Table 2. Continue.

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

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

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

Table 3. Continue.

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

Table 3. Continue.

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

(Source: BRKB 2019).

Table 4. Yearly germplasm distribution from BRRI Genebank.

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

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

Conclusion

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

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

Fitrahtunnisa and Muji Rahayu

INTRODUCTION

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

Upland rice mostly belonging to local varieties has been cultivated from generations by the local community. Local rice with specific characteristics generally has low yield potential, late maturity, logging and less response to fertilization input. Therefore, local varieties are less economic value than improved varieties. On the other hand, a number of local varieties have been identified as sources of genes controling grain quality, resistance to pests and diseases and tolerance to suboptimal environmental stress (Singh et al. 2000). The local varieties are stable and small grains favored by farmers and consumers (Iskandar 2001). A number of studies reported that many local varieties have low amylose content equivalent to glutinous rice (Silitonga 2004; Sutoro et al. 2010), suggesting their high economic value.In addition, high genetic diversity in local rice plants can be useful for varieties improvement. Further identification of important characters found in local varieties is needed for optimal utilization in breeding programs (Hairmansis et al. 2005).

Gumantar is one of villages in Kayangan Subdistrict, North Lombok Regency, West Nusa Tenggara where people still cultivate local rice in wide area of more than 25 hectares each year. Local rice cultivation comprises special activities, i.e. lowland rice (called *pare rau*) which is the process from collecting seeds in the barn, determining when they want to plant until returning it to the granary (after harvest) must pass through a traditional ceremony. Notable, some community's cultural with the customary practices to maintain food security in this regency could be a good lesson for next generation. This article reviews how to manage local rice resources from West Nusa Tenggara that have been registered their own DOIs.

Agro-geographical Condition of Gumantar Village

Gumantar Village is dominated by paddy fields consisting of 50 ha of technical irrigation, 438 semi-technical irrigation, 70 ha of public settlements, 275 ha of moor and the rest is forest. The topography of Gumantar stretches from the south which is a hilly land that has great potential for the development of plantation crops such as coffee, cacao, cashew etc., while lowland rice are grown below hill. In the northern part is a coastal area which is as a land boundary.

Similarly to other villages in North Lombok Regency, Gumatar has experienced two seasons, dry and rainy season. Food crops such as rice, corn, soybeans and other legumes can grow well. Lowland improved rice varieties are grown two times a year, in contrast, local rice are once only per year with cropping system with other food crops.

Customs Attached to the Local Rice Cultivation

Cultivation of local rice can be the most important activities for the community in the Gumantar. Local people produce local rice grains which are not traded for any reason. During the rainy season, improved varieties sometime are planted with local varieties in the same paddy field of rainfed land and also intercropped with vegetable crops, local maize varieties, beans, cassava, millet and *buleleng*. Planting time is determined based on the deliberations by traditional leaders. Three stages should be undertaken when planting local rice as follows:

1. Menepung

Menepung is the first stage of local rice cultivation which is only carried out by the customary leader.

2. Melulur

Melulur is the second stage of local rice cultivation carried out by traditional leaders.

3. Meruntut

Meruntut is the stage of local rice planting done by local rice farmers in the village. This is next step after *menepung and melulur*.

The field location for rice planting each year changes depending on the customary deliberations which consider the existence of pest and land. This is understood since plants are threatened by monkeys, birds and a pest of "*gayas caterpillar*" which can reduce yield. Local wisdom still maintained is the use of natural pesticides, such as *Maja* fruit. The crushed fruit is mixed with water then sprayed on plants.

Challenges of Local Rice Cultivation

Local rice germplasm which has long been cultivated enables to adaptation to varied environments. Consequently, local varieties with superior characters need to be preserved (Sitaresmi et al. 2013). Development of upland or lowland rice is very important to increase national rice production, but the productivity is still low.

The problem faced by farmers in upland rice is the lack of availability of superior varieties and seeds (Soerjandono and Robi'in 2012). In general, local varieties (Sunjaya 2011) are suitable in marginal land, resistant to several pests and diseases and high adaptability, with low yield (Ahadiyat 2011). Unfortunately, most farmers cultivate upland rice using minimal effort (Wahyuni et al. 1999; Toha et al. 2001). With the benefit of superior local varieties and cultivation techniques, upland rice productivity can be increased. In addition, the availability of good seeds could encourage the adoption of more productive cultivation technology.

Most farmers planting upland rice use their own production seeds from previous years. Observation of the quality of seeds used shows only 50% have good quality (germination> 80% and vigor> 70%). Seeds generally have been infected by 10 types of fungus and carried by seeds (Wahyuni et al. 1999). The unavailability of upland rice seeds on the market affects this farmer culture. Growing upland rice for consumption and seed were done once a year in rainy season. Upland rice seeds must be stored for 6-8 months until used. As reported by Wahyuni et al. (2006), the upland rice seeds produced in irrigated fields in the dry season have higher yields and a better quality of seed compared to that on dry land in rainy season. Up to 3 months of storage, all seeds produced in the dry season still have vigor above 92%.

Characterization of Local Rice Varieties Commonly Grown by Farmers

Local rice in this regency needs to be explored their information with several ways for sustainable use. Field survey is useful for coordination with prospective cooperative farmers using snowball sampling method. In determining the sample, one or two samples are selected first, additional samples are chosen based on how well the information could be provided. The number of samples could be increased and the total numbers of samples are obtained after the information obtained is saturated. Coordination were conducted with related agencies such as Agriculture Faculty of Mataram University, Department of Agriculture and Plantation of West Nusa Tenggara and other research organizations for collecting information related to distribution, productivity, diversity and existing cultivation techniques. Field survey with farmers to characterize local rice varieties is presented in Figure 1.

