NUSANTARA BIOSCIENCE
Vol. 9, No. 3, pp. 237-242
August 2017

ISSN: 2087-3948
E-ISSN: 2087-3956
DOI: 10.13057/nusbiosci/n090301

Characterization and clustering of agronomic characters of several soybean genotypes

M. MUCHLISH ADIE♥, AYDA KRISNAWATI♥♥
Indonesian Legumes and Tuber Crops Research Institutes, Jl. Raya Kendalpayak Km 8, Malang 65101, East Java, Indonesia. Tel./Fax. +62-341-801468/+62-341-801496, ♥email: mm_adie@yahoo.com, ♥♥email: my_ayda@yahoo.com.

Manuscript received: 17 November 2016. Revision accepted: 5 June 2017.

Abstract. *Adie MM, Krisnawati A. 2016. Characterization and clustering of agronomic characters of several soybean genotypes. Nusantara Bioscience 9: 237-242.* The development of improved soybean variety in Indonesia is mostly derived from crossing (51.19%), which requires the availability of gene source to serve as the parental stock. Characterization of 150 soybean genotypes was conducted in Probolinggo, Indonesia, from February to May 2016. The research was arranged in a randomized block design with two replicates. Clustering of agronomic characters was carried out using cluster analysis. The grouping was based on plant age characters (vegetative phase duration, generative phase duration, generative and vegetative ratio, days to maturity), growth characters (plant height, number of filled pods, number of empty pods, number of branches, number of nodes), and seed characters (100-seed weight and seed yield plant^{-1}), which resulted in 10 groups/clusters. Cluster I, II and III consisted of 47, 80, and 13 genotypes, respectively; whereas other clusters consisted of one up three genotypes, respectively. Each cluster represents specific characters. Cluster IV that consisted of three genotypes showed a late maturity (83.5-88.5 days), high number of pods (81.8-83.3 pods plant^{-1}) and high yield plant^{-1} (21.76-25.78 g plant^{-1}), but have small seed size (12.24-13.75 g 100 seed^{-1}). Cluster VI consisted of one genotype, and characterized by large seed size (16.79 g 100 seed^{-1}) and high yield plant^{-1} (15.76 g). Cluster IX (1 genotype) was characterized by early maturity (73 days), unbranched, but produced relatively low yield. The preference of soybean consumer in Indonesia is high yield, in addition to early maturity (< 80 days), and large seed size (>14 g 100 seed^{-1}). Soybean genotypes within cluster IV, VI, and IX are valuable as gene source in the development of superior soybean varieties in Indonesia.

Keywords: Agronomic character, cluster, seed yield

INTRODUCTION

High yielding varieties, as a component of cultivation technologies, are still become the most preferred and most rapidly adopted by users. In addition to high yield, development of soybean varieties in Indonesia is intended to produce varieties with general and specific objectives. The general soybean breeding objectives are to develop large seed size and early maturing soybean varieties, while the specific objectives are to generate soybean varieties with good adaptation to abiotic stress, biotic stress, and high nutrients content (protein, fat, isoflavones, etc.).

The development of improved variety requires the availability and diversity of genetic resources. Moreover, the Indonesian government has released as many as 84 soybean varieties, of which 51.19% were generated through crossbreeding processes. This indicates that genetic diversity plays an important role as gene sources in varietal development. Efforts to broaden the genetic diversity can be achieved through the characterization of soybean genotypes from various sources. In the USA, more than 70% released variety was originated from seven crossbreeding using nine unique parents (Chen et al. 2004). These genetic resources play a major role in soybean improvement and serve as the basis for the introduction of new genes to improve productivity, crop quality, and to increase resistance to diseases, pests, and stresses imposed by natural environments.

