emphasize the complexity, we should be alert to the fact that agriculture does not stand on its own, nor do technological developments take place autonomously; it always interacts with developments in the economy, society and politics. In addition, the food systems of the various countries are intertwined in numerous ways, from the trade in raw materials to products. A large part of the economic value-added of food is at the farms but in final food processing and in retail, and at the end of the food chain is the consumer, whose needs and demands also influence the production and supply of food. On the other hand, companies in the food chain can exert considerable political and social influence, effecting consumer demand. It is therefore a highly complex system and to investigate its future requires many different factors and a large degree of uncertainty must be considered (De Wilde 2016).

Having learnt from various intelligence providers and trend observers, the four drivers are technology, energy and environment, economics and politics, and social and health. Meanwhile the twelve common megatrends across the four drivers are disruptive technology developments, changing energy mix, shortage of resources, climate change, knowledge and information society, economic shifts, globalisation, new norms, multi polar world, demographic shift, urbanization and mobility, health and wellness demands. The drivers and megatrends impacting on agriculture mentioned above is probably not complete, however, it serves to highlight pertinent considerations regarding the future of agriculture, and as

guidance of views in the 4AR, which serve as agriculture's pivotal role in the UN's SDGs. More specifically, the second goal of the SDGs, that aims to end hunger, achieve food security and improved nutrition and promote sustainable agriculture. Improving and increasing food production solely will not work to end hunger. Well-functioning markets, increased incomes for smallholder farmers, equal access to technology and land, and additional investments all play a role in creating a vibrant and productive agricultural sector that builds food security (United Nations 2017).

The 4IR for Agricultural Sector and Its Impacts

As previously discussed, the goal for the agricultural sector is no longer simply to maximize productivity, but to optimize across a far more complex landscape of production, rural development, environmental, social justice and food consumption outcomes. However, there remain significant challenges to developing national and international policies that support the wide emergence of more sustainable forms of land use and efficient agricultural production. The lack of information flow between scientists, practitioners and policy makers is known to exacerbate the difficulties, despite increased emphasis upon evidence-based policy. However, the 4IR with its fundamental concept plays fundamental roles and leveraging factor to achieve the ultimate goals of agriculture sectors. Moreover, the recent trends of technologies behind the 4IR as leveraging factors, give specific challenges for agricultural sector, agricultural business models, agricultural rural development, agricultural innovation platforms with two choices, adaptation or transformation into digital systems by utilizing of some of the recent trends of fundamental technologies.

Smart farming, smart agriculture, precision farming, and precision agriculture need to adjust to meet growing food demand, it is necessary to develop more productive and sustainable farming systems. Agriculture needs substantial increase in investment to meet the growing demand for food, adjust to changing dietary patterns and make farming systems sustainable. Mechanization and advanced inputs are essential for the transformation of farming systems. Considerable research efforts have been spent on the development of models in the agricultural sector in many countries. However, the applications of agricultural innovative models to individual farms is still limited, despite the many advantages of smart agriculture; the way in which these could be achieved within the dimensions of productivity, profitability and sustainability remains unclear (O' Grady and O' Hare et al 2017). Policy makers need to launch calls for proposals to further promote start-ups based on 4IR technologies and even to support Small and Medium Enterprises (SMEs) to invest in these technologies to keep up with the coming technological revolution, and to be competitive and at the forefront of other economic realities. Moreover, a training process must be planned to lead to effective solutions for farms, responding to the needs and interactions of the operating contexts of farmers. The ability to apply data along the agricultural supply chain can permit a productive growth of existing agricultural processes towards innovative farming.

The processes being pursued by industry are also influencing the food production process in agriculture. Recent industrialization of the agricultural production process has led to major environmental concerns, e.g., soil degradation, erosion, compaction, and pollution. This translates into a loss of soil quality and of the eco-systemic services that the soil has guaranteed us over time. Some evidence of this dramatic

situation of soils can be found in different parts of the world, offering some potential solutions. Understanding how industrial techniques are managing agriculture has resulted in soil degradation that should be updated. In this sense, the 4IR should include not only technological innovation but also environmental issues. In this sense, United Nations objectives include economic sectors as both responsible and useful actors for sustainable development. Therefore, natural resources, e.g., soil, in the primary sector must be treated in accordance with sustainability criteria in order to advance towards increasingly sophisticated technological development.

The recent debate about innovation reveals that the economic sectors differ among them. This review permits to explore and reflect on the current state of art, comparing agriculture and industry. While industry 4.0 is, today very advanced both from the scientific and research standpoint and from the practical attitude, since many firms apply it, Agriculture 4.0 is still restricted and put off in theory, and not widely implemented yet. The 4IR in agriculture is still limited to rare pioneering firms, and farmer best practices. For this reasons, policy makers and decision makers are suggested to invest on technological progress and offer to all the economic sectors (e.g., industry and agriculture) different ways to promote innovative and even sustainable development following United Nation Sustainable goals. In such a background, Industry and Agriculture 4.0 can offer numerous advantages for large enterprises, while SMEs often face some difficulties. For this reasons, policy makers should offer policies supporting a technological and advanced enlargement of SMEs making them more competitive in the marketplace.

Concluding Remarks and Future Perspective

The impacts of the 4IR in Agriculture create new literacies on data, technology, and humanity. Smart and precision farming, smart and precision agriculture, which have been developed earlier in the previous industrial revolution have been improved with the latest and recent trends of technologies in the 4IR.

The overview indicates that societal consent respect to agriculture should not be industrialized. The utilization of the 4IR enlightens the agriculture sector as business opportunity where modernization of agricultural processes plays an important role in current market demand. The digitalization of private sector with public sector with revolution of ICT helps to implement 4AR in developing countries.

Recommendations for best practices in agricultural systems in developing countries with the incremental efforts from adaptation to transformation: 1) Managing agriculture big data covering plant genome, geospatial, soil, agricultural-climate, supply chain, and market, 2) Adoption of the recent trends of technologies as part of the 4IR, 3) Managing Infrastructure of ICT, 4) Managing agile organization, 4) Shifting the collaboration into open science and open innovation, 5) Moving from research system to innovation system, 6) Managing human resource and building capacity through training and socialization across societies, 7) Complying the triple bottom-line principles: economic, social, and environment in the application of the latest and recent trends of technologies to achieve SDG.

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GLOBAL INFORMATION SYSTEM ON PLANT GENETIC RESOURCES FOR FOOD AND AGRICULTURE: THE USE OF DIGITAL IDENTIFIER

Muhamad Sabran and Marco Marsella

INTRODUCTION

Plant genetic resources are very important resources to cope with climate changes and to secure the ever growing world population. An in-depth analysis on countries interdependence on PGRFA demonstrates that national food supplies and production systems are highly interdependent worldwide in regard to plant genetic resources (Palacios 1997; Khoury et al. 2015). Countries strongly depend on crops whose genetic diversity largely originates from outside their borders, both in their food supplies and in their production systems. Acknowledging this interdependence, members of the Food and Agriculture Organization enter into The International Treaty on Plant Genetic Resources for Food and Agriculture.

The Treaty is a legally binding international agreement dealing with the sustainable management of plant genetic resources for food and Agriculture (ITPGRFA 2010). It established a multilateral system both to facilitate access to plant genetic resources for food and agriculture and to share the

benefits arising from the utilization of such resources (Sabran and Bhatti 2016; Sabran 2018). Multilateral in this context means that a global pool of plant genetic resources for food and agriculture are shared and managed jointly by all contracting parties to the Treaty.

The Multilateral System (MLS) on access and benefit sharing is facilitated through the standard Material Transfer Agreement (sMTA) (ITPGRFA 2006). The sMTA requires that all available passport data and any other associated non confidential descriptive information, shall be made available with the PGRFA provider and the recipient shall make available all non-confidential information that results from research and development carried out on the material, through the information system provided for in Article 17 of the Treaty. Article 17 of the Treaty also requested contracting Parties to cooperate to develop and strengthen a global information system to facilitate the exchange of information, based on existing information systems, on scientific, technical and environmental matters related to plant genetic resources for food and agriculture (ITPGRFA 2015).

Global Information System

The Multilateral System of access of genetic materials grows quickly, in particular since the introduction of the online sMTA (easy-sMTA) (ITPGRFA 2012). However, the rapidly growing material exchanges through easy-sMTA did not yet include the sharing of the associated information as required by article 17 mentioned above. The Treaty secretariat have developed a global information system (GLIS) to make such information more easily transferable, accessible and available for a long time, more accurately associated to the PRGFA at hand and is accrued as the PGRFA is transferred, studied and improved. It was designed to

become the "Google" for the PGRFA community and router to existing systems for information on PGRFA and other resources of interest for the community.

The GLIS can be described as in figure 1 below. The provider transfers the PGRFA with easy-sMTA to the recipient along with the non-confidential information. The recipient, as obliged in the sMTA, return any information resulted from research and development on the PGRFA material transferred to GLIS. In addition other third parties, if any, can also provide additional information on the PGRFA materials. The GLIS then transmit the information to the provider as well as to the world-wide web so that it becomes accessable by the global PGRFA community. This information pooling and sharing are made possible by the assignation of a permanent unique identifier to the PGRFA material which uniquely and permanently identified the material.

Digital Object Identifier (DOI) as Permanent Unique Identifier (PUID)

A Permanent Unique Identifier (PUID) is a text string that unambiguously and permanently identifies a single object of interest. The key of PUIDs are:

- ***Uniqueness***: unambiguously identify a specific object or intellectual asset. In context of plant genetic resources, an object is a sample of genetic which are not necessarily homogeneous. A sample that has been transferred by SMTA from provider to recipient will be change administratively, legally and scientifically, and therefore has to be treated a new object differ with the original sample since they are held under different legal conditions and, in addition, genetic materials change through mutation, genetic drift, deliberate or unintentional selection, cross-contamination with pollen or

seed or plant of other varieties and will further diverge with time. This is particularly true for landraces and crop wild relatives, which are typically genetically heterogeneous, so an accession or variety in a collection of genetic materials is often not a homogeneous sample of seeds.

- ***Permanence***: the same object will be forever associated to the same identifier. If an object, in this case a sample of genetic resources is no longer available, its identifier cannot be used to identify another sample.
- ***Opacity***: nothing about the associated object should be inferable by the structure of the identifier.
- ***Actionability/resolvability***: a defined procedure for name resolution exists to access the information associated to the object once the identifier is known and
- ***Discoverability***: given details of an object, it is possible to retrieve its identifier.

The digital object identifier (DOI) system provides an infrastructure for persistent unique identification of any types object. A DOI name is permanently assigned to an object to provide a resolvable persistent network link to current information about that object, including where the object, or information about it, can be found on the Internet. While information about an object can change over time, its DOI name will not change. A DOI name can be resolved within the DOI system to values of one or more types of data relating to the object identified by that DOI name, such as a URL, an e-mail address, other identifiers and descriptive metadata.

The DOI system enables the construction of automated services and transactions. Applications of the DOI system include but are not limited to managing information and documentation

location and access; managing metadata; facilitating electronic transactions; persistent unique identification of any form of any data; and commercial and non-commercial transactions. The content of an object associated with a DOI name is described unambiguously by DOI metadata, based on a structured extensible data model that enables the object to be associated with metadata of any desired degree of precision and granularity to support description and services. The data model supports interoperability between DOI applications. It obvious from the above description, that the DOI is unique, permanent, opaque, resolvable and recoverable, and hence is permanent unique identifier.

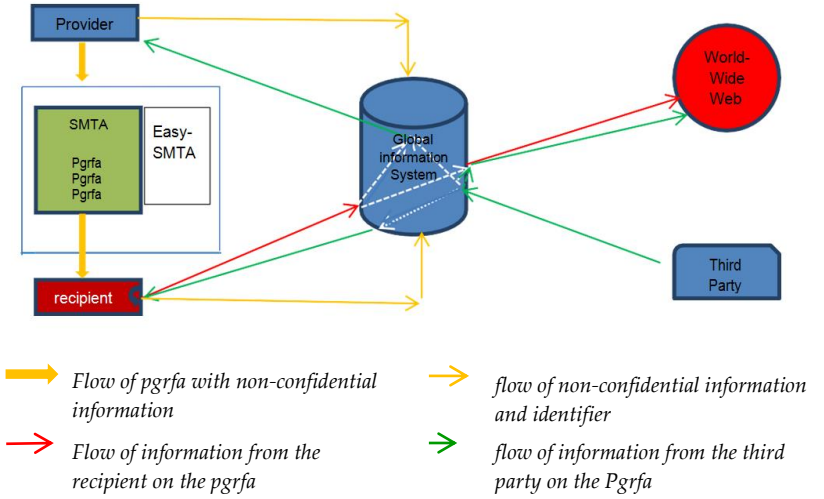

Figure 1. Exchange of PGRFA and information with easy-SMTA.

Descriptors

A global online survey on metadata descriptors have been conducted by the ITPGRFA secretariat (ITPGRFA 2011) to have agreeable minimum set of metadata descriptors on PGRFA,

which are required to assign a DOI to PGRFA material shared under the MLS System. This process has involved consultation with some 200 experts from 98 institutions in 62 countries. Organizations include, but are not limited to, national programs, research institutions, universities, FAO National Focal Points, DivSeek, ECPGR, USDA, CGIAR centres and the private sector. The 202 respondents of the survey are of different well-balanced areas of expertise and include researchers (32%), breeders (18%), gene bank curators (18%), national focal points (14%), information specialists (14%), geneticists (2%) and bioinformaticians (2%). The global survey content builds upon the results of the Expert Consultation on PUIDs set up by the Secretariat in March 2015 regarding the International Crop Information System (ICIS) and the FAO/Bioversity Multi-Crop Passport Descriptors (MCPD) (FAO/Bioversity 2015). There have been strong consensuses on classification of descriptor as follows (ITPGRFA 2017).

Mandatory descriptor. Values for these descriptors must be provided for every sample of PGRFA in GLIS; the holder is not given the option to enter "unknown", "not applicable" or "other", or to leave the field empty; a sample cannot be registered until valid values have been entered for all mandatory fields. Examples of Mandatory descriptors are location of the holder of PGRFA, genus or species and the method by which the holder obtained the PGRFA.

Highly recommended descriptor. These descriptors are applicable to all types of PGRFA. Valid values must be entered if known, but missing values are allowed, so omission of values does not prevent sample registration. These descriptors are highly recommended since they are basically the information demanded by the PGRFA community or potential recipient.

Context-dependent descriptor. These are applicable only to certain types of PGRFA. Their use is highly recommended in the appropriate context, i.e. values should be given if available and applicable. This descriptor intended to enhance data quality through helping the registrant to enter correct data. They do not correspond to the "importance" of the descriptors. A mandatory descriptor is not necessarily more important than a highly recommended or context-dependent descriptor. For example, the name of a variety or the country of provenance of a sample may be considered critically important; but they are not always known or applicable and therefore cannot be treated as mandatory.

To accommodate the diversity of systems and standards used by different holders of PGRFA, no restrictions are placed on the value of context-dependent descriptor other than it must be used to distinguish the sample from those held by the registrant and will not be re-used for future samples. It may, for example, be an identifier that has been created in accordance with a syntax defined by the holder for specific purpose of identifying the sample in his/her records. There are many forms and terms for such identifiers used by different communities, such as accession ID [ACCENUMB], Selection ID, Selection Number, Derivative name, Population ID, Seed lot ID, Catalogue entry, Designation, Preferred Name, Preferred ID, Permanent Unique ID [PUID] etc.

If samples are acquired from other sources, the recipient may use whatever identifier given by the provider. There are many forms, such as cultivar name or common name or the provider's own sample ID [DONORNUMB]) or even a sample ID created by a collector when collecting a sample from *in situ* conditions [COLLNUMB]. GLIS will register an error if we attempt to register a second sample with the same sample unique identifier; and a warning if this sample unique identifier duplicates any other identifier that has been registered for another sample. The

practice of identifying samples using the identifier supplied by the provider is deprecated in many cases. Any organization with a formal germplasm data management system would and should assign its own internal identifiers to the germplasm it manages. The option is included only to accommodate communities without such formal germplasm data management system.

Multi-Country Construction of a Test Platform for Allocation of Unique Identifier

Under the leadership of Indonesia, a Multi-Country Project aims at the adoption of permanent unique identifiers to add value and facilitate the use of PGRFA for the benefit of plant breeders and farmers have been implemented since 2016. The project presents a participatory and science-based methodology with multi-country approach, involving both national and international institutions with demonstrated experience, capacity, mandate and willingness to make a step forward in this area for the benefit of the rice community, first, but also for the benefit of other crop communities and PGRFA networks. The overall objective of the project is to bridge the gap between the information requirements of genebank curators, rice breeders and more targeted upstream biological researchers, to support applied germplasm curation, forward-looking rice breeding programs and strategic rice research. Whereas, the specific objective is to adopt and implement the agreed method for the assignation of global, permanent and unambiguous identification of rice accessions and the development of a platform to establish automatized system-to-system connections to add value to the material being transferred within and from the Multilateral System.

The project was targeted to all ex situ collection of rice (*Oryza* spp.) at institutions with advanced database capability. This includes not only accessions conserved in ex situ gene bank collections managed in accordance with international gene bank standards, but also working collections of genetic stocks, pre-breeding materials, and other bred and elite materials developed by researchers and breeders, not necessarily managed under standard gene bank but with some sort of documentation system exists.

During three years of the project implementation, software was developed, and database in participating countries was upgraded. Along with the availability of guidelines for DOI adoption, the DOI system was implemented. Metadata information of accessions of participating countries was aggregated to the PGRFA and this will make the material discoverable. The exposion of the aggregation information in MLS expected to support broader use of PGRFA. There were three targeted output for the Project, i.e.:

1. A developed plug-in to facilitate the connection with a central metadata registry to facilitate the assignation of permanent unique identifiers to the PGRFA material (which was consisted of two main activities i.e. the development guidelines for adoption of DOI).
2. Updated genebank data base software supporting the management of information related to the transfer of material with the SMTA with additional function to automatically register and identify the accession. The output was achieved through training activities where the rice database was adjusted and upgraded and followed by the DOI assignation for the software implementation. Two international training batchs were conducted and the DOI system was implemented in the 13 participating countries. A total of 155.040 rice

accessions were assigned with DOI, including 124.597 rice accessions from the International Rice Research Institute and 21.300 accessions from African Rice Center.

3. Software disseminated at national and international fora, such as focus group discussion (FGD), workshops, conferences, and web portal development. Three national focus group discussion and three international workshops were conducted, and a web portal has been established.

The project has completed the three main outputs. A Software was developed to facilitate the DOI connection and registration system to the Global Information System (GLIS) metadata center (https://ssl.fao.org/glis/) managed by the ITPGRFA-FAO Secretariat. An Integration Toolkit, or shortly called as Toolkit is a plugin designed and packaged to technically run the DOI connection and registration process to the GLIS-FAO metadata center. The initial version of Toolkit v1.0.0 was tested at IRRI, Los Banos, Philippines in October-November 2017. The method to run the Toolkit v1.0.0 and DOI registration are compiled and published, i.e., Format for batch registration of DOIs in the Global Information System; Integration Toolkit Version 1.0.0: Integration Toolkit and Installation and operation manual; Data required for the assignation of Digital Object Identifiers v2.1; GLIS_XML_integration_protocol_3.4 and guidelines for the optimal use of Digital Object Identifiers v2.

Thirteen genebanks data base software from 13 countries have been upgraded through International training. The genebanks are as listed in Table 1. Three national Focus Group Discussions and three international workshops were conducted, and a web portal has been established to disseminate the software and the DOI registration.

The Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development (ICABIOGRAD), an Indonesian Research Institution that run the project contributed to the software development by assigning DOI for 849 rice accessions in the testing phase of the Software. At the end of the project a total of 155.040 rice accessions have been assigned with DOI including 124.597 accessions from IRRI and 21.300 accessions from African Rice Center. The list of these accessions can be found at the GLIS portal of the ITPRFA-FAO (https://ssl.fao.org/glis/).

Table 1. Gene bank institutions participated in DOI international training 2019.

Country	Institution	World Information Early Warning System (WIEWS)	Permanent Identifier (PID)	No. of accession
INDONESIA	Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development (ICABIOGRAD), IAARD, Ministry of Agriculture.	IDN179	00AQ17	1245
INDIA	Indian Council of Agriculture Research, National Bureau of Plant Genetic Resources.	IND001	00AS28	1512
MALAYSIA	Program of Genetic Resources and Germplasm Conservation Management (GB1) Genebank Seed and Centre, MARDI Seberang Perai, Malaysia.	MYS005	00AP70	715
PHILIPPINES	Genetic Resources Division (GRD) Philippine Rice Research Institute (PhilRice), Philippines.	PHL158	00AS26	1016

Table 1. Continue.

Country	Institution	World Information Early Warning System (WIEWS)	Permanent Identifier (PID)	No. of accession
BANGLADESH	Genetic Resources and Seed Division, Bangladesh Rice Research Institute (BRRI).	BGD002	00BA47	70
BHUTAN	National Biodiversity Centre, Ministry of Agriculture and Forests, Bhutan.	BTN026	00AS31	60
LAO PDR	Rice Research Center (RRC), National Agriculture and Forestry Research Institute (NAFRI).	LAO018	00AY57	439
SRI LANKA	Plant Genetic Resources Center (PGRC).	LKA036	00BA45	3499
PAKISTAN	Plant Genetic Resources Program, Bio-resources Conservation Institute, National Agricultural Research Centre (NARC).	PAK001	00BA39	50
CAMBODIA	Cambodian Agricultural Research and Development Institute (CARDI).	KHM010	00BA37	10
MYANMAR	The Seed Bank of Myanmar Department of Agricultural Research (DAR).	MMR015	00BA41	47
BURUNDI	Burundi Genebank (BGB), Institut des Sciences Agronomiques du Burundi (ISABU).	BDIZMB048016	00BA43	188
ZAMBIA	National Plant Genetic Resources, Zambia.	ZMB048	00AS30	264
Total				9.105

Table 2. GLIS descriptor and multi crop passport descriptor (MCPD V.2.1).

1. Mandatory descriptors		
GLIS descriptor	GLIS descriptor	MCPD equivalent for genebanks
M01. Location where the sample is held	The location where the PGRFA is maintained	Institute code [INSTCODE]
M02. Sample unique identifier	The identifier that the registrant use to identify their PGRFA sample to distinguish it from other PGRFA	Accession number [ACCENUMB]
M03. Date	Date on which the registrant became the holder	Acquisition date [ACQDATE]
M04. Method	What event occurred on that date (In M03) that resulted in you becoming the sample holder	N/A
M05. Genus or crop name	Genus or common crop name.	Specify one or both genus [GENUS] common crop name [CROPNAME]
2. Highly recommended descriptors		
R01. Targets	One or more URLs where further information about the sample can be obtained	N/A
R02. Biological	This describes the conditions of provenance of the sample	Biological status of accession [SAMPSTAT]
R03. Additional taxonomic category	Species: specific epithet of the scientific name Species authority: authority for the specific epithet Sub taxa: any additional infra-specific taxon: subspecies, variety, form, Group Sub taxon authority: Authority for the sub taxon	Species [SPECIES] Species authority [SPAUTHOR] Sub taxon [SUBTAXA] Sub taxon authority [SUBTAUTHOR]
R04. Names	R04. Names one or more registered names or other designations, such as the name of a landrace, traditional variety or modern cultivar, or some other name or designation used to identify a breeder's selection or elite line or variety	Accession name [ACCENAME]

Table 2. Continue.

R05. Other identifiers	Any other identifiers, including permanent unique identifiers that have been assigned to identify the sample. It does not include identifiers for other samples that you believe maybe similar to this sample	Persistent unique identifier [PUID]
R06. MLS status	The status of the sample with regard to the Multilateral System of Access and Benefit-Sharing (MLS) of the International Treaty on Plant Genetic Resources for Food and Agriculture	MLS status of the accession [MLSSTAT]
R07. Physical existence	Describes whether the sample is still available or permanently lost after being registered	N/A
3. Context-dependent descriptors		
3.1 Material you acquired from someone else		
C01. DOI of provider's sample	DOI of the sample held by the provider	N/A
C02. Provider's location	Location or name of the person or organization that provided the sample to you	Donor institute code [DONORCODE] Donor institute name [DONORNAME]
C03. Provider's sample unique identifier	Unique identifier used by the provider to identify the sample under the provider's management	Donor accession number [DONORNUMB]
C04. Country of provenance	The country in which the sample was either collected or bred or selected or the first country in the known history of the sample.	Country of origin [ORIGCTY]
3.2 Material previously collected from *in situ* conditions		
C05. Collector's location	Location of the home base of the person(s) or organization(s) that originally collected the sample from *in situ* conditions	Collecting institute code [COLLCODE] Collecting institute name [COLLNAME] Collecting institute address [COLLINSTADDRESS]
C06. Collector's sample unique identifier	Identifier assigned by the collector(s) to the sample collected	Collecting number [COLLNUMB]

Table 2. Continue.

C07. Collecting mission identifier	The identifier, if any, of the mission during which the sample was collected	Collecting mission identifier [COLLMISSID]
C08. Location where sample was collected	Location information below the country level that describes where the sample was collected	Location of collecting site [COLLSITE]
C09. Latitude	Latitude of the location where sample was collected	Latitude of collecting site [DECLATITUDE] [LATITUDE]
C10. Longitude	Longitude of the location where sample was collected	Longitude of collecting site [DECLONGITUDE] [LONGITUDE]
C11. Uncertainty	Uncertainty of the latitude/longitude coordinates of the location	[COORDUNCERT]
C12. Geodetic datum	The geodetic datum or spatial reference system upon which the latitude/longitude coordinates of the collecting location are based	Coordinate datum [COORDDATUM]
C13. Georeferencing method	The method used to estimate latitude/longitude coordinates of the location where the sample was collected]	Georeferencing method [GEOREFMETH]
C14. Elevation	Elevation of collecting site	Elevation of collecting site [ELEVATION]
C15. Collecting date	Date on which the sample was collected	Collecting date of sample [COLLDATE]
C16. Collecting source	A description of the nature of the location where the sample was collected	Collecting/acquisition source [COLLSRC
3.3 Material is a derived variant		
DOI of the variable sample	If available, the DOI of the sample from which you derived the current sample	N/A
3.4 Material is a novel distinct PGRFA created by you		
C18. DOI(s) of ancestral sample(s)	List of the DOIs of any samples that you acquired from others and that you used to create this novel distinct PGRFA	N/A
3.5 Material bred		
C19. Breeder's location	Location where the material was bred	Breeding institute name [BREDNAME]
C20. Ancestry	The pedigree or other description of the ancestry of the sample and how it was bred	Ancestral data [ANCES]

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CHAPTER 2.
RIGHTS, CONSERVATION AND USES OF PLANT GENETIC RESOURCES

Genetic Resources, particularly plant genetic resources (PGR), are the heritage of mankind. However, countries have sovereign rights over PGR found in their territories. Unfortunately, many genetic resource-rich countries have low capacity to conserve and sustainably use the genetic resources; whereas technology-rich countries that have the capacity and capabilities of conserving and utilizing PGR in general are poor in genetic resources. To bridge this gap the international community has agreed on several provisions that enable the genetic resources-rich countries to exercise their sovereign right over PGR and facilitate the technology-rich countries to access the plant genetic proposes. Two international agreements in this issue are the Nagoya protocol of the United Nation Convention on Biological Diversity and the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) established by members of the United Nation Food and Agriculture Organization.

Both the Nagoya Protocol and the ITPGRFA facilitate access of PGR and sharing the benefits arising from their uses. The Nagoya Protocol facilitates the bilateral agreement between the provider and the recipient; whereas the ITPGRFA facilitates multilateral

system of access and benefit sharing, with a standard material transfer agreement (sMTA). Moreover, both Nagoya Protocol and the ITPGRFA aimed at conserving and sustainably use plant genetic resources. Conservation of PGR can be *in situ* and *ex situ*. In the ITPGRFA, more emphasis is given to the *ex situ* conservation since they are under the control of governments. Almost every country has a genebank to conserve their plant genetic resources. There are more than 1.750 genebanks in the world, which cover more than 7.2 million accessions. Each genebank has their own information system. It is therefore important to discuss the genebanks as introduction to the big data in plant.

DYNAMIC AND IMPLICATION OF RIGHTS ON PLANT GENETIC RESOURCES

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INTRODUCTION

Indonesia is well known as a megabiodiversity country after Brazil. Being one of element of biodiversity, genetic resources (GR) are basically a variety of types and quantities of genetic material in a major species and their relatives. Their direct utilization through farmer domestication and selection, and breeding has benefited in the supply of food and raw materials for agriculture-based industries. The role of plant genetic resources (PGR) has been started since the beginning of the development of agriculture, of which superior local varieties involving wild relatives produced with contribution of farmers. Farmers selected seeds or other plant material for their own needs and contributed to provide varied local varieties adapted to specific location and different environment.

The development of world agriculture has increased rapidly since the 1960s and 1970s to become the first Green Revolution which was supported by many improvements in plant genetics and supporting technologies. During this period a number of International Agricultural Research Centers (IARCs) were established and followed by the establishment of gene banks along accompanied by breeding research and cultivation

technology. As a result, an extraordinary increase in world food production in developing countries was able to save from hunger.

The second Green Revolution that began in 2005 was supported by the development of biotechnology. Biotechnology researches produce many leaps, but require investment in human resources and facilities, and expensive operational budget. Because of numerous results and findings which provide new opportunities, the adoption of biotechnology is inevitable. In fact, the green revolution also indirectly increased the chances of threats to the existence and genetic diversity. This is caused by the widespread of improvement of genetic varieties which allow their narrow genetic centered on specific food crops (rice, corn and wheat) and diminished superior local varieties from other commodities, as undergone in Indonesia at present. According to Ogwu et al. (2014), declined genetic diversity is affected by many factors such as population growth and urbanization; land, sea and air pollution; changes and loss of origin habitat; climate change; disease attacks; invasion foreign species; patent rights on plants; replacement of local varieties with improved varieties; and vulnerability and genetic erosion.

Patent rights are made for the purpose to safeguard one's invention. However, when a right on genetic resource is unfair, it could harm farmers. Convention on Biological Diversity (CBD) is a milestone in the recognition of state rights in the utilization of PGR. CBD was accompanied by various conventions on the regulation of PGR such as ITPGRFA, the Cartagena Protocol, and the Nagoya Protocol, the International Union for the Protection of New Varieties of Plants (UPOV) and Trade-Related Aspects of Intellectual Property Rights (TRIPS) agreement related to the World Trade Organization (WTO). CBD has been implemented through agreements for the development of ITPGRFA which

PGR management will be carried out together with sustainable conservation.

The progress of conventional breeding technology based on Mendel's Law is the main pillar of the green revolution supported by food research institutions. In addition to food crops, breeding technology has encouraged researches and breeding programs of other agricultural commodities. This effort also encourages the development of agricultural IPRs as an appreciation, compensation and protection for the rights of breeders. US Agriculture has imposed a patent on plants in 1930 to encourage invention of plants. In contrast, Europe and several other countries including Indonesia do not acknowledge patents on organisms (except microbes). In several European countries in 1961, the right on PGR to breeders and organizers through had been thought the establishment of UPOV. The development of breeders' rights in UPOV was increasingly tighter through improving the regulatory agreement in 1978, and finally in 1991 which was more stringent.

To date, genetic improvement technology is developing more rapidly, supported by sophisticated equipment, and large investment cost, as consequence, protection of the right on PGR through IPRs is necessary (Kock and Gould 2011). Innovation is influenced by protection of IPRs as incentives and freedom of intervention according to the IPRs. This review discussed general information of dynamic of rights on plant genetic resources, access and benefit sharing (ABS) and IPRs of plant genetic resources, and related issues to their disputes and biopiracy.

Dynamic of Rights on PGR

Biodiversity addresses the diversity of species and taxa, species and their relatives, and ecosystems. Breeding program

implied to utilize the diversity of PGR and wild relatives in developing new varieties. Genetic improvement of varieties require gene pool which can be distinguished into primary, secondary, tertiary and quaternary (Hammer et al. 2003; Haussmann et al. 2004), which has crossing ability from easy to difficult and need supporting technology, respectively.

Concerned about the ongoing erosion of PGR, subsequently, the Food Agriculture Organization (FAO) in 1965 established a Panel of Experts in Plant Exploration and Introduction which advised on issues of PGR and made guidelines for their conservation (Esquinas-Alcazar et al. 2012). Based on the recommendations from Conference on Human Environment in Sweden, most countries considered PGR as the rights of human beings (Brahmi and Tyagi 2017). In 1983 the International Undertaking on Plant Genetic Resources (IUPGR) was established. Its resolution stated the importance of PGR to breeding and research, and GR is valuable materials for human kind. The spirit emphasizes no limitation for anyone to access them (Sullivan 2004; Hufler and Lefeber 2011; Esquinas-Alcazar et al. 2012). According to Muller (2018), in addition to conserve PGR, IUPGR also began to function in accessing and utilizing PGR. The next important change is the existence of the CBD Convention in 1992 document article 15 which stipulates state sovereignity over PGR in its territory. However, Kamau (2009) emphasized that a state's right to PGR does not mean that there is an effort to block access, but rather the rights and obligations of the state to regulate access and utilization of them in a sustainable manner.

The PGR across regions is a manifestation of their recognition of as a common property of mankind. In Indonesia, some commodities such as coffee, pepper, tea, oil palm were introduced from other countries while sugar cane, banana, durian

and clove were originally from Indonesia, and are free to be grown in other countries. Likewise, the development of new plants from the new world (the Americas) such as corn, cassava, sweet potatoes, chili, tomatoes, cocoa, makes Indonesia the main producer of several commodities. Thus, human rights on PGR and to boost food production are very important through extensive access to PGR.

Crop improvement via breeding has led to change in the views of various countries over the increased important role of PGR in agricultural development. The importance of food security causes every country to strive for increased productivity and quality of agricultural products through the application of technology. In addition to genetic improvement technologies, soil improvement technologies such as organic fertilization and chemistry, pest and disease control with pesticides, irrigation, and other technologies continue to be developed. This change allowed the state to have the right to PGR, as supported by CBD (Brahmi and Tyagi 2017). This convention is marked by changes of IUPGR on PGRFA by FAO which are not binding to the Commission on Genetic Resources for Food and Agriculture (CGRFA). The management of PGRFA is more systematic and make PGR a public area.

The development of PGR management among nations occurred in 2001, after the 31st FAO Conference with the establishment of ITPGRFA which was approved by many countries, and came into force since 2005. This Treaty was ratified through the 2006 Act. The important issue of The Treaty is granting of rights on PGR power to farmers for their efforts to conduct domestication and selection of local varieties. According to the 1978 UPOV, local varieties were considerably open access because the requirements for uniformity and stability were not met. UPOV 1978 version still allows farmers to replant seeds that

are protected by their Plant Variety Protection (PVP Rights) (article 6). However, UPOV in 1991, article 15.2 stipulates the choice for the state to implement it or not. The privileges of farmers to save or exchange with others are increasingly reduced, while exemption breeders are narrowed in scope.

Indonesia has actively participated in the formation and ratification of ITPGRFA. As stated in Annex 1 from ITPGRFA, which includes 64 food and feed crops, the existence of supporting institutions mainly related to the function of the world gene pool. Clearly, recognition of farmers' rights is based on the historical reality of the role of farmers in producing local varieties. Additionally, development of the right to PGR underwent rapid changes along with the development of breeding technology. Several countries mastered in breeding technology and seed industry had agreed to grant rights on PGR resulting from modern breeding, called as breeder rights.

Significant changes to the right on PGR occurred after the WTO agreement on TRIPS in 1994. This agreement binds all WTO members to the application of IPRs, including patents. Article 27.3 (b) mentions the obligation to introduce IPRs for plants especially patents or effective forms of *sui generis* or both (Sullivan 2004). In the previous era, countries outside of UPOV and the US were not obliged to provide patent or sui generis, in contrast after the agreement, all WTO countries must protect PGR (Zerbe 2015). Moreover, TRIPS needs to be following up by WTO countries including Indonesia. Indonesia does not grant patents to living things except microbes, while for plants, a protection system for sui generis varieties has been adopted by issuing the 2005 Law. Conversely, countries such as the US have implemented IPR protection like patents, utility patents and plant variety protection.

Access and Benefit Sharing

The right on PGR has many implications, especially how a country, company or other party can access these them for various purposes (research, food, and commercial use). International rights on PGR are regulated in several conventions. The CBD along with the Nagoya Protocol regulates the state's rights on PGR in a country. In addition, the ITPGRFA and Nagoya Protocol conventions differ, where ITPGRFA regulates 64 food and feed commodities, while Nagoya protects all commodities and traditional knowledge. The ITPGRFA basically regulates the PGR of certain food and agriculture, in particular the mechanism of access to PGRFA, benefit sharing, and world gene pool development. This convention is primarily intended to support food security and efforts to protect farmers' rights on PGR.

In relation to PGR utilization, the development of biosciences and bioindustries opens opportunities for wider utilization of functional food products, medicines, and modern industrial materials, including bioprospecting, thus not limited to food, traditional medicine, and other industrial raw materials (Pisupati and Bavikatte 2014). For this reason, the increasing world attention to PGR has been accelerated by establishment of various institutions dealing with PGR, increased research activities, and the development of transfer mechanisms or benefit mobilization of PGR by various parties. According to Pisupati and Bavikatte (2014), there are three important principles in the effort to utilize world GR for commercial interests, namely: 1) benefits can be monetary or non-monetary, 2) the need to develop benefit sharing mechanisms, and 3) ABS must support conservation and sustainable use. Related to the acquisition of monetary and non-monetary benefits, an appropriate system is needed. The development of facilitative systems such as South Africa and

Bhutan is a good example to be developed rather than a protective system. The development of a model of ABS needs to pay attention to three factors, i.e. 1) simplicity and sustainability in comparison to providing large compensation but it is rare, 2) a cooperative approach needs to be prioritized compared to competition, and 3) the priority of giving incentives compared to prioritizing penalties.

IPRs of PGR

IPRs are basically the rights given by the state to the inventors for original work and creativity to protect from those who are not entitled to receive economic benefits. In the beginning, IPRs developed following the industrial revolution, and then continued to be developed through the creation of various new invention products to meet human needs. The use of IPRs on crops, globally related to world trade, began with an agreement in the Uruguay Round in Doha 1993 concerning the Agreement on TRIPS of the WTO. In the article 27.3 (b), it stated the use of patent of crops or Sui generis or their combinations (World Bank 2006). The most widely adopted forms of sui generis are the rights on PVP Rights or breeders right developed in the UPOV.

Patents are an important and strongest form of IPRs compared to others. The development of patent adoption of living things is a controversial issue that continues to the present which has only been adopted in the US, Japan and Australia (Kock and Gould 2011; Ogwu et al. 2014). The US has permitted plant patents since 1930 (Aoki 2009). While the use of patents for IPRs protection has not yet been accepted by many other countries. Patent plants can be applied in all plants, parts of plants or DNA sequences. Oxfam (2018) considers its importance to examine the development of the number and scope of patents in relation to world food needs.

He implied that plant patents prevented further research and breeding, and prevented farmers from using freely produced technologies.

Although the TRIPS agreement places plant patents as an option, both in generic and its combination, many countries choose *sui generis* for protection of IPRs. Indonesia is a country that does not adopt patentability in plants. In countries that allow plant patents, there are a variety of principles of what permissible is or not. Europe is a group of countries that do not allow patenting of plant varieties, but allows everything generic even though it only applies to a number of plants (Kock and Gould 2011).

As an alternative to patents, the rights to protect plant varieties or breeders' rights are mostly chosen by various countries including Indonesia. Some countries use breeders' rights and are pioneered by Europe which develops IPRs on other forms of plants (*sui generis*) through the establishment of UPOV. The UPOV Convention develops the IPR protection system in the form of breeders' rights which differ from patent. The right to protection of plant varieties (PVP rights) is centered on the protection of the multiplication of varieties through seeds and products. Kock and Gould (2011) argue that IPRs based on PVP differ in principle from patents. The principle of patents is that 1) invention, which is a technological improvement that previously did not exist and is different from in conventional breeding, 2) novelty on patents is absolute, but novelty in PVP is marketable only, and 3) inventive or non boviousness stage, meaning that there are creations (unexpectedly). The list of world organization related to IPRs is presented in Table 1.

Indonesia and other ASEAN countries have yet to become a member of UPOV. The rights of breeders in Indonesia are based on Law No. 29, 2000 concerning PVP. Many PVP rights in

Indonesia are similar to the 1978 version of the UPOV convention. The main differences include article 7 which recognizes local varieties. Notably, Indonesia has not protected IPR plants by *sui generis* non UPOV. According to Shashikant and Meienberg (2015), UPOV 1991 was not in line with ITPGRFA in the context of the protection and application of farmers' rights. Article 15.2 basically does not allow farmers to exchange and sell seeds freely. Likewise, article 15.1 stated allowance of the production of seeds and replanting them only for self-consumption (subsistence). The absence of recognition of the farmers right implicitly or explicitly includes legal protection need to be an important consideration for the decision not to become a member of UPOV.

Table 1. World organizations on IPRs.

Convention on Biological Diversity (CBD)		World Trade Organization (WTO)	World Intellectual Property Organization (WIPO)		Food Agriculture Organization (FAO)-UN
Nagoya Protocol : Access and benefit sharing	Cartagena Protocol: Bio safety	Trade-Related Aspects of Intellectual Property Rights (TRIPS)	Patent Cooperation Treaty (PCT), Substantive Patent Law Treaty	Inter-Governmental Committee on IPR and GR, Traditional knowledge and Folklore	The International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA)
Plant genetic resources	Genetic engineering products	Breeders right, patent, trademark, trade secret	IPRs harmony	Traditional knowledge, PGR and Folklore	Access facilitation, farmers right

Source: World Bank (2006).

Disputes and Biopiracy of PGR

Disputes and biopiracy of PGR are important issues which often occur, especially the PGR owned by developing countries utilized by other unauthorized parties. The parties include companies, research institutions, universities or even other countries. One important issue about the GR dispute involving Indonesia was the use of the avian influenza virus which happened a few years ago by the WHO. The incident occurred during the 2006 pandemic, in which Indonesia refused to submit samples of avian influenza viruses because of perceived injustice. The virus, which is more virulent (clade 2) than that in neighboring country (Vietnam), could produce more effective vaccines. While, vaccine companies from Australia sell them to Indonesia with high price and without benefit sharing. Such incident had broad implications of changes in governance facing a pandemic in the world involving the WHO and WHA.

The dispute on PGR can be seen when a US company registered a patent on a superior local rice variety, called Basmati from the Indian subcontinent which caused high reactions from various parties in India and other countries. Since these superior varieties are yielded by a long selection of farmers, that was awarded farmers right. However, the company claims have implications for the closed access of farmers, especially Basmati-producing farmers to their technology.

Biopiracy of PGR is directed to the interests of food, medicine, industrial materials and biofuels. As an example, tomatoes developed from marker assisted breeding was patented. The tomatoes and wild relatives were collected by developed countries long before the CBD, and collected *ex situ* on gene banks. Another case was herbicide-resistant sorghum which was improved by introducing genes from Bolivian grass from Bolivia

which were patented by one of the US state universities with Dupont. The university did not mention where the genetic material came from. According to the Nagoya Protocol, the access of parties (users) should be informed and submitted to competent authorities in Bolivia as provider, after submitting a PIC, approval MAT's to complete MTA and other bilateral agreements. More various cases regarding the biopiracy of PGR in the world were reported (Hammond 2013).

Future Perspective

The management of PGR must be strengthened; therefore, increased environmental problems need to be solved, involving international conventions. The development of relations between nations needs to be addressed to the regulation of rights on PGR, which need various conventions such as CBD, ITPGRFA, Cartagena Protocol, Nagoya Protocol, UPOV) and TRIPS. This is done in proper manner and accompanied by national legislation in each country, including Indonesia. In Indonesia, ABS has been implemented on PGR. The ABS protocol contributes to protect comprehensively Indonesian PGR and secures the sharing benefit to Indonesia being a country with high PGR. With the ABS, scope of PGR terminology could be broadening their utilization including their derivatives. Indonesia is not yet a member of UPOV which applies the plant protection with IPR and related issues to breeders right and farmers right. Dispute and biopiracy of PGR should be solved with strong national legislation and support of relevant international conventions such as CBD, ITPGRFA and Nagoya Protocol. Biopiracy of PGR ownership through a patent without permission or absence to mention the origin should provide compensation to the rightful party.

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EFFICIENT AND EFFECTIVE MANAGEMENT AND USE OF GENETIC RESOURCE IN INDONESIA

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INTRODUCTION

Indonesia, like many other countries, faces similar challenges in agriculture, which include increased demographics that boost food demand, excessive usage of natural resources, climate change that reduces productivity in agriculture, massive food wastes, and other environmental threats. Population growth, rapid urbanization and changes in diet preferences cause an increase in food demand and agriculture therefore must keep up to produce sufficient nutritious food to face such challenges in an enviromentally sustainable manner (Roa et al. 2016). This can be done by reducing yield gap through sustainable intensification and improved crop management, increasing yield protential through plant breeding, and reducing crop loses by improving harvesting and post harvest procedures. Plant breeding has contributed to increased productivity by systematically creating new genotypes using plant genetic diversity, especially genetic resources with superior adamaksptation, to fulfill the need of

society, provide resource for the production system and the demand of nature in the target environment (Lee 1988).

Indonesia is rich in biodiversity and is also known as a megadiversity country. Species diversity has been reported in the 4th National Biodiversity Report, and the number of plant species in the country positions Indonesia in the world's big five. Not only in plant genetic diversity, Indonesia also posesses a high number of genetic resources for cattle and poultry. The importance of biodiversity for the future of Indonesia has been shown by the decision to ratify the United Nations Convention on Biological Diversity (UNCBD) into Law No. 5 in 1994. The three main objectives of the convention are (i) the conservation of biological diversity, (ii) sustainable use of its components, and (iii) fair and equitable sharing of benefits arising from use of genetic resources.

Genetic resources provided the basic building blocks to improve the productivity, resilience and nutritional compositions of organisms (Roa et al. 2016), because genetic resources correspond to the genetic potential of an organisms (Wilkes 1992). Genetic resources are the basis of agricultural production and significant economic benefits resulted from their conservation and use (Rubenstein et al. 2005). Collection of genetic resources means mantaining the gene pool out of harm's way. Genetic resource generally can be conserved *in situ* and *ex situ*. Although *in situ* conservation is by far the most effective way to protect endangered species, it is evident that not all species can be efficiently preserved at their natural habitats (Witzenberger and Hockkirch 2011). *Ex situ* conservation is the maintenance of species outside their natural habitats. *Ex situ* conservation can also be defined as the conservation of components of biological diversity outside their natural habitat (Oqwu et al. 2014).

Types of *ex situ* conservation includes seed genebank, field genebank and *in vitro* culture. The components of *ex situ* conservation consist of material acquisitions, management of physical materials, management of information and handling of legal issues (Anumalla et al. 2015). *Ex situ* conservation allows the reintroductions of an organism in area where they had been lost through environmental degradation, displacement and war, but the stored materials need to be readily accessible, well documented, characterized and evaluated and are relatively safe from external threats.

Among the various types of *ex situ* conservation, seed storage in seed genebank is the most convenient for long-term conservation (Le and Pritchard 2009; Hammer and Teklu 2008), because seeds, especially the ortodox ones, can be conserved at low relative humidity and temperature for long time (Westengen et al. 2013). Seed genebanks can conserve and mantain genetic resources that are threatened in their habitat and make them accessible. Seed genebanks therefore not only requires proper infrastructure but also efficient management of safety backup, regeneration, characterization, distribution, and data management (Engels and Visser 2003), whereas the pre-requisite for the utilization of genetic resources is the availability of information from characterization and evaluation of genetic resources (Khoury et al. 2010). The global challenges related to *ex situ* seed genebank include the lack of sufficient funds, facilities and staff, regeneration backlog and genetic integrity loss, diluted political support, lack of adequate genetic resource characterization and evaluation, regular updating of genebank information system, incomplete diversity coverage and inadequate genebank capacity, deteorating genebank support, unbalanced support, lack of proffesional trainning and genebank collapse (Fu 2017). In Indonesia, some of those challenges will be

addressed by system rationalization and coordination, the use of similar procedures and approved identification system and robust digital system.

System Rationalization and Coordination

Genebank operation can be classified into 3 services i.e. genetic resource conservation, distribution and information assembly and management (Westengen et al. 2013). Genetic resource conservation includes collection and storage (Peaters and Galwey 1988, Wang et al. 2017). Conceptually, germplasm collection methods must capture maximum variation (Rao 2004), therefore the collection ideally includes landraces, advanced/ improved strains (varieties) and wild relatives found in different areas. As a result, germplasm collection can be very expensive.

Indonesia is a country with a large diversity of genetic resources and the countries actually is responsible for their conservation and sustainable use and enshrine them as a local wisdom and historical heritage to ensure the sustainable development of the nation (Annonia et al. 2008). However, in the case of Indonesia, a single institution probably will not be able to conserve all genetic resources found around the nation. The constraint is not only the required budget, but also the time and space. Genetic resources have been conserved *ex situ* by some research institutes and universities under the coordination of the Indonesian agency for agricultural research and development as the focal point (Sutoro 2008), but this arrangement has not worked properly. Clearer directions must be developed to optimize the genetic resource management at the whole region. In addition, it is important to establish a national network between the national commission and its stakeholders, but unfortunately such infrastructure has not been established yet.

Good coordination between the national commission and its stakeholders must be developed, so that genetic resource can be efficiently and effectively utilized. We propose that the national commission must be facilitated with a very robust computer system and a large seed genebank that can store core collections and their accompanying informations. Whenever possible, the location of the national commission must be situated close to a biological garden. Genetic resources can be classified based on their utilization, for instance food crops, industrial crops, small and large animals. The national commission has the responsibility to communicate with international stakeholders and the result must be reported to national stakeholders. National stakeholders must be coordinated by their local governments, preferably provincial governments. Similar to the national commission, local commission must be supported by a robust computer system which can communicate ssecurely to national commission. Important elements of *ex situ* conservation include the management of physical materials, such as handling, storage, monitoring, regeneration and distribution, and also management of information such as passport data, phenotypic and omics data, database, user interface and website (Anumalla et al. 2015). Such activities generally are conducted by seed genebanks or other institutions such as universities or private seed companies that manage *ex situ* genetic resource conservations, but local governments must monitor all genetic resources that are managed at the region. Each seed genebank or other *ex situ* genetic resource conservations have the responsibility to collect, distribute, and manage at least the genetic resources originated from their regions. Other intitutions around the nation can utilize those genetic resources by requesting directly to the genebank or through the national and local commission.

Utilization of Uniform Procedures for Genetic Resource Management

The availability of information regarding the characteristics of genetic resource strored in ex situ genebank has been accepted as a pre-requisite for their utilization (Khoury et al. 2010). There are a number of information associated with genebank, including passport, characterization, evaluation, environmental, genetic and molecular data. The more information available about the genetic resources, the more useful the genetic resources will be for the stakeholders (Diez et al. 2019).

Passport data normally contain the origin or source of the genetic resources. Environmental data must be included in the passport, especially now due to the development of Geographical Information System (GIS). Accurate information is very important because there is a link between geographical region and the genetic resource characteristics. Genetic resource characterization records morphologically distinctive and identifiable characteristics among accessions. Such characteristics should be highly heritable, easily visible and have similar expressions in different environments. International standards, which are known as descriptors, have been established by IPBGR or Biodiversity, but they mostly exist in very important commodities.

Genetic resource evaluation is very similar to characterization because it is related to agronomic description, but it is for traits which are more sensitive to environment or controlled by multigenic factors, but are generally also important in plant improvement. Each seed genebank has different methods to document such characteristics. Evaluation is an important activity to discover useful resources and predict their genetic potential and breeding value, especially for materials that are currently

underutilized (Wang et al. 2017). Evaluation data include productivity, reaction to biotic and abiotic stresses, agronomic attributes and time to flower and harvest.

Another type of information which is most promising for modern users are genetic and molecular data. Radically different approaches to data management and lack of sharing within and across sectors due to fundamentally different objectives and low level of mutual trust must be avoided. To effectively work towards a better data sharing, two aspects need to be in place. First, a data standard and guidance on what is required to promote optimal data management need to be formulated. Secondly, data should be managed according to FAIR principles, where all data should be findable, accessible, interoperable and reusable.

Utilization of Approved Identification System

Several stakeholders have highlighted the importance of creating and adopting permanent unique identifiers for genetic resources due to the difficulties found during collaboration on conservation, research, and breeding in the absence of a common standard and the difficulty in finding information associated with genetic resources (FAO 2018).

Passport data contain basic description of an accession. In every passport data there must be an identification number, which is intended to serve as a unique identifier for the accessions within a genetic resource collection. This number, once assigned, can never be reassigned. Even when that accession becomes extinct its assigned number is still not available for re-use. This number is assigned by each institute when an accession is entered into its genetic resource collection along withaccesion name, genus name, country of origin, acquisition date and code

of the institute where the accession is maintained, but passport code for accession number must be unique. Although there are several international system for passport code for genetic resource such as DOI system, FAO WIEWS (World Information and Early Warning System) database and WIEWS Institute codes, FAO/Bioversity Multi-crop Passport Descriptors (MCPD), genesys extensions to MCPD, and GRIN, some countries and international institutions develop their own unique identifier such as Japan with their NIASGBdb (National Institute of Agrobiological Sciences Genebank Database). In the case of Indonesian genebank management system, all stakeholders must agree on an identification system. With such agreement, genetic resources will be easier to manage and utilize.

Robust Digital System

Data management systems are vital to track accessions for management purpose and for adding beneficial value to accessions for their efficient utilization. Better management system within genebank as well as integrated information system will aid in identifying unique genetic resources, but it must be supported by a robust digital information system. Hovewer, successful construction of a robust and integrated digital information system must overcome several constraints, such as availability of the technology, infrastructure and knowledge base and the paucity of accession-level information, as well as continued support from stakeholders for the maintenace of the resulting information system (Kuory et al. 2010).

