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Plant Genetic Resource Management in Indonesia

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Abstract

The loss of genetic resources which sustain people is now widely recognized to be critical; therefore, plant genetic resources have to be intensively managed. Plant genetic resource materials need to be conserved in crop research institutes as base and working collections. *Ex situ* conservation has been carried out with cold storage of seeds of plant genetic resources, while plant genetic resources propagated by vegetative organs are conserved in the field and *in vitro*. To increase public awareness, the National Committee of Genetic Resources promotes the importance of managing genetic resources. The morphological characters of plant genetic resources that have been collected in seed-field banks should be measured, and their resistance to biotic and abiotic stresses and their nutritional values should be evaluated. Germplasm accessions to develop core collections or for preliminary evaluations can be selected using cluster analysis involving quantitative plant characteristics. Plant genetic resources have been used as materials for agricultural research.

Introduction

Plant domestication began with the recognition and utilization of plant diversity by early farmers. This process occurred in various environments with diverse sets of native species which formed the foundation for the present diversity of agricultural crops. Further evolution occurred with the transfer of plant materials over wide areas, followed by their adaptation to differing local conditions. This process of recognizing and exploiting plant diversity for domestication continues to the present day and should remain an important element in crop preservation and adaptation to different environments.

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Indonesia is a country which has a large diversity of plant genetic resources. The loss of genetic resources which sustain people is now widely recognized as being critical. The endangerment or extinction of some species has occurred because of several factors including land uses, modern agriculture, availability of instant foods in the market, and people's consumption patterns. Modern agriculture is known to have caused erosion in diversity, especially inhabitants or landraces that have adapted to their ecosystems over long periods. Overexploitation of certain species and development activities disturbing habitats have caused the near extinction of certain species, which suggests the importance of *ex situ* conservation of such species (Moeljopawiro and Suprahtomo, 2007). It is essential that plant genetic resources be well conserved for use by present and future generations (Rao and Riley, 1994; Sastrapraja and Balakhrishna, 2002).

Plant genetic resources in Indonesia have been conserved by research institutes based on their national mandates, and this is coordinated by the Agency of Agricultural Research and Development (AARD). The collection, exploration, characterization, and evaluation of plant genetic resources have been consistently carried out. Plant genetic resources have been conserved mostly through *ex situ* conservation.

Institutions and regulations

Institutions intensively involved in managing plant genetic resources in Indonesia are mostly crop research institutes under the AARD, Ministry of Agriculture Research Institute managing plant genetic resources are listed in Table 1.

To increase public awareness, one of the activities conducted by the National Committee of Genetic Resources is to promote the importance of managing genetic resources in Indonesia. With increased public awareness, stakeholders should conserve the genetic resources in their area. Stakeholders can conduct conservation activities in their area with coordination of an institution, like a regional committee on genetic resources at the provincial level. It is important to coordinate the conservation of genetic resources at the national level by establishing a national network between the national committee and regional committees, because only with good coordination can well-planned conservation be conducted. Since 2001, the National Committee on Genetic Resources has encouraged genetic resource stakeholders at the provincial level to establish a network. As a result, to date, 17 regional committees have been established. One of the activities in networking was conducted at a congress of the Regional Committee on Genetic Resources in Balikpapan

(East Kalimantan Province) and a second congress in Pekanbaru, Riau Province (Nurhadi and Thohari, 2007).

Table 1. Research institutes managing plant genetic resources in Indonesia

1	Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development (ICABIOGRAD)
2	Rice Research Institute (RRI)
3	Legume and Tuber Crops Research Institute (LTCRI)
4	Corn and other Cereals Research Institute (CCRI)
5	Ornamental Research Institute (ORI)
6	Vegetables Research Institute (VRI)
7	Fruit Research Institute (FRI)
8	Coconut and Palmae Research Institute (CPRI)
9	Citrus and Subtropical Fruit Research Institute (CSTFRI)
10	Center for Estate Crops Research Institute (CECRI)
11	Medicinal and Spice Crops Research Institute (MSCRI)
12	Oil Palm Research Institute (OPRI)
13	Tobacco and Fiber Crops Research Institute (TFCRI)

Legal norms in relation to policy and legislation may be sought within traditional systems, science, and technology as well as international conventions (Moeljopawiro and Suprahtomo, 2007). Indonesia has already ratified several conventions through Law no. 5 in 1994 for ratifying the United Nations Convention on Biological Diversity, Law no. 29 in 2000 for Plant Variety Protection, Law no. 21 in 2004 on the Ratification of the Cartagena Protocol on Biosafety to the Convention on Biological Diversity, and Law no. 4 in 2006 on the accession of the International Treaty on Plant Genetic Resources for Food and Agriculture.

Collection, conservation, and evaluation

Plant genetic resources include landraces, advanced/improved cultivars, and wild relatives of crop plants. Landraces which are distinct local types adapted to the many variants and interactions of natural and cultural environments are probably the most important among plant genetic resources (Rao and Riley, 1994). Exploration activities for collecting indigenous genetic materials have been done to protect and save these endangered species. Exploration has been done in almost every province but in only a part of the area due to budget limitations. The number of collections of plant genetic resources

resulting from exploration/collection and introduction of managing research institutes under AARD is presented in Table 2.

Table 2. Plant genetic resource collections under AARD, Ministry of Agriculture, Indonesia

Crops/Institute	No. of accessions
Cereals, legumes, and tuber crops (ICABIOGRAD)	10,563
Medicinal and spices-industrial (MSCRI, TFCR, and CPRI)	3590
Ornamentals (ORI)	961
Vegetables (VRI)	1507
Fruits (FRI and CSTFRI)	799
Estate crops (CECRI and OPRI)	
Coffee	1292
Cacao	570
Sugarcane	6009
Tea	870
Cinchona	600
Rubber	9130
Oil palm	7788

Organization abbreviations are defined in Table 1.

Ex situ conservation for seeds consists of cold storage, with seed viability being monitored yearly. *Ex situ* conservation of vegetatively propagated materials, such as tuber crops which are difficult to propagate by seed, is generally carried out in the field. *Ex situ* conservation of sweet potatoes, taro, and cassava has been done in the field and *in vitro*. Methods of *in vitro* conservation procedures have been applied to taro, sweet potato, and cassava germplasm. The following are the procedures of *in vitro* conservation that have been used for taro, sweet potato, and cassava (Nurwita, 2007).

Explants of taro were sterilized with 70% alcohol for 10 minutes, and 1.5% chlorine as a disinfectant for 10 minutes, and then grown in Murashige-Skoog (MS) medium for 2 months. Sterilized explants were grown in MS medium + 1 mg/l Benzyladenine (BA), and stored in MS medium + 4% mannitol for *in vitro* conservation.

Explants of sweet potato were sterilized with 70% alcohol for 5 minutes, 0.05% HgCl for 3 minutes, and 1% chlorine as a disinfectant for 5 minutes, and then grown in MS medium for 2 months. Sterilized explants were grown in MS medium + 1 mg/l BA, and stored in MS medium + 4% mannitol for *in vitro* conservation.

Explants of cassava were sterilized with 70% alcohol for 10 minutes, and 0.5% chlorine as a disinfectant for 5 minutes, and then grown in MS medium for 2 months. Sterilized explants were grown in MS medium + 0.1 mg/l gibberellins acid (GA) + 0.02 mg/l BA + 0.01 mg/l naphthalene acetic acid (NAA), and stored in MS medium + 0.1 mg/l GA + 0.02 mg/l BA + 0.01 mg/l NAA + 2% mannitol for *in vitro* conservation.

Conservation *in vitro* described above could be used for 10~18 months, and then crops have to be transferred to new medium to maintain their viability.

Morphological characters of most of the collection have been measured. Evaluations of plant characters observed mostly follow guidelines published by the IPGRI. Evaluation of plant genetic resources resistant to biotic (pests and diseases) and abiotic stresses (drought, iron toxicity, and acidic soils), and nutritional value have also been identified for several accessions of the germplasm collection.

Germplasm selection for the core collection

Germplasm accessions to develop a core collection or for preliminary evaluation can be selected using cluster analysis involving quantitative plant characteristics. The characteristics of a large number of accessions collected by research institutes holding plant genetic resources have to be evaluated. The genetic resources contained in germplasm collections are the basis for future progress in developing new varieties. Developing more-efficient methods for evaluating germplasm collections should help to speed up utilization of plant genetic resources. A core collection approach can be used to improve the efficiency of identifying valuable genes in germplasm collections (Corley et al., 2000).

Frankel (1984) proposed the core collection concept to denote a set which contains germplasm accessions with minimum repetitiveness, while retaining at the same time most of the genetic diversity of the principal collection. Characteristics of accessions selected in a core collection must represent the entire collection. The core collection can be determined based on qualitative and quantitative plant characters through cluster analysis. Cluster analysis is a technique of partitioning a set of accessions into clusters such that accessions within a cluster are homogeneous but are heterogeneous among clusters.

The number of groups or clusters can be determined by considering the percentage similarity, when the number of clusters is unknown. Accession samples can be obtained from each group using a constant or proportional strategy (van Hintum, 2000). The proportional

strategy allocates accessions to a group in proportion to the number of accessions in each group. The validation process usually involves comparisons between core collections and the entire collection.

Studies of germplasm accession selection for a core collection have been done for mungbean germplasm (Sutoro, 2008). Quantitative characters from 513 accessions used for the cluster analysis were flowering and harvesting times, branch number, seed number per pod, pod and seed numbers per plant, 100 seed weight, seed weight per plant, the ratio of seed weight to total dry matter, and plant height. Results of the correlation analysis among variables showed that several variables were significantly correlated. Euclidean distances used in the cluster analysis among variables were independent (Chatfied and Collins, 1980). All principal component scores were used as input variables for the cluster analysis.

Cluster analysis was performed using all principal component scores and considering 70% similarity. Results of the analysis showed that many clusters had only one member of an accession. In developing a method of defining a core collection, all of the populations sampled should be represented in the core, and as much of the diversity as possible from each population should be represented. Because all populations must be represented, each population will not necessary contribute to the core in the same proportion as it contributes to the entire collection (Skinner et al., 1999). For certain studies, genetic analysis with molecular or field evaluation of accession requires 96 samples for efficiency (electrophoresis requires 96 lines for running a molecular analysis). Distribution of accession numbers for each cluster can be determined but at least one member of an accession must be selected as a member of the core collection, while the rest can be allocated by a proportional strategy.

Samples can be validated by comparing the mean and variance of characters in the different groups of the core collection with those of groups from which they were derived (van Hintum *et al.*, 2000). A comparison between the core collection and the entire collection can be carried out using characteristics that were involved in establishing the core or using characteristics that were not used in its development.

To evaluate how well those 96 accessions of the core collection represent the entire collection, the mean and variance of each character in the core collection (accessions of which were selected at random) were compared with the corresponding mean and variance of the entire collection. Pairwise comparisons of the mean and variance of each trait indicated that most of the means and variances of the plant characters did not significantly differ between the core collection and entire collection. Correlations (data not shown) of

flowering time with branch number and seed weight significantly differed between the core collection and entire collection, but the directions were similar.

Development of the core collection is better when using molecular techniques, because they are not affected by environment factors, but molecular analyses are relatively costly.

Utilization of plant genetic resources

Numbers of accessions of plant genetic resources requested by researchers or students/universities during 2007 and 2008 were served by ICABIOGRAD as shown in Table 3. The recipients of plant genetic resources have to sign a material transfer agreement. The recipient agrees to use the materials for research purposes only, and not for any commercial use. Germplasm requested by a user generally has certain characters such as being susceptible, resistant, or tolerant to biotic and abiotic factors.

Table3. Numbers of accessions of plant genetic resources (germplasm) in ICABIOGRAD requested by researchers and students in 2007 and 2008

Crops	Number of accessions requested	
	2007	January~September 2008
Rice	154	29
Corn	10	6
Sorghum	5	-
Peanuts	27	-
Soybeans	200	28
Mungbean	42	12
Sweet potatoes	-	150

Utilization of plant genetic resources for commercial use by private companies to produce new varieties occurred in 2005. The local variety of peanuts belonging to a farmer group was used as a source of genetic material to obtain a new variety. These local varieties were registered with the Plant Protection Variety Office, Ministry of Agriculture. Negotiations between farmers and the company were mediated by the local government to obtain benefits for using local varieties. As a result of the negotiations, the farmers received a budget from the company for their input production, such as tractors and other facilities.

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