Asian Journal of Plant Sciences

ISSN 1682-3974

science alert

ANSInet
an open access publisher
http://ansinet.com

OPEN ACCESS **Asian Journal of Plant Sciences**

ISSN 1682-3974
DOI: 10.3923/ajps.2022.440.447

Research Article

Effect of Agronomic and Morphological Characteristics of *Glycine max* L. Merrill in Advanced Separation

Anna Satyana Karyawati, Naomi Geoviani Buyung and Budi Waluyo

Department of Agronomy, Faculty of Agriculture, Brawijaya University, Jl. Veteran, Malang 65145, East Java, Indonesia

Abstract

Background and Objective: Assembly of soybean varieties through crossbred is an effort to recombine genetic to obtain a superior genotype. Genotypic clustering and character diversity assessment is the base for selection. The objective of the research was to group 30 genotypes as a result of crossbred and 6 parents based on agro morphological characters. **Materials and Methods:** The research was conducted from March-May, 2019 at Malang, Indonesia. The research used Randomized Block Design (RBD) by 3 replications. Materials of the research include 6 parents and 30 genotypes resulting from crossbred of 6 parents that are designed diallel, such as Anjasmoro (AJM), Tanggamus (TGM), Argopuro (AGP), Grobogan (GBG), Brawijaya 1 (UB 1) and Brawijaya 2 (UB 2). **Results:** Results for analysis of variance used Principal Component Analysis (PCA) by Pearson correlation coefficient approach and 5 principal components were obtained and contributed to cumulative diversity values of 60.92%. The clustering analysis is based on Agglomerative Hierarchical Clustering (AHC) with similarity of Pearson correlation coefficient and agglomeration method of unweighted pair group method average (UPGMA and it generated 6 principal groups, which spread with a similarity coefficient of 98.15%. **Conclusion:** The appearance of morphological characters in each main component is classified into 5 components. The dendrogram results were classified into 2 major groups, the group I, which contained the GBGXTGM genotype and group II, which contained 35 genotypes. The distinction between groups I and II was made based on differences in leaf length, compound leaf width and leaf area.

Key words: Clustering, crossbred, diversity, genetic distance, morphological, PCA, soybean

Citation: Karyawati, A.S., N.G. Buyung and B. Waluyo, 2022. Effect of agronomic and morphological characteristics of *Glycine max* L. Merrill in advanced separation. Asian J. Plant Sci., 21: 440-447.

Correspo nding Author: Budi Waluyo, Department of Agronomy, Faculty of Agriculture, Brawijaya University, Jl. Veteran, Malang 65145, East Java, Indonesia

Competing Interest: The authors have declared that no competing interest exists.

Data Availability: All relevant data are within the paper and its supporting information files.

INTRODUCTION

Soybean (*Glycine max* (L.) Merrill) is an essential commodity in Indonesia, not only for agroindustrial material, for example, fermented soybean cake (tempe), tofu, soy sauce, soy milk and for feed industries by Pujiwati *et al.*[1]. Soybean contains some nutrients, which are good for health, such as protein, carbohydrates, vitamins and minerals. Dry soybean contains 36% protein, 19% oil, 35% carbohydrate, 5% mineral and other substances including vitamins by Salimi *et al.*[2]. Along with the increased awareness of the society about health and nutritive foods and followed by the rapid growth of population, it makes the demand for soybean in Indonesia increases as well Bøhn and Millstone[3]. High demand for soybean was not counterbalanced with sufficient production so that the government should import it to fulfill the domestic demand for soybean by Zikri *et al.*[4].

An effort to increase soybean production is through plant breeding. Inbreeding the plant, genetic diversity is very important for breeding material by Liu *et al.*[5]. Diversity could be increased through crossbred by extending genetic diversity, however, it is expected that a combination of the parental traits will be able to produce variety as expected. Diversity is useful to find out the grouping pattern of genotype population and specific character of each genotype group so that it can be used for parents selection to assembly new superior variety by Malek *et al.*[6]. Genetic diversity in a population can be used as a guide to select the parents in artificial crossbred to establish hybrid population as selection material by Torres *et al.*[7].

Evaluation on genetic grouping can be used as a base in selecting potential parents in the breeding program by Gwinner *et al.*[8]. Information of genetic distance and relationship is highly required in establishing basic population to assembly superior variety by Khan *et al.*[9]. The relationship between 2 individuals or populations could be measured following the similarity of characters by the assumption that different characters are caused by different genetic structures El-hashas[10]. Characters on creatures are controlled by a gene. Gene is a fraction of DNA in which its activity (expression) could be observed through the change of morphological character as a result of environmental influence He *et al.*[11]. Cluster analysis agglomerates genotypes, which have the closeness of a certain character that can be seen clearly and separate individuals that have a different character based on an algorithm of minimum distance method with the main input of distance matrix between the objects pair by Neisse *et al.*[12]. Relationship analysis based on morphological characters will be perfect if it used character description that has stable and high heritability values. The objectives of the research were grouping genotypes and character diversity of soybean from the crossbred.

