



Characterization, Genetic Diversity, and Clustering of Common Bean (*Phaseolus vulgaris* L.) Accessions Based on Seed Yield and Related Traits



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TWENTY-SEVEN accessions of common bean were evaluated for their performance and genetic diversity based on 11 seed yield and related traits, with the aim to identify diverse accessions with greater performance to exploit the heterotic potential in hybrid combinations between them, with the possibility to obtain superior segregants in subsequent generations. The study was carried out at El-Dalgamon village, Kafr El-Zayyat, El-Gharbiya Governorate, Egypt, during the two successive summer seasons of 2016 and 2017. The accessions were arranged in a complete block design with three replications. The Tocher optimization method and unweighted pair group method with arithmetic mean (UPGMA), were used for clustering based on Mahalanobis D^2 statistic as a dissimilarity measure. The results indicated a wide genetic variability for all traits. The accessions were grouped into five clusters by Tocher's method. Cluster I was the largest, comprised 22 accessions, cluster II, which included the accessions NGB17827 and NGB17823, had the maximum inter-cluster distances with the other clusters, while each of the remaining three clusters contained only one accession. There was an agreement between UPGMA hierarchical clustering and Tocher optimization method. To obtain superior recombinants in segregating generations, we suggest investigating the crossing combinations of Giza 6 with, NGB17817, either of NGB17823 or NGB17827, and the desired accessions from cluster I, such as NGB17806, NGB17814, NGB17816, and NGB18054. Plant height, number of pods per plant, pod length, and seed yield per plant, were the most important traits for the genetic diversity.

Keywords: Common Bean, Genetic Variability, Mahalanobis D^2 , Tocher Optimization, UPGMA, Hierarchical Clustering.

Introduction

Beans (*Phaseolus vulgaris* L.), originated in Latin America, is one of the most important vegetable crops grown in the world. It is consumed for its dry or immature seeds, and as a vegetable for its leaves and immature pods. It has high morphological variability with diverse cultivation methods, and adaptation to many environments (Broughton et al., 2003). As a self-pollinated crop ($2n=2x=22$), it has a narrow genetic background consisting of homozygous lines which can be released directly for cultivation or may be involved in hybrid combinations to select superior segregants in segregating generations (Mishra et al., 2010). The

cultivated area of dry bean in Egypt was 39.67 thousand hectares with a total production of 98.13 thousand tonnes (FAOSTAT, 2017).

The grouping based on genetic diversity for a set of genotypes into similar subgroups helps to distinguish the divergent genotypes in order to hybridize between them to exploit the heterotic potential and to create subsequent segregating populations with a high degree of heterozygosity, which would act as a base for efficient selection with high opportunity for selecting superior segregants. However, it is not practical to evaluate all combinations among a large number of accessions. Instead,

it is appropriate to work on a limited number of genotypes which is expected to be promising. Thus, predictive methods such as multivariate analysis could be applied for the genetic diversity prediction (Bhering et al., 2017).

The cluster analysis is a multivariate method that simultaneously evaluates multiple traits. Such analysis estimates the dissimilarity between the parents using either the Euclidean distance or the generalized Mahalanobis distance (Bhering et al., 2017). Many researchers reported that, the Mahalanobis distance is an effective method to estimate the degree of genetic diversity among genotypes (Mishra et al. 2010, Razvi, 2011, Hossain et al., 2013, Verma et al., 2014, and Sharma et al., 2019). The most common clustering methods in plant breeding, are optimization methods such as the Tocher optimization method (Rao, 1952) and hierarchical methods such as unweighted pair group method with arithmetic mean (UPGMA) (Sokal and Michener, 1958). Both of such clustering methods have been used to estimate the genetic diversity in beans (Ceolin et al., 2007, Barelli et al., 2009, Razvi, 2011, Carvalho et al., 2016, da Silva et al., 2017, de Souza et al., 2017, Lyngdoh et al., 2018, Wani et al., 2018, and Sharma et al., 2019). Moreover, it is necessary for plant breeders, to distinguish the most contributing traits towards the genetic diversity, to consider them as selection criteria and discard those with a little contribution.

The production of common bean in Egypt, depends on the available commercial cultivars, with -to the authors' knowledge-few reported attempts to evaluate newly introduced germplasm under local environments (Mohamed, 1997). Therefore, it is important to evaluate new germplasm to distinguish the most divergent and productive accessions. Such accessions maybe released as newly superior pure lines or included in hybridization programs to exploit the heterosis in their offspring and obtain transgressive segregation in the later generations. Consequently, this study aimed to 1) evaluate the agronomic performance of 26 common bean accessions obtained from The Nordic Genetic Resource Center in addition to Giza 6, the local commercial cultivar, 2) assess the variability and genetic diversity among such accessions, and 3) determine the relative contribution of 11 seed yield and related traits to the genetic diversity.

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Materials and Methods

Plant materials

The genetic materials consisted of twenty-six common bean accessions obtained from The Nordic Genetic Resource Center (NordGen), in addition to, Giza 6, the commercial local cultivar (Table 1 and Fig. 1). The accessions were preliminarily screened for disease resistance for two generations. Then, they were evaluated during the two summer seasons of 2016 and 2017 at El-Dalgamon village, Kafr El-Zayyat, El-Gharbia Governorate, Egypt. Each accession was sown manually in four rows of 4 m long and 70 cm wide and the planting date for the two years was 4th March. The experimental design was a randomized complete block design with three replicates.

Ten plants from the two middle rows of each plot were labeled for data collection, and 0.5 m on each side of the rows were discarded. Eleven agronomic traits were evaluated according to the International Board for Plant Genetic Resources (IPGR, 1982). The traits measured were, plant height, measured from the cotyledon scar to the plant tip, number of leaves per plant, averaged from 10 plants, number of days to flowering, as the number of days from emergence until flowering of 50% of the plants, number of racemes per plant, averaged from 10 plants, number of days to maturity, as the number of days from emergence until maturity of 90 % of the pods, number of mature pods per plant, as an average of 10 harvested plants, pod width, measured from the middle of the mature pod for an average of 10 randomly taken pods, pod length, measured as an average from the exterior distance from the pod tip to the peduncle for 10 randomly taken mature pods, number of seeds per pod, as an average number of seeds from 10 randomly taken mature pods, 100-seed weight, as the weight of 100 dry seeds at a moisture content of 12-14% from 10 plants, and seed yield per plant, as the total weight of seeds from 10 plants divided by 10. The collected data of the studied accessions were used in another study conducted by AlBallat and Al-Araby (2019).

Data analysis

The mean values of the recorded data were subjected to analysis of variance and F-test for each trait. The expectations of mean squares, environmental variance, phenotypic variance, genotypic variance, and coefficients of variation for each trait were estimated according to Singh and Chaudhary (1985) as follows,

TABLE 1. Identification number, code number, name, type, and origin of investigated 27 common bean accessions including 26 accessions from the Nordic Genetic Resource Center (NordGen) and Giza 6, the Egyptian local commercial cultivar.⁽¹⁾

Number	Accession code	Accession name	Type	Origin
1	NGB9300	ØIJORD	Advanced cultivar	Norway
2	NGB17801	HALLANDSBÖNA	Primitive	Sweden
3	NGB17803	SLOALYCKE	Primitive	Sweden
4	NGB17805	MOR KRISTIN	Primitive	Sweden
5	NGB17806	SARDAL	Primitive	Sweden
6	NGB17807	HARPLINGE	Landrace	Sweden
7	NGB17808	RYSK KEJSARBONA	Primitive	Sweden
8	NGB17809	BERNADINA	Primitive	Sweden
9	NGB17810	PETTERSSON	Landrace	Sweden
10	NGB17812	STÅSHULT	Primitive	Sweden
11	NGB17813	HANNAS STRIMMIGA	Primitive	Sweden
12	NGB17814	SVEA	Landrace	Sweden
13	NGB17815	SANDA	Primitive	Sweden
14	NGB17816	GULLSPANG	Landrace	Sweden
15	NGB17817	MORBRORS GRONA	Landrace	Sweden
16	NGB17821	FISKEBY	Advanced cultivar	Sweden
17	NGB17823	SIGRID	Landrace	Sweden
18	NGB17824	KULLA	Landrace	Sweden
19	NGB17825	SIGNE	Landrace	Sweden
20	NGB17826	PERSSON	landrace	Sweden
21	NGB17827	EXTRA-HATIF DE JUILLET	Advanced cultivar	France
22	NGB18054	GULBONA FRAN OSTERGARN	Landrace	Sweden
23	NGB20198	DAGMAR	Landrace	Sweden
24	NGB20200	ELNA	Landrace	Sweden
25	NGB21935	LAU	Primitive	Sweden
26	NGB24332	THORNGRENS BONA	Primitive	Sweden
27	-----	Giza 6	Commercial cultivar	Egypt

⁽¹⁾, According to Sesto (2019).



