DEVELOPMENT OF SORGHUM CORE COLLECTION BASED ON PHENOTYPIC TRAITS IN ICABIOGRAD GENEBANK

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ABSTRACT

Core collection is a subset of accessions from a larger collection that maximizes the possible genetic diversity of a species with minimum redundancy. The development of core collection is usually applied in the genebank to efficient the handling of hundreds or thousands collection of germplasm. In this study we aimed to develop a core collection in sorghum germplasm using phenotypic data. The phenotypic data of 20 morpho- agronomic traits of 220 accessions of sorghum were used to develop the core collection carried out by the PowerCore program. The resulted core collection was consisted of 36 accessions (16%) with value of mean difference percentage (MD%), variance difference (VD%), coincidence rate (CR%), and variable rate (VR%) of 5.96%, 43.06%, 96.3%, and 137.01% respectively. These values indicated that the variation available in the initial collection has been preserved in the core collection. The development of core collection is an important suggestion for genebank manager to give better directions for germplasm management and facilitate further research for germplasm enhancement and plant breeding program.

Keywords: accession, diversity, germplasm, morpho-agronomic, PowerCore

INTRODUCTION

As a country known of its mega biodiversity, Indonesia has unspoken responsibility to maintain and preserve the diversity of genetic resources. The genetic resources play a key role in contributing the sustainable development of human living. Thus, the preservation of genetic resources become important since various aspect of human living cannot be detached from the utilization of genetic resources.

The preservation of genetic resources may come in two ways, i.e. in-situ conservation and ex-situ conservation in the form of a genebank. Most of research institute in Indonesia which deals with crop improvement usually has a genebank to store the genetic material. These genebanks are varying in size, function, facilities, and program sustainability depend on the budget available for the conservation activity. However, Indonesian Agency of Agriculture Research and Development (IAARD) under the Ministry of Agriculture is an official representative of Indonesian government that has responsibility to conserve, manage and utilize the plant genetic resources for food and agriculture (PGRFA). The main institution under IAARD which deals with PGRFA conservation is Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development (ICABIOGRAD). In performing the responsibility,

ICABIOGRAD genebank possesses an adequate and advanced genebank facilities such as long-term storage (cold storage -20 ^{0}C, RH 40%), short-term storage room (19 ^{0}C, RH 40%), seed quality testing laboratory, seed processing machines, germinator, and in-vitro storage room. Recently, a total of 11683 accessions comprises from no less than 30 species are conserved by ICABIOGRAD genebank (http://biogen.litbang. pertanian.go.id/plasmanutfah/). These accessions are conserved in the form of seed genebank, field genebank, and in-vitro genebank based on their reproductive system, generatively or vegetatively

However, handling a diverse and huge collections is not a simply task. Most of genebank manager often troubled by how to run the routine activity of conservation with minimal budget allocation but must provide maximum information about the potential of the collection. Therefore it is widely known that conservation of PGRFA is a costly and less profitable activity. To overcome this problem, an effective and efficient genebank management should be applied by genebank manager and their staff to ensure that germplasm is well-conserved.

One approach that can be applied to increase the effectiveness and efficiency of the conservation is through development of core collection. The concept of core collection is firstly proposed by Frankel and Brown (1984) as a subset of accessions from a larger collection that maximizes the possible genetic diversity of a species with minimum redundancy. Initially the core collection is used to monitor genetic drift during preservation, identify gaps in genetic diversity, and managing redundancy within the collection. But later core collection is used by genebank community to promote and maximize the utilization of germplasm stored to other users such as breeders and researchers (Brown, 1989; Upadhyaya & Ortiz, 2001).

Considering the importance of core collection development in handling genebank collection, thus we aimed to develop the core collection for sorghum germplasm in our genebank. The crop selection was based on the collection size and the availability of phenotypic data. Result from this study is expected to provide better direction for genebank manager to maximize the utilization of collection while ensuring its sustainability. For genebank users such as breeders and researchers, the core collection can be used as basis information for crop improvement program.

MATERIALS AND METHODS

The sorghum germplasm collection of ICABIOGRAD genebank was used as plant material for this study. Most of the collections are cultivars collected from abroad and the remaining are improved varieties and local varieties from several provinces in Indonesia. From this collection, 220 accessions were chosen based on their identification level and availability of morpho-agronomic data. The morpho-agronomic characterization of sorghum plant was performed based on descriptors for sorghum developed by IBPGR and ICRISAT (1993). Twenty traits were observed and measured which consist of six vegetative traits (plant height, stalk juiciness, leaf midrib colour, number of leaves, leaf width, leaf length), six inflorescence and fruit traits (days to flowering, glume colour, shattering, panicle length, panicle stalk length, number of panicle branches), and eight seed traits (grain colour, 100-seed weight, grain number per panicle, days to harvesting,

wet panicle weight, dry panicle weight, grain weight per panicle, grain weight per plot). The development of sorghum core collection was carried out by PowerCore program version 1.0 as proposed by Kim *et al*. (2007). This program used advanced M (maximization) strategy with heuristic search which selects the accessions with higher diversity representing the total coverage of trait state present in the entire collection. Thus the size of core collection depends on the levels of variability and redundancy of entire collection.

RESULTS AND DISCUSSION

ICABIOGRAD genebank conserves 259 accessions of sorghum germplasm which originated from local region in Indonesia and from correspondence with abroad genebank/researchers. Most of these accessions were acquired from abroad and accounted for 77.27% in the initial collection. The remaining was local and improved variety of Indonesia (Table 1). From these collections, a total of 220 accessions has been fully characterized their morpho-agronomic traits based on sorghum plant descriptor developed by ICRISAT. Therefore, based on this data we developed a core collection of ICABIOGRAD sorghum germplasm.

The PowerCore program through its M (maximization) method and heuristic search identified 36 accessions (16.4%) out of 220 accessions for the core collection (Table 2). All regions were covered in the core collection developed and the numbers of accessions originated from abroad were accounted for majority (66.67%) similar with the initial collection that previously described. However, the proportion of improved variety in the core collection was higher than that in the initial collection. The core collection developed has the same distribution frequency over all the categorical germplasm and retain most of the morpho-agronomic variations found in the initial collection although the number of accessions within the core is more than 10% from the initial collection as proposed by Brown (1989) (Table 1).

Table 1. Distribution frequency comparison of origin of accessions between the initial collection and the core collection among nine regions per categories

Region per category	Initial collection		Core collection	
	Number	%	Number	%
Africa	10	4.55	2	5.56
USA	14	6.36	3	8.33
Southeast Asia	9	4.09	3	8.33
India	137	62.27	16	44.44
Java. Indonesia	20	9.09	4	11.11
Kalimantan, Indonesia	2	0.91	1	2.78
Lampung, Indonesia	1	0.45	1	2.78
Nusa Tenggara, Indonesia	19	8.64	3	8.33
Improved varieties	8	3.64	3	8.33
Total	220	100.00	36	100.00

Table 2. The sorghum core collection of ICABIOGRAD genebank developed with the PowerCore program through maximization strategy with heuristic search

No	Origin	Acc. no	Acc. name
1	Africa	05005-00872	IS 18551
2	Africa	05005-00875	TU B7
3	USA	05005-00578	867.171
4	USA	05005-00728	M-3
5	USA	05005-00742	ISIAP DORADO
6	Southeast Asia	05005-00001	SIL 75
7	Southeast Asia	05005-00013	8309/199026
8	Southeast Asia	05005-00053	3568/199040
9	ICRISAT	05005-00736	GAMBELA
10	ICRISAT	05005-00746	GJ-35-15-15
11	ICRISAT	05005-00756	ICSV-LM-89522
12	ICRISAT	05005-00760	LB5
13	ICRISAT	05005-00774	ICSV 89037
14	ICRISAT	05005-00776	ICSV 89106
15	ICRISAT	05005-00803	ICSV 93030
16	ICRISAT	05005-00807	ICSV 93034
17	ICRISAT	05005-00814	ICSV 93041
18	ICRISAT	05005-00819	ICSV 93047
19	ICRISAT	05005-00837	ICSR 60
20	ICRISAT	05005-00838	ICSR 70
21	ICRISAT	05005-00850	ICSR 143
22	ICRISAT	05005-00878	RED OCHULI
23	ICRISAT	05005-00880	ICSR 154
24	ICRISAT	05005-00884	KSB II
25	Java, Indonesia	05005-00911	HERMADA COKLAT
26	Java, Indonesia	05005-00905	KOLOT
27	Java, Indonesia	05005-00123	KEMPUL PUTIH 82 R10
28	Java, Indonesia	05005-00886	DEMAK 2 (GAJAH)
29	Kalimantan, Indonesia	05005-00914	14 (LOKAL KALTIM)
30	Lampung, Indonesia	05005-00921	RUMBIA (LOKAL LAMPUNG)
31	Nusa Tenggara, Indonesia	05005-00933	BATAR AINARUP MEAN 1
32	Nusa Tenggara, Indonesia	05005-00891	BUTTER AINARUP 1
33	Nusa Tenggara, Indonesia	05005-00896	BUTTER MEAN
34	Improved Variety	05005-00900	SELAYER 1
35	Improved Variety	05005-00902	SELAYER 3
36	Improved Variety	05005-00730	KERIS

Comparative values for the ranges, means, and variances of 20 morpho-agronomic traits among the ICABIOGRAD sorghum initial and core collection are presented in Table 3. The core collection covers the range of variation for each trait. The t-test results indicate the presence of homogeneity of means between the initial collection and the core collection for 19 (95%) of the 20 traits analyzed. Thirteen (65%) of the traits had homogenous variances between the initial and core collection as revealed by Lavene's test (Lavene, 1960). The remaining seven traits that had heterogeneous variances, all of them showed

greater variances in the core collection than in the initial collection, i.e. leaf midrib colour, leaf width, glume colour, panicle length, wet panicle weight, dry panicle weight, and grain weight per plot.

To comparably evaluate the phenotypic traits properties between the initial collection and the core collection we used the MD%, the VD%, the CR%, and the VR% parameter. Over the entire 20 morpho-agronomic traits, the MD% was 5.96% indicates the mean difference between initial and core collection is less. The VD% was 43.06% indicates the variance difference between the two collections is relatively high. The VR% was 137.01% indicates the comparison of variation values coefficient of the 20 morpho-agronomic traits measured in the initial collection and core collection. To indicate whether the distribution ranges of the morpho-agronomic traits are well represented, we used the CR% parameter and in this study we obtain 96.3% for this parameter. For the last result, the coverage value for the resulting core collection was 100% since all classes over the 20 morpho-agronomic traits are retained.

The MD% between the initial collection and the core collection for 20 morpho-agronomic traits (5.96%) was far less than the significance level of 20% as described by Hu *et al*. (2000). The value of MD% obtained from this study similar to the average of core collections developed by *Kim et al*. (2007) and Agrama *et al.* (2009). The VD% of the core collection (43.06%) was less than that of the core collection in litchi (Sun *et al*., 2012) but higher than USDA rice mini-core collection (Agrama *et al*., 2009). Along with the value of the VD%, the VR% value obtained from this study (137.01%) also higher than that reported in rice or litchi (Agrama *et al*., 2009; Sun *et al*., 2012).

According to Hu *et al*. (2000), the core collection with larger VD% and VR% is considered to provide a good representation of the genetic diversity of the initial collection. Thus based on the VD% and the VR% we developed the core collection of sorghum that well-represented. Whereas the MD% value indicates the mean differences among the initial and the core collection, thus the less MD% value is the best since it shows that the mean of the core collections selected is similar to the mean of the entire collection (Kim *et al*., 2007). The last parameters to evaluate the core collection as proposed by Hu *et al*. (2000) is the CR% value that no less than 80%. This value indicates the distribution ranges of the phenotypic traits that retained in the core collection. In this study we obtained the CR% value as 96.3% similar to those in rice and litchi core collection (Agrama *et al*., 2009; Sun *et al*., 2012).

Table 3. Comparison of range, mean, and variance between the ICABIOGRAD sorghum entire collection and the core collection for 20 morpho-agronomic traits.