Figure 1. Survey of local rice under the local rice barn (lumbung) (left) and interview with local farmer (right).

Genetic diversity estimation can be done based on characterization and identification in phenotypic and genotypic levels. Today's superior varieties are produced via conventional breeding programs or non conventional breeding using seeds from existing genetic resources. Each rice variety has certain traits whose can be used to be introgressed with one another (Liu et al. 2007). Morphological characteristics that are often used as a differentiator of rice cultivars are plant height, number of productive tillers, stem color, leaf color, leaf surface, number of grain per panicle, grain form, grain color and grain surface (Lesmana et. al. 2004). The morphological characters in the vegetative phase can be used as a descriptor includes the stems and leaves. The character of local varieties commonly identified are number of tillers, plant height, stem surface type, stem surface color, number of nodes and internodal length while leaf character is the length and color of ligula and the color of leaf strands (Irawan and Purbayanti 2008).

Three local rice varieties from Gumantar Village, Kayangan District, North Lombok Regency have been characterized and registered as superior local rice. The three varieties are pare jarak, pare putek and pare nanas that have characters as presented in Table 1.

Table 1. Characters of three local rice varieties in West Nusa Tenggara.

Character of local rice	Pare Jarak	Pare Putek	Pare Nanas
Plant			
Plant habitus	Erect	Erect	Erect
Plant height	148 – 150 cm	175 cm	158-161 cm
Days to maturity (days)	135	135	135
Stem			
Number of tillers per plant	2	2	2
Culm	Erect	Erect	Erect
Stem thickness	0.63 cm	0.82 cm	0.70 cm
Stem colour	Purple striped	Green	Green
Leaf			
Length of blade	61.2 cm	67 cm	68 cm
Width of blade	2.7 cm	2.5 cm	2.8 cm
Pubescence	Medium	Medium	Medium
Leaf attitude	Erect	Erect	Erect
Flag leaf attitude	Descending	Descending	Horizontal
Colour of leaf collar	Light green	Light green	Light green
Leaf color	Green	Green	green, purple at the tip
Sheath color	Purple striped	Green	Purple striped
Height of ligule	2.2 cm	2.5 cm	3 cm
Colour of ligule	Purple striped	Purple striped	Purple striped
Shape of ligule	*2-cleft*	*2-cleft*	*Acute-acuminate*
Panicle			
Length of main axis	32.2 cm	44 cm	37 cm
Panicle type	Between compact and medium	Medium	Between compact and medium
Secondary panicle branches	Few	Few	Few
Panicle shaft	Straight	Straight	Straight
Grain			
Awn	Present	Present	Present
Colour of apiculus	Blackish purple	White	Reddish
Lemma length	4.1 cm	8.12 cm	6.92 cm
Grain length	0.86 cm	0.82 cm	0.81 cm
Grain width	0.32 cm	0.36 cm	0.34 cm
Weight of 100 grains	3.90 gr	3.66 gr	3.78 gr

The genetic complexity is greater, therefore its is expected that in many cases multiple genetic paths can lead to the same phenotypic output. Genetic properties along with environmental factors such as elevation, temperature, humidity, soil type and soil fertility can cause the change of plant morphology performance. Strong effect of genetic factors will not show morphological diversity even plants are grown in different region (Suranto 2001). Each local rice variety has similarity or different characteristics which indicate their relationship pattern (Irawan and Purbayanti 2008).

Local rice evaluation is carried out on vegetative and generative growth phase and their yields. In multiple environments for a wide range of adaptation. Since nowadays farmers prefers to cultivate improved varieties that have emerged with various advantages compare to local varieties, thus encouraging the utilization of local varieties is necessary. Therefore, AIAT West Nusa Tenggara through the management of local plant genetic resources program provides technology assistance for highland rice cultivation and fertilizer subsidy assistance.

Figure 3. Evaluate and purify local rice varieties.

Assigning DOIs on Local Rice Varieties

Digital Object Identifiers (DOIs) is the assignation of global identifiers as the permanent and unambiguous method for the identification of million accessions including rice. DOI program is also developing a platform to establish automatized system to connections to add value to the material being transferred within and from the Multilateral Syste, to meet both scientific needs and legal obligations of the Standard Material Transfer Agreement (SMTA). In 2018, the three local rice varieties from West Nusa Tenggara have been registered (Table 2).

Table 2. Register number of three local rice varieties.

Items	Pare Jarak	Pare Putek	Pare Nanas
DOI register number	05020-30719	05020-30720	05020-30721
Ministry of Agriculture register number	358/PVL/2017	359/PVL/2017	360/PVL/2017

In addition to DOI registration, in 2017 the three local rice varieties have been registered by the local government through AIAT, West Nusa Tenggara to the Ministry of Agriculture as a local variety of North Lombok Regency.

Based on Permentan Basic Law No. 01/Pert/SR.120/2/2006, the terms of the Local Variety Registration are:

1. Registration form of local varieties that have been filled in and signed by the regent/mayor/governor or organization/ institution designated or established teams (according to the geographical distribution of local varieties) on stamped paper
2. Photos mentioned in the description printed in color on paper matte finish, which is necessary to clarify the description

3. Letter of appointment or formation team by regent/mayor/ governor (in accordance with the geographical distribution of local varieties) to the Organization/Institution designated or established team, if the local variety registration is filed by the institution/regional institutions.