The seed yield of soybean, which consists of several components, including the number of plants per unit area, pods number per plant, seeds per pod, seed number and seed size, depends mainly on the soybean genotype used (Sumarno and Zuraida 2006; Susanto and Adie 2006; Showkat and Tyagi 2010). Genetic variability can be analyzed using various methods such as agronomic and biochemical traits, and molecular marker polymorphisms. Valliyodan et al. (2015) performed a landscape analysis of genomic diversity and trait discovery of 106 soybean genomes representing the wild, landraces, and elite lines, and obtained 10 million high-quality SNPs. This approach is very useful in the genomic aspects. Information from this study provides a valuable resource for understanding soybean genome structure and evolution, and can also facilitate trait dissection leading to sequencing-based molecular breeding. Characterization of several soybean genotypes in terms of abiotic stresses revealed PI 416937 as a drought-tolerant genotype. The drought-tolerant genotype was reported to be able to maintain its leaf turgidity as a result of efficient extraction of soil water by a larger and fibrous root system (Patterson and Hudak 1996). Hao et al. (2012) performed a genome-wide association analysis detecting significant single nucleotide polymorphisms for chlorophyll and chlorophyll fluorescence parameters in soybean (*Glycine max*) landraces. The previous study by Vollmann (2000) showed that selection of early maturing soybean genotypes with improved seed protein content appears to be feasible and is only limited by the moderately negative correlation between protein content and seed yield.

A previous study by Navabi et al. (2014) on the genetic diversity in dry bean varieties released between 1930 and 2010 revealed that the pedigree-based estimate of genetic diversity for all dry bean varieties was 0.93. This result indicated a narrow genetic diversity among the Canadian beans of Andean origin (kidney and cranberry beans) suggesting that the breeding efforts for these market classes would benefit from the introduction of new genetic diversity. In kidney bean (*Phaseolus vulgaris* L.), Khanal et al. (2015) obtained an accession named Dynasty, with the characteristic as a mid to late season maturity cultivar with excellent yield potential, superior seed size, and good cooking quality.

Genetic diversity is important for crop improvement (Malek et al. 2014). Variations among agronomic and yield-related characters in soybean offer the most effective selection for particular characters. The objectives of the present study were to characterize and classify 150 soybean genotypes based on agronomic characters.

MATERIALS AND METHODS

Research material

A total of 150 soybean genotypes which consisted of 145 soybean genotypes and five soybean popular varieties in Indonesia (Burangrang, Argomulyo, Grobogan, Anjasmoro, and Dega 1) were used in this study. These soybean genotypes were derived from a selection of various soybean crossing with different genetic background.

Field research

The experiment was conducted in dryland in Probolinggo (East Java, Indonesia) during the dry season (February-May 2016) at an elevation of 10 m asl, climate type C2 based on Oldeman system, and Alfisol soil type. The experiment was arranged in randomized completely block design, with 150 treatments and two replicates. Each genotype was planted in 1.2 m × 4.5 m, plant spacing was 40 cm × 15 cm, two plants hill^{-1}. The soil management was optimally performed and drainage channel was made. Planting system was done using individually planted (*tugal*) direct seeded, 2-3 seeds hole^{-1} and only two plants hole^{-1} were retained at 12 days after planting onward. Fertilizer of 250 kg Phonska ha^{-1} and 100 kg SP 36 ha^{-1} was applied prior to sowing. Crop maintenance consisted of optimal irrigation, pest and disease control, and weeding.

Observation

The observed data consisted of vegetative phase duration, generative phase duration, vegetative and generative ratio, days to maturity, plant height, number of filled pods, number of empty pods, number of branches, number of nodes, 100 seed weight, and seed yield plant^{-1}. The vegetative phase duration was the period started from the seed emergence until the opening of the first complete flower while the generative phase duration was the period started from the emergence of the first complete flower until pod maturation.

Data analysis

Data were analyzed using an ANOVA for a randomized block design (Gomez and Gomez 1984). Accessions diversity was determined by Principal Component Analysis (PCA) to identify the principal traits. Furthermore, the PCA values were used for cluster analysis. PCA and cluster analysis were performed using Minitab 14 program (McKenzie and Goldman 2005).

RESULTS AND DISCUSSION

Result

Analysis of variance showed significant variation among the 150 soybean genotypes. The CV values ranged from 3.96 to 23.61% (Table 1). This indicates that there were variations in particular agronomic characters, thus allowing us to perform grouping of the genotypes based on their agronomic characters.

