

Assessment of genetic variability and heritability of elite faba bean (*Vicia faba* L.) landraces based on yield and yield-related characters in Northern Sudan

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ABSTRACT

The effectiveness of selection in any crop depends on the magnitude of the available genetic variability in the gene pool of the species. In this study, 11 faba bean genotypes (eight genotypes and three checks) were assessed for agronomic performance, extent of genetic variability and heritability under irrigation conditions. The study was carried out at Dongola Research Station Farm in the Northern State of Sudan during two winter seasons 2020/2021 and 2021/2022. A randomized complete block design with four replications was used. The combined analysis of variance revealed the presence of significant ($P \leq 0.01$) and wide range of variation among the tested genotypes for most of the characters. Mean squares due to the interaction between the genotype and season were highly significant for most of the characters studied. The genotypes no. 5 and 2 gave significantly heavier seed weight than the two checks, Basabeer and Shendi. The maximum seed yield ton per hectare was recorded on genotypes; C.2/2 (4.18 t ha^{-1}) followed by Elarkey 82 (4.11 t ha^{-1}) and Gelass 36 (4.11 t ha^{-1}) while the minimum (2.89 t ha^{-1}) was obtained from C.3/3. These genotypes out – yielded the check Turkey in seed yield, with average yield advantages amounting to 22.0, 20.7 and 20.7%, respectively. Also, same genotypes exceeded the check Shendi by 9.3, 8.8 and 8.8%, respectively. The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all characters indicating the influence of environmental factors. The phenotypic coefficient of variation was higher for plant height (cm), number of pods per plant and 100-seed weight (g). Subsequent combined high genotypic coefficient of variation (GCV), high heritability (H^2) and high genetic advance as present of mean (GAM) were recorded for the number of seeds per pod (7.75%, 79.30% and 33.18%), seed yield (t ha^{-1}) (12.75%, 60.91% and 60.48) and hundred seed weight (22.26%, 23.64% and 3.82%), which denotes, these characters can be improved through direct selection easily than other characters.

Keywords: Faba bean, characters, genetic variability, seed yield.

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INTRODUCTION

Legumes are an important source of protein in many countries of the world and the countries of the Near East and North Africa, and they are an essential source for some of them (Tewodros et al., 2015; Gemechu et al., 2016). Alhajj et al. (2019) stated that China is one of the largest producers of studies to confirm that the Mediterranean basin is the original home of faba bean,

followed by Egypt is considered one of the main Arab countries in the production of studies to confirm that the Mediterranean basin is the original home of seed faba bean, and it is next to Ethiopia.

Faba bean (*Vicia faba* L.) is one of the most important crops of the leguminous family Fabaceae, and its importance stems from its use as food for humans

because its pods and seeds contain essential nutrients important for humans, such as carbohydrates, amino acids, vitamins, fatty substances and several other nutrients (Gnanasambandam et al., 2012; Sallam et al., 2015). As well as their seeds contain a high protein content (Kumar, 2016), which makes this crop of nutritional importance necessary to compensate for the high price of animal protein (Fekadu et al., 2012).

In Sudan, faba bean is one of the primary grown and consumed legume crops. It constitutes the primary human nutrition, supplying high-quality proteins essential for a balanced diet for the daily breakfast and dinner of the millions of people who cannot afford meat as a source of protein in both rural and urban areas (Osman et al., 2014). In many parts of Sudan, faba beans are served in several types of dishes such as stewed faba bean (Fuel Musalah), deep-fried cotyledon paste with some vegetables and spices (Taamia or Falafel), and faba bean soup with bread and cheese whey (Fata). Additionally, the crop is an imperative source of income for the farmers in the country (Salih and Mohamed, 1992). However, the demand for this nutritious legume crop is growing, fuelled by rapid population growth in the country, which led to an enormous gap between supply and demand. In Sudan, faba bean is traditionally cultivated on the banks of the Nile River north of latitude 18.50°N in the Northern and Nile States, where temperature is moderately cooler and winter longer (Salih and Mohamed 1992). However, to meet the ever-increasing demand for faba beans in Sudan, its production was extended into the warmer areas at latitudes lower than 15°N, where the climate is marginally suitable. In these areas, faba bean yield is far below the potential (Gasim et al., 2013), mainly because of the biological limitations of the traditional cultivars and poor management practices as well as the effect of abiotic (especially temperature) and/or biotic (diseases and pests) stresses.

Genetic variability of yield and yield components in the breeding material must be estimated for increasing the grain yield of faba bean. Yet, genetic variability doesn't show the heritable portion of traits. Heritability indicates the magnitude of the inheritance of traits but does not indicate the amount of genetic progress (Georgieva et al., 2016). For this reason, estimation of heritability coupled with genetic advancement is essential for breeding programmes (Fikreselassie and Seboka, 2012; Sharma et al., 2017). High broad-sense heritability was observed in days to flowering, plant height, number of pods per plant, 100-seed weight and seed yield per plant (Bakhiet et al., 2015; Sheelamary and Shivani, 2015). Some studies reported that great genetic variation in seed mineral concentration was found among faba bean and common bean genotypes regarding seed mineral contents (Talukder et al., 2010; Baloch et al., 2014). Genotypic evaluation is significant for mineral concentration and can be increased by selection among genotypes (Baloch et al., 2017).