The registration along with sMTA allows the local rice to be better known for its information and material transfer in the global level.

Conclusions

The management of local rice resources cannot be separated from the culture of the local people with their inherent habits. DOIs is persisten identifiers that could be useful for managing the utilization of local rice varieties. Both of them work together in preserving the genetic resources of local rice plants to strengthen the food security in West Nusa Tenggara.

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STATUS OF PLANT GENETIC RESOURCES CONSERVATION AND DIGITAL OBJECT IDENTIFIERS REGISTRATION FOR RICE GERMPLASM IN ZAMBIA

Graybill Munkombwe

INTRODUCTION

Plant genetic resources consist of a diversity of genetic material contained in both traditional and modern varieties grown by farmers as well as wild relatives of crops and other wild plant species used by humans for different purposes including food, fibre, clothing, timber and medicines. The conservation and sustainable utilisation of this resource is the key to improve agricultural productivity and sustainability, thereby contributing to food security and national development. For many years, farmers and farming communities have contributed to the evolution of crops by combining genes in new and different ways to form varieties suited to their needs. Mutations that might arise in various places and the region of domestication generate new diversity that is noticed and made use of by a farmer, thus adding a valuable trait to the crop. Historically, plant genetic resources have provided the crucial raw material used in modern scientific plant breeding. They are the natural resource which have allowed crops to be adapted to different environments and uses, and which will allow them to respond to the new challenges of the next century.

Plant genetic resources conservation has been evolving in an effort to meet the dynamic challenges of conservation. Currently there has been a global need of sharing plant genetic resources for food and agriculture (PGRFA) in the multilateral system because all countries largely depend on PGRFA that originated elsewhere (FAO 2009). Both the International Treaty on plant Genetic Resources for Food and Agriculture (ITPGRFA) and the Convention on Biological Diversity (CBD) emphasize a continuum between the conservation and sustainable utilisation, along with facilitated access and equitable sharing of benefits arising from use (CGRFA 2013). It is from this background that gene banks are required to make available as many PGRFA accessions as possible along with their associated information to users. The sharing of germplasm and its associated information in the multilateral system poses a challenge on identification and tracking of PGRFA where there is no common standard of identification. The common standard of identification of PGRFA accessions that has been accepted by FAO is the use of Digital Object Identifiers (DOIs) (FAO 2017). This paper highlights the status of plant genetic resources conservation, digital object identifiers (DOIs) registration in Zambia, importance of DOIs and future plans for DOIs registration in Zambia.

Diversity of Conserved Plant Genetic Resources Accessions

Zambia possesses a wide range of plant genetic resources of cultivated plant species, their wild relatives and useful wild plant species. There are approximately 100 plant species that are cultivated in Zambia (GRZ 2015). Out of these, about 15% are indigenous, which include sorghum, millets, cowpea, Bambara groundnut, sesame and a number of vegetable species. About 75% of these are exotic and 7% of those are naturalized, such as maize, beans, groundnuts, cassava, sweet potato, mango and avocado. These crops have undergone adaptation that has led to the generation of unique and valuable crop genetic diversity that has played and continues to play an important role in agricultural productivity and contributing to household food and nutritional security. Wild relatives of crops found in Zambia include those of rice, cowpea, sorghum, a range of cucurbits, kenaf and sesame species. A wide range of indigenous vegetable species and fruit trees that may be semi-cultivated or gathered from the wild are also found throughout the country. Conservation priorities for the National Plant Genetic Resources Centre (NPGRC) are in line with the priorities of the Zambia Agriculture Research Institute (ZARI) which focus on major traditional food crops. The priorities are also influenced by the availability of facilities for conservation. This perhaps explains the initial bias towards seed crops as opposed to root, tuber, fruit and plantation crops, which are propagated using vegetative materials.

There are 6.640 accessions of seed samples in the seed store at present that have been collected from around the country since 1989 when the national gene bank was established (Figure 1), against the initial number of 1479 accessions in 1989 covering about 40 different crop/plant species found in Zambia (ZARI 2018). This indicates an increase in number of accessions by more than three folds.

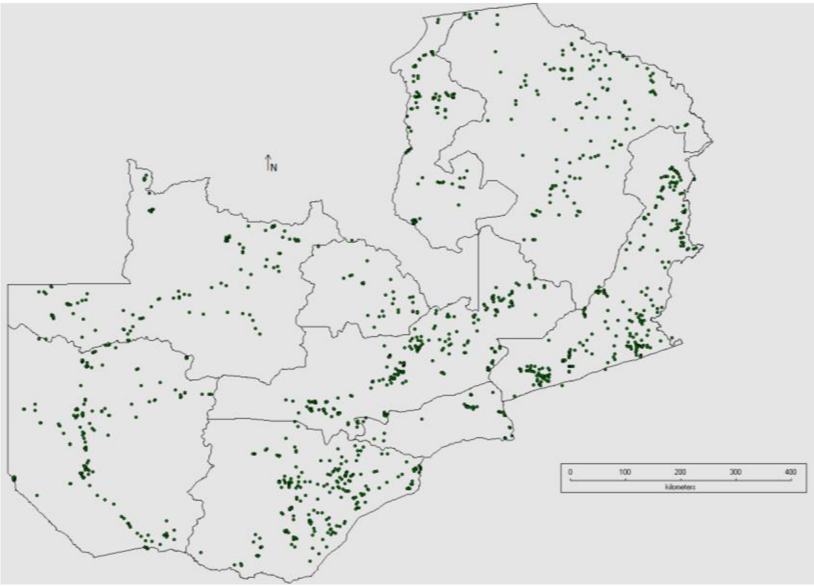

Figure 1. Map showing germplasm collection in Zambia.

Rice Profile in Zambia

Status of rice in national policies

Ministry of Agriculture has reviewed the first National Rice Development Strategy (NRDS) to align it to the National Agriculture Investment Plan (NAIP), where the main policy objective for the crops development component is to increase sustainable crop production, productivity and value addition for a diversified range of competitive crops apart from maize. Ministry of Agriculture's Crop Diversification Programme also recognizes rice as one of the strategic commodities that contributes to food security, and with a potential to significantly increase incomes and employment among rural producers. Hence government's decision to include rice as one of the nine crops supported by the Farmer Input Support Programme (FISP). The nine crops include maize, rice, sorghum, ground nuts, soya beans, beans, sunflower, cotton and orange maize. Rice is also one of the crops that is included in the Statutory Instrument of 2015 as a designated crop. Of all the staple food crops in Zambia, currently rice is the only one with a deficit and the amount of this deficit has been increasing every year (GRZ 2016).

Status and trends of rice production

Rice is becoming an important staple food in Zambia. In the last 5 years, the crop has seen a steady increase in demand and its growing importance is evidenced by its current status as a strategic food crop. However, the demand for rice exceeds production and the deficit is met through imports mainly from Asia. According to Ministry of Agriculture/Central Statistics Office Crop Forecasting data, Zambia over the last 5 years has been producing on average about 44.500 MT of paddy rice (approximately 29.000 MT in milled rice) annually. However, consumption stands at about 60.000 MT (approximately 39.000 MT in milled rice). In recent years, the country has been importing between 5.000 and 20.000 MT of milled rice annually, mostly from Asia to meet domestic demand (GRZ 2016). Zambia's inability to produce rice to self-sufficiency level is due to a number of challenges facing the rice sub sector.

Implementation of Digital Object Identifiers in Zambia

The DOIs are a permanent method of identifying PGRFA accessions. Previously PGRFA accessions have been assigned new identifier numbers each time they are shared between gene banks. Each gene bank would assign its unique identifying number using its system. This has been causing some challenges in identifying a shared material. Using the DOI system PGRFA accessions do not need the assignment of new numbers. The system brings various opportunities such as; institutes can easily share materials and track them if they wish, PGRFA accessions information is made accessible easily and PGRFA accessions that are duplicated across gene banks can be identified (FAO 2017).

Through the support of the Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development (ICABIOGRAD) in cooperation with ITPGRFA-FAO, Zambia NPGRC has 329 rice accessions with DOIs, representing 76.69% of the total rice collection in the gene bank. The rice collection comprises both cultivated and wild species collected around the country (Figure 2). The wild species include *Oryza longistaminata, O. barthii* and *O. brachyantha,* while the cultivated species only comprises *O. sativa*.

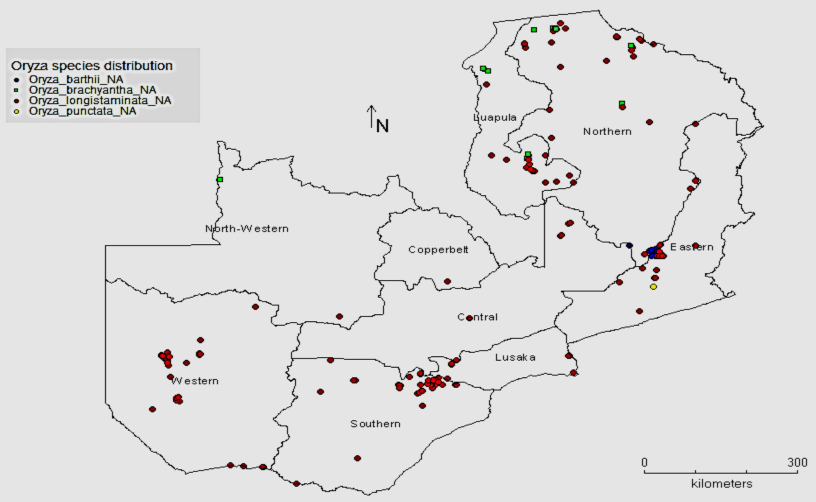

Figure 2. Distribution of *Oryza* species in Zambia.

A total of 2000 accessions along with their passport data are being processed for DOIs registration before the end of 2019. Among these accessions are 100 rice, 450 maize, 100 cowpea, 450 sorghum, 200 beans, 300 finger millet and 400 cucurbits. The NPGRC intends to have all the accessions listed in the Annex 1 of the ITPGRFA registered as soon as possible after government approval.

Concluding Remarks

While the global community is busy requiring facilitated access to rice and crops species germplasm, the need for information associated to these materials cannot be over emphasized. The use of digital object identifiers as the common standard of identification of PGRFA accessions will in the long run enhance genetic information identification and sharing.

Acknowledgements

I wish to thank the Indonesian Center for Agricultural biotechnology and Genetic Resources Research and Development in cooperation with the ITPGRFA-FAO secretariat for supporting my participation in International workshops and conferences on the application of Digital Object Identifier for rice germplasm.

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RICE GENETIC RESOURCE MANAGEMENT FOR SUPPORTING INDONESIA AGRICULTURE IN INDUSTRIAL 4.0: CASE STUDY IN INDONESIAN CENTER FOR RICE RESEARCH

Indria Wahyu Mulsanti, Trias Sitaresmi, and Nani Yunani

INTRODUCTION

Biodiversity can be divided into three levels, i.e. ecosystem level diversity, species level and genetic level. An ecosystem is a unit formed by reciprocal relationships between living things (biotic components) and their environment (abiotic components). Each ecosystem has characteristics of a physical environment, chemical environment, vegetation type, and specific types of animals. The diversity of environmental conditions causes different types of living things to inhabit them. Such diversity is referred to as ecosystem level diversity. Species-level diversity is indicated by the presence of different types of plants, animals, and microorganism Genetic resources as a form of biodiversity are a genetic material that has the ability to inherit. Indonesia, being as a tropical country, is endowed with an enormous rice genetic resource because of its geographical condition, diverse ecosystem and rich agricultural heritage linked with various ethnic. This country consists of islands scattered along the equator (Prijono 2013). With the high level of biodiversity in Indonesia, the potential of rice genetic resources variability is abundant and its distribution covers various regions. Each region in Indonesia has several unique rice accessions, which are often different from one to another. These rice genetic resources are potential as parental lines to develop new varieties through breeding program. This review describes the conservation, optimizing the utilization through breeding and increasing the involvement of the rice collections in Indonesian Center for Rice Research (ICRR) in national/international integrated database system.

Rice Genetic Collection for Breeding Program In ICRR

Rice germplasm collection in ICRR majorly consists of local, wildtype, domesticated and introduced lines. Newly improved varieties which have been released that currently popular are derived from ICRR germplasm collection. For example, Inpago 11 were developed from two accessions which are tolerant to drought tolerant and resistant to blast. One of three parental lines of Inpari 38, a rainfed variety, was identified as drought resistant line. Inpari 42 and Inpari 43 GSR, are found to be resistant to *rice ragged stunt virus* (RRSV) and *rice grassy stunt virus* (RGSV), in which they were derived from introduced lines from INGER program. Munawacita variety is produced from induced mutation of Kewal local variety having a good eating/cooking quality from Banten. The latest released varieties based on local germplasm improvement were Rindang 1 and Rindang 2 that were derived from local Si Macan and Batutegi and Cimelati, respectively.

Table 1. The utilization of ICRR rice genetic resources collection for developing new variety through breeding (2000-2017).

No.	Line code	Crossing scheme	Released variety	Year released	Number of Acc.
1	KAL9414D-BJ-63-1	Siam unus/Cisokan	Margasari	2000	2
2	KAL9420D-BJ-270-3	Siam Unus/Dodokan	Martapura	2000	2
3	B10384-MR-1-8-3	Memberamo//IR66160/Memberamo	Cimelati	2001	1
4	B8055F-KN-6-2	Mahsuri/Kelara	Mendawak	2001	1
5	B9645E-MR-89-1	Lusi/B7136E-MR-22-1-5	Sintanur	2001	1
6	S4362F-KN-2-1-2	Shintha/IR64//IR64	Batang Lembang	2003	2
7	S3429-4D-PN-1-1-2	Ciliwung/Cikapundung//IR64	Cigeulis	2003	3
8	B1924-1e-5-2	Setail/Way Apo Buru//Widas///Widas	Aek Sibundong	2006	3
9	B9852E-KA-66	Batang Ombilin/IR9884-54-3	Inpara 1	2008	1
10	B10214F-TB-7-2-3	Pucuk/Cisanggarung/Sita	Inpara 2	2008	2
11	TB490C-TB-1-2-1	Batutegi/Cigeulis/Ciherang	Inpago 4	2010	3
12	BP3244-2E-8-8-3-3-1*B	TB168E-TB-4-0-1/Widas//IR64	Inpari 15 Parahyangan	2011	2
13	B13138-7-MR-2-KA-1	IR69502-6-SKN-UBN-1-B-1-3/ KAL-9418F//Pokhali/Angke	INPARI 29 Rendaman	2012	2
14	IR79971-B-162-B-B	Wayrarem/Vandana	Inpago Lipigo 4	2014	2
15	B12151D-MR-11	UPLLRI/IRAT 13	Inpago 11 Agritan	2015	2
16	B12497E-MR-45	IR688886B/BP68*10/Selegreng/ Guarani/Asahan	Inpari 38 Tadah Hujan Agritan	2015	3
17	B12825E-TB-1-25	BP342B-MR-1-3/Dendang// IR69502-6SKM-UNB-1-B1	Inpari 39 Tadah Hujan Agritan	2015	2
18	BP2836-3E-KN-11-2-1	Limboto/Towuti//Ciherang	Inpari 41 Tadah Hujan Agritan	2015	3
19	Zhongzu 14	Huangxinzhan/Fenghuazhan	INPARI 42 Agritan GSR	2016	3
20	Huanghuazhan	WuFengZhan/IRBB5/ WuFengZhan	Inpari 43 Agritan GSR	2016	4
21	IPPHTI-14	Kebo/Ciherang	Inpari 44 Agritan GSR	2016	2

Table 1. Continue.

No.	Line code	Crossing scheme	Released variety	Year released	Number of Acc.
22	Taiken		Tarabas	2017	1
23	BP13816D-6-KLB-10-4-1*-B	Varietas Kewal Balik Semah diradiasi sinar gamma dengan dosis 0,20kGy dari Co^{60}	Munawacita	2017	1
24	B12056F-TB-1-29-1	Selegreng/Si Macan	Rindang 1	2017	2
25	B12480D-MR-7-1-1	Batutegi/CAN//IR60080/Cimelati	Rindang 2	2017	2
	Total				53

Rice Genetic Resources Conservation

The conservation of genetic resources is an important issue concerning the human population worldwide. Introduction lines, as well as domesticated and chronic weed infestation have significant effects on plant diversity which reflects in reduction of their genetic diversity. Rice genetic resources provide different basic raw materials and contribute to supply new genetic information useful for breeding programs and for developing high yield crops resistant to biological and environmental stresses (Rao 2004).