The evaluated 150 soybean genotypes were grouped into characters associated with plant duration (vegetative phase duration, generative phase duration, generative and vegetative ratio, days to maturity), growth characters (plant height, number of filled pods, number of empty pods, number of branches, number of nodes), and seed characters (100 seed weight, seed yield plant^{-1}) (Table 2). The average vegetative phase duration was 32.54 days, generative phase duration was 45.01 days, generative and vegetative ratio was 1.39, days to maturity was 77.5 days, plant height was 48.31 cm, number of filled pods plant^{-1} was 42.65 pods, number of empty pods plant^{-1} was 2.06 pods, number of branches plant^{-1} was 2.38, number of nodes plant^{-1} was 10.07, 100 seed weight was 15.25 g, and seed dry weight plant^{-1} was 13.41 g. Skewness value for all characters was positive, except for number of branches, which indicates that most of the tested genotypes were centralized on the right side, thus have an opportunity to perform better than the average value. On the contrary, most genotypes tended to have relatively a few number of branches.

The grouping of 150 soybean genotypes based on agronomic characters resulted in 10 clusters (Table 3, Figure 1). Cluster I consisted of 47 genotypes, characterized by the relatively short stem and large seed size. Cluster II, as the largest cluster members (80 genotypes), had characteristics of a short stem and a high number of nodes. Cluster III (13 genotypes) had a medium stem and heavier seed per plant. Cluster IV (three genotypes) had characteristics of long duration of the vegetative phase, late maturity, high number of filled pods plant^{-1} and also high yield plant^{-1}. Cluster V with only two genotype members had characteristics of long duration of the generative phase, late maturity, and medium seed size.

Cluster VI (one genotype) was characterized by the long duration of generative phase and large seed size. Cluster VII (one genotype) was characterized by a high number of filled pods, a few empty pods, and high yield. Cluster VIII (one genotype) had a low number of filled pods. Cluster IX (one genotype) was characterized by the short duration of the vegetative phase, high G/V, very early days to maturity, and a few number of branches. The last cluster, cluster X (one genotype) was characterized by a long stem and a high number of nodes (Table 3).

Table 1. Analysis of variance of 150 soybean genotypes in 2016

Observed variables	Mean square		CV (%)
	Replication	Genotype	
Vegetative phase duration (V) (day)	74.00333^{**}	9.08682^{**}	5.25
Generative phase duration (G) (day)	19.76333^{*}	5.99644^{**}	3.99
G/V ratio	0.05796^{**}	0.00974^{**}	4.59
Days to maturity (day)	170.25333^{**}	24.89360^{**}	3.96
Plant height (cm)	38.30613^{ns}	73.51535^{**}	10.59
Number of filled pods plant^{-1}	282.65813^{ns}	238.28127^{**}	21.83
Number of empty pods plant^{-1}	0.05205^{ns}	0.21088^{**}	27.55
Number of branches plant^{-1}	1.28053^{ns}	1.13594^{**}	27.77
Number of nodes plant^{-1}	3.63000^{ns}	2.01104^{**}	9.35
100 seed weight (g)	18.72001^{**}	5.02741^{**}	8.78
Seed weight plant^{-1} (g)	72.42253^{**}	21.47234^{**}	23.61

Note: ** = significant at 1% probability level (p<0.01), * = significant at 5% probability level (p<0.05).

Table 2. Descriptive statistic of 150 soybean genotypes in 2016

Observed variables	Range	Mean	Std	Skewness
Vegetative phase duration (V) (day)	29.00-38.50	32.54	2.131	0.407
Generative phase duration (G) (day)	42.00-51.50	45.01	1.731	1.784
G/V ratio	1.23-1.55	1.39	0.069	0.082
Days to maturity (day)	73.00-88.50	77.55	3.528	1.163
Plant height (cm)	33.40-67.80	48.31	6.063	0.268
Number of filled pods plant^{-1}	22.00-83.30	42.65	10.915	1.222
Number of empty pods plant^{-1}	0.20-5.40	2.06	1.039	0.684
Number of branches plant^{-1}	0.50-3.90	2.38	0.754	-0.244
Number of nodes plant^{-1}	7.50-14.30	10.07	1.003	0.452
100 seed weight (g)	11.59-21.23	15.25	1.585	0.708
Seed weight plant^{-1} (g)	6.48-25.78	13.41	3.277	0.882