No	Trait	Entire collection			Core collection			Test	
		Range	Mean	Variance	Range	Mean	Variance	t-test	Lavene's
1	Plant height	92.00 - 392.00	196.44	56.35	92.00 - 361.00	211.03	60.19	NS	NS
2	Stalk juiciness	0.00 - 7.00	3.55	2.08	0.00 - 7.00	3.11	2.38	NS	NS
3	Leaf midrib colour	1.00 - 5.00	2.18	0.60	1.00 - 5.00	2.50	0.94	NS	S
4	Number of leaves	6.00 - 17.00	11.93	2.49	6.00 - 17.00	11.41	2.81	NS	NS
5	Leaf length	51.60 - 93.00	70.99	7.65	53.00 - 93.00	69.40	8.45	NS	NS
6	Leaf width	4.00 - 18.60	8.30	1.53	5.10 - 18.60	8.00	2.42	NS	S
7	Days to flowering	49.00 - 87.00	73.85	7.31	49.00 - 85.00	73.00	8.45	NS	NS
8	Glume colour	1.00 - 7.00	6.01	0.64	1.00 - 7.00	5.83	1.11	NS	S
9	Shattering	3.00 - 7.00	5.52	1.39	3.00 - 7.00	5.17	1.54	NS	NS
10	Panicle length	7.60 - 57.40	31.33	5.90	7.60 - 57.40	30.87	8.80	NS	S
11	Panicle stalk length	0.00 - 32.80	10.03	6.60	0.00 - 30.20	11.42	7.55	NS	NS
12	Number of panicle branches	4.90 - 117.00	51.73	13.29	4.90 - 115.00	52.29	18.08	NS	NS
13	Grain colour	1.00 - 6.00	3.82	1.44	1.00 - 6.00	4.00	1.64	NS	NS
14	100-seed weight	1.04 - 9.28	2.26	0.74	1.14 - 9.28	2.47	1.36	NS	NS
15	grain number per panicle	162.40 - 8562.60	2299.54	992.13	162.40 - 8562.60	2404.43	1564.08	NS	NS
16	days to harvesting	80.00 - 119.00	99.86	6.99	81.00 - 119.00	99.56	7.51	NS	NS
17	wet panicle weight	89.20 - 361.14	126.46	30.35	98.00 - 361.14	150.84	64.92	S	S
18	dry panicle weight	69.56 - 324.44	103.32	23.55	75.44 - 324.44	114.85	48.85	NS	S
19	grain weight per panicle	25.34 - 183.04	66.69	19.91	41.08 - 183.04	75.84	32.31	NS	S
20	grain weight per plot	108.00 - 2146.00	882.20	421.38	108.00 - 2146.00	842.56	471.31	NS	NS

NS=not significant at 0.05 probability, S=significant at 0.05 probability

Means were tested using t-test and variances were tested by Lavene's test for homogeneity between the entire collection and core collection of ICABIOGRAD sorghum collection

All of the parameters used for evaluating the development of core collection are important to be highlighted for anyone working in core collection development especially for genebank manager. Since the core collection which is developed from diverse origins may giving a better directions for germplasm management within the genebank such as conservation strategies, mass-screening for biotic and abiotic stress and direction for conducting further germplasm exploration activity to richness the diversity of the collection (Upadhyaya & Ortiz, 2001; Agrama *et al*., 2009). For research community, the core collection might better facilitate further research for germplasm enhancement and plant breeding program i.e. selecting potential parents for crossing and association studies. It also facilitates studies on linkage maps and QTL analysis, genomic variations, and mining favorable alleles within the genome (Zhao *et al*., 2010; Belaj *et al*., 2012).

CONCLUSION

Based on the value of the MD%, the VD%, the VR% and the CR%, the core collection of 36 sorghum accessions presented in this study is a good representative subset of the ICABIOGRAD sorghum collection. Besides that the core collection also showed 100% of coverage for 20 phenotypic traits since all classes in the initial collection is retained in the core collection developed. Therefore this sorghum core collection should be considered as sound representation of sorghum genetic diversity in ICABIOGRAD genebank and it is available to the research community worldwide.

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