Conservation of plant genetic resources can be performed *in situ* or *ex situ*. *In situ* conservation conducted through the maintenance of plant species in their natural habitat, as well as the conservation of domesticated and cultivated species on the farm or in the surroundings where they have developed their distinctive characteristics (Brush 1995). *Ex situ* conservation is an approach that involves the activity of removal genetic resources from the original habitats or natural environments. However, in relation to evolution, *ex situ* conservation is static, thus, it may reduce the adaptive potential of the wild species and their populations in the future because seed samples are isolated from the environments where microevolution occurred (Bellon et al.

1998). *Ex situ* conservation is a viable way for saving plants from extinction, and in some cases, it is the only possible strategy to conserve certain species (Ramsay et al. 2000).

Collecting germplasm is the first step in *ex situ* conservation and important for the use of the material by breeders. Increased genetic resources collection can be conducted through exploration of local varieties and wild rice species or introduction. ICRR has performed active exploration activity from 2012-2018 to collect local rice varieties in several province in Indonesia (Figure 1).

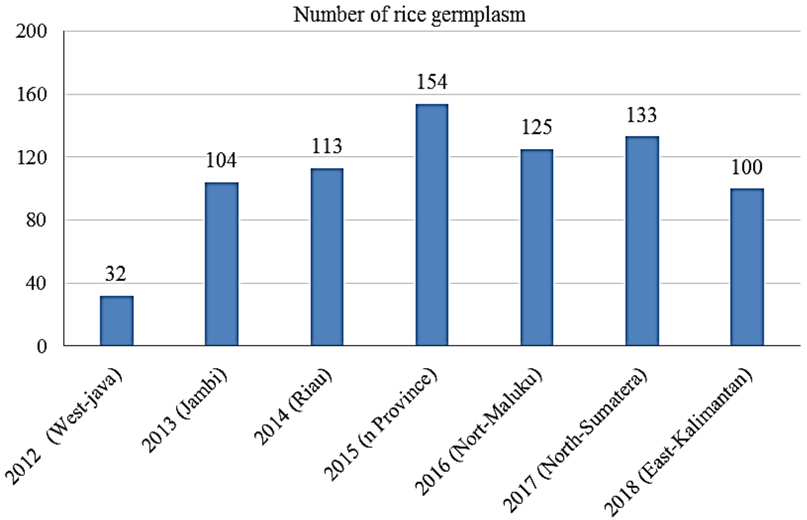

Figure 1. Number of rice germplasm accession obtained from exploration on different years at different province in Indonesia.

Optimizing Rice Genetic Resources Utilization

Realizing the importance of rice germplasm collection to optimizing breeding program, a systematic collection of rice germplasm is essentially required. Characterization and evaluation is the main key to understand the genetic potential for breeding activities. Table 2 presents the number of germplasm collection had been evaluated for the last 5 years. Considering the total number of rice germplasm collection, we need to accelerate the number of rice accession to be characterized rapidly. Biotic and abiotic stresses are still a threat to rice productivity and sustainability. The major challenge is to overcome these constraints and produce high yielding rice varieties with multiple resistances to biotic and abiotic stresses possessing improved grain quality and nutritive value.

Table 2. The number ICRR rice genetic resources evaluated from 2015-2018 for biotic and abiotic stress.

Evaluation	Year					On going 2019
	2014	2015	2016	2017	2018	
Biotic Stress						
Brown Planthopper	100	100	100	100	151	100
Bacterial Leaf Streak	60	100	100	100		
Bacterial Leaf Blight	60	100	100	100	151	100
Blas	60	100	100	100	151	100
Stem borer	60	100	100			
Tungro	60	100	100	100	151	100
Abiotic Stress						
Al-toxicity			150		151	
Salinity	129	150	150	150		150
Fe-toxicity		150	150			100
Anaerobic germination						200
Drought	154	150	150			
Submerge	154	150	150			
Shading		150	100			
Total accessions number	60-154	100	100	100-150	151	100-200

The use of resistant varieties is the cheapest and most effective method in controlling major pests and diseases. On the other hand, the selection pressure due to changes in the environment causes dynamic changes of disease races and pest biotypes in the environment. Hence, it is important to maintain the continuation of breeding to resistances for pest and disease, for that we need new sources of genes as sources of resilience. Some of ICRR germplasm collection had been identified for biotic and abiotic stress (Table 3 and 4).

Table 3. Local rice germplasm collections resistant to pests and/or plant diseases.

No.	Pest and diseases resistance	Accessions
1.	Bacterial leaf blight (BLB)	Bandang Buyur, Gembang, Genjah Welut, Ibu, Jembar, Katik Ana, Kaya Merah, Keriting, Ketan Garut, Kuntu Kuranyi, Pandan Wangi Leher II, Lumbu, Mashuri, Mentri, Natrom, Omad, Omas, Rembang, Sekemiling, Serepet Tinggi, Sunting Beringin
2.	Blas	Gampai, Jogja, Padi Banten, Popot, Pulut Cantung, Nipon
3.	Brown Planthopper	Si Rendah Putiih, Torondol Kuning, Ampek Panjang, Ase Puteh, Badik, Bapuk, Bidai, Bintang Landang, Buban, Bulang, Bulu Hideung, Buntok, Cecek Beleleng, Cempo Telouluk, Cere Beurem
4.	Tungro	Horeng, Jenai, Ketan Langgar Sari, Lumbuk, Menyan, Sagi, Cantik Manis, Cao, Danau, Tempe, Dewi Surya, Gebrang, Kangkungan, Ketan, ketan gabel, Lege Pisah, Lima Bulan kamang, Mayang Terurai

(BBPadi, 2010).