Note: Std = standard deviation

Table 3. Grouping of 150 soybean genotypes based on agronomic characters in 2016

Cluster	Number of genotypes	Characteristic
I	47	Short plant, large seed size
II	80	Short plant, high number of nodes
III	13	Medium plant height, heavy seed weight
IV	3	Long duration of vegetative phase, late maturity, high number of filled pods, heavy seed weight
V	2	Long duration of generative phase, late maturity, medium seed size
VI	1	Long duration of generative phase, large seed size
VII	1	High number of filled pods, a low number of empty pods, heavy seed weight
VIII	1	A low number of filled pods
IX	1	Short duration of vegetative phase, high G/V, early days to maturity, a few number of branches
X	1	High plant, high number of nodes

Table 4. Range of agronomic characters of each cluster in 2016

Cluster	Range										
	Vegetative phase duration	**Generative phase duration**	**G/V ratio**	**Days to maturity (day)**	**Plant height (cm)**	**No. of filled pods plant^{-1}**	**No. of empty pods plant^{-1}**	**No. of branches plant^{-1}**	**No. of nodes plant^{-1}**	**100 seed weight (g)**	**Seed weight plant^{-1} (g)**
I	29.0-36.5	43.0-49.0	1.28-1.52	73.5-85.5	33.4-48.0	27.0-37.8	0.3-4.0	0.7-3.0	7.5-10.5	13.67-19.65	6.48-13.6
II	29.0-36.5	44.0-49.0	1.28-1.52	74.0-84.5	42.7-56.5	34.0-52.1	0.2-4.7	1.3-3.9	8.8-12.3	11.59-19.98	7.26-17.32
III	33.0-37.0	42.0-48.0	1.24-1.49	73.5-85.0	47.8-59.8	55.6-63.6	0.5-5.0	2.6-3.6	10.3-11.9	13.09-16.01	14.80-20.51
IV	36.0-38.5	47.5-51.0	1.27-1.36	83.5-88.5	50.4-56.9	81.8-83.3	0.5-2.6	3.5-3.7	11.2-12.5	13.42-14.78	21.76-25.78
V	36.0-37.5	51.0-51.5	1.36-1.43	87.5-88.5	48.5-48.6	55.0-59.7	0.8-1.6	2.9-3.5	10.1-10.9	12.24-13.75	15.03-16.54
VI	37.0	51.0	1.38	88.0	56.5	49.3	1.6	2.7	11.2	16.79	15.76
VII	34.0	48.0	1.42	82.0	56.0	71.9	0.3	3.4	11.1	13.48	21.53
VIII	35.5	47.5	1.34	83.0	53.6	27.8	1.1	1.1	10.0	15.28	9.87
IX	29.0	44.0	1.52	73.0	58.4	28.1	1.3	0.5	11.8	15.01	8.1
X	31.5	44.0	1.44	74.5	61.8	50.3	0.8	1.7	14.3	15.85	14.41