MATERIALS AND METHODS

Study area: The research was conducted from March-May, 2019 at the experimental field of Brawijaya University in Agro Techno Park, Malang, East Java Province, Indonesia. The location of the research is at 7°21'-7°31' South latitude and 110°10'-111°40' East longitude at altitude 330 masl, the average temperature is 25°C-30°C and has Alfisol soil.

Methodology: The research used Randomized Block Design (RBD) by 3 replications. Materials of the research include 6 parents and 30 genotypes resulting from crossbred of 6 parents that are designed diallel, such as Anjasmoro (AJM), Tanggamus (TGM), Argopuro (AGP), Grobogan (GBG), Brawijaya 1 (UB1) and Brawijaya 2 (UB2). There are 36 beds on each replication, each bed comprises 60 plants and spacing 15×40 cm. Fertilizer application uses NPK by formulation (16:16:16) and dose 250 kg ha^{-1}. Disease and pest control are conducted preventively.

Observation on qualitative characters was conducted on colours of hypocotyls, hair, flower, middle leaf shape, lateral leaf shape, growth type, branching pattern, pod colour, glossy level of pod colour, seed size, seed shape, testa colour on seed, glossy seed, hilum colour and funicle colour. Observation on quantitative characters was conducted against the width of the leaflet, length of the leaflet, width of compound leaves, length of compound leaves, wet weight of the plant, dry weight of the plant, leaf area, flowering time, root length (rooting), number of root nodule, number of effective root nodule, number of stomata, amount of chlorophyll, number of vein bundle, plant height, stem diameter, number of leaves, number of branches, number of fertile nodes, pod maturity, harvest time, number of filled pod, number of empty pods, number of total pods per plant, number of seeds per plant, weight of seeds per plant, weight of 100 seeds and yield.

Statistical analysis: The maximum diversity of morphological characters and agronomy, which comprise qualitative and quantitative characters, is determined by the following Principal Component Analysis (PCA) with Pearson's correlation type. The number of the principal components, which affect total diversity, is determined by eigenvalue >1. Characters that contribute to maximum diversity are determined by factor loadings >0.5. Clustering analysis and genetic distance are done by involving qualitative and quantitative characters, which significantly contribute to diversity based on PCA analysis. Grouping and genetic distance are conducted by cluster analysis that is based on Agglomerative Hierarchical Clustering (AHC) similarities using Pearson's correlation coefficient by Aglomerasi Unweighted Pair-Group Method Average (UPGMA) method. PCA and AHC use XLSTAT software version 2009.3.02.

RESULTS

Qualitative character on 36 genotypes of soybean: Observation of qualitative character on 36 genotypes of soybean (Table 1) was conducted following the descriptor guide by the International Union for the protection of new varieties of plants. Result of observation on hypocotyls colour from 36 genotypes of soybean, there are 2 colours, purple and green, 30 genotypes have purple hypocotyls and 6 genotypes have green hypocotyls. Observation on the hair colour of the stem, there are 2 colours, brown and green, which are dominated by brown colour for 30 genotypes and white for 6 genotypes. The growth type and branching pattern of soybean are dominated by determinate growth type and semi-erect branching pattern. The determinate growth type shows that after flowering, the vegetative phase will stop and the flowering will take place simultaneously but the flowering period may not take long.

Results of observation on middle leaf shape and lateral leaf shape, there are 3 types of middle leaf shape,

Table 1: Colours of hypocotyls, hairs on stem, growth type and branching pattern of 36 genotypes