Fig. 1. Dry seeds color and size of 27 investigated common bean accessions, numbered according to Table 1.

TABLE 2. Form of the analysis of variance and expectations of mean squares.

Source of variation	d.f.	M.s	Expected mean squares
Replications	(r-1)	MS_r	$\sigma_e^2 + G\sigma_r^2$
Genotypes	(G-1)	MS_G	$\sigma_e^2 + r\sigma_g^2$
Error	(G-1)(r-1)	MS_e	σ_e^2

Environmental variance = Error Mean Square (MS_e)

Phenotypic variance (σ^2_p) = (MS_G)/r

Genotypic variance (σ^2_g) = ($MS_G - MS_e$)/r

Environmental coefficient of variation (ECV) = $\{(MSe^{1/2})/\bar{x}\} \times 100$

Genotypic coefficient of variation (GCV) = $\{(\text{Genotypic variance}^{1/2})/\bar{x}\} \times 100$

Where, r= number of replications, \bar{x} = The mean of a trait, MS_G =genotypes mean square.

The means were compared by the Scott-Knott method (Scott and Knott, 1974) at the 5% probability level. The accessions were clustered with Tocher's optimization method (quoted by Rao, 1952), and UPGMA hierarchical method (Sokal and Michener, 1958), based on the generalized Mahalanobis D^2 distance (Mahalanobis, 1936), as a dissimilarity measure. Singh's criterion (Singh, 1981) was applied to estimate the relative contribution of each trait to genetic diversity from the number of times that each trait appeared in the first rank. All statistical analyses were performed using GENES software (Cruz, 2016).

Results and Discussion

Genetic variability

Genetic variability provides the basis for selection. Therefore, it is essential for successful plant breeding programs, because, the hybrids between diverse lines, generally display greater heterosis than those between closely related ones. There were significant differences ($p < 0.01$) among the accessions for all traits (Table 3), suggesting the presence of significant genetic variability which could be exploited through selection. In this respect, Correa et al. (2015) and Razvi et al. (2018) found similar results, also da Silva et al. (2017) found significant differences ($P < 0.05$) for all traits, except number of seeds per pod.

The phenotypic variances were either equal to or slightly higher than their corresponding genotypic variances for all traits, this suggests a large genetic variation with little environmental one, indicating that the genotypic variation was the major contributor to the total variation for all traits with minimum influence of the environment.

Consequently, the selection among the genotypes is expected to be effective.

The environmental coefficients of variation (ECV) were less than 20% for all traits in the two years, indicating medium to high precision in environmental control (Cruz et al., 2004 as cited in Correa et al., 2015). This agrees with Correa et al. (2015). The genotypic coefficient of variation (GCV) reflects the relative change in a trait through selection. In this respect, seed yield per plant, plant height, number of pods per plant, number of racemes per plant, and number of leaves per plant had the highest genotypic coefficient of variation in both years, indicating greater variability in these traits. On the contrary, number of days to flowering and number of days to maturity had the lowest values. In this regard, Raffi and Nath (2004) found highest GCV for 20-seed weight (42.19%), followed by seed yield per plant (39.35%) while, number of days to 50% flowering and number of days to maturity had the lowest ones. Also, Lyngdoh et al. (2018) found high GCV for seed weight per pod (144.87%), plant height (91.35%), and number of leaves per plant (30.92%).

The ratio between genotypic coefficient of variation and environmental coefficient of variation (GCV/ECV) was larger than the unit for all traits, with high estimates, therefore, it is additional evidence that the traits are promising for successful selection (Correa et al., 2015 and Vaz et al., 2017). The high genetic variations are probably due to the nature of the investigated genetic materials, since they are genebank germplasm, consist of landraces and advanced cultivars which widely differ in their traits. Accordingly, our results meet the expectations of such materials.

TABLE 3. Mean square and genetic parameters for 11 seed yield and related traits in 27 common bean accessions evaluated in 2016 and 2017 summer seasons.

Traits	Mean squares (M.S)	Phenotypic variance	Genotypic variance	Environmental coefficient of variation (ECV)	Genotypic coefficient of variation (GCV)	GCV/ECV ratio
First year (2016)						
Plant height	5874.81**	1958.27	1957.57	3.41	104.31	30.59
Number of leaves per plant	74.98**	24.99	24.89	3.82	34.47	9.02
Number of days to flowering	14.70**	4.90	4.84	1.03	5.28	5.15
Number of racemes per plant	30.84**	10.28	9.96	12.83	41.49	3.23
Number of days to maturity	78.19**	26.06	25.50	2.27	8.81	3.88
Number of pods per plant	1084.54**	361.51	358.70	14.25	92.96	6.52
Pod width	0.13**	0.04	0.04	1.86	16.02	8.60
Pod length	6.47**	2.16	2.15	1.40	13.17	9.44
Number of seeds per pod	2.76**	0.92	0.90	4.86	20.50	4.22
100-seed weight	153.85**	51.28	50.43	4.31	19.14	4.44
Seed yield/plant	87.19**	29.06	28.91	19.88	157.01	7.90
Second year (2017)						
Plant height	6080.83**	2026.94	2025.54	4.57	100.27	21.92
Number of leaves per plant	66.00**	22.00	21.85	4.46	31.49	7.06
Number of days to flowering	15.01**	5.00	4.92	1.17	5.33	4.55
Number of racemes per plant	33.92**	11.31	11.20	7.62	44.49	5.84
Number of days to maturity	73.17**	24.39	23.91	2.11	8.56	4.06
Number of pods per plant	1046.05**	348.68	347.50	9.35	92.56	9.90
Pod width	0.12**	0.04	0.04	1.83	15.50	8.46
Pod length	6.46**	2.15	2.15	1.23	13.00	10.59
Number of seeds per pod	2.41**	0.80	0.79	4.54	19.73	4.35
100-seed weight	155.57**	51.86	50.25	5.75	18.58	3.23
Seed yield/plant	63.16**	21.05	20.96	17.21	147.76	8.59

*and **, Significant at 1% and 5%, respectively, by F test.

Agronomic performance

The highest plant height average was recorded in two climbing-types accessions viz., NGB17827 and NGB17823, in both years (Table 4 and Table 5) with values of 195.2 cm & 193.3 cm, respectively in the first year and 201.8 cm & 196.5 cm in the second year, followed by bush-type accessions, viz., NGB17808, NGB17816, NGB20198, NGB24332, and Giza 6. Also, the highest number of leaves per plant was observed in NGB17823, NGB17827, NGB21935, and Giza 6 in both years.

For number of days to flowering in the first year, the accessions, NGB17801, NGB17806, NGB17808, NGB17809, NGB17810, NGB17814, NGB17815, NGB17817, NGB17824, NGB18054, NGB20198, NGB20200, and NGB24332 were the most early-flowering accessions with values ranged from 39.0 to 40.3 days. Also, the same accessions except NGB17809 had the lowest desirable values in the second year.

The highest number of racemes per plant in the first and the second year was recorded by the accessions, NGB17806, NGB17816, NGB17821, NGB17823, NGB17827, and NGB18054. The most early-mature accessions in the first year were, NGB17801, NGB17803, NGB17805, NGB17808, NGB17812, NGB17813, NGB17815, NGB17817, NGB17824, NGB17826, NGB20198, NGB20200, and NGB24332. The same accessions in addition to NGB17814 were the earliest in the second year. Approximately 50% of accessions in each year (13 accessions in the first year and 14 accessions in the second year) had the least number of days to maturity, making them the highest early-mature accessions. In contrast, NGB9300, NGB17823, NGB17827, and Giza 6 were the most late-mature accessions.

TABLE 4. Mean performance for 11 seed yield and related traits in 27 accessions of common bean evaluated in 2016 summer season, El-Gharbiya Governorate, Egypt.