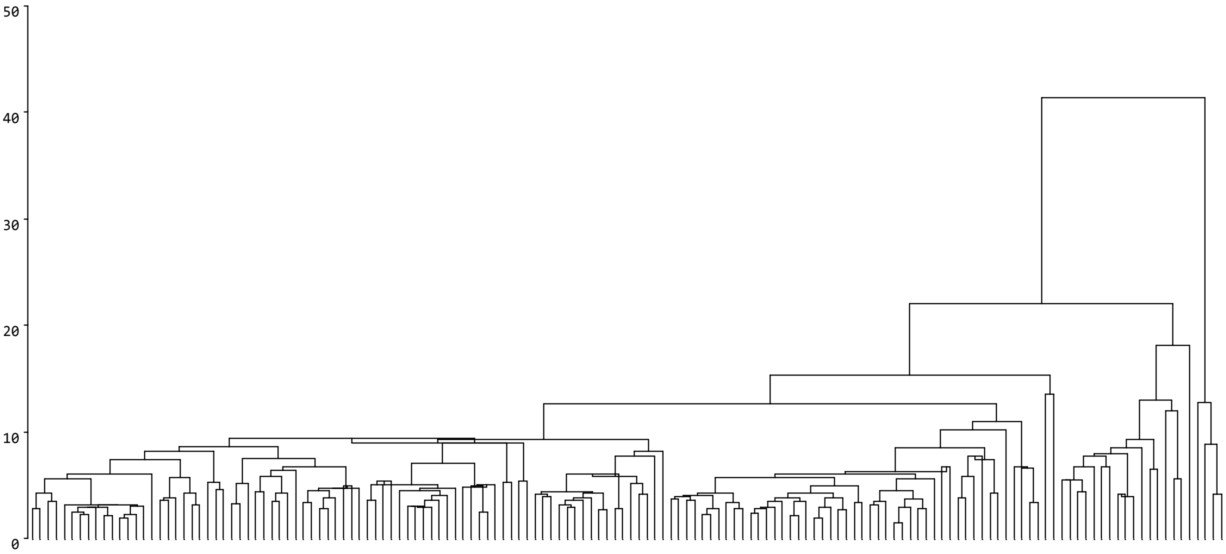

Figure 1. Grouping 150 soybean genotypes based on agronomic characters

Discussion

Plant age, growth, and seed characters of the 150 soybean genotypes were genetically greatly varied. By using cluster analysis, the 150 soybean genotypes were grouped into 10 clusters using 11 morphological traits. Morphological characterization of the existing genetic variation has been used in various researches. For example, Dayaman (2007) investigated 45 soybean accessions from different geographical areas and screened for their genetic diversity using 22 morphological traits. The investigation revealed out the accessions into six clusters. Another study by Diazcarrasco et al. (1986) grouped seventeen soybean varieties based on days to maturity, plant height, and seed yield plant^{-1}. Rasaily et al. (1986) characterized twenty soybean genotype characters based on plant height, number of branches, pods plant^{-1} and seed yield plant^{-1}. For agro-morphological traits, 94 accessions were grouped into seven different clusters at similarity coefficient of 0.52 by using Unweighted Pair Group Method with Arithmetic Mean (UPGMA) (Moe 2012). By using cluster analysis, Salimi et al. (2012) also successfully identified genotypes TNH56 and BP which are drought tolerant, and these genotypes could be used as a source of germplasm for breeding for drought tolerance.

In this study, 150 soybean genotypes were grouped into 10 clusters. Cluster I, II, and III consisted of 47, 80, and 13 genotypes, respectively; or about 93.33% of the total tested genotypes. Meanwhile, the other eight clusters consisted of only one up to three genotypes each. This indicates that some agronomic characters of the 150 genotypes have a narrow diversity. This finding is quite different from that of Malik et al. (2011), who found a high level of diversity on morphological traits (leaf area, pods plant^{-1}, branches plant^{-1}, 100-seed weight and grain yield plant^{-1}) on 92 soybean genotypes evaluated in Pakistan. Kaga et al. (2012) also found highly heterogeneous accessions and comprised of accessions from Nepal, Pakistan, Myanmar and China. These accessions generally flowered very late in the experimental field and had primitive characters such as twining, elongated stem and small seeds. By using RAPDs, Li and Nelson (2001) found that the mean genetic distance within accession from China was much larger than that within Japan or South Korea, but smaller than that between China and Japan or South Korea. Meanwhile, Oda et al. (2015) evaluated the combination of six microsatellite primers, which were able to distinguish the 21 cultivars used in that study; and those microsatellite markers showed less biased estimates compared to the estimates obtained by the parentage coefficient and phenotypic characters in studies on genetic diversity.

Study of genetic diversity is important to determine the genetic diversity of a population and to explore the superior character in order to support the development of improved varieties. Similarly, Paterson et al. (1991) stated that evaluation of genetic diversity would promote the efficient use of genetic variations in the breeding program. Genetic diversity and relationships among breeding materials are also of essential information for a plant breeder to improve an efficient crop variety. The genetic diversity study is important not only for crop improvement but also for efficient management and conservation of germplasm resources (Tahir and Karim 2011). The detection of genetic diversity can be done through analysis of morphological characterization and genetic markers. In this research, morphological characters (vegetative phase duration, generative phase duration, vegetative and generative ratio, days to maturity, plant height, number of filled pods, number of empty pods, number of branches, number of nodes, 100 seed weight, and seed yield plant^{-1}) were used to reveal the genetic diversity among 150 soybean genotypes. Some researchers stated that plant morphology-based approach is easier and cheaper, but the phenotypic appearance of the characters is strongly affected by the environment (Bohn et al. 1999; Maric et al. 2004), on the contrary, Ozkaya et al. (2006) stated that genetic marker approach such as random amplified polymorphic DNA (RAPD), amplified fragment length polymorphism (AFLP), simple sequence repeat (SSR), and inter-simple sequence repeat (ISSR) are not much affected by the environment.

In this study, each cluster exhibited a morphological characteristic that differed among clusters. Within each cluster, a number of genotype was successfully identified with the shortest duration of vegetative phase (29 days), the longest duration of generative phase (51-51.5 days), high G/V ratio (1.52), early days to maturity (73 days) and late maturity (87.5-88.5 days), long plant stem (61.8 cm), high number of filled pods plant^{-1} (81.8-83.3 pods), a few number of empty pods plant^{-1} (0.3 pods), a few number of branches plant^{-1} (0.5 branches), high number of nodes plant^{-1} (14 nodes), large seed size (16.79 g 100 seeds^{-1}), and high seed yield plant^{-1} (21.76-25.78 g). Moreover, each cluster described two or more determinant characters. For example, cluster V was characterized by late maturity (83.5-88.5 days) and relatively small seeded-size, i.e. 12.24-13.75 g 100 seeds^{-1}. On the contrary, cluster VI was characterized by days to maturity of 88 days but had large seed size, i.e. 16.79 g 100 seeds^{-1}. This implies that days to maturity within those clusters was similar, except the seed size. Those characters could serve as gene source for soybean's genetic improvement since studies on genetic diversity not only serve as a basis for understanding the genetic basis of soybean of different gene pools, but also to help identify new sources of genes to increase the productivity and quality of the soybean (Fu et al. 2007). The identified character for each cluster depends on the genetic material used or is also determined by the origin of the gene source used. According to Peric et al. (2014), a great similarity was usually found, primarily between the varieties come from the same institution because these varieties, generally, were developed from the same crosses.

In Indonesia, soybean was categorized as a secondary crop. Hence, most of the cultivars were planted after paddy. In such condition, the plant age preferred by farmers is early days to maturity (under 80 days). In addition, soybeans with large seeded size (>14 g/100 seeds) are used as raw material for tempeh. Thus, improvement of soybean's genetic potency in Indonesia could use the superior characters existed in each cluster identified in the present study.

We concluded from the present study that based on agronomic characters, the 150 genotypes were successfully clustered into 10 clusters, each cluster has its own agronomic characteristics related to days to maturity, growth, and seed. The soybean users in Indonesia prefer soybeans with high yield, early maturity, and large seed size. Genotypes in the group IV, VI, and IX were potentially used as gene sources for the development of improved soybean variety in Indonesia.

ACKNOWLEDGEMENTS

We thank Arifin who has assisted in data acquisition during the field research. This research was supported by Indonesian Agency for Agricultural Research and Development (IAARD), the Indonesian Ministry of Agriculture, Jakarta.

REFERENCES

Bohn M, Utz HF, Melchinger AE. 1999. Genetic diversity among winter wheat cultivars determined on the basis of RFLPs, AFLPs and SSRs and their use for predicting progeny variance. Crop Sci 39: 228-237.

Chen YW, Nelson RL. 2004. Genetic variation and relationships among cultivated, wild, and semiwild soybean. Crop Sci 44: 316-325.

Dayaman V. 2007. Diversity analysis in soybean (*Glycine max* L.) using morphological and simple sequence repeat (SSR) markers. Master of Science in Biotechnology, Department of Plant Molecular Biology and Biotechnology, Centre for Plant Molecular Biology, Tamil Nadu Agricultural University, India.

Diazcarrasco H, Abreuferrer S, Velazquez O, Garcia O. 1986. Similarities between some agronomic characters in soybean. Ciencias de la Agricultura 27: 108-113.

Fu YB, Peterson GW, Morrison MJ. 2007. Genetic diversity of Canadian soybean cultivars and exotic germplasm revealed by simple sequence repeat markers. Crop Sci 47: 1947-1954.

Gomez KA, Gomez AA. 1984. Statistical Procedures for Agricultural Research. 2nd ed, John Wiley and Sons, New York.

Hao D, Chao M, Yin ZT, Yu D. 2012. Genome-wide association analysis detecting significant single nucleotide polymorphisms for chlorophyll and chlorophyll fluorescence parameters in soybean (*Glycine max*) landraces. Euphytica 186: 919-931.

Kaga A, Shimizu TT, Watanabe S, Tsubokura Y, Katayose Y, Harada K, Vaughan DA, Tomooka N. 2012. Evaluation of soybean germplasm conserved in NIAS Genebank and development of mini core collections. Breed Sci. 61: 566-592.