Genotype♀×♂	WHp	WBB	TP	PP	BDT	BDL	WB	WP	KWP	UBj	BB	WT	KB	WH	WF
AJM×TGM	U	CT	D	SE	T	PO	U	CK	Tr	S	Gp	K	Ks	CM	BdT
AJM×AGP	H	P	D	SE	T	PO	P	HK	G	S	BT	K	Ks	CT	BdT
AJM×GBG	U	CT	D	SE	T	PO	U	CK	Tr	S	BT	K	Ks	CT	BdT
AJM×UB1	U	CT	D	SE	O	RO	U	HK	G	S	BT	K	Ks	CM	BdT
AJM×UB2	U	CT	D	SE	T	PO	U	CK	Tr	S	BT	K	Ks	CT	BdT
TGM×AJM	H	P	D	SE	T	PO	P	HK	G	S	BT	K	Ks	CT	BdT
TGM×AGP	U	CT	D	SE	T	PO	U	CK	Tr	S	B	K	Ks	CM	BdT
TGM×GBG	U	CT	D	SE	T	PO	U	HK	G	S	G	K	Ks	CT	BdT
TGM×UB1	U	CT	D	SE	T	PO	U	HK	G	S	BT	K	Ks	CM	BdT
TGM×UB2	U	CT	D	SE	T	PO	U	HK	G	S	BT	K	Ks	CT	SdT
AGP×AJM	U	CT	D	SE	O	RO	U	CK	Tr	S	BT	K	Ks	CT	BdT
AGP×TGM	H	P	D	SE	O	RO	P	HK	G	S	BT	K	Ks	CT	BdT
AGP×GBG	H	P	D	SE	L	L	P	HK	G	S	B	K	Ks	CM	BdT
AGP×UB1	U	CT	D	SE	T	PO	U	HK	G	S	BT	K	Ks	CT	BdT
AGP×UB2	H	P	D	SE	L	L	P	Ht	G	S	BT	K	Ks	CM	BdT
GBG×AJM	U	CT	D	SE	O	RO	U	HK	G	S	BT	K	Ks	CT	BdT
GBG×TGM	U	CT	D	SE	T	PO	U	CK	Tr	B	BT	K	Ks	CT	BdT
GBG×AGP	U	CT	D	SE	T	PO	U	CK	Tr	B	BT	K	Ks	CM	BdT
GBG×UB1	U	CT	D	SE	T	PO	U	HK	G	S	BT	K	Ks	CT	BdT
GBG×UB2	U	CT	D	SE	T	PO	U	CK	Tr	S	BT	K	Ks	CT	BdT
UB1×AJM	U	CT	D	SE	T	PO	U	CK	Tr	S	BT	K	Ks	CM	BdT
UB1×TGM	U	CT	D	SE	T	PO	U	HK	G	S	BT	K	Ks	CT	BdT
UB1×AGP	U	CT	D	SE	T	PO	U	HK	G	S	BT	K	Ks	CT	BdT
UB1×GBG	U	CT	D	SE	T	PO	U	HK	G	S	Lj	K	Ks	CT	BdT
UB1×UB2	U	CT	D	SE	O	RO	U	Ht	G	S	B	K	Ks	CM	BdT
UB2×AJM	U	CT	D	SE	O	RO	U	HK	G	S	BT	K	Ks	CT	BdT
UB2×UB1	U	CT	D	SE	T	PO	U	CK	Tr	S	BT	K	Ks	CT	BdT
UB2×AGP	U	CT	D	SE	T	PO	U	HK	G	S	BT	K	Ks	CT	BdT
B2×GBG	U	CT	D	SE	T	PO	U	HK	G	S	BT	K	Ks	CT	BdT
UB2×UB1	U	CT	D	SE	O	RO	U	HK	G	S	BT	K	Ks	CT	BdT
AJM	U	CT	D	SE	T	PO	U	CK	Tr	B	G	K	Ks	CM	BdT
AGP	H	P	D	SE	L	L	P	Ht	G	B	B	K	Ks	CM	BdT
GBG	U	CT	D	SE	T	PO	U	CK	Tr	B	BT	K	Ks	CT	BdT
TGM	U	CT	D	SE	T	PO	U	HK	G	S	BT	K	Ks	CT	BdT
UB1	U	CT	D	SE	O	RO	U	HK	G	B	BT	K	M	CM	BdT
UB2	U	CT	D	SE	T	PO	U	CK	Tr	B	BT	K	Ks	CT	BdT

AJM: Anjasmoro variety, AGP: Argopuro variety, GBG: Grobogan variety, TGM: Tanggamus variety, UB1: UB1 line, UB2: UB2 line, Whp: Hypocotyls colour, WBB: Hair colour on stem, TP: Growth type, PP: Branching pattern, BDT: Middle leaf shape, BDL: Lateral leaf shape, WB: Flower colour, WP: Pod colour, KWP: Glossy pod colour, Ubj: Seed size, BB: Seed shape, WT: Testa colour, KB: Glossy seed, WH: Hilum colour, WF: Funicle colour, U: Purple, H: Green, CT: Dark brown, P: White, D: Determinate, SE: Semi erect, T: Triangular, O: Ovoid, L: Lanceolate, PO: Pointed ovate, RO: Rounded ovate, CK: Yellowish brown, HK: Brownish black, Ht: Black, Tr: Bright, G: Dark, S: Medium, B: Big, Gp: Flat, BT: Ovoid, B: Round, Lj: Oval, K: Yellow, Ks: Dull, M: Glossy, CM: Light brown, BdT: Different from testa and SdT: Same with testa

Table 2: Minimum value, maximum value, mean value, standard of deviation, variance and coefficient of variation on 28 quantitative characters of soybean

Characters	N	Minimum	Maximum	Mean	Std. dev	Varian	Coef. variations
Width of leaflet (cm)	36	4.65	7.75	6.52	0.73	0.53	11.17
Length of leaflet (cm)	36	9.17	11.92	10.47	0.66	0.44	25.94
Width of compound leaves (cm)	36	17.67	23.42	20.36	1.48	2.18	7.26
Length of compound leaves (cm)	36	12.83	33.25	15.04	3.25	10.53	21.59
Wet weight (g)	36	4.63	19.74	12.85	3.41	11.62	26.52
Dry weight (g)	36	1.61	5.63	3.92	0.88	0.77	22.40
Leaf area	36	55.83	155.50	108.44	22.34	498.92	20.60
Flowering time	36	28.00	38.00	34.28	2.29	5.23	6.67
Rooting length (cm)	36	25.58	44.33	32.71	4.63	21.42	14.15
Root nodule	36	8.83	34.33	17.52	5.63	31.70	32.14
Effective root nodule	36	5.83	25.33	13.43	4.29	18.44	31.97
Number of stomata	36	25.00	47.00	36.96	5.98	35.73	16.17
Amount of chlorophyll	36	37.03	47.70	42.74	2.41	5.83	5.65
Number of vein bundle	36	10.50	20.00	14.18	1.84	3.39	12.98
Plant height (cm)	36	30.00	63.50	45.02	6.46	41.73	14.35
Diameter of stem (mm)	36	7.50	13.50	9.51	1.41	1.98	14.77
Number of leaf	36	10.00	24.83	17.32	3.15	9.91	18.17
Number of branch	36	1.67	4.83	3.15	0.83	0.69	26.30
Number of fertile node	36	7.83	14.00	11.25	1.36	1.85	12.08
Pod maturity	36	76.00	89.00	84.25	2.51	6.31	2.98
Harvest time	36	79.00	92.00	87.19	2.55	6.50	2.92
Number of filled pod	36	33.92	105.25	69.70	15.59	243.09	22.37
Number of empty pod	36	1.75	7.08	2.99	0.93	0.87	31.22
Number of pod per plant	36	41.00	108.75	72.69	15.45	238.82	21.26
Number of seed per plant	36	72.00	255.83	164.70	41.93	1.758	25.46
Weight of seed per plant (g)	36	14.76	28.53	21.25	3.45	11.90	16.24
Weight of 100 seeds (g)	36	10.14	20.30	13.41	2.45	5.99	18.25
Yield ($t\ ha^{-1}$)	36	1.89	3.65	2.72	0.44	0.19	16.24

namely triangular, ovoid and lanceolate as well as 3 types of lateral leaf shape, namely pointed ovate, rounded ovate and lanceolate. The colour of the soybean flower is dominated by purple for 30 genotypes and white for 6 genotypes. Such purple and white flowers are conditioned by dominant/recessive allele from locus W1. There are 3 types of pod colour for soybean, namely black, yellowish-brown and brownish-black, in which 3 genotypes are black, 14 genotypes are brownish yellow and 19 genotypes are brownish-black. For the glossy level of pod colour, 13 genotypes look glossy bright and 23 genotypes look glossy dark. There are 2 sizes of soybean seed that are observed, medium and big, 29 genotypes dominate the medium size and 7 genotypes dominate the big size. Four types of seed shape being observed, namely ovoid, round, oval and flat.

Testa colours of 36 genotypes, which are being observed are yellow. The glossy seed of the soybean is dominated by dull seeds over 34 genotypes and 2 genotypes have glossy seeds. The hilum is a part of the seed coat that attaches to the seed stalk, there are 2 types of hilum colour from 36 genotypes that are observed, namely dark brown for 24 genotypes and light brown for 12 genotypes. The funicle is part of the seed coat in the middle of the hilum and from 36 genotypes that are being observed, the funicle colour of 35 genotypes are different from the testa and 1 genotype has the same funicle colour as a testa.

Quantitative characters on 36 genotypes of soybean: Results of the analysis on 28 quantitative characters from 36 genotypes of soybean showed the highest coefficient of variation is for root nodule, 32.14 and the lowest coefficient of variation is for harvest time, 2.92 (Table 2). The coefficient of variation values show diversities of character. Coefficients of variation values, which are relatively homogenous, imply that selection on a population has not been effective to improve the character and vice versa.

Principal component analysis on 36 genotypes of soybean based on agromorphology characters: Results of PCA diversity evaluation on 40 agronomic characters from 36 genotypes of soybean have been obtained. Five principal components that have eigenvalue >1 with cumulative variability of 60.92% (Table 3). The 1st Principal Component (PC_1) has eigenvalue 8.50 contributes to maximum diversity of 21.24%. Characters that contribute to PC_1 include middle leaf shape, lateral leaf shape, wet weight, dry weight, effective root nodule, number of leaves, number of filled pod, number of pod per plant, number of seed per plant, weight of

Table 3: Principal component values on 40 morphological characters of soybean

Characters	PC$_1$	PC$_2$	PC$_3$	PC$_4$	PC$_5$
Hypocotyls colour	0.40	**0.69**	0.20	-0.25	-0.09
Hair colour	0.40	**0.69**	0.20	-0.25	-0.09
Seed size	-0.43	0.36	0.32	0.25	0.16
Middle leaf shape	**0.58**	0.40	0.15	-0.19	0.09
Lateral leaf shape	**-0.62**	**-0.50**	-0.19	0.18	-0.04
Flower colour	0.40	**`0.69**	!qq!~	-0.25	-0.09
Pod colour	0.42	-0.20	-0.18	-0.29	-0.45
Glossy level of pod colour	0.26	**-0.53**	-0.22	-0.12	-0.27
Seed shape	0.39	0.26	-0.39	-0.09	-0.16
Glossy level of seed	0.03	0.12	**0.52**	0.03	0.35
Hilum colour	0.34	0.19	-0.47	-0.11	-0.48
Funicle colour	-0.10	-0.02	0.21	0.37	0.04
Width of leaflet	0.28	0.42	**0.62**	-0.16	-0.10
Length of leaflet	-0.07	-0.39	0.34	**0.59**	-0.45
Width of compound leaves	-0.17	-0.37	0.29	**0.53**	-0.41
Length of compound leaves	0.25	-0.09	0.07	0.47	-0.46
Wet weight	**0.58**	0.13	0.34	0.12	-0.31
Dry weight	**0.61**	0.18	0.30	0.07	-0.35
Leaf area	0.33	0.26	**0.57**	0.24	-0.12
Flowering time	0.34	**-0.66**	0.37	-0.39	0.23
Rooting length	0.08	-0.21	-0.33	0.44	0.35
Root nodule	0.14	0.23	0.41	0.25	**0.61**
Effective root nodule	**0.55**	-0.04	0.32	0.21	0.25
Number of stomata	0.00	0.27	**-0.51**	-0.31	0.03
Chlorophyll	-0.49	0.16	0.12	-0.25	-0.23
Vein bundle	-0.25	**-0.63**	0.09	-0.22	0.08
Plant height	-0.03	-0.48	0.25	-0.13	-0.12
Stem diameter	0.26	-0.29	0.42	-0.23	-0.38
Number of leaf	**0.71**	-0.30	0.01	0.08	0.00
Number of branch	0.47	0.09	-0.44	0.21	0.29
Number of fertile node	0.05	-0.46	0.02	-0.25	-0.20
Pod maturity	0.37	**-0.68**	0.38	-0.36	0.21
Harvest time	0.37	**-0.68**	0.36	-0.37	0.24
Number of filled pod	**0.86**	-0.25	-0.26	0.08	0.10
Number of empty pod	-0.25	0.36	-0.38	-0.20	-0.04
Number of pod per plant	**0.85**	-0.23	-0.29	0.07	0.10
Number of seed per plant	**0.88**	-0.19	-0.28	0.17	0.08
Weight of seed per plant	**0.71**	0.23	-0.15	0.27	0.10
Weight of 100 seeds	**-0.69**	**0.53**	0.20	0.05	-0.06
Yield	**0.71**	0.23	-0.15	0.27	0.10
Eigenvalue	**8.50**	**6.25**	**4.13**	**2.86**	**2.64**
Variability (%)	**21.24**	**15.61**	**10.33**	**7.14**	**6.59**
Cumulative (%)	**21.24**	**36.86**	**47.19**	**54.33**	**60.92**

Numbers in bold are the influential character values due to factor loading >0.5

seed per plant, weight of 100 seeds and yield. Analysis of the 1st Component (PC$_1$) shows the highest diversity effect in comparison with other components. The 2nd Principal Component (PC$_2$) with eigenvalue 6.25 contribute to maximum diversity of 15.61%. Characters that contribute to PC$_2$ include hypocotyls colour, hair colour, lateral leaf shape, flower colour, glossy level of the pod colour, flowering time, vein bundle, pod maturity, harvesting time and weight of 100 seeds. The 3rd Principal Component (PC$_3$) has eigenvalue 4.13 and contributes to maximum diversity of 10.33%. Characters that contribute to PC$_3$ include the glossy level of seed, leaflet width, leaf area and the number of stomata. The 4th Principal Component (PC$_4$) has an eigenvalue of 2.86 and a diversity value of 7.14%. Characters that contribute to PC$_4$ include leaflet length and width of a compound leaf. While the 5th Principal Component (PC$_5$) has an eigenvalue of 2.64 and contributes to maximum diversity of 6.59% and only 1 character that contributes to diversity, the root nodule.

Based on the result for analysis of variance on the principal components, it results from different values of the factor loading, so that, the character contribution which