Accessions	Plant height (cm)	Number of leaves/plant	Number of days to flowering	Number of racemes/plant	Number of days to maturity	Number of pods/plant	Pod width (mm)	Pod length (cm)	Number of seeds/pod	100-seed weight (g)	Seed yield/plant (g)
NGB9300	17.2 i	10.6 h	45.7 a	6.6 d	67.0 b	16.2 e	1.0 i	12.5 c	4.2 f	28.9 g	2.3 e
NGB17801	26.2 f	10.4 h	40.0 e	7.8 d	54.0 e	15.0 e	1.3 f	9.4 h	3.5 h	37.5 e	1.4 f
NGB17803	24.5 g	13.4 e	41.0 d	5.2 e	54.0 e	10.1 f	1.5 b	11.3 e	4.3 f	35.1 f	1.3 f
NGB17805	26.5 f	14.8 e	41.0 d	5.5 e	54.0 e	10.9 f	1.3 e	11.0 e	4.2 f	41.6 d	1.1 f
NGB17806	24.2 g	14.0 e	40.0 e	9.6 c	60.0 c	19.5 d	1.3 f	12.0 d	5.2 d	33.7 f	3.0 d
NGB17807	28.9 e	11.3 g	44.0 b	8.0 d	57.0 d	19.8 d	1.1 h	10.8 f	5.3 d	38.2 e	2.7 e
NGB17808	39.2 c	16.1 d	39.7 e	6.1 e	54.0 e	13.3 e	1.5 b	11.0 e	4.0 g	41.4 d	1.3 f
NGB17809	27.9 e	16.0 d	40.3 e	7.4 d	56.0 d	16.1 e	1.0 i	11.9 d	4.7 e	38.0 e	2.0 e
NGB17810	29.5 e	11.5 g	40.0 e	5.9 e	57.0 d	11.9 f	1.2 g	11.1 e	5.6 c	29.8 g	2.2 e
NGB17812	29.3 e	10.0 h	41.0 d	4.0 e	54.0 e	6.6 f	1.1 h	11.9 d	4.3 f	51.4 a	0.6 f
NGB17813	29.4 e	12.2 f	42.0 c	6.1 e	54.0 e	12.4 f	1.4 c	12.2 d	4.0 g	39.9 d	1.2 f
NGB17814	26.3 f	13.0 f	40.0 e	6.7 d	56.0 d	13.2 e	1.0 i	11.9 d	4.3 f	30.9 g	1.9 e
NGB17815	31.2 e	14.3 e	40.0 e	5.1 e	54.0 e	11.6 f	1.5 b	11.3 e	3.5 h	46.8 b	0.9 f
NGB17816	42.2 b	13.9 e	43.7 b	12.3 b	57.0 d	26.8 c	1.0 i	10.7 f	6.3 b	33.6 f	5.0 c
NGB17817	24.2 g	12.3 f	40.0 e	5.7 e	55.0 e	14.1 e	1.3 f	15.5 a	6.2 b	44.5 c	2.0 e
NGB17821	38.0 d	12.6 f	43.7 b	11.0 c	57.0 d	29.5 c	1.1 h	10.4 g	4.6 e	31.6 g	4.2 c
NGB17823	193.3 a	29.4 a	46.0 a	13.9 b	73.0 a	78.5 b	1.1 i	11.2 e	7.5 a	26.4 h	22.3 a
NGB17824	19.7 h	10.6 h	40.0 e	5.1 e	54.0 e	11.6 f	1.5 b	9.0 i	4.0 g	38.6 e	1.2 f
NGB17825	35.9 d	12.3 f	43.7 b	5.1 e	57.0 d	11.9 f	1.6 a	8.2 k	4.1 g	37.0 e	1.3 f
NGB17826	28.3 e	10.9 g	41.0 d	5.3 e	54.0 e	10.7 f	1.3 e	12.5 c	4.6 e	35.4 f	1.4 f
NGB17827	195.2 a	29.4 a	46.0 a	18.1 a	67.0 b	87.5 a	1.0 j	10.5 g	5.5 c	23.0 i	21.1 b
NGB18054	36.1 d	11.2 g	39.0 e	10.7 c	57.0 d	29.7 c	1.5 b	11.0 e	5.1 d	34.3 f	4.4 c
NGB20198	39.7 c	14.6 e	40.0 e	6.5 d	54.0 e	13.9 e	1.4 d	10.3 g	4.8 e	33.0 f	2.0 e
NGB20200	25.1 g	12.0 f	40.0 e	5.2 e	54.0 e	7.7 f	1.1 h	10.5 g	3.8 h	50.1 a	0.6 f
NGB21935	27.1 f	19.0 c	41.0 d	6.4 d	56.0 d	14.0 e	1.5 b	10.5 g	3.5 h	36.0 e	1.4 f
NGB24332	41.0 b	14.1 e	40.0 e	8.8 d	54.0 e	20.9 d	1.3 e	8.7 j	3.5 h	33.9 f	2.2 e
Giza 6	39.2 c	20.9 b	45.3 a	7.2 d	67.0 b	16.7 e	1.6 a	13.4 b	4.8 e	50.9 a	1.6 f

Means followed by the same letter do not differ significantly by the Scott-Knott test ($P < 0.05$).

TABLE 5. Mean performance for 11 seed yield and related traits in 27 accessions of common bean evaluated in 2017 summer season, El-Gharbiya Governorate, Egypt.

Accessions	Plant height (cm)	Number of leaves/plant	Number of days to flowering	Number of racemes/plant	Number of days to maturity	Number of pods/plant	Pod width (cm)	Pod length (cm)	Number of seeds/pod	100-seed weight (g)	Seed yield/plant (g)
NGB9300	18.2 i	10.5 i	46.0 a	6.1 g	64.3 c	16.9 e	1.0 g	12.5 c	4.0 h	29.9 e	2.3 e
NGB17801	28.7 g	11.5 h	40.0 e	7.2 f	54.3 f	17.1 e	1.3 d	9.5 i	3.8 h	37.6 c	1.7 f
NGB17803	26.4 g	13.4 f	40.7 d	5.4 h	54.0 f	10.7 g	1.5 b	11.3 e	4.3 g	34.6 d	1.3 f
NGB17805	29.1 g	15.0 e	41.0 d	6.0 g	54.3 f	10.0 g	1.4 d	11.0 f	3.9 h	46.5 b	0.9 g
NGB17806	28.8 g	14.0 f	40.0 e	9.8 d	60.0 d	17.7 e	1.3 d	12.0 d	5.0 e	35.6 d	2.5 e
NGB17807	31.5 f	11.5 h	43.3 b	7.9 e	56.3 e	21.1 d	1.0 g	10.7 g	4.8 e	38.9 c	2.6 e
NGB17808	40.9 d	16.1 e	39.3 e	5.5 h	54.0 f	16.6 e	1.6 a	11.0 f	3.4 i	43.6 b	1.3 f
NGB17809	31.0 f	15.3 e	41.0 d	7.1 f	56.0 e	18.5 e	1.0 g	12.0 d	4.9 e	38.2 c	2.4 e
NGB17810	29.9 g	11.6 h	39.7 e	6.1 g	56.3 e	12.8 f	1.2 e	11.1 e	5.7 c	30.9 e	2.4 e
NGB17812	32.6 f	10.4 i	41.0 d	3.5 i	54.0 f	5.9 h	1.2 f	12.0 d	4.2 g	52.7 a	0.5 g
NGB17813	32.3 f	12.9 g	42.0 c	6.6 f	54.0 f	14.3 f	1.4 c	12.3 c	3.8 h	40.3 c	1.3 f
NGB17814	27.1 g	14.0 f	39.3 e	6.6 f	55.0 f	13.0 f	1.0 g	12.0 d	4.3 g	32.1 e	1.8 f
NGB17815	32.3 f	14.4 f	40.0 e	3.8 i	54.0 f	6.7 h	1.5 b	11.3 e	2.9 j	47.2 b	0.4 g
NGB17816	45.7 c	15.2 e	43.7 b	13.6 c	56.7 e	23.3 d	1.0 g	10.8 g	5.6 c	33.4 e	3.9 d
NGB17817	24.6 h	12.9 g	39.7 e	6.1 g	55.0 f	15.5 e	1.3 d	16.0 a	6.3 b	46.4 b	2.1 e
NGB17821	37.6 e	13.7 f	44.0 b	8.7 e	57.0 e	18.8 e	1.2 f	10.9 f	4.5 f	32.8 e	2.6 e
NGB17823	196.5 b	28.6 a	46.0 a	15.4 b	73.0 a	78.7 b	1.1 f	11.2 e	6.9 a	27.3 f	20.0 a
NGB17824	21.1 i	11.5 h	40.0 e	4.8 h	54.0 f	10.1 g	1.5 b	9.0 j	3.7 h	39.8 c	0.9 g
NGB17825	36.2 e	11.4 h	43.3 b	4.8 h	57.0 e	12.5 f	1.6 a	8.3 k	3.9 h	37.8 c	1.3 f
NGB17826	29.7 g	11.9 h	41.0 d	5.5 h	53.3 f	10.3 g	1.3 d	12.5 c	4.7 f	36.3 d	1.3 f
NGB17827	201.8 a	26.7 b	45.7 a	17.7 a	65.3 c	84.8 a	1.0 g	11.0 f	5.3 d	26.2 f	17.1 b
NGB18054	39.9 d	14.3 f	39.7 e	10.6 d	57.0 e	33.5 c	1.5 b	11.1 e	5.3 d	34.5 d	5.2 c
NGB20198	40.4 d	13.9 f	40.0 e	6.9 f	54.3 f	16.3 e	1.3 d	10.5 h	4.3 g	32.9 e	2.2 e
NGB20200	27.7 g	13.0 g	40.0 e	5.3 h	54.0 f	7.8 h	1.1 f	11.0 f	3.8 h	50.7 a	0.6 g
NGB21935	31.4 f	17.3 d	41.0 d	6.8 f	56.0 e	12.8 f	1.5 b	10.5 h	3.8 h	36.5 d	1.3 f
NGB24332	44.1 c	14.3 f	40.0 e	8.5 e	54.0 f	21.1 d	1.3 d	9.5 i	4.2 g	36.0 d	2.4 e
Giza 6	46.4 c	25.5 c	45.7 a	6.8 f	68.3 b	17.0 e	1.6 a	13.5 b	4.3 g	51.6 a	1.4 f

Means followed by the same letter do not differ significantly by the Scott-Knott test ($P < 0.05$).

The highest number of pods per plant was recorded in NGB17806, NGB17807, NGB17816, NGB17821, NGB17823, NGB17827, NGB18054, and NGB24332 in the first year, whereas, the same accessions except NGB17806 and NGB17821 had the highest values in the second year as well. Regarding pod width, the accessions NGB17803, NGB17808, NGB17813, NGB17815, NGB17824, NGB17825, NGB18054, NGB21935, and Giza 6 had the highest averages, indicating that they have wider pods than the other accessions. In the concern of pod length, NGB17817 followed by Giza 6, NGB9300, NGB17826, in the first year in addition to NGB17813 in the second year had the longest pods. Concerning the number of seeds per pod, the highest values in the first year were recorded by NGB17823 (7.5) followed by NGB17806, NGB17807, NGB17810, NGB17816, NGB17817, NGB17827, and NGB18054, while in the second year, the same accessions in addition to NGB17809, NGB17821, and NGB17826 had the highest values.

Regarding the 100-seed weight, it ranged from 23.0 to 51.4 g in the first year and from 26.2 to 52.7 g in the second year. The highest values were recorded in the two years for the accessions, NGB17812, NGB20200, and Giza 6 followed by NGB17805, NGB17808, NGB17815, and NGB17817, revealing that they had larger seeds than the other accessions. The lowest values in both years were recorded in NGB17823 and NGB17827, indicating that they had smaller seeds compared with the other accessions. In this concern, Singh (1989) divided the seed size into three categories, small (<25 g/100-seed), median (25-40 g/100-seed) and large (> 40 g/100-seed). Based on this classification, we found that, the seed size in the first year was, median for 19 accessions and large for seven accessions, while only one accession had small seeds. Whereas, in the second year, the accessions were classified as median (19 accessions) and large (eight accessions). These findings are consistent with Lima et al. (2012) and Boros et al. (2014) who found that most genotypes were median. For the same accessions of the present study, AlBallat and Al-Araby (2019) reported significant negative correlation between 100-seed weight and each of number of pods per plant and number of seeds per pod. Similarly, Nienhuis and Singh (1986) and Boros et al. (2014) found negative correlation between the seed size and each of number of pods and number of seeds.

Considering at least 3.5 g/plant as a selection criterion, the highest average of seed yield per plant in the first year was found in NGB17823 (22.3 g) followed by NGB17827 (21.1 g), NGB17816 (5.0 g), NGB17821 (4.2 g), and NGB18054 (4.4 g). Whereas in the second year the best performing accessions were, NGB17823 (20.0 g), NGB17827 (17.1 g), NGB18054 (5.2 g), and NGB17816 (3.9 g).

Genetic diversity

The genetic divergence between parents is indicative of heterotic expression in progenies (Falconer, 1960). Mahalanobis D^2 Statistic is one of the efficient techniques to estimate the genetic divergence. It defines the best parental lines, since it measures the intra-cluster and inter-cluster distances between groups, which helps in the selection of genetically divergent parents for hybridization programs. When selecting parents based on D^2 statistic, we should consider, the selection of clusters with the maximum distance, the selection of well-performed genotypes within such clusters, and the relative contribution of each trait to the total diversity (Singh, 2001).

The dissimilarity measures estimated by the Mahalanobis distance ranged from 67.48 (NGB17813 and NGB17826) to 56767.55 (NGB9300 and NGB17827) in the first year and from 73.03 (NGB17814 and NGB17809) to 26936.3 (NGB17817 and NGB17827) in the second year, indicating a large genetic diversity among the accessions (Table 6). The correlation between the dissimilarity matrices of the two years was high (0.97) and highly significant by Mantel test (Mantel, 1967) indicating the agreement between the values of the two years.

The Mahalanobis D^2 distance obtained between the accessions NGB17813 and NGB17826 (67.48) and the distance between NGB17814 and NGB17809 (73.03) (Table 6) were the lowest distances in the first year and the second year, respectively. Therefore, the accessions having such distances were considered the most similar. On the contrary, the accessions NGB9300 and NGB17827 (56767.55) in the first year, as well as NGB17817 and NGB17827 (26936.3) in the second year, were the most divergent accessions, as each pair of them had the highest distance among other distances.

There was a high frequency of pairs with the greatest distances when one of the components was either NGB17827 or NGB17823 in the

first year and NGB17827 in the second year, suggesting high genetic dissimilarity between each of them and the other accessions. On the other hand, the shortest distances were observed, when the accessions NGB17808, NGB17826, and NGB17814 in the first year and NGB17801, NGB17805, and NGB17826 in the second year took part as one of the accessions

pair, indicating smaller genetic dissimilarity between each of them and the other accessions. In this respect, many researchers employed D^2 statistic as a dissimilarity measure in their studies, for example, Razvi et al. (2018) grouped 13 genotypes into two distinct groups, whereas, Sharma et al. (2019) grouped 169 genotypes into eight groups.

TABLE 6. Measures of the higher and lower genetic dissimilarity between the accessions by the Mahalanobis distance in 27 common bean accessions evaluated for seed yield and related traits in 2016 and 2017 summer seasons, El-Gharbiya Governorate, Egypt.

Genotypes ¹	1 st year (2016)		2 nd year (2017)	
	longest distance	shortest distance	longest distance	shortest distance
G1	56767.6 (G 21)	478.113 (G 12)	20680.4 (G 21)	402.682 (G 8)
G2	52490.4 (G 17)	192.407 (G 18)	14647.4 (G 21)	105.32 (G 26)
G3	52769.5 (G 21)	108.619 (G 4)	18658.7 (G 21)	76.6372 (G 4)
G4	52321 (G 21)	108.619 (G 3)	18129.4 (G 21)	76.6372 (G 3)
G5	51662.8 (G 21)	149.61 (G 20)	17687.5 (G 21)	189.5 (G 9)
G6	50496.2 (G 17)	235.558 (G 9)	14686.4 (G 21)	81.1212 (G 16)
G7	45180.6 (G 21)	115.708 (G 13)	16615.9 (G 21)	165.427 (G 4)
G8	51876.4 (G 17)	76.3912 (G 12)	17480.1 (G 21)	73.0366 (G 12)
G9	50162.1 (G 21)	137.61 (G 12)	15847.1 (G 21)	189.5 (G 5)
G10	50762 (G 21)	278.456 (G 24)	18350.7 (G 21)	170.482 (G 20)
G11	49717.4 (G 21)	67.4875 (G 20)	18927.2 (G 21)	89.2563 (G 20)
G12	52584.3 (G 17)	76.3912 (G 8)	18412 (G 21)	73.0366 (G 8)
G13	48844.9 (G 21)	115.708 (G 7)	19294.1 (G 21)	196.791 (G 7)
G14	43265.4 (G 17)	157.133 (G 16)	12848.1 (G 21)	232.78 (G 6)
G15	52902.1 (G 21)	879.116 (G 20)	26936.4 (G 21)	1394.16 (G 20)
G16	44908 (G 17)	157.133 (G 14)	14875 (G 21)	81.1212 (G 6)
G17	56622.9 (G 1)	397.678 (G 21)	24974.9 (G 15)	278.26 (G 21)
G18	55639.4 (G 17)	192.407 (G 2)	16411.9 (G 21)	123.581 (G 2)
G19	48332.3 (G 17)	358.985 (G 26)	13749.7 (G 21)	304.678 (G 18)
G20	50360.7 (G 21)	67.4875 (G 11)	19241.8 (G 21)	89.2563 (G 11)
G21	56767.6 (G 1)	397.678 (G 17)	26936.4 (G 15)	278.26 (G 17)
G22	42943.9 (G 21)	162.652 (G 23)	13815.9 (G 21)	237.217 (G 23)
G23	45274.6 (G 17)	155.651 (G 7)	14279.2 (G 21)	147.893 (G 2)
G24	53951.2 (G 17)	239.091 (G 6)	17653.7 (G 21)	154.335 (G 4)
G25	52390.8 (G 17)	217.51 (G 3)	17725.6 (G 21)	151.902 (G 4)
G26	45288.6 (G 17)	358.985 (G 19)	12520 (G 21)	105.32 (G 2)
G27	46445.2 (G 21)	1181.55 (G 7)	23117.1 (G 21)	987.016 (G 11)

¹G1, NGB9300, G2, NGB17801, G3, NGB17803, G4, NGB17805, G5, NGB17806, G6, NGB17807, G7, NGB17808, G8, NGB17809, G9, NGB17810, G10, NGB17812, G11, NGB17813, G12, NGB17814, G13, NGB17815, G14, NGB17816, G15, NGB17817, G16, NGB17821, G17, NGB17823, G18, NGB17824, G19, NGB17825, G20, NGB17826, G21, NGB17827, G22, NGB18054, G23, NGB20198, G24, NGB20200, G25, NGB21935, G26, NGB24332, G27, Giza 6.

Tocher's optimization method of clustering

In Tocher optimization method (Rao, 1952), the most similar pairs of parents will create the first group, to which, the new parents may be added, so that, the mean dissimilarity measures within each group should be less than the mean distances between any groups (Bhering et al., 2017). The cluster analysis using Tocher's optimization method in each year grouped the twenty-seven accessions into five groups (Table 7). In the first year, cluster I was the largest, comprising 81.48% of the total accessions (22 accessions), whereas, cluster II included the accessions NGB17823 and NGB17827, while each of Giza 6, NGB17817, and NGB9300, was located individually in group III, group IV, and group V, respectively. The constituents of each group were repeated in the second year except for the accession NGB9300, which was in the fifth group in the first year whereas it came within the first group in the second year. Also, the accession NGB17825 was in the first group in the first year, while it came in the third group in the second year.

The grouping of the accessions into different clusters is important for selecting parents since the accessions from divergent clusters are relatively distant. Thus, it is expected to obtain high heterotic effects and desirable transgressive segregants in subsequent generations if they were intercrossed together (Sharma et al., 2019). Many researchers reported that Tocher's optimization method is efficient for diversity assessment in common bean, for instance, Barelli et al. (2009) used Tocher method to group 35 genotypes into 10 groups, in which one group comprised 31.42 % of genotypes. Similarly, Carvalho et al. (2016) used Tocher method to group 24 genotypes into three groups, where, approximately 92% of the genotypes located in one group. Also, Wani et al. (2018) studied the genetic diversity of 10 genotypes of common bean and found four groups with Tocher optimization method based on Mahalanobis distance. Whereas, Ceolin et al. (2007) reported that 18 genotypes were grouped into three, five, four, and five groups in four years of study.

TABLE 7. The Tocher clustering pattern of 27 common bean accessions based on 11 seed yield and related traits and Mahalanobis D² dissimilarity matrix in 2016 and 2017 summer seasons, El-Gharbiya Governorate, Egypt.

Clusters	Number of accessions	Accessions (2016 season)	Accessions (2017 season)
I	22	G11, G20, G5, G3, G4, G13, G9, G8, G12, G10, G6, G24, G23, G7, G2, G25, G16, G22, G18, G14, G26, G19	G11, G20, G5, G3, G4, G13, G9, G8, G12, G10, G6, G24, G23, G7, G2, G25, G16, G22, G18, G14, G26, G1
II	2	G17, G21	G17, G21
III	1	G27	G19
IV	1	G15	G27
V	1	G1	G15

G1, NGB9300, G2, NGB17801, G3, NGB17803, G4, NGB17805, G5, NGB17806, G6, NGB17807, G7, NGB17808, G8, NGB17809, G9, NGB17810, G10, NGB17812, G11, NGB17813, G12, NGB17814, G13, NGB17815, G14, NGB17816, G15, NGB17817, G16, NGB17821, G17, NGB17823, G18, NGB17824, G19, NGB17825, G20, NGB17826, G21, NGB17827, G22, NGB18054, G23, NGB20198, G24, NGB20200, G25, NGB21935, G26, NGB24332, G27, Giza6

The genotypes within the same cluster are less divergent than those in different clusters, the most distant clusters show the maximum divergence. The maximum intra-cluster distance was found in cluster I (691.197 and 732.90) followed by cluster II (397.678 and 278.26) in the first and the second year, respectively (Table 8 and Figure 2), suggesting that the genotypes in such clusters are more heterogeneous. Therefore, the selection of parents within cluster I or cluster II for hybridization would be effective. While the intra-cluster distance in cluster III, cluster IV and cluster V were (0.0), as each of them contains only one accession.

In the first year, cluster II & cluster V had the greatest inter-cluster distance (56695.21) followed, in descending order, by the distances between cluster II & cluster IV (52239.20), cluster I & cluster II (49470.866), cluster II & cluster III (45800.03), cluster III & cluster V (3051.84), cluster I & cluster IV (2369.13), cluster I & cluster III (2287.13), cluster IV & cluster V (1912.58), cluster III & cluster IV (1657.57), and cluster I & cluster V (1298.20). Also, in the second year, cluster II & cluster V had the maximum inter-cluster distance (25955.64) followed by the distances between cluster II & cluster IV (22117.799), cluster I & cluster II (16190.43), cluster II & cluster III

(13240.01), cluster III & cluster V (7501.75), cluster III & cluster IV (3562.70), cluster I & cluster V (3460.85), cluster IV & cluster V (2193.67), cluster I & cluster IV (1975.95), and cluster I & cluster III (1496.91).

These results suggest the importance of the accessions in cluster II since the largest distances occurred when cluster II was involved in the estimation of the distances between clusters. The high inter-cluster distance values indicate that genotypes in different clusters are highly divergent, probably due to geographical or reproductive barriers. While the lower values suggest more closely related genotypes which suggest that these genotypes were derived from a common original ancestor (Hossain et al., 2013 and Wani et al., 2018).

The inter-cluster distances and the mean performance of the accessions should be considered together as the genetically divergent parents may not have the best combining ability unless they also have good performance of the traits being improved (Vaz et al., 2017). Consequently, the crossing between the best performing genotypes from diverse clusters is recommended. Thus, the hybrid combinations between Giza 6, NGB17817, NGB17823, or NGB17827, in addition to, the desired accessions from cluster I, are expected to give high heterotic effects.

TABLE 8. Average distance of intra (underlined) and inter-cluster centroids among five clusters of 27 common bean accessions grouped by Tocher optimization method in 2016 and 2017 summer seasons, El-Gharbiya Governorate, Egypt.

Clusters	Number of distances	Mean	
		First year (2016)	second year (2017)
I	231	691.197	732.90
I × II	44	49470.866	16190.43
I × III	22	2287.134	1496.91
I × IV	22	2369.13	1975.95
I × V	22	1298.202	3460.85
II	1	397.678	278.26
II × III	2	45800.034	13240.01
II × IV	2	52239.2	22117.80
II × V	2	56695.214	25955.64
III	1	0.00	0.00
III × IV	1	1657.573	3562.70
III × V	1	3051.838	7501.75
IV	1	0.00	0.00
IV × V	1	1912.577	2193.67
V	1	0.00	0.00

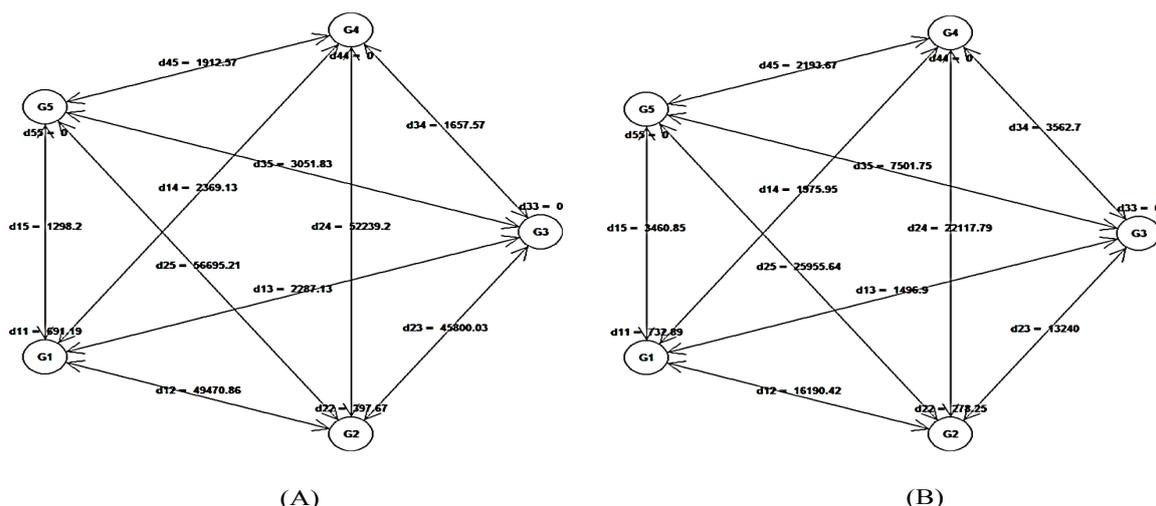


Fig. 2. Clustering diagrams formed by Tocher's method representing the intra and inter-cluster distances among five clusters of common bean accessions of 2016 (A) and 2017 (B) summer seasons, based on Mahalanobis D^2 dissimilarity matrix.

Although Giza 6 is well adapted to the Egyptian environment and has greater seed weight, it has low seed yield potential in comparison with the other accessions. Furthermore, it is among the most late-mature accessions. Therefore, it could be improved by the hybridization with bush-type accessions from cluster I such as, NGB17816 or NGB18054 which are early mature and has greater seed yield. Also, NGB17806 and NGB17814 showed greater performance than Giza 6 for seed yield and maturity traits, in addition, they have white seed color, which is favorable by local consumers. Consequently, they could be intercrossed with Giza 6. Moreover, NGB17823 and NGB17827 are promising accessions, since they are the most divergent accessions forming one cluster and have good agronomic performance, therefore they could be released, after further examinations, as climbing genotypes for cultivation under greenhouse during the winter season.

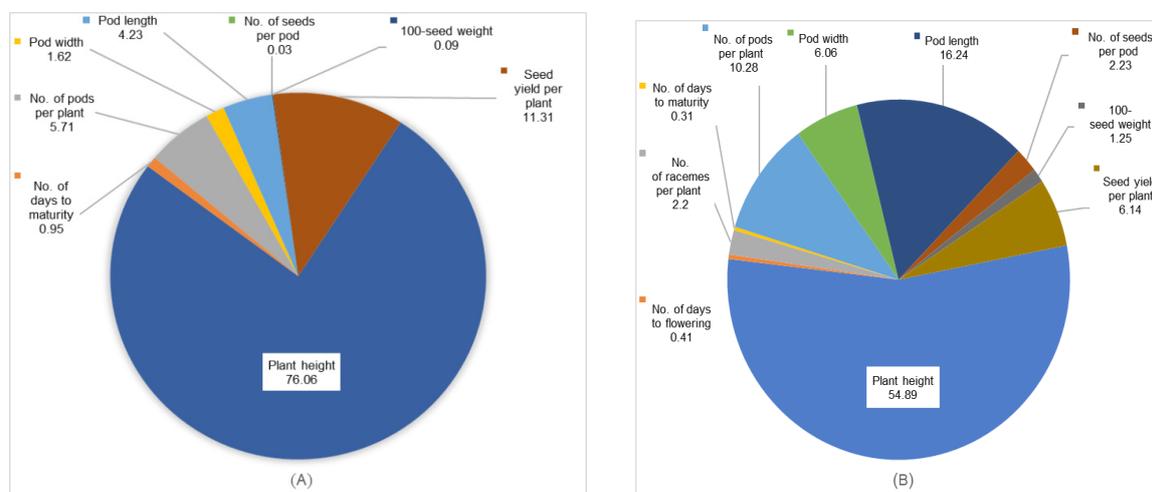
It is important to determine the relative contribution of the traits to accessions diversity, to focus only, on the most important traits and ignore those with a little contribution (da Silva et al., 2017). Plant height, number of pods per plant, pod length and seed yield per plant, were the most important traits for the genetic diversity in both years (Table 9 and Fig. 3), revealing their importance in the selection of the common bean germplasm. Plant height participated by about 75 % of the divergence in the first year and by more

than 50 % in the second year, while there was an increase of the participation of the other traits in the second year compared with its contribution in the first year. Also the arrangement of their importance had been changed, suggesting that the environmental conditions probably affected these traits. The contribution of number of leaves per plant to the genetic divergence was 0 % in both years, which reveal that it is unimportant for the diversity and may be rejected as a selection criterion. In this concern, AlBallat and Al-Araby (2019), investigated the correlation and path analysis for the same accessions and traits under study and recommended the direct selection of plant height and number of pods per plant, in order to improve seed yield per plant.

In this regard, number of pods per plant had the maximum contribution value (35.85%) followed by number of seeds per pod (35.50 %), seed yield (15.86 %), and 100-seed mass (12.77 %) as reported by de Souza et al. (2017). Whereas the traits contribution reported by Carvalho et al. (2016) were, plant height at maturity (31.71%), number of days to maturity (16.52 %), number of pods per plant (4.09 %) and number of seeds per pod (0.12 %). Moreover, Haralayya et al. (2017) found that plant height and pod length were the most important traits, while, pod width contribution was 0.0 %. The variation between our results and the findings of the other researchers probably due to the difference of genetic materials, studied traits, and the environmental conditions.

TABLE 9. The percent contribution of 11 seed yield and related traits to the total divergence in 27 accessions of common bean in 2016 and 2017 summer seasons, El-Gharbiya Governorate, Egypt.

Traits	Contribution to the diversity (%)	
	First year (2016)	Second year (2017)
Plant height	76.06	54.89
Number of leaves per plant	0.00	0.00
Number of days to flowering	0.00	0.41
Number of racemes per plant	0.00	2.20
Number of days to maturity	0.95	0.31
Number of pods per plant	5.71	10.28
Pod width	1.62	6.06
Pod length	4.23	16.24
Number of seeds per pod	0.03	2.23
100-seed weight	0.09	1.25
Seed yield per plant	11.31	6.14

**Fig. 3.** The percent contribution of 11 seed yield and related traits to the total divergence in 27 accessions of common bean evaluated in 2016 (A) and 2017 (B) summer seasons, El-Gharbiya Governorate, Egypt, according to Singh (1981).