Khanal R, Smith TH, Michaels TE, Pauls KP. 2016. Dynasty kidney bean. Can. J Plant Sci 96: 215-217.

Li Z, Nelson RL. 2001. Genetic diversity among soybean accessions from three countries measured by RAPDs. Crop Sci. 41: 1337-1347.

Malik MA, Rafii MY, Afroz MSS, Nath UK, Mondal MMA. 2014. Morphological characterization and assessment of genetic variability, character association, and divergence in soybean mutants. Sci World J. 2014, DOI: 10.1155/2014/968796.

Malik MFA, Ashraf M, Qureshi A, Khan MR. 2011. Investigation and comparison of some morphological traits of the soybean populations using 132 cluster analysis. Pakistan J Bot 43 (2): 1249-1255.

Maric S, Bolaric S, Martincic J, Pejic I, Kozumplik V. 2004. Genetic diversity of hexaploid wheat cultivars estimated by RAPD markers, morphological traits and coefficient of parentage. Plant Breed 123: 366-369.

McKenzie J, Goldman R. 2005. The Student Guide to MINITAB Release 14. Pearson Higher Education. Minitab Inc., NY.

Moe S. 2012. Relationships of Soybean (*Glycine max* L.) Accessions based on Agro-morphological, Physiological Traits and DNA Polymorphisms. [Thesis]. Program in Crop Science, Suranaree University of Technology, Thailand.

Navabi A, Balasubramanian P, Pauls KP, Bett K, Hou A. 2014. Genetic diversity of the Canadian dry bean varieties released since 1930: A pedigree analysis. Crop Sci 54: 993-1003.

Oda MC, Sediyama T, Matsuo E, Cruz CD, de Barros EG, Ferreira MFS. 2015. Phenotypic and molecular traits diversity in soybean launched in forty years of genetic breeding. Agron Sci Biotechnol 1: 1-9.

Ozkaya MT, Cakir E, Gokbayrak Z, Ercan H, Taskin N. 2006. Morphological and molecular characterization of Derik Halhali olive (*Olea europaea* L.) accessions grown in Derik-Markin province of Turkey. Scientia Horticulturae 108: 205-209.

Patterson RP, Hudak CM. 1996. Drought-avoidant soybean germplasm maintains nitrogen-fixation capacity under water stress. Plant Soil 186: 39-43.

Paterson AH, Damon S, Hewitt JD, Zamir D, Rabinowitch HD, Lincoln SE, Lander ES, Tanksley SD. 1991. Mendelian factors underlying quantitative traits in tomato: Comparison across species, generations and environments. Genetics 127 (1): 181-197.

Peric V, Nikolic A, Babic V, Sudaric A, Srebric M, Dordevic V, Drinic SM. 2014. Genetic relatedness of soybean genotypes based on agromorphological traits and RAPD markers. Genetika 46: 839-854.

Salimi S, Samiezade H, Abadi GM, Moradi. S 2012. Genetic diversity in soybean genotypes under drought stress condition using factor analysis and cluster analysis. World Appl Sci J 16: 474-478.

Showkat M, Tyagi SD. 2010. Correlation and path coefficient analysis of some quantitative traits in soybean (*Glycine max* L. Merrill.). Res J Agric Sci 1: 102-106.

Sumarno, Zuraida. 2006. Correlative and causative relationship between yield components and grain yield of soybean. Jurnal Penelitian Pertanian Tanaman Pangan 25 (1): 38-43. [Indonesian]

Susanto GWA, Adie MM. 2006. Pathway Analysis and its Implication on the Soybean Selection in the Development of Production of Legume and Tuber Crops Supporting Food Self-Sufficiency. Indonesian Center for Food Crops Research and Development, Bogor. [Indonesian]

Tahir NAR, Karim HFH. 2011. Determination of genetic relationship among some varieties of chickpea (*Cicer arietium* L) in Sulaimani by RAPD and ISSR markers. Jordan J Biol Sci 4 (2): 77-86.

Vollmann J, Fritz CN, Wagentristl H, Ruckenbauer P. 2000. Environmental and genetic variation of soybean seed protein content under Central European growing conditions. J Sci Food Agric 80: 1300-1306.