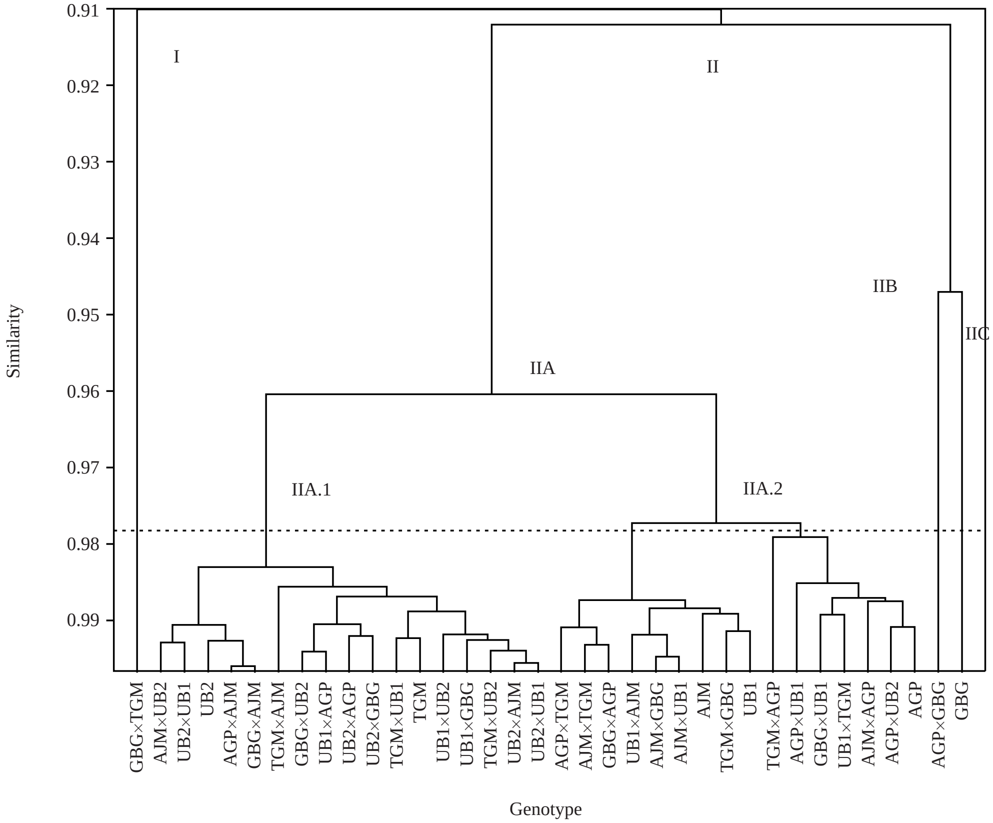

Fig. 1: Dendrogram of 36 soybean genotypes based on 40 morphological characters

affects diversity is also different. Some characters above have a strong influence in determining the character role on diversity and besides that, some characters above highly the effect on grouping among genotypes.

Clustering analysis on 36 genotypes of soybean: The result of the dendrogram shows that 36 genotypes of soybean are divided into 2 main groups, namely group I and II by the coefficient of similarities range 91-99% and genetic distance 9%, which shows a close relationship over the observed genotypes. A high coefficient of similarity indicates that the genetic distance between genotypes is getting closer. Based on the dendrogram analysis in Fig. 1, Group I and II show the result of clustered together on a coefficient of 91.3%. Group I only comprises of a genotype, GBG×TGM, which separates in similarity level 91.3%. While group II comprised 35 genotypes. Separating group I and group II was due to different characters that include the length of the leaflet, width of compound leaves and leaf area. Such morphological characters have significantly differentiated the GBG×TGM genotype and other genotypes. GBG×TGM genotype has the highest values for leaflet length, the width of compound leaves and leaf area in comparison with other genotypes. Group II establishes 3 major subgroups that include group IIA, IIB and IIC. Those 3 subgroups were separated at a similarity level of 91.5%. Group IIA comprises 33 genotypes, group IIB just comprises of one genotype, AGP×GBG and group IIC comprises of GBG genotype that assembles at similarity level 95%. Group IIB is separated from groups IIA and IIC because it has some characters, such as wet weight, dry weight, leaf area and root nodule. While group IIC is separated from groups IIA and IIB because it has the characters of leaflet length, flower initiation, effective root nodule, stomata, a bundle of vessels, number of leaves, pod maturity, harvest age, number of the filled pod, number of the empty pod, number of planting pod, number of planting seed and weight of 100 seeds. Group IIA establishes subgroups, IIA.1 and IIA.2 that were separated at a similarity level of 96.4%. Group IIA.1 comprises of 17 genotypes that include AJM×UB2, UB2×UB1, UB2, AGP×AJM, GBG×AJM, TGM×AJM, GBG×UB2, UB1×AGP, UB2×AGP, UB2×GBG, TGM×UB1, TGM, UB1×UB2, UB1×GBG, TGM×UB2, UB2×AJM and UB2×UB1. Moreover, group IIA.2 comprises of 16 genotypes that include AGP×TGM, AJM×TGM, GBG×AGP, UB1×AJM, AJM×GBG, 9JM×UB1, AJM, TGM×GBG, UB1, TGM×AGP, AGP×UB1, GBG×UB1, UB1×TGM, AJM×AGP, AGP×UB2, AGP, AGP×GBG and GBG.

DISCUSSION

Result of observation on hypocotyls colour from 36 genotypes of soybean, there are 2 colours, purple and green. Soybean cultivars with purple hypocotyl have purple flowers, while green hypocotyl will produce white flowers by Jeong *et al.*[13]. Soybean cultivars generally have purple and white flowers by Dorneles *et al.*[14]. The flowers are usually found at the end of the soybean stem and have a medium plant height Dai *et al.*[15]. In addition to flowers, soybeans also have a variety of different colours of pods. Bhartiya *et al.*[16] stated that there are 3 colour classifications of pods in soybean plants, namely black, brown and tan. On the other hand, Wu *et al.*[17] described the shape of the seed that could be measured, including the height, length and depth of the seed. When the cotyledons in soybean embryos have entered maturity, the skin colour of soybean seeds is green, yellow and dark yellow by Myers *et al.*[18]. However, the yellow colour generally dominates the soybean seed coat. The difference in genotypic response to genotypic and environment that is observed in deviation of standard CV (%) by Sabri *et al.*[19]. Coefficients of variation values show that the great roles of variability are due to genotype and environmental conditions. Based on the results of the research by Khan *et al.*[20], they indicated quantitative properties that show wide varieties (high difference level) in 115 genotypes of soybean.

Principal Component Analysis (PCA) is a multivariate analysis that can be used to look for the character of a plant, which has maximum contribution to diversity by Hssaini *et al.*[21]. Worede *et al.*[22] suggested that diversity values of characters on the 1st component have relatively high values due to the higher value of the component, the greater role that must be played by the character in diversity. Iqbal *et al.*[23] suggested that the character value of the principal component has factor loading $\geq$0,750, which means that the character has a very strong influence on diversity. Character value, which has factor loading 0,500$\leq\times<$0,750, means that the character is sufficiently influential. Character value <0,500 is less influential in diversity.

Clustering analysis is applied to determine objects that are being observed following characteristics belonging to the specific plant, the relationship between objects using similarity measurement when both objects have the closest distance so that they will be joined into a cluster and vice versa Salimi *et al.*[2]. The distance closeness indicates that both objects have characteristic similarities by Khan *et al.*[9].

Goodarzi *et al.*[24] the genotypes grouping into some clusters is determined following the genetic similarity of each genotype, which is used to find out its genetic distance. Genotypes in different clusters indicate that the genetic distance relationship is far, while genotypes in the same cluster have a close genetic distance. Character similarity analysis among groups to interpret genetic distance accurately, so that it would be able to design new genotype efficiently by Salimi *et al.*[2].

Cluster analysis based on the characteristics of a plant can be used to determine the kinship. This is demonstrated by the dendrogram results in this study, which indicated that 36 soybean genotypes were classified into 2 major groups, namely groups I and II, with a similarity coefficient of 91-99 percent, which is close to 100% with a genetic distance of 9%. The genetic distance between groups I and II appears to be close based on observed genotypes.

CONCLUSION

Diversity on 36 soybean genotypes based on 40 qualitative and quantitative characters have formed 5 principal components that have eigenvalue >1 with total cumulative diversity of 60.92%. Results of genotype grouping generate 6 groups using AHC (Analysis Hierarchical Clustering). Separating the genotype groups was due to different characters that include the length of the leaflet, width of compound leaves and leaf area. The coefficient of similarity on 6 groups was 98.15% and indicated the genotypes have very similar appearances but they are still distinguishable.

SIGNIFICANCE STATEMENT

This study demonstrates the possible synergistic effect of the assembly of soybean varieties through cross-breeding to obtain a superior genotype. This study will help the researcher to uncover the critical areas of grouping 30 genotypes as a result of crossbred and 6 parents based on agro morphological characters. Thus, we can get a new theory on clustering and principal component analysis based on agronomic and morphological characteristics in the advanced segregating population of soybean (*Glycine max* L. Merrill).

REFERENCES

1. Pujiwati, I., N. Aini, S.P. Sakti and B. Guritno, 2018. The effect of harmonic frequency and sound intensity on the opening of stomata, growth and yield of soybean (*Glycine max* (L.) Merrill). Pertanika J. Trop. Agric. Sci., 41: 963-974.