Beyond cold room and the laboratories, greenhouses and regeneration field, there is a wealth of information that must accompany the diverse collection. This information includes everything from where and when a seed was collected, and who

requested and recieve the sample (Cole et at. 2012). Information related to an accession will therefore contain a wealth of data, big in size, heterogeneous among different accessions, complex and sometimes unstructured. There were theoretically no adequate systems that existed for logging and tracking all those data as well as the metadata related to genetic resource. However, a robust data management system along with big data analysis can probably be the best approach to solve the constraint of genetic resource management and use. Big data means large data sets with the features like high velocity, volume and variety, which are difficult to process using traditional database management and analytical methods (Ma et al. 2014). Because big data technology generally refers to three aspects of technical evaluation including automated paralel computation, data management scheme, and data mining analytics, robust digital information system with big data analysis is better equipped to solve the future constraints on the efective and efficient utilization of genetic resources.

Concluding Remarks

Optimal, efficient and effective utilization of genetic resources can be approached through system rationalization and coordination, using similar procedures, approved identification system, and robust digital system.

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CHARACTERIZATION OF BUTTERFLY PEA AS A MODEL OF UNDERUTILIZED CROP MANAGEMENT IN INDONESIA

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INTRODUCTION

Indonesia is one of the tropical countries known as megabiodiversity country rich in plant genetic resources (PGR). PGR is very important for keeping balance ecosystems and biosphere life system. The lost and erosion of PGR, which have been due to human activities, caused the unbalance ecosystems on earth which in turn affect human life. PGR must be evaluated for their useful characteristics and be well described to be of use for farmers and breeders. There also proposed strategy to make it easier to locate useful varieties and genes in collections by developing properly identified core sub-sets of larger collections, through the development of better database.

Underutilized crops suffer from a lack of dedicated research centers which leads to unavailability of centralized and organized database. Research on underutilized crops requires identification data of the places where the crops are grown, planted and used as food, feed or in commercialized products. This will lead to the

detection of existing value chains and communities that are involved. Butterfly pea is an underutilized crop, although there are many publications regarding butterfly pea but the database have not been systematically available. Butterfly pea is a member of the Leguminosae (Fabaceae) family, Phaseoleae tribe, and Clitoriinae subtribe, found in many countries worldwide (NPGS 2008). Butterfly pea has a diploid chromosome number of 2n = 16 (Joson and Ramirez 1991). The development of butterfly pea in Indonesia is still very low both from the cultivation and utilization. The planting of butterfly pea buds is still irregular in most areas. Indonesia needs Plant Genetic Resources (PGR) inventory so that butterfly pea can be recorded and easily monitored and managed.

Big data are immense data sets that can be analyzed to reveal patterns and trends in PGR. The growth in the digital universe and the data available provide PGR facilities with information that can be used to develop targeted conservation-breeding programs and for long-term future planning for utilization of butterfly pea. The needs for PGR stakeholder's cooperation are to accelerate PGR data collection, open public access and its conservation program. Habitat destruction by modernization requires the state to create support systems, regulations, and adequate research funding incentives for PGR.

Butterfly pea has not been developed much since there is no study of diversity of its varieties so it becomes one of the factors that cause low quality of anthocyanin information on the plants. Efforts to develop butterfly pea such as by using superior varieties, proper cultivation mode, and improvement of genetic potential are suggested. Characterization is a way to recognize butterfly pea. Graduate School of Padjadjaran University collaborated with Sensient Inc. has conducted research on the characterization and utilization of butterfly pea. The objectives of

this research were to obtain information on genetic distance and genetic diversity of butterfly pea originated from Indonesia on morphological traits. Morphological trait can be used as significant indicators for specific genes and gene markers in chromosomes.

Big Data: Discovering the Value of an Underutilized Crop

The current advancement of research on big data in plant science and underutilized crops is crucial. Significantly it can help in mitigating the effects of global problems like climate change, nutrition deficiency, food security and to decrease developing countries dependency on imported crops. Every crop can have many varieties. Local names, synonyms, and landrace names are different and can define certain crops. Most of their varieties have their genetic sequences stored in gene banks. This is not the case for most underutilized crops. For underutilized crop like butterfly pea, most of the names have not been documented. Their varieties, landrace and cultivar names and their cropping patterns are not well documented. Solving this problem requires an expert study on underutilized crop names.

Big data analytics for underutilized crop is essentially an outcome of developments across three major components of the digital revolution (Kune et al. 2016): (i) new digital data sources, (ii) more computing power (faster processors and networks, massive storage, parallel processing, cloud computing) and (iii) higher level analytics (machine learning, deep learning, natural language processing, visualization). Together, they enable creation of novel value by leveraging massive, structured, and unstructured data to generate powerful insights into complex phenomena. Unstructured data does not conform to a pre-defined schema and cannot be easily searched or processed in

traditional database systems. Sensors, search engines and social media are examples of sources of unstructured data (text, documents, images, videos, etc.). Only 5% of all data in the world is structured data (Gandomi and Haider 2015), underscores the wide scope and significance of big data technologies.

Large volume, accession (variety) and velocity are three basic characteristics of big data of underutilized crops. Volume refers to size of data, while variety encompasses multiple data sources, variables, formats and heterogeneity (structured/unstructured data). Velocity refers to the frequency at which data is acquired, which can vary from seconds to years. Data veracity (uncertainty), variability (inconsistency) and value are also often included as additional characteristics of big data. Such data are too large to be stored or processed on a single computer using traditional software and database architectures (tables, excel sheets, SQL databases). While the size/volume of big data gets popular attention, the heterogeneity of sources, formats and lack of structure present its most difficult challenges (Davenport 2014). The key idea of big data therefore also includes novel methods used for data integration, storage, processing, visualization and analyses. A definition which covers all these aspects is: Big Data, which is data of such large size and complexity (large number of variables and diversity of their sources, structures, frequencies, and scales), that they require new computer and data architectures, techniques, algorithms, and analytics to manage and extract value and hidden knowledge (adapted from Schönberger and Cukier 2013).

Big Data and Climate Smart Agriculture creating value from big data involves five distinct steps: (i) data acquisition and storage, (ii) information extraction and cleaning, (iii) data integration, (iv) modeling and analysis, and (v) interpretation and deployment (Jagadish 2015). Specific big data technologies

analyze textual, video and audio data and link them to other data. Similarly, to deal with high volume, variety and velocity aspects of big data, machine learning technologies are used to rapidly fit, optimize and predict data. Further, as big data are too large to store in any single central database, technologies for parallel storage and processing among several computers are deployed for faster and more balanced output. Finally, the visualization tools of big data enable users to interact with underlying algorithms, assess and interpret outcomes of analysis and communicate with stakeholders.

Big Data of Butterfly Pea: Characterization and Utilization

In Indonesia, butterfly pea (*Clitoria ternatea*) is considered to as an underutilized crop. It has a wide range of diversity (Karuniawan et al. 2017). For example, butterfly pea comes in a variety of colors such as purple, dark blue, light blue, pink, and white. Aside from its stunning beautiful flowers used as ornamentals, butterfly pea can also be used as vegetable, forage, cover crop, natural colorant, and medicinal plant (Gomez and Kalamani 2003; FAO 2012; Hariadi et al. 2018). Butterfly pea's blue and purple flowers are rich in anthocyanins, which are beneficial antioxidants (Hariadi et al. 2018; Suebkhampet and Sotthibandhu 2012). In addition, it also contains flavonoids, alkaloids, saponins and tannins, which make butterfly pea a good candidate as a medicinal plant (Chauhan et al. 2012; Lijon et al. 2017). Because of its many potential uses, butterfly pea could become a very important crop in Indonesia with the aid of breeding and crop improvement programs.

Graduate School of Padjadjaran University collaborated with Sensient Inc. has conducted research on the characterization and utilization of butterfly pea. The study used 89 butterfly pea

germplasm accessions collected from all over Indonesia. Each accession was planted on a 5 m^2 plot with a spacing of 1 m x 1 m. Manure was used as a basic fertilizer with a rate of 2 tons/ha. NPK was applied 3 months after planting with a rate of 200 kg/ha.

Field experiments were laid out using Randomized Complete Block (RCBD) with two replications across two different environments, i.e. lowland and upland. Genetic diversity was estimated using cluster analysis and principle component analysis (PCA) using NTSYSpc version 2.1. (Rohlf 2001). Fifteen agro-mprpological traits were emplyoed to assess the diversity.

Characterization of Butterfly Pea

Table 1 shows the results of the PCA using 89 butterfly pea germplasm accessions based on agro-morphological traits. Eleven axes were obtained with eigenvalues in the range of 1.05-3.95 with cumulative contributions reaching 71.36%. According to Jeffers (1967), the number of principal components (PCs) used is determined by an eigenvalue of more than one. Thus, the number of axes that have values greater than one explains cumulative factors and the genetic diversity present among these accessions.

Table 2 shows the contribution of each agro-morphological trait to the genetic diversity of 89 butterfly pea germplasm accessions. On this table, only the four principal components (PCs) that contribute significantly to the genetic diversity of the 89 accessions are displayed. As a general rule, if the value of a trait is > 0.5, it has a significant influence on genetic diversity (Jolliffe 2002). This has been confirmed by other researchers (Sitepu el al. 2011; Setiawati et al. 2015; Karuniawan et al. 2016; Maulana et al. 2018). PC1 showed a huge influence in diversity. On PC 1, there are seven traits that influence genetic diversity

with a contribution of 14.62%. They are LW, FW, WFFP, LS, PL, NTP and SL. On PC 2, there are three traits that give an effect of 9.42%, i.e., PL, SL and SD. On PC 3, there are three traits that have an effect of 7.93%, i.e., PH, W1FF and GH. On PC 4, there are two traits that influence diversity by 6.47%, namely LW and FW. Traits with positive effects have maximum contributions on genetic diversity (Haydar et al. 2007; Solankey and Singh 2018).

Table 1. Eigenvalue, percent, and cumulative values of 89 butterfly pea germplasm accessions from Indonesia.

PC	Eigenvalue	Percentage	Cumulative
1	3.95	14.62	14.62
2	2.54	9.42	24.04
3	2.14	7.93	31.97
4	1.75	6.47	38.44
5	1.51	5.60	44.04
6	1.45	5.36	49.40
7	1.37	5.08	54.48
8	1.22	4.52	59.00
9	1.19	4.39	63.40
10	1.10	4.08	67.47
11	1.05	3.89	71.36

Table 2. Contribution of each agro-morphological trait to the genetic diversity of 89 butterfly pea germplasm accessions from Indonesia.

	PC1	PC2	PC3	PC4
PH	0.168	0.377	**0.692**	0.074
LL	-0.144	-0.144	-0.271	-0.106
LW	**0.557**	-0.001	-0.181	**0.607**
FL	-0.177	-0.100	-0.147	-0.052
FW	**0.569**	-0.038	-0.171	**0.647**
CL	-0.206	0.395	0.437	0.210
W1FF	0.450	-0.410	**0.520**	-0.441
EW100FF	-0.250	0.367	0.278	0.127
WFFP	**0.609**	-0.312	0.244	-0.017

Table 2. Continue.

	PC1	PC2	PC3	PC4
WTFF	-0.358	0.172	0.108	0.124
FC	0.278	-0.250	0.416	-0.412
PN	-0.161	0.146	0.214	0.145
LS	**0.608**	-0.380	0.288	0.213
GH	-0.305	0.238	**0.513**	0.306
PL	**0.604**	**0.545**	-0.090	-0.233
PW	-0.236	0.078	0.084	0.165
NPP	0.494	-0.228	0.049	0.028
WPP	-0.332	-0.010	-0.024	0.148
NTP	**0.560**	0.052	-0.217	0.195
WTP	-0.132	-0.110	-0.195	-0.082
SL	**0.503**	**0.751**	-0.214	-0.206
SW	-0.204	-0.095	-0.195	-0.030
SD	0.268	**0.664**	-0.079	-0.326
NSP	-0.134	-0.157	-0.282	-0.139
WSP	0.448	0.282	-0.221	-0.087
W100S	-0.235	0.019	0.041	0.115
WTS	0.338	-0.110	0.089	0.043

Note: PH: Plant Height; LL: leaf lenght; LW: leaf width;FL: Flower lenght; FW: Flower width; CL: Calix length; EW100FF: estimated weight of 100 fresh flower; WFFP: weight of fresh flower per plant; WTFF: weight of total fresh flower; FC: flower color; PN: petal number or type of flower; LS: leaf shape; GH: growth habit; PL: Pod length; PW: Pod width; NPP: number of pod per plant; WPP: weight of pod per plant; NTP: number of total pod; WTP: weight of total pod; SL: Seed length; SW: Seed width; SD: Seed diameter; NSP: Number of seed per plant; WSP: Weight of seed per plant; W100S: Weight of 100 seeds; WTS: weight total seed.

Figure 1 Shows the dendogram generated from the cluster analysis performed on 89 butterfly germplasm accessions from Indonesia. Genetic diversity ranged from 0.47-7.64. Sitepu et al. (2011) stated that if the Euclidian value is greater than one, it has a wide genetic diversity. This was also observed by Karuniawan et al. (2017) on butterfly pea with values ranging from 0.0-4.79. Similar observations were reported in wild sweet potato (Setiawati et al. 2015), cassava (Karuniawan et al. 2017), and orange-fleshed sweet potato F1 population (Maulana et al. 2018).

Thus, based on this study, the 89 butterfly pea germplasm accessions from Indonesia have a broad genetic diversity.

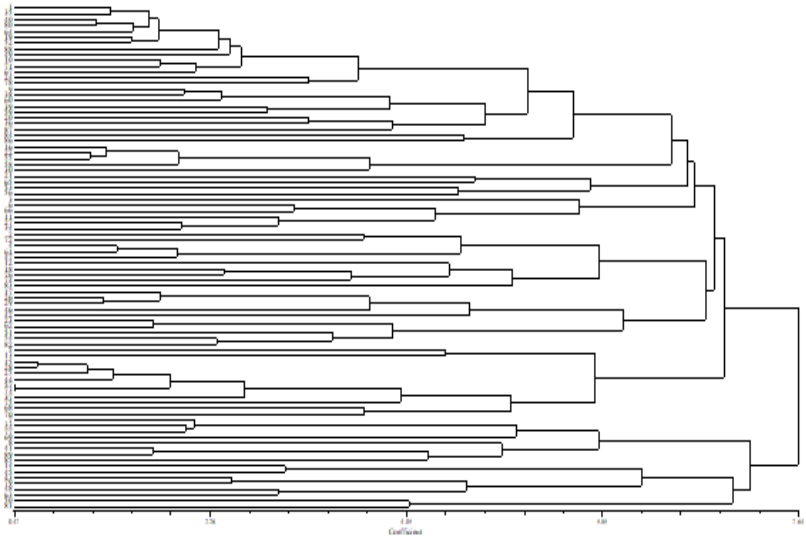

Figure 1. Dendrogram of 89 butterfly pea germplasm accessions from Indonesia.

Cluster analysis based on agro-morphological traits was also used to identify the degree of similarity and relationships among the 89 butterfly pea germplasm accessions studied. Based on the dendogram in Figure 1, the 89 accessions can be divided into two main clusters, namely I and II. Accessions that are in the same cluster are homogeneous groups based on the traits tested. This was also reported by Safitri et al. (2012) in secondary crops and by Maulana et al. (2018) in sweet potato.

In the first cluster, there are two sub-clusters, IA and IB. IA sub-cluster is divided into IA1 and IA2 sub-clusters. Sub-cluster IB is also divided into IB1 and IB2 sub-clusters. Furthermore, Sub-cluster IA1 consists of 39 butterfly germplasm accessions.

Accessions that were very similar in this subclass were accession numbers 22 and 55. Sub-cluster IA2 consists of 20 butterfly pea germplasm accessions, with accession numbers 26 and 29 being the most similar. Sub-cluster IB1 consists of two accessions only, while sub-cluster IB2 consists of 10 butterfly pea germplasm accessions with accession numbers 57 and 73 being the most similar. In the main cluster II, there are two sub-clusters; IIA and IIB. Each sub-cluster is divided into two sub-clusters (i.e IIA1, IIA2, IIB1 and IIB2). Sub-cluster IIA1 consists of four butterfly germplasm accessions. Sub-cluster IIA2 consists of four butterfly germplasm accessions. Sub-cluster IIB1 consists of six accessions and sub-cluster IIB2 consists of two accessions. In each sub-cluster the germplasm accessions are very similar.

Germplasm accessions that are in the same sub-cluster have very similar agro-morphological traits. However, germplasm accessions that are very similar to each other but are placed in different sub-clusters could be due to phenotyping error. Accuracy in cluster analysis is dependent on the number of traits observed. Thus, the more traits included in the analysis, the better it is to distinguish among germplasm accessions (Rohlf 2001). This study shows that there is broad genetic diversity available among the 89 butterfly germplasm accessions from Indonesia.

Concluding Remarks and Future Perspective

Big data is very important to inventory plant genetic resources, especially underutilized crop. This research attempted to utilize agro-morphology of underutilized crop of butterfly pea for database inventory. Characterization using principal component analysis (PCA) and cluster analysis show that the 89 butterfly pea germplasm accessions from Indonesia have a broad

genetic diversity. The availability of broad genetic diversity in butterfly pea is essential for further improvement by providing options for the breeders to create improved varieties with traits such as yield, pest resistance and tolerance to environmental stresses. The ability to develop improved butterfly pea varieties further bolsters its potential to become an economically important crop in Indonesia.

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SUSTAINABLE USE OF CASSAVA GENETIC RESOURCES IN TANZANIA THROUGH GENETIC DATABASES

Gladness Temu and Joseph Ndunguru

INTRODUCTION

As the world population continues to grow it is estimated that overall food production will need to increase by 60-70 percent by 2050 in order to feed about 9 billion people (FAO 2009). This has necessitated more innovations in agriculture and wider uses of plant genetic resources (PGRs). Plant genetic resources was defined by FAO (1989), referring to it as the economic, scientific or societal value of heritable materials contained within and among plant species. They include materials used in cytogenetic, evolutionary, physiological, biochemical, pathological or ecological research on the one hand, and accessions evaluated for their agronomic or breeding propensities on the other.

Cassava (*Manihot esculenta* Crantz), also known as manioc, tapioca, or yuca, is a valuable crop with diverse genetic resources (GRs) found in landraces, accessions, improved cultivars, breeder's released materials and cassava wild relatives. The crop is extensively cultivated as an annual crop in tropical and

subtropical regions for its edible starchy tubers that serves more than 800 million people in Sub Saharan Africa and Asian subcontinent (Nassar et al. 2010). Cassava is the third largest source of carbohydrates in the world (Fauquet and Fargette 1990) and is a popular African crop, it is cultivated in the Western, Eastern, Central and Southern parts of Africa. However, global climate change introduces stresses such as elevated heat, coldness, drought and flooding, which threaten sustainable cassava cultivation. Biotic stresses, especially viruses such as Cassava Mosaic Disease (CMD) caused by cassava mosaic begomoviruses (CMBs) and Cassava Brown Streak Disease (CBSD) caused by cassava brown streak viruses (CBSVs), are considered as major threats to cassava production in many growing regions worldwide (Kanju et al. 2007; Legg et al. 2015; Tomlinson et al. 2018).

Various cassava germplasm have been characterized for a variety of traits and exploited for breeding new varieties adapted to climate change for sustainable agriculture. For instance, characterization of germplasm at the molecular level to detect candidate genes for useful traits offers the possibility to apply them in marker assisted selection (MAS) within breeding programmes (Perez-de-Castro et al. 2012). The survey of allelic diversity within such genes from cultivated and wild accessions followed by analyses of their particular effects permits the selection of the most efficient allele combinations. However, for breeders to access and utilize this kind of information, some concerted efforts are required to establish a knowledge exchange database or genetic databases due to the huge data obtained during genome sequencing. This alone is not adequate since the improved plant materials themselves should be available for proper exchange among and between breeders, scientists, researchers and farmers to obtain the benefits of the GRs.

Therefore, the International Treaty for Plant Genetic Resources for Food and Agriculture (ITPGRFA) has introduced a sustainable standardized and automated one-stop shops for PGRFA information around the world though the Global Information System (Alercia et al. 2018). This tool facilitates easy access to information on various crops for research, training and breeding through the use of Digital Object Identifiers (DOIs), which was designed for easy identification and tracking of plant germplasm worldwide. This review discusses the GRs available in cassava, established cassava GRs databases, permanent linking of cassava materials with digital identifiers for benefit sharing and a way forward to access and utilize these genomic tools by African scientists.

Cassava Genetic Resources in Tanzania and Climate Change Challenges

Cassava is an important subsistence food crop in Tanzania, ranked second only to maize, and sometimes considered as a famine reserve when cereals fail due to cassava's drought tolerance (Kapinga et al. 2005). More than 80% of the total production in Tanzania is used as a primary source of calories, while the remaining are utilized for animal feed, starch making and exportation (Kapinga et al. 2005). Farmers grow diverse cassava genotypes rich in allelic variations, some of them already widely exploited and many more remain unexploited. The available cassava GRs represent a critical resource that can be employed in breeding for the future of this crop. Over the years, several genomic tools have been used to characterize cassava germplasm available in Tanzania, such as the use of Random Amplified Polymorphic DNA (RAPD) and Amplified Fragment Length Polymorphism (AFLP) (Fregene et al. 2003; Herzberg et al. 2004), Short Sequence Repeats (SSR) (Lyimo et al. 2012;

Elibariki et al. 2013; Pariyo et al. 2013), Single Nucleotide Polymorphism (SNP) (Mtunguja et al. 2017), and Quantitative Trait Loci (QTLs) (Masumba et al. 2017).

However, the genetic base of many landraces and their wild relatives, in which breeding is based on, have been threatened by various factors such as genetic erosion and stress induced by global climate change (Hammer and Teklu 2008). CMD and CBSD for instance, have caused the disappearance of cassava landraces. In Tanzania, cassava landraces that were very popular in the 1990s are no longer available after being wiped out by these two viral diseases. The disappearing cassava landraces include Rushura, Rwakitangaza, Msitu Zanzibar and Aipin Valenca, mainly because of their high susceptibility to CMD and CBSD (Ndunguru et al. 2005). These viral diseases also eliminated susceptible cassava landraces in other countries also such as Uganda, Kenya, Rwanda, Burundi and the Republic of Congo (Otim-Nape et al. 1994; Sseruwagi et al. 2004). In Uganda, the outbreak of CMD pandemic in 1998 resulted in the disappearance of a cassava landrace called Ebwanatereka, which was widely distributed in the country in the 1980s (Otim-Nape et al. 1994b). Another common cause of reduction in diversity is the replacement of landraces by modern cultivars (van de Wouw et al. 2010). Cassava was introduced to Africa by Portuguese traders from Southern and Central America in the 16th century. It has undergone genetic modifications as well as genetic erosions that resulted in the loss of some genetic diversity. Several factors contribute to genetic erosion and loss of biodiversity, such as modern cultivation, deforestation, wildfire, as well as pests and diseases. Genetic erosion (also known as genetic depletion) is a process where the gene pool of a population diminishes when reproductive individuals die off before reproducing resulting in the loss of a phenotype or even the whole species. Genetic erosion

occurs because each individual organism has many unique genes which get lost when it dies without getting a chance to breed (Hammer and Teklu 2008).

Since climate change can contribute to the loss of crop biodiversity, plant conservation is very critical and sustainable use of GRs available in any plant is necessary (Hammer and Teklu 2008). Breeding new varieties that can withstand climate change is critical in order to increase agricultural productivity and meet the food security challenges. However, development of new improved cassava varieties is a long term and expensive process due to its long breeding cycles. Genetic improvement of any crop also depends on the capability to successfully utilize the existing genetic resources, including related wild species. Similarly, collection, conservation and utilization of PGRs and their global sharing are essential components of international crop improvement programmes (Alercia et al. 2018). Thus, to improve the available cassava germplasm and minimize genetic erosion and loss of biodiversity, several genomic databases have been established by various teams of researchers and scientists. To promote access and sustainable utilization of these databases for cassava germplasm improvement in Africa, it must be coupled with capacity building and technology transfer since a huge knowledge gap exists between the scientists who develop these genomic information and the intended users.

Cassava genetic resources database initiatives

Over the past decade, there has been an ongoing effort for exploration, exploitation and manipulation of PGRs, through the use of new technologies that generate and analyze big data (Perez-de-Castro et al. 2012; Halewood et al. 2018). Plant breeders and other scientists can potentially leverage these technologies to

significantly increase the efficiency and effectiveness of breeding programs for improved cassava for sustainable agriculture. Data from genetic diversity studies, genome wide association studies, next generation sequencing and others, have enabled the establishment of cassava genetic databases by various teams. Next generation sequencing has enabled the creation of genome-wide molecular tools such as bulk identification of markers and high-throughput genotyping strategies, for breeders to incorporate into existing breeding methods (Lorenz et al. 2011). In order to tap into this useful information, consolidated efforts to assure access and utilization of both genomic data and physical materials related to the genebank and databases is crucial (Halewood et al. 2018). Examples of the cassava database initiatives (Table 1) includes the International Cassava Information System, which is an ontology-driven cassava database (ICASS database), Cassavabase.org, Cassava online archive (http://cassava.psc.riken.jp/), the Integrated Breeding Platform (IBP), Phytozome (a portal hosting genome databases) and the Cassava Genome Hub, which is an integrated web-based database for communicating and sharing genomic, transcriptomic, metabolomic, genetic and breeding resources to enable basic and transformational research in cassava genetic improvement.

Similarly, a Benefit Sharing Fund cassava project co-funded by FAO-ITPGRFA at Tanzania Agricultural Research Institute, Mikocheni (2016-2019) intended establishes a knowledge exchange database as one of its outputs. The project evaluated the adaptation of cassava germplasm to biotic and abiotic stresses caused by global climate change. Through this project, more than 150 cassava local varieties and breeder's released materials were evaluated with respect to resistance and tolerance to elevated cold, heat, drought, cassava mosaic disease, cassava brown streak

disease and cassava bacterial blight, and utilize them in breeding programmes to obtain new cassava varieties adapted to climate change for sustainable agriculture. Within this project, useful candidate genes, markers for marker-assisted breeding, and predictive models for different biotic and abiotic stresses in cassava were identified using RNAseq and Restriction Associated DNA (RAD) markers. The project generated data that were used to develop a knowledge exchange database that can be accessed at BIOCAS-FAO webpage (http://www.biocas-fao.com/). These platforms along with so many others have very useful genotypic data that can be used by researchers, scientists and breeders in their efforts to improve cassava germplasm worldwide.

Table 1. Cassava GR and genetic databases.

Sn	Database	Remarks	Link
1.	Cassava Online Archive	Provides cassava mRNA sequences and ESTs currently available from NCBI (Genbank/EMBL/DDBJ) and their annotations	http://cassava.psc.riken.jp/
2.	ICASS	An ontology-driven cassava database	-
3.	Phytozome	The database and portal hosting the genome database	https://phytozome.jgi.doe.gov/
4.	Cassavabase.org	NextGen Cassava Breeding project	https://www.cassavabase.org/
5.	Cassava Genome Hub	A web-based database for communicating and sharing genomic, transcriptomic, metabolomic, genetic and breeding resources for cassava	https://www.cassavagenome.org/
6.	Biocas-FAO CG database	Cassava candidate gene database for abiotic and biotic stresses	http://www.biocas-fao.com/ http://www.biocas-fao.com/molecular-analyses/candidate-gene-detection/
7.	Integrated Breeding Platform (IBP)	Gives access to forefront technology and quality services for both traditional and modern breeding activities	https://www.integratedbreeding.net/

Genotypic characterization to identify useful molecular markers in plant materials through genome sequencing are increasingly being used in research and breeding programs (Halewood et al. 2018). The genetic data can be applied in pre-breeding and breeding programs, conservation and other purposes in crops genetic improvements (Hammer and Teklu 2008). DNA sequencing of thousands of varieties, accessions, landraces, crop wild relatives, improved varieties and hybrids normally generates a comprehensive data that can be used for crop improvements (Halewood et al. 2018). Different approaches are available but the demand for crops tolerant to biotic and/or abiotic stresses as well as other good agronomic traits requires intervention through innovative approaches in breeding, to incorporate the desired traits in farmer's or industry-preferred materials. The use of candidate genes and breeding models greatly facilitates the availability of desired traits to incorporate into crop germplasm through marker-assisted selection (Perez-de-Castro et al. 2012). Ultimately, delivery of improved varieties to farmers must pass through repeated cycles of field evaluations-wet laboratory-dry laboratory supported by big data databases (Figure 1).

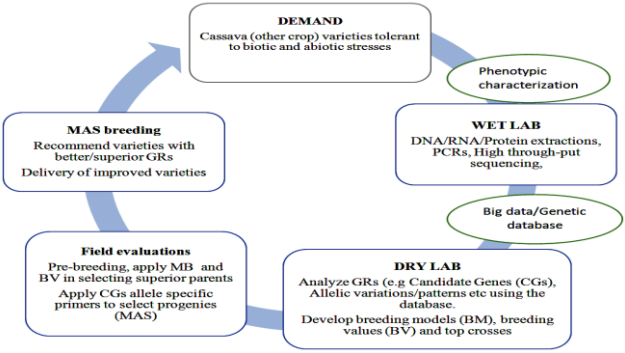

Figure 1. Simplified schematic illustration of the GRs analysis and database for MAS breeding.

Ambiguity in Plant Genetic Resources Identities

In traditional agro ecosystems especially in Africa, farmers grow an enormous diversity of crop landraces that need to be conserved for their sustainable utilization in agriculture (Turyagyenda et al. 2012; Kombate et al. 2017). Sustainable management of these genetic resources is crucial. However, different communities use different naming systems so some varieties end up having different names in different communities while the same name may refer to different varieties. It is also very common for breeders to release plant materials with 'special names' or codes that are unfamiliar to farmers. When farmers receive those materials they normally change the names to somewhat simpler names when they like the material's good agronomic performance. This leads to confusion regarding the purity and identity of some varieties, making it difficult to trace and attribute the varieties to different farmers or communities (Kapinga et al. 2005). To avoid this confusion, having a permanent digital identification of crop varieties will facilitate tracing and sustainable use of the GRs, even if the common name/s are changed at some point in the future. Digital object identifier (DOI) is a standard system that can be used to identify plant germplasm worldwide, which can promote access and utilization of GRs sustainably (Alercia et al. 2018). DOIs are used as Permanent Unique Identifiers (PUID) in the context of the Global Information System (GLIS) of Article 17 of the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA). Therefore, during cassava (or any other crop) material exchange, the digital identifiers will unambiguously and permanently identify the exchanged materials across local and international organizations. This permanent identification will facilitate sustainable utilization and conservation, and prevent mixing or duplication of the cassava

genetic materials in farmer's hands and cassava genebanks. Exchange of new germplasm provides an opportunity to breeders to incorporate these GRs into the available germplasm through evaluations, selection and hybridization to produce new varieties that will be resistant to CMV and CBSV (Tumwegamire et al. 2018).

Empowering African Scientists with Genomic Tools

In addition to the establishment of genetic resources databases, there is a need to empower African scientists with genomic resource tools so that they can use them to access and use genomic data for crop improvement in Africa. Africa is endowed with a huge genetic resource base and its biodiversity is largely underutilized. Modern molecular biology techniques such as whole genome sequencing and deep sequencing are emerging as the go-to tools for biologists. The number of plant genomes with published sequences has grown significantly within the past five years and some of the remaining genomes are currently being sequenced. Ideally, the crop's whole genome data should be used for to mine useful genes for agricultural improvements. The challenge now lies in promoting the access and utilization of that database by African scientists, since the majority of them lack the knowledge and skills to access, analyze, interpret and make use of the datasets (Karikari et al. 2015). Consequently, most of the genomic data is being used by scientists from advanced laboratories for publications in high impact journals and not by African scientists for agricultural improvement. The majority of the sequenced plants however comprise important food and cash crops in Africa. Thus there is an urgent need to empower African scientists (breeders, biotechnologists, biologists, entomologists and geneticists) on how to access and make use of the whole genome data not only of cassava but also for other food and cash

crop improvement in Africa. This can be done through technology transfer trainings, acquisition of bioinformatics software's and mentoring programs. The demand for such trainings is so huge in Africa. This will lead to improved African agricultural productivity through the application of modern science and technologies, enhanced African human resource capacity, as well as enhanced regional and national/international collaboration among scientists to work towards providing practical solutions to African farmers through the application of modern biotechnologies as well as science-based decision making by policy makers.

Concluding Remarks and Future Perspectives

Advances in biotechnology have offered a new arsenal of methods to effectively utilize plant genetic resources. Despite the available potentials to utilize valuable PGRs in Africa, there is a need for more capacity building for access and sustainable utilization of genomic tools and genetic databases. In addition, the use of digital identifiers can be greatly beneficial since both information and crop materials can be traced, which promotes efficient and sustainable exchange and utilization of GRs. To harness these technologies, African scientists must be empowered and strong collaboration need to be extended to achieve the development of improved crop varieties for farmers.

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CONSERVATION AND EXPLORATION OF PLANT GENETIC RESOURCES IN VIETNAM

Dang Toan Vu and The Duc Ngo

INTRODUCTION

Vietnam has been recognized as one of the world's most prosperous, rich and diverse countries in plant genetic resources (PGR). Diverse climatic conditions endowed the country's flora with both tropical and temperate plants. In addition, thousands of years of agricultural practice by 54 ethnic groups largely enriched its crop genetic resources with great numbers of local cultivars and landraces. Vietnam is in the center of origin of various crops, such as rice, taro, banana, jack fruit, mango, coconut, tea, local onion, some citrus and their wild relatives that have agricultural and social values (Nguyen and Luu 2002).

There are more than 800 plant species grown for food, medicine and construction materials in largely diversified agro-systems throughout the country, including 41 starchy food crops, 95 non-starchy food crops, 105 fruit plants, 55 vegetables, 44 oil plants, 16 fiber crops, 12 beverage plants, 181 medicinal plants, 39 spice plants, 29 cover plants and bare hill re-greening, 50

ornamentals, 49 woody plants and 5 shading plants (Nguyen 2000; Pham and Luu 2008). Recently, agricultural crops have been divided into three main groups: 1) local varieties, specialty and traditional varieties; 2) new varieties created by breeding; and 3) imported varieties.

Vietnam is richly endowed with plant genetic resources, particularly for rice, taro and bananas. This unique genetic reservoir provides the foundation for further development and improvement of rice, root crops and banana worldwide. Traditional agricultural practices have assisted in maintaining native species. With the long history of rice cultivation, Vietnamese have accumulated a rich indigenous knowledge for use and management of rice resources. Rice varieties are grown for different purposes and under different systems. Similarly, farmers have maintained various taro varieties for diverse preferred traits and use.

Currently, Vietnamese government has initiated and directed the development of a green and sustainable economy. However, the reality shows that Vietnam's economy has grown rapidly, bringing many socio-economic benefits and also putting pressure on conservation of plant resources. Moreover, the population in Vietnam reached over 90 million in 2015, making Vietnam one of the most populous countries in Asia, which creates a great demand for bio-resources as well as land use. Besides, the global context also poses new challenges and opportunities, the degree of climate change becomes more serious and creates increasing negative effects on the conservation of plant resources. Therefore, conservation and sustainable exploitation and utilization of plant genetic resources become more urgent.

Plant Genetic Resources Conservation

Collection of plant genetic resources

Since early 1990s, collection of plant germplasm in Vietnam such as rice, banana, cassava, sweet potato, yam, taro, and citrus has been undertaken through different national and international projects. Exotic germplasm have also been introduced from other countries and organizations such as Russia, India, China, Germany, CIP, AVRDC and IRRI. In total, 37.820 accessions of 430 species have been collected in Vietnam (36.324 accessions), and from other countries and organizations (1.496 accessions). We have divided the collection into different collected periods. The collected germplasm in Vietnam at the periods before 1996, 1996-2000, 2001-2005, 2006-2010, 2011-2015 and 2016-now were 8.175, 5.325, 6.500, 5.174, 11.000 and 150 accessions, respectively. The exotic germplasm at the periods before 1996, 1996-2000, 2001-2005, 2006-2010, 2011-2015 and 2016-now were 970, 20, 185, 321, 190, and 0 accessions, respectively (Table 1). The funding sources for germplasm collection were from national and international projects (Nguyen and Luu 2002).

Table 1. Collection of germplasm at Plant Resources Center and its network members.

Collection period	Vietnam germplasm	Exotic germplasm	Total
Before 1996	8.175	970	9.145
1996-2000	5.325	20	5.345
2001-2005	6.500	185	6.685
2006-2010 IV	5.174	321	5.495
2011-2015	11.000	190	11.190
2016-now	150	0	150
Total	36.324	1.496	37.820

Sources: Plant Genetic Resources for Food and Agriculture, annual project report from 2006 to 2019.

Germplasm conservation

Agricultural germplasm has been conserved at Plant Resources Center (PRC) and its network members by both *ex situ* and *in situ* conservation methods.

1. Ex situ conservation

A total of 38.338 accessions are conserved at PRC and its network members, of which more than 26.000 accessions from 120 species are conserved at seed banks with short, medium and long term conditions, including graminaceus collection (11.356 accessions), vegetables, spice collections (8.859 accessions) and legumes collection (6.296).

Moreover, field collections are used to conserve tuber crop collection comprising 3.570 accessions, fruit and industrial crop collection with 7.633 accessions from 310 species (Table 2), mushroom collections (78 accessions), flower collection (434 accessions), as well as forage and land recovery crop collection with 102 accessions. *In vitro* genebanks are conserving 157 accessions of taro and stevia. Some germplasms have been duplicated at PRC and its network members.

2. In situ/on farm conservation

In situ/on farm conservation plays an important role for improving the crop genetics and it is part of the conservation and management of plant genetic resources for food and agriculture in Vietnam.

In Vietnam, *in situ* conservation has been implemented by Plant Resources Center since 2010. The purposes is to conserve endemic crops from special regions of the country. In situ

conservation of 67 endemic crops have been done for crops like local pumelo, lychee, and local vegetable germplasm in Hung Yen, Ha Noi, NinhBinh, Nam Dinh, and Lang Son provinces (Luu et al. 2004; Vu et al. 2011).

Table 2. List of agricultural germplasm conservation at PRC and its network members.

No.	Crop Types	Sources	Total	Conservation methods*
1.	Graminaceus	Local and exotic	11.356	*Ex situ*, DNA
2.	Vegetable, spice and mushroom	Local and exotic	8.947	*Ex situ, in vitro*
3.	Fruit, industrial crop	Local and exotic	7.633	*Ex situ, in situ*, DNA
4.	Tuber crop	Local and exotic	3.570	*Ex situ, in vitro*
5.	Legume	Local and exotic	6.296	*Ex situ*
6.	Flower	Local and exotic	434	*Ex situ, in vitro*
7.	Soil improvement and forage crops	Local	102	*Ex situ*
	Total		38.338	

**Some germplasms have been duplicated at PRC and its network members.*
Sources: Plant Genetic Resources for Food and Agriculture report, annual project report, 2019.

Germplasm Characterization and Evaluation

The description and evaluation criteria for each crop are used by all members in the national PGR network. In total, 44.116 accessions have been evaluated for agronomic characteristics, and 27.169 accessions were evaluated for quality, salinity or drought tolerance, pest or disease resistance, genetic diversity or sub-species classification. Until 2006, 12.908 accessions were characterized, with 10.400 accessions have data for more than ten morphological traits, and 7000 accessions were evaluated for pests and diseases resistance. DNA analysis was carried out on 320 accessions of citrus and mango. Genetic diversity was evaluated for several accessions of local rice "Tam thom", bean

"daunhonhe" and *Cucurbita sp*. From 2007 to 2010, 11.230 accessions (77,9%) were characterized, and 10.380 accessions (72%) were characterized for more than ten morphological traits. Evaluation was performed on 12.044 accessions, including 420 rice accessions for quality (amylose content, gelatinization temperature, flavour and aroma), 6.000 rice accessions for sub-species classification, and 389 accessions (rice, taro and bean) for genetic diversity. From 2011 to 2015, a total of 18.336 accessions were characterized for morphological traits and 6321 accessions were evaluated, including 2765 accessions for quality, 1366 accessions for salinity or drought tolerance, 1190 accessions for pest or disease resistance, and 1000 accessions for genetic diversity. From 2016 until now, 1.642 accessions were characterized morphologically and 1.484 accessions were evaluated, including 380 accessions for quality, 492 accessions for salinity or drought tolerance, 552 accessions for pests or diseases resistance, and 60 accessions for genetic diversity (Table 3).

Table 3. Germplasm characterization and evaluation.

No.	Characteristic	No. of accessions*				Total
		Until 2006	2007-2010	2011-2015	2016 now	
A	Morphological characterization	12.908	11.230	18.336	1.642	44.116
B	Evaluation	7.320	12.044	6.321	1.484	27.169
	Quality		420	2.765	380	3.565
	Salinity, drought Tolerance			1.366	492	1.858
	Pests and diseases Resistance	7.000	5226	1.190	552	13.968
	Genetic diversity	320	398	1.000	60	1.778
	Sub-species classification: Rice		6.000			6.000

**Several accessions were characterized or evaluated twice or more.*
Sources: PGRFA, annual project report from 2006 to 2019.

PGR Information and Data Management

The software for data management has been developed to version GB2.5 for managing the data at the national genebank. Moreover, the database has been updated in the PRC website (http/www/prc.org.vn) for general users.

Passport, characterization and evaluation data has been exported to the GB2.5 software. Currently, 52.888 modules of passport data; 36.777 modules of morphological characteristic data, 15.336 modules of evaluation data have been updated in the GB2.5 software. The morphological characteristic data, evaluation data and digital pictures of germplasm and passport data by 2006 contained 12.514, 7.000, 3.500 and 8.561 modules, respectively. At the period of 2007-2010, the number of morphological characteristic data, evaluation data and digital pictures of germplasm and passport data were 10.380, 5.226, 0, 20.001 modules, respectively. At the period of 2011-2015, the number of morphological characteristic data, evaluation data and digital pictures of germplasm and passport data were 11.880, 1.930, 46.632 and 19.133 modules, respectively. And at the period of 2016-now the number of morphological characteristic data, evaluation data and digital pictures of germplasm and passport data were 2.003, 1.480, 18.250, 93 modules, respectively (Table 4).

Table 4. The plant genetic resource data collected at National Genebank.

No.	Data	Digital modules				Total
		Until 2006	2007-2010	2011-2015	2016 now	
1.	Morphological characteristic	12.514	10.380	11.880	2.003	36.777
2.	Evaluation	7.000	5.226	1.930	1.480	15.336
3.	Digital pictures of germplasm	3.500	0	46.632	18.250	93.732
4.	Passport	8.561	20.001	19.133	93	52.888

Sources: Plant Genetic Resources for Food and Agriculture, annual project report from 2006 to 2019.

In national and local research institutions, biotechnology and traditional methods have both been used in crop improvement. More than 1.000 accessions from *ex situ* collections have been utilized for selection and breeding purposes every year (Pham and Luu 2008; Le, La and Tran 2013). As a result, more than 160 new commercial varieties originated from the national PGR system have been developed and recognized nationally. A number of local promising lines or varieties have been recovered, propagated and reintroduced to agricultural production. Until 2006, 11 local promising lines/varieties were reintroduced to farmers, including 3 rice, 4 taro, 1 vegetable, 1 bean and 2 flower crops. From 2010 to 2013, 61 local promising lines/varieties were reintroduced to farmers, including 17 rice, 4 maize, 5 taro and 11 fruit crops (orange, mandarin, grapefruit and persimmon), 3 vegetables, 21 industrial crops (MOST 2013).

To protect local promising lines/varieties and their products, geographical indications (GI) protection has been developed in the legal, policy, and socio-economic system in Vietnam. As of September 2018, there were 53 plant products with registered geographical indications in Vietnam, including fruits (25), rice (7), tea (3), coffee (2) and others (16) (Pick, Marie-Vivien and Kim 2017).

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PRESENT AND FUTURE ASPECT OF *IN VITRO* CONSERVATION RESEARCH IN IAARD

Ika Roostika, Nurwita Dewi, Mastur, and Toto Hadiarto

INTRODUCTION

Indonesia is an archipelago of around 9 million km^2 which is located between two oceans and two continents with a total of around 17.500 islands. This geographical condition caused the country to become a megabodiversity country. Flora in Indonesia is estimated to around 25% of flowering plant species in the world with a number of species reaching 20,000 species, 40% of which are endemic or native to Indonesia. Indonesia is also listed as one of the Vavilov centers, which is the center of the distribution of genetic diversity agricultural crops such as bananas (*Musa* spp.), nutmeg (*Myristica fragrans*), cloves (*Syzygium aromaticum*), durian (*Durio* spp.) and rambutan (*Nephelium* spp.). At present there are around 240 species of plants declared rare, most of which are species of cultivated plants (Kusmana and Hikmat 2015).

Several factors such as climate changes and rapid human growth which leads to increase in industrial area and destruction of habitat may cause extinction of species. It is estimated more than 99% species that ever lived to be extinct (Steams et al. 2000).

Therefore, genetic diversity needs to be conserved urgently, including plant species. Plant genetic diversity is an essential source of genes for improved varieties and for their direct use as a source of food, feed and energy.

Preservation of plant genetic resources can be done *in situ* and *ex situ*. In *in situ* conservation, plant species are recovered in their present habitat to a state whereby the species are capable to grow without further human intervention (Heywood 2017). However, *in situ* conservation is rarely undertaken in tropical countries. On the other hand, e*x situ* conservation can be complemented by a genebank. Conservation of plants with orthodox seeds can be carried out in the long term through the application of low temperature and humidity. The conservation of recalcitrant seed plants is not appropriate to use this method due to their low survival under low temperature and humidity. Moreover, vegetative propagated plants require specific conservation approach for sustainable use.

Vegetative propagated plant germplasms of various tuber crops could be found in Indonesia to the species level, such as in Dioscorea, namely *D. alata, D. hispida*, *D. esculenta, D. acuelata* and *D. bulbifera*, as well as Amorphophallus, namely *A. campanulatus, A. mulleri* and *A. Oncophyllus* (Flach and Rumawas 1996). Genetic diversity is also found at the plant variety/accession level, such as in sweet potato (*Ipomoea batatas*) and cassava (*Manihot esculenta*), including minor tuber crops such as arrowroot (*Marantha arundina*), canna (*Canna edulis*), tuberose (*Coleus tuberosus*), taro (*Colocasia esculenta* and *Xanthosomas agittifolium*). Field conservation will require large areas, labor and costs, besides the risk of losing certain genotypes due to their narrow adaptability to biotic and abiotic stresses. In addition, difficult maintenance of the genetic purity of each genotype is faced in the field due to the natural characters of plants which produce tuber, rhizome and

stolon. The most suitable method for these vegetative propagated plants is the *in vitro* conservation technique (Danso and Ford-Llyod 2011).

In vitro collection management has been operated in several genebanks in the world. International Potato Center (CIP) in Peru is one of the largest *in vitro* genebank mainly to conserve sweet potato and canna (Tay 2000; Panta 2009). International Center for Tropical Agriculture (CIAT) collects more than 5000 cassava genotypes. International Transit Center (ITC) in Belgium conserves worldwide banana germplasm (Panis 2009), both with minimal growth and cryopreservation methods. Centre for Pacific Crops and Trees-Secretariat of the Pacific Community (CPCT-SPC) in Fiji has the highest number od *in vitro* collection of taro (Secretariat of the Pacific Community 2002). International Institute of Tropical Agriculture (IITA) collects about 1.000 accessions of *Dioscorea* spp. (IITA 2012) with a minimal growth method.

Indonesian Agricultural Agency for Research and Development (IAARD) has built genebank facilities in 2012 which is is under the management of Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development (ICABIOGRAD). This genebank has a mandate to conserve agricultural genetic resources. Recently, this genebank is proposed as the national genebank, while other local genebanks deal to certain crops as assigned by the IAARD. Given the importance of these genebanks in Indonesia, conservation approaches should be addresses for its management strategy. This review discus the implementation of *in vitro* conservation researches and future strategy for developing management of minimal growth conservation and cryobanking in IAARD genebank.

Current Status of *In Vitro* Conservation Research in IAARD

The agricultural plant *in vitro* conservation research in IAARD is performed for specific application. The research is aimed to provide in vitro conservation methods to properly maintain and manage plant species in the genebank routinely. The methods include storage, regeneration and mainly post storage. In vitro conservation methods may be reintroduced to plants with vegetative propagation. The application would be more effective when administered for plants with high genetic diversity within species or varieties. *In vitro* conservation methods are also important to be applied on endangered crops even if they have low genetic diversities such as endemic plants.

The *in vitro* conservation researches in IAARD started in 1980s, were especially conducted by Indonesian Center for Estate Crops Research and Development (ICECRD) mainly to medicinal plants. Since 1990s the programs have been further performed by ICABIOGRAD and majorly manages tuber crops. To date, a number of significant findings have been achieved in the tuber crops research programs using *in vitro* conservation by minimal growth method and cryopreservation for many purposes. The suitable method for specific tuber crop is able to prolong its preservation and to multiply many accessions to be stored in the genebank or exchanged to other genebanks/users. Examples of research topics dealing with *in vitro* conservation by minimal growth method in ICABIOGRAD is presented in Table 1. The *in vitro* conservation using minimal growth method were applied in sweet potato, dioscorea, pruatjan, tuberose, cassava, pineapple, banana, pumelo, taro, and sugarcane, (Figure 1). In addition to the minimal growth method, several commodities were cryopreserved, particularly on pineapple, sweet potato, cassava, pruatjan, banana, and sugarcane (Figure 2). Other complementary approaches in molecular and genetic levels could

be beneficial to support the conservation of these plant genetic resources.

Table 1. List of research of *in vitro* conservation by minimal growth method in ICABIOGRAD.

No.	Commodity	Result	Application	References	Remarks
1.	Sweet potato (*Ipomoea batatas*)	6-10 months preservation period, using 4% mannitol	Has been applied in IAARD genebank	Sunarlim *et al.* (1999)	Appropriate for many accessions of sweet potato
2.	Sweet potato (*Ipomoea batatas*)	18 months preservation period by using 3 mg/L paclobutrazol and 5 g/L sucrosa 5	-	Roostika and Sunarlim (2001)	Potential to be be applied to prolong preservation period
3.	Cassava (*Manihot utilissima*)	Using 4% mannitol	-	Sunarlim *et al.* (2002)	High level of senes-cence
4.	Cassava (*Manihot utilissima*)	Preservation period 12 months, using modified basal medium and 1-3 mg/L paclobutrazol	Has been applied for germplasm exchange to CIP	Unpublished	150 cassava accessions have been transferred
5.	Cassava (*Manihot utilissima*)	9 months preservation period by using 3.4 μM paclobutrazol	-	Diantina *et al.* (2015)	-
6.	Yam *(Dioscorea alata)*	Using paclobutrazol or ancymidol	-	Sunarlim *et al.* 2002	-
7.	Gadung (*Dioscorea hispida*)	Using WPM media	-	Adil *et al.* (2003)	Preservation on growth media
8.	Gembili *(Dioscorea esculenta)*	10 months preservation period, using paclobutrazol	-	Sunarlim and Roostika (2004)	-
9.	Gembili *(Dioscorea esculenta)*	Preservation on regeneration media	-	Hutami, *et al.* (2014)	-
10.	Taro (*Colocasia esculenta*)	Using 4% manitol	-	Dewi (2002); Dewi *et al.* (2012)	-
11.	Taro (*Colocasia esculenta*)	Preservation period 12-24 months by using 4% mannitol	Has been applied in IAARD genebank	Dewi (2012)	To conserve 200 taro accessions

Table 1. Continue.

No.	Commodity	Result	Application	References	Remarks
12.	Tuberose (*Coleus tuberosus*)	12 months preservation period, using media dilution without sucrose	-	Roostika *et al.* (2005)	-
13.	Belitung *(Xanthosoma sagitti-folium)*	Using 2 mg/L paclobutrazol	Has been applied in IAARD genebank	Sabda and Dewi (2016)	To conserve 5 accessions
14.	Pruatjan (*Pimpinella pruatjan*)	10 months preservation period, using 2.5% sucrose	-	Roostika *et al.* (2008)	Endemic & endangered medicinal plant
15.	Pruatjan (*Pimpinella pruatjan*)	Using media dillution and paclobutrazol	-	Roostika *et al.* (2009)	The method could not prolong preservation period, residual effect was remained after 6 months recovery
16.	Pamelo *(Citrus maxima)*	5 months preservation period, using 2% sorbitol	-	Dewi, *et al.* (2010)	Using three different varieties
17.	Pineapple (*Ananas comosus*) cv Smooth Cayenne	10 months preservation period, using 4% mannitol	-	Roostika *et al.* (2012)	Synseed with 3% Na-aliginate encapsula-tion
18.	Banana (*Musa paradisiaca*)	12 months preservation period, using 4% mannitol		Unpublished	-
19.	Kantung semar *(Nepenthes* spp.*)*	6 months preservation period, using 3% sorbitol	-	Damayanti *et al.* (2011)	*N. mirabilis, N. gracilis,*
20.	Sugarcane (*Saccharum officinarum*)	12 months preservation period, using 2-4 mg/L paclobutrazol	Will be applied in IAARD genebank	Roostika *et al.* (2018)	4 groups of sugarcane accessions (POJ, superior varieties & introduction from Queensland, USA & Mexico)

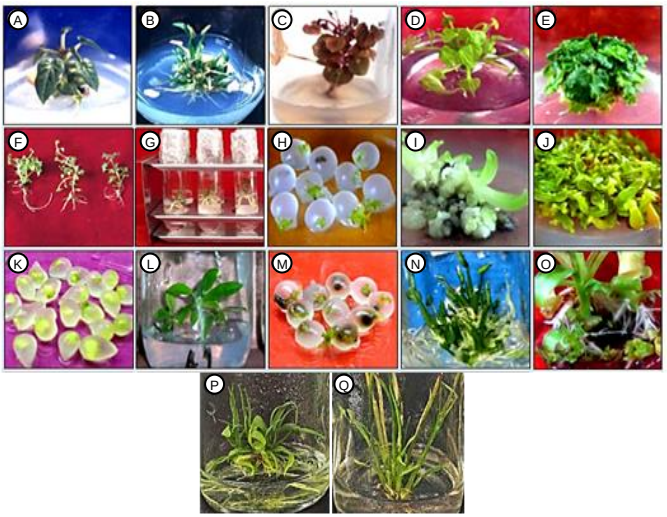

Figure 1. *In vitro* conservation researches of plant commodities using minimal growth method: sweet potato (A dan B), dioscorea (C dan D), pruatjan (E), tuberose (F), cassava (G), pineapple (H, K, and M), banana (I and O), pumelo (L), taro (N), and sugarcane (P and Q).

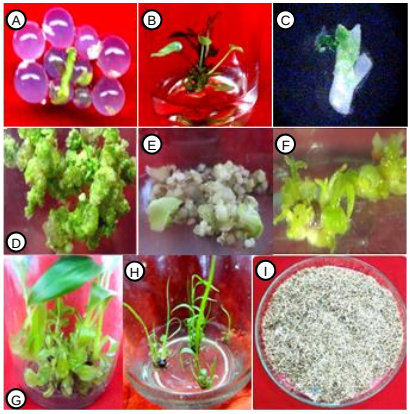

Figure 2. Several commodities in cryopreservation research: pineapple (A), sweet potato (B), cassava (C), pruatjan (D), banana (E and G), sugarcane (F, H and I).

Table 2. List of research of *in vitro* conservation by cryopreservation in ICABIOGRAD.

No.	Commodity	Result	Application	References	Remarks
1.	Sweet potato (*Ipomoea batatas*)	Shoot tips culture failed to regrow after cryopreservation by vitrifi-cation and encapsulation-vitrification technique	-	Roostika (2003)	Using two local varities and one introduced variety
2.	Cassava (*Manihot utilissima*)	Shoot tips culture could be cryopreserved by vitrification technique with low level of regrowth (1.7%)	-	Roostika *et al.* (2004)	-
3.	Cassava (*Manihot utilissima*)	33-67% regrowth after cryopreservation by dehydration-vitrificication	-	Diantina (200	Two accessions were studied
4.	Yam *(Dioscorea alata)*	Shoot tips culture failed to regrow after cryopreservation	-	Hutami *et al.* (2014)	-
5.	Pruatjan (*Pimpinella pruatjan*)	40% shoot tips could regrow after cryopreservation by vitrification technique	-	Roostika *et al.* 2007	-
6.	Pruatjan (*Pimpinella pruatjan*)	10% shoot tips could regrow after cryopreservation by encapsulation-vitrification technique	-	Roostika *et al.* 2008	-
7.	Banana (*Musa paradisiaca*)	Embryogenic calli and somatic embryos could be cryopreserved by vitrification technique with 80% regrowth	-	Roostika *et al.* (2010)	Model plant: cv Dwarf Parfit
8.	Banana (*Musa paradisiaca*)	High proliferating meristems could be cryopreserved by vitrification technique with 10% regrowth	-	Roostika *et al.* (2014)	Cultivated variety: Rajakinalun
9.	Sugarcane (*Saccharum officinarum*)	40% shoot tips of variety PS 864 could regrow after cryopreser-vation by vitrification technique	-	Roostika *et al.* (2015)	Using cultivated variety PS 864
10.	Sugarcane (*Saccharum officinarum*)	Cryotherapy could eliminate 33% SCSMV and 100% other Poty-virus from sugarcane tissues	-	Roostika *et al.* (2015)	The virus detection was conducted by RT-PCR
11.	Sugarcane (*Saccharum officinarum*)	Vitrification technique succeed to cryopreserve shoot tips of several accessions (PS 864, PSJK 922, Q 998, USA2, POJ 1027) with different level of regrowth (%)	Will be applied in IAARD genebank	Roostika *et al.* (2018)	The method is still optimized and evaluated

Constraints on the Implementation of Cryopreservation Researches

One of the responsibilities of ICABIOGRAD is to manage agricultural genetic resources including agricultural crops conservation in the genebank. Several components of the genebank include: (1) Genetic resources, which are plant germplasm which consits of local varieties, wildtype species, introduced varieties, and elite varieties obtained from breeding programs; (2) Human resources which include operators, skills and capabilities; (3) Facilities that consist of buildings, fields, laboratories, storages and information technology; (4) Management which includes laboratory standardization and networking with national or international institutions.

In vitro conservation activities in ICABIOGRAD started in 2012 (Dewi et al. 2014) with targeted commodities of major tuber crops (sweet potatoes, cassava and taro) using minimal growth techniques. However, at present the number of the *in vitro* conserved accessions is still limited due to: (1) Limited number of operator/technician, (2) Limited skills and experiences of the operators, (3) limited operating time because operators are also engaged to other tasks, (4) unorganized management system, (5) limited number of accession target to be conserved using *in vitro* culture (50-100 accessions/year). Consequently, it might require tens of years to conserve all accessions. Along with increasing accession due to the acquisition of new local germplasm, introduced germplasm, and the released new varieties from breeding, thus, the number of managed accessions will be greater which needs a management strategy.

To increase the role of IAARD genebank, especially long-term conservation of genetic materials with recalcitrant seeds and vegetative propagated crops, mastery of cryopreservation

methods and equipment are necessary. Expertise and standard cryopreservation procedures for various commodities and types of explants could be helpful for long term implementation. Plant cryopreservation studies have been initiated at ICABIOGRAD since 2000s, unfortunately these studies are not sustainable (Table 2). Priority setting and fund efficiency are reasons for discontinuing these studies for several years. However, paradigm of IAARD has shifted to Biodiversity and Ecology.

Future Strategy for *In Vitro* Conservation for Managing IAARD Genebank

To sustain the genebank routine activities needs human resources, utilities and management. Standard and best practices for the IAARD genebank management of in vitro collections should be increased in order give public service more widely in both local and international levels. All policies and technical standards are to gain quality improvement in the IAARD genebank's technical dan operational performance.

The performance of IAARD genebank can be developed by proposing several solutions andfaction plans as follows (1) Increasing human resource capacity, especially technicians who operate routine conservation activities in the genebank, (2) Creating a well-organized conservation team with defined distribution of roles, (3) Determination of clear and proportional target of the number of accessions that need to be conserved annually, (4) Giving professional services to users while considering the economic benefits and also science and technology development, (5) Promoting cooperation of plant conservation research by distributing assignments and responsibilities in conserving genetic resources according to the germplasm categories through biotechnological approaches with

other research organizations (species and wild species by Indonesian Institute of Sciences and Bogor Botanical Garden, landraces and local varieties by IAARD genebank, and new elite varieties by Indonesian Center for Testing development of seed quality of agricultural and horticultural crops), (6) Engagement of local communities in appreciating the importance of plant conservation, and (7) Enactment of safety back-up collection in national genebank of IAARD. These needs commitment from all plant conservation research institutes, genebanks, nature reserves and the government to successfully sustain and conserve plant genetic resources.

The genebank facilities of IAARD were built under the management of ICABIOGRAD with the mandate to conserve agricultural genetic resources. *In vitro* has been the main conservation approach of IAARD genebank. The relevant research aimed to provide *in vitro* conservation methods for the genebank management as a routine activity, including storage, regeneration and post storage. Several limiting factors have been identified which should be solved andsome feedbacks were suggested. A high commitment should be prioritized by all plant conservation research institutes, nature reserves and the government to effectively implement the proposed startegies and action plan offered.

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IMPROVEMENT OF RICE RESISTANT TO IMPORTANT RICE VIRUS DISEASES WITH THE BENEFIT OF INDONESIAN LOCAL VARIETIES

Ifa Manzila, Tri Puji Priyatno, Puji Lestari, and Mastur

INTRODUCTION

Indonesia is the world's third-largest rice producer and consumer after China and India. Being as the staple food, rice is consumed over 90% of Indonesian people, and the source of livelihood for about 17.8 million households or about 71.2 million people in the late 2015 (SI 2015). Annual per capita rice consumption declined from 107.7 kg/year in 2002 to 96.5 kg/year in 2016. On the other hand, national rice production increases every year since 1993-2016 with a growth rate of 2.1% per year. There have been concerns, however, the rice imports may surge in the future due to the increasing population. Indonesian Rice Research Istitute (IRRI) estimates that Indonesia will require 38% of more rice within 25 years, indicating that adjusting of increased rice higher than 6 t/ha from present national rice yield (4.6 t/ha) is urgent to fill the gap. To avoid huge imports, most rice policies in Indonesia have been aimed at achieving rice self-

sufficiency by increasing the production (IRRI 2010). The Indonesian government sets the targeted production to be 10 million ton of annual rice surplus for 2015 and subsidies fertilizer to farmers who own less than 0.5 ha for paddy field (SI 2015).

To increase national production, the rice breeding program in Indonesia has also been focused to improve varieties with high yielding potential, resistance to major pests and diseases, early maturity and eating quality. Rice disease was one of the major barriers of increasing and sustaining rice productivity. In recent years, the attacks of rice diseases caused by viruses cause severe incidence in Indonesia. There are five viruses reported to directly impact to rice production in Indonesia, and most of them are transmitted by either plant or leaf hoppers (Ling 1972; Hibino 1996). Insect vector for the rice grassy stunt tenuivirus (RGSV), rice ragged stunt phytoreovirus (RRSV), and rice stripe tenuivirus (RSV) are transmitted by plant hopper, while rice tungro and rice gall dwarf phytoreovirus (RGDV) are transmitted by leafhoppers. Rice tungro, RGSV, and RSSV usually occured in the endemic hot spot where continuous rice cultivation exist every year. In the favourable environmental conditions along with high populations of vector insects, virus attacks can cause a lot of losses of rice yield in Indonesia.

The most effective and economical way to control disease is resistant varieties that play a key role in world rice productivity (Bonman et al. 1992). However, these resistant varieties against rice viruses are not long durable as a result of diverse virus strains. So far, most rice breeding effort is intensive to develop resistant varieties especially to RGSV and RRSV. This effort should focuse to insect vector that is more destructive effect compared to transmitted-viruses. Moreover, the incidence of rice tungro, RGSV and RRSV are always found in endemic areas of brown planthopper (BPH) where the most serious attack was

occurred in 2010 and caused 38.881 ha rice plant to be infected and 2.309 ha hopperburn (Ditlin 2010). In fact, no modern rice varieties planted in a wide area in Indonesia was reported resistant to RRSV, RGSV, RSV, and RGDV, in exception of Inpari HDB and Inpari Blas varieties to be resistant to tungro (Manzila and Priyatno 2015). The resistant gene in Inpari HDB and Inpari Blas was obtained from *Oryza rufipogon* introduced to IR64 (Manzila and Priyatno 2015). Since the genetic sources of viral resistance genes are still limited, an extensive effort to evaluate existing rice germplasm is needed in order to find new resistance genes from local rice varieties.

Rice Virus Diseases Problems in Indonesia

Virus is one of the important pest and disease organisms in rice in Indonesia after rats, stem borer, and bacterial leaf blight (BLB). The widespread attack of rice virus disease reached 5% to 10% per year of overall rice damage caused by pest incidence (Figure 1). Out of five of viruses often attack rice plant in the fields, the most dominant diseases are tungro, RGSV and RRSV.

In Indonesia, the incidence of tungro attacks began rapidly in 1970s after the introduction of high yielding varieties susceptible to tungro. In 1969-1992, tungro disease was reported infect rice in Sumatra, Kalimantan, Sulawesi, Bali, Java, Nusa Tenggara, Maluku, Irian Jaya with a total planted area of 244.904 ha (Hasanuddin et al. 1987). In 1995, tungro outbreak occurred in Surakarta, resulting in hopperburn rice plant area of 12.340 ha with losses of Rp. 25 billion (Puslitbangtan 1995). During 2000-2015, the annualy widespread of tungro incidence is between 6.000-8.000 ha and about 1-2% of the damaged area was hopperburn. The reports of RGSV and RRSV incidences are always combined with the widespread attacks of brown

planthopper, as insect vector of both viruses. This condition is probably a consequence of the destructive status caused by BPH which is higher than virus infection to be transmitted. In contrast to tungro, plant damage caused by insect as vector is less than virus infection. Therefore, the development of rice resistant against the three types of viruses should use different control strategy addressed to either virus or vector or both of the Two.

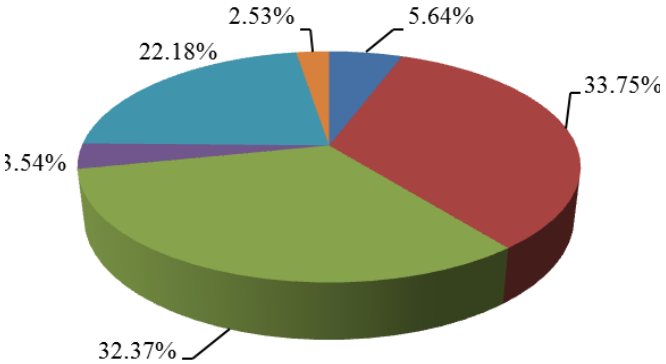

Figure 1. The incidence of rice pest and disease important in Indonesia.

The Potential of Viral Disease Resistance Source on Indonesia Landraces

The rice crop of Oryza sativa species was originated from Asian continent (LIPI 2014). In the past, the Asian Continent was a unified land and then separated into thousands of islands, including the Nusantara archipelago, which has a specific agroecosystem condition. According to Sastrapradja et al. (1989), Indonesia has 47 distinct agroecosystem that create different growing environment conditions for many rice germplasm across Indonesian island. Through farming activities, farmers have produced thousands of local varieties adaptive to specific agroecosystems. In addition, Indonesia is also the habitat of a

number of wild rice species, such as *O. meyeriana, O. granulate, O. longiglumis, O. offidinalis, O. schlechteri, O. ridleyi* and *O. rufipogon* (Vaughan 1994).

Currently, the Genebank of the Indonesian Agency for Agricultural Research and Development (IAARD) has collected 6.184 local rice varieties from different parts of Indonesia, and approximately 3.500 accessions have been characterized and used as a source of genes or parental lines to develop high yielding varieties (Las et al. 2004; Kurniawan 2015). Rice accessions collection also has been packaged into a spatial map based on geographical information system (GIS) which is accessible to public (Figure 2). The spatial maps of rice genetic resources are important database for the development of monitoring and early warning systems of rice genetic resources management in Indonesia. From this collection, IAARD has successfully released 183 new rice varieties with high productivity and good quality characters, and also tolerance to abiotic and biotic stresses (PPVTPP 2017). Hawkes et al. (2000) suggested that the elements of germplasm functioned as a genetic resource are (1) wild strains in the native habitat of cultivated plants, (2) local varieties, (3) old varieties which are not used anymore and the strains produced by breeders that have no commercial value, but still have useful genes for plant breeding, and (3) gene pool, ie germplasm accessions containing useful genes to establish modern varieties through plant breeding programme.

Some of Indonesian local rice varieties are also important for the improvement of rice resistance against viral diseases, such as tungro, RGSV, and RRSV. The identification of resistance genes has been done before (Ling 1972). There are 51 Indonesian local varieties reported resistant to viruses, especially tungro (Table 1). Utri Merah is one of rice germplasm that has been widely used for the improvement of elite varieties resistant against tungro.

The tungro resistance genes in Utri Merah have been used on crossbreed of IR61009-37-2-1-1///IRI 1561-228-3-3/Utri Merah//IR1561-228-3-3 to produce Tukad Petanu variety (Ladja and Widiarta 2012). The tungro resistance gene in Balimau White is also used to improve resistance traits of IR64. In addition to Utri Merah and Balimau Putih, Tetep is also one of the local variety resistant to virus that has not been studied previously. According to Choi (2004), the lines produced from hybridization with Utri Merah showed consistently resistance to tungro strains in different countries. According to Darajat et al. (2004), Utri Merah has a number of genes which are capable to inhibit the development of RTBV tungro virus particles and two recessive genes resistant to RTSV. The tungro resistance genes in Balimau Putih and Utri Rajapan are also identified as recessive gene (Choi 2004). Recessive genes in Utri Merah are located on chromosome 7 (Coi et al. 2009) and sized 200 kb in the region between 22.05 Mb and 22.25 Mb, which is associated with initiation translation factor (*EIF4G*) (Lee et al. 2010).

Figure 2. Spatial map of Indonesian rice germplasm collected in national gene bank (www.bbsdlp.litbang.pertanian.go.id/sdgp/).

Table 1. Response of Indonesian rice landraces against rice viruses.

No.	Rice germplasm	Resistance status to			References
		Tungro	RGSV	RRSV	
1.	Mentik Wangi	-	R	-	Suprihanto et al. 2015
2.	Rojolele	-	MR	-	Suprihanto et al. 2015
3.	Tetep	R	R	R	Hasanudin 1987; Suprihanto et al. 2015
4.	Kamba Kolori	MR	-	-	Hamzah et al. 2015
5.	Kamba Wuasa	MR	-	-	Hamzah et al. 2015
6.	Kamba Bulili	R	-	-	Hamzah et al. 2015
7.	Kamba Tomado	R	-	-	Hamzah et al. 2015
8.	Balimau Putih	MR	-	-	Hasanuddin 1987
9.	Betrik	MR	-	-	Hasanuddin 1987
9.	Tjempo Kijik	MR	-	-	Hasanuddin 1987
10.	Palasitahari	MR	-	-	Hasanuddin 1987
11.	Sigadis	MR	-	-	Hasanuddin 1987
12.	Ase kute	MR	-	-	Suprihanto et al. 2010
13.	Bawi	MR	-	-	Suprihanto et al. 2010
14.	Galur	MR	-	-	Suprihanto et al. 2010
15.	Hitam	MR	-	-	Suprihanto et al. 2010
16.	Hawara Batu	MR	-	-	Suprihanto et al. 2010
17.	Incak Labu	MR	-	-	Suprihanto et al. 2010
18.	Jalawara	MR	-	-	Suprihanto et al. 2010
19.	Jambu	MR	-	-	Suprihanto et al. 2010
20.	Jambuan	MR	-	-	Suprihanto et al. 2010
21.	Jambi Galah	MR	-	-	Suprihanto et al. 2010
22.	Ketan Baniar	MR	-	-	Suprihanto et al. 2010
23.	Kangkungan	MR	-	-	Suprihanto et al. 2010
24.	Ketan Hideung	MR	-	-	Suprihanto et al. 2010
25.	Lapang	MR	-	-	Suprihanto et al. 2010
26.	Mavas	MR	-	-	Suprihanto et al. 2010
27.	Mentri	MR	-	-	Suprihanto et al. 2010
28.	Padi Merah	MR	-	-	Suprihanto et al. 2010
29.	Si Pola	MR	-	-	Suprihanto et al. 2010
30.	Si Geupay	MR	-	-	Suprihanto et al. 2010
31.	Torondol Kuning	MR	-	-	Suprihanto et al. 2010
32.	Tangkawa	MR	-	-	Suprihanto et al. 2010
33.	Deli	R	-	-	Suprihanto et al. 2010
34.	Jeluang	MR	-	-	Suprihanto et al. 2010
35.	Cipeundeuy A	MR	-	-	Suprihanto et al. 2010
36.	Cinta Kasih	MR	-	-	Suprihanto et al. 2010

Table 1. Continue.

No.	Rice germplasm	Resistance status to			References
		Tungro	RGSV	RRSV	
37.	Cere Hideung	MR	-	-	Suprihanto et al. 2010
38.	Intan	R	-	-	Ou 1965
39.	Sigadis	R	-	-	Ou 1965
40.	Dara	R	-	-	Rivera et al. 1968
41.	Peta	R	-	-	Ou 1965
42.	Bengawan	R	-	-	Ou 1965
43.	Tjeremas	R	-	-	Ou 1965
44.	Tjina	R	-	-	Ou 1965
45.	Tjina 417	R	-	-	Ou 1965
46.	Salak 2885	R	-	-	Ling 1969
47.	Fadjar	R	-	-	Ling 1969
48.	Tjahaja	R	-	-	Ling 1969
49.	Mas	R	-	-	Ling 1969
50.	Utri Merah	R	R	R	Suprihanto et al. 2015
51.	Utri Rajapan	R	-	-	

R= resistance; MR=moderate resistance; S=susceptible

Strategies of Improving Rice Varieties Resistant to Virus Disease (On Going Project)

The effectiveness of improved rice resistance against viruses needs to be done not only against the virus itself but also its vector insects. The plants that are only resistant to the vector solely will rapidly be broken and damaged by the high selection pressure of insect vector development. While rice viruses have large variety of strains and enable to change rapidly by pressure selection of resistant varieties grown in the field. Therefore, the development of rice resistant to viruses should be multigenic, suggesting conducting gene pyramiding. As for improving the resistance to tungro, plants must be resistant to both types of virus causes, RTBV and RTSV. Although single infection by RTBV or double infection by RTBV-RTSV is more potential to decrease the rice productivity than single infection by RTSV,

however, RTSV is a key factor in tungro epidemic in rice fields. RTSV is a helper virus for RTBV to be transmitted to other plants by vector insects.

Improvement of rice resistant virus also should be synergized with their endurance properties against other major diseases in rice plants, such as BLB and blast diseases. Currently more than 40 blast resistant genes (Pi) (Imbe et al. 2000; Inukai et al. 1994), 20 resistant genes BLB (Xa) (Chen et al. 2002; Khush et al. 1999) and rice tungro resistance genes (Azzam et al. 2002) have been identified. Although these resistance genes have not been used significantly in commercial varieties, the diversity of resistance genes has been well utilized through the development of differential varieties for pathogen characterization, namely near isogenic lines (NIL). NILs that carry individual resistance genes provide an efficient way to detect the alteration of pathogen virulence genes associated with their specific resistance genes. This approach is particularly useful in determining the correct resistance genes for introduction into plants.

Future Perspective

Improvement the host plant resistance is being considered as the best approach to handle rice virus diseases. Rice cultivars containing monogenic resistance gen to a specific pathogen strain often become susceptible over time due to the emergence of new virulent strain. In an attempt to increase resistance durability in fields, crop improvement requires a continuous pipeline of new resistance genes (Nicaesi 2014). During the evolution and artificial selection processes, a significant portion of beneficial alleles have been left behind in the landraces and wild species which can be used for the development of better rice varieties (McCouch et al. 2007).

Although using virus resistance genes from Indonesian local varieties successfully improve resistance in elite varieties, defence responses, and the signal transduction leading to activation of defence responses in rice, the whole story is still far from clear. Studies of the molecular biology of virus resistance will be helpful in understanding virus resistance gen mechanism in controlling rice disease caused by virus. Availability of rice genomic database for the public undoubtedly can accelerate research on rice disease resistance on molecular biology side. Identification of candidate gene through rice functional genomics has great potential for developing durably resistant varieties. Molecular breeding can help in the introduction of durably blast-resistant rice cultivars thereby sustaining rice yields.

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CHAPTER 3.
BIG DATA ON GENOMIC FOR CROP IMPROVEMENT

Agricultural biotechnology trends in plants shifted in the past decade from conventional breeding to new breeding techniques at present. The key of the new techniques were the underlying molecular mechanisms, a product-based approach, precision breeding and potential application of agricultural techniques of synthetic biology, genome editing and gene drives. In addition to these new techniques, genome sequencing of plant genetic resources (PGR) enable faster breeding and complements phenotype-based selective breeding. A large number of this information is digitalized and stored in data repositories which are freely accessible to the public and will accelerate the dematerialization of PGR.

In Indonesia, the PGR diversity richness should be exploited for breeding purposes to develop superior cultivars of important crops. Next-generation sequencing (NGS)-based DNA variation discovery is facilitated by the availability of genome reference maps of important crop species, to map genetic variations contained within a genetic resource collection of a crop species using a cheaper whole-genome re-sequencing technology. In Indonesia, the genome of a number of important crops have been resequenced to develop molecular markers to expedite crop improvement. As the data keeps building up and create big data, phenomics supported by metabolomics and genomics are

increasingly used and put in good uses in the effort to address the causes of desired traits and their subsequent applications in breeding programs.

Advances in sciences, both in the field of molecular biology and information technology, have enabled new understandings of genetic resources and biological processes which lead to an ongoing fundamental paradigm shift. The phenomenon of big data resulting from genomic sequencing has emerged as a consequence of NGS technologies that are capable to generate large data sets in biotechnological research. Technical progress in such big data generation and management has opened previously unexplored possibilities for research, the development of new products, and leads to even more data being generated at an unprecedented speed. While there will always remain a reliance on genetic materials, one may observe a trend that research and development activities using genetic material are increasingly supplemented or substituted by computerized research activities based on digital sequence information (DSI). The rise of big data raises specific legal challenges in terms of data ownership and intellectual property, data stewardship and governance as well as technology transfer and licensing.

AGRICULTURAL BIOTECHNOLOGY TRENDS AND THE DIGITAL TRANSFORMATION OF PLANT GENETIC RESOURCES

Puji Lestari, Muhamad Sabran, and Mastur

INTRODUCTION

Plant genetic resources (PGRs) are raw materials usually used by plant breeders to create new crop. Economic value of any particular PGRs must not remain a matter of conjecture, but needs to be calculated. Moreover, the primary value of plant genetic resources for food and agriculture (PGRFA) lies in the fact that these could be used to improve productivity. However, challenges of agriculture like biotic (such as new pests and diseases) or abiotic (such as climate change) stresses bring an idea for better adapted crop varieties. For these constrains, PGRs are an essential component of all such improvements. More than three-quarters of the increased crop productivity of the past three decades is majorly the result of breeding scheme, and it continuously depends on PGRs. This gives PGRs an incalculable insurance value as the primary source for breeders, researchers and other users who have to adapt the most important crops under changing production conditions. Utilization of PGRs through plant breeding may include advanced technologies (European Commission 2017; Sabran 2016).

Biotechnological trends in agriculture from conventional to new breeding techniques have been progressively achieved. These new techniques generate and analyze large genotypic and phenotypic data that need acceleration, crop improvement and especially for synthesizing genetic materials. In particular, high-throughput platforms which are important for synthesizing genetic materials are clearly revolutionizing biology. Thedevelopment of techniques in genomics, transcriptomics and other omics has been followed in parallel with other methods in molecular state of cells and organisms, for prediction phenotypic traits in an automated manner (Furbank and Tester 2011), and moreover, for re-engineering the content and function of living systems (Noman et al. 2016). Thus, the emerging opportunities take advantage of the PGRs to generate data and synthesis across disciplines.

Rapid generation of large quantity of big data allows describing biological systems, from simple data to big data, and the analysis and interpretation of these data to change the transformed biology into an information-rich science (Halewood et al. 2018). Such increasing bioinformatics and computational capacities for analysis process and further use of the big data sets in modern plant science and breeding, which may affect less use of PGR material, have been described as 'dematerialization' of PGR. The term and concept of 'dematerialization' of PGR was created by the first Secretary of the International Treaty on PGR for Food and Agriculture (ITPGRFA), Dr Shakeel Bhatti, in the report to Fifth Session of the ITPGRFA Governing Body in 2013 (http://www.fao.org/3/a-be587e.pdf). It was later elaborated by the FAO Commission on Genetic Resources for Food and Agriculture (http://www.fao.org/3/my588en/my588en.pdf) and many others. Some authors have suggested that this next trend for the information of PGRs to be extracted, processed and exchanged will probably be detached from the physical material (Traore 2018). Notably, the advances of new breeding techniques,

synthetic biology, and plant genomics have shifted the balance of value of material and knowledge. This review describes agricultural biotechnological trends and new breeding techniques and synthetic biology, accessible information systems on genomics and genetic sequences for the public, detached to physical materials, and the dematerialization and its implication to the international communities.

Agricultural Biotechnological Trends

Conventional breeding techniques in plants

There is a wide range of conventional breeding techniques (CBTs) in plants (EFSA Panel on Genetically Modified Organisms 2012). These CBTs included simple selection, sexual crosses, intraspecies and interspecies crossing, bridge crosses, hybridization for vigour, somatic hybridization, mutation breeding, and doubled haploids and polyploidy induction. Genetic materials in the form of seeds, seedlings, organ tissues of plant are used in the CBTs with its specificity, as reflected by how the method of crop improvement is conducted.

Simple selection can be applied in preferred plants based on the desirable traits as commonly done from the past. The resulting product like variety or population, usually maintains some heterogeneity relative to the global population (Centre for Biosafety and Sustainability 2016), and almost all are widely used (Borrelli et al. 2014; Sakuma, Salomon, and Komatsuda 2011). This simple selection is accelerated by sexual crossing, which frequently is used in plant breeding (Van De Wiel et al. 2016; Xia 2009). Both of these techniques bring together desired traits found in different plant varieties through cross-pollination. On the other hand, intraspecies and interspecies crossing involves plant

varieties which have already been selected for distinct desired traits, or with wild relatives expressing desired traits, then selection of progeny (Khan 2015). Marker-assisted selection (MAS), which is based on the molecular markers closely associated to the specific trait (Kadirvel et al. 2015; Zhang et al. 2014) have been used, and in some cases, automated phenotyping platforms have also been used (Jin and Nassirou 2015). Bridge crosses techniques are used when a direct cross between two species is impossible, an intermediate crossing with a third species which may bridge the crossing barrier is needed (Van De Wiel et al. 2016). Based on hybridization, an example is a technique of hybridization for vigour which involves a sexual crossing on the basis of the exploitation of heterosis that is the phenotypic superiority of a cross over the parents. If high inbred varieties are crossed with other inbred varieties, very vigorous and large sized progenies probably result from the effect of heterosis (Lippman and Zamir 2007). For somatic hybridization, it relies on tissue culture of plants to combine genes from different plant varieties that are sexually incompatible. Somatic cells from two varieties are stripped of their protective cell walls and the protoplasts are pooled. Other technique called as mutation breeding, is spontaneous DNA mutations naturally occur and result in the expression of a novel and desirable trait. Plant breeders attempt to accelerate these events by mutations (Suprasanna, Mirajkar and Bhagwat 2015) and selection for rare desirable traits. Mutation breeding involves exposing plants or seeds to physical or chemical mutagenic agents, which induce random changes in DNA sequences throughout the genome (Singh and Singh 2015).

The conventional breeding techniques demonstrated their high dependence on physical PGRs in all process. A high number of accessions or varieties have been the main materials used in these techniques. Eventhough these conventional breeding

techniques are not relatively difficult to conduct, specific approach sometimes are needed for specific plants in order to gain an optimal yield.

Established techniques of genetic modification in biotechnology

The development of established techniques of genetic modification (ETGM) in biotechnology till 1980s enabled the insertion of genetic information into an organism. The gene pool available for improving new varieties can be expanded beyond sexually compatible species (Committee on Identifying and Assessing Unintended Effects of Genetically Engineered Foods on Human Health 2004). The most common ETGM used in plants employs recombinant nucleic acids (Borém et al. 2014). A DNA sequence corresponding to a desired trait is combined with other genetic elements, which enable its expression in the recipient.

Diverse techniques exists for the introduction of heritable material into cells with some specificities according to use in plants. Methods are available for genetic transformation of plant cells, which either need to remove the cell wall (Pacher and Puchta 2016; Royal Society 2016) or allow to transfer nucleic acids into cells. Plants can be regenerated from single cells or protoplasts. Efficiency may depend on the tissue from which the cells were obtained and also on the species or even the cultivar used. If such single plant cells are transformed with exogenous DNA, then regenerated into complete fertile plants, transgenic plants are obtained, and these transgenic plants display new characters (European Commission 2017).

This description showed that even though ETGM manipulates DNA sequence in the process, genetic transformation steps require plants cells as physical materials. In this technique, nucleotide sequences in targetted genes are also importantly used

to be inserted into the host genome. Notable, these approaches which involve the plant materials and its associated sequence information are more advanced than the hybridization and mutation, indicating the decreased attachment of the raw materials of plants.

New breeding techniques of agricultural biotechnology

Scientific progress has enabled to develop a new generation of techniques, often referred to as 'New Breeding Techniques' (NBT). The NBT describes a diverse technique, some of which differ from transgenic methods (EASAC, 2015). Some of them are a refinement of CBT and insert genetic material derived from a sexually compatible species, or combination with ETGM. Some of the NBT result in new plants that contain only point mutations and are indistinguishable from varieties produced through CBT. Whereas several NBT are restricted to plants, particularly the recent techniques of genome editing (Lüthi et al. 2012; OECD 2016). In this review, the NBT methods clearly described how these techniques start to minimize the use of genetic materials, especially RNA-dependent DNA methylation (RdDM) and genome editing (Kamburova et al. 2017).

RdDM allows breeders to result plants varieties with desired traits without foreign DNA sequences and no changes in the nucleotide sequence of the genome. The technique relies on a natural process of enzymatic addition of a small chemical group (e.g. methyl) to nucleotides. Foreign genetic material is introduced to these plants to induce gene silencing.

Genome editing technique is a precise alteration of a DNA sequence in a cell, or to achieve random changes at precise locations. The cell's DNA recombination/repair system activated with the use of a site-directed nuclease (SDN), exogenous nucleic acid molecule (oligonucleotide), or the combination of both aided

this technique achievement (Royal Netherlands Academy of Arts and Sciences 2016). Oligonucleotide directed mutagenesis (ODM) technique can contribute to introduce natural allelic variations which could be also obtained by crossing but needs long process. However, genome modification has become more widely applicable via the development of SDNs that cut DNA at selected target sites producing what are called double-stranded breaks (DSBs). The techniques following the development of RNA-directed SDNs based on the bacterial CRISPR system and CRISPR-associated (Cas) nucleases (Jinek et al. 2012; Schiml and Puchta 2016).

Genome editing mainly manipulates genome which contains a huge nucleotide variation in plants species. These techniques have advanced rapidly the development of new plant varieties with the advantages of the genes in the genome controlling the desired traits. It indicates that sequence information which can be obtained from public domain or other sources are very crucial. This information does not need to meet the persons who produce the data or its genetic materials owning the information.

Application of NBT in synthetic biology

Synthetic Biology combines modern biotechnological techniques, computer science and other areas to engineer new organisms/plants which do not occur in nature and which can function (Scientific Committee (SCHER/SCENIHR/SCCS) 2015). In comparison to modern biotechnology like ETGM, the novelty of synthetic biology lies in the systematic use of engineering approaches to design artificial organisms (Raimbault, Cointet, and Joly 2016).

For this NBT, genetic engineering and information of complete genomes sequences are very important so that large functional DNA molecules can now be synthesized efficiently and without

using natural template (Lusser et al. 2011). Some examples are to add a metabolic pathway is in Golden Rice (Paine et al. 2005), and adaptation of pathways in maize (Naqvi et al. 2011). To result these products, combinatorial transformation and introduced transgenic constructs are performed simultaneously through a biolistic approach followed by selecting plants that express targeted transgenes. Moreover, to make real full potential of plant synthetic biology, techniques to provide control over the genetic code enabling desired modifications in DNA sequences level in living plant cells is required. This such control is possible, hence the advances synthetic biology is beneficial from the advantages of genome editing (Baltes and Voytas 2015).

Synthetic biology uses large sets of genes encoding complete biochemical pathways from one organism that are introduced in a new production organism. This technique is able to synthesize new organisms or plants based on the genetic sequences which do not need the belonging genetic materials. Detachable information from the provider becomes higher compared to other NBTs. Thus, synthetic biology denotes important shift towards using less physical materials or called as dematerialized PGRs.

Information System on Genomic and DNA Sequences

At present, advance techniques have facilitated to sequence genomes of plants species in rapid way and faster pace, then process, digitalize and store all the information in online databases (DBs). This progressive DBs because high-throughput and low cost genome sequencing technologies have begun to produce new insights of agriculture. New data are able to interrogate the molecular biology of desired traits from DNA to protein. Genotyping,exome sequencing, transcriptome analysis and whole-genome sequencing, enable the interpretation of new genetic data to be more meaningful. Notable, the rapidly moving

tools in bioinformatics significantly contribute to agriculture and transform them from basic science to practice as a result of more big genomic data generated (Chen and Coppola 2018). All these useful information could be specific and details but others show more generic (Table 1). Therefore, some of the DB are addressed on certain species but others deal with more common plant species in integrated system.

Table 1. List of genomic and genetic DBs.

DATABASE	URL
Repositories	
NCBI (GenBank)	http://www.ncbi.nlm.nih.gov/
EMBL-EBI	http://www.ebi.ac.uk/
DDBJ	http://www.ddbj.nig.ac.jp/
INSDC	http://www.insdc.org/
RefSeq	http://www.ncbi.nlm.nih.gov/RefSeq/
VEGA	http://vega.sanger.ac.uk/
CCDS	http://www.ncbi.nlm.nih.gov/CCDS/
Genome browsers	
Ensembl	http://www.ensembl.org/
UCSC Genome Browser	http://www.genome.ucsc.edu/
NCBI MapViewer	http://www.ncbi.nlm.nih.gov/mapview/
Projects (in genome browsers section)	
ENCODE (project)	http://www.genome.gov/10005107
1000 Genomes	http://www.1000genomes.org/
Species and taxa specific databases	
Rat Genome Database	http://rgd.mcw.edu/
Mouse Genome Informatics	http://www.informatics.jax.org/
ZFIN, Zebrafish Model Organism Database	http://zfin.org
FlyBase, Drosophila and other species	http://flybase.org/
VectorBase, invertebrate vectors of human disease	http://www.vectorbase.org/
WormBase, C. elegans and related nematodes	http://www.wormbase.org
Gramene, crop grasses and other plants	http://www.gramene.org
TAIR, Arabidopsis	http://www.arabidopsis.org/
SGD, Saccharomyces Genome Database	http://www.yeastgenome.org/
IMG, Integrated Microbial Genomes	http://img.jgi.doe.gov/

The DBs of genomic and DNA sequences accessible freely to public, lead to foster scientific communication among scientists in a multi-disciplinary research group composed of computer scientists, molecular biologists, biochemists, structural biologists and other fields. This information gives important contributions to basic science and serves as a wellspring of new methods for applied research activities. One of a comprehensive database like The National Center for Biotechnology Information (NCBI) could be a good example of DB providing access to genomic information. A lot of whole genome of plant species are available. In this DB, problems including gene organization, sequence analysis, and structure prediction are explored. Being as the genBank DNA sequence database, Entrez NCBI's search and retrieval system provide users with integrated access to sequence, mapping, taxonomy, and structural data. A more detailed analyzed sequence in graphical views of sequences and chromosome maps can also be accessed (www.ncbi.nlm.nih.gov).

A first genomic database established by Indonesian Agency for Agricultural Research and Development (IAARD) in Indonesia is called Pusat Genom Pertanian Indonesia (PGPI, http://genom.litbang.pertanian.go.id). As an initial start, there are 11 plant species with their genome sequences and/or genome wide genotypic data that have been the main content on this DB. Since big data of genome sequences could be compressed in an interface friendly web, user can easily access GenomeBrowser and retrieve some interested information for their own purposes. All of DBs and software tools are available to provide an alternative way to access for text or other information searching.

These easy access of genomic information and DNA sequences of plants make it possible to use them for many basic and applied researches in agriculture. Recently, many groups of public and private partnership connect and share their databases. This

shared information of genomic and DNA sequences lead to 'dematerialization of PGRs because it is made accessible, and separated from genetic materials of plants which they stem from. Automatically they are more isolated away from the provider having the data and information.

Dematerialization of PGRs and Its Implication

The effectiveness and efficient utilization of PGRs is a result of the increasing trend for the available information of genetic materials for plant breeders after analyzing and processing. Characterization and evaluation of genotypic and phenotypic characters of variety/accessions of plants are more progressive with the support of bioinformatics and computation as well as freely accessible DBs. The available PGRs collection in genebanks worldwide can be genetically characterized to enhance genomic information for further research and development. The NBTs may also assist plant breeders to make breeding results more precise and create a shorter cycle. Genomics and advanced DNA sequencing technologies facilitate high-density genotyping in many crops. The genomic information related to detailed genes can support modern breeding and synthetic biology. Important research on many crops is underway, addressing on important desirable traits in agriculture.

The advances of plant genomics have shifted the balance of value of plant material and knowledge. Once the intangible knowledge about PGRs becomes more important for plant innovation than the PGRs material itself, the intellectual property becomes more relevant for regulating use of the PGRs than the access and benefit sharing (ABS). However, the accelerating speed of technological achievement, based on the exchanged information about the accessions of genetic material, is gradually

detached from the physical exchange of the PGRs. This could reduce the use of the physical material its self and lead to dematerialized uses of PGR data (Bhatti 2013). Furthermore, the high speed of technological innovation derived from synthetic biology and genomic technologies might imply the International Treaty the importance of mining plant genomic information for gene editing or other purposes in agriculture. However, relevant policies should widely recognize the constantly evolving technologies and be set by the relevant international legal instruments (CBD 2018; ITPGRFA 2018).

Dematerialization of PGRs impacts many aspects in scientific and international agreements. All DBs of these important genetic sequences and information should be managed and controlled in proper manner for users. The dematerialization of PGRs also makes IPRs more important for all PGR work and can also be employed to facilitate patenting of new inventions.

This issue must be reflected in relevant legal frameworks to advance with legal certainty. The challenges for the Treaty (International Treaty on Plant Genetic Resources for Food and Agriculture/ITPGRFA) from the dematerialization of PGRs include that plant breeding is not focused longer on genetic material as raw materials. Moreover, addressing the non-material values of PGRs should be enhanced by the Treaty that can continue to add value for breeders and scientists by facilating innovative uses of PGRs and associated data. The Treaty has already addressed the dematerialization of the use of PGRs via the Secretary's report, vision paper and ongoing implementation processes of its Global Information System. How to define new data standards is needed to make it easier to exchange, access and interpret them. A coherent implementation of ABS and IPRs is needed, which takes into account the specificity of PGRFA needs of plant breeding and other research purposes. The

International Treaty that facilitates the sustainable use of PGRs on breeding is rapidly changing. The entry into force of the Nagoya Protocol and an increasing dematerialization of the use of PGRs bring significant changes in future plant breeding. The Treaty responds to these changes via the enhancement of the Multilateral System and the launch of the Global Information System. As a consequence, plant breeding for major crops becomes more knowledge-intensive. An implication for breeders is that in the future they will need to address legal encumbrances to their breeding activity deriving from both ABS frameworks applicable to their genetic material and from the IPRs. Integrated solutions for dealing with the various facets of rights and obligations in PGRFA need to be done in an efficient and comprehensive manner (ITPGRFA 2018; Traore 2018).

Future Perspective

Biotechnological trend in agriculture moves from conventional to new breeding techniques including genome editing, genetic engineering and synthesis of biological systems, through the development of new technologies that generate, analyse and exploit big data. Users and scientist could leverage these capacities to efficiently utilise PGRs, however NBT tends toward the direction where the physical material use decreases. Opportunities for generating a big data and publicly accessed genomic data and information become wider and open to the deployment of the new invention without attaching the genetic materials.

New opportunities and the challenges in the dematerialization of PGRs use, will play an important role to increase and strengthen the partnerships between plant breeders, seed gene banks, curators, scientists, farmers and donors. Additionally, this

can strengthen the global technical and policy framework for the big data and sequence information of important PGRFA. Data sharing through the Global Information System of the Treaty (the GLIS) and introduced IPRs of genomics data and related information must be highly addressed (ITRPGRFA 2019). A clear and transparent rule may act as a powerful incentive for the sharing of added-value information in this domain for all involved stakeholders.

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DIGITAL SEQUENCE INFORMATION – LEGAL QUESTIONS FOR PATENT, COPYRIGHT AND TRADE SECRET PROTECTION AND SHARING OF GENOMIC SEQUENCING DATA

Claudia Seitz

INTRODUCTION

Innovation in plant breeding is dependent on specific knowledge, the development and application of new technologies, access to GR, and capital to utilize those factors. Progress in molecular biology has lead to the science of genomics and resulted in new techniques such as gene editing, synthetic biology, bio-nanotechnology and other evolving technologies which can be considered increasingly as transformative tools for biological systems and may be used to enhance production in the pharmaceutical, agricultural, food and biotechnology sectors for new diagnosis methods, personalized medicine, new breeding techniques to improve plant varieties and animal breeds. In addition, in the last several decades digitalization has become a major trend in the sector of GR. New characterization techniques for GR and new capabilities for collections of bioinformatics data

resulting from innovation in bioinformatics, the use of artificial intelligence and the use of digital trust technologies, have become possible at reduced cost and have already created rapid scientific and technological progress.

The combination of both innovations in molecular biology and bioinformatics has lead to new possibilities but also to new legal questions. The sequencing of genetic material and the DSI of GR have raised a variety of questions (Reichman et al. 2016). First of all, the terminology and different types of DSI on GR need to be defined. Besides questions regarding potential implications of the use of DSI on GR for conservation of biological diversity and their sustainable use and for the fair and equitable sharing of the benefits arising out of the utilization of GR there are in addition several other practical legal questions. Especially the question of protection and sharing of DSI and the resulting tension is not yet answered. The present paper shall therefore address and highlight a few remarks on the definition of DSI, its protection under the current IP system and the scope of application of the current ABS systems for sharing DSI.

Terminology and Scope of Digital Sequence Information

The transition from biological material to sequence data has led to intensive discussions on international level concerning the question how to address sequence data and whether the regulations concerning access to GR, their sustainable use and the fair and equitable sharing of benefits arising from the use shall apply to sequence data (CBD 2016). These discussions are simultaneously taking place in multiple fora, such as the Convention on Biological Diversity (CBD 1992) and its Nagoya Protocol of 2010 (Secretariat of the Convention on Biological Diversity 2011), in the FAO International Treaty on Plant Genetic

Resources for Food and Agriculture (ITPGRFA) (FAO 2009), in the World Health Organization (WHO) on the Pandemic Influenza Preparedness Framework (World Health Organization 2016), which not only uses sequence data but also other information connected with genes and related information, as well as in the UNESCO International Bioethics Committee (International Bioethics Committee 2016).

So far there is no precise terminology of DSI. The Conference of the Parties to the CBD in 2016 in Cancun adopted a decision that uses the term DSI already but left the clarification of the terminology as a subject of further discussion in a study and an Ad Hoc Technical Expert Group (CBD 2016). The term DSI is currently undefined, still not used in a uniform way and interpreted differently by different stakeholders. In a narrow definition, it covers only sequence data, however, according to a broader definition it seems to include other related information such as annotations and interpretation data. In its broadest interpretation DSI could comprise all immaterial, electronically saved data on GR, whereas GR is defined according the Art. 2 of the CBD as genetic material of actual or potential value and genetic material is defined as any material of plant, animal, microbial or other origin containing functional units of heredity. The term genetic refers to the physical carrier of hereditary information, i.e. the deoxyribonucleic acid (DNA) and the ribonucleic acid (RNA).

It is not yet clear whether the term digital sequence information should only cover DNA or RNA sequences or whether it should be interpreted in a broader way to cover even protein sequences. The term of sequencing could be defined as the process of determining and documenting the order of nucleotides or nucleobases on a given fragment of DNA or RNA, which are the building blocks of the chromosomes of organisms

(Sollberger 2018). The lack of clarity in the definition of DSI causes problems in the current discussion since the subject matter is not clear which also causes a lack of common understanding and legal uncertainty. Thus, the terminology as well as the scope of information which shall be covered by this definition is currently subject to a debate on an international level.

At the fourteenth Conference of the Parties to the CBD, held in November 2018 in Egypt, an Ad Hoc Technical Expert Group (AHTEG) was extended to continue work on DSI of GR resources under the CBD and the Nagoya Protocol in the context of a post-2020 global biodiversity framework (Tsioumani et al. 2018). In a decision, the Conference of the Parties (COP) recognized that access to and use of DSI contributes to scientific research, and that further capacities to access, uses, generates, and analyze DSI is needed in many countries. In addition, the COP noted that some parties have adopted domestic measures that regulate the access to and use of DSI as part of their ABS frameworks, and that there is a divergence of views among parties regarding benefit-sharing from the use of DSI. Therefore, the COP further decided (i) to establish a science and policy-based process, which involves inviting governments and others to submit their views and information to clarify the concept, including relevant terminology and scope, and if and how domestic ABS measures consider DSI, and on benefit-sharing arrangements from commercial and non-commercial use of DSI; (ii) to invite governments and others to submit information on capacity-building needs; and (iii) to establish an extended AHTEG. Finally the COP requested the Secretariat to synthesize submissions, and commission studies on the concept and scope of DSI, ongoing developments in the field of traceability, public and, to the extent possible, private databases of DSI and how domestic ABS measures address benefit-sharing arising from commercial and

non-commercial use of DSI. The AHTEG is to consider the synthesis of views, develop options for operational terms and their implications to provide conceptual clarity, identify key areas for capacity building, and submit the outcomes for the consideration of the working group on the post-2020 framework.

Digital Sequence Information and Intellectual Property

In the context of intellectual property (IP) protection of DSI, patents, copyright and trade secret protection raise the most interesting IP protection issues as the full eligibility of this information subject matter for coverage under either regime is currently not clear and free from doubt. Genetic sequencing and DSI as such are generally not an invention. Thus, under most patent laws and as a general principle, mere products of nature and discoveries, where no human innovation is involved, are not patentable. Since the decision of the US Supreme Court in the Myriad case in 2013 (United States 2013) it is now widely acknowledged that the mere identification of a genetic sequence as such is not patentable since it is a discovery and not an invention. In addition, a scientific discovery as such is, by definition, universal and must remain accessible to everyone.

In the European Union (EU), however, the EU Biotechnology Directive (European Union 1998) of 1998, does not generally exclude patents on gene sequences isolated from nature. According to Art. 3.2 of the Directive the definition of biological material includes any material containing genetic information and capable of reproducing itself or being reproduced in a biological system. Art. 5.2 constitutes that elements isolated from the human body, including sequences and partial sequences of a gene, may constitute a patentable invention, even if the structure of that element is identical to that of a natural element. Art. 1.1

and 3.1 of the EU Directive constitutes, however, that a patent is granted for an invention which are new, involve an inventive step and which are susceptible of industrial application. Thus, a patent under the EU Directive requires an invention as well.

Also copyright protection of DNA sequence information seems to be a weak protection. Although this information may be copyrightable as a "work", if it is original, in principle there is no specific protection in place. An analogy to the copyright of the source code of computer software programs can be drawn, since the algorithms which constitute the source code can be protected under copyright laws. The question, however, remains, to what extent a DNA sequence is comparable to an algorithm of a software program. The mere detection of sequence information may not be comparable whereas the encoding functions of DNA sequences and their recombination within the scope of synthetic biology could be considered as similar to algorithms of software programs since this constitutes not a mere detection but a new and human designed combination of sequences to create something new and innovative. If the focus is on codes of DNA sequences it could be argued that sequence information could fall under the category of literary works since it could be compared to words, characters, numbers, symbols or signs that express something specific like a specific kind of language. However, if the DNA sequence is just the expression of a natural functionality it seems to be difficult to apply copyright laws to this information which is similar to literary works. In addition, there is neither case law on copyright protection of DNA sequences so far nor an existing copyright law which explicitly mentions genomic data or DSI or any other form of data of genetic resources.

According to the "WIPO Guide in IP Issues in ABS-agreements", copyright protection may arise when advanced characterization data about GR are created, such as DSI, however,

whether copyright applies is subject to applicable law (Abs Capacity Development Initiative 2018). In addition, the guide explains that the ways in which copyright and other IP are asserted for sequence information and its applications, in different sectors and under different scenarios, together with the implications for ABS, including monitoring, have been identified in existing fact-finding and scoping studies as one important area among several which warrant further and deeper investigation.

Since patent and copyright laws seem not to cover DSI at all or at least sufficiently, one could think about know-how protection of sequence data as a kind of a trade secret. In this case, however, special precautionary measures need to be in place in order to protect the secrecy of the information. If the data, however, is made publicly available in a public database or platform there is no precautionary measure in place and thus no secret information which could be kept protected.

As a result it is clear that the current IP system does not cover explicitly DSI although the importance of DSI in the innovation process and in the management and production of GR-based products is evident and increasingly growing and the results of the innovation process could lead to claims of ownership of relevant processes and products. The background of this legal situation is the different role of IP on the one side and GR and DSI on the other: The objective of IP is to protection innovation and creativity, whereas the objective of GR policy and DSI is according to the Nagoya Protocol access and benefit sharing. DSI results from GR and research with both may lead to IP rights and there are multiple interfaces between to two sides but the underlying objectives for protection and thus their regulation are different.

Access and Benefit Sharing

Recently, a debate has emerged whether to apply existing regulations on access to GR resulting from the Nagoya Protocol and its implementation on regional and national level to DSI and, if so, to what extent (CBD 2016; Karger 2018; Sollberger 2018; Spranger 2017). Besides the unclear terminology and scope of DSI, as already explained, the questions that are currently discussed in this context are, whether the existing ABS system applies to DSI and, if so, to what extent and, if not, whether a completely different ABS system modelled on Art. 10 Nagoya Protocol is needed to address the transformation from biological material to sequence data sufficiently and appropriately in order to meet the underlying public policy requirements of the CBD and the Nagoya Protocol. This discussion. whether and how DSI is covered by the Nagoya.

Protocol, is of fundamental importance for the ABS system since DSI allows to have access to genetic data independent from access to the biological material for GR research. This leads to the consequence that there is no need for travelling to a country or entity providing a particular GR, to start negotiations with this country under the ABS system and to sign appropriate agreements if the coded characteristics of the GR can be downloaded from an electronic database or portal of DSI.

Currently, in most jurisdictions sequence information downloaded from public databases is not covered by the Nagoya Protocol. However, some countries such as Brazil have their own national access legislation to GR which also cover rights over DSI. Whereas sequence information can be downloaded from public databases without any obligations by the ABS system some argue that DSI is already covered by the Nagoya Protocol or that its provisions should be adapted to cover sequence information.

This current debate is leading to an unclear legal position and causes legal uncertainty.

Whereas the negotiation history of the Nagoya Protocol and its objectives make it seem clear and leave no doubt that DSI is the result of sequencing activities on GR and thus should be considered as the results of research and development activities or as a form of utilization of GR according to Art. 2 of the Nagoya Protocol. it is still unclear to what extent the ABS system applies to DSI (Secretariat of the Convention on and Biological Diversity 2010).

Conclusion

The fundamental and radical transition from material to data is unique in history. It brings along a lot of changes and possibilities for the global research and use of genetic material. The technological use of DSI in a rapidly changing scientific environment, however, requires solutions and answers to legal, policy and scientific implications of regulating DSI, which is becoming an increasingly complex challenge. Whereas one could argue that genetic sequences do not fall into the scope of the Nagoya Protocol, since free sharing of DSI is a common scientific practice, and that any other solution would be counterproductive for global research – and especially in the pharmaceutical sector would be dangerous for public health – the answer is not that easy. Besides the need for a common terminology on an international, regional and national level on DSI and what should be covered by this term, there should be a discussion on the question whether a specific (IP) protection sui generis should be established to protect DSI. New innovations may create new needs for protection through new uses of existing IP law, IP-related technological protection measures for GR and DSI or

through similar *sui generis* protection rights. Finally, there should be an open discussion on the question whether provisions of the Nagoya Protocol should be amended to address the regulation of DSI and to clarify the questions regarding the applicability of the current ABS system. The possibility of the production of functional biologics which are produced automatically from digitally transmitted DNA sequences, has the potential to replace biological material and will increasingly enhance research and development processes in a wide range of sectors. In an age of synthetic biology, when an organism can theoretically be made artificially by using genetic sequencing and the resulting information from a public database, questions arise about the importance of biological material and the functionality of the current ABS system.

Although, it is currently not yet possible to synthesize from scratch more complex organisms, such as crops, the increasing importance of the replacement of biological material by data is evident: By combining sequence data with new and innovative gene editing technologies, such as gene editing with CRISPR/Cas9, the importance of sequence data is obvious, since a specific DNA sequence can be used by introduction into another organism without access to the biological material, where the specific DNA results from. Presently this can be done without negotiating any material transfer agreement under the current ABS system.

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NGS-BASED GENOMIC CHARACTERIZATION OF AGRICULTURALLY IMPORTANT PGR TO SUPPORT NATIONAL BREEDING PROGRAM

I Made Tasma

INTRODUCTION

Indonesia is recognized as the second richest megabiodiversity of the world. This includes plant genetic resources (PGR) of agriculturally importance. The PGR diversity determines the future of Indonesian agriculture. Few examples of PGR of Indonesian origins include rice, durian, banana, sugar cane, mangosteen and sweet potato. The PGR diversity needs to be explored to obtain genes, QTLs of interests for crop and animal breeding purposes. This can be done by the use of high throughput next generation sequencing (NGS) and high throughput SNP array technologies. Genes (DNA markers) are used for crop improvement in breeding programs. This paper describes the recent progress and achievement of plant genome re-sequencing projects at the Indonesian Agency for Agricultural Research and Development (IAARD). This manuscript describes the characterization of national agriculturally important crop

species at genomic level based on whole genome sequencing technology using NGS platform. The crops characterized include soybean, maize, oil palm, cacao, chili pepper, potato, banana and *Jatropha curcas*.

A Brief Review of the IAARD Advanced Genomic Research Program

IAARD missions include developing superior crop cultivars using the available breeding techniques. The methods should be able to manipulate PGR collection richness in efficient and effective manners. This manipulation would be facilitated by the current genomic technology by using the high throughput genetic platforms. Since the end of 2010, the IAARD has been equipped with such high throughput sequencing platform (i.e. the NGS system, Illumina HiSeq2000) and also a high throughput SNP array reader (Illumina iScan). The objectives of genomic research of IAARD were to: (1) sequence and re-sequence national priority crops and animals; the sequence data will be used for gene and SNP discovery and SNP chip development; (2) dissect economically important genes (QTLs) of economically important traits (e.g. yield, biotic and abiotic stress tolerance, nutritional values, etc.) of the national priority crops and animals using high throughput marker e.g. SNP markers; and (3) develop superior lines (cultivars, superior animals) of priority traits (e.g. yield, meat production and quality) of the national priority crops and animals through molecular breeding techniques.

Table 1. Genomic data status of targeted crops and animals studied at the ICABIOGRAD (Tasma et al. 2012). The study was started in fiscal year of 2010.

Crop	Reference genome sequence	SNP marker	Research activities
Oil palm	Not available	Not available	Design marker
J. curcas	Not available	Not available	De novo sequencing
Cacao	Available	Not available	Design marker
Soybean	Available	Not available	Design marker
Rice	Available	Available	Association analysis
Cow	Available	Available	Association analysis
Maize	Available	Available	Association analysis
Banana	Available	Not available	Design marker
Potato	Available	Not available	Design marker
Chili pepper	Available	Not available	Design marker

The genetic platforms have been utilized to sequence, re-sequence, and genotype national high priority crops and animals (Table 1). The crops and animals studied included rice, soybean, cacao, oil palm, physic nut, banana, maize, potato, chili pepper and cows. For crops with no reference genome sequence yet available, a *de novo* sequencing and genome assembly project were performed. This includes *de novo* sequencing project of oil palm (as in the year of 2010 the genome reference sequence of oil palm was not yet available at that time) and *Jatropha curcas*. If genome reference sequences were available but SNP markers were not available, a re-sequencing project was commenced to obtain SNP databases of the crops. This was done for crops and animal such as soybean, cacao, banana, potato and chili pepper. For crops and animals with reference genome sequence and SNP markers available, a high throughput genotyping and trait association studies were accomplished. This mainly was done in rice, maize, and cows. The genomic status of the crop and animals studied at IAARD is as shown in Table 1.

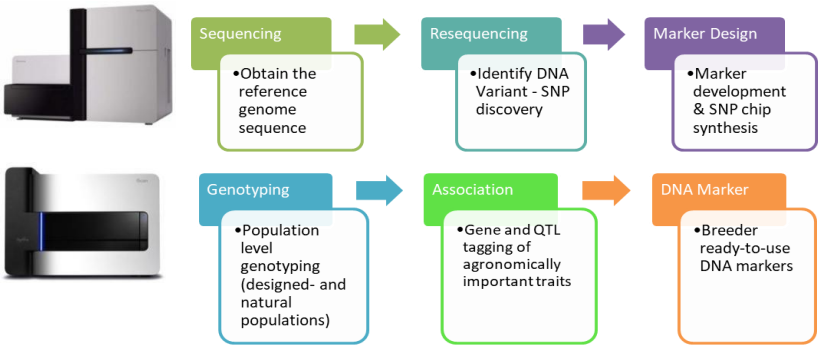

Figure 1. Strategy of advanced genomic studies at IAARD (Tasma et al. 2012; Tasma 2015; Tasma et al. 2018). Two high throughput genetic platforms (HiSeq2000 and iScan) have been applied in the research to support genomic-based breeding programs of priority crops at IAARD.

To meet the IAARD genomic research goals, we have designed a general strategic scheme of advanced genome research at ICABIOGRAD as shown in Figure 1. The NGS sequencing platform has been oriented to conduct *de novo* sequencing, re-sequencing, and genotyping by sequencing (GBS). While the high throughput SNP array reader is subjected for high throughput genotyping to expedite gene and QTL discoveries of important traits to be applied in a breeding program of the respective crops.

De Novo Sequencing of PGR Species to Develop Reference Genome Sequences

De novo sequencing is to define the genome sequence of a particular crop species the first time (Van et al. 2012; Danaval et al. 2012; Tasma 2017). *De novo* sequencing is intended to develop reference genome sequence of a particular crop species of interest. The reference genome will be used as a guidance to

analyze genomic variations among individual genotypes of the species member using a simpler and cheaper method known as resequencing genome project (Tasma 2015; Tasma 2016).

A reference genome is required for each target species for genomics scientists to leverage the power of modern genome technologies in agricultural research. To produce and annotate the first genome sequence of any individual in a species, chromosomal DNA is broken up into billions of pieces, from 500 to 30.000 base pairs in length, and a complex set of specialized DNA libraries over many months are produced (Varshney et al. 2009; Wetterstrand 2011). High cost long read sequence data is then generated from the complex DNA libraries and a map of long contiguous chromosomal regions is reconstructed with a *de novo* sequence assembly computer. Long read sequences enable the computer programs to assemble through the tens of thousands of repetitive elements typically present in plant genomes, which in turn results in longer sequence scaffolds. Long sequence scaffolds have more utility to researchers than short sequence scaffolds. Once lengthy sequence scaffolds have been produced, expressed regions of the genome are typically annotated with millions of sequences generated from RNA libraries also using long read sequencing technologies. Similar to *de novo* genome sequencing, long read sequencing technology is also preferred over Illumina short read sequencing for the construction of the first-draft of the transcriptome, because long reads when assembled are more likely to result in full-length transcripts, which are most useful for gene model construction.

High quality (i.e., long and accurate) reference sequences are far more expensive to produce than genome re-sequencing data sets (Wetterstrand 2011). Moreover, research teams generally never complete reference projects but are engaged in a process of continually improving and releasing more consolidated and more

accurate genome builds over time. For example, in the United States, even though the first reference genome sequence of man was completed in 2002, today an estimated 300 scientists are engaged in editing the reference human sequence, which is now in its 19th build. The more accurate the reference sequence is for a given species, the more powerful each low cost re-sequencing study becomes.

In researching a particular crop species, scientists often are required to produce 3 to 5 reference genome sequences from multiple species which are related to the crop (Varshney et al. 2009). For example, in maize (*Zea mays*), a reference genome sequence was produced from B73, MO17, as well as from the popcorn variety (Schnable et al. 2009). Likewise in rice (*Oryza sativa*), reference genome sequences have been produced from the niponbare, indica (Yu et al. 2002) and japonica (International Rice Genome Project) varieties. In cacao (*Theobroma cacao),* reference genome sequences have been produced from the Belizean Criollo (Argout et al. 2011) and Matina 1-6 cultivars. In Oil Palm, private groups have produced reference genome sequences from three *E. guineensis* palms with pisifera, dura, and tenera fruit types and from the related *E. Oleifera* oil palm. Reference genome sequences of several agriculturally important plant species have been reported (Table 2).

The IAARD have conducted *de novo* sequencing of two crop species, oil palm and physics nut (*Jatropha curcas*) to provide reference genome maps of the two crops (Tasma et al. 2014b). The oil palm genome reference map, however, was published in 2013 (Singh et al. 2013) and the analyzed sequence data obtained from three oil palm genotypes conducted by IAARD were used as re-sequenced data to discover genomic variations of the oil palm genomes. SNP and INDEL markers have been developed from the sequence data to support breeding programs of oil palm. *De*

novo sequencing project of *Jatropha curcas* genome was conducted in collaboration with Seoul National University (Korea) and Kasersart University (Thailand). *J. curcas* genome reference map has been completed that becomes a high value resource to support breeding programs of this oil-bearing crop species. Millions of SNPs and Indels have been discovered by aligning the reference sequences with other genotypes of the Indonesian physic nut accessions. These would be very important marker resources for expediting physic nut breeding programs.

Table 2. Plant species of agriculturally importance in which their reference genome sequences have been available (Van et al. 2012; Danaval et al. 2012; Tasma 2015; Tasma et al. 2018).

Plant species	Scientific name	Genome size (Mbp*)
Rice	*Oryza sativa* ssp *indica*	430
	O. sativa ssp *japonica*	430
Soybean	*Glycine max*	1.115
Maize	*Zea mays*	2.300
	Zea mays spp. *parviglumis*	2.100
Sorghum	*Sorghum bicolor*	730
Cassava	*Manihot esculenta*	760
Papaya	*Carica papaya*	372
Cucumber	*Cucumis sativus*	367
Potato	*Solanum tuberosum*	844
Banana	*Musa accuminata*	472.2
Apple	*Malus domestica*	742.3
Strawberry	*Fragaria vesca*	240
Grape	*Vitis vinifera*	487
Watermelon	*Citrullus lanatus*	450
Melon	*Cucumis melo* L.	430
Tomato	*Solanum lycopersicum*	900
Green beans	*Phaseolus vulgaris*	486.9
Cacao	*Theobroma cacao*	430
Cotton	*Gossypium raimonddi*	750
Oil palm	*Elaeis guineensis*	1.800
Castor nut	*Ricinus communis*	350

**1 Mbp (Mega base pair) = 10^6 base pairs.*

Resequencing of PGR Genomes of Agriculturally Important Crops to Identify Genomic Variation

Once a set of reference genome exists, scientists can re-sequence a second or third individual from the same species using very low-cost short read technologies, such as the Illumina HiSeq-2000 platform (Varshney et al. 2009; Tasma 2016). Individual reads from a short read project are not necessarily assembled to one another, but rather are mapped back to the reference genome to identify genetic differences that exist between the reference sequence and the sequence of the second individual. In this way a list of differences can be recorded, and these genetic differences are used to explain differences between varieties within a species, such as yield, disease resistance, flowering time, drought and flood tolerance etc. Re-sequencing projects can be used to survey variation with a species, to conduct genotyping by whole genome sequencing studies, to build high resolution genetic maps, and to generate genome wide association maps.

Genome re-sequencing analysis was done to identify DNA variations of national priority crops and animals, marker SNP collection of which, has not been available. Whole genome of various superior accessions of the priority crop species were re-sequenced and genome variations (e.g. SNP and INDEL) were identified by aligning the genome reference sequence with those of the re-sequence data of the crop species under study. The type of crop accessions sequenced was Indonesian accessions and varieties to discovered genes and QTL adaptable to Indonesian tropical climates. The collected SNPs and INDELs from the studies have been validated, maintained in a database and be used in marker discovery analyses. The validated SNP markers will be selected based on genetic merits and GR characterization and future breeding objectives. The selected SNPs then are

arranged in condensed manner in a chip containing low-to-high density SNP markers. The markers selected in such a way to meet scientific needs for discovering genes and GR evaluation of the respective crop or animal under study.

IAARD has focused on nine priority crop species important for Indonesian agriculture. The crops under study included rice, maize, soybean, oil palm, cacao, banana, chili pepper, potato and physics nut (*Jatropha curcas*). The genetic materials used in the genomic analyses were the parental breeding materials (i.e. the parents of breeding programs that were used in cultivar development of the targeted traits in each crop or animal species). The genetic materials analyzed also included other genetic materials of specific interest for the respective RIs important for their future breeding programs. The RIs also develop mapping populations based on traits of interest and as the targeted trait improvement for each crop and animal species.

The number of genetic materials used in this study ranged from three to 20 genotypes of each respective crop and animal species. The genomic DNA of the selected genotypes was deeply-resequenced using an NGS HiSeq platform to result in high quality reads. Genome coverage of this whole genome sequencing study ranged.

from 27 to 1.185 genomes (Table 3). The high quality DNA sequences resulted from this study were aligned with the reference sequence of each respective crop and animal species. The alignment identified genome-wide DNA variations in each crop and animal species unde study. The alignment was done by using software Bowtie2 (Langmead and Salzberg 2012). The sequencing alignment was then followed by genome variation characterization by using computer software Mpileup within Samtools (Li et al. 2009). Anotation of the location and effect prediction of the identified SNP/INDEL were conducted using

software snpEff (Cingolani et al. 2012). Finally, a genetic diversity analysis of the five genome sequences was conducted by using software DarWin (Perrier and Jacquemoud-Collet 2006). The types of genomic variations identified from this study included SNPs, INDELS, and SSRs. DNA variations discovered from this experiment were as presented in Table 3.

Table 3. DNA variations observed based on alignment results of the NGS-derived re-sequence data to the respective reference map of the crop and animal species under study (Tasma et al. 2014; Satyawan et al. 2014; Tasma et al. 2015; Tasma 2016; Tasma et al. 2018).

Crop/animal species	Genom size (Mb)*	Number of genotypes sequenced	Average genome coverage**	DNA variation frequency observed***	Total DNA variations observed		Total
					SNP	INDEL	
Soybean	1,115	5	33	288	2,690,000	459,000	3,150,000
Maize	2,300	4	27	634	2,805,145	240,526	3,247,037
Banana	472.9	14	47	57	5,159,450	571,885	5,731,335
Cacao	430	5	77	121	2,326,088	362,081	2,688,169
Oil palm	1,800	3	109	197	3,032,200	303,109	3,335,331
Chili pepper	2,649	6	69	101	24,760,787	1,316,987	26,077,774
Potato	844	6	27	160	4,166,472	339,372	4,505,844
Physic nut	450	3	125	1,185	92,007	nd	92,007
Total and range values		46	27-125	57-1,185	45,032,149	3,592,960	48,625,109

Gene-Based Genomic Variations Observed Among the Crop Species Under Study

Breeders are of utmost interest in obtaining DNA variations located within the exons (protein coding regions) to design functional markers useful for breeding programs. Two types of DNA variations were observed from exons. The frist was synonymous SNPs and INDELS (DNA variations that do not change proteins sequences due to the changes of bases in the site of observed SNP or INDEL). The second was non-synonymous SNPs and INDELS (DNA variations that change the amino acid

sequences of the proteins due to the changes in the sites of the observed SNPs/INDELS).

The majority of the variations observed were located outside the genes, i.e. upstream, downstream, intergenic regions of the genes (Table 3). Among the DNA variations observed only a small portion was located within the exons (protein coding regions) (Table 4).

Table 4. Location of DNA variations observed within the genome of each crop species under study (Tasma et al. 2014; Satyawan et al. 2014; Tasma et al. 2015; Tasma et al. 2016).

Crop species	Number and percentage of genomic variation observed at different parts of the genome					
	Upstream gene	Downstream gene	Intergenic region	Intron	Exon	Other sites*
Soybean	55.870	1.174.917	1.393.216	381.701	95.154	53.343
(*Glycine max)*	(29.757%)	(26.367%)	(31.586%)	(8.654%)	(2.157%)	(1.209%)
Maize	1.698.426	1.772.088	2.563.804	663.812	230.412	349.914
(*Zea mays)*	(23.34%)	(24.35%)	(35.23%)	(9.12%)	(3.17%)	(4.81%)
Banana	869.078	855.128	774.327	391.795	48.382	34.535
(*Musa accuminata*)	(29.83%)	(28.761%)	(26.043%)	(13.177%)	(1.627%)	(1.161%)
Cacao	469.623	360.497	404.919	28.995	1.3462	500.348
(*Theobroma cacao)*	(29.93%)	(22.98%)	(25.81%)	(18.48%)	(0.86%)	(2.11%)
Oil palm	584.063	551.772	2.782.751	492.316	55.870	4.804
(*Elaeis guineensis)*	(13.062%)	(12.34%)	(62.232%)	(11.01%)	(1.249%)	(0.0107%)
Chili pepper	1.589.861	1.486.165	25.071.638	532.184	180.234	388.18
(*Capsicum annum)*	(5.44%)	(5.081%)	(85.72%)	(1.82%	(0.16%)	(1.33%)
Potato	1.625.886	1.932.527	2.450.034	1.123.125	654.923	369.317
(*Solanum tuberosum*)	(19.94%)	(23.70%)	(30.04%)	(13.77%)	(8.03%)	(4.527%)
Physic nut	1.225	1.492	90.652	326	500	1.407
(*Jatropha curcas)*	(1.33%)	(1.51%)	(96.06%)	(0.35%)	(0.53%)	(1.597%)
Range of percentage	1.33-29.83	1.51-26.37	25.81-96.06	0.35-25.68	0.53-8.03	0.01-4.80

Other sites included splice site acceptor, splice site donor, UTR 3 primer, UTR 5 primer.

Genomic Data Base Development on PGRs of Agriculturally Important Crop Species

The IAARD has developed genome browsers covering genomic and phenotypic data of rice, soybean, maize, cacao, oil palm, physic nut, chili pepper, potato and cows. The genome browsers contain genome wide resequencing data of each

respective crop and animal species, SNP and INDELS information (gene or non-gen SNPs and INDELS) across the genome including the sequence information where the SNPs and INDELS located, etc. The genome browsers are being incorporated into the IAARD open-to-public genome database (http://genom.litbang.pertanian.go.id). This database is a very important resource for crop and animal scientists (geneticists, plant and animal physiologists and breeders) interested in finding particular genes and genetic markers of particular traits of the respective crop and animal species covered by the IAARD genome database. The genome resources should provide the basic data for developing breeding resources to expidate national breeding programs of the national priority crop and animal species.

Figure 3. Genomic data base containing millions of genetic variations resulted from genomic characterization of various agriculturally important crop species of national priority assessed with NGS Hiseq2000 (Rijzaani et al. 2016; Tasma et al. 2018).

Breeding Programs Based on PGR Genomic Data

The DNA markers (i.e. SNPs, INDELS) linked to the traits of interest would be used in breeding programs through marker-assisted selection (MAS) and genomic selection methods. Such methods would be able to exploit our plant and animal GR richness for developing superior plant and animals in a more efficient and effective manners that will support national programs on food self-sufficiency and food security for human kinds.

In plants and animal breeding programs, it has been commonly practiced to tag traits with molecular markers. More classical genomic tools have been successfully used to tag many important agronomic traits with more classical DNA markers such as RFLP, AFLP and SSR markers. The markers linked to the traits then are used in a molecular breeding program to select individual plants or animals having the trait of interest. Such marker-assisted selection (MAS), marker-assisted backcrossing (MAB) become very common to be applied in recent years to expedite breeding programs. More recently with the ability to map plant genome with dense molecular markers (i.e. SNPs), genomic selection (GS) technique becomes more popular for plant and animal breeders.

The GS is defined as the simultaneous selection for many thousands of markers, covering the entire genome so that all genes are expected to be in linkage disequilibrium with at least some of the markers (Meuwissen et al. 2001). The GS is very compatible with the recent genotyping technologies using NGS and high throughput SNP genotyping methods in which the marker assay can cover thousands and even few millions SNP markers. This technology becomes more feasible with a drop in genotyping costs, has GS become feasible, attracting the attention

of crop and perennial plant breeders (Bernardo and Yu 2007). Genome-wide and cost-efficient marker systems are needed to apply GS in plants. Furthermore, dedicated GS breeding populations with effective population sizes (N_e) of around 20–50 individuals must be adopted to increase the extent of LD and fit into currently achievable genotyping densities of a few hundred markers per Morgan. In genetically heterogeneous populations still encompass large amounts of genetic variation for sustained genetic gains, recent experimental results in outbred plants, indicate that GS has better predictive ability than the classical polygenic model (Lee et al. 2008). A GS scheme has been tested in several crop plants where predictive equations for multiple traits are developed on the basis of high density genotyping and precise phenotyping of several hundred individual plants of a discovery population (training set) involving N_e in the range of 15–50. Selection accuracy of the predictive models is then assessed in a validation population, targeting the application of early GS at the individual plant level in progeny trials. This technique, once accomplished will be very accurate in selecting individual plants having the trait of interest and can be done in a faster, more predictable and more precise manner.

Future Perspectives

Future breeding program demands interesting challenges to develop crop varieties with multiple traits. This is due to the significant effect of global warming affecting crop cultivations in the field. Breeders should develop high productivity crops with lower water availability, tolerant to abiotic and biotic stresses (e.g., drought; aluminum and iron toxicity, flood; more dynamic disease and insect pest development and patterns; more nutritious crop products; etc.). Breeders need to develop crop cultivars in a time frame basis to provide plant materials to

address the product demand and environmental problems. Indonesia has high PGR diversity that should be characterized in efficient, effective, and comprehensive manners to obtain genes of interest for plant breeding purposes. The NGS technology expedites gene and marker discoveries for traits of interest. Genomic-based breeding program should result in more variable crop cultivars and plant products that can be resulted in a faster and precise manner. In addition, the advanced technology should also be able to use of PGR richness in comprehensive manner in plant breeding program. Indonesian government, therefore, needs to allocate more resources to be allocated in the genomic-based plant breeding program to assure the national food self-sufficiency program be successful.

Conclusion

IAARD has sequenced the whole genomes of 46 genotypes covering eight agriculturally important crop species. A total of 48.625.109 DNA variations consisted of SNP, insertion and deletion (INDEL) were obtained from the NGS-based sequence data. The genomic variations have been deposited in the national genomic data base that can be accessed for research purposes. PGR characterization at the genome level is useful mainly in developing breeding resources to be used in gene discovery and marker development useful to expedite plant breeding program of agriculturally important crop species. The genome database containing genetic variations derived from 39 PGR of nine crop species will be useful for scientific as well as product development derived from the crop species. A more comprehensive genomic characterization of PGR would be more useful in supporting future breeding program. With the development and the lower cost of sequencing technology the genome sequencing will be affordable by the more common

laboratories of the world. The NGS-based PGR characterization technology, therefore, will become routine activities in the future. The Indonesian government needs to be aware on this type of technology to be able to use its PGR richness in more efficient and comprehensive manners for breeding and product development purposes to support the food, feed and bioenergy self-sufficiency programs to be successful.

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TOWARDS BUILDING THE BIG DATA OF SHALLOT: PHENOMIC, METABOLOMIC AND GENOMIC

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INTRODUCTION

Shallot (*Allium cepa* var *ascalonicum*) is an important commodity, especially in Asia including Indonesia. Shallot is consumed in both fresh and processed forms. The use of shallot has been widely known as a flavoring in food or used as an ingredient in herbal medicines (Grubben and Denton 2004). Demands for shallots in Indonesia and in the international markets continue to increase from year to year. Therefore efforts are needed to fulfill these needs through increased production. Unfortunately, in Indonesian the production of shallot is heavily reliant on very limited number of varietieslike Bima Brebes. In fact, the yield of this variety has been decreasing from year to year. In addition, the use of seed bulb for propagation has contributed to the narrowing genetic diversity of shallot in Indonesia.

Breeding is a very urgent thing to do and genetic diversity studies are important in optimizing plant-breeding programs

toward high yielding and high bulb quality shallot varieties. Genetic diversity could be analyzed using morphological characters, chemical characters, and molecular markers (Wahyuni *et al*. 2013). The main objective of this study was to get the information regarding the genetic diversity of 59 shallot genotypes and initiating the construction of big data for shallot in Indonesia. Thirty five morphological traits (macroscopic and microscopic), ability to produce flower, untargeted metabolomics approach using CG-MS and LC-MS, and some random and gene analog-based markers were used to portray the diversity of our shallot collection. Further, the acquired data were used to identify flowering related genes in shallot and to identify the defense mechanism in shallot against pathogens.

All Genetic Markers Reveal the High Genetic Diversity of Shallot in Indonesia

Our results showed that our shallot genotypes have high genetic diversity (Figure 1, Figure 2, and Figure 3). Cluster analysis of 40 genotypes of shallot divided them into two main groups based on the coefficient of dissimilarity of 0.59 (21 morphological traits) and also two main groups based on the coefficient of dissimilarity of 0.48 (14 morphological bulb traits). Principal component analysis based on morphological characters showed that there were three main components that could explain 62.10% of the total diversity.

Untargeted metabolomic analysis of shallot bulb using GC-MS can detect a total of 326 metabolite compounds. Based on the heatmap of 326 metabolites, the metabolites are grouped into two groups, group A and group B (Figure 3). Group A consists of three metabolite compounds, namely *cycloartenol* (*triterpenoid*), *palmitic acid* (*fatty* acid), *octadecadienoic acid* (*fattyacids*). Group B

comprises compounds that are only found in one or several genotypes. The heatmap divided shallot genotypes into two groups. Group 1 contains genotypes which only have *palmitic acid* and *octadecadienoic acid* compounds. While group 2 contains genotypes which only have *palimitic acid* and *cycloartenol*. Some sulfur compounds found in some genotypes in this study were *methylsulfanyl-4,5,6,7-tetrahydro-benzo[c]thiophene* (BM26), *nonadecane* (BM29), *allyl-dimethylcyclopropane* (BM45), *lanosterol* (BM47), *stearic acid* (BM60) and *propyl alcohol* (BM21). Cluster analysis classified the genotypes into two main groups with a dissimilarity coefficient of 0.41. Eigenvector of the four main components could be used to reduce the 229 original characters to 24 main characters.

We also found that not all of shallot genotypes can naturally produce flower. Therefore more efforts are needed to induce flowering ability in those genotypes. Flowering is important to transfer desirable traits from one genotype to others during the breeding process. Moreover, the ability to produce flower and TSS (True Seed of Shallot) is also esential during the germplasm collection and preservation. So far, we could only store 18% shallot genotypes as TSS (Table 1), while the rest were stored as bulbs. The bulbs always cause problem since they can only be stored in relatively short periods.

Resistance gene analog-based markers could also be used to support the morphological and metabolites characterization in evaluating the genetic diversity of shallot (Herlina et al. 2018). The diversity and population structure of shallots has also been detected by resistance gene-derived markers. Six polymorphic *R* gene-derived markers (Acepa-1, Acepa-2, Acepa-3, Acepa-4, Acepa-5 and Acepa-6) were developed and applied to analyse the genetic diversity of shallots in Indonesia. These loci produced a total of 963 alleles with an average of 0.51 ± 0.77 alleles per

marker. The polymorphic information content value ranged from 0.2784 to 0.5236 with an average of 0.36015 (Herlina et al. 2019).

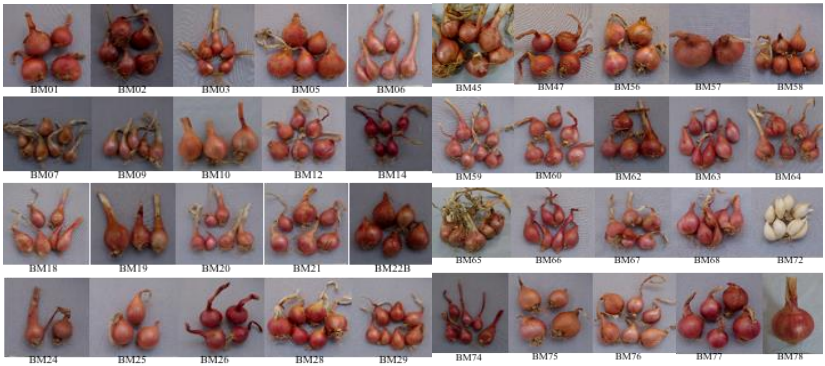

Figure 1. Morphological diversity of shallot bulb in our collection.

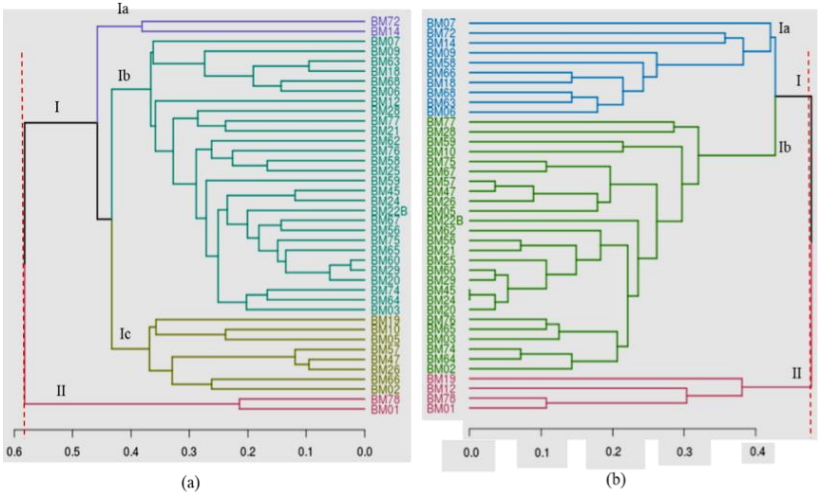

Figure 2. Cluster analysis of shallot diversity based on morphological and molecular characters.

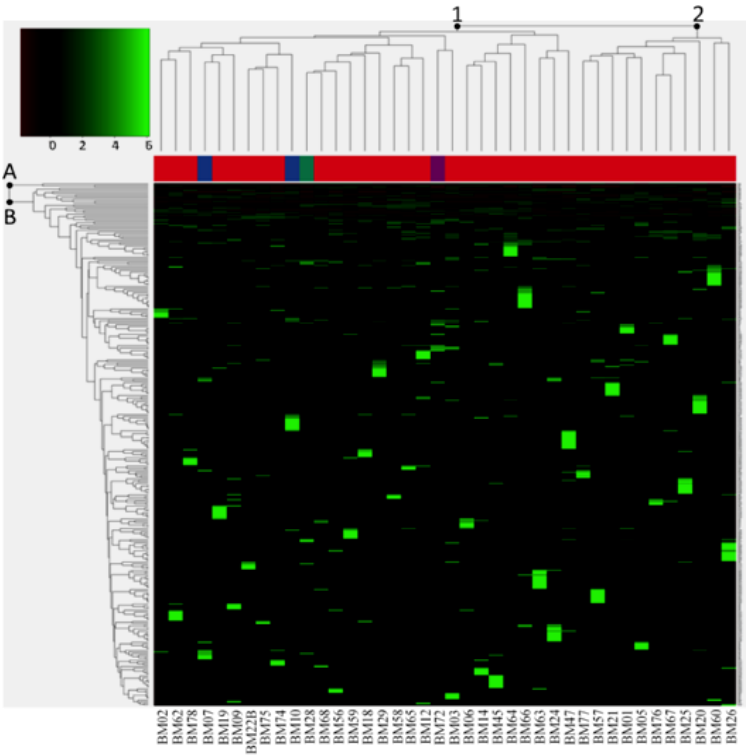

Figure 3. Cluster analysis of shallot diversity based on metabolite contents.

Table 1. Storage systems of shallot genotypes in our collection.

Geno	Collection material		Geno	Collection material		Geno	Collection material	
	Bulb	TSS		Bulb	TSS		Bulb	TSS
BM 01	√	-	BM 35	√	√	BM 60	√	-
BM 02	√	√	BM 36	√	-	BM 61	√	-
BM 03	√	√	BM 40	√	-	BM 62	√	-
BM 05	√	√	BM 41	√	√	BM 63	√	-
BM 06	√	-	BM 42	√	-	BM 64	√	-
BM 07	√	-	BM 43	√	-	BM 65	√	-
BM 08	√	-	BM 44	√	√	BM 66	√	-
BM 09	√	-	BM 45	√	-	BM 67	√	-
BM 10	√	-	BM 46	√	-	BM 68	√	-

Table 2. Continue.

Geno	Collection material		Geno	Collection material		Geno	Collection material	
	Bulb	TSS		Bulb	TSS		Bulb	TSS
BM 12	√	√	BM 47	√	-	BM 69	√	-
BM 14	√	-	BM 49	√	-	BM 70	√	-
BM 15	√	√	BM 50	√	-	BM 71	√	-
BM 16	√	-	BM 51	√	-	BM 72	√	-
BM 18	√	-	BM 52	√	-	BM 73	√	-
BM 19	√	√	BM 53	√	-	BM 74	√	-
BM 20	√	-	BM 54	√	-	BM 75	√	-
BM 21	√	√	BM 55	√	-	BM 76	√	-
BM 24	√	-	BM 56	√	-	BM 77	√	-
BM 25	√	√	BM 57	√	-	BM 78	√	-
BM 26	√	-	BM 58	√	-	BM 79	√	-
BM 29	√	-	BM 59	√	-			

Molecular Diversity of the Flowering Related Gene (Leafy) on Shallot

Since the flowering ability of shallot is very important for breeding purpose and propagation, we turned our focus to this aspect. Marlin et al. (2018) used the previously described material to study flowering in shallots. Flowering initiation in shallot has predictably been associated to the function of LEAFY (LFY) gene. This gene has been reported as the flowering meristem identity, and a potential indicator of plant flowering ability. Marlin et al. (2018) identified the diversity of shLFY (shallot-LFY) gene in five shallot genotypes in relation to their flowering pattern, and compared them to homologous sequences from Allium relatives. Genomic DNA from the 5 genotypes was amplified using novel primers (F/5′-GACCCAACAGACCCCTAC-3′ and R/5′-TTAGAACATAGAGGACACAGAG-3′), resulting in shLFY gene sequences with fragment lengths between 1.161 and 1.253 bp. These fragments were found to contain 3 exons with 2 introns.

The sequences of shLFY from 5 shallot genotypes confirm the existence of genetic polymorphism among shallot genotypes. The result of sequence analysis based on genomic and amino acid sequences identified 3 groups of shLFY genes in shallot. The first group consists of a single member, bm1LFY (Bentanis), which corresponds to naturally flowering type. The second group contains bm2LFY (Bima Brebes) and bm4LFY (Tajuk), which correspond to inducible flowering type. The third group comprises bm3LFY (Ilokos) and bm5LFY (Sumenep), corresponding to the non-flowering shallot type. The ShLFY sequence encodes a putative protein of 363 amino acids, with ~ 99% homology to the Allium cepa LEAFY and > 95% homology to LEAFY proteins from other higher plants. The shLFY protein in the 5 shallot genotypes also showed homology with FLORICAULA/LFY protein from referenced Allium relatives.

Identification of Defense Mechanisms Against Stress in Shallot

Using the previously described materials, we identified some important resistance traits in shallot, such as resistance to *Fusarium oxysporum*, *Colletotrichum gloeosporioides* and adaptability in tidal swampland. Aprilia et al. (2019) found that two shallot genotypes, Batu Ijo and Rubaru or Sumenep, were resistant to *F. oysporum.* Recently, Kurnianingtyas et al. (2019) identified that the Sumenep variety was the most resistant to *C. gloeosporioides,* with a disease severity of 30.19%, while the Biru lancor variety was the most susceptible with a disease severity of 95.05%. Laboratory tests indicated that the resistance to *C.gloeosporioides* might be related to the thickness of the palisade tissue (R=0.80). This research also showed a possible relationship between resistance to *C. gloeosporioides* and metabolite productions. We detected that carbamic acid, an elicitor compound in the jasmonic

acid transduction pathway, was highly correlated with the resistance. Similar approach has also been done by Galingging et al. (2018) to detect metabolite contents of shallot genotypes that might be related to the adaptation of shallot to extreme conditions like tidal swampland.

Concluding Remarks and Future Perspective

Genetic diversity of shallot in Indonesia can be considered as high. This diversity should be exploited further in breeding programs to make shallot production more sustainable by reducing chemical usages for controlling pest and diseases in Integrated Pest Management system (Maharijaya and Vosman 2015). Our materials are available in the form of commercial and near commercial varieties of shallot. Thus, we can avoid breeding constraints introduced by the use of wild relatives for breeding, such as hybrid sterility and low crossing ability, as well as the retention of undesirable agronomic traits (Hajjar and Hodgkin 2007). However, there are still some important issues to be solved, such as induction of flowering ability from desirable genotypes for breeding purposes. Networking and collaboration are urgently needed and databases should be developed to be made available and accessible for related institutions.

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CHAPTER 4.
DIGITAL OBJECT IDENTIFIER FOR PLANT GENETIC RESOURCES MANAGEMENT

The Digital Object Identifier (DOI) is defined as a character string used to identify intellectual property in the digital environment. The DOI system was established to provide a framework for managing intellectual content, including activities such as linking users to content owners, facilitating electronic commerce and enabling automated copyright management for all types of media. A DOI name is permanently assigned to an object, to provide a persistent link to current information about that object, including where the object, or information about it, can be found. The DOI system consists of four components: identifier, resolution, metadata or description and policy. The value of DOI system lies in its combination of resolution, metadata and policy.

The Global Information System (GLIS) is established by the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) of the United Nations Food and Agriculture Organization (UN-FAO) to facilitate agricultural researchers, plant breeders and farmers to access relevant information related to plant genetic resources for food and agriculture (PGRFA) around the world. GLIS is expected to become a one-stop shop for easy access to information on seeds

and other crops materials for research, training and plant breeding. On the other hand, the development and promotion of the use of the established system of DOI is also needed as several communities have highlighted the importance of creating and adopting Permanent Unique Identifiers to improve the identification of PGRFA. It is expected that DOI will be the international standard for identifying and documenting PGRFA materials uniquely and permanently, as well as facilitating data interoperability among different systems.

Multi-country Construction of a Test Platform for the Development and Allocation of Unique Identifiers for Rice Germplasm is a collaborative project between the Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development (ICABIOGRAD), the Indonesian Agency for Agricultural Research and Development (IAARD), ITPGRFA-FAO Rome and IRRI in the Philippines. It was financed by Benefit Sharing Fund of the ITPGRFA and was intended to promote the use of DOI for rice germplasm management and exchanges among participating countries.

DOI can be used as an identifier for PGRFA material managed by individuals, groups and organizations. DOI identifies PGRFA materials, not the associated data. Therefore, if the data associated with the PGRFA materials changes, the holder must correct the data without changing the DOI. DOI also has direct association with the holder of PGRFA materials. When a material is transferred, assigning a new DOI is usually recommended because the material is potentially placed under different legal and quality management conditions. However, when the recipient publishes results, they must refer to the recipient's DOI, not the provider's.

It is important to include basic data or information related to PGRFA materials as well, which is known as DOI metadata. DOI

metadata is essential for identifying PGRFA materials and providing an overview of the nature or category of the PGRFA materials. Adopting the DOI does not mean replacing existing systems with a new one. Both DOI and local identifiers can still be used to manage the identity of PGRFA materials, as well as becoming main references in online publications and articles. However, if the PGRFA material is transferred across different organizations, then local identifiers will not be sufficient to be used as material identifiers. A unique global identifier system such as DOI is preferable in such cases to facilitate access globally. Once the PGRFA material is given a DOI, the DOI metadata of this material will be uploaded to GLIS and can be accessed by global users. This is one of the advantages, where the assignation the DOI will significantly improve the visibility of PGRFA-related data.

Although tested for rice germplasm as a pilot project, the DOI registration for other PGRFA is the same and straight forward. Several countries have registered non-rice germplasm from their gene bank successfully. The DOI system also improved the plant genetic resources management since it will also keep track of the movement of accessions in the genebanks. In addition, registration of the accession in the DOI system for some countries help them to consolidate their accession since each DOI number should serve as unique identifier for each accession in the collection.

ACCELERATING DOI REGISTRATION OF PGRFAs FROM ASIAN AND AFRICAN COUNTRIES THROUGH INTEGRATION-TOOLKIT DISSEMINATION

Hakim Kurniawan, Nurul Hidayatun, and M. Sabran

INTRODUCTION

The DOI is defined as a character string used to identify intellectual property in the digital environment (Information Standards Quarterly 2004). The DOI system was established to provide a framework for managing intellectual content, including activities such as linking users to content owners, facilitating electronic commerce and enabling automated copyright management for all types of media. A DOI name is permanently assigned to an object, to provide a persistent link to current information about that object, including where the object, or information about it, can be found (Paskin 2010). The DOI system consists of four components: identifier, resolution, metadata or description and policy. The value of DOI system lies in its combination of resolution, metadata and policy (Chandrakar 2006).

The Global Information System (GLIS) is established by ITPGRFA of the United Nations (FAO) to facilitate agricultural researchers, plant breeders and farmers to access relevant information related to plant genetic resources for food and agriculture (PGRFA) around the world. GLIS is expected to become a one-stop shop for easy access to information on seeds and other crops materials for research, training and plant breeding. On the other hand, the development and promotion of the use of the established system of Digital Object Identifiers (DOI) is also needed as several communities have highlighted the importance of creating and adopting Permanent Unique Identifiers for improved identification of PGRFA. It is expected that DOI will be the international standard for identifying and documenting PGRFA materials uniquely and permanently, as well as facilitating data interoperability among different systems.

Multi-country Construction of a Test Platform for the Development and Allocation of Unique Identifiers for Rice Germplasm is a collaborative project between the Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development (ICABIOGRAD), the Indonesian Agency for Agricultural Research and Development (IAARD) Indonesia, ITPGRFA-FAO Rome and IRRI in the Philippines. It is financed by Benefit Sharing Fund and intended to promote the use of DOI for rice germplasm management and exchanges among participating countries. To facilitate DOI batch-registration of large collections of PGRFA, an Integration-Toolkit, is developed and disseminated during the implementation of the project.

DOI for Easier Management of PGRFAs

DOI can be used as an identifier for PGRFA material managed by individuals, groups and organizations. DOI identifies PGRFA materials, not the associated data. Therefore, if the data associated with the PGRFA materials changes, the holder must correct the data without changing the DOI. DOI also has direct association with the holder of PGRFA materials. When a material is transferred, assigning a new DOI is usually recommended because the material is potentially placed under different legal and quality management conditions. However, when the recipient publishes results, they must refer to the recipient's DOI, not the provider's.

It is important to include basic data or information related to PGRFA materials as well, which is known as DOI metadata. DOI metadata is essential for identifying PGRFA materials and providing an overview of the nature or category of the PGRFA materials. Adopting the DOI does not mean replacing existing systems with a new one. Both DOI and local identifiers can still be used to manage the identity of PGRFA materials, as well as becoming main references in online publications and articles. However, if the PGRFA material is transferred across different organizations, then local identifiers will not be sufficient to be used as material identifiers. A unique global identifier system such as DOI is preferable in such cases to facilitate access globally. Once the PGRFA material is given a DOI, the DOI metadata of this material will be uploaded to GLIS and can be accessed by global users. This is one of the advantages, that assignation the DOI will significantly improve the visibility of PGRFA-related data.

Important Data for Assignation of DOI

The object associated with a DOI name is described unambiguously by DOI metadata. Assignment of a DOI name requires the registrant to record metadata describing the object to which the DOI name is being assigned (Paskin 2010). DOI metadata is essential for providing a basic description of the characteristic of the PGRFA materials, thus users can easily screen and select based on their own needs. There is a minimum requirement for data sets, called descriptors, which need to be provided for assignation of DOI.

Descriptors associated to the DOI in GLIS can be categorized as core descriptors and additional descriptors. Core descriptors are data sets which are essential for GLIS to perform its main functions. Parts of the core descriptors are fundamental for assignation of DOI (mandatory descriptors), while others should be provided if available (highly-recommended descriptors) to get the advanced functions of GLIS. On the other hand, additional descriptors are complementary data sets which can be relevant depending on some values inputed in the mandatory descriptors (Alercia et al. 2018).

DOI Registration of PGRFAs

In general, there are 3 methods to do DOI registration i.e. manually on the GLIS web site (suitable for small collections or editing), using Excel tables (for medium size collections), and using the XML protocol (for all types of collections). Manual registration through website supports registration and update, whereas Excel tables supports registration but not update.

Contrary to manual registration and Excel batch registration options, the XML protocol offers greater flexibility. It supports

registration and update, offers a system-to-system integration option, contains simple message structure, easy to implement and maintain, reduces human errors and minimizes human intervention. This method also has an extensive data validation and reporting feature, with very fast running time during the execution (over 3 messages per second). Nevertheless, stakeholders are welcome to implement their own software layer, or adopt the Toolkit to minimize the effort.

Assignation of DOI to PGRFA typically involves the following steps (Kurniawan et al. 2019):

1. Installation of the Toolkit in a local machine and configure it. The latest version of Toolkit v2.0.3 offers much simpler procedures for installation and configuration. The configuration includes creation of a local database to be used for storing PGRFA data to be uploaded into GLIS and obtain DOI after the registration is successful.
2. Installation of supporting software. The Toolkit is a Java-based application; therefore, it needs Java Runtime Environment to run properly. The other essential software is database management software such as DBeaver or My SQL Workbench. That software is all opensource and can be freely downloaded from their official websites.
3. Data preparation in a standard datasheet in Excel format. All required data regarding PGRFA is compiled and has to be inputted according to the standard datasheet.
4. Data importing and mapping. Data importing is conducted to move the validated PGRFA data from Excel format into the local database managed by the Toolkit. Data mapping is conducted as it is necessary for the additional data to be moved into particular tables in the database.

5. Deploying the Toolkit and starting to upload the PGRFA data for DOI registration.
6. Store the registered DOI for PGRFA into local database.

Integration-Toolkit Development and Dissemination

The Integration Toolkit, henceforth abbreviated as Toolkit, was developed to help those unwilling or unable to implement their own XML solution and implement the XML message processing. The Toolkit uses JDBC database as data source and destination, giving it more flexibility to manage PGRFA datasets as well as obtained DOI. The Toolkit is also expected to become a bridge to guarantee compliance with GLIS XML Protocol and compatibility with any future GLIS updates such as transfer transaction and SMTA reporting.

The Toolkit comprised two main components: the database containing the information to be provided to GLIS and for storing the responses from GLIS and the XML communication layer that formats the information in the database into XML messages that GLIS can accept and respond to. It is important to note that the Toolkit performs no validation on the data that are read from the database, so mistakes like duplicate materials will be processed as well. If there is any error, it will be GLIS that will return the corresponding error messages.The initial version of Toolkit v1.0.0 was released in 2017. Testing of the Toolkit was carried out at IRRI, Los Banos, Philippines in October-November 2017. Two ICABIOGRAD staffs worked together with staffs from IRRI's Crop Research Informatics Laboratory. During the testing of the Toolkit, a total of 849 accessions of Indonesian rice were registered to obtain DOI.

After the Toolkit testing and implementation in IRRI, a newer version of Toolkit v1.0.1 was released. Toolkit v1.0.1 was disseminated at the 1st DOI International Training Course in Bogor, Indonesia, at 23 April – 1 May 2018. In this training course, 16 participants from 7 countries (Indonesia, Malaysia, Philippines, India, Bhutan and Zambia) were present. The training aimed to socialize the Toolkit v1.0.1 software for batch-registration of DOI on rice accessions. During the training, registration of DOI rice collections from each participating country was also conducted. It is expected that the DOI registration of rice collections will continue to be carried out by each participant after they returned to their respective institutions. Some participants still encountered problems during the implementation of Toolkit v1.0.1. There were two common problems faced by the participants during the implementation of DOI registration using Toolkit v1.0.1:

1. Toolkit v1.0.1 can only be run in Linux operating system and some of its supporting software demand very high storage space and computer memory capacity
2. Toolkit v1.0.1 is executed by using command prompts, which is quite difficult to understand for common genebank managers.

However, all participants were satisfied and appreciated the training course program. DOI is a new system to be implemented in rice germplasm management and exchange, and this was the first technical training course which provides very technical knowledge on how to assign and manage DOI to support the management and exchange of rice germplasm. Although some participants encountered problems during the training and did not successfully assign DOI to their rice accessions, they continued the registration after the training. Resource persons from ICABIOGRAD and IRRI continued to provide technical

assistance to participants from all participating countries. Later, the Toolkit has been improved to overcome the complicated configuration and high resources requirement. The newest version (Toolkit v2.0.3) was released in 2018, and it had been successfully disseminated at the second DOI International Training Course in Yogyakarta, Indonesia from 26 April-3 May 2019. In this training course, 14 participants from 8 countries (Indonesia, Bangladesh, Pakistan, Myanmar, Cambodia, Lao PDR, Sri Lanka and Burundi) were present.

Registered DOI Achievement of Participating Countries

Currently, 8.419 accessions of PGRFAs from 13 countries have been assigned DOI. Detailed breakdown of the number of PGRFA accessions from each participating country is presented in Table 1 and Table 2. So far, Indonesia has registered as many as 1.369 PGRFA materials to obtain DOIs. Registration was done in 2017 (849 accessions), 2018 (351 accessions) and 2019 (169 accessions). In 2019, non-rice crops such as sweet potato, cassava, pigeon pea, banana, forages, citrus and maize were also included for the registration.

Since ICABIOGRAD is considered as the National Focal Point for PGRFA management in Indonesia, DOI registration of PGRFA collections from all domestic institutions is done under the coordination of ICABIOGRAD. Most of the PGRFA material is stored in the Genebank of ICABIOGRAD-IAARD, and some of them were contributed by other institutions under the IAARD, i.e.:

1. Assessment Institute for Agricultural Technology (AIAT) of Central Kalimantan (96 accessions of rice).
2. Assessment Institute for Agricultural Technology (AIAT) of East Kalimantan (10 accessions of rice).
3. Assessment Institute for Agricultural Technology (AIAT) of South Sumatera (55 accessions of rice).
4. Assessment Institute for Agricultural Technology (AIAT) of Yogyakarta (55 accessions of rice).
5. Assessment Institute for Agricultural Technology (AIAT) of West Nusa Tenggara (4 accessions of rice).
6. Indonesian Center for Rice Research (ICRR) (14 accessions of rice).
7. Indonesian Legumes and Tuber Crops Research Institute (ILETRI) (12 accessions of pigeon pea).
8. Indonesian Tropical Fruits Research Institute (ITFRI) (10 accessions of banana).
9. Indonesian Research Institute for Animal Production (IRIAP) (18 accessions of forages crops).
10. Indonesian Citrus and Subtropical Fruits Research Institute (ICSFRI) (12 accessions of citrus).
11. Indonesian Cereals Research Institute (ICERI) (20 accessions of maize).

Table 1. Registration status of participating countries after the first DOI training in 2018.

Country	WIEWS	Institution	Registered DOI		Crop
			During training	After training	
Indonesia	IDN179	Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development (ICABIOGRAD)	262	20	Rice
	IDN179	Assessment Institute for Agricultural Technology (AIAT) of Central Kalimantan	96	-	Rice
	IDN179	Assessment Institute for Agricultural Technology (AIAT) of South Sumatera	55	-	Rice
		Assessment Institute for Agricultural Technology (AIAT) of East Kalimantan	0	10	Rice
	IDN179	Assessment Institute for Agricultural Technology (AIAT) of Yogyakarta	0	55	Rice
		Assessment Institute for Agricultural Technology (AIAT) of West Nusa Tenggara	0	4	Rice
Zambia	ZMB048	National Plant Genetic Resources	60	269	Rice
Philippines	PHL158	Genetic Resources Division (GRD), Philippine Rice Research Institute (PhilRice)	0	1.016	Rice
India	IND001	Indian Council of Agricultural Research, National Bureau of Plant Genetic Resources	1.513	-	Rice
Malaysia	MYS005	Program of Genetic Resources and Germplasm Conservation Management (GB1) Genebank Seed and Centre, MARDI	0	708	Rice
Bhutan	BTN026	National Biodiversity Centre, Ministry of Agriculture and Forests	60	-	Rice
Total			1.895	2.082	

Table 2. Registration status of participating countries after the second DOI training in 2019.

Country	WIEWS	Institution	Registered DOI		Crop
			During training	After training	
Indonesia	IDN179	Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development (ICABIOGRAD)	5	30	Rice
			12	-	Sweet potato
			6	-	Casssava
	IDN179	Indonesian Legumes and Tuber Crops Research Institute (ILETRI)	12	-	Pigeon pea
	IDN179	Indonesian Tropical Fruits Research Institute (ITFRI)	10	-	Banana
	IDN179	Indonesian Research Institute for Animal Production (IRIAP)	18	-	Forages
	IDN179	Indonesian Citrus and Subtropical Fruits Research Institute (ICSFRI)	12	-	Citrus
	IDN179	Indonesian Cereals Research Institute (ICERI)	20	-	Maize
	IDN179	Indonesian Center for Rice Research (ICRR)	14	-	Rice
	IDN179	Agro-technology Innovation Center, Gadjah Mada University (AIC-GMU).	5	-	Bean
			5	-	Winged bean
			5	-	Yard long
			5	-	bean
			5	-	Snow pea
			5	-	Eggplant
					Pumpkin
Bangladesh	BGD002	Genetic Resources and Seed Division, Bangladesh Rice Research Institute (BRRI)	70	-	Rice
Lao PDR	LAO018	Rice Research Center (RRC), National Agriculture and Forestry Research Institute (NAFRI)	47	393	Rice
Sri Lanka	LKA036	Plant Genetic Resources Center (PGRC)	94	3.402	Rice

Table 2. Continue.

Country	WIEWS	Institution	Registered DOI		Crop
			During training	After training	
Pakistan	PAK001	Plant Genetic Resources Program, Bio-resources Conservation Institute, National Agricultural Research Centre (NARC).	50	-	Rice
Cambodia	KHM010	Cambodian Agricultural Research and Development Institute (CARDI)	10	-	Rice
Burundi	BDI016	Burundi Genebank (BGB), Institut des Sciences Agronomiques du Burundi (ISABU)	188	-	Rice
Myanmar	MMR015	The Seed Bank of Myanmar Department of Agricultural Research (DAR)	49	-	Rice
Total			617	3,825	

ICABIOGRAD (Indonesia), PhilRice (Philippines), MARDI (Malaysia), RRC-NAFRI (Lao PDR) and PGRC (Sri Lanka) are the most active gene banks who continue to assign DOI to their PGRFA collection after the training courses. The PGRFA materials that have been registered so far from those gene banks are 1.369 accessions (ICABIOGRAD), 1.016 accessions (PhilRice), 708 accessions (MARDI), 440 accessions (RRC-NAFRI), and 3.496 accessions (PGRC). There are also 30 vegetable accessions (5 accessions each of bean, winged bean, yard long bean, snow pea, eggplant and pumpkin) being registered, which are managed by Agro-technology Innovation Center, Gadjah Mada University (AIC-GMU).

Concluding Remarks and Future Perspective

DOI system is very useful to be implemented in germplasm collection management and exchanges. Therefore, it should also be implemented for other crops in the gene bank collection. Some accessions of non-rice crops from ICABIOGRAD-IAARD Indonesian genebank had been successfully registered for DOI during the project implementation. The DOI system and the Toolkit have been disseminated to 13 participating countries from Asia and Africa. However, there is still a great chance to expand it to more participating countries in the future.

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GENOMIC INFORMATION AS A POTENTIAL DESCRIPTOR OF GENETIC RESOURCES

Dani Satyawan

INTRODUCTION

Object identifier is an essential requirement in the management of genetic resources collection, as it provides information regarding the identity of each accession for both genebank managers and users. The digital object identifier (DOI) project aims to create a global standard in identifying plant genetic resources for agriculture (PGRFA) and provides a link between information that are available for a material and that material stored in a collection (Alercia et al. 2018). Currently, DOI contains several mandatory descriptors regarding taxonomic identity, date and method of procurement, as well as the location of the collection. Additional descriptors can also be added, but at the moment the suggested descriptors mostly contain geographical information.

While useful in multiple ways, geographical information quite often is just a snapshot of the current whereabouts of a PGRFA. This is because many PGRFA were introduced materials instead of native plants that evolve over a long period of time in a particular location. The absence of good record-keeping in many

locations means that PGRFA exchange and introduction were often unnoticed. Thus, it is possible that materials collected from distant areas are actually closely related, which reduces their utility to be used as parental lines in breeding programs due to their low genetic diversity.

For breeding applications, geographical information can be useful in breeding programs for specific locations, such as drought-prone high altitude lands, swampy lands, and natural habitats of specific pathogens. However, geographical descriptor typically focuses on aiding in finding a location rather than providing agronomically relevant information about that location. Thus, breeders interested in materials adapted to certain environmental types will need to do more work to obtain the environmental characteristics of certain geographical locations.

Another notably useful type of information for breeders that are also absent in the descriptor is phenotypic information. This is understandable because phenotypic data is greatly influenced by the environment where they are scored. Thus, a good performance in one environment is not always a good predictor of similarly good performance in another location. This inconsistent nature makes it an unreliable identifier. The number of phenotypic characteristics that can be scored reliably is also limited, which means that a lot of PGRFA will have the same phenotypic descriptions. Hence, phenotypic data alone will not be able to function as unique identifiers for PGRFA.

On the other hand, genotypic data in the form of DNA sequence information can serve as a better identifier and descriptor. DNA sequence variation is the underlying cause of phenotypic variation, which is of great interest to plant breeders and farmers. Using recent advances in genomics research, it is possible to predict the phenotypes of a PGRFA at a reasonable accuracy using its DNA sequences (Hickey et al. 2017). The

number of DNA variation in the genome of an organism is also more abundant, making it easier to find sequences that are unique and can be used as identifiers for individual PGRFA. The cost of DNA sequencing also tends to decrease while the genome's function becomes better characterized as time progresses (Van El et al. 2013), making DNA information more attractive as future descriptors and identifiers for PGRFA collection. This review discussed the capacity of current knowledge in genomics to be used as a descriptor and identifier of PGRFA, the technical challenges that need to be considered, as well as expected progress that can promote the utilization of genomic data in PGRFA management.

Current Capabilities of Genome Analysis

The cost of whole genome sequencing has gradually decreased and the choice of sequencing technology has expanded in recent years. As a result, many institutions have assembled high quality reference genomes for economically important PGRFA (table 1). High quality references are important because current sequencing technologies have not been able to read a complete plant genome uninterrupted from start to end. Reference genomes are usually assembled from overlapping short reads, which produces gaps in a large part of the genome, especially in highly repetitive regions in the chromosomes (Alkan, Sajjadian and Eichler 2011). Recent genome assemblies typically combined high quality short reads with long reads sequencing technologies to minimize missing sequences and better sequence fidelity across the whole genome (Shi et al. 2016).

Once a reference genome is assembled, the genome sequences of other accessions from the same species can be read more easily as their sequences can be deduced from their alignment with the

reference genome. Consequently, many institutions have now sequenced a large number of PGRFA collections. One notable example is the 3000 rice genome project at the International Rice Research Institute, which sequenced 3048 rice accessions obtained from all over the world in IRRI genebank collection (Li, Wang and Zeigler 2014). The resulting sequence data was subsequently used to deduce the phylogenetic relationship among all of the accessions, and can be used as a context and reference when more rice accessions are sequenced and analyzed (Wang et al. 2018).

Table 1. List of crops with assembled reference genomes by 2013 (Michael and Jackson 2013).

Scientific name	Common name	Year	Chromosome (#)	Size (Mb)	Assembled (%)	Gene (#)	Journal	PMID
Oryza sativa	Rice	2005	12	389	95	37544	Nature	16100779
Populus trichocarpa	Black cottonwood	2006	19	485	84	45555	Science	16973872
Vitis vinifera	Grape	2007	19	475	103	30434	Nature	17721507
Carica papaya	Papaya	2008	9	372	99	28629	Nature	18432245
Sorghum bicolor	Sorghum	2009	10	818	90	34496	Nature	19189423
Zea mayes	Maize	2009	10	2300	89	32540	Science	19965430
Glycine max	Soybean	2010	20	1115	87	46430	Nature	20075913
Ricinus communis	Castor bean	2010	10	320	102	31237	Nature Biotechnology	20729833
Malus x domestica	Apple	2010	17	742	81	57386	Nature Genetics	20802477
Jatropha curcas	Jatropha	2010	NA	380	75	40929	DNA Research	21149391
Theobroma cacao	Cocoa	2011	10	430	76	28798	Nature Genetics	21186351
Fragaria vesca	Strawberry	2011	7	240	87	34809	Nature Genetics	21186353
Phoenix dactylifera	Date palm	2011	18	658	58	28890	Nature Biotechnology	21623354
Solanum tuberosum	Potato	2011	12	844	86	39031	Nature	21743474
Cucumis sativus	Cucumber	2011	7	367	88	26587	PlosOne	21829493
Brassica rapa	Chinese cabbage	2011	10	485	59	41174	Nature Genetics	21873998
Cannabis sativa	Hemp	2011	?	820	96	30074	Genome Biology	22014239
Cajanus cajan	Pigeon pea	2011	11	833	72	48680	Nature Biotechnology	22057054
Solanum lycopersicum	Tomato	2012	12	900	84	34727	Nature	22660326
Cucumis melo	Melon	2012	12	450	83	27427	PNAS	22753475

Table 1. Continue.

Scientific name	Common name	Year	Chromosome (#)	Size (Mb)	Assembled (%)	Gene (#)	Journal	PMID
Linum usitatissimum	Flax	2012	15	373	85	43484	Plant Journal	22757964
Musa acuminata malaccensis	Banana	2012	11	523	90	36542	Nature	22801500
Gossypium raimondii	Cotton D	2012	13	880	88	40976	Nature Genetics	22922876
Azadirachta indica	Neem	2012	NA	364	NA	20169	BMC Genomics	22958331
Hordeum vulgare	Barley	2012	7	5100	98	30400	Nature	23075845
Citrullus lanatus	Watermelon	2012	11	425	83	23440	Nature Genetics	23179023
Triticum aestivum	Wheat	2012	21	17000	22	94000	Nature	23192148
Gossypium raimondii	Cotton D	2012	13	880	84	37505	Nature	23257886
Prunus mume	Chinese plum	2012	8	280	85	31390	Nature Communication	23271652
Pyrus bretschneideri	Pear	2013	17	527	97	42812	Genome Research	23149293
Cicer arietinum	Chickpea	2013	8	738	72	28269	Nature Biotechnology	23354103
Hevea brasiliensis	Rubber tree	2013	18	2150	52	68955	BMC Genomics	23375136
Prunus persica	Peach	2013	8	265	86	27852	Nature Genetics	23525075
Aegilops tauschii	Wheat DD	2013	7	4360	97	43150	Nature	23535592
Triticum urartu	Wheat AA	2013	7	4940	94	34879	Nature	23535596

Using association analysis, DNA segments that correlate with several important traits were identified (Huang et al. 2012). In the future, as this kind of information and the results of individual gene function studies accumulate, they can be used as the basis to predict traits using DNA sequence data. Many research groups are currently developing prediction algorithms that utilize such data in conjunction with DNA variation data (Spindel et al. 2016). Some of those predictive algorithms were even deemed good enough to be used in breeding programs to aid or even replace physical evaluation in the field (Heffner et al. 2010). Breeders and farmers who try to find plant accessions that carry certain traits

will be able to use such algorithms to select potential parental candidates among thousands of materials stored in genebanks.

DNA sequences also carry information that can be used to identify the organism that carry the DNA (Čandek and Kuntner 2015). Several toolkits were developed to identify the taxonomic identity of an organism based on the DNA sequence of parts of its genome (Liu et al. 2017). The availability of whole genome sequences enable this analysis to not only identify which species the sample belongs to, it even indicates the population and families the sample is most closely related to. Using whole genome sequence data from more than 3000 well-characterized rice accessions from IRRI as reference points, it is now possible to predict the origin and subpopulation of recently sequenced rice accessions, as well as elucidate their pattern of genetic admixture and ancestry (Wang et al. 2018). This will be useful when intellectual property dispute arises from the utilization of genetic resources.

DNA sequence data can also be used to overcome a common problem experienced by genebanks, namely the presence of redundant and duplicated samples. Such problem arose because plant variety exchange is relatively common across many regions, which means that several plants cultivated in different areas under different cultivar names are actually the same plant material. Lack of proper documentation system and sample maintenance management also often cause mislabeling of genebank accessions. Duplicated samples increase the cost of genetic resource maintenance while offering little value for those interested in utilizing genebank collection. DNA sequence data can easily identify and eliminate such accessions, thus improving the efficiency of genebank management (Singh et al. 2019).

Challenges of Incorporating Genomic Information

Although genomic information has several intrinsic advantages, its application as descriptors or passport data presents some new challenges for the systems that are currently used in most genebanks. For a start, the size of genome information is significantly larger than the data currently inputted as descriptors in genebank database system. Such large information necessitates the use of specialized computers, network, and software to ensure smooth and immediate access of the DNA information. All of those equipments can represent a significant investment that is out of reach for most genebanks. Fortunately, specialized cloud computing platforms and network providers that can handle such demand is becoming more ubiquitous and hopefully will become more economically viable for genebanks in the immediate future (Langmead and Nellore 2018).

Alternatively, genomic DNA variation data can be compressed by focusing only on DNA sequences that are different from the reference genome sequence. Trait variations arise from DNA sequences that are different between each accession, and even in different species like humans and bonobo DNA sequence variations only account for less than 2% of the genome (Prüfer et al. 2012). Thus, a large portion of the genomic data that are identical in all members of the species can be excluded to reduce the size of incorporated genomic DNA data. However, exclusive use of variable DNA sequences also necessitates the inclusion of sequence coordinate data to provide information regarding the location of the DNA variation. Those coordinate data can also significantly increase file size and add another type of data that computers need to read and decipher.

Another potential hurdle is that DNA information is relatively opaque and specialized software is required to translate DNA sequence data into more useful information, such as sample identity and potential ability to express useful traits. Currently, there is no single software that can provide all of that information from DNA sequence data, as most available softwares were designed to do specific types of sequence analysis. Genebanks intending to provide DNA analysis services therefore must also provide various DNA analysis programs and provide support to their users on how to operate that software. This can create a significant burden as some of those software also require specific training to operate and specific computer hardware to run (Schneider et al. 2010).

Potential users with no background knowledge in bioinformatics may also feel discouraged when faced with complex software and analysis pipelines. Current software that can predict traits from DNA sequence data also cannot do so in a highly accurate manner (Spindel et al. 2015). Although it can still be useful in some applications, the inaccuracy can be problematic for some crops that are expensive to maintain as every mistake represents a significant investment loss for the recipient. However, as the function of each part of the genome is gradually being elucidated, it can be expected that the prediction accuracy will improve in the future. This of course assumes that such studies will be funded in the future, while in reality not all crop species are allocated sufficient funding for even basic genetic research. A lot of less popular tropical crops do not yet have proper reference genomes and have rarely been the subject of genetic studies. For such orphaned crops, DNA information usefulness may come further away in the future.

Expected Progress in the Field of Genomics

It is clear that a reference genome is needed for maximum utilization of genomic information. The good news is that aside from the ever-decreasing sequencing cost, new sequencing technologies have also been developed which greatly assist in reference genome assembly, such as long read sequencing technologies and optical mapping (Dong et al. 2013; Rhoads and Au 2015). Higher quality reference genomes had been generated using combinations of sequencing technologies at a quicker pace and lower cost, which improves the chance that even orphaned crops will soon have their own high quality reference genomes. This had been initiated in the 1000 plant genome project, which sequenced only the genes or expressed portion of all DNA in the genome of 1000 plant species (Matasci et al. 2014). An even more ambitious project to sequence the full genome of 10.000 plant species, protists, and algae is also underway and is expected to be completed by the year 2023 (Cheng et al. 2018).

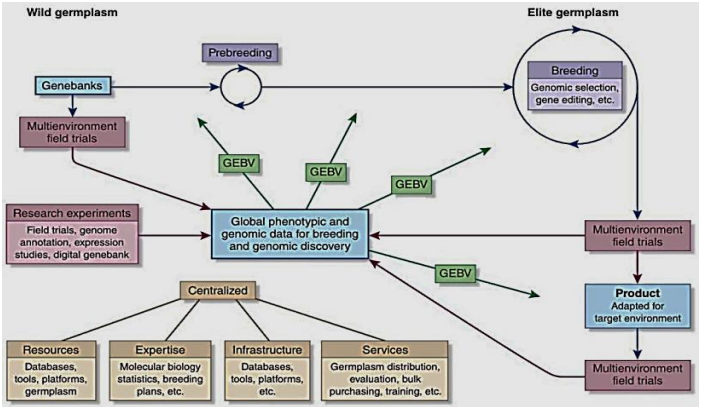

Figure 1. Proposed global framework for combining animal and plant breeding approaches to accelerate genetic gain through coordinated phenotyping, sequencing, genomic prediction, and genome editing (Hickey et al. 2017).

Those reference genomes will need to be accompanied by comprehensive annotation regarding the function of each segment of the genome. Thus, some forms of automation may be needed to complete such a massive undertaking (Cheng et al. 2018). The result may be rudimentary, but it will be a good foundation for researchers to perform genetic analysis later on. The inter-relatedness of all organisms on earth and the fact that DNA code is relatively universal also mean that data from one species sometimes translate well when applied to closely related species (Proost et al. 2009). Thus, software that predict trait from DNA information could be applicable not only to the species it was originally designed for, but also for other species related to that species.

On the software side, improvements need to be made on the usability, accuracy, and integration aspect. Hickey et al. (2017) proposed a global framework to integrate phenotypic and genomic data generated from coordinated research experiments to increase genebank utilization and incorporate genomic prediction into plant breeding programs (Figure 1). The approach also integrate best practices from animal breeding, such as selection based on genomic estimated breeding values (GEBV), to accelerate product generation in plant breeding. The collaborative aspect will also encourage standardization and consistency, which contrasts to the highly fragmented and specialized software development found in today's environment.

Lastly, the advent of genome editing technology will enable plant improvement that is based on genomic information without the need for physical genetic resources (Roa et al. 2016). When such technology becomes easy to implement, transfer of genetic information becomes more important than the genetic materials themselves. Consequently, genebanks may no longer need to keep as many collection of plant materials as they do today and

replace some of the collections with their genetic information instead. The use and management of DNA information are therefore inevitable and the sooner we figure out how to do it efficiently, the smoother the transition will be.

Conclusion

The use of genomic DNA information as one of the descriptors for genetic resources carries some intrinsic advantages that are beneficial for PGRFA management and utilization. Although currently available technology and infrastructure may prevent its effective implementation immediately, research progress in the field of computing and genomics can speed up its feasibility. Genomic information gradually becomes an important element in modern breeding programs and may eventually eliminate the need for seeds to be used as parental materials when genome editing technique becomes sufficiently advanced for regular applications. Consequently, genebanks need to start incorporating DNA information in their workflow to stay relevant and the formulation and adoption of DOI can be used as a starting point to develop such a system.

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CURRENT AND FUTURE OF DOI IMPLEMENTATION IN THE LAO NATIONAL GENEBANK

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INTRODUCTION

Lao national genebank (LNGB) is located in Phonthong village, Xaythany district, Vientiane capital, Lao People Democratic Republic (Lao PDR). LNGB was established in 1995 under The Rice Research Center of National Agriculture and Forestry Research Institute (NAFRI). It is the main genebank in Lao People's Democratic Republic (Lao PDR) which has function for seeds conservation in certain conditions. Recently, there are many crops conserving inside, such as rice, maize, sorghum and millet. Among those mentioned crops germplasm, rice is the biggest number as 14.000 accessions conserved in the genebank. Rice is a staple food of mostly peoples in the world (Mohanty 2013), and most people in Lao depend on it as their staple food and rice dominates agricultural production. Since 1995, NAFRI and International Rice Research Institute (IRRI) conserved all of rice accessions throughout the country.

During the collection, the genebank provided many accessions of rice for users. However, it is difficult to track the provided

samples from users. Therefore the Digital Object Identifier (DOI) now has been chosen as problem solver to provide a globally unique and permanent mechanism to track and identification of germplasms. DOI is a standardized alphanumeric string that is assigned by a registration agency and provides a persistent link to the location of information about the object on the internet (Paskin 2010). Digital object identifier (DOI) was first introduced to LNGB manager through the DOI Implementation training in Bali, Indonesia 2019. In this paper, we will describe the implementation of DOI in Lao National Genebank.

Collection and Conservation of PGRFA in the Lao PDR

Rice germplasm in Lao was started to explore for conservation and utilization in 1970s. Another 1000 rice germplasm were collected from 1991 to 1994 (Roder et al. 1996). IRRI regarded a set of 13.192 samples collected from 1995 to 2000 as being representative of the PGRFA throughout the country (Rao et al. 1996). However there was no genebank available in the country to conserve those genetic materials. National institutions of Lao in collaboration with international organizations have taken measures to identify and conserve valuable genetic material for future use. With the aid of international funding organization, ARC under NAFRI has initiated biodiversity programmes for several crops including rice. There is a joint project namely "Rice Biodiversity Project for Rice Germplasm Collection" between Lao's Ministry of Agriculture and IRRI called the Lao-IRRI project until 1993 (Thepphavong & Sipaseuth 2007).

The objectives of the Lao components of Lao-IRRI project were collect traditional rice varieties cultivated under diverse agroclimate conditions and under different ecosystems throughout the country, collect wild and spontaneous

interspesific hybrids between wild and cultivated forms of rice, preserve the collected wild and cultivated forms in appropriate storage facilities at NARCin Sythany Distric of Vientiane Municipality, conserve a duplicate set of the germplasm collection at the International Rice Genebank (IRG) at IRRI, and make the germplasm collection available for utilization in Lao PDR and elsewhere (Bounphanousay et al. 2000). The National Genebank was established in 1995. Collection of rice germplasm started in 1993 and lasted till 2000, and approximately 14.000 samples of rice germplasm were collected.

Distribution of Rice Germplasm to Users

There is big collection of rice germplasm throughout the country during 1993 to 2000, and the rice germplasm are not only conserved in the LNGB, but also in IRRI (Rao et al. 2006). Some of rice germplasms are conserved in the LNGB for future purposes, and some of them were provided to the users for research purpose (Table 1).

Current DOI Implementation

The current progress of DOI Implementation in the LNGB is there are 440 rice accessions were registered and obtained with DOI number (https://ssl.fao.org/glis/entity/search) since the genebank manager of LNGB was participated in DOI training in Bali, Indonesia in 2019. However, compare to the whole rice germplasm collection in the LNGB Genebank, only 2.9% accession registered in DOI system and 97.1% have not yet assign to DOI.

Table 1. Distribution of rice germplasm in the LNGB.

Users	Germplasm requested	Reference
1	Rice	Bounphanousay et al. 2008
2	Rice	Kanyavong 2012
3	Rice	Boualaphanh et al. 2011
4	Rice	Vilayheuang et al. 2016

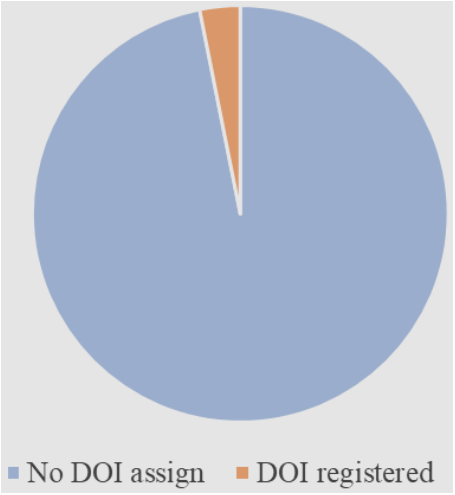

Figure 1. Showing the ratio between rice samples DOI registered and non-DOI.

Concluding Remarks and Future Perspective

In Lao PDR, most of food crops germplasm collections are conserved in the National Genebank. However, some of them were distributed to users and the germplasm tracking system was not yet available. Recently, 440 rice accessions were registered for DOI which could enable genebank to tracking on it. Even though, only few percent of number of accession registered compare to the whole collection, but it presenting the beginning of DOI

implementation in LNGB. In the future, all accessions of rice and other crops are planning to be registered. Thus, capacity building programmes both national and international for LNGB staffs should be considered in order to increase the implementation of DOI in LNGB.

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DIGITAL OBJECT IDENTIFIERS FOR EASY ACCESS OF INFORMATION AND EXCHANGE OF GERMPLASM

Min San Thein

INTRODUCTION

Myanmar is one of the centers of genetic diversity of rice and varietal group which spreads along the Himalayas from Iran to Myanmar consists of very diverse varieties (Glaszmann 1986). Some plants species exist in different pytopeographic regions with great antiquity and famous of its richness. However loss of crop genetic diversity for many reasons in the country has warned to conserve them in proper ways. At present more than 12000 accessions of different crop germplasms are being conserved in Myanmar Seed Bank. The diverse germplasm collection, however, are challenged for crop improvement through breeding programs for desirable traits in national level. Therefore exchange of germplasm and related information become crucial, and Digital Object Identifiers (DOI) can play a key role in this issue. By using the DOI standards, users will be able to identify and document their plant material uniquely and permanently, and will facilitate data interoperability among different systems (Alercia et al. 2018).

Germplasm Information in Myanmar Seed Bank

Myanmar Seed Bank (MSB) was established in 1990 by a grant of JICA of Japanese government and Myanmar government. During 1990-1992, a number of scientists from international organizations visited Myanmar to discuss further to explore for he compete of germplasn collection, conservation and management of plant genetic resources. Systematic genebank activities such as exploration, characterization, cold storage and database were started in 1997. Collections of landraces for different crops are used in collaboration of international organizations. Currently, a total of 8056 rice accessions along with other crop genetic resources (Table 1) are being conserved in *ex situ* collection in MSB (Annual Report 2019). At the beginning, information on data passport and characterization data is available only in hard copy catalogues. These limitations suggest a better management in the next period.

In 2009 the FAO Regional Project (GCP/RAS/240/JPN) has been designed for Strengthening Information on Plant Genetic Resources in Asia including MSB, called as National Information Sharing Mechanism Global Plan of Action (NISM-GPA). The website of NISM-GPA provides limited information related to plant genetic resources since they were not a big digitised data set like data passport and characterization data. Since Myanmar is a member of International Treaty on Plant Genetic Resources for Food and Agricultural (ITPGRFA), its participation should be inclusion of multilateral system by exchanging information and material of germplasm for food and agriculture. In this regard, huge data sets of rice and other crop germplasms conserved in the MSB should be available in the network of global genebanks. Collaboration between Myanmar with neighboring countries and developed countries are also important to achieve food security.

Table 1. Number of *ex situ* germplasm accessions in Myanmar Seed Bank (2019).

Sr. no.	Crop group	Number of accessions
1	Rice	8056
2	Legume	1578
3	Cereal	2238
4	Oilseed	800
5	Others	166
Total		12838

Training on Software Testing to Support DOI Implementation

To increase the capacitiy building, Myanmar participated in the 2nd International Training on Software Testing to Support DOI Implementation which was held in Yogyakarta, Indonesia during 26 April-3 May 2019. The training course lasted one week and was attended by genebank managers, database specialists and instructors from 8 countries (Figure 1). The participants have learned genetic resources related law, treaty such as ITPGRFA and Nagoya Protocol and have practiced installation of global information system (GLIS) toolkit v.2.0.3, operation of manual, input of huge data sets and software testing, finally have studied the implementation of DOIs then the registration of the data for exchanging information and germplasm material among genebanks. This training is beneficial for Myanmar particularly to support genetic resources management which could be involve in global information system.

Figure 1. Participants of the 2nd International Training on Software Testing to Support DOI Implementation on Rice Germplasm.

Global Information System for Germplasm Utilization

In the past, crop germplasms was managed at the genebank. Over the years, other systems such as EURISCO, SINGER and GRIN have been developed and integrated databases from various genebanks together with powerful tools for accessing and searching germplasm accessions information (Sebastian and Mackay 2009). At present, Global Information System (GLIS) comes into force of the ITPGRFA and it will contribute to access and benefit sharing of such information available to all contracting parties of the Treaty that can be as a user-friendly internet portal/gateway to information at the accession level (Quek 2009). Thus, near the future germplasm material and its related information will be easily accessed by the stakeholders of genetic resources.

Acknowledgment

The author would like to thanks the Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development (ICABIOGRAD), for inviting to participate in the 2nd International Training on Software Testing to Support DOI Implementation on Rice Germplasm that was held in Yogyakarta, Indonesia on 26 April – 3 May 2019.

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ROLE OF DIGITAL OBJECT IDENTIFIERS FOR NETWORKING AND MANAGING DATA TO AGRICULTURE BIODIVERSITY'S FUTURE

Bigirimana Jean Claude and Mbonihankuye Cyrille

INTRODUCTION

Burundi gene bank (BGB) was established in 2004, thus prior activities have been devoted on bringing together resources and skills needed for the genebank management. The main objectives of BGB are (1) to collect and conserve plant genetic resources of traditionally grown; (2) to strengthen scientific and technical capacities for the sustainable management of plant genetic diversity; (3) to establish and improve the use of data on plant genetic resources in Burundi; (4) to raise a public authorities' awareness on the importance on these resources in agricultural research plans to the national level and worldwide (ISABU 2009).

At more than one decade, data on Burundi plant genetic resources for food and agriculture (PGRFA) remain inaccessible for use by researchers and breeding programs worldwide. This is inconsistent with the objectives of the International Treaty on

Plant Genetic Resources for Food and Agriculture (ITPGRFA) on the use of genetic resources and the fair and equitable sharing of benefits derived from their use, in harmony with the Convention on Biological Diversity (CBD) for sustainable agriculture and food security. The challenge of BGB was not to be able for long time to share information to potential users on the actuality of PGRFA diversity. Even though plant materials were conserved, rational use has not been much facilitated. Due to lack of a reliable system for sharing descriptive information on biodiversity, information of PGRFA from scientific users has not been collected properly

International Cooperation on Plant Conservation

The Institut des Sciences Agronomiques du Burundi (ISABU) built a Genebank of Burundi (BGB) as recommended by the Government. It works in close collaboration with scientific and technical partners facilitated by international agencies which are involved in agricultural research.

At the beginning, funding was jointly provided by the Government for long-term and by the Swedish International Development Agency (SIDA) in short term. International funding was executed through EAPGREN (East African Plant Genetic Resources Network) covering Burundi, Eritrea, Ethiopia, Kenya, Madagascar, Rwanda, Sudan and Uganda. The collaboration work were with Nordgen (Nordic Genetic Bank-Sweden) which strengthened scientifically and technically network; Bioversity International; and Global Crop Diversity Trust (Bashaasha et al. 2010). BGB also collaborated with universities and multidisciplinary organizations involved in protection of the environment in national level. Importantly, Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and

Development (ICABIOGRAD) invited BGB to participate in the training for the Digital Object Identifier (DOIs) assignation to rice germplasm. Through this training, Burundi has been suggested to assign DOIs for plant accession to be accessed on global scale through FAO's Global Information System (GLIS) (https://ssl.fao.org/glis). This web portal provides user-friendly tools to develop a dynamic system of exchange and access to information. It helps researchers, breeders, farmers and other users to access the relevant scientific and technical information.

Profile of PGRFA Collections Conserved in the BGB

Since the BGB inception in 2004, there is significant progress in the inventory and collection of accessions of traditional food crop species across the country. These activities resulted in collection of 2044 accessions grouped in 43 species including 987 accessions of beans and 229 of sorghum in which the two crops have large traditional gene pools in Burundi. There are also 219 accessions of rice, 130 of maize, 143 of cassava, 204 of banana, 57 of groundnut, 67 of finger millet and 326 accessions for other species especially vegetables (Figure 1). Grains are then stored in freezers at-18°C (ISABU, 2018).

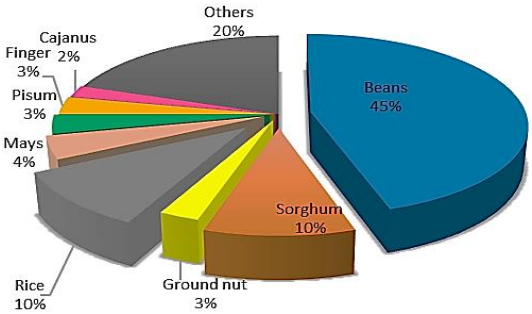

Figure 1. Proportions of seeds of several plant species stored in the Burundi Genebank

Germplasm accessions are duplicated and hermetically packaged in aluminium bags to be stored as active collections accessible at any time for studies and used for breeding programs. Copies of accessions have been sent to international gene banks as a security collection for long-term use. Burundi PGRFA collections are conserved in two international gene banks i.e. 439 accessions of 11 crops are kept at Svalbard Global Seed Vault (SGSV-Norway) and 283 accessions of beans are deposed at IITA (Nigeria). As many as 124 accessions of rice have been sent to Africa rice for molecular characterization (ISABU 2018). Diversity of vegetative propagated cultivars such as cassava, yam and taro are conserved on farm. These crops are used for food security and resilience to climate change as a result of their ability to drought adaptation (Bigirimana et al. 2016). Data of all these accessions have been recorded for long time and saved in Excel format and also identified by geographic coordinates.

Importance of the DOI Registration on Burundi Gene Bank: Case Study on Rice Germplasm

Burundi faced a problem on data documentation system. The lack of reliable digit data challenged the BGB for recording characterization in the safe way. The recording data with DOI could contribute to track and update data base on genetic resources and be consulted by scientific users around the world. Digitalization of genetic resources information is particularly an answer to the BGB gap.

Burundi's participation to training on DOI implementation in Indonesia in 2019 has enhanced the capacity building of its staff for improving and adjust database to provide comprehensive information to users. Registration on DOI addresses issues related to informations needed by curators, breeders for their

breeding programs, and researchers to support germplasm conservation and utilization. Sharing data from BGB with the Global Information System facilitates easy access of informations related to crops diversity for research activities and breeding programs. The digitalization database could be beneficial for:

- Gene bank managers: to evaluate and quantify the degree of variability among accessions in gene bank;
- Breeders: to grasp and use existing diversity to develop more effective breeding strategies and achieve the goals of producing high yield to feed current and future generations;
- The government*:* develop in partnership with farmers and other managers of plant genetic resources conservation priorities to maintain the diversity.

The training DOI implementation introduced the digital system for rice germplasm management for conservation and exchange purposes. Testing the software to support the implementation of DOI is focude on rice because this plant species is one of most important crop widespread around the world. The key topics developed were: (1) software installation and configuration of the toolbox; (2) data setting in conformity with required standard compatible with the toolkit; (3) Importing data from the adapted file; (4) application of toolkit V2.0.3 (on a GLIS test server); (5) Storing DOI Recording Results; (6) Error handling after registration (GLIS 2019). The training allowed each participant to establish and test the software through humble manipulations, improve database and DOI registration of accessions. Training manuals and GLIS toolkit V.2.0.3 for guidance in setting up and operationalization of the software were provided.

Progress on Documentation and Data Sharing on Burundi PGRFA

During 12 years of data recording, BGB had not yet found any electronic documentation network to share and consult data (ISABU 2018). Geographical coordinates and identity of preserved accessions were not available for various scientific uses and for agricultural development purposes. Data have been for long time non-exchangeable efficiently between BGB with any regional or international gene banks. The use of data sharing tool became a new and fascinating element for the BGB managers. A total of 188 accessions of rice have been assigned their DOI to be available online after the training held in Yogyakarta-Indonesia 2019 (https://glistest.planttreaty.org/glis/entity/list-own). This allows plant genetic resources users and providers to find more information on material transfer if necessary. Due to this new skill, two activities are underway of preparation in Burundi to increase a number of digitalized accessions: (1) Knowledge sharing session for the team in charge of managing BGB data and local collaborators; the experience sharing will focus on use of the software and the recording data on DOI and error handling; (2) An upgrading data on conserved germplasm, particularly missing information on PGRFA will be adjusted to facilitate future DOI registration.

Concluding Remark and Future Perspective

The Global Information sharing system on PGRFA offers easy access to information on PGRFA for research and breeding. Boosting the Big Data of PGRFA is a way to make data managers be aware on the use of digital object identifiers (DOIs) to find solution on problems related to the lack of information exchange on plant material. For Burundi, this approach can strengthens

cooperation in term of biodiversity conservation. Registration with the DOI of data from the BGB is likely to improve the profile of the BGB PGRFA. The software tested to support the DOI application will facilitate the documentation and data sharing in Burundi. Promoting the use of DOIs suitable for identifying plant genetic material around the world will be performed in Burundi.

As the ITPGRFA facilitates access and benefit sharing through the establishment of information and genetic resources exchange scheme in a multilateral system, the BGB plan to: (i) set the germplasm data of all food crops in use for food or conserved according to required standard for registration with DOI. Preparation will be completed on each crop to overcome the challenge of lack of documentation on Burundi PGRFA and information sharing weakness on plant material kept in BGB or on farm; (ii) to set up a specific team in charge of data processing once approved by the scientific committee of ISABU. The team will be in charge of data processing and boosting for sharing information on GLIS.

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PHILRICE GEMS DATABASE: ITS UPGRADE AND IMPACT

Malvin Duldulao, Marilyn Ferrer, Maria Cristina V. Newingham, Jonathan Niones, Xavier Greg Caguiat, Loida Perez, and Gabriel Romero

INTRODUCTION

Access to genetic resources and information held at genebanks are essential for current and future needs of rice improvement programs. Genebanks are responsible not only for the integrity of the samples they maintained but also with the data associated to the accessions (Richards and Volk 2015). The Philippine Rice Research Institute (PhilRice) Genebank serves as the national repository of 7.129 accessions of traditional landraces and other foreign-sourced rice genetic materials. It has enormous amount of data that was organized into a standard database format to enable strategic management for effective use and enhancement (Arlett et al. 2007). The Germplasm Management System (GEMS) was developed to facilitate access of information and to support complex processes in managing rice collections. It runs as a stand-alone database focused for internal use in the genebank operations. GEMS is also a central repository of all integrated data on passport, morpho-agronomic characterization, grain quality, pests, diseases, and abiotic stress reactions.

In order to optimize its use in rice conservation and management, it was upgraded into advanced version 'GEMS v2.0'. System architecture was redesigned, and new functions were added in synchronization with the current documentation needs of the genebank. This paper presents the significant impact of system upgrade from the perspective of genebank's operational efficiency

System Improvement

The overall architecture of GEMS was redesigned to cater system improvements: establishment of data validation rules and error-trapping mechanism, automation of procedures that covers the full range of activities in managing germplasm, implementation of barcode technology for seed inventories and distribution, and adaptation of Digital Object Identifier (DOI) for improved tracking of germplasm movement.

GEMS v2.0 is designed to document the two main operational procedures of the PhilRice Genebank: (i) genebank's management per se (acquisition, conservation, regeneration, inventory, and distribution), and (ii) germplasm management per se (passport, characterization, biotic, abiotic, and grain quality evaluation), which nested sub-operational procedures (Figure 1).

Figure 1. The sub-operational procedures in the genebank (a), and system architecture of GEMS v2.0 in stand-alone mode (b).

Genebank Operations

GEMS v2.0 serves as decision-support for genebank curators on daily operations to monitor seed inventory, determine regeneration priorities, generate germplasm status reports, and process germplasm requests. This transition ensures sufficiency of viable stocks and preservations of the germplasm's genetic integrity that would allow researchers and breeders to draw on a stable reference: a sample that would be, as much as possible, genetically unchanged since its storage (Peres 2016).

The inventory features of the GEMS allow proper documentation to monitor the quantity and viability of seeds to carry out regeneration and distribution. The system was designed to issue a warning as seed reaches critical level: below 50 grams in terms of amount and less than 85% in viability. It automatically highlights accessions to alert genebank curator to limit further distribution of such accessions until they are regenerated.

Inventory management adapted the barcoding system to eliminate labelling mistakes such as transposition of numbers which are common in hand-written labels. The most space-efficient linear symbol of Code 128 (subset C) was used as labelling paradigm. This machine-readable barcode label enables the system to acquire data via scanning seed packets thereby facilitating ease of updating seed stocks during seed distribution (Fig 2).

Seed and germplasm data requests processed primarily depending on the amount of seed stocks, viability status of the germplasm requested, and availability of information. This transaction requires the requestor to fill-up a "Request Form" and provide personal information, seeds/data to be requested, purpose and date of request, and acceptance to the Standard Material Transfer Agreement (SMTA) if applicable. All requests

has assigned tracking number and documented in the 'Requests' tab of the system.

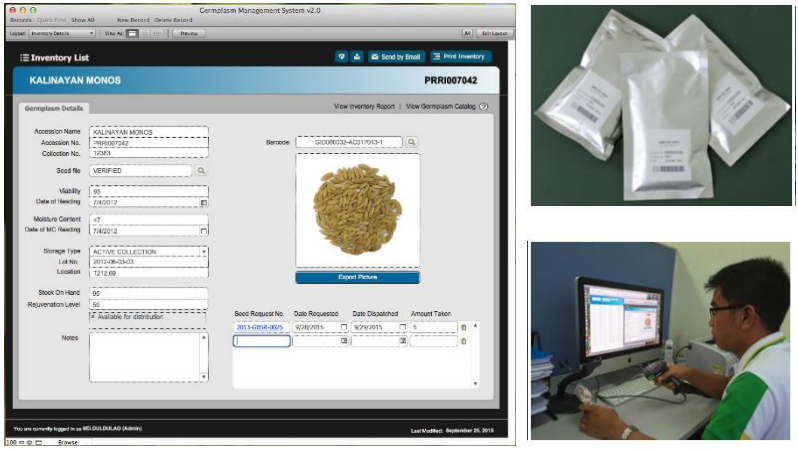

Figure 2. Scanning of seed packets with computer generated barcode labels.

Monitoring the use of PGR is one of the many responsibilities of genebank curators, but often this information is not reported or relayed back to the genebanks (Ruas 2017). GEMS v2.0 now provides capability to alert genebank curators to verify receipt of materials and record feedbacks after the expected time of delivery. Furthermore, the DOI-assigned germplasm will allow the use of material to be tracked, thus meeting the legal obligations of the SMTA and monitor the impact of genebank collections in utilization in research and breeding programs.

Germplasm Data

As part of data integrity checks, all data entry in the database is now executing validation rules for all parameters described for each germplasm collection. This mechanism ensures that dataset meets certain conditions before allowing it to commit the changes

in the system. It automatically intercepts encoding errors and warns the user that invalid entry has been entered, thus, integrity and accuracy of rice germplasm data is maintained.

Passport data includes basic information of the collected material (*e.g* accession name, collecting number, collecting date, name of collector/donor, and place and date of collection, etc). To identify individual samples, a unique germplasm identification (GID) and collection number were assigned when passport data is encoded in the 'Registration' tab of the GEMS v2.0. Some other basic information consisting of 36 descriptor states will be encoded in the 'Collecting Data' tab (Fig 3). The system was also adjusted and complemented with DOI through registration to the Global Information System of the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) comprising of 1.016 accessions.

In addition to passport data, the database also contains morphological-data based from standard rice descriptors published by Alercia (2011). To facilitate ease of data entry and data viewing, the 'Characterization Data' tab of the GEMS v2.0 was organized into two groups (quantitative and qualitative data) separated by three views for vegetative, reproductive and post-harvest data (Fig 3). This consists of 58 parameters essential to facilitate preliminary selections of end-users for direct use or as parental in breeding programs. The system has the capability to automate the selection of materials to be included in the planting plan during Wet Season (WS) trials. Auto-selection of entries is based mainly on availability of morpho-agronomic characterization data, seeds stock and viability.

Table 1. List of parameters gathered at different rice growth stages.

Rice growth stage		Descriptor		
Vegetative				
	1	Basal leaf sheath color	7	Leaf blade pubescence
	2	Leaf sheath anthocyanin coloration	8	Auricle color
	3	Leaf blade anthocyanin coloration	9	Collar color
	4	Leaf blade distribution of anthocyanin	10	Ligule shape
	5	Leaf blade intensity of green color	11	Ligule color
	6	Leaf blade attitude (penultimate leaf)	12	Flag leaf (early)
Early reproductive				
	13	Culm habit (angle)	23	Awn distribution
	14	Culm kneeing ability	24	Awn color (early)
	15	Culm anthocyanin coloration on nodes	25	Panicle main axis attitude
	16	Culm underlying node color	26	Panicle branches attitude
	17	Culm internodes anthocyanin	27	Panicle secondary branching
	18	Culm underlying internodes color	28	Panicle exertion
	19	Flag leaf attitude (late)	29	Culm lodging resistance (culm strength)
	20	Stigma color	30	Heading days
	21	Lemma and palea color(early)	31	Days to maturity
	22	Lemma color of apiculus (early)		
Harvest and post harvest				
	32	Panicle shattering	44	Flag leaf width (cm)
	33	Panicle threshability	45	Culm length (cm)
	34	Awn color (late)	46	Culm number per plant
	35	Lemma and palea pubescence	47	Culm diameter at basal internode (mm)
	36	Lemma and palea color(late)	48	Panicle number per plant
	37	Apiculus color (late)	49	Panicle length of the main axis (cm)
	38	Sterile lemma color	50	Awn length (cm)
	39	Caryopsis: pericarp color	51	Sterile lemma length (mm)
	40	Endosperm type	52	Spikelet fertility
	41	Leaf length (cm)	53	Grain length (mm)
	38	Sterile lemma color	54	Grain width (mm)
	39	Caryopsis: pericarp color	55	Grain weight of 100 grains (g)
	40	Endosperm type	56	Caryopsis length (mm)
	41	Leaf length (cm)	57	Caryopsis width (mm)
	42	Leaf width of blade (cm)	58	Caryopsis shape (length/width)
	43	Flag leaf length (cm)		

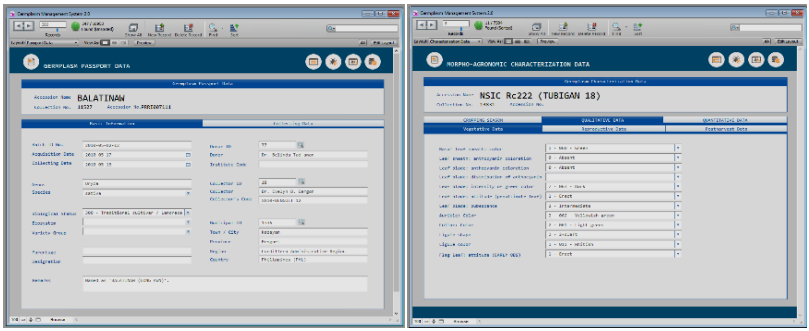

Figure 3. Passport and morpho-agronomic data tab of GEMS v2.0.

Grain quality evaluation is one of the primary considerations for both consumers and breeders which will be encoded under 'Grain Quality Data' tab (Fig 4). This consist of data on milling recovery, physical attributes and physicochemical properties of the grain covering 14 parameters based from the grain quality classification on National Cooperative Test (NCT) Manual for Rice (2014).

Germplasm evaluations on abiotic and biotic stresses are significant in identifying resistant cultivars under unfavourable conditions. Data from the evaluation of germplasm against important biotic and abiotic stresses are to be encoded in the 'Stress Evaluation' tab (Fig 4).This was categorized into four categories namely: bacteria (rice blast, bacterial leaf blight), virus (sheath blight, rice tungro induced, rice tungro field reactions), insect pests (brown planthopper, green leafhopper, stemborer) and abiotic stresses (zinc, drought, salinity).

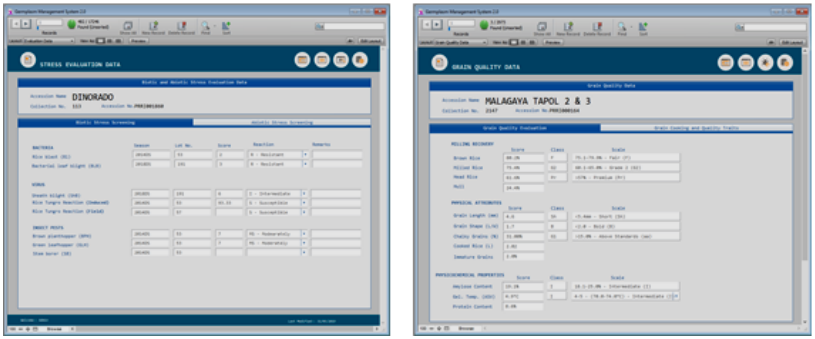

Figure 4. Grain quality and stress evaluation data tab of GEMS v2.0.

The GEMS v2.0 was upgraded from FileMaker 4.0 (FM4.0) into a new cross-platform relational database-FileMaker Pro 12 Advanced and can be accessed internally upon request. The choice of using FileMaker software was prompted due to the previous data loss of in the Windows PC-based programs being plagued by software virus. As a commercial package, FileMaker Pro has extensive documentation (http://www.filemaker.com) and continually offers other features such as searching and report generation.

Corrections and changes will inevitably make in any database (McLaren et al. 2005). GEMS v2.0 has administration controls which allow assigning specific privileges to users. The system administrator has the 'admin privilege' and has the overall control to the system, while users have 'read-write privilege' that can modify but cannot delete records. Every change in a record is logged at 'System Logs' tab and can be undone if required. This feature protects the system from unauthorized modifications and possible security risks.

Concluding Remarks and Future Perspective

A new version of PhilRice Genebank in-house documentation system called 'GEMS v2.0' was launched in 2017. System upgrade was done wherein data validation was performed to ensure that system coding and source data migrated successfully. GEMS v2.0 with new system functions and user interface delivers significant impact in the genebank operational efficiency. Efforts are continuously being done to improve its data content and to ensure high quality germplasm data. To date, the web-based version of GEMS v2.0 is in alpha-testing and expected to access within the domain of PhilRice network by October 2019. Through this online interface, researchers and breeders can access information about the characteristics of rice varieties for rice varietal improvement programs.

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MARDI AGROBIODIVERSITY INFORMATION SYSTEM (AGROBIS) TO SUPPORT GENETIC RESOURCES FOR FOOD AND AGRICULTURE (PGRFA) CONSERVATION IN MALAYSIA

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INTRODUCTION

Malaysia is rich in biological diversity, harboring some 185000 species of fauna, more than 15000 species of flowering plants. Of about 1500 genera to be found are over 2500 tree species, 3000 species of orchids, 500 species of ferns, 60 species of grasses and bamboos, and many others (Abdullah et al. 2015). However, only a handful of the 15000 species has been utilized for food production. It has been reported that only about 300 species native to the country have been exploited and utilized (Ali et al. 2017).

Being the lead agency in spearheading the agricultural technology development in the country, MARDI has been identified as the national focal point for research and management of agrobiodiversity since the year 1996 (Abdul Shukor et al. 2013). Since then, Management and Utilization of Biological Resource Programme under the Strategic Resource Research Centre of MARDI have been given the task to undertake the national responsibility in the conservation, characterization, evaluation and utilization of crop genetic resources (Nordin et al. 2011). Genebank and Seed Centre were established after MARDI restructuring. The Management of Genetic Resources and Germplasm Conservation Program have been established to coordinate the management of genetic resources and germplasm at MARDI. Now, the management of all seed and germplasm collections at MARDI stations throughout the country is under the supervision of Agrobiodiversity & Environment Research Centre. The main objective within the programme is to mitigate the loss of agrobiological resources in the country through their judicious management and utilization in support of sustainable national food and agriculture development. In addition, the other functions of the programme are to gather and disseminate information on the nation's agrobiodiversity; to conduct research and development in areas relevant to management and sustainable utilization of agrobiological resources and to position MARDI as the national reference center for agrobiodiversity.

MARDI Initiatives on PGRFA Information Systems

Malaysia in implementing the Convention on Biological Diversity (CBD) that ratified in 1994 and currently, to support the Sustainable Development Goals (SDGs), always works on strategies in order to have adequate information on our biodiversity online. Agrobiodiversity research in MARDI, as a

subset of biodiversity, generates great volumes of data. It comprises data from PGRFA, Animal genetic resources for food and agriculture (AnGR), and arthropods of importance to agriculture and microbial culture collection. In addition, this information is important for government at all levels, and also needed by users of the agricultural sectors, such as researchers, farmers, seed companies and education institutions. As a part of our National Biodiversity Strategies and Action Plans (NBSAPs), accessible information on this is online.

As for PGRFA particularly, in MARDI's genebank, researchers actively regenerate and multiply seeds, as well as screen PGRFA materials for different characteristics. These activities generate huge data. Before the year 2000, this data was not disseminated extensively and therefore the data was not accessible to breeders who are working for improving genetic resources. The information on characterization and evaluation work were normally kept only as hard copies, otherwise on the researcher's computer. MARDI realizes that was about time to supply this information and needs to develop its own information systems.

In 2002, MARDI has established Rice GeneBank Information System (RGBIS) and the system was developed for MARDI Rice Genebank operations. Subsequently, several individuals stand-alone were developed using Microsoft Access and Visual Basic 6 interface, such as *Nephelium lappaceum* (rambutan), *Mangifera odorata* (kuini), medicinal plants, arthropods and microbes. This database was a stand-alone database because of researchers involved wanted to protect unique characters of each agrobiodiversity group, especially for the plant group.

MARDI then developed a database information system known as MARDI Agrobiodiversity Information System (AgrobIS). The development of AgrobIS was taking into account that MARDI had several separate databases for specific projects or collections.

Apart from non-centered systems, these separate databases also make it difficult to access information. AgrobIS supports multiple collections of different datasets by using object-hierarchical design to enable inter-relational between each of agrobiodiversity components even with different data format such as a database, pictures and geographical data.

PGRFA data in AgrobIS do not follow the Multi-Crop Passport Descriptors (MCPD) because the data provider involved in the AgrobIS development is suggested for a system that enables them to develop their own descriptors based on the descriptors by IPGRI (Bioversity International). The central reference of the AgrobIS for PGRFA is the accession which is an anchor for the information belonging to the species. To give an impression about the scope of AgrobIS, the most important categories of Figure 1 is briefly described Tosiah (2013) as follows:

1. Passport data – contains basic information of the collection, such as, accession number, collector's name, collection date, cultivar name, and donor name
2. Environment and site – consist of data or information on sites where the accession is collected
3. Management – consists of information on how the collection being managed, duplicated area, preservation techniques and other related information
4. Characterization – data and information on characters of vegetative growth, leaf, inflorescence, fruits and seeds
5. Evaluation – data and information on pest status, fruiting times, biochemical contents, cytology characters and molecular markers.

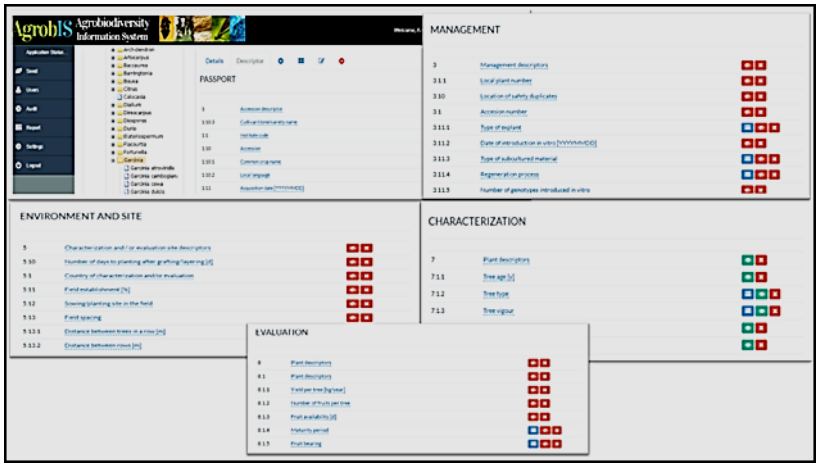

Figure 1. PGRFA data categories in AgrobIS Interface for descriptors.

PGRFA cluster includes several components which are fruits, rice, traditional vegetables, herbs, medicinal plants, floriculture, palms and tubers groups. To date, there are 17.243 accessions were registered into AgrobIS. AgrobIS development has brought several benefits, especially in PGRFA conservation, mainly its encouraged utilization of conserved PGRFA by providing specific information of crop accession to the public that can be potentially used in crop improvement or as a new source for food and income. This also helps to support the key task of genebank which is to provide seeds to breeders, scientists and the public.

MARDI has developed The Seed Management Information System (SMIS) which is designed for MARDI Seed Genebank to manage the plant genetic resources stored in a seed genebank in the proper way. The system provides with a powerful data entry, flexible, and easy-to-use and linked to AgrobIS. It was developed in 2014 under the MEGA Project Fund. The objective of the project is to upgrade the system from "stands-alone" database, to the web-based system with easy access, integrated and

comprehensive database system. This system contains information on varieties, quality attributes, seed regeneration, seed viability, and seed request status. This information is important to reduce the limitations and constraints in efficiently conserving the material in seed genebank and to allow easy access of the germplasm by researchers in MARDI or other universities and research institutes.

In the Eleventh Malaysia Plan (11 MP), MARDI has developed MARDI Rice Genebank Dashboard where allows breeders to search and retrieve information on specific accessions based on selected traits; and the information on rice germplasm were pulled from AgrobIS. The dashboard is able to provide information on rice germplasm focusing on high-yield, pest and diseases, and quality and specialty.

AgrobIS Data Available Globally

The Global Crop Diversity Trust (GCDT) has invited MARDI to adopt standards for data management and exchange through Genesys, which is the global online portal on PGRFA in the genebanks. In this project, MARDI's genebank has successfully developed an internal standard operating procedure (SOP) for preparing characterization and evaluation datasets for publication. Additionally, a very clear and relatable title to each of datasets, an explanation and description of the datasets, the location of where the research was conducted, the methodologies, the name list of researchers and supporting staffs involved in the creation of the dataset, and the precise descriptors used for the characterization or evaluation were created.

The rice germplasm data in AgrobIS were extracted and annotated in accordance with Multi-crop Passport Descriptors Version 2.1 (MCPD V.2.1) to build 22 rice metadata and datasets

and published in Genesys catalogue. There 22 datasets that have been shared from AgrobIS into the Genesys portal: (1) Morphological characterization of rice accessions-off planting season 2012, (2) Morphological characterization of rice accessions-off planting season 2013, (3) Morphological characterization of rice accessions-main planting season 2013/2014, (4) Morphological characterization of rice accessions-off planting season 2014, (5) Morphological characterization of rice accessions-main planting season 2014/2015, (6) Morphological characterization of rice accessions-off planting season 2015, (7) Morphological characterization of rice accessions-main planting season 2015/2016, (8) Morphological characterization of rice accessions-off planting season 2016, (9) Morphological characterization of rice accessions-main planting season 2016/2017, (10) Evaluation of rice accessions for bacterial leaf blight (BLB) during the off planting season 2016, (11) Evaluation of rice accessions for bacterial leaf blight (BLB) during the off planting season 2015, (12) Evaluation of rice accessions for bacterial leaf blight (BLB) during the off planting season 2013, (13) Evaluation of rice accessions for bacterial leaf blight (BLB) during the off planting season 2011, (14) Evaluation of rice accessions for bacterial leaf blight (BLB) during the off planting season 2009, (15) Evaluation of rice accessions for bacterial leaf blight (BLB) during the main planting season 2015/2016, (16) Evaluation of rice accessions for bacterial leaf blight (BLB) during the main planting season 2014/2015, (17) Evaluation of rice accessions for bacterial leaf blight (BLB) during the main planting season 2011/2012, (18) Evaluation of rice accessions against Brown Plant Hopper (BPH), (19) Characterization of quality traits in rice, (20) Evaluation of rice accessions against Foliar Blast Disease (FBD), (21) Evaluation of rice accessions for bacterial leaf blight (BLB) during the main planting season 2013/2014, and (22)

Evaluation of rice accessions for bacterial leaf blight (BLB) during the main planting season 2009/2010.

Besides, MARDI has also involved in adoption and implementation of the Digital Object Identifier (DOI) which is a `permanent unique identifier created for all genetic resources registered in the Global Information System (GLIS). It is highly opaque and more robust than other permanent unique identifiers. Under the project *"W3B-PR-29-Indonesia: Multi-country Construction of a Test Platform for the Development and Allocation of Unique Identifiers to Rice Germplasm, linking the MLS information infrastructure and the DivSeed repository"*, MARDI has registered the DOI for 727 rice accessions. The accessions that registered by DOI in MARDI rice germplasm includes MARDI released varieties, landraces, and introduced varieties from IRRI.

Concluding Remarks

In the era of Industrial 4.0 and Big Data, the AgrobIS will be continually upgraded with the current tools and systems. The awareness of the public, scientific community, especially the breeders and the agricultural scientists on the existence and importance of AgrobIS will be increased. Publishing AgrobIS data in the Genesys alongside with DOIs will help to contribute in the documentation of PGRFA and the way of how to exchange this information globally. The involvement and contribution of AgrobIS in both projects showed the commitment of MARDI for data sharing mechanism established by the Treaty.

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THE IMPLEMENTATION OF DIGITAL OBJECT IDENTIFIER ON GERMPLASMS AT THE GENEBANK OF CARDI

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INTRODUCTION

Inherence from official concern voiced the need for conservation of plant genetic resources (PGR) in 1930, Food and Agriculture Organization (FAO) had promoted conservation, exchange and utilization of germplasms, and consequently set international guidelines in 1963. Rapid loss of diverse farmer landraces in 1970s forced into acceleration of PGR collection and establishment of genebanks which were expanded globally through the International Board for Plant Genetic Resources (IBPGR), formed by the Consultative Group on International Agricultural Research (CGIAR) (FAO 1997). Therefore, there are more than 1.700 genebanks around the world conserving over 7 million plant accessions (Singh 2012). In the context of Cambodia, the Cambodian Agricultural Research and Development Institute (CARDI) under the Ministry of Agriculture, Forestry and Fisheries of Cambodia has installed deep freezers for short-term conservation since 1989 for *ex situ* condition. Meanwhile, Genebank of CARDI stock approximately

7.000 accessions of rice germplasm and 1.600 accessions of wild rice and non-rice crops.

Genebank plays an important role in the conservation, availability and use of plant genetic diversity for crop improvement to meet the present and future demand for food production (FAO 2014). Genebanks make valuable resources utilizable for crop improvement through the acquisition, *ex situ* conservation and sharing of unique germplasm. Collecting plant genetic resources for food and agriculture (PGRFA) is important, however, the quality and management of the information associated with PGRFA is also as imperative as the material itself (https://www.genebanks.org/news-activities/news/dois/). Chauvet (1993) said "The efficiency of a genetic resources conservation network lies in the availability of materials and data." Some management aspects have been increasingly recognized as crucial to sustainable maintenance and optimal utilization of high-quality germplasm. Sharing accession information and making it publicly available for potential germplasm users is important to facilitate and support the use of the collection.

Every genebank created unique code for identifying each accession at theirown genebank. However, when contributing and sharing information of its PGRFA around the globe, there are problems with accession numbers which have the same identifying code but different materials. This is the global issue genebanks facing (https://www.genebanks.org/news-activities/news/dois/). Thus, the community agreed on the need of accurately and permanently identifying PGRFAs with global unique identifier. The Secretariat of ITPGRFA conducted a study on available technologies, a survey among over 200 experts worldwide, and a further validation study with 23 selected experts. Ultimately, the adoption of Digital Object Identifiers (DOIs) by the Scientific Advisory Committee (SAC) on the Global Information System. DOIs have now been chosen to provide a

globally unique and permanent mechanism for identifying germplasm. The Secretariat of the International Treaty provides them free of charge for the entire PGRFA community participating in the Global Information System (FAO 2019). The Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development (ICABIOGRAD), in collaboration with the Secretariat of the ITPGRFA have lounged "The 2nd International Training on Software Testing to Support DOI Implementation" conducted on April 26th – May 3rd, 2019 with participants from 8 different countries including Cambodia. With the global information sharing of PGRFA assigned by DOIs, how Genebank of CARDI, Cambodia, respond to implementing DOI system in germplasm management and registration of Cambodian PGRFAs to Global Information System (GLIS).

Digital Object Identifiers

The DOI system has been developed and implemented in a range of publishing applications since 2000. DOIs were introduced by the International DOI Foundation and have largely been used for scholarly publications, datasets and commercial videos. It is widely used with over 190 million DOIs assigned (https://www.doi.org/faq.html). A DOI is a standardized alphanumeric string that is assigned by a registration agency and provides a persistent link to the location of information about the object on the Internet. Importantly, DOIs coexist with other identifiers, such as the ones already used by genebanks, allowing curators to keep their current systems in place. The Digital Object Identifiers (DOI) system provides identifiers which are persistent, unique, resolvable, and interoperable and capable of managing content on digital networks in automated and controlled ways (Paskin 2010). For these reasons, the ITPGRFA has made decision on adoption of Digital Object Identifiers (DOIs) by the Scientific

Advisory Committee (SAC) on the Global Information System for accurately and permanently identifying PGRFAs. DOIs have now been chosen to provide a globally unique and permanent mechanism for identifying PGRFAs (FAO 2019). Now DOIs hold great promise for tracking the use of germplasm (Paskin 2010).

Status of Genebank of CARDI

Isolation from rest of the world for 30 years started from late 60's to early 90's, Cambodia has never constructed a genebank (Sahai et al. 1992) until 1989 that the Cambodian Agricultural Research and Development Institute (CARDI) under the Ministry of Agriculture, Forestry and Fisheries of Cambodia has installed deep freezers for short-term conservation of rice germplasm with support from the Cambodian-IRRI-Australia Project (CIAP) (Javier et al. 1999). Cambodia would have a great irreplaceable loss of the native varieties of rice, if IRRI genebank did not receive the 55 viable rice varieties from Cambodia and later send a team to conduct the first collection, characterization, and conservation of 765 rice accessions at IRRI in 1972-1973 (Sahai et al. 1992). Through the CIAP project, CARDI has continued to collect, conserve, and characterize its traditional germplasms. Further,a total of 765 accession of first rice collection by IRRI and 2.842 accessions in four catalogues have been characterized, but there are remaining 3.400 samples which need to be characterized. Approximately 1.600 samples of wild rice and non-rice crops are collected and conserved in genebank of CARDI (CARDI 2018) (Table1).

Table 1. Wild and non-rice crops conserved in Genebank of CARDI in 2018.

No.	Common name	Scientific name	Conservation type	No of Samples
1	Wild rice	*Oryza rufipogon Griff.*	*Seed Bank*	295
2	barley	*Triticum aestivum*	*Seed Bank*	3
3	Maize	*Zea mays L.*	*Seed Bank*	58
4	Sorghum	*Sorghum bicolor*	*Seed Bank*	29
5	Okra	*Abelmoschus ficulneus*	*Seed Bank*	5
6	Sessame	*Sesamum indicum*	*Seed Bank*	13
7	Mungbean	*Vigna radiata*	*Seed Bank*	14
8	Soybean	*Glycine max*	*Seed Bank*	19
9	Groundnut	*Arachis hypogaea*	*Seed Bank*	16
10	Wild bean	*Vigna radiata*	*Seed Bank*	137
11	Watermelon	*Citrullus lanatus*	*Seed Bank*	43
12	Wax gourd	*Benincasa hispida*	*Seed Bank*	27
13	Pumpkin	*Cucurbita maxima*	*Seed Bank*	94
14	Cucumber	*Cucumis sativus*	*Seed Bank*	195
15	Sponge gourd	*Luffa acutangula*	*Seed Bank*	14
16	Bottle gourd	*Lagenaria siceraria*	*Seed Bank*	3
17	Bitter melon	*Momordica charantia*	*Seed Bank*	3
18	Wing bean	*Psophocarpus tetragonolobus*	*Seed Bank*	3
19	Tomato	*Solanum lycopersicum*	*Seed Bank*	37
20	Chili	*Capsicum annuum*	*Seed Bank*	180
21	Eggplant	*Solanum melongena*	*Seed Bank*	49
22	Mango	*Mangifera indica. L.*	*Field*	26
23	Fruit tree	Fruit tree	*Field*	30
24	Papaya	*Carica papaya*	*Seed Bank*	1
25	Cassava	*Manihot esculenta*	*Field*	28
26	Sweet potato	*Ipomoea batatas*	*Field*	36
27	Yam	*Oxalis tuberosa*	*Field*	1
28	Lesser yam	*Dioscorea esculenta*	*Field*	1
29	Potato	*Solanum tuberosum*	*In vitro*	4
30	Taro	*Colocasia esculenta*	*Field*	7
31	Banana	*Musa spp*	*Field + in vitro*	153
32	Sugarcane	*Saccharum officinarum. L.*	*Field*	34
33	Wild sugarcane	*Saccharum spontaneum*	*Seed Bank*	3
34	Cotton	*Gossypium hirsutum*	*Seed Bank*	1
35	Skouy	N/A	*Seed Bank*	1
36	Lotus	*Nelumbo nucifera*	*Seed Bank*	5
37	Ornamental plants	Ornamental plants	*In vitro*	5
	Total			1.573

Present Aspect of DOI Implementation in the GeneBank of CARDI

The 2nd International Training on Software Testing to Support DOI Implementation was conducted in Indonesia in order to introduce the DOI system, to transfer technical knowledge on DOI registration by using DOI Toolkit for managing rice genetic resources to genebank managers. Through the training, Genebank of CARDI has registered 10 accessions of rice germplasm on GLIS (Table 2). The DOI availability of Cambodian PGRFA in GLIS indexed in the ITPGRFA database will allow the genebank to preserve its database and facilitate international interest on exchange and utilization of Cambodian PGRFAs. The DOIs uniquely assigned to PGRFAs will provide breeders with a seamless way to find information and enable breeders and researchers to easily cite PGRFAs in scientific publication and documentation. This is useful for Cambodian breeders who are using our germplasms in breeding purpose and facing difficulty in citation and providing history of breeding materials. The remaining of crops germplasms are planned to be assigned their DOIs on GLIS.

Table 2. DOIs assignation of 10 accessions of Cambodian rice germplasms registering in the GLIS.

DOI	WEIWS code	Local ID	Creation method	Taxonomy
10.18730/SBCGX	KHM010	3458	Acquisition	*Oryza sativa* L.
10.18730/SBCHY	KHM010	3459	Acquisition	*Oryza sativa* L.
10.18730/SBCJZ	KHM010	3460	Acquisition	*Oryza sativa* L.
10.18730/SBCK*	KHM010	3461	Acquisition	*Oryza sativa* L.
10.18730/SBCM~	KHM010	3462	Acquisition	*Oryza sativa* L.
10.18730/SBCN$	KHM010	3463	Acquisition	*Oryza sativa* L.
10.18730/SBCP=	KHM010	3464	Acquisition	*Oryza sativa* L.
10.18730/SBCQU	KHM010	3465	Acquisition	*Oryza sativa* L.
10.18730/SBCR0	KHM010	3466	Acquisition	*Oryza sativa* L.
10.18730/SBCS1	KHM010	3467	Acquisition	*Oryza sativa* L.

Concluding Remarks

DOIs are the key to standardizing the identification of germplasm, facilitating information sharing and ensuring more effective use of the collection in genebank. PGRFAs with assigned DOIs will be easier to discover through digital means. The adoption of DOI system will not only help genebank of CARDI, but genebank around the globe to preserve its database online, to be able to track specific accessions to scientific publications and documents, and to share its PGRFAs with the world. Preserving PGRFA database on GLIS enable developing countries, where database managing system impossible to be installed and stop from data loss.

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SIGNIFICANCE OF DIGITAL OBJECT IDENTIFIERS FOR PLANT GENETIC RESOURCES MANAGEMENT AND UTILIZATION

Asif Javaid

INTRODUCTION

Plant Genetic Resources for Food and Agriculture (PGRFA) are vital for modern plant breeding. They are essential in the efforts to increase agricultural productivity for food security. PGRFAs provide genetic traits required to deal with crop pests and diseases as well as dealing with changing climate conditions. They are also important for marginal environments in order to develop crop varieties that can adapt to difficult conditions. However, due to many reasons, plant genetic diversity is disappearing at alarming rates and 80-90 percent loss is reported in major crops over the past century (Andersen 2016).

Effective conservation and sustainable utilization of PGRFA are thus critically important for the food security of the world. *Ex situ* conservation of PGRFA began in mid-twentieth century when the importance of conservation of agricultural biodiversity was realized (Diez et al. 2018). Genebanks for PGRFA have the responsibility to collect, regenerate, conserve, characterize, evaluate, document and distribute germplasm (Tyagi and

Agrawal 2015). Genebanks also provide infrastructure for storage, a platform for sharing, and opportunity for better access and utilization of the germplasm. More than 1700 genebanks around the world stock over seven million plant accessions, of which only a small number are characterized and few are ever used for crop improvement. Since genebanks are expensive to establish and manage, there should be efficient genebank management system for the conservation and sustainable use of PGRFA (Singh et al. 2019). Utilization of PGRFA for research and breeding purposes requires thoroughly cataloged passport data and information about agronomic, biochemical and genomic traits of genebank accessions (Anglin et al. 2018). Modern phenotyping and genotyping technologies have enhanced the capacities of genebanks to perform their work but also raise questions as to how big data from plants should be managed and shared (Popova 2018).

Commercial use of PGRFA by corporate sectors is increasing, followed by demands of intellectual property rights. There are also demands for protection of the rights of farmers and local communities and ensuring a fair and equitable sharing of benefits arising from the use of these resources. The international community has responded to these developments with several regimes including the Convention on Biological Diversity (CBD), the Agreement on Trade Related Aspects of Intellectual Property Rights (TRIPS) of the World Trade Organization and the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA). These regimes affect the management of PGRFA (Andersen 2016).

One important element of PGRFA management is accession number, which is a unique identifier assigned to each germplasm accession in a genebank. Since different genebanks have different systems of identifiers and data handling, many accessions in the

genebanks are duplicates. Such information are often lost when the material is transferred from one holder to another. Different users of PGRFA, such as researchers and plant breeders, often follow different methods to assign identifiers to their materials. It results in a lack of standardization, which complicates the exchange of PGRFA data between researchers and plant breeders worldwide. The Global Information System of ITPGRFA aims to provide a standardized system of Digital Object Identifiers (DOIs) for plant genetic resources for food and agriculture (PGRFA) information around the world. It also facilitates easy access to information on PGRFA for research, training and plant breeding (Alercia 2018).

National Genebank of Pakistan

Pakistan is blessed with a vast diversity of plant genetic resources from different agro-climatic ecologies. Pakistan lies in the Central Asiatic Center of Diversity and in the vicinity of Near Eastern and Indian Centers of Diversity. Conservation of plant genetic resources at national level is required to supply the National Agricultural Research System (NARS) with germplasm. Germplasm collection was started in Pakistan during the 1970s. Bio-resources Conservation Institute (BCI) of Pakistan Agricultural Research Council (PARC) is established at National Agricultural Research Center (NARC), Islamabad, for exploration, collection, conservation, evaluation and distribution of PGRFA. More than a hundred plant collecting missions in Pakistan have collected indigenous germplasm from Pakistan for conservation and distribution. In addition, to meet the need and requirements of breeders and researchers, PGRFA were also acquired from abroad. National Genebank at BCI holds 38259 accessions of 400 plant species. These conserved genetic resources are distributed to breeders and researchers for utilization.

National Genebank of Pakistan distributes about 7000 accessions per year.

Germplasm Evaluation

Plant genetic resources without evaluation data do not serve the purpose of crop improvement. Identification of superior PGRFA saves the time and labor required for successful crop breeding. Germplasm evaluation also aids utilization and the planning for future collection missions. Evaluation Laboratory of BCI has characterized and evaluated more than half of the PGRFA conserved in the Genebank using standard protocols from Bioversity International. It identified genotypes for various traits of economic importance and enhanced the pace of crop development. Hidden treasures of germplasms tolerant to biotic and abiotic stresses have been uncovered. Markers for quality in wheat and disease resistance in peas have also been successfully utilized.

The Evaluation Laboratory has also identified elite crop germplasm lines with economically important characters like early maturity, yield components and resistance to biotic and abiotic stresses. National Genebank of Pakistan has made these elite germplasm lines available to education and research institutes for utilization in crop improvement.Biochemical evaluation of germplasm using SDS-PAGE and molecular evaluation using RAPD and SSR is also conducted to study the genetic diversity in germplasm of different crops.

Data Management and Integration

Genebank database maintains the passport data of germplasm accessions in National Genebank of Pakistan, while germplasm

evaluation data is maintained by scientists working on different crops. The users of plant genetic resources conduct experiments in an effort to utilize germplasm to improve agricultural productivity. There is substantial variability in the quantity of experiments and the quality of data produced among different users. The potential uses of data from plant genetic resources are enormous for crop improvement. Future uses of agricultural trial databases will likely be driven by the increased links between genotype and phenotype to improve selection and use of germplasm. The combination of agronomic data from field trials with genomic data shows promise for developing next generation breeding. However, fragmentation, lack of organization and inaccessibility of agricultural trial data hinder their use and application for resolving problems in agriculture (Hyman et al. 2017).

Efforts are continuously being made for data integration. Several studies have suggested that Digital Object Identifiers (DOIs) can play an important role in data integration for management and use of plant genetic resources. Diez et al. (2018) discussed the strategies for improving Spanish Plant Genetic Resources Network, by identifying major shortcomings including the lack of efficient coordination in the distribution of species among genebanks, too many genebanks, existence of detected and undetected duplicates, insufficient rate of regeneration, insufficient phenotyping, genotyping and epiphenotyping, unsatisfactory rate of use by end users and insufficient funding. One of the suggested tasks is to develop user-friendly platforms to access germplasm documentation, including a unified system of descriptors and classification categories. Additionally, it was suggested that the use of digital object identifier (DOI) system would connect different data sources and increase the traceability of accession use.

Wambugu et al. (2018) reviewed the real and potential application of the current advances in genomic technologies in improving the utilization of plant genetic resources. The actual and potential application of these genomic approaches are in plant identification, phylogenetic analysis, analyzing the genetic value of germplasm, facilitating germplasm selection in genebanks, as well as instilling confidence in international germplasm exchange system. It was suggested that the genebanks can benefit from the current advances in genomic technologies through greater collaboration with the user community. Some of the linkages and collaborations that have been established include DivSeek and Global Information System (GLIS). The assignment of Digital Object Identifiers (DOIs) as permanent identifiers of PGRFA makes it easier to share PGRFA information, by easily and unambiguously referencing PGRFA samples across organizations.

The Wheat@URGI portal has been developed to provide the international community of researchers and breeders with access to the bread wheat reference genome sequence produced by the International Wheat Genome Sequencing Consortium. Genome browsers, BLAST, and InterMine tools have been established for in-depth exploration of the genome sequence along with additional linked datasets including physical maps, sequence variations, gene expression, and genetic and phenomic data from other international collaborative projects already stored in the GnpIS information system. The genetic resources stored in GnpIScoreDB also have the unambiguous identification of the accession using Digital Object Identifier (DOI) and a rich set of associated data (Alaux et al. 2018).

Genebank users should be in a position to identify and select germplasm from the global genepool based on a combination of passport, genotypic and phenotypic data. The Musa Germplasm

Information System (MGIS), the database for global *ex situ*-held banana genetic resources, has been developed to address those needs. Accession-based data has been enriched with publications, genotyping studies and associated genotyping datasets reporting on germplasm use. Banana germplasm identified by accession numbers will be complemented soon by Digital Object Identifiers (DOI) following the specifications of ITPGRFA (Ruas et al. 2017).

Concluding Remarks and Future Perspective

Efficient PGRFA database management system is necessary in genebanks. Genebanks use accession numbers for activities like collecting, regenerating, conserving, characterizing, evaluating, documenting and distributing germplasm. Once the accessions are distributed to users, their traceability becomes difficult because the user may use the same accession numbers or assign new accession numbers to the accession. DOI (Digital Object Identifier) is a unique identifier that identifies digital objects. Once DOI is assigned to a germplasm accession, the physical location of accessions may change, but the DOI assigned to that accession will never change. Thus DOI improves the traceability of accessions and their use. DOIs may also help resolve issues like intellectual property rights and access and benefit-sharing. Studies are being conducted on PGRFA for agronomic, physiological, biochemical and molecular characters by different research groups. Data and information generated during these studies should be integrated as in Wheat@URGI portal (Alaux et al. 2018) and MGIS (Ruas et al. 2017) using DOIs. It may help researchers and plant breeders to select PGRFA according to their goals.

The second International Training on Software Testing to Support DOI Implementation on Rice Germplasm was held in

Indonesia during April, 2019. During this training, GLIS Toolkit v.2.0.3 was used for assigning DOIs to rice germplasm accessions in National Genebank of Pakistan. The same software can be used to assign DOIs for germplasm accession from other crops. National Genebank of Pakistan is working on the development of new database management system for genetic resources. FAO Multi-crop Passport Descriptors (MCPD V.2.1) with DOIs as persistent unique identifiers are suggested to be used for development of new database management system (Alercia et al. 2015).

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CHAPTER 5.
DIGITAL OBJECT IDENTIFIER FOR RICE GERMPLASM

Rice is one of the major food crops that contribute to food security and almost 20 percent of all the world's holdings of rice germplasm are included in the multilateral system of access and benefit sharing of the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA). Nevertheless, these accessions are maintained in collections distributed around the world and their discoverability and use is hindered by this fragmentation of location and database systems. Additionally, other important information associated with those rice accessions, which are highly relevant and required for plant breeding, is often disconnected from the collection database. The International Community has tried in the last decade to agree on a common approach to facilitate the establishment of an automated and meaningful links through the adoption of permanent unique identifiers.

Ambiguous germplasm identification and difficulties in tracing pedigree information also created constraints in rice improvement programs that involve exchanges of genetic resources. To address these constraints, a permanent unique identifier for each germplasm is needed. One such identifier is the Digital Object Identifier (DOI). The DOI is a permanent unique identifier that has specific advantages over other identifying systems, i.e. it is highly opaque and more robust than other

permanent unique identifiers. Indonesia has applied the DOI to its rice germplasm collection based on the guidelines developed by the secretariat of the ITPGRFA. The DOI will keep track of the movement of Indonesian rice germplasms and can be used to further reveal the variations in the germplasms.

DIGITAL OBJECT IDENTIFIERS FOR INDONESIA RICE GERMPLASM

Muhamad Sabran, Nurul Hidayatun, and Hakim Kurniawan

INTRODUCTION

The mutual interdependence of different countries and regions in relation to plant genetic resources has been recognized by scientific communities (Palacios 1998). An in-depth analysis on interdependence on Plant Genetic Resources for Food and Agriculture (PGRFA) between countries demonstrated that national food supplies and production systems are highly interdependent worldwide in regard to plant genetic resources (Khoury et al. 2015). Countries strongly depend on crops whose genetic diversity largely originates from outside of their borders, both for their food supplies and their production systems. The global average of the degree of countries' dependence on crop genetic diversity originating from outside their borders is 68.7% across food supply variables, 69.3% across production variables, and 68.9% across all variables for all countries.

Acknowledging the inter-dependence among countries on plant genetic resources for food and agriculture, FAO member countries agreed to commit to an International Treaty on Plant

Genetic Resources for Food and Agriculture (International Treaty on Plant Genetic Resources for Food and Agriculture 2009). The Treaty established a Multilateral System (MLS) on access of 64 crops considered to be important for food security and climate change adaptation, and benefit sharing arising from their uses. In such multilateral system, contracting parties, international organizations and any natural and legal persons contribute to a virtual gene pool of the 64 crops. The transfer of genetic materials in the system are managed with a standard material transfer agreement (SMTA).

The SMTA requires that all available passport data and any other associated non-confidential descriptive information shall be made available in conjuction with the PGRFA provided. The recipient shall make available all non-confidential information that results from research and development carried out on the material to the multilateral system, through the information system specified in Article 17 of the treaty. However, rapidly growing material exchanges through SMTA had not yet included the sharing of associated information as required by Article 17 mentioned above.

Information System and Permanent Unique Identifier on PGRFA

There are many systems of inventory management and/or workflows of genetic resources available. One example is information systems in genebanks like GRIN GLOBAL and GENRES (https://www.genres.de/), that contains documentations on each accession and their origin, maintenance record of viability and health, genetic integrity of seeds or clones, etc. (Weise et al. 2017). Genesys (www.genesys-pgr.org), SINGER and

WIEWS (http://www.fao.org/wiews), and information systems for specific crops across genebanks such as ICIS and IRIS.

The global information system (GLIS) developed by the Treaty Secretariat aims to make such information more easily transferable, accessible, available for a long time, more accurately associated to the PRGFA at hand, and is accrued as the PGRFA is transferred, studied and improved. It is designed to become the "Google" for the PGRFA community and a gateway to existing systems for information on PGRFA and other resources of interest in the community. The global information system needs a permanent unique identifier for each accession so that they can be tractable and traceable.

A Permanent Unique Identifier (PUID), as a minimum definition, is a text string that unambiguously and permanently identifies a single object of interest (International Treaty on Plant Genetic Resources for Food and Agriculture 2015). The key characteristics of PUIDs are:

1. Uniqueness: unambiguously identify a specific object or intellectual asset
2. Permanence: the same object will be forever associated to the same identifier (always valid)
3. Opacity: nothing about the associated object should be inferable by the structure of the identifier
4. Actionability/resolvability: a defined procedure for name resolution exists to access the information associated to the object once the identifier is known
5. Discoverability: given details of an object, it is possible to retrieve its identifier

A Digital Object Identifier (DOI) (International DOI Foundation 2018) is a PUID with a number of specific advantages

over other identifying systems, *i.e.* it is highly opaque and more robust than other PUIDs. The system is based on ISO and ANSI standards, thus ensuring a solid foundation and a controlled environment. It is managed by the International DOI foundation, widely used, accommodates existing identifiers, has a flexible and extensible metadata structure, and supports advanced features.

Guideline for the Use of DOI for PGRFA

In order to use DOI effectively, a consensus regarding minimum set of metadata descriptors for PGRFA has to be decided by the PGRFA communities. Through an electronic survey that involved 200 experts from 98 institutions in 62 countries, followed by several consultations, the community had agreed on a set of discriptors for assigning DOI to PGRFA. The data required for assignation of DOI (the descriptors) are grouped into core descriptors, which consist of mandatory descriptors and highly recommended descriptors, and additional descriptors (International Treaty on Plant Genetic Resources for Food and Agriculture 2017).

The values for mandatory descriptors must be inputted for every PGRFA material in GLIS. The holder is not given the option to enter "unknown", "not applicable" or "other", nor to leave the field empty. The PGRFA cannot be registered until valid values have been entered for all mandatory fields. These descriptor consist of organization, individual or legal entity conserving the PGRFA (MO1), PGRFA unique identifier within specific collection (e.g. genebank)(M02), the date at which the PGRFA was acquired (M03), the method by which the PGRFA was acquired (M04), and scientific or crop name (M05).

The method by which the PGRFA are obtained (M04) can be one of the following:

1. Acquisition: the acession was acquired from other sources, such as ex situ or in situ collection, local market, research collaborator, or any other sources outside the holding genebank, breeding or research program.
2. In-house copy: the PGRFA are created by subsampling or taking a harvest from another material that is under the holder's management, with the intent that the new PGRFA should be, as much as possible, a genetic copy of the parent, and the holder wishes to register a new DOI for the new PGRFA rather than use the DOI of the parent.
3. In-house variant: the PGRFA were created by subsampling or taking a harvest from another material that is under the holder's management. They are a subset of genetically variable (segregating and/or physical mixture) parents.
4. Novel distinct PGRFA: The PGRFA is a novel variety, breeding material, or research material that had been created from one or more parental samples under the holder's management, distinct from its parents, through a process that includes at least one innovative step such as crossing, mutation, or genetic modification.
5. Observation-Natural: the PGRFA material was in situ or on farm and it appeared on the holder's land without any intervention.
6. Inherited: The PGRFA were inherited from the holder's predecessor, without knowing how it was acquired or created.

There are also some highly recommended descriptors, although they are not mandatory, for the assignation of DOI such as : link to associated information, i.e. one or more URLs where

further information about the PGRFA can be obtained (RO1), DOI(s) of progenitor(s) (RO2), biological status (RO3), additional taxonomic category, i.e., finer level of classification from the scientific names given in M05 (R04), names, i.e., one or more registered names or other designation such as a landrace, traditional variety or modern cultivar, or some other name or designation used to identify a breeder's selection or elite line or variety (R05), other identifiers (R06), MLS status, i.e. the status of the PGRFA with regard the multilateral system of ABS of the ITPGRFA (R07), Historical PGRFA, i.e., to indicate whether or not the material identified by the DOI currently exist (R08). In addition to those core descriptors, there are other descriptors that depend on the method by which the material are obtained as given in M04. Different values of M04 required different sets of additional descriptors. The DOI with the above descriptors for its assignation will facilitate access to the information about PGRFA.

An issue that was intensively discussed during the consultation is the definition of the "object" that needs to be identified with DOI for the purposes of the Global Information System. Defining the type of object to be identified requires a definition of what type or degree of difference (or change) is sufficient to require assignment of a new DOI. This needs a clear consensus for the term 'change'. More concretely, when a sample is transferred with SMTA from a provider to a recipient, should the provider's and recipient's samples be considered as the same object (and therefore share the same DOI) or to be different (and therefore have different DOIs)?

The provider's samples and recipient's samples from the same original material are separated following transfer, and for administrative, scientific, legal, and professional reasons must be treated as different objects. They are managed as separate entities under different administrative procedures, and unless the

provider's sample was previously acquired with SMTA, they are held under different legal conditions. In addition, since genetic materials change through mutation, genetic drift, deliberate or unintentional selection, cross-contamination with pollen or seeds or plants of other varieties, or even simple mislabeling, the two samples will be genetically different; and they will diverge further with time. This is particularly true of landraces and crop wild relatives, which are typically genetically heterogeneous, so an accession or variety in a collection of genetic materials is often not a homogeneous sample of seeds. Documenting them as separate objects is essential to resolve questions that may arise over use or misuse, genetic identity, or attribution of data.

The main issue for discussion here is whether using the DOI for this purpose is in accord with the needs of the Global Information System. Choosing to assign the same DOI to the provider's and the recipient's samples implies a judgment that genetic differences between them are too small to warrant treating them as separate objects. Consequently, it would be necessary to agree to a threshold for the degree of genetic divergences between two samples where they can still be considered as the same object. Further agreements would need to be reached on what evidence would be required to determine whether they are different objects. Possible categories of evidence include (a) genetic characteristics such as DNA fingerprints, (b) phenotypic characteristics such as visible morphological traits, (c) records of germplasm management including sample sizes, and environments and processes used for germplasm maintenance and seed multiplication, or (d) the germplasm holder's subjective assessment. The issues described above have been resolved by allowing to assign DOI even to the in-house copy of the other accession as long as the method by which the PGRFA was acquired is reflected in the new DOI (in this case in-house copy, as outlined in descriptor M04).

International Rice Information System

The International Crop Information System (ICIS) (www.icis.cgiar.org), is a database system for the management and integration of global information on genetic resources and crop improvement. It was developed by CGIAR and its collaborative partners. The International Rice Information System (www.iris.irri.org) is the implementation of ICIS for rice (McLaren et al. 2005). The system consists of database design, controlled vocabularies, and software, which are applied to rice data. The IRIS contains the genealogy management system which documents the method of progeny creation, including generative (crossing/hybridization, induced mutation, and genetic modification), derivative (selection, separation of component from mixture), and maintenance (seed multiplication, sub-sampling) methods.

Linking DOI to the IRIS

The DOI assigned to rice germplasms needs to be linked with the IRIS (or ICIS in general) in addition to its registration in the Global Information System (GLIS). Providers submit a request to the GLIS through a web service by providing the local germplasm ID and passport data (according to the DOI metadata specification of GLIS). If no IRIS Germplasm Identifier Data (GID) is found in the provider's database, then a parent entry for the germplasm will be created in IRIS (in addition to the registration in GLIS) with minimal passport data and link it to the provider's database. The DOI server (GLIS) assigns a new DOI to the rice accession and this DOI is then added to: (1) the provider's own database and (2) the IRIS central database.

The provider submits a request to GLIS with DOI and recipient ID, and the system (GLIS) assigns a new DOI to the recipient's sample and issues a service call to create a new entry for the recipient's sample in IRIS with: GID, DOI, minimal passport data, and a link to the provider's DOI. If the recipient's database is enabled, a germplasm record with DOI and passport data is added to the recipient's own database. If the material is not already registered, the provider can register it "on the fly" by providing the necessary information in the transfer request message. GLIS will first register the material, assign it a DOI and then proceed with the transfer as described above.

DOI for donor and recipient could perhaps be resolved by assigning separately one type of DOI where a type of object is defined as the original source material following the MCPD concept of COLLNUMB and the Darwin Core Occurrence concept (using the Darwin Core occurrence ID descriptor), and another type of DOI where its type of object is the actual germplasm material of the genebank-accession that is shipped in response to a seed request. The "COLLNUMB/occurrence ID-DOI" identifier name would be the same for both provider and recipient samples and correspond (in object-type definition) to the MCPD concept of COLLNUMB. The "germplasm-material-type-of-DOI" identifier name would be different for the provider and recipient samples and correspond (in object-type definition) to the core MCPD concept of ACCENUMB. This resembles the normal procedure of genebanks today where even a germplasm sample received from another genebank institute is assigned a new accession number (ACCENUMB) upon registration in the recipient genebank database. An obstacle for using this approach in GLIS is that the original source material (COLLNUMB) for genebank accessions is very often not known.

Another way to solve this is by exploring the different point of view between providers and recipients respectively. From the point of view of the provider, the provider's sample identifier (DOI) corresponds to the ACCENUMB identifier in the provider's own database, and the recipient sample identifier (DOI) will correspond to the "ACCENUMB-to-be" in the recipient's own information system. From the point of view of the recipient (and subsequent registration of the SMTA event in the recipient's own database) the provider's sample identifier corresponds to the MCPD DONORNUMB concept, and the recipient sample identifier (the material that is shipped) corresponds to the ACCENUMB concept with respect to registration in the recipient's own database. The GLIS SMTA component would thus need to take care to register both the provider's sample DOI and the recipient's sample DOI for each SMTA material transaction.

Documentation of passport data requires special attention, because it provides critical data or information for discriminating the germplasm materials. The higher the number of discriminants, the better its power to differentiate germplasm with DOIs. Therefore, the provider has to explore multiple potential traits to be used as reliable discriminant characters. In addition, as in Darwin Core, DOI is referenced for the present existence of germplasm materials in a genebank collection as well as the germplasm sample when it was first taken at the time of collection.

In the case of germplasm uses by contracting parties or other users, how can the DOI and other related data to the germplasm materials be tracked?

The Global information system that will be developed is expected to have the ability to trace the DOIs and related data to the germplasm materials exchanged by the MLS, and will

compile these information for reporting to the MLS. Since the DOI will be centralized in GLIS (Global Information System), interested users and or any third parties will have the opportunity to further search and trace any related data to the germplasm material that is already shared in the MLS. It is important to note that accession number and DOI are the two different systems. Accession numbers are locally assigned and directly related to materials maintained in an *ex situ* germplasm collection, whereas DOI in this context is a globally unique identifier to be used to identify germplasm exchanged across multiple institutions.

DOI Applied to Indonesia Rice Germplasm

A successful rice breeding program requires genetic diversity to obtain improved variety with desired traits of economic importance. Germplasm characterization at morphological and molecular level will enable rice breeders to exploit genotypic diversity for conservation and further crop improvement (Thomson et al. 2009). Morphological variations can be used to classify rice into two major subspecies, japonica and indica. Typical grain characteristics and optimum environment between the two are distinctive. Another subspecies, the tropical japonica, has broad grains and thrives under tropical conditions and possesses specific morphology. Based on morphology and molecular analyses, scientists also try to sort rice into different cultivar groups, namely temperate japonica, aromatic, aus etc. (Garris et al. 2005). Morphologically, rice differs with respect to vegetative characters, leaf, culm, panicle, and seed properties during their growth stages, and these are important for guiding selection process in breeding.

Recent rice cultivars in Indonesia have more than 2000 ancestors and very complicated pedigree. IRRI cultivars contributed the largest proportion of the genetic background of Indonesian cultivars. Rice cultivars having the genetic background of IR64 or having kinship to IR64 were planted in 50.6% of the total rice cultivation area in Indonesia. Cluster analysis using coefficients of parentage divided Indonesian cultivars into 5 groups: Cisadane, Ciapus, IR8, Sintanur and Kalimas group.

Rice germplasms in Indonesia is managed by various institutions under the Indonesian Agency for Agricultural Research and Development (IAARD, Ministry of Agriculture), Indonesian Institute of Sciences (IIS), and Universities under the Ministry of Education and Culture. Rice germplasm collections in each institution are maintained because they are related to research and development activities. The largest rice germplasm collection is in IAARD with a total collection of 7,728 accessions. They are managed by the Indonesian Center for Rice Research (ICRR, 3,396 accessions) and Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development (ICABIOGRAD, 4,332 accessions). There is an additional ICABIOGRAD's collection of more than 8,000 accessions, which is deposited in IRRI genebank. The ICABIOGRAD genebank currently manages 4,332 accessions of rice, which consists of landraces (3,513 accessions), introduced varieties (357 accessions), wild rice (93 accessions) and others (369 accessions). ICABIOGRAD is the central genebank that holds a basic collection for rice germplasm. ICRR has a collection of 3,231 accessions, which consists of landraces (1,729 accessions), introduced varieties (1,287 accessions), wild rice (50 accessions), as well as elite varieties (165 accessions). Rice germplasm collection is also carried out by IIS and several universities.

However, the collection status in these institutions is still not completely inventoried.

Rice germplasm collection data in each institution is still managed using different database systems at the moment. There is no central database system that connects those institutions for accessing and sharing data. ICABIOGRAD has begun to coordinate rice germplasm data management in Indonesia. A prototype of website portal had been built since 2016 for the purpose of sharing agricultural genetic resources data. However, the coordination was still limited within the scope of the IAARD (Ministry of Agriculture).

Through the portal, it is possible to access collection and characterization data of agricultural genetic resources collected in ICABIOGRAD genebank. Until now, there have been a lot of access and exchanges of genetic resources material being carried out among the institutions within and outside the IAARD. Almost all of these material exchanges occured between domestic institutions.

Since 2017, a total of 1,366 accessions of rice and other crops collected in IAARD genebank have been registered to obtain the DOI. Most of those accessions were landraces, and they are maintained in ICABIOGRAD and some Assessment Institute for Agricultural Technology (AIAT). There are also minor accessions maintained in the gene bank of Agro-inovation Center, Gadjah Mada University (Table 1).

Table 1. Rice and non-rice accessions collected in IAARD gene bank which have been registered for the DOI.

Holding institution	Number of accessions	Year of DOI registration
ICABIOGRAD	849	2017
ICABIOGRAD	111	2018
AIAT of South Sumatera	55	2018
AIAT of Central Kalimantan	96	2018
ICABIOGRAD	70	2019
ICRR	14	2019
ILETRI	12	2019
ITFRI	10	2019
IRIAP	18	2019
ICSFRI	12	2019
ICERI	20	2019
AIC-GMU	30	2019
AIAT of Yogyakarta	55	2019
AIAT of West Nusa Tenggara	4	2019
AIAT of East Kalimantan	10	2019
Total	1,366	

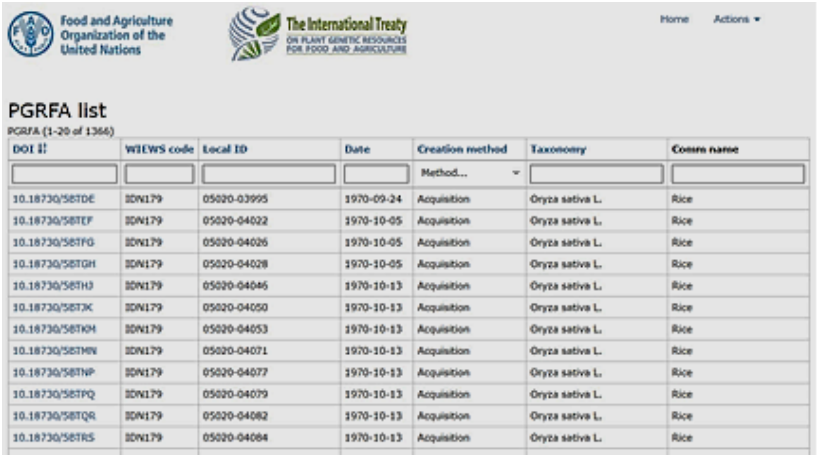

Figure 1. Recent status of DOI registration of the Indonesian PGRFAs accessions as shown in GLIS website.

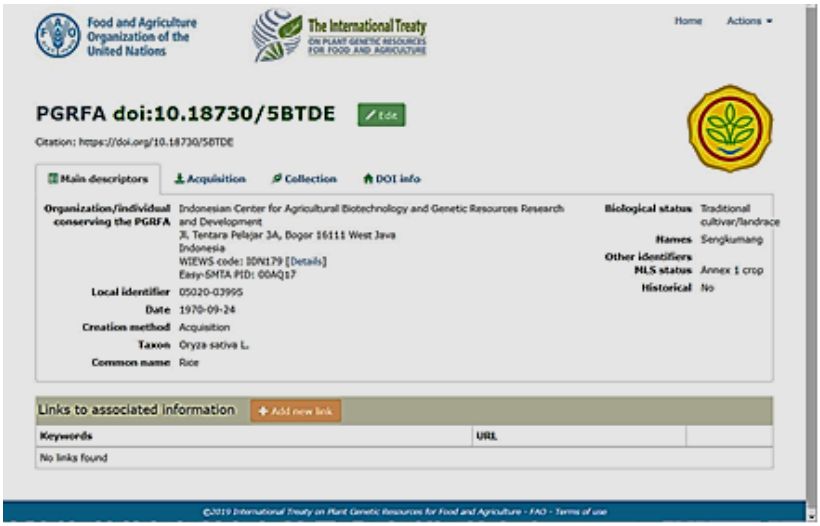

Figure 2. Detail information for citation of a single accession of PGRFA.

As ICABIOGRAD-IAARD is a National Focal Point for managing agricultural genetic resources, therefore the DOI registration of domestic institutions was done under the coordination of ICABIOGRAD-IAARD. Technical assistances for DOI registration of agricultural germplasms collected in various institutions is still continuing even a collaborative project between IAARD and ITPGRFA-FAO has been ended in July 2019.

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DIVERSITY OF DOI REGISTERED RICE LANDRACES FROM SOUTHEAST ASIA FOR GENETIC IMPROVEMENT

Dwinita Wikan Utami, Puji Lestari,
Rerenstradika Tizar Terryana, and Karden Mulya

INTRODUCTION

Rice is the most widely consumed as a staple food for a large part of the world's human population, especially in Southeast Asia. This plant species is the agricultural commodity with the third-highest worldwide production. Currently, the majority of all rice production comes from China, India, Indonesia, Bangladesh, Vietnam, Thailand, Myanmar, Pakistan, Philippines, Korea and Japan. Asian farmers including those in Southeast Asia still yield for 87% of the world's total rice production (Worldatlas 2017). Rice landrace is defined as a traditional variety with a high capacity to tolerate biotic and abiotic stresses, resulting in high yield stability and an intermediate yield level under a low input agricultural system. Landraces covering a domesticated, locally adapted (Jones et al. 2008) or traditional variety (Camacho et al. 2005) have developed over time, through adaptation to its natural and cultural

environment of agriculture and pastoralism, and due to isolation from other populations (Sponenberg 2000).

Rice landraces possess wide diversity, which needs to be properly characterized for their use in genetic improvement. They have been preserved by indigenous farmers to the commercially bred cultivars developed during the green revolution. Harlan (1975a) was stated that landraces are balanced populations in equilibrium with both the environment and pathogens, and are genetically dynamic. Each landrace has particular properties or potential characteristics: early maturity, adaptation to particular soil types, resistance or tolerance to biotic and abiotic stresses, and increased grains number which potential for crop improvement through breeding approach (Das et al. 2013). For this reason, the management of the information of landraces is as important as the material itself associated with genetic resources for food and agriculture. The complicated problems arise when some landrace accessions were shared to different place. It becomes difficult to track relationships as these genetic resources are shared, duplicated and further used, causing limitation of the capacity to associate new information to the accessions attributable to generating it. Digital Object Identifiers (DOI) has now been chosen to provide a globally unique and permanent mechanism for identifying germplasm which is important to multilateral system. A DOI is a standardized alphanumeric string that is assigned by a registration agency and provides a persistent link to the location of information about the object on the Internet (unlike URLs, which can lose connectivity if they are not updated). Importantly, DOIs coexist with other identifiers, such as the ones already used by gene banks, allowing curators to keep their current systems in place (https://www.genebanks.org/news-activities/news/dois/).

This review described how the diversity of DOI registered Asian landraces, particularly those originating from Southeast Asia can be exploited and made readily available for use by breeders and the scientific communities. It highlighted DOI as a mean of research in genetic improvement to traceable the rice genetic resources for held in trust. An attempt was made to discuss the diversity of rice landraces in Southeast Asia on specific-trait characters and a special case of the diversity of shared rice landraces from multiple countries could be utilized through breeding for genetic improvement. Finally, ways of centralizing and unifying genetic resources and their potential associated traits for specific trait characters through the conservation of germplasm and the development of databases are proposed. It is clear that more efforts are necessary to exploit genetic diversity of rice landraces in Southeast Asia to achieve sustainable production in the future.

Genetic Diversity of DOI Registered Rice Landraces on Specific-Trait Characters

Rice landraces DOI registered diversity

The genetic variability found within landraces affords the possibility of genetic flexibility. Landraces have the potential to adapt to local field conditions, changing environments and farming practices (McCouch 2004). Moreover, the genetic diversity of traditional/landrace varieties is the most immediately useful and economically valuable component of rice biodiversity (Wood and Lenné 1997). To efficiently conserve, manage and use such germplasm resources, an understanding of structure, apportionment and dynamics of local landrace variation is required. Several studies have examined genetic variation and

differentiation among rice landrace varieties (Fukuoka et al. 2006).

Germplasm identification using DOI has been globally adopted. DOI system for genetic resources, including rice landraces adopted by Scientific Advisory Committee (SAC) on the Global Information System (GLIS) has been applied in the management and the exchange of plant genetic resources for food and agriculture. This system has also been implemented on the total 85 accessions rice landraces from Southeast Asia countries, under 'Benefit-Sharing Fund of the International Treaty on Plant Genetic Resources for Food and Agriculture' Project funded by European Union through multi country project of FAO. All these accessions were registered into DOI system as showed on: http://biogen.litbang.pertanian.go.id/codevelopment/list-of-the-indonesian-local-cultivars-of-rice and in the multilateral system (https://ssl.fao.org/glis/). They were originated from: Lao PDR (17 accessions), Philippines (17 accessions), Malaysia (19 accessions) and Indonesia (20 accessions) and 3 check varieties from the four countries (total 12 varieties) which have been characterizedand included in the 3000 Rice Genome Project in International Rice Research Institute (IRRI) database (http://iric.irri.org/resources/3000-genomes-project).

Observation of all accessions from each country was diverse based on morphological characters. Based on principle component analysis, several characters contributed the most on total diversity (Figure 1). The characters and their contribution (%) are plant height (72.5%), length of ligule leaf (79.4%), color of leaf sheath (92.7%), color of collar leaf (85.7%) and color of auricle leaf (87.9%).

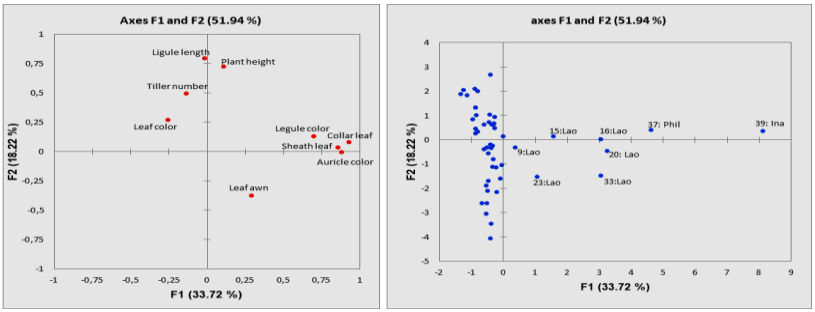

Figure 1. A. A distribution pattern of the morpho-agronomical characters contributed to the diversity on all accessions rice landraces from four Southeast Asian countries.; B. Relative positions of the accessions of rice landraces from four Southeast Asian countries: Mal=Malaysia; Ind: Indonesia; Phil=Philippine and Lao PDR.

Based on Principal Coordinate Analysis (PCoA) plotting, in general, landraces from the Philippines were clustered in same quadrant with landraces from Lao PDR, indicating relatively close genetic distance. While Malaysia landraces were clustered in the same quadrant with landraces from Indonesia. The accessions plotted in the same or closely coordinates indicated in low diversity (Mahbub et al. 2016). Therefore the PCoA plotting was applicable to analyse the genetic diversity among the accessions (Shankar et al. 2009). The closely related landraces from the two countries apparently reflect their ecological similarities (Burns and Strauss 2011).

Specific-traits characterization related with the breeding targets

The integration of physical and biological characters is the ultimate goal for characterization, as this would lead to an improved assessment of where particular types of environments are present (McLaren and Wade 2000). Morphological characterization generates important information that serves as

the basis for selecting the accessions, either for direct use by farmers, use as parents in breeding programs or for varied scientific investigations, including gene discovery (Engels and Mba 2014).

Since physiological understanding of patterns of genotype adaptation is required for the identification of useful traits conferring an adaptive advantage in particular conditions, using the representative reference lines could provide the first step in the characterization process (McLaren and Wade 2000). The agro-climatic classification for rice and rice-based cropping systems has been widely adopted. This is based on the length of the rice-growing season, months in which surface flooding and disease incidence can be maintained (Oldeman and Frere 1982).

Southeast Asia region's hot and humid climate during the long and heavy monsoon season provide the most favourable agro-ecological environment for rice cultivation as well as diseases development. Cianjur district in West Java, Indonesia, is one specific lowland environment which is appropriate for rice landraces characterization due to the endemic status in all season for Bacterial Leaf Blight (BLB) disease. Therefore, this environment is appropriate for characterization of rice landrace accessions from Southeast Asia on the specific trait of BLB resistance (Figure 2).

Figure 2. Characterization of rice landraces from Southeast Asia in BLB's endemic lowland in Cianjur, West Java, Indonesia.

BLB is found to be one of the most destructive diseases of rice in many Southeast Asia countries. The disease starts with water soaked lesion on the tip of the leaves, and the lesion increases in length downwards and turns into yellow to straw coloured stripes with wavy margins. Lesions may be developed at one or both edges of the leaves or along the mid rib. In humid areas, on the surface of the young lesions, yellowish, opaque and turbid drops of bacterial ooze may be observed in the early morning (Mew and Gonzales 2002). This disease becomes a serious problem because many high yielding varieties, which are managed with high nitrogen levels and close spacing, have inadequate resistance to the pathogen.

Characterization for specific trait in BLB's endemic area of rice landraces originated from Lao PDR, Philippines, Malaysia and Indonesia showed diverse performance. Based on standard scoring produced by IRRI (2002) for BLB's resistance (score 1 to 9), around 40% from the total accessions were resistance (score 1 and score 3) to natural inoculum in Cianjur's environment (Figure 3A). It seems the diversity was generated by spatial factors because they are originated from different countries with

different environment. Frankel and Soule' (1981) reported that one of the former on genetic diversity of landraces was attributable by diverse spaces and reproductive isolation. The rice landraces accessions characterized were separated from different places and constrained on their genetic transfer between each accession.

Among the resistance cluster, there were also diversity between origin of country with score 3 resistance accession being dominant (Figure 3B). Rice landrace accessions from Lao PDR which have the major resistance (score1) were the most susceptible comparing those from other countries. Notable, the genetic diversity of landraces within populations was generated by heterogeneity in time associated with both short term variations between seasons and by longer-term climate, biological and socio-economic changes (Frankel and Soule' 1981).

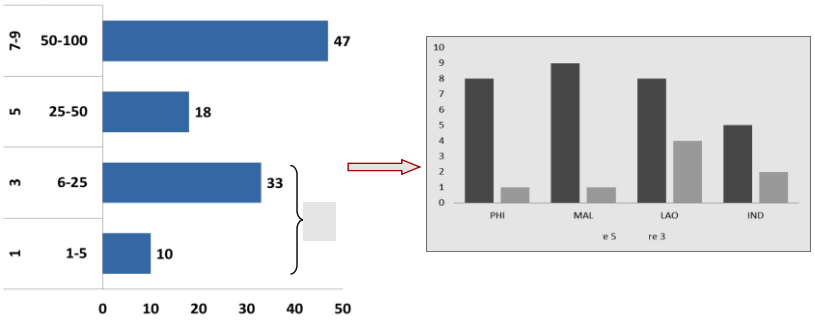

Figure 3. A. Distribution of BLB's resistance responds on rice landraces from Southeast Asia. B. The resistance group (s-1:score1 and s-3: score 3) in each country.

Finding Allelic Variation for Targets Traits Among Landraces

Conservation of all gene pools is a high priority for sustaining food security and coping with current and future climate change effects. Not only must landraces be conserved, but so should local varieties that have been replaced by new and more productive ones. Older varieties, due to the emphasis on landraces and more exotic materials, must not be forgotten, as well as other breeding materials, need to be conserved as a source of genetic diversity. Despite the enormous efforts made by national and international programs to conserve landrace diversities, eventually the conservation of germplasm and characterization of key traits will provide specific information to breeders that will promote the use of genetic resources by the scientific community.

Allele mining, being a tool at identifying allelic variation of relevant traits, is important to identify genes of known function and basic DNA sequence, therefore, genetic resources collections may be screened for allelic variation (Bhullar et al. 2010) using different molecular technologies. Isolation of important alleles from landraces and other genetic resources has been referred to as a source of functional allelic diversity and differential allelic frequency in comparison to modern breeding lines (material selected through breeding but not yet a variety) and varieties. This information will be highly valuable for enriching the genetic diversity within breeding programs. Discovery of new markers associated with key traits through genome-wide association studies (GWAS) will greatly benefit the scientific community, particularly after validation of important markers associated with complex traits (Lopes et al. 2015; Sukumaran et al. 2015).

Allele mining for BLB resistance on rice landraces was accomplished by specific markers for dominant major gene of

BLB resistance, Xa7, based on previous genomic map: 27.7-28.0 Kb on chromosome 6 (Chen et al. 2008; Proter et al. 2003; Utami et al. 2017). These specific markers could be applied to screen the rice accessions for allele mining purpose (Figure 4).

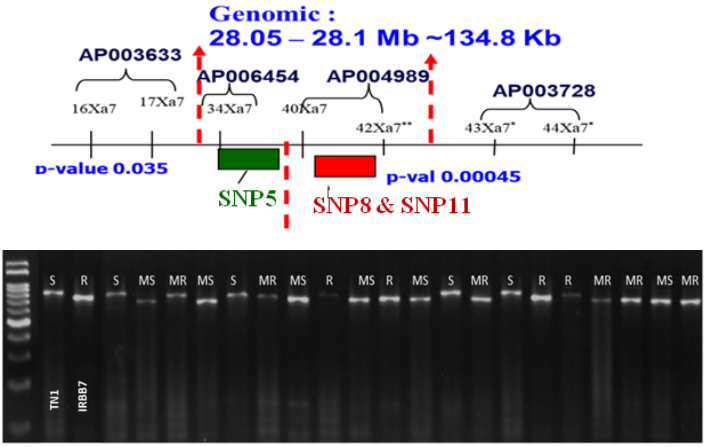

Figure 4. Allele mining of Xa7 gene by using the specific designed molecular markers based on fine map of the gene.

DOI Registered-Genetic Diversity and Allelic Variation into Gene Bank Database

Genetic diversity is the main source of variability in any crop improvement program. It serves as a reservoir for identifying superior alleles controlling key agronomic and quality traits through allele mining/association mapping. The assessment and conservation of diversity landraces have to be based on allelic variation at one or more loci. It will link to characterization activity to find the unique combinations of alleles which result in unique or distinct phenotypes. The discovery of abiotic stress at tolerant alleles in landraces of rice clearly shows the importance of conserving and exploring landrace germplasm as a mean to

identify genomic based to find beneficial alleles for enhancing adaptation and productivity in stress-prone environments (Dwivedi et al. 2016).

The characteristics of landraces in relation to the magnitude of allelic and genetic diversity in contrast to cultivars are considered to be significantly more genetically diverse (Fowler and Mooney 1990). Thus, a landrace is a 'highly variable population in appearance' (Harlan 1975b), 'highly diverse populations and mixtures of genotypes' (Hoyt and Brown 1992), 'genetically heterogeneous' (Villa et al. 2006), 'not genetically uniform and containing high levels of diversity' (FAO 1998), 'local diverse crop varieties' (Brush 1999), 'heterogeneous crop populations' (Hoyt and Brown 1992) and 'materials with variable levels of heterogeneity'. The diversity of landraces was influenced by allelic variation which as a key priority traits in breeding programs.

The ability of accession landraces which have DOI registered is potential to undergo rapid adaptation or utilization for genetic improvement. As consequence, the utilization of rice landraces for genetic improvement could be traceable the rice genetic resources for holding it in trust and confidence. The next important thing is the DOI's label was coexisting with other identifier, such as in gene bank management.

Concluding Remarks and Future Perspective

Loss of genetic diversity has been recognized as a genetic bottleneck imposed on crop plants during domestication and through modern plant-breeding practices. Allelic variation of genes originally found in the wild but gradually lost through domestication and breeding has been recovered only by going back to landraces. Landraces have potentially new allelic variation that should be exploited in rice breeding.

Several strategies to retain diversity found in rice landraces from Southeast Asia are available and must be implemented. The first strategy is measuring diversity to establish core collections where genetic diversity is maximized with minimum repetition and in intermediate generations of a breeding programme to conserve genetic variability for selection in later generations. The second is addressing the allelic variation for key traits in breeding programmes where the importance of keeping diversity has been well established. Allele mining for traits and alleles of interest (finding 'new' allelic variation for known functional genes among landraces and linkages or pleiotropic between new alleles for known functional genes and grain yield) will be highly valuable for enriching the genetic diversity within breeding programmes. Phenotypic variation and related genetic association for specific traits through large-scale and precision phenotyping can be coupled with GWAS for the identification of new markers. The third strategy is using the DOI's label, utilization of rice accession landraces which could be traceable in trust and worthwhile for gene bank management. Finally, the unified development of databases and promotion of data sharing among physiologists, pathologists, scientists, national programmes and breeders through linkages with gene banks will greatly benefit on rice improvement for adaptation to climate change worldwide.

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DIGITAL OBJECT IDENTIFIERS (DOI) FOR LOCAL RICE GENETIC RESOURCES OF CENTRAL KALIMANTAN

Susilawati and Muhamad Sabran

INTRODUCTION

Central Kalimantan which consists of 13 regencies and one city has two main agro ecosystems, namely dry land (including rainfed) and swamp land (both tidal, swampy and peat land). There are many diverse local rice genetic resources found in this area. The characteristics of the rice plants are very high, high and medium. The grains are slim, small, round, long, hairy, grain color reddish, golden or blackish, etc. Responses to biotic and abiotic stresses are resistant to stem borer, blast disease, inundation, shade tolerant and tolerant to certain acidity levels. Local rice is generally 5-6 months old, and is widely planted by local people for consumption, seed production and traditional ceremonies (Susilawati et al. 2014). They are widely developed and utilized. Several rice accessions were also threatened with extinction and some are no longer be found. More than 170 local rice accessions from Central Kalimantan have been explored. Some have been characterized and collected at Genebank of Indonesian Center for Agricultural

Biotechnology and Genetic Resources (ICABIOGRAD) and Assessment Institute for Agricultural Technology (AIAT) of Central Kalimantan (Susilawati et al. 2017). Some of local rice accessions also have been registered by Center for Plant Variety Protection and Agricultural Licensing (PPVTPP).

In the management of genetic resources in AIAT of Central Kalimantan, the system of documentation and information on explored and collected local rice genetic resources are still limited to passport data (data relating to the origin of germplasm material) and characterization data (data relating to morphological and agronomy characters), as well as information on resilience and/or tolerance to biotic and abiotic stresses, which are compiled based on field information. At present the information system has been developed with a computer-based Decision Support System (DSS). In this system information on genetic resources that are explored and collected can be known for their distribution and existence, and equipped with cultivation information and recommendations for development and utilization and their level of suitability (Bhermana and Susilawati 2018). Local rice data information systems arranged in the form of a database system will be good and may ease the process in entering data into storage media, data validation during the entry stage, flexibility in the operation of data entry and access, data availability is always up to date and allows for rapid exchange of data (Kurniawan et al. 2004).

The development of food crop germplasm data base using the Digital Object Identifiers (DOI) system was introduced. The DOI has been adopted by the Scientific Advisory Committee (SAC) on the Global Information System (GLIS) and applied in the management and exchange of Plant Genetic Resources for Food and Agriculture (PGRFA). For the trials in Indonesia, local rice commodities from Central Kalimantan are also used as model

plants. Implementation of the DOI system that is standard ISO 26324 would be application of all genetic resources of food crops (PGRFA) commodities. Indonesia, which is trusted as a coordinator for software development (GLIS-Toolkit) in order to support the implementation of the DOI system, has collaborated with the ITPGRFA-FAO Secretariat in Rome, Italy and the International Rice Research Institute (IRRI) in the Philippines to conduct dissemination and technical training to several ITPGRFA-FAO signatory countries.

This paper is a review of some of the results in the Central Kalimantan AIAT management of local rice genetic resources, which aims to provide information on the existence and availability of its local rice germplasm that can be exchanged and utilized in scientific development, through registration in the DOI system.

Exploration and Characterization of Local Rice Genetic Resource of Central Kalimantan

Exploration of food crops, especially local rice, has been carried out since 2013 and continues to be expanded. In 2013 exploration of genetic resources was carried out in the yard, then since 2014 exploration of food crops, especially local rice, has been carried out on various land agroecosystems, both in swamp land, such as tidal, swampy and peatland and dryland including rainfed land (Susilawati et al. 2015). Until April 2019 as many as 171 local rice accessions from Central Kalimantan have been explored, they consist 35 accessions (2013), 43 accessions (2014), 32 accessions (2015), 20 accessions (2016), 12 accessions (2017), 10 accessions (2018) and 19 accessions (2019). Based on its distribution, around 63% of accession is explored from dryland rice and 37% is from swamp land (Susilawati et al. 2018). Most of

the exploration results have been collected at Genebank of ICABIOGRAD, and some are collected simply in Central Kalimantan AIAT.

Characterization performed on collected local rice is still limited to morphological or agronomic traits, which consists of leaf surface, flag leaf position, leaf neck color, leaf ear color, leaf book color, leaf strand color, leaf midrib color, leaf tongue color, leaf length, leaf width, stem segment color, stiffness of the stem, panicle type, pan panicle, panicle length, sterile lemma, lemma and palea color, sterile lemma color, color of grain tip, grain edge feather, color of the end of grain, color pistil head, class variety, flowering age, harvest age, number of tillers, plant height, habitus and loss (FAO 1996; IRRI 1996). Evaluation on amylose content, resistance to bacterial leaf blight, resistance to white-striped leaf pests, resistance to pests, resistance to aluminum poisoning and resistance to drought, were not carried out. This is due to the limitation of human resources to manage genetic resources and other facilities contained in Central Kalimantan AIAT.

Besides having specific characters of varieties, some local rice accessions that are explored and collected, have good adaptability to sub-optimal land. Rice accession explored from dryland agroecosystems, with the main constraints of low soil pH and high Al content (Kochian 1995), proved to be able to withstand these conditions. Even though it is known that high Al solubility can inhibit root growth and function, and therefore, the condition can reduce production between 25%-85% (Herrera and Estrella 2003). Two dryland local rice varieties known as Sentang variety from the Kapuas district and Sahuwi from the district Lamandau have a mechanism to defend themselves in these clenched conditions by extending their roots to soil pH 4.0 while the condition of the land is quite dry.

In the case of swamp agroecosystem, two varieties known as Siam Epang from Kotawaringin Timur district and Brenti from Pulang Pisau district may survive in the conditions of Fe poisoning by an excluder mechanism, which is a mechanism by which plants are able to accumulate excessive Fe^{2+} ions at the root, and inhibit the entry of excessive Fe^{2+} ions into the root zone (Marschner 1995). In addition, in the inundated conditions, all plants are also able to survive by forming new roots as their adaptability mechanism. This condition is in accordance with Yang et al. (2005), which states that the excluder mechanism contained in plants is related to ethylene production in roots. Ethylene in the form of small and gas-shaped molecules has a function to help the development of aerenchyma in the roots and also the formation of new roots as a way of adapting plants to stagnant conditions.

Management of Local Rice Genetic Resources Specific Location

The management system of genetic resources, especially local rice in Central Kalimantan AIAT has been carried out, among others, by compiling passport data (data relating to the origin of germplasm material), characterization data (data relating to morphological and agronomic characters) and information on resilience/tolerance to biotic and abiotic stresses, which are compiled based on field information. In information based on passport data, specifically for local rice, data is divided into local rice data specific to swamps and dryland, as shown in Table 1 and Table 2.

Table 1. Local rice genetic resources specific on swamp land of Central Kalimantan.

No.	Accesion number	Accesion name	Village	Sub Distric	District	Harvest time	Rice type
1	0041	Brenti	Tahai Jaya	Maliku	Pulang Pisau	130	White Rice
2	0042	Buntut kuda	Tahai Jaya	Maliku	Pulang Pisau	130	White Rice
3	0043	Kahayan	Tahai Jaya	Maliku	Pulang Pisau	130	White Rice
4	0044	Karang Dukuh	Palingkau	Dadahub	Kapuas	125	White Rice
5	0045	Kencana	Tahai Jaya	Maliku	Pulang Pisau	130	White Rice
6	0046	Lemo	Tahai Jaya	Maliku	Pulang Pisau	130	White Rice
7	0047	Pentet,	Tahai Jaya	Maliku	Pulang Pisau	130	White Rice
8	0048	Pikat	Tahai Jaya	Maliku	Pulang Pisau	130	White Rice
9	0049	Siam Banjar	Palingkau	Dadahub	Kapuas	125	White Rice
10	00410	Siam Epang	Palingkau	Dadahub	Kapuas	125	White Rice
11	00411	Siam Landak	Palingkau	Dadahub	Kapuas	125	White Rice
12	00412	Siam Lantik	Palingkau	Dadahub	Kapuas	125	White Rice
13	00413	Siam Mutiara	Dadahup	Dadahub	Kapuas	125	White Rice
14	00414	Siam Pedang	Palingkau	Dadahub	Kapuas	125	White Rice
15	00415	Siam Pudak	Palingkau	Dadahub	Kapuas	125	White Rice
16	00416	Siam Sekonyer	Kumai	Kumai	Arut Selatan	125	White Rice
17	00417	Siam Unus	Palingkau	Dadahub	Kapuas	125	White Rice
18	00418	Bajang	Palingkau	Dadahub	Kapuas	125	White Rice
19	00419	Balimau	Buntut Bali	Tewang SG	Katingan	125	White Rice
20	00420	Banyu Bilis	Buntut Bali	Tewang SG	Katingan	125	White Rice
21	00421	Barinsai	Palingkau	Dadahub	Kapuas	125	White Rice
22	00422	Behas bahandang	Jabiren	Jabiren Raya	Pulang Pisau	125	Red Rice
23	00423	Bulan	Palingkau	Dadahub	Kapuas	125	White Rice
24	00424	Buntut Raja	Palingkau	Dadahub	Kapuas	125	White Rice
25	00425	Cirendah	Buntut Bali	Tewang SG	Katingan	125	White Rice
26	00426	Gadabung	Timpah	Timpah	Kapuas	125	White Rice

At present the a computer-based information system has been developed by *Decision Support System* (DSS). In this system, information on explored and collected genetic resources is equipped with a map of whereabouts and their distribution. In addition, it is equipped with cultivation information and

recommendations for its development and utilization (Bhermana and Susilawati 2018). PC-based Microsoft Access applications used in developing database systems with DSS are built as planning databases that are used for logical data structures in helping decision makers for planning and management (Hirouchi and Kosaka 1984). This application is also effective for database management systems (DBMS) (Oktarina and Kuswantoro 2011).

Table 2. Local rice genetic resources specific on upland of Central Kalimantan.

No.	No accesion	Name accesion	District	Status accesion	Old of Harvest	Rice type
1	0151	Garagai	Kapuas	Lokal	130	White Rice
2	0152	Humbang Inai	Katingan	Lokal	130	White Rice
3	0153	Kalanis	Katingan	Lokal	130	White Rice
4	0154	Kowong	Katingan	Lokal	130	White Rice
5	0155	Kumpang Emas	Lamandau	Lokal	130	White Rice
6	0156	lokal Gilai	Lamandau	Lokal	130	White Rice
7	0157	Lungkuh Tamuun	Barut	Lokal	130	White Rice
8	0158	Manyahi	Kapuas	Lokal	130	White Rice
9	0159	Mungkolandik	Gunung Mas	Lokal	130	White Rice
10	01510	Pahakung	Lamandau	Lokal	130	White Rice
11	01511	Siam Gunung	Barut	Lokal	130	White Rice
12	01512	Sibung rendah,	Katingan	Lokal	130	White Rice
13	01513	Talun Bajang	Barito Utara	Lokal	130	White Rice
14	01513	Talun Bitik	Barito Utara	Lokal	130	White Rice
15	01514	Tambangan	Barito Utara	Lokal	130	White Rice
16	01515	Tampui	Lamandau	Lokal	130	White Rice
17	01516	Umbang putih,	Katingan	Lokal	130	White Rice
18	01517	Buyung	Katingan	Lokal	130	White Rice
19	01518	Garagai	Kapuas	Lokal	130	White Rice
20	01519	Garu	Barito Utara	Lokal	130	White Rice
21	01520	Gilai	Lamandau	Lokal	130	White Rice
22	01521	Goyang pinggul	Barito Utara	Lokal	130	White Rice
23	01522	Humbang Inai	Lamandau	Lokal	130	White Rice
24	01523	Kalanis	Katingan	Lokal	130	White Rice
25	01524	Karang Dukuh	Kapuas	Lokal	130	White Rice
26	01525	Karundang	Kapuas	Lokal	130	White Rice

Regarding the availability of information maps, the application of geographic information systems (GIS) called Q-GIS 3.4 is also used to supplement databases in spatial format. In addition to facilitating, improving, storing, and displaying data, the application can also be used to update data and utilization in the future (Eswaran et al. 1992; Goodchildet al. 1992; Bhermana et al. 2002; Son and Rajendra 2008). As part of the GIS, a basic reconnaissance-scale land system map of land systems is also used to identify land suitability for each local rice plant genetic resources (PGR) in accordance with its habitat. This is beneficial for the development of in situ and *ex situ* according to the similarity of landforms, soil, vegetation, and relative climate uniform (FAO 1993; Suharta 2007).

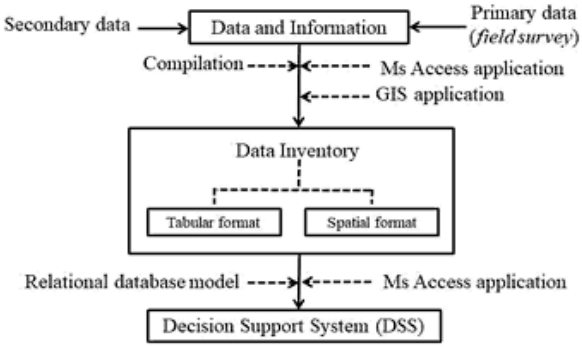

Figure 1. Diagram of DSS preparation procedure.

DOI Registration and Utilization of Central Kalimantan Local Plant Genetic Resources

DOI has been currently chosen for the mechanism of providing and identifying unique and permanent germplasm globally. In Indonesia the development of a food crop germplasm database with DOI system was introduced. This digital object identifier has also been adopted by the Scientific Advisory

Committee (SAC) on the Global Information System (GLIS) and applied in the management and exchange of Plant Genetic Resources for Food and Agriculture (PGRFA). Implementation of the DOI system that is standard ISO 26324 would be application to all PGRFA commodities. Indonesia, which is trusted as a coordinator for software development (GLIS-Toolkit) to support the implementation of the DOI system, has collaborated with the ITPGRFA-FAO Secretariat in Rome, Italy and the International Rice Research Institute (IRRI) in the Philippines to conduct dissemination and technical training to several ITPGRFA-FAO signatory countries. For the trials in Indonesia, local rice commodities from Central Kalimantan were used as model plants. This trial resulted in 96 local rice accessions from Central Kalimantan were registered with DOI (Table 3).

From a number of local rice accessions from Central Kalimantan, there is one local variety, namely Siam Mutiara from Kapuas district that has been used as an parental line in plant breeding The government has also released the R1 variety Dadahup,a progeny of Siam Mutiara. One other variety, Siam Epang from the East Kotawaringin district, has been bleached as a local superior variety. In addition, as many as five local varieties have been fingerprinted by ICABIOGRAD, and as many as 10 local rice varieties have been registered with the Center for Plant Variety Protection and Agricultural Licensing, with evidence in the form of a register of plant varieties (Susilawati et al. 2018). In 2019 there will be 10-15 registered local rice varieties.

Conclusion

1. The genetic resources of local rice in Central Kalimantan are spread in two main agroecosystems, namely dryland and swampland.

2. Management of local rice genetic resources that have been carried out is compiling passport data, characterization data, and information on resistance to biotic and abiotic stresses, as well as computer-based information systems by Decision Support System that is able to provide spatial information on the distribution of genetic resources, cultivation information and recommendations for compliance.
3. A total of 96 local rice accessions from Central Kalimantan have also been managed through the Digital Object Identifiers, so as to encourage the use of local rice PGR globally for the benefit of scientific knowledge.

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THE FOUR YOGYAKARTA'S LOCAL RICE SUPERIORITY REGISTERED BY DIGITAL OBJECT IDENTIFIER

Setyorini Widyayanti, Kristamtini, and Nurul Hidayatun

INTRODUCTION

Indonesia is one of megadiversity country which has a diverse genetic resource: Rice is one of food crop genetic resources. Regional conditions (soil, rainfall type), Indonesia's topography and climate are very diverse, that contribute to rice accessions diversity which developed in each region of Indonesia. Some information states that rice is not an Indonesia native's plant. It is believed that rice have been first domesticated in Yang tse river valley, Hunan province, China in 5000-4000 BC and then referenced into Ganges river valley, which is around India and Sri Lanka, Korea, Japan and Southeast Asia (Indonesia, Malaysia, Philippines) (Vaughan et al. 2008; Gross and Zao 2014). In Indonesia, rice cultivation was spreading from west to eastern end sovereign part. It is not certainly known which one of Indonesia's territory that first made rice cultivation.

Rice does not consist only white rice, there is also rice accession which produces another colored rice, such as yellow, red, brown, purple and black rice (Sanghera et al. 2013). The color is due to anthocyanin pigment accumulated in the pericarp layer,

seed shell or aleurone (Kristamtini 2014). Colored rice is a type of rice that has existed over long period. Colored rice is believed to have special features because it has a high nutrient content which can control various diseases and also it can extend longevity of life (Kushwaha 2016). Red rice has been consumed by the people in India, Sri Lanka and Bhutan on their special days and traditional ceremonies, whereas in China, black rice is only consumed by the royal family (king) hence black rice is also called forbidden rice, king's rice or prized rice (Sanghera et al. 2013; Oikawa et al. 2015; Kushawa 2016). In 2014, Yogyakarta Assessment Institute for Agricultural Technology (AIAT) has conducted an exploration, inventory and identified 76 Yogyakarta local rice accessions (Sudarmaji 2014; Kristamtini et al. 2015). Yogyakarta is one of the provinces in Indonesia.It is located in central Java, and cover an area of 3,185.80 km²and It lies between 7°33'–8°12' South Latitude and 110°00'–110°50' East Longitude of Greenwichand stretches from 0-2,911 m above sea level (above sea level) (BPS 2014). Typology of Yogyakarta is quite diverse consisting of Mount Merapi area, lowland areas, coastal sandy land and mangrove area which contribute greatly to the existing of genetic resources diversity (Bappeda 2009). With the diversity of agro-ecosystem, it is possible that Yogyakarta have colored rice genetic resources.

The 76 local rice accessions consisted of white rice, red rice, black rice and sticky rice. Genetic resources management of AIAT consist of exploration, identification, characterization, evaluation and utilization so that it will not disappear or become extinct. Beside preserving and protecting genetic resources from extinction and biopiracy, the government has provided a legal law through a mechanism for registering both local varieties and breeding activity with the enactment of Law No. 29 of 2000 concerning Protection of Plant Varieties, government law No. 13

of 2004 concerning Registration of Plant Varieties and the Ministry of Agriculture Decree No. 67/2006 concerning the preservation and utilization of genetic resources (PPVTPP 2015).

An effort to improve conservation and sustainable use of food and agricultural genetic resources were also made by FAO (Food and Agriculture Organization) which is a United Nation organization. The exploration to identification activities of AIAT Yogyakarta were funded by FAO's Benefit Sharing Fund under the International Treaty of Plant Genetic Resources for Food and Agriculture (ITPGRFA), multicountry activities. This kind of platform is expected to reduce the information gap between gene bank curators, rice breeders and researchers who are involved in agricultural cultivation for supporting transfer of technology and information of genetic resources for developing a new variety. The platform also supports applied germplasm curation and forward-looking rice breeding programs and strategic rice research.

Sharing information regarding to plant genetic resources, especially annex-1 group of plants, has been carried out by countries who already signed the ITPGRFA treaty using a diverse data storage application system. To provide an easy genetic resources data information access between those countries, a digital system identification was needed. Multi-country construction of a test platform for development and allocation of unique identifiers for rice germplasm is a research activity coordinate by Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development (ICABIOGRAD), which make an effort to adopt and implement digital object identifier (DOI) as a global, unique, no-bias identities and develop a platform to establish automatized system to system connection to add value to the material being transferred within and from the Multilateral System (MLS), thus

meeting both scientific needs and legal obligation of the Standard Material Transfer Agreement (SMTA).

The purpose of this paper is to provide information on the characteristics and superiority of four Yogyakarta colored rice cultivars which has been registered in a digital information system.

Digital Object Identifier (DOI) on Plant Genetic Resources

Indonesia is one of the countries which have ratified ITPGRFA in 2006. One consequence of ITPGRFA is that every country member agreed to establish a multilateral system of access and benefit sharing of plant genetic resource, which is efficient, effective, transparent, fair and in an equitable way. Instruments which can be used for information dissemination applications are Digital Object Identifier (DOI).

DOI is a permanent instrument that can be used to recognize or mark an electronic document. DOI is generally a series of unique and fixed codes (persistence) consisting of different numbers and letters on each object (entity). DOI can be used on all electronic documents, and currently it has been used to identify genetic resources accessions.

Rice is one of the commodities listed in Annex 1 of ITPGRFA and are listed as the main food commodities in many countries. However, rice genetic resources collection is not yet fully accessible in various treaty signatory countries. This is allegedly caused by the lack of information systems that support data access. Therefore, the dissemination of rice genetic resources diversity through DOI implementation is expected to be a part of an information system that supports, eases and facilitates data access.

AIAT Yogyakarta has successfully exploring, invented and carried out 76 Yogyakarta local rice. From identification and characterization activity, until the end of 2014, there were 55 accession of Yogyakarta local rice that was ready to be registered in the DOI system. The results have been registered into ICABIOGRAD registration system.

The 55 accession of Yogyakarta local rice which uploaded in ICABIOGRAD registration system have a variety of features. A few of them are now rare or only be found in a specific location in Yogyakarta. Another specific feature is a distinguished pericarps color (white, red or black pericarp color). Other accessions provide a specific fragrant aroma. Some of it are local rice accessions which have a potential value such as high production. There were also accessions which are specific on irrigated rice, upland rice also sticky rice. Information related to Yogyakarta local rice digital numbering can be accessed through https://ssl.fao.org/glis/. Yogyakarta local rice which has been registered through the ICABIOGRAD digital numbering system is listed in local ID numbers 05020-30654 up to numbers 05020-30708 (Widyayanti et al. 2018).

Morphological Characters of Yogyakarta Local Rice Registered by DOI

AIAT Yogyakarta has already explored and carried out 76 Yogyakarta local rice accessions. 55 local rice accessions have been fully identified and registered in DOI through ICABIOGRAD registration system. Registered accessions consisted of 5 accessions of red rice, 5 accessions of black rice, 30 accessions of white rice, and 15 accessions of sticky rice.

According to Indonesian Ministry of Agriculture Decree, 4 Yogyakarta local rice accessions which have been assigned with

DOI have been released as a local superior variety. The four rice varieties are 1) Mandel Handayani which has been released into local superior variety through Indonesian Ministry of Agriculture Decree number 2227/Kpts/SR.120/5/2009, May 19, 2009; 2) Segreng Handayani which has been released into local superior variety through Indonesian Ministry of Agriculture Decree, number 2226/Kpts/SR.120/5/2009, May 19, 2009; 3) Cempo Merah Sleman through Indonesian Ministry of Agriculture Decree number 126/HK.540/C/03/2019, March 6, 2019 which was released as a local superior variety under the name of Sembada Merah and 4) Pari Ireng through Indonesian Ministry of Agriculture Decree number 125/HK.540/C/03/2019, dated March 6, 2019 which was released as a local superior variety under the name of Sembada Hitam.

Mandel Handayani and Segreng Handayani are specific local red rice variety from Gunungkidul. Gunungkidul is one of Yogyakarta's district area which mainly consists of dry land, and thus both rice varieties are commonly cultivated as an upland rice. Sembada Merah is red rice and Sembada Hitam is black rice, both of them are from Sleman, one of Yogyakarta's district area. Sembada Merah and Sembada Hitam are commonly cultivated as irrigated rice. Four of Yogyakarta colored rice are registered in ICABIOGRAD local ID number05020-30660; 05020-30666; 05020-30707 and 05020-30707 (Table 1).

Table 1. Identification of DOI, local ID, type and origin of 4 Yogyakarta colored rice varieties.

Accessions	DOI	Local ID	Type of rice	Area origin
Mandel Handayani	10.18730/SF1F	05020-30660	Upland rice	Gunungkidul, Yogyakarta
Segreng Handayani	10.18730/SF1N4	05020-30666	Upland rice	Gunungkidul, Yogyakarta
Sembada Merah	10.18730/SF2Y8	05020-30707	Irrigated rice	Sleman, Yogyakarta
Sembada Hitam	10.18730/SF2Z9	05020-30708	Irrigated rice	Sleman, Yogyakarta

Sources: Kristamtini et al. (2015); Widyayanti et al. (2018).

Descriptions of morphological characters of the 4 Yogyakarta specific colored rice varieties are presented in Table 2 and Figure 1. Although morphological characters observations are strongly influenced by the environmental conditions in which they growth, these observations are considered the most accurate for identifying the phenotypic performance of individuals or groups of plants (Kristamtini et al. 2015). According to morphological character, plant height of red rice from both Gunungkidul (Mandel Handayani and Segreng Handayani) and Sleman (Sembada Merah) has a medium-sized plant (110-130 cm for irrigated rice and 90-125 cm for upland rice) (Komnas Plasma Nutfah 2003). Similarly, Sembada Hitam has a medium plant height (125 cm). Medium-sized plant height is preferred by farmers, because of easier harvesting process.

Figure 1. Morphology performance of grain and rice seeds of 4 Yogyakarta colored rice.

Table 2. Description of the morphological character of 4 Yogyakarta specific colored rice varieties.

Characters	Accessions			
	Mandel Handayani	Segreng Handayani	Sembada Merah	Sembada Hitam
Days of maturity (day)	115	112	111	140
Plant height (cm)	141.00	93.50	91.00	125.00
Number of productive tillers	2 – 5	8	10 – 15	10 – 15
Number of full grainsper panicle	193	143	112	141
Yield potential (t/ha)	4.50	4.00	6.00	6.00
Weight of 1000 seeds (g)	27.00	24.33	26.67	24.00
Plant shape	slightly curved erect	erect	erect	erect
Feet color	green	purple	purple	green
Culm color	green	purple	green	green
Leaf blade color	colorless	colorless	purple lines	purple lines
Ligule color	colorless	colorless	puple lines	white
Flag leaf	semi-erect	erect	erect	erect
Grain shape	round	slender	slender	slender
Grain loss	easiest	easiest	Easy	moderate
Culm strenght	very weak	weak	strong	strong
Grain color	yellow	Reddish yellow	Straw yellow	Black with yellow lines
Pericarp color	Red to endosperm	Red	Red	Black

Sources: Kementerian Pertanian (2009; 2009a; 2019; 2019a).

Days to maturity is relatively similar between the red rice accessions (Mandel Handayani, Segreng Handayani and Sembada Merah) which is around average of 112 days so that it is classified as early maturity rice (105-124 days). Sembada Hitam is classified as medium-days to maturity rice (125-150 days) (BB Padi 2009). The number of productive tillers of Mandel

Handayani and Segreng Handayani is relatively small (<5-9 tillers). However, Mandel Handayani has greater number of productive tiller than Segreng Handayani. This is directly proportional that Mandel Handayani has higher yield potential than Segreng Handayani.

Pests and Diseases Resistance of Yogyakarta Local Superior Rice Varieties Registered by DOI

The main pests and diseases that usually attack rice cultivation in Indonesia are rice stem borer, brown planthopper, blast and bacterial leaf blight. Pests and diseases attack in all stages of growth in rice cultivation. If these pests and diseases were attacking in generative phase it could decline rice production.

Several efforts that could be considered effective for controlling pest and disease can be done through improved cultivation techniques, such as using healthy seeds, plant spacing, proper fertilization, environmental sanitation and prevention activity (Sudir et al. 2012). Other effort to prevent pests and diseases can be done by cultivating resistant varieties. Most of resistant varieties can be found in local varieties. Local varieties are believed to have resistance genes that can be used in breeding program.

The scoring observation showed that Mandel Handayani and Segreng Handayani were somewhat resistant of rice stem borer, sheath blight and bacterial leaf blight. The analysis using insect feeding behavior instrument namely electrical penetration graph (EPG) showed that Sembada Hitam followed by Sembada Merah have resistance to brown planthopper (Pemerintah Kabupaten Sleman 2018).

The resistance results analysis to bacterial leaf blight both through scoring intensity of disease progression and by using quantitative assessment indicators; namely AUDPC (Area Under Disease Progress Curve) with 2 weeks observation showed that Sembada Merah and Sembada Hitam AUDPC's value are lower than Ciherang's national variety. This indicated that Sembada Merah and Sembada Hitam have resistance to bacterial leaf blight (Pemerintah Kabupaten Sleman 2018).

These results are in line with Sutoro et al. (2018), which state that Yogyakarta specific colored rice varieties contain resistance gene to blast and bacterial leaf blight. Sembada Hitam has a *Pii* resistance gene against blast and Xa7-LD40 gene against bacterial leaf blight. Sembada Merah has resistance gene (Xa4-LD6) against bacterial leaf blight.

Physical and Chemical Properties of Yogyakarta Specific Colored Rice Varieties Registered by DOI

Despite of having specific morphological characteristics, the four Yogyakarta specific colored rice varieties also have specific physical and chemical quality characters. The character of physical quality can be assessed through grain and milled rice.

The physical quality character of milled rice can be determined through the percentage of head rice, percentage of broken rice, brewers, chalkiness and biological damaged kernel (Indrasari et al. 2016), which in Indonesia must standardize as SNI No. 01-6128-2008 in 2008. According to this standard, head rice is a rice grain with a greater size than or equal to 0.75 parts of whole rice grains. Head rice is a component of physical quality of rice which directly affects the level of consumer acceptance. The results of laboratory analysis showed the percentage of head rice: Segreng Handayani (86.95%), Mandel Handayani (82.63%) and Sembada Merah (80.63%) and smaller Sembada Hitam (68.85%).

Table 3. The physical quality character of milled rice of 4 Yogyakarta specific colored rice varieties.

Physical quality of milled rice	Accessions			
	Mandel Handayani	Segreng Handayani	Sembada Merah	Sembada Hitam
Head rice (%)	82.63	86.95	80.63	68.85
Broken rice (%)	10.59	12.94	19.27	30.82
Brewers (%)	2.14	0.11	0.11	0.33
Chalkiness (%)	4.64	0.08	2.58	2.81
Damaged kernel (%)	0	0	0.47	0

Sources: Purwaningsih et al. 2008; BPTP Yogyakarta 2018; Pemkab Sleman 2018.

High percentage of broken rice, which occurs in mostly in Sembada Hitam, causes declining level of consumer acceptance, because consumers are less interested in the physical condition of rice that is not intact. The higher percentage of broken rice and brewers will decrease its economic value. Broken rice is a rice grain with has larger size than 0.2 to smaller than 0.8 parts of whole rice grains, and brewers is a rice grain with smaller size less than 0.2 parts of whole grains of rice. Mandel Handayani, Segreng Handayani, Sembada Merah and Sembada Hitam rice percentages still fulfill quality standards at all quality levels (SNI 2008).

Chalkiness is a brown rice which has white chalky and soft textured due to physiological factors, including greenish kernel (immature grains) which is harvested when the rice is not yet optimum. The four of Yogyakarta local superior rice varieties has chalkiness rice: Mandel Handayani (4.64%), Segreng Handayani (0.08%), Sembada Merah (2.58%) and Sembada Hitam (2.81%). Based on SNI 2008, chalkiness rice that meets the standards quality is Segreng Handayani, Sembada Merah and Sembada Hitam which have a maximum content of chalkiness of 3% of sample weight.

Biological damaged kernel is a damaged kernel caused by mechanical, physiological and pathological factors (SNI 2008; Febriandi 2017). The four of Yogyakarta specific colored rice varieties still meet the SNI 2008 quality standard of rice, which has the maximum standard grain damage of 3% of sample weight.

The chemical quality character of the four varieties is presented in table 4. Chemical quality characteristics are needed to determine the nutrient content that shows the quality of rice that can fulfill nutritional needs. The nutritional of rice which can indicate the level of glutinous rice is amylose content. The higher the amylose content, the lower the glutinous rice level. According to Damardjati (1988), the classification of amylose content is divided into waxy (1-2%), very low (2-9%), low (10-20%), intermediate (20-25%) and high (25-30%).

Sembada Hitam has the lowest amylose content (5.89%) so the rice texture is very glutinous but not waxy like sticky rice. Sembada Merah has 21.42% of amylose content so that the texture of rice is relatively glutinous. Mandel Handayani and Segreng Handayani are upland rice, with 28.77% and 29.55% amylose content, respectively, and are still classified as glutinous textured rice which tends to be rather hard.

Nutrient content that is a feature characteristic of colored rice is anthocyanin content. Anthocyanin is a phenolic compound that belongs to flavonoid group. The color difference formed in rice pericarp is influenced by the composition of the anthocyanin compounds. Anthocyanin functions as an antioxidant that has healthy benefit, such as preventing premature aging, protecting the stomach from damage, inhibiting tumor cell development, anti-inflammatory and anticancer compounds, preventing obesity and diabetes, improving brain memory, preventing neurological diseases and warding off free radicals (Kushwaha 2016).

Sembada Hitam's anthocyanin content showed the highest value (369.5μ/100g) compared to the red rice varieties. This is in line with the opinion of Sutharut and Sudarat (2012), which states that the highest anthocyanin content is found in black rice when compared to other colored anthocyanin rice or white rice.

Table 4. The chemical quality characteristics of milled rice of 4 Yogyakarta specific colored rice varieties.

Chemical quality parameters	Accessions			
	Mandel Handayani	Segreng Handayani	Sembada Merah	Sembada Hitam
Water content (%)	12.64	14.38	11.83	13.60
Ash content (%)	1.24	1.18	0.88	0.43
Protein (%)	10.2	9.25	9.04	5.51
Fat (%)	2.19	2.50	1.59	1.85
Crude fiber (%)	3.46	3.97	0.45	5.77
Amylose (%)	28.77	29.55	21.42	5.89
Amilopektin (%)	40.59	40.58	45.65	-
Starch (%)	69.36	70.03	67.07	89.05
Anthocyanin (cyanidin-3-glucosida μ/100g	nd	nd	1.2	369.5

Sources: Purwaningsih et al. 2008; Kristamtini et al. 2018; Pemerintah Kabupaten Sleman 2018; nd = not identified.

Concluding Remarks and Future Perspective

Four Yogyakarta specific colored rice varieties with its superiority in morphological characters, resistance to certain pests and diseases, physical and chemical quality characters have been assigned with the DOI system and thus, they can be included into Multi-Lateral System for ABS. Complete information is expected to be related to the diversity of genetic resources of rice, especially colored rice. Information related to Yogyakarta genetic resources diversity can be used as an ingredient of crossbreeding inmodern breeding programs.

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DOI IMPLEMENTATION ON RICE GERMPLASMS OF BRRI GENEBANK: PRESENT AND FUTURE ASPECTS

Armin Bhuiya, Md. Shahjahan Kabir, and Md. Khalequzzaman

INTRODUCTION

Global warming and climate change is harshly affecting biodiversity around the world. Bangladesh is blessed with diverse economically important plant genetic resources as it belongs within the geographical domain of Indian mega center of origin and also located near the Chinese mega center of origin (Hossain et al. 2014). These resources have high potential genetic variations, which can provide tremendous contribution in plant breeding to overcome various challenges by developing new varieties with high yield, biotic and abiotic stress tolerance etc.

Sharing or exchange of plant genetic resources (PGRs) has gained high attention worldwide to address certain environmental challenges, mitigate global hunger and achieve food security. Different organizations have different locally assigned identifiers for their PGRs, which can create confusions when these PGRs are transferred across organizations. Such problem can be minimized by a globally unique, persistent

identifier such as Digital Object Identifier (DOI), which should maintain consistency over time, and provide proper recognition of rights and obligations as well as facilitating access to research outcomes produced by subsequent recipients of the materials (Alercia et al. 2018). Though DOI is only very recently introduced in Bangladesh, BRRI Genebank has pioneered in the registration of germplasms to obtain DOI in GLIS.

Background

International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) of the United Nations (FAO) is facilitating research, conservation and exchange of germplasms worldwide through the development and promotion of the use of Digital Object Identifiers (DOIs), which is an international standard to identify plant germplasm worldwide. The Treaty defines PGRFA as any genetic material of plant origin of actual or potential value for food and agriculture. This broad definition encompasses not only accessions conserved in genebanks and PGRFA conserved *in situ*, but also breeding lines, research materials, and protected modern varieties (Alercia et al. 2018).

Bangladesh has several National Biodiversity strategies and action plans for the conservation and sustainable use of plant genetic resources for food security, and modern agricultural practice like National Agriculture Policy-2018, National Biodiversity Strategy and Action Plan of Bangladesh 2016 to 2021, Access and beneficiary policy, Biosafety Guidelines of Bangladesh-2007, National Biosafety Framework-2007 and 7th Five Year Plan. It already has collaboration with FAO, IRRI, CIMMYT, ICRISAT, SAARC, AFACI, CIP, ICARDA and AVRDC for germplasm exchange and plant improvement for climate resilience. Bangladesh also has SMTA with AFACI and CGIAR institutes (Salam 2018).

Genebanks worldwide are conserving millions of accessions, some of which are duplicates but most carry valuable information associated with them. Sometimes this information is lost during the transfer of the material from one holder to another. Different user communities such as plant breeders, data curators, researchers and extension officers follow different methods to assign identifiers. This lack of standardization complicates the exchange of PGRFA data worldwide and creates challenges for effective conservation and sustainable use of PGRFA. Several communities (genebank community, genomics community, plant breeders, journal editors etc.) have emphasized the importance of creating and adopting Permanent Unique Identifiers for improved identification of PGRFA for better collaboration for conservation, research and breeding. By using the DOI standards adopted by the Governing body of the International Treaty, users will be able to identify and document their plant material uniquely and permanently and this will facilitate data interoperability among different systems. DOIs can be used to identify PGRFA held by any individual or organizations including genebanks, plant breeders, geneticists, other plant scientists, extension officers, seed companies, plant variety protection offices, gardeners, farmers, landowners and land managers (Alercia et al. 2018).

According to Alercia et al. 2018, DOI system brings the following new opportunities for users:

1. It exposes the material to the public or collaborators in a format that can be resolved by humans as well as computers
2. It enables information on the materials to be harvested by robots searching publications and online databases that refer to the PGRFA by its DOI and thus making them more readily available

3. It facilitates access to the information about the PGRFA and related PGRFA by pointing to websites and systems where detailed information is created, maintained and made available to the public
4. It provides a simple way of for recipients of material under an SMTA to comply with their obligations under the provisions of Article 6.9[3]of the SMTA, simply by using the DOI in their publications and online datasets to refer to the material received
5. It helps developers of PGRFA to maintain their records and comply with their obligations under SMTA article 6.5[b]
6. It enables families of PGRFA to be identified and thus jointly searched. For example, it enables a genebank manager to easily find all publications and online datasets created by recipients of accessions from the genebank
7. It provides a simple reliable mechanism to identify accessions that are duplicated across genebank
8. It facilitates interoperability between databases, by providing a single common standard for sample identification used by all communities
9. It enables collaborating laboratories, should they wish to track samples between them with any appropriate degree of precision while each laboratory continues to use its own in-house sample tracking system, providing assurance that they are working on the same material.

DOI Application in Bangladesh

Bangladesh Rice Research Institute (BRRI) has pioneered the registration of DOI for germplasms in Bangladesh. BRRI has 8578

germplasms registered as accession conserved in genebank (Table 1). A total of seventy germplasms were registered during the training program of "The 2nd International Workshop and Training on Software Testing to Support DOI Implementation" held at ICABIOGRAD, Indonesia on 26/04/19 to 2/05/2019 (Table 2). These are BRRI developed HYVs with special features. Most of these varieties are not only in high demand at farmers' field, but also have frequent utilizations and incorporation in new breeding programs (Table 3).

Table 1. Present status of BRRI genebank collection.

Variety/Line	Accession (no.)
Indigenous *indica* (Local)	5373
Indigenous *indica* (Pure Line)	857
Local *indica* varieties and breeding lines	565
Exotic *indica* (IRRI, China, USA, Turkey etc.)	1610
Japonica (Korea, Japan, Taiwan, N. China)	103
Wild rice (4 species)	46
Unknown	24
Total	8578

(Source: GRS Division, BRRI, 2019).

Table 2. List of BRRI germplasms registered in the GLIS.

Sl.No.	WIEWS	PID	Genus	NAME	Acc. No.	DOI
1	BGD002	00BA47	Oryza	BR-1	6865	10.18730/SBP66
2	BGD002	00BA47	Oryza	BR-3	4759	10.18730/SBP77
3	BGD002	00BA47	Oryza	BR-10	7089	10.18730/SBP88
4	BGD002	00BA47	Oryza	BR-11	6707	10.18730/SBP99
5	BGD002	00BA47	Oryza	BR-14	6872	10.18730/SBPAA
6	BGD002	00BA47	Oryza	BR-16	6874	10.18730/SBPBB
7	BGD002	00BA47	Oryza	BR-21	6199	10.18730/SBPCC
8	BGD002	00BA47	Oryza	BR-22	7090	10.18730/SBPDD
9	BGD002	00BA47	Oryza	BR-23	7091	10.18730/SBPEE
10	BGD002	00BA47	Oryza	BR-24	4276	10.18730/SBPFF

Table 2. Continue.

Sl.No.	WIEWS	PID	Genus	NAME	Acc. No.	DOI
11	BGD002	00BA47	Oryza	BR-25	4277	10.18730/SBPGG
12	BGD002	00BA47	Oryza	BR-26	4278	10.18730/SBPHH
13	BGD002	00BA47	Oryza	BRRI dhan27	4408	10.18730/SBPJJ
14	BGD002	00BA47	Oryza	BRRI dhan28	4409	10.18730/SBPKK
15	BGD002	00BA47	Oryza	BRRI dhan29	4410	10.18730/SBPMM
16	BGD002	00BA47	Oryza	BRRI dhan30	4411	10.18730/SBPNN
17	BGD002	00BA47	Oryza	BRRI dhan31	4412	10.18730/SBPPP
18	BGD002	00BA47	Oryza	BRRI dhan32	4413	10.18730/SBPQQ
19	BGD002	00BA47	Oryza	BRRI dhan33	7092	10.18730/SBPRR
20	BGD002	00BA47	Oryza	BRRI dhan34	7093	10.18730/SBPSS
21	BGD002	00BA47	Oryza	BRRI dhan36	6879	10.18730/SBPTT
22	BGD002	00BA47	Oryza	BRRI dhan37	7094	10.18730/SBPVV
23	BGD002	00BA47	Oryza	BRRI dhan38	7095	10.18730/SBPWW
24	BGD002	00BA47	Oryza	BRRI dhan39	7096	10.18730/SBPXX
25	BGD002	00BA47	Oryza	BRRI dhan40	7097	10.18730/SBPYY
26	BGD002	00BA47	Oryza	BRRI dhan41	7098	10.18730/SBPZZ
27	BGD002	00BA47	Oryza	BRRI dhan42	6214	10.18730/SBQ0*
28	BGD002	00BA47	Oryza	BRRI dhan43	6215	10.18730/SBQ1~
29	BGD002	00BA47	Oryza	BRRI dhan44	7099	10.18730/SBQ2$
30	BGD002	00BA47	Oryza	BRRI dhan45	6880	10.18730/SBQ3=
31	BGD002	00BA47	Oryza	BRRI dhan46	7100	10.18730/SBQ4U
32	BGD002	00BA47	Oryza	BRRI dhan47	6881	10.18730/SBQ50
33	BGD002	00BA47	Oryza	BRRI dhan48	7980	10.18730/SBQ61
34	BGD002	00BA47	Oryza	BRRI dhan49	7101	10.18730/SBQ72
35	BGD002	00BA47	Oryza	BRRI dhan50	6882	10.18730/SBQ83
36	BGD002	00BA47	Oryza	BRRI dhan51	7319	10.18730/SBQ94
37	BGD002	00BA47	Oryza	BRRI dhan52	7320	10.18730/SBQA5
38	BGD002	00BA47	Oryza	BRRI dhan53	7321	10.18730/SBQB6
39	BGD002	00BA47	Oryza	BRRI dhan54	7322	10.18730/SBQC7
40	BGD002	00BA47	Oryza	BRRI dhan55	7323	10.18730/SBQD8
41	BGD002	00BA47	Oryza	BRRI dhan56	7324	10.18730/SBQE9
42	BGD002	00BA47	Oryza	BRRI dhan57	7325	10.18730/SBQFA
43	BGD002	00BA47	Oryza	BRRI dhan58	8001	10.18730/SBQGB
44	BGD002	00BA47	Oryza	BRRI dhan59	8002	10.18730/SBQHC
45	BGD002	00BA47	Oryza	BRRI dhan61	8004	10.18730/SBQJD
46	BGD002	00BA47	Oryza	BRRI dhan62	8005	10.18730/SBQKE
47	BGD002	00BA47	Oryza	BRRI dhan63	8006	10.18730/SBQMF
48	BGD002	00BA47	Oryza	BRRI dhan64	8007	10.18730/SBQNG

Table 2. Continue.

Sl.No.	WIEWS	PID	Genus	NAME	Acc. No.	DOI
49	BGD002	00BA47	Oryza	BRRI dhan65	8008	10.18730/SBQPH
50	BGD002	00BA47	Oryza	BRRI dhan66	8009	10.18730/SBQQJ
51	BGD002	00BA47	Oryza	BRRI dhan67	8010	10.18730/SBQSM
52	BGD002	00BA47	Oryza	BRRI dhan68	8011	10.18730/SBQVP
53	BGD002	00BA47	Oryza	BRRI dhan69	8012	10.18730/SBQXR
54	BGD002	00BA47	Oryza	BRRI dhan71	8049	10.18730/SBQYS
55	BGD002	00BA47	Oryza	BRRI dhan72	8050	10.18730/SBR0V
56	BGD002	00BA47	Oryza	BRRI dhan73	8051	10.18730/SBR2X
57	BGD002	00BA47	Oryza	BRRI dhan74	8158	10.18730/SBR3Y
58	BGD002	00BA47	Oryza	BRRI dhan75	8159	10.18730/SBR5*
59	BGD002	00BA47	Oryza	BRRI dhan76	8160	10.18730/SBR8=
60	BGD002	00BA47	Oryza	BRRI dhan77	8161	10.18730/SBRA0
61	BGD002	00BA47	Oryza	BRRI dhan78	8164	10.18730/SBRC2
62	BGD002	00BA47	Oryza	BRRI dhan79	8202	10.18730/SBRF5
63	BGD002	00BA47	Oryza	BRRI dhan80	8203	10.18730/SBRH7
64	BGD002	00BA47	Oryza	BRRI dhan82	8588	10.18730/SBRMA
65	BGD002	00BA47	Oryza	BRRI dhan83	8589	10.18730/SBRPC
66	BGD002	00BA47	Oryza	BRRI dhan84	8590	10.18730/SBRRE
67	BGD002	00BA47	Oryza	BRRI dhan86	8592	10.18730/SBRTG
68	BGD002	00BA47	Oryza	BRRI dhan87	8593	10.18730/SBRWJ
69	BGD002	00BA47	Oryza	BRRI dhan88	8594	10.18730/SBRYM
70	BGD002	00BA47	Oryza	BRRI dhan89	8595	10.18730/SBRZN

Table 3. Examples of use of BRRI varieties to develop new high yielding varieties.

DOI	Variety Name	Pedigree	Parentage	Special Features
10.18730/SBPAA	BR14	BR319-1-HR28	IR5(D)/**BR3**	-
10.18730/SBPKK	BRRI dhan28	BR601-3-3-4-2-5	**BR6** (IR28)/ Purbachi	3 weeks earlier than BRRI dhan29. Suitable for flood prone area.
10.18730/SBPPP	BRRI dhan31	BR1725-13-7-1-6	**BR11**/ ARC10550	5-6 days earlier than BRRI dhan11
10.18730/SBPQQ	BRRI dhan32	BR4363-3-8-1-2-4	**BR4**/BR2626	-
10.18730/SBPVV	BRRI dhan37	BR4384-2B-2-2-HR3	Basmati (D)/ **BR5**	Aromatic rice, High Protein content

Table 3. Continue.

DOI	Variety Name	Pedigree	Parentage	Special Features
10.18730/SBPWW	BRRI dhan38	BR4384-2B-2-2-4	Basmati (D)/ **BR5**	Aromatic rice, plants are stronger than Basmati
10.18730/SBPYY	BRRI dhan40	BR5331-93-2-8-3	IR4595-4-1-15/ **BR10**	Moderately salt tolerant (8dS^{-m} at seedling stage)
10.18730/SBPZZ	BRRI dhan41	BR5828-11-1-4	**BR23**/ BR1185-2B-16-1	Moderately salt tolerant
10.18730/SBQ0*	BRRI dhan42	BR6058-6-3-3	**BR14**/ IR25588-7-3-1	Short duration variety, drought tolerant
10.18730/SBQ1~	BRRI dhan43	BR5543-5-1-2-4	**BR24**/ **BR21**	Short duration variety, drought tolerant
10.18730/SBQ2$	BRRI dhan44	BR6110-10-1-2	**BR10**/**BRRI dhan31**	Appropriate for Tidal area
10.18730/SBQ3=	BRRI dhan45	BR5877-21-2-3	**BR2**/TETEP	-
10.18730/SBQ4U	BRRI dhan46	BR5226-6-3-2	**BR11**/ Shawrnalata// ARC14766A	Low GI (Glycaemic Index) variety
10.18730/SBQ83	BRRI dhan50	BR6902-16-5-1-1	**BR30**/IR67684B	Aromatic, Premium Quality Rice (PQR)
10.18730/SBQA5	BRRI dhan52	IR85260-66-654-Gaz2	**BR11**/ IR40931-33-1-3-2	Submergence tolerant and High elongation
10.18730/SBQB6	BRRI dhan53	BR5778-156-1-3-HR14	**BR10**/ **BR23**// BR847-76-1-1	Moderately salt tolerant
10.18730/SBQFA	BRRI dhan57	BR7873-5*(NIL)-51-HR6	**BR11**/CR146-7027-224	Drought escaping variety
10.18730/SBQGB	BRRI dhan58	BRRI dhan29-SC3-28-16-4-HR2	Somaclonal variation of **BRRI dhan29** (Developed by tissue culture)	7-10 days earlier than BRRI dhan29
10.18730/SBQJD	BRRI dhan61	BR7105-4R-2	IR64419-3B-4-3/ **BRRI dhan29**	Salt tolerant variety
10.18730/SBQKE	BRRI dhan62	BR7517-2R-27-3	Zirakatari/BRRI dhan39	Medium Zinc enriched variety (19.8mg/kg)
10.18730/SBQMF	BRRI dhan63	BR7358-30-3-1	Amol-3/**BRRI dhan28**	Aromatic variety
10.18730/SBQSM	BRRI dhan67	BR7100-R-6-6	IR61247-3B-8-2-1/ **BRRI dhan36**	Salt tolerant variety (8dS^{-m} whole lifecycle)

Table 3. Continue.

DOI	Variety Name	Pedigree	Parentage	Special Features
10.18730/SBR0V	BRRI dhan72	BR7528-2R-19-HR10	BR7166-4-5-3/ **BRRI dhan39**	Zinc enriched variety (22.8mg/kg)
10.18730/SBR2X	BRRI dhan73	IR78761-B-SATB1-28-3-24	**BRRI dhan40**/ NSIC Rc106 (IR61920-3B-22-1-1)	Salt tolerant variety (8dS^{-m} whole lifecycle)
10.18730/SBR3Y	BRRI dhan74	BR7671-37-2-2-3-7	**BRRI dhan29**/ IR68144	Zinc enriched variety (24.2mg/kg)
10.18730/SBRF5	BRRI dhan79	BR9159-8-5-40-14-57	**BRRI dhan49***6/ **BRRI dhan52**	Submergence tolerant
10.18730/SBRPC	BRRI dhan83	BR6848-3B-12	**BR24**/BR1890-12-2-1-1-HR45	Medium drought tolerant
10.18730/SBRRE	BRRI dhan84	BR7831-59-1-1-4-5-1-9-P1	**BRRI dhan29**/IR68144 //**BRRI dhan28** ///**BR11**	High Zinc enriched variety (27.6mg/kg)
10.18730/SBRWJ	BRRI dhan87	BR(Bio)9786-BC2-132-1-3	**BRRI dhan29**/ *Oryza rufipogon*	7 days early than BRRI dhan49
10.18730/SBRYM	BRRI dhan88	BRRI dhan29-SC3-28-16-10-8-HR1(Com)	**Somaclonal variation of BRRI dhan29**	3-4 days early than BRRI dhan28
10.18730/SBRZN	BRRI dhan89	BR(Bio)9786-BC2-59-1-2	**BRRI dhan29**/ *Oryza rufipogon*	3-4 days early than BRRI dhan29 and higher yield

(Source: BRKB 2019).

Table 4. Yearly germplasm distribution from BRRI Genebank.

Year	Germplasm Distributed (Number)	Stakeholder
2010-11	1050	Research institutes, Universities, MS and PhD students, Plant Breeding Division of BRRI for hybridization, different divisions of BRRI for screening against different biotic and abiotic stresses, DAE, BADC, NGOs, Seed producing organizations etc.
2011-12	6495	
2012-13	617	
2013-14	790	
2014-15	1192	
2015-16	1523	
2016-17	2315	
Total	13982	

From table 4, it is clear that every year there is a huge demand for germplasms for research and development of novel varieties from institutions outside the Genebank or collection holder. Once the germplasms leave the genebank, it is very difficult to track where it is being used and what exactly is the outcome of the research. DOI will help to track by whom, where and how these germplasms are being or will be used in future.

Conclusion

Different genebanks are using different identification system for their germplasms. This sometimes creates confusion when the germplasms are shared among different organizations. As DOI provides unique numbers for all the germplasms, it eliminates this problem and ease the sharing of PGRFA among stakeholders. Thus, even though DOI is a new development, but it already has immense importance for conservation, utilization and exchange of PGRFA not only in Bangladesh but also around the globe. So, this is high time for Genebanks to register their germplasms with DOI to assist global collaboration to achieve food security.

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MANAGEMENT OF LOCAL RICE RESOURCES ASSIGNED THEIR DOIS ORIGINATING FROM WEST NUSA TENGGARA

Fitrahtunnisa and Muji Rahayu

INTRODUCTION

Rice (*Oryza sativa* L.) is a food crop that plays an important role in Indonesia's economic sector. Rice is consumed by approximately 90% of Indonesia's population as a daily staple food. This plant is mostly grown in the fields with irrigation system throughout the season, and some of them are planted in moorings and newly opened forest land which is commonly called as upland rice or "gogo" (Sulistyono et al. 2002). Upland rice could be potential in Indonesia's dry land (BKPRN 2012), as consequence, their role in national supply becomes increasingly important (Rahayu et al. 2006).

Upland rice mostly belonging to local varieties has been cultivated from generations by the local community. Local rice with specific characteristics generally has low yield potential, late maturity, logging and less response to fertilization input. Therefore, local varieties are less economic value than improved varieties. On the other hand, a number of local varieties have been identified as sources of genes controling grain quality,

resistance to pests and diseases and tolerance to suboptimal environmental stress (Singh et al. 2000). The local varieties are stable and small grains favored by farmers and consumers (Iskandar 2001). A number of studies reported that many local varieties have low amylose content equivalent to glutinous rice (Silitonga 2004; Sutoro et al. 2010), suggesting their high economic value.In addition, high genetic diversity in local rice plants can be useful for varieties improvement. Further identification of important characters found in local varieties is needed for optimal utilization in breeding programs (Hairmansis et al. 2005).

Gumantar is one of villages in Kayangan Subdistrict, North Lombok Regency, West Nusa Tenggara where people still cultivate local rice in wide area of more than 25 hectares each year. Local rice cultivation comprises special activities, i.e. lowland rice (called *pare rau*) which is the process from collecting seeds in the barn, determining when they want to plant until returning it to the granary (after harvest) must pass through a traditional ceremony. Notable, some community's cultural with the customary practices to maintain food security in this regency could be a good lesson for next generation. This article reviews how to manage local rice resources from West Nusa Tenggara that have been registered their own DOIs.

Agro-geographical Condition of Gumantar Village

Gumantar Village is dominated by paddy fields consisting of 50 ha of technical irrigation, 438 semi-technical irrigation, 70 ha of public settlements, 275 ha of moor and the rest is forest. The topography of Gumantar stretches from the south which is a hilly land that has great potential for the development of plantation crops such as coffee, cacao, cashew etc., while lowland rice are

grown below hill. In the northern part is a coastal area which is as a land boundary.

Similarly to other villages in North Lombok Regency, Gumatar has experienced two seasons, dry and rainy season. Food crops such as rice, corn, soybeans and other legumes can grow well. Lowland improved rice varieties are grown two times a year, in contrast, local rice are once only per year with cropping system with other food crops.

Customs Attached to the Local Rice Cultivation

Cultivation of local rice can be the most important activities for the community in the Gumantar. Local people produce local rice grains which are not traded for any reason. During the rainy season, improved varieties sometime are planted with local varieties in the same paddy field of rainfed land and also intercropped with vegetable crops, local maize varieties, beans, cassava, millet and *buleleng*. Planting time is determined based on the deliberations by traditional leaders. Three stages should be undertaken when planting local rice as follows:

1. Menepung

Menepung is the first stage of local rice cultivation which is only carried out by the customary leader.

2. Melulur

Melulur is the second stage of local rice cultivation carried out by traditional leaders.

3. Meruntut

Meruntut is the stage of local rice planting done by local rice farmers in the village. This is next step after *menepung and melulur*.

The field location for rice planting each year changes depending on the customary deliberations which consider the existence of pest and land. This is understood since plants are threatened by monkeys, birds and a pest of "*gayas caterpillar*" which can reduce yield. Local wisdom still maintained is the use of natural pesticides, such as *Maja* fruit. The crushed fruit is mixed with water then sprayed on plants.

Challenges of Local Rice Cultivation

Local rice germplasm which has long been cultivated enables to adaptation to varied environments. Consequently, local varieties with superior characters need to be preserved (Sitaresmi et al. 2013). Development of upland or lowland rice is very important to increase national rice production, but the productivity is still low.

The problem faced by farmers in upland rice is the lack of availability of superior varieties and seeds (Soerjandono and Robi'in 2012). In general, local varieties (Sunjaya 2011) are suitable in marginal land, resistant to several pests and diseases and high adaptability, with low yield (Ahadiyat 2011). Unfortunately, most farmers cultivate upland rice using minimal effort (Wahyuni et al. 1999; Toha et al. 2001). With the benefit of superior local varieties and cultivation techniques, upland rice productivity can be increased. In addition, the availability of good seeds could encourage the adoption of more productive cultivation technology.

Most farmers planting upland rice use their own production seeds from previous years. Observation of the quality of seeds used shows only 50% have good quality (germination> 80% and vigor> 70%). Seeds generally have been infected by 10 types of fungus and carried by seeds (Wahyuni et al. 1999). The

unavailability of upland rice seeds on the market affects this farmer culture. Growing upland rice for consumption and seed were done once a year in rainy season. Upland rice seeds must be stored for 6-8 months until used. As reported by Wahyuni et al. (2006), the upland rice seeds produced in irrigated fields in the dry season have higher yields and a better quality of seed compared to that on dry land in rainy season. Up to 3 months of storage, all seeds produced in the dry season still have vigor above 92%.

Characterization of Local Rice Varieties Commonly Grown by Farmers

Local rice in this regency needs to be explored their information with several ways for sustainable use. Field survey is useful for coordination with prospective cooperative farmers using snowball sampling method. In determining the sample, one or two samples are selected first, additional samples are chosen based on how well the information could be provided. The number of samples could be increased and the total numbers of samples are obtained after the information obtained is saturated. Coordination were conducted with related agencies such as Agriculture Faculty of Mataram University, Department of Agriculture and Plantation of West Nusa Tenggara and other research organizations for collecting information related to distribution, productivity, diversity and existing cultivation techniques. Field survey with farmers to characterize local rice varieties is presented in Figure 1.

Figure 1. Survey of local rice under the local rice barn (lumbung) (left) and interview with local farmer (right).

Genetic diversity estimation can be done based on characterization and identification in phenotypic and genotypic levels. Today's superior varieties are produced via conventional breeding programs or non conventional breeding using seeds from existing genetic resources. Each rice variety has certain traits whose can be used to be introgressed with one another (Liu et al. 2007). Morphological characteristics that are often used as a differentiator of rice cultivars are plant height, number of productive tillers, stem color, leaf color, leaf surface, number of grain per panicle, grain form, grain color and grain surface (Lesmana et. al. 2004). The morphological characters in the vegetative phase can be used as a descriptor includes the stems and leaves. The character of local varieties commonly identified are number of tillers, plant height, stem surface type, stem surface color, number of nodes and internodal length while leaf character is the length and color of ligula and the color of leaf strands (Irawan and Purbayanti 2008).

Three local rice varieties from Gumantar Village, Kayangan District, North Lombok Regency have been characterized and registered as superior local rice. The three varieties are pare jarak, pare putek and pare nanas that have characters as presented in Table 1.

Table 1. Characters of three local rice varieties in West Nusa Tenggara.

Character of local rice	Pare Jarak	Pare Putek	Pare Nanas
Plant			
Plant habitus	Erect	Erect	Erect
Plant height	148 – 150 cm	175 cm	158-161 cm
Days to maturity (days)	135	135	135
Stem			
Number of tillers per plant	2	2	2
Culm	Erect	Erect	Erect
Stem thickness	0.63 cm	0.82 cm	0.70 cm
Stem colour	Purple striped	Green	Green
Leaf			
Length of blade	61.2 cm	67 cm	68 cm
Width of blade	2.7 cm	2.5 cm	2.8 cm
Pubescence	Medium	Medium	Medium
Leaf attitude	Erect	Erect	Erect
Flag leaf attitude	Descending	Descending	Horizontal
Colour of leaf collar	Light green	Light green	Light green
Leaf color	Green	Green	green, purple at the tip
Sheath color	Purple striped	Green	Purple striped
Height of ligule	2.2 cm	2.5 cm	3 cm
Colour of ligule	Purple striped	Purple striped	Purple striped
Shape of ligule	*2-cleft*	*2-cleft*	*Acute-acuminate*
Panicle			
Length of main axis	32.2 cm	44 cm	37 cm
Panicle type	Between compact and medium	Medium	Between compact and medium
Secondary panicle branches	Few	Few	Few
Panicle shaft	Straight	Straight	Straight
Grain			
Awn	Present	Present	Present
Colour of apiculus	Blackish purple	White	Reddish
Lemma length	4.1 cm	8.12 cm	6.92 cm
Grain length	0.86 cm	0.82 cm	0.81 cm
Grain width	0.32 cm	0.36 cm	0.34 cm
Weight of 100 grains	3.90 gr	3.66 gr	3.78 gr

The genetic complexity is greater, therefore its is expected that in many cases multiple genetic paths can lead to the same phenotypic output. Genetic properties along with environmental factors such as elevation, temperature, humidity, soil type and soil fertility can cause the change of plant morphology performance. Strong effect of genetic factors will not show morphological diversity even plants are grown in different region (Suranto 2001). Each local rice variety has similarity or different characteristics which indicate their relationship pattern (Irawan and Purbayanti 2008).

Local rice evaluation is carried out on vegetative and generative growth phase and their yields. In multiple environments for a wide range of adaptation. Since nowadays farmers prefers to cultivate improved varieties that have emerged with various advantages compare to local varieties, thus encouraging the utilization of local varieties is necessary. Therefore, AIAT West Nusa Tenggara through the management of local plant genetic resources program provides technology assistance for highland rice cultivation and fertilizer subsidy assistance.

Figure 3. Evaluate and purify local rice varieties.

Assigning DOIs on Local Rice Varieties

Digital Object Identifiers (DOIs) is the assignation of global identifiers as the permanent and unambiguous method for the identification of million accessions including rice. DOI program is also developing a platform to establish automatized system to connections to add value to the material being transferred within and from the Multilateral Syste, to meet both scientific needs and legal obligations of the Standard Material Transfer Agreement (SMTA). In 2018, the three local rice varieties from West Nusa Tenggara have been registered (Table 2).

Table 2. Register number of three local rice varieties.

Items	Pare Jarak	Pare Putek	Pare Nanas
DOI register number	05020-30719	05020-30720	05020-30721
Ministry of Agriculture register number	358/PVL/2017	359/PVL/2017	360/PVL/2017

In addition to DOI registration, in 2017 the three local rice varieties have been registered by the local government through AIAT, West Nusa Tenggara to the Ministry of Agriculture as a local variety of North Lombok Regency.

Based on Permentan Basic Law No. 01/Pert/SR.120/2/2006, the terms of the Local Variety Registration are:

1. Registration form of local varieties that have been filled in and signed by the regent/mayor/governor or organization/ institution designated or established teams (according to the geographical distribution of local varieties) on stamped paper
2. Photos mentioned in the description printed in color on paper matte finish, which is necessary to clarify the description

3. Letter of appointment or formation team by regent/mayor/ governor (in accordance with the geographical distribution of local varieties) to the Organization/Institution designated or established team, if the local variety registration is filed by the institution/regional institutions.

The registration along with sMTA allows the local rice to be better known for its information and material transfer in the global level.

Conclusions

The management of local rice resources cannot be separated from the culture of the local people with their inherent habits. DOIs is persisten identifiers that could be useful for managing the utilization of local rice varieties. Both of them work together in preserving the genetic resources of local rice plants to strengthen the food security in West Nusa Tenggara.

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STATUS OF PLANT GENETIC RESOURCES CONSERVATION AND DIGITAL OBJECT IDENTIFIERS REGISTRATION FOR RICE GERMPLASM IN ZAMBIA

Graybill Munkombwe

INTRODUCTION

Plant genetic resources consist of a diversity of genetic material contained in both traditional and modern varieties grown by farmers as well as wild relatives of crops and other wild plant species used by humans for different purposes including food, fibre, clothing, timber and medicines. The conservation and sustainable utilisation of this resource is the key to improve agricultural productivity and sustainability, thereby contributing to food security and national development. For many years, farmers and farming communities have contributed to the evolution of crops by combining genes in new and different ways to form varieties suited to their needs. Mutations that might arise in various places and the region of domestication generate new diversity that is noticed and made use of by a farmer, thus adding a valuable trait to the crop. Historically, plant genetic resources have provided the crucial

raw material used in modern scientific plant breeding. They are the natural resource which have allowed crops to be adapted to different environments and uses, and which will allow them to respond to the new challenges of the next century.

Plant genetic resources conservation has been evolving in an effort to meet the dynamic challenges of conservation. Currently there has been a global need of sharing plant genetic resources for food and agriculture (PGRFA) in the multilateral system because all countries largely depend on PGRFA that originated elsewhere (FAO 2009). Both the International Treaty on plant Genetic Resources for Food and Agriculture (ITPGRFA) and the Convention on Biological Diversity (CBD) emphasize a continuum between the conservation and sustainable utilisation, along with facilitated access and equitable sharing of benefits arising from use (CGRFA 2013). It is from this background that gene banks are required to make available as many PGRFA accessions as possible along with their associated information to users. The sharing of germplasm and its associated information in the multilateral system poses a challenge on identification and tracking of PGRFA where there is no common standard of identification. The common standard of identification of PGRFA accessions that has been accepted by FAO is the use of Digital Object Identifiers (DOIs) (FAO 2017). This paper highlights the status of plant genetic resources conservation, digital object identifiers (DOIs) registration in Zambia, importance of DOIs and future plans for DOIs registration in Zambia.

Diversity of Conserved Plant Genetic Resources Accessions

Zambia possesses a wide range of plant genetic resources of cultivated plant species, their wild relatives and useful wild plant species. There are approximately 100 plant species that are

cultivated in Zambia (GRZ 2015). Out of these, about 15% are indigenous, which include sorghum, millets, cowpea, Bambara groundnut, sesame and a number of vegetable species. About 75% of these are exotic and 7% of those are naturalized, such as maize, beans, groundnuts, cassava, sweet potato, mango and avocado. These crops have undergone adaptation that has led to the generation of unique and valuable crop genetic diversity that has played and continues to play an important role in agricultural productivity and contributing to household food and nutritional security. Wild relatives of crops found in Zambia include those of rice, cowpea, sorghum, a range of cucurbits, kenaf and sesame species. A wide range of indigenous vegetable species and fruit trees that may be semi-cultivated or gathered from the wild are also found throughout the country. Conservation priorities for the National Plant Genetic Resources Centre (NPGRC) are in line with the priorities of the Zambia Agriculture Research Institute (ZARI) which focus on major traditional food crops. The priorities are also influenced by the availability of facilities for conservation. This perhaps explains the initial bias towards seed crops as opposed to root, tuber, fruit and plantation crops, which are propagated using vegetative materials.

There are 6.640 accessions of seed samples in the seed store at present that have been collected from around the country since 1989 when the national gene bank was established (Figure 1), against the initial number of 1479 accessions in 1989 covering about 40 different crop/plant species found in Zambia (ZARI 2018). This indicates an increase in number of accessions by more than three folds.

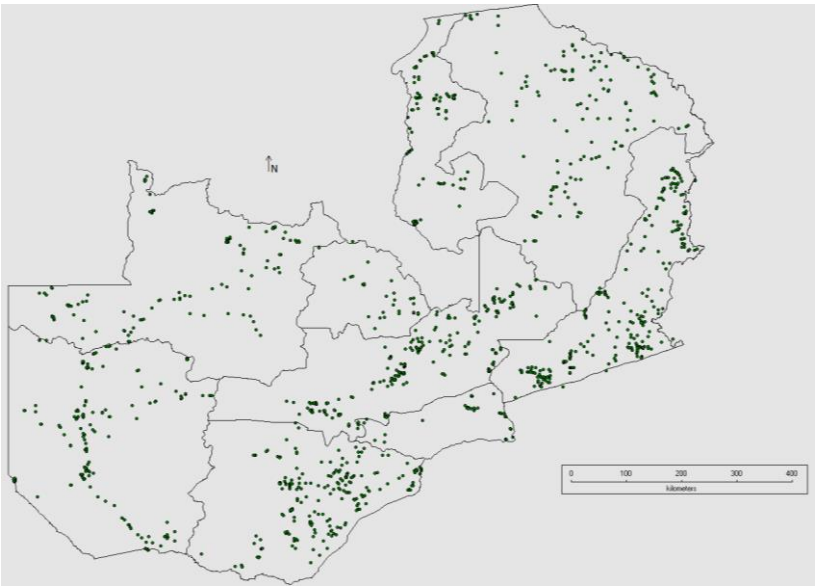

Figure 1. Map showing germplasm collection in Zambia.

Rice Profile in Zambia

Status of rice in national policies

Ministry of Agriculture has reviewed the first National Rice Development Strategy (NRDS) to align it to the National Agriculture Investment Plan (NAIP), where the main policy objective for the crops development component is to increase sustainable crop production, productivity and value addition for a diversified range of competitive crops apart from maize. Ministry of Agriculture's Crop Diversification Programme also recognizes rice as one of the strategic commodities that contributes to food security, and with a potential to significantly increase incomes and employment among rural producers. Hence government's decision to include rice as one of the nine crops

supported by the Farmer Input Support Programme (FISP). The nine crops include maize, rice, sorghum, ground nuts, soya beans, beans, sunflower, cotton and orange maize. Rice is also one of the crops that is included in the Statutory Instrument of 2015 as a designated crop. Of all the staple food crops in Zambia, currently rice is the only one with a deficit and the amount of this deficit has been increasing every year (GRZ 2016).

Status and trends of rice production

Rice is becoming an important staple food in Zambia. In the last 5 years, the crop has seen a steady increase in demand and its growing importance is evidenced by its current status as a strategic food crop. However, the demand for rice exceeds production and the deficit is met through imports mainly from Asia. According to Ministry of Agriculture/Central Statistics Office Crop Forecasting data, Zambia over the last 5 years has been producing on average about 44.500 MT of paddy rice (approximately 29.000 MT in milled rice) annually. However, consumption stands at about 60.000 MT (approximately 39.000 MT in milled rice). In recent years, the country has been importing between 5.000 and 20.000 MT of milled rice annually, mostly from Asia to meet domestic demand (GRZ 2016). Zambia's inability to produce rice to self-sufficiency level is due to a number of challenges facing the rice sub sector.

Implementation of Digital Object Identifiers in Zambia

The DOIs are a permanent method of identifying PGRFA accessions. Previously PGRFA accessions have been assigned new identifier numbers each time they are shared between gene banks. Each gene bank would assign its unique identifying number using its system. This has been causing some challenges

in identifying a shared material. Using the DOI system PGRFA accessions do not need the assignment of new numbers. The system brings various opportunities such as; institutes can easily share materials and track them if they wish, PGRFA accessions information is made accessible easily and PGRFA accessions that are duplicated across gene banks can be identified (FAO 2017).

Through the support of the Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development (ICABIOGRAD) in cooperation with ITPGRFA-FAO, Zambia NPGRC has 329 rice accessions with DOIs, representing 76.69% of the total rice collection in the gene bank. The rice collection comprises both cultivated and wild species collected around the country (Figure 2). The wild species include *Oryza longistaminata*, *O. barthii* and *O. brachyantha,* while the cultivated species only comprises *O. sativa*.

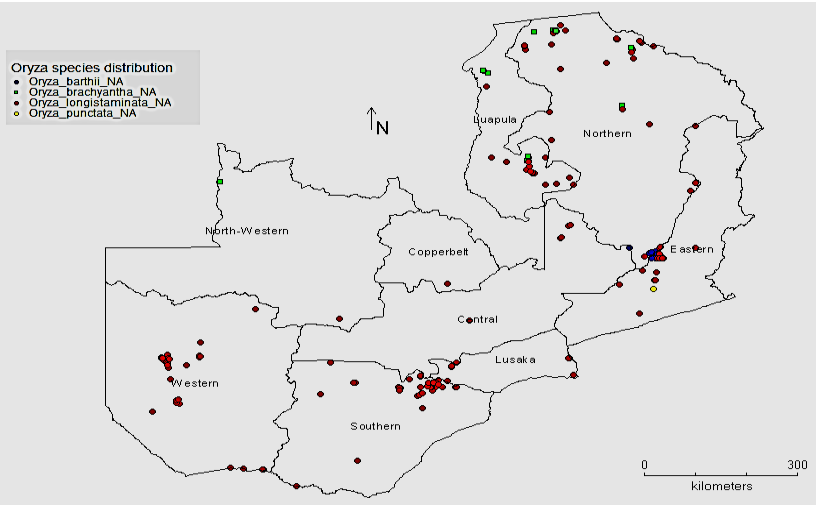

Figure 2. Distribution of *Oryza* species in Zambia.

A total of 2000 accessions along with their passport data are being processed for DOIs registration before the end of 2019. Among these accessions are 100 rice, 450 maize, 100 cowpea, 450 sorghum, 200 beans, 300 finger millet and 400 cucurbits. The NPGRC intends to have all the accessions listed in the Annex 1 of the ITPGRFA registered as soon as possible after government approval.

Concluding Remarks

While the global community is busy requiring facilitated access to rice and crops species germplasm, the need for information associated to these materials cannot be over emphasized. The use of digital object identifiers as the common standard of identification of PGRFA accessions will in the long run enhance genetic information identification and sharing.

Acknowledgements

I wish to thank the Indonesian Center for Agricultural biotechnology and Genetic Resources Research and Development in cooperation with the ITPGRFA-FAO secretariat for supporting my participation in International workshops and conferences on the application of Digital Object Identifier for rice germplasm.

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RICE GENETIC RESOURCE MANAGEMENT FOR SUPPORTING INDONESIA AGRICULTURE IN INDUSTRIAL 4.0: CASE STUDY IN INDONESIAN CENTER FOR RICE RESEARCH

Indria Wahyu Mulsanti, Trias Sitaresmi, and Nani Yunani

INTRODUCTION

Biodiversity can be divided into three levels, i.e. ecosystem level diversity, species level and genetic level. An ecosystem is a unit formed by reciprocal relationships between living things (biotic components) and their environment (abiotic components). Each ecosystem has characteristics of a physical environment, chemical environment, vegetation type, and specific types of animals. The diversity of environmental conditions causes different types of living things to inhabit them. Such diversity is referred to as ecosystem level diversity. Species-level diversity is indicated by the presence of different types of plants, animals, and microorganism Genetic resources as a form of biodiversity are a genetic material that has the ability to

inherit. Indonesia, being as a tropical country, is endowed with an enormous rice genetic resource because of its geographical condition, diverse ecosystem and rich agricultural heritage linked with various ethnic. This country consists of islands scattered along the equator (Prijono 2013). With the high level of biodiversity in Indonesia, the potential of rice genetic resources variability is abundant and its distribution covers various regions. Each region in Indonesia has several unique rice accessions, which are often different from one to another. These rice genetic resources are potential as parental lines to develop new varieties through breeding program. This review describes the conservation, optimizing the utilization through breeding and increasing the involvement of the rice collections in Indonesian Center for Rice Research (ICRR) in national/international integrated database system.

Rice Genetic Collection for Breeding Program In ICRR

Rice germplasm collection in ICRR majorly consists of local, wildtype, domesticated and introduced lines. Newly improved varieties which have been released that currently popular are derived from ICRR germplasm collection. For example, Inpago 11 were developed from two accessions which are tolerant to drought tolerant and resistant to blast. One of three parental lines of Inpari 38, a rainfed variety, was identified as drought resistant line. Inpari 42 and Inpari 43 GSR, are found to be resistant to *rice ragged stunt virus* (RRSV) and *rice grassy stunt virus* (RGSV), in which they were derived from introduced lines from INGER program. Munawacita variety is produced from induced mutation of Kewal local variety having a good eating/cooking quality from Banten. The latest released varieties based on local germplasm improvement were Rindang 1 and Rindang 2 that

were derived from local Si Macan and Batutegi and Cimelati, respectively.

Table 1. The utilization of ICRR rice genetic resources collection for developing new variety through breeding (2000-2017).

No.	Line code	Crossing scheme	Released variety	Year released	Number of Acc.
1	KAL9414D-BJ-63-1	Siam unus/Cisokan	Margasari	2000	2
2	KAL9420D-BJ-270-3	Siam Unus/Dodokan	Martapura	2000	2
3	B10384-MR-1-8-3	Memberamo//IR66160/Member amo	Cimelati	2001	1
4	B8055F-KN-6-2	Mahsuri/Kelara	Mendawak	2001	1
5	B9645E-MR-89-1	Lusi/B7136E-MR-22-1-5	Sintanur	2001	1
6	S4362F-KN-2-1-2	Shintha/IR64//IR64	Batang Lembang	2003	2
7	S3429-4D-PN-1-1-2	Ciliwung/Cikapundung//IR64	Cigeulis	2003	3
8	B1924-1e-5-2	Setail/Way Apo Buru//Widas///Widas	Aek Sibundong	2006	3
9	B9852E-KA-66	Batang Ombilin/IR9884-54-3	Inpara 1	2008	1
10	B10214F-TB-7-2-3	Pucuk/Cisanggarung/Sita	Inpara 2	2008	2
11	TB490C-TB-1-2-1	Batutegi/Cigeulis/Ciherang	Inpago 4	2010	3
12	BP3244-2E-8-8-3-3-1*B	TB168E-TB-4-0-1/Widas//IR64	Inpari 15 Parahyangan	2011	2
13	B13138-7-MR-2-KA-1	IR69502-6-SKN-UBN-1-B-1-3/ KAL-9418F//Pokhali/Angke	INPARI 29 Rendaman	2012	2
14	IR79971-B-162-B-B	Wayrarem/Vandana	Inpago Lipigo 4	2014	2
15	B12151D-MR-11	UPLLRI/IRAT 13	Inpago 11 Agritan	2015	2
16	B12497E-MR-45	IR688886B/BP68*10/Selegreng/ Guarani/Asahan	Inpari 38 Tadah Hujan Agritan	2015	3
17	B12825E-TB-1-25	BP342B-MR-1-3/Dendang// IR69502-6SKM-UNB-1-B1	Inpari 39 Tadah Hujan Agritan	2015	2
18	BP2836-3E-KN-11-2-1	Limboto/Towuti//Ciherang	Inpari 41 Tadah Hujan Agritan	2015	3
19	Zhongzu 14	Huangxinzhan/Fenghuazhan	INPARI 42 Agritan GSR	2016	3
20	Huanghuazhan	WuFengZhan/IRBB5/ WuFengZhan	Inpari 43 Agritan GSR	2016	4
21	IPPHTI-14	Kebo/Ciherang	Inpari 44 Agritan GSR	2016	2

Table 1. Continue.

No.	Line code	Crossing scheme	Released variety	Year released	Number of Acc.
22	Taiken		Tarabas	2017	1
23	BP13816D-6-KLB-10-4-1*-B	Varietas Kewal Balik Semah diradiasi sinar gamma dengan dosis 0,20kGy dari Co^{60}	Munawacita	2017	1
24	B12056F-TB-1-29-1	Selegreng/Si Macan	Rindang 1	2017	2
25	B12480D-MR-7-1-1	Batutegi/CAN//IR60080/Cimelati	Rindang 2	2017	2
	Total				53

Rice Genetic Resources Conservation

The conservation of genetic resources is an important issue concerning the human population worldwide. Introduction lines, as well as domesticated and chronic weed infestation have significant effects on plant diversity which reflects in reduction of their genetic diversity. Rice genetic resources provide different basic raw materials and contribute to supply new genetic information useful for breeding programs and for developing high yield crops resistant to biological and environmental stresses (Rao 2004).

Conservation of plant genetic resources can be performed *in situ* or *ex situ*. *In situ* conservation conducted through the maintenance of plant species in their natural habitat, as well as the conservation of domesticated and cultivated species on the farm or in the surroundings where they have developed their distinctive characteristics (Brush 1995). *Ex situ* conservation is an approach that involves the activity of removal genetic resources from the original habitats or natural environments. However, in relation to evolution, *ex situ* conservation is static, thus, it may reduce the adaptive potential of the wild species and their populations in the future because seed samples are isolated from the environments where microevolution occurred (Bellon et al.

1998). *Ex situ* conservation is a viable way for saving plants from extinction, and in some cases, it is the only possible strategy to conserve certain species (Ramsay et al. 2000).

Collecting germplasm is the first step in *ex situ* conservation and important for the use of the material by breeders. Increased genetic resources collection can be conducted through exploration of local varieties and wild rice species or introduction. ICRR has performed active exploration activity from 2012-2018 to collect local rice varieties in several province in Indonesia (Figure 1).

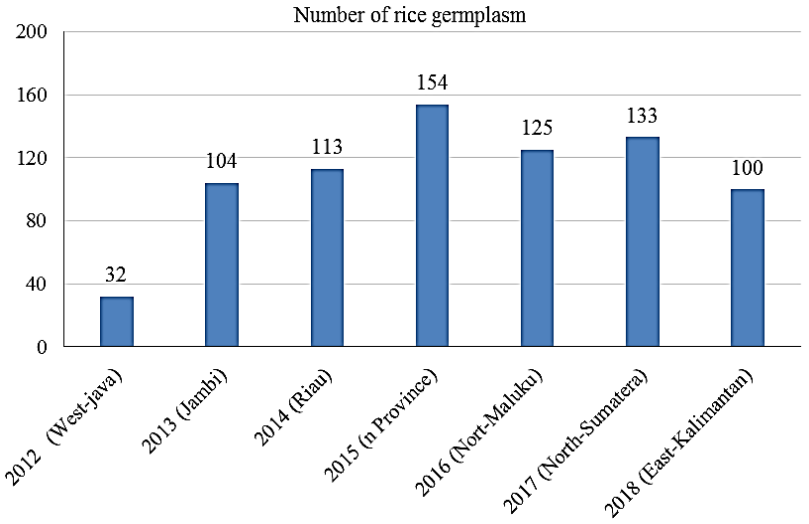

Figure 1. Number of rice germplasm accession obtained from exploration on different years at different province in Indonesia.

Optimizing Rice Genetic Resources Utilization

Realizing the importance of rice germplasm collection to optimizing breeding program, a systematic collection of rice germplasm is essentially required. Characterization and evaluation is the main key to understand the genetic potential for breeding activities. Table 2 presents the number of germplasm collection had been evaluated for the last 5 years. Considering the total number of rice germplasm collection, we need to accelerate the number of rice accession to be characterized rapidly. Biotic and abiotic stresses are still a threat to rice productivity and sustainability. The major challenge is to overcome these constraints and produce high yielding rice varieties with multiple resistances to biotic and abiotic stresses possessing improved grain quality and nutritive value.

Table 2. The number ICRR rice genetic resources evaluated from 2015-2018 for biotic and abiotic stress.

Evaluation	Year					On going 2019
	2014	2015	2016	2017	2018	
Biotic Stress						
Brown Planthopper	100	100	100	100	151	100
Bacterial Leaf Streak	60	100	100	100		
Bacterial Leaf Blight	60	100	100	100	151	100
Blas	60	100	100	100	151	100
Stem borer	60	100	100			
Tungro	60	100	100	100	151	100
Abiotic Stress						
Al-toxicity			150		151	
Salinity	129	150	150	150		150
Fe-toxicity		150	150			100
Anaerobic germination						200
Drought	154	150	150			
Submerge	154	150	150			
Shading		150	100			
Total accessions number	60-154	100	100	100-150	151	100-200

The use of resistant varieties is the cheapest and most effective method in controlling major pests and diseases. On the other hand, the selection pressure due to changes in the environment causes dynamic changes of disease races and pest biotypes in the environment. Hence, it is important to maintain the continuation of breeding to resistances for pest and disease, for that we need new sources of genes as sources of resilience. Some of ICRR germplasm collection had been identified for biotic and abiotic stress (Table 3 and 4).

Table 3. Local rice germplasm collections resistant to pests and/or plant diseases.

No.	Pest and diseases resistance	Accessions
1.	Bacterial leaf blight (BLB)	Bandang Buyur, Gembang, Genjah Welut, Ibu, Jembar, Katik Ana, Kaya Merah, Keriting, Ketan Garut, Kuntu Kuranyi, Pandan Wangi Leher II, Lumbu, Mashuri, Mentri, Natrom, Omad, Omas, Rembang, Sekemiling, Serepet Tinggi, Sunting Beringin
2.	Blas	Gampai, Jogja, Padi Banten, Popot, Pulut Cantung, Nipon
3.	Brown Planthopper	Si Rendah Putiih, Torondol Kuning, Ampek Panjang, Ase Puteh, Badik, Bapuk, Bidai, Bintang Landang, Buban, Bulang, Bulu Hideung, Buntok, Cecek Beleleng, Cempo Telouluk, Cere Beurem
4.	Tungro	Horeng, Jenai, Ketan Langgar Sari, Lumbuk, Menyan, Sagi, Cantik Manis, Cao, Danau, Tempe, Dewi Surya, Gebrang, Kangkungan, Ketan, ketan gabel, Lege Pisah, Lima Bulan kamang, Mayang Terurai

(BBPadi, 2010).

Table 4. Local rice germplasm collections tolerant to abiotic stress.

No.	Abiotic stress tolerance	Accessions
1.	Drought	Bulang, Buban, Beton, Cempo, Abang Ner; Merni
2.	Salinity	Si Putih; Lahatan Jambu
3.	Low temperature	Cere Beureum; Padi Gunung/Huma; Tejo

(BBPadi 2010).

The molecular screening of local varieties using genotypic markers will provide sufficient knowledge on traits of tolerance among the local accession on molecular level. It will help the breeders to develop strategic breeding programmes in order to produce elite lines (Chungada et al. 2016). The screening using specific molecular marker will enable to identify and characterize each variety separately.

Shifting to 4.0 era, is to identified large scale and thoroughly, especially on genetic traits. ICRR initiated by conducting DNA finger printing in 2015. We used 45 Indonesian varieties consisting of 32 local varieties, 5 improved variety and 8 control The results were able to verify local variety Gulabed from the farmer plantation, which were similar to Gulabed accession in ICRR collection and different with other varieties grown in the farmers area (BB Padi 2015). Furthermore, from 32 local varieties that has been evaluated, we were able to identify local varieties harbouring gene resistance to Xa7 and Xa4 by using SSR marker (BB Padi 2016).

The utilization of local lines/varieties in breeding programs are frequently recommended, with the aim to expanding the genetic background in order to breed superior variety (Berthaud et al. 2001; Cooper et al. 2001). Local varieties are great source of genetic diversity, which can be used to improve the quality and quantity of rice grain. Nafisah et al. (2007) used local rice as parental line to obtain the resistance trait to bacterial leaf blight

(*Xanthomonas oryzae*). Some potential lines which have multigenic resistance to BLB have been produced. Abdullah (2006) used wild rice and local rice as parental line to obtain new type of rice variety and potential lines with better morphological and physiological properties.

National/International Integrated Database System of Rice Genetic Resources

Agricultural development started shifting to industrial 4.0 to achieve food security. In this level, agriculture research is catalyzed by major technological advance in genetic and information system. ICRR has started to develop germplasm management based on Agriculture 4.0. Development of information system towards agriculture 4.0 may be done in two methods : 1) Development of a Mini Core collection, as a strategy to increase the efficiency of germplasm evaluation and management; 2) Assigning digital object identifier (DOI), which is software has been developed as part of global information system.

Core collection establishment

In order to optimize the use of the genetic resource, two step could be utilized in germ plasm management, which are 1) genotypically evaluate all accessions to understand its genetic diversity and population structure and 2) develop a core collection, which captures most of the genetic diversity (Nayak et al. 2014). The large sizes of rice germplasm collections complicate the characterisation, evaluation, utilisation and maintenance of the conserved germplasm. The approach of forming core collections was introduced to increase the efficiency of characterisation and utilisation of collections, while preserving as

much as possible the genetic diversity of the entire collection (Brown 1989). Frankel (1984) defined a core collection as a limited set of accessions representing, with minimum repetitiveness. A core collection that is an essence set of the entire collection with maximized genetic diversity and minimized redundancy is essential for its utilization (Brown 1989). Based on the purposes for which they are formed, Odong et al. (2013) classified core collection into three types or categories, i.e. core collections representing (1) individual accessions; (2) extremes; and (3) distribution of accessions in the whole collection).

Such a core collection for ICRR rice germplasm collection would provide a subset of representative accessions and can facilitate extensive examination at phenotypic, physiological and genetic levels. Thus, it could substantially utilize for rice breeding programs. At the moment ICRR initiating to form a core collection of the germplasm collection. Therefore, it is necessary to clearly define criteria for the evaluation of the quality of core collections and to relate the different types of core collections to those criteria. For example, a core collection for the purpose of capturing accessions with rare values of the desired trait(s) (i.e. high resistance to pest or high yield) should be evaluated differently from one developed to represent the genetic diversity in the collection.

Developing global information system

Indonesia has been ratified ITPGRFA since 2006. In consequence, contracting parties had to share their genetic resource on multilateral scheme. Accordingly, integrated data management will be needed. Global information system requires the availability of adequate supporting devices that can be accessed multilaterally. The hindrances on germplasm exchange

in Indonesia are difficulties on searching data information. In the case of ICRR gene bank, some problems identified are: the data of ICRR's germplasm collection were not available online because of gap information of the germplasm (between user and germplasm management division); database system between institutions of managing germplasm are not well integrated in the platform system differences (Hakim Kurniawan 2019, personal communication).

Two Principal of database will be used by ICRR as an early step toward developing Global Information System, in which: 1) Passport Database; database would contain all genetic resource passport data; 2) Integrated Database Management System; all other available information regarding the characteristics of each accession. ICRRR's passport data was classified according to origin into following conceptual fields (Yamasaki et al. 2016); Location: details of where the original germplasm was collected; Storage: information about how the germplasm is preserved, location within the cold storage. In the future, this data will be linked to database system; Collection status: logistic details such as current availability; Sample status: type of sample (bulk, panicle), viability, and quantitative/qualitative information about germplasm unit; Origin: details information how the germplasm was collected.

Genebank collections around the world hold the genetic material need to breed to cope uncertain environment. Digital Object Identifier (DOI) have now been chosen to provide a globally unique and permanent mechanism for identifying germplasm. A DOI is standardized alphanumeric string that is assigned by a registration agency and provides a persistent link to the location of information about the object on the internet (https://www.genebanks.org/news-activities/news/dois/). ICRR has been started for implementation of Digital Object Identifier

(DOI) by registered 14 accessions. This identifier contains data relevant to storage, collection, status, sample type, sample status and origin.

Future Perspective

Development of information system towards agriculture 4.0 in Indonesian Center for Rice Research may be done in two methods:

- Development of a mini core collection, as a strategy to increase the efficiency of germplasm evaluation and management.
- Development of global information systems through multilateral projects, a digital object identifier (DOI).

These are the initial step for realizing an integrated database system that can adequately manage the expected information to protect and utilize genetic resources.

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EPILOGUE
FUTURE CHALLENGES IN THE MULTILATERAL SYSTEM ON ACCESS AND BENEFIT SHARING OF PLANT GENETIC RESOURCES

The International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) is a legally binding international agreement dealing with the sustainable management of plant genetic resources for food and Agriculture. It established a multilateral system both to facilitate access to plant genetic resources for food and agriculture (PGRFA) and to share the benefits arising from the utilization of such resources. The Multilateral System (MLS) on access and benefit sharing is facilitated through the standard Material Transfer Agreement (sMTA). The sMTA requires that all available passport data and any other associated non confidential descriptive information, shall be made available with the PGRFA provider and the recipient shall make available all non-confidential information that results from research and development carried out on the material, through the information system provided for in Article 17 of the Treaty. Article 17 of the Treaty also requested contracting parties to cooperate to develop and strengthen a Global Information System (GLIS) to facilitate the exchange of information, based on existing information systems, on scientific, technical and environmental matters related to PGRFA.

The assignation of Digital Object Identifier (DOI) is intended as a means to implement the Article 17 of the Treaty, in particular the obligation of the recipient to provide information that results from research and development using the accessed materials. It is important to invite parties and other holders of material to use the DOIs of the GLIS and to share difficulties that may be encountered for capacity building for placing material in the MLS or in sharing germplasm with other parties. This kind of information is important since it will have the provider to keep track of their materials not only on locational or institutional holding aspects but also the scientific advancement of the materials. It will also help scientific community to gain information on the genetic materials will be used for research. It is our hope that any parties or individuals involve in exchanges of genetic materials register their materials in the DOI system and provides information on the materials not only mandatory information but also highly recommended information.

Information that might need to be shared in the DOI is the genetic sequence data (GSD) or genetic sequence information (DSI). The next generation of DNA sequencing, deep phenotyping approach, and sophisticated bioinformatics tools enable the comprehensive characterization of genetic diversity of crops. Statistical models can be constructed to predict the breeding value of an individual, given its genomic composition; an optimal breeding scheme can be designed in the light of such predictions. Accurate prediction is enhanced not only by access to more data, but to more variation in the available data and information.

The sharing of DSI might raise new issue in the benefit sharing. The inequities in the distribution of benefits derived from the commercial use of genetic resources determine the underlying provision on access and benefit sharing in the ITPGRFA and the Nagoya Protocols of the CBD. The issue of

sharing benefits derived from the use of DSI has already made its way onto a number of international agendas, with developing regions calling for new negotiated benefit-sharing rules. Updating information on availability of material in the MLS, and to identify the genetic material to make available in the MLS together with relevant nonconfidential characterization and evaluation data could be addressed and need to be presented in many fora.

There is a need for novel approaches to promote both monetary and nonmonetary benefit sharing for both PGRFA and its derived GSD and associated information. It is challenging to develop globally applicable, legally binding access and benefit sharing (ABS) norms that are a custom fit for emerging areas of scientific practice. There is a risk that new efforts at the level of the United Nations to develop a one-size-fits-all, ABS policy solution with respect to DSI could inadvertently end-up perpetuating disincentives for sharing, accessing, and using genetic resources and information, including DSI. This approach could involve identifying and endorsing best practices, developing voluntary guidelines and model ABS agreements. Another approach would entail extending the scope of the Nagoya Protocol and the ITPGRFA to apply to genomic sequence data and other types of digital data related to PGR, in addition to material genetic resources. Under the predominant model for national implementation of the Nagoya Protocol, parties seeking access to a data base containing genome sequences or other PGR-related digital data would need to negotiate an ABS agreement, which could include any number of conditions. Moreover, the technological breakthroughs that have created enhanced interest and value for DSI.

Muhamad Sabran and Puji Lestari

BOOSTING THE BIG DATA OF PLANT WITH DIGITAL IDENTIFIER

Data and information add value to plant genetic resources collection. Technologies for generating and analyzing large quantities of genotypic and phenotypic data are evolving at accelerating rates. This high volume of data is beyond the capacity of the traditional data processing software to deal with. In the era of big data, one of the significant challenges faced by scientists and plant breeders is the need to access information about plant genetic resources quickly and efficiently. The International Treaty on Plant Genetic Resources for Food and Agriculture established global information system in support of the multilateral system of access on plant genetic resources and the sharing of the benefit arising from their use. One innovative approach in the global information system is the assignation of Digital Object Identifiers to crop germplasm. This identifier may function as "google" in plant genetic resources for food and agriculture, i.e. by knowing the identifier one can find all information on accession of plant genetic resources assigned with such identifier.

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