The high genotypic coefficient of variation (GCV) is an indication of the less influence of environmental factors in the expression of traits and the higher chance to improve the traits through selection breeding (Ejigu et al., 2016). While the higher phenotypic coefficient of variation (PCV) values than the genotypic coefficient of variation (GCV) implies a greater influence of environmental factors for the phenotypic expression of these traits that make it difficult or practically impossible to exercise selection based on the phenotypic performance of the genotypes to improve the traits (Mesfin, 2019).

A high estimate of heritability (H^2) was reported for hundred seed weight and grain yield in faba bean genotypes at varied environments and several genotypes (Bakhiet et al., 2015; Sharifi, 2015; Hamza et al., 2017; Mesfin et al., 2021).

Hence, the objectives of this study were to estimate genetic variability and heritability among seed yield and yield-related characters of elite 11 faba bean genotypes.

MATERIALS AND METHODS

Description of the study area

The field experiment was conducted at Dongola Research Station Farm, Northern State Sudan, during the two winter seasons 2020/2021 and 2021//2022. It is located within latitude 19°11' N, longitude 30°29' E and altitude 227m. The Northern State occupies the distant Northern part of the Republic of Sudan and lies between latitudes 16°- 22° N and longitudes 20°- 32° E. The state was cited within the desert region of the Sudan. The soil of the experimental site (classified as high terrace) was alkaline soil with a high content of CaCo₃ (Yassin and Sami, 2014).

Experimental materials

The materials used for the present study comprise a total of 11 genotypes of faba bean (*Vicia faba* L.). Eight faba bean genotypes are advanced breeding lines, and three released faba bean varieties: namely the Basabeer, Shandi and Turkey, were included as checks. Among eight genotypes three genotypes were chosen from the Hudeiba breeding program, and five faba bean landraces were collected from different farmers' fields from the Merowe locality. The pedigree of the genotypes used in this study is presented in Table 1.

Cultural practices

Land preparation

During two seasons the field was prepared by disk ploughing, harrowing and leveling. After two days of

Table 1. Faba bean (*Vicia faba* L.) landraces and their collection site used in the study.

No.	Genotype/cultivar	Collection site	Pedigree
1	C.2/2	-	H.93 x Wahab
2	Elarkey 82	Village Elarkey	Landrace - single plant selection, 2015/2016 - entry no. 82
3	C.3/3	-	W.Habashi x Egy53
4	C.5	-	BB.7 x Egy53
5	Gelass 35	Village Gelass	Landrace - single plant selection, 2015/2016 - entry no. 35
6	Basabeer	-	Released commercial variety
7	Elarkey 48	Village Elarkey	landrace - single plant selection, 2014/2015 - entry no. 48
8	Shendi	-	Released commercial variety
9	Turkey	-	Released commercial variety
10	Gelass 36	Village Gelass	Landrace - single plant selection, 2015/2016 - entry no. 36
11	Gelass 2	Village Gelass	Landrace - single plant selection, 2015/2016 - entry no. 2

leveling, the land was ridged.

Sowing

The plot size was 5 ridges 5 m long spaced at 0.60 m. Two seeds were sown in holes spaced at 20 cm along both sides of the ridge. The plot area was 15 m². Sowing was done during mid-November in both seasons. The plants were irrigated equally at 10 to 12 days intervals. The crop took a total of about 11 irrigations during the growing period. Nitrogen was added as urea (46%) at a rate of 43 kg N/ha in the 3rd week from sowing. Weeds were manually controlled every two weeks during the first two months after sowing. Yield data were collected from an area of 8.28 m² (the inner three rows and the inner 4.6 meter ridge length) for each experimental plot.

Experimental Design

The experiment was laid out as a randomized complete block design (RCBD) with four replications.

Data collection

During the two winter seasons, observations were taken on ten plants randomly selected in a plot. Data were recorded on the following vegetative and reproductive characteristics.

Vegetative characters

- (i) Days to 50% flowering: It was recorded as the number of days from sowing to the date when 50 % of the plants in a plot bore at least one flower.
- (ii) Days to 90% maturity: It was estimated as days from sowing to the date when 90% of the leaves in the row turned yellow and green pods became black.
- (iii) Plant height: It was measured from ground level to the top of the plant at maturity. An average of ten plants was recorded in centimeters (cm).

Reproductive characters

- (i) Number of pods per plant: Pods of 5 randomly taken plants were counted to estimate the number of pods per plant.
- (ii) Number of seeds per pod: It was calculated by dividing the total number of seeds per plant (of the sample) by the total number of pods.
- (iii) 100-seed weight (g): Hundred seeds were taken randomly from each plot and weighed using a sensitive balance.
- (iv) Seed yield (t ha⁻¹): At maturity, plots were harvested by hand, and seed yield t ha⁻¹ was determined.

Data analysis and procedures

All measured parameters were subjected to analysis of variance (ANOