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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

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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.

We wish to thank the secretariat of the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) for funding the conference and the preparation of this book and the Director General of the Indonesian Agency of Agriculture Research and Development (IAARD) for publishing the book through the IAARD press and the Director of Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development (ICABIOGRAD) for funding the final printing and multiplication of the book.

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.

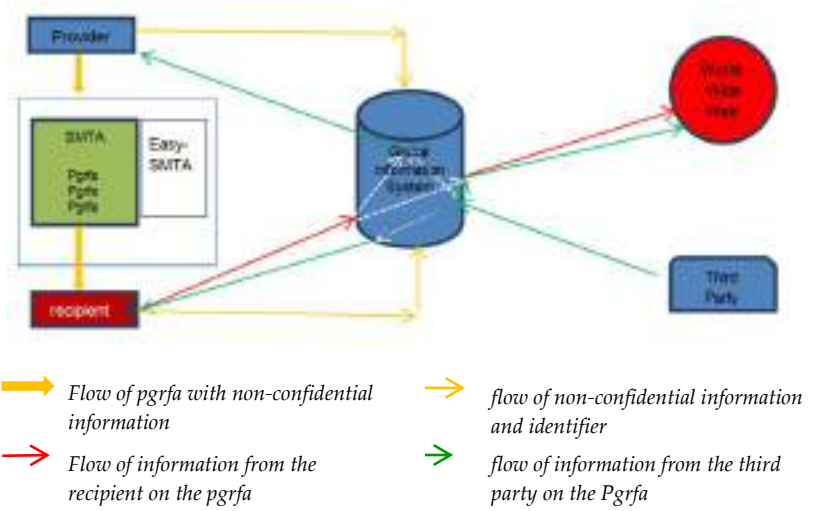

Figure 1. Exchange of PGRFA and information with easy-SMTA.

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.

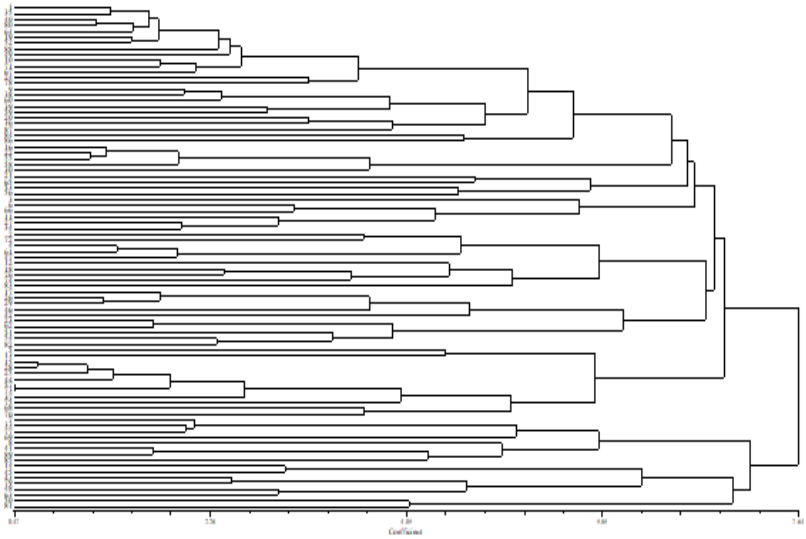

Figure 1. Dendrogram of 89 butterfly pea germplasm accessions from Indonesia.

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)

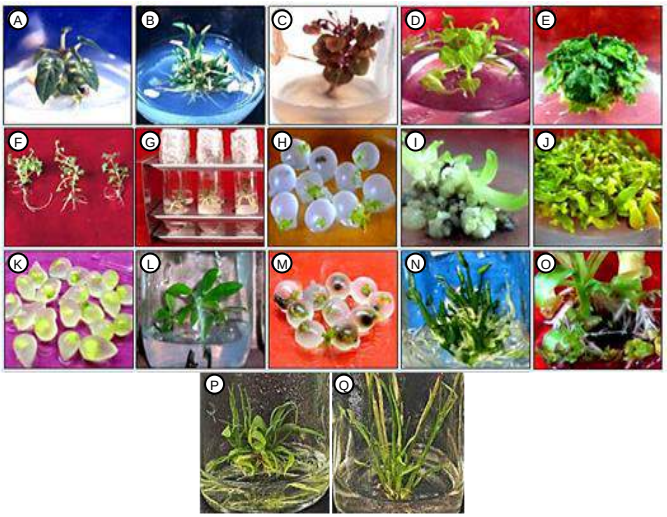

Figure 1. *In vitro* conservation researches of plant commodities using minimal growth method: sweet potato (A dan B), dioscorea (C dan D), pruatjan (E), tuberose (F), cassava (G), pineapple (H, K, and M), banana (I and O), pumelo (L), taro (N), and sugarcane (P and Q).

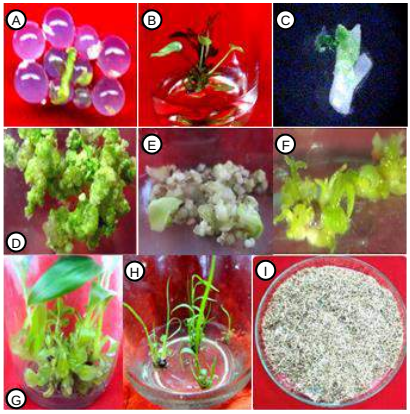

Figure 2. Several commodities in cryopreservation research: pineapple (A), sweet potato (B), cassava (C), pruatjan (D), banana (E and G), sugarcane (F, H and I).

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.

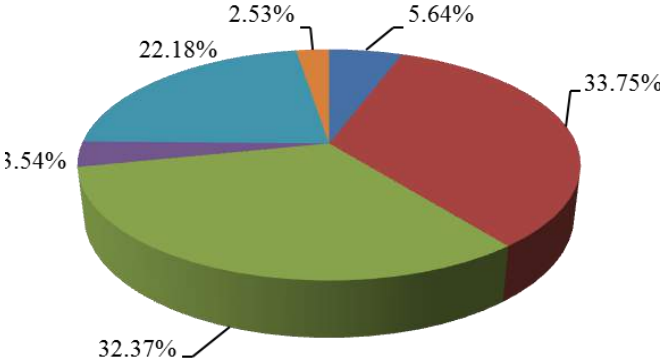

Figure 1. The incidence of rice pest and disease important in Indonesia.

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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