Hierarchical clustering

In the hierarchical methods such as unweighted pair group method with arithmetic mean (UPGMA) (Sokal and Michener, 1958), a dendrogram of several levels are formed to represent the grouping pattern of the accessions, so that, a cluster of similar genotypes is formed first and the distances of the others are calculated relative to such group (Bhering et al., 2017).

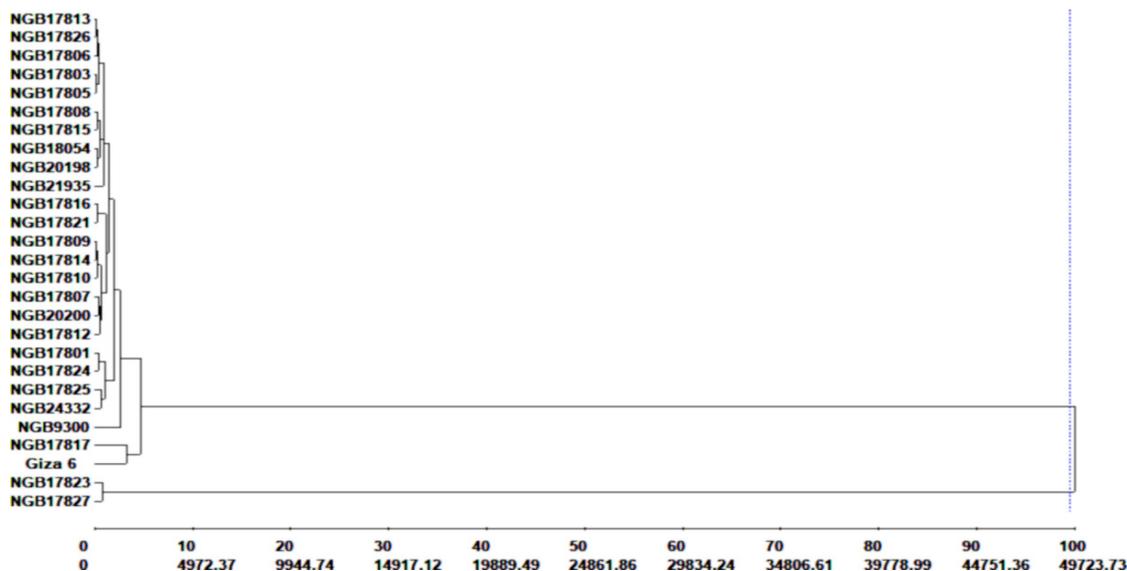
The dendrogram obtained by the UPGMA method for the two years (Fig. 4. A and B) considering the cut in accordance with Mojena method (Mojena, 1977), allowed the 27 accessions to be grouped into two main distinct groups, the first group comprised the accessions NGB17823 and NGB17827 whereas the second group comprised the other accessions. This

indicates that the accessions NGB17823 and NGB17827 are closely related to each other while they are divergent compared with the other accessions. To further investigate the clustering pattern, we excluded the group I, which contain two accessions, and repeated the analysis with the second group with 25 accessions, in order to distinguish the sub-clusters located within it.

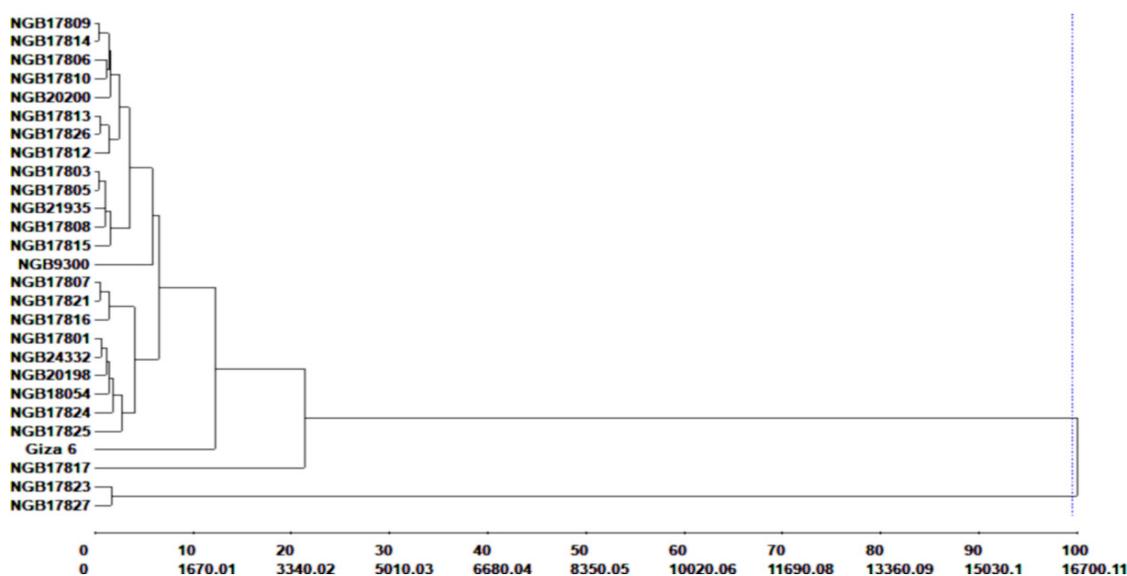
The second level of UPGMA analysis for the first year (Figure.5.A), allowed the formation of four groups, each of the accessions Giza 6, NGB17817, and NGB9300 is located individually in three different subgroups, while the fourth group comprised the remaining 22 accessions. Accordingly, the overall UPGMA analysis for the first year revealed the formation of five groups, two main groups, one of them was divided into four

subgroups. Thus, the results of UPGMA analysis considering the number and content of groups are in line with the clusters formed by Tocher optimization method. In such a case, the use of both grouping methods confirmed the diversity pattern between accessions. The UPGMA dendrogram of the second year (Figure.5.B) formed three groups, one of them consisted of 23 accessions, while each of the accessions, Giza 6 and NGB17817 were located individually in two

separate subgroups. Consequently, the results of the UPGMA analysis in the second year are the formation of two main groups, one of them subdivided into three subgroups, which confirmed the results of Tocher method except for the accession NGB17825 which was located solely in a separate group in Tocher method, which is probably due to the difference of grouping criteria in the two grouping methods.

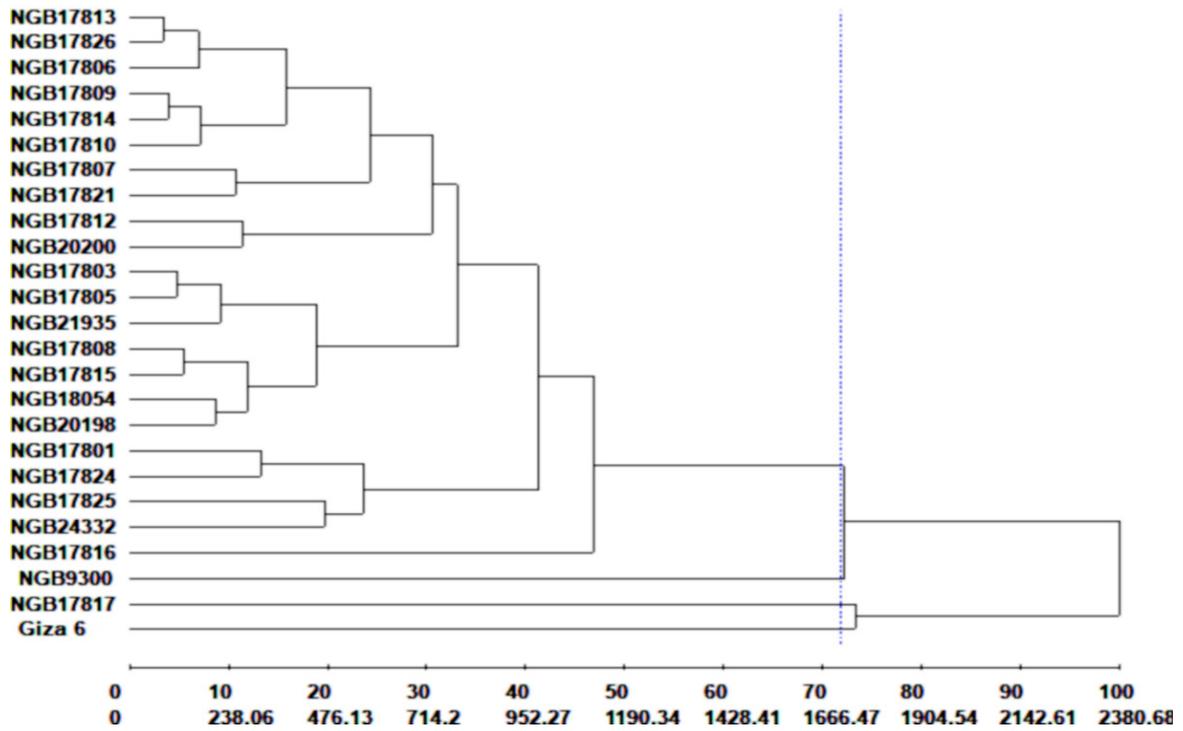


(A)

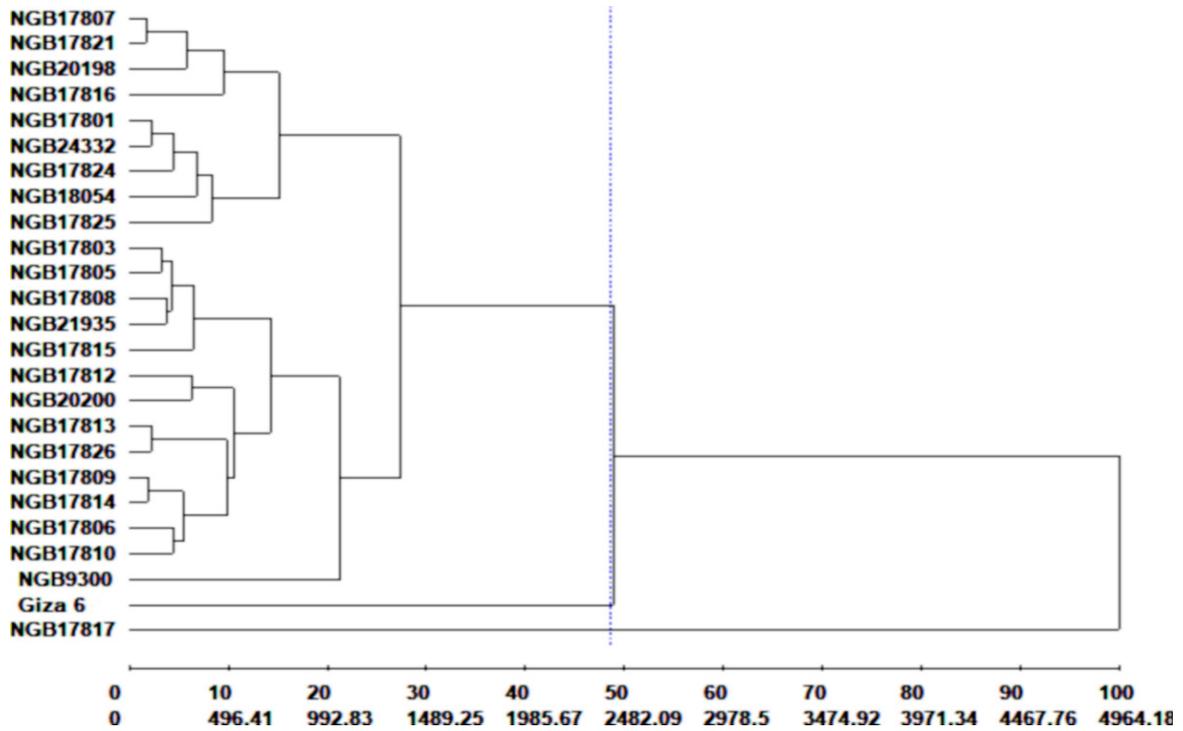


(B)

Fig. 4. UPGMA clustering dendrogram for 11 seed yield and related traits in 27 accessions of common bean evaluated in 2016 (A) and 2017 (B) summer seasons, El-Gharbiya Governorate, Egypt. The dotted line indicates the cut-off point according to Mojena (1977).



(A)



(B)

Fig.5. UPGMA clustering dendrogram for 11 seed yield and related traits in 25 accessions of common bean evaluated in 2016 (A) and 2017 (B) summer seasons, El-Gharbiya Governorate, Egypt. The dotted line indicates the cut-off point according to Mojena (1977).

Our results agree with those obtained by Carvalho et al. (2016) since he found that 24 accessions of common bean were grouped into three groups by Tocher optimization method or UPGMA method. Also, Vaz et al. (2017) reported that four groups were formed for 29 genotypes of the bush snap bean by either grouping methods.

In general, there was an agreement between the two years for all study parameters, as we conducted this study during the summer seasons of two successive years. However, we think that, if the experiments were conducted during different seasons, such as, autumn or winter season under protected cultivation, or under locations with different climatic conditions, the results might differ. Also, most studied accessions were from one germplasm resource, which might limit the formation of more distinct groups. The results are of practical importance since it forms the basis for the selection of superior diverse genotypes for future research, which could involve the hybridization between the desired accessions with greater performance and diversity. It would also be interesting to evaluate such accessions along with other ones from different resources, under various seasons and locations. Further examination with molecular techniques, might help to deeply understand the clustering pattern of such accessions.

Conclusions

The results indicated a wide genetic variability for all traits. In general, the accessions have been grouped into five distinct clusters. To obtain superior recombinants in segregating generations, we recommend investigating the crossing combinations of Giza 6 with, NGB17817, either of NGB17823 or NGB17827, and the desired accessions from cluster I, such as NGB17806, NGB17814, NGB17816, and NGB18054. Furthermore, we think that, NGB17823 and NGB17827 are suitable for the production under greenhouse conditions because of their indeterminate growth habit and high seed yield potential, therefore, they need further studies under such conditions in the winter season. Plant height, number of pods per plant, pod length and seed yield per plant were the most important traits for the genetic diversity.

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Conflicts of interest

The authors declare that there are no conflicts of interest related to the publication of this study.

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التوصيف، التنوع الوراثي، والتجميع العنقودي لتراكيب وراثية من الفاصوليا العادية بناء على محصول البذور والصفات المتعلقة به

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تم استخدام 27 تركيباً وراثياً من الفاصوليا العادية واختبارها من ناحية السلوك الانتاجي والتباين الوراثي فيما يتعلق باحدى عشرة صفة تشمل محصول البذور الجافة والصفات المتعلقة به، بهدف تحديد افضل التراكيب الوراثية المتباينة وراثياً وذلك لاستكشاف قوة الهجين في التهجينات فيما بينها ولبيان إمكانية الحصول على انحرافات فائقة في الأجيال التالية. تم اجراء الدراسة في قرية الدلجمون، مركز كفر الزيات بمحافظة الغربية بمصر وذلك خلال الموسم الصيفي لكل من العامين 2016 و 2017. تم توزيع التراكيب الوراثية في تصميم قطاعات كاملة عشوائية في ثلاث مكررات، تم استخدام طريقة Tocher وطريقة UPGMA لتقسيم التراكيب الوراثية إلى مجموعات متباينة وذلك بناء على طريقة Mahalanobis كمقياس لمدى التباعد الوراثي. أظهرت النتائج وجود مدى واسع من التباينات الوراثية لكل الصفات. وتم تجميع التراكيب الوراثية في خمسة مجموعات باستخدام طريقة Tocher، كانت المجموعة الأولى هي الأكبر حيث ضمت 22 تركيباً وراثياً، في حين أن المجموعة الثانية ضمت كلا من التركيبين NGB17823 و NGB17827 وفي نفس الوقت اتسمت هذه المجموعة بأكبر مسافة تباعد بينها وبين المجموعات الأخرى، بينما ضمت كل من المجموعات الثلاثة المتبقية تركيباً وراثياً واحداً. بصفة عامة اتفقت طريقة UPGMA مع طريقة Tocher. وبناء على النتائج، نقترح التهجين بين كل من الصنف التجاري جيزة 6 مع كل من التراكيب الوراثية NGB17817 أو أياً من التركيبين NGB17823 أو NGB17827 بالإضافة الى التراكيب المرغوبة من المجموعة الأولى مثل، NGB17806، NGB17816، NGB17814، وNGB18054. كانت أكثر الأصفات أهمية للتباين الوراثي هي صفات ارتفاع النبات وعدد القرون الناضجة للنبات وطول القرن الناضج و محصول البذور للنبات.