2. Salimi, S., H.S. Lahiji, G.M. Abadi, S. Salimi and S. Moradi, 2012. Genetic diversity in soybean genotypes under drought stress condition using factor analysis and cluster analysis. World Appl. Sci. J., 16: 474-478.
3. Bøhn, T. and E. Millstone, 2019. The introduction of thousands of tonnes of glyphosate in the food chain-an evaluation of glyphosate tolerant soybeans. Foods, Vol. 8, 10.3390/foods8120669.
4. Zikri, I., S. Safrida, E. Susanti and R.A. Putri, 2020. Analysis of trend and determinant factors of imported soybean in the period of 2003-2022. Adv. Food Sci., Sustainable Agric. Agroindustrial Eng., 3: 17-24.
5. Liu, Z., H. Li, Z. Wen, X. Fan and Y. Li *et al*., 2017. Comparison of genetic diversity between Chinese and American soybean (*Glycine max* (L.)) accessions revealed by high-density SNps. Front. Plant Sci., Vol. 8. 10.3389/fpls.2017.02014.
6. Malek, M.A., M.Y. Rafii, M.S.S. Afroz, U.K. Nath and M.M.A. Mondal, 2014. Morphological characterization and assessment of genetic variability, character association, and divergence in soybean mutants. Sci. World J., Vol. 2014. 10.1155/2014/968796.
7. Torres, A.R., A.K. Grunvald, T.B. Martins, M.A. dos Santos, N.G. Lemos, L.A.S. Silva and M. Hungria, 2015. Genetic structure and diversity of a soybean germplasm considering biological nitrogen fixation and protein content. Sci. Agricola, 72: 47-52.
8. Gwinner, R., T.A. Setotaw, M. Pasqual, J.B. dos Santos, A.M. Zuffo, E.V. Zambiazzi and A.T. Bruzi, 2017. Genetic diversity in Brazilian soybean germplasm. Crop Breed. Appl. Biotechnol., 17: 373-381.
9. Khan, M.R.A., F. Mahmud, M.A. Reza, M.M. Mahbub, B.J. Shirazy and M.M. Rahman, 2017. Genetic diversity, correlation and path analysis for yield and yield components of pea (*Pisum sativum* L.). World J. Agric. Sci., 13: 11-16.
10. El-Hashash, E., 2016. Genetic diversity of soybean yield based on cluster and principal component analyses. J. Adv. Biol. Biotechnol., Vol. 10. 10.9734/jabb/2016/29127.
11. He, H., D. Huang, W. Pang, D. Sun and Q. Wang *et al*., 2018. Plasma-induced amorphous shell and deep cation-site S doping endow TiO_2 with extraordinary sodium storage performance. Adv. Mater., Vol. 30. 10.1002/adma.201801013.
12. Neisse, A.C., J.L. Kirch and K. Hongyu, 2018. AMMI and GGE biplot for genotype × environment interaction: A medoid–based hierarchical cluster analysis approach for high–dimensional data. Biome. Lett., 55: 97-121.
13. Jeong, N., K.S. Kim, S. Jeong, J.Y. Kim and S.K. Park *et al*., 2019. Korean soybean core collection: Genotypic and phenotypic diversity population structure and genome-wide association study. PLoS One, Vol. 14. 10.1371/journal.pone.0224074.
14. Dorneles, J.B., I.R. Carvalho, T.D.S. Martins, N.B. Moura, J.A.G. da Silva and F. Lautenchleger, 2020. Two decades of national registry of soybean cultivars: Updates and perspectives. Commun. Plant Sci., 10: 85-96.
15. Dai, J., R. Zhang, B. Wei, Z. Nie and G. Xing *et al*., 2017. Key biological factors related to outcrossing-productivity of cytoplasmic-nuclear male-sterile lines in soybean [*Glycine max* (L.) merr.]. Euphytica, Vol. 213. 10.1007/s10681-017-2054-6.
16. Bhartiya, A., J.P. Aditya, R.S. Pal, N. Chandra, L. Kant and A. Pattanayak, 2020. Bhat (black soybean): A traditional legume with high nutritional and nutraceutical properties from NW himalayan region of India. Indian J. Trad. Knowledge, 19: 307-319.
17. Wu, J., L. Wang, J. Fu, J. Chen and S. Wei *et al*., 2019. Resequencing of 683 common bean genotypes identifies yield component trait associations across a North-South Cline. Nat. Genet., 52: 118-125.
18. Myers, J.R., M. Aljadi and L. Brewer, 2018. The importance of cosmetic stay green in specialty crops. Plant Breed. Rev., 42: 219-256.
19. Sabri, R.S., M.Y. Rafii, M.R. Ismail, O. Yusuff, S.C. Chukwu and N.A. Hasan, 2020. Assessment of agro-morphologic performance, genetic parameters and clustering pattern of newly developed blast resistant rice lines tested in four environments. Agronomy, Vol. 10. 10.3390/agronomy10081098.
20. Khan, M., M. Karim, M. Haque, A. Karim and M. Mian, 2015. Variations in agronomic traits of soybean genotypes. SAARC J. Agric., 12: 90-100.
21. Hssaini, L., H. Hanine, R. Razouk, S. Ennahli, A. Mekaoui, A. Ejjilani and J. Charafi, 2019. Assessment of genetic diversity in Moroccan fig (*Ficus carica* L.) collection by combining morphological and physicochemical descriptors. Genet. Resour. Crop Evol., 67: 457-474.
22. Worede, F., T. Sreewongchai, C. Phumichai and P. Sripichitt, 2014. Multivariate analysis of genetic diversity among some rice genotypes using morpho-agronomic traits. J. Plant Sci., 9: 14-24.
23. Iqbal, Z., M. Arshad and M. Ashraf, T. Mahmood and A. Waheed, 2008. Evaluation of soybean [*Glycine max* (L.) Merrill] germplasm for some important morphological traits using multivariate analysis. Pak. J. Bot., 40: 2323-2328.
24. Goodarzi, F., R. Darvishzadeh, A. Hassani and A. Hassanzaeh, 2012. Study on genetic variation in Iranian castor bean (*Ricinus communis* L.) accessions using multivariate statistical techniques. J. Med. Plants Res., 6: 1160-1167.