Table 4. Local rice germplasm collections tolerant to abiotic stress.

No.	Abiotic stress tolerance	Accessions
1.	Drought	Bulang, Buban, Beton, Cempo, Abang Ner; Merni
2.	Salinity	Si Putih; Lahatan Jambu
3.	Low temperature	Cere Beureum; Padi Gunung/Huma; Tejo

(BBPadi 2010).

The molecular screening of local varieties using genotypic markers will provide sufficient knowledge on traits of tolerance among the local accession on molecular level. It will help the breeders to develop strategic breeding programmes in order to produce elite lines (Chungada et al. 2016). The screening using specific molecular marker will enable to identify and characterize each variety separately.

Shifting to 4.0 era, is to identified large scale and thoroughly, especially on genetic traits. ICRR initiated by conducting DNA finger printing in 2015. We used 45 Indonesian varieties consisting of 32 local varieties, 5 improved variety and 8 control The results were able to verify local variety Gulabed from the farmer plantation, which were similar to Gulabed accession in ICRR collection and different with other varieties grown in the farmers area (BB Padi 2015). Furthermore, from 32 local varieties that has been evaluated, we were able to identify local varieties harbouring gene resistance to Xa7 and Xa4 by using SSR marker (BB Padi 2016).

The utilization of local lines/varieties in breeding programs are frequently recommended, with the aim to expanding the genetic background in order to breed superior variety (Berthaud et al. 2001; Cooper et al. 2001). Local varieties are great source of genetic diversity, which can be used to improve the quality and quantity of rice grain. Nafisah et al. (2007) used local rice as parental line to obtain the resistance trait to bacterial leaf blight

(*Xanthomonas oryzae*). Some potential lines which have multigenic resistance to BLB have been produced. Abdullah (2006) used wild rice and local rice as parental line to obtain new type of rice variety and potential lines with better morphological and physiological properties.

National/International Integrated Database System of Rice Genetic Resources

Agricultural development started shifting to industrial 4.0 to achieve food security. In this level, agriculture research is catalyzed by major technological advance in genetic and information system. ICRR has started to develop germplasm management based on Agriculture 4.0. Development of information system towards agriculture 4.0 may be done in two methods : 1) Development of a Mini Core collection, as a strategy to increase the efficiency of germplasm evaluation and management; 2) Assigning digital object identifier (DOI), which is software has been developed as part of global information system.

Core collection establishment

In order to optimize the use of the genetic resource, two step could be utilized in germ plasm management, which are 1) genotypically evaluate all accessions to understand its genetic diversity and population structure and 2) develop a core collection, which captures most of the genetic diversity (Nayak et al. 2014). The large sizes of rice germplasm collections complicate the characterisation, evaluation, utilisation and maintenance of the conserved germplasm. The approach of forming core collections was introduced to increase the efficiency of characterisation and utilisation of collections, while preserving as much as possible the genetic diversity of the entire collection (Brown 1989). Frankel (1984) defined a core collection as a limited set of accessions representing, with minimum repetitiveness. A core collection that is an essence set of the entire collection with maximized genetic diversity and minimized redundancy is essential for its utilization (Brown 1989). Based on the purposes for which they are formed, Odong et al. (2013) classified core collection into three types or categories, i.e. core collections representing (1) individual accessions; (2) extremes; and (3) distribution of accessions in the whole collection).

Such a core collection for ICRR rice germplasm collection would provide a subset of representative accessions and can facilitate extensive examination at phenotypic, physiological and genetic levels. Thus, it could substantially utilize for rice breeding programs. At the moment ICRR initiating to form a core collection of the germplasm collection. Therefore, it is necessary to clearly define criteria for the evaluation of the quality of core collections and to relate the different types of core collections to those criteria. For example, a core collection for the purpose of capturing accessions with rare values of the desired trait(s) (i.e. high resistance to pest or high yield) should be evaluated differently from one developed to represent the genetic diversity in the collection.

Developing global information system

Indonesia has been ratified ITPGRFA since 2006. In consequence, contracting parties had to share their genetic resource on multilateral scheme. Accordingly, integrated data management will be needed. Global information system requires the availability of adequate supporting devices that can be accessed multilaterally. The hindrances on germplasm exchange in Indonesia are difficulties on searching data information. In the case of ICRR gene bank, some problems identified are: the data of ICRR's germplasm collection were not available online because of gap information of the germplasm (between user and germplasm management division); database system between institutions of managing germplasm are not well integrated in the platform system differences (Hakim Kurniawan 2019, personal communication).

Two Principal of database will be used by ICRR as an early step toward developing Global Information System, in which: 1) Passport Database; database would contain all genetic resource passport data; 2) Integrated Database Management System; all other available information regarding the characteristics of each accession. ICRRR's passport data was classified according to origin into following conceptual fields (Yamasaki et al. 2016); Location: details of where the original germplasm was collected; Storage: information about how the germplasm is preserved, location within the cold storage. In the future, this data will be linked to database system; Collection status: logistic details such as current availability; Sample status: type of sample (bulk, panicle), viability, and quantitative/qualitative information about germplasm unit; Origin: details information how the germplasm was collected.

Genebank collections around the world hold the genetic material need to breed to cope uncertain environment. Digital Object Identifier (DOI) have now been chosen to provide a globally unique and permanent mechanism for identifying germplasm. A DOI is standardized alphanumeric string that is assigned by a registration agency and provides a persistent link to the location of information about the object on the internet (https://www.genebanks.org/news-activities/news/dois/). ICRR has been started for implementation of Digital Object Identifier

(DOI) by registered 14 accessions. This identifier contains data relevant to storage, collection, status, sample type, sample status and origin.

Future Perspective

Development of information system towards agriculture 4.0 in Indonesian Center for Rice Research may be done in two methods:

- Development of a mini core collection, as a strategy to increase the efficiency of germplasm evaluation and management.
- Development of global information systems through multilateral projects, a digital object identifier (DOI).

These are the initial step for realizing an integrated database system that can adequately manage the expected information to protect and utilize genetic resources.

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EPILOGUE

FUTURE CHALLENGES IN THE MULTILATERAL SYSTEM ON ACCESS AND BENEFIT SHARING OF PLANT GENETIC RESOURCES

The International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) is a legally binding international agreement dealing with the sustainable management of plant genetic resources for food and Agriculture. It established a multilateral system both to facilitate access to plant genetic resources for food and agriculture (PGRFA) and to share the benefits arising from the utilization of such resources. The Multilateral System (MLS) on access and benefit sharing is facilitated through the standard Material Transfer Agreement (sMTA). The sMTA requires that all available passport data and any other associated non confidential descriptive information, shall be made available with the PGRFA provider and the recipient shall make available all non-confidential information that results from research and development carried out on the material, through the information system provided for in Article 17 of the Treaty. Article 17 of the Treaty also requested contracting parties to cooperate to develop and strengthen a Global Information System (GLIS) to facilitate the exchange of information, based on existing information systems, on scientific, technical and environmental matters related to PGRFA.

The assignation of Digital Object Identifier (DOI) is intended as a means to implement the Article 17 of the Treaty, in particular the obligation of the recipient to provide information that results from research and development using the accessed materials. It is important to invite parties and other holders of material to use the DOIs of the GLIS and to share difficulties that may be encountered for capacity building for placing material in the MLS or in sharing germplasm with other parties. This kind of information is important since it will have the provider to keep track of their materials not only on locational or institutional holding aspects but also the scientific advancement of the materials. It will also help scientific community to gain information on the genetic materials will be used for research. It is our hope that any parties or individuals involve in exchanges of genetic materials register their materials in the DOI system and provides information on the materials not only mandatory information but also highly recommended information.

Information that might need to be shared in the DOI is the genetic sequence data (GSD) or genetic sequence information (DSI). The next generation of DNA sequencing, deep phenotyping approach, and sophisticated bioinformatics tools enable the comprehensive characterization of genetic diversity of crops. Statistical models can be constructed to predict the breeding value of an individual, given its genomic composition; an optimal breeding scheme can be designed in the light of such predictions. Accurate prediction is enhanced not only by access to more data, but to more variation in the available data and information.

The sharing of DSI might raise new issue in the benefit sharing. The inequities in the distribution of benefits derived from the commercial use of genetic resources determine the underlying provision on access and benefit sharing in the ITPGRFA and the Nagoya Protocols of the CBD. The issue of sharing benefits derived from the use of DSI has already made its way onto a number of international agendas, with developing regions calling for new negotiated benefit-sharing rules. Updating information on availability of material in the MLS, and to identify the genetic material to make available in the MLS together with relevant nonconfidential characterization and evaluation data could be addressed and need to be presented in many fora.

There is a need for novel approaches to promote both monetary and nonmonetary benefit sharing for both PGRFA and its derived GSD and associated information. It is challenging to develop globally applicable, legally binding access and benefit sharing (ABS) norms that are a custom fit for emerging areas of scientific practice. There is a risk that new efforts at the level of the United Nations to develop a one-size-fits-all, ABS policy solution with respect to DSI could inadvertently end-up perpetuating disincentives for sharing, accessing, and using genetic resources and information, including DSI. This approach could involve identifying and endorsing best practices, developing voluntary guidelines and model ABS agreements. Another approach would entail extending the scope of the Nagoya Protocol and the ITPGRFA to apply to genomic sequence data and other types of digital data related to PGR, in addition to material genetic resources. Under the predominant model for national implementation of the Nagoya Protocol, parties seeking access to a data base containing genome sequences or other PGR-related digital data would need to negotiate an ABS agreement, which could include any number of conditions. Moreover, the technological breakthroughs that have created enhanced interest and value for DSI.

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BOOSTING THE BIG DATA OF PLANT WITH DIGITAL IDENTIFIER

Data and information add value to plant genetic resources collection. Technologies for generating and analyzing large quantities of genotypic and phenotypic data are evolving at accelerating rates. This high volume of data is beyond the capacity of the traditional data processing software to deal with. In the era of big data, one of the significant challenges faced by scientists and plant breeders is the need to access information about plant genetic resources quickly and efficiently. The International Treaty on Plant Genetic Resources for Food and Agriculture established global information system in support of the multilateral system of access on plant genetic resources and the sharing of the benefit arising from their use. One innovative approach in the global information system is the assignation of Digital Object Identifiers to crop germplasm. This identifier may function as "google" in plant genetic resources for food and agriculture, i.e. by knowing the identifier one can find all information on accession of plant genetic resources assigned with such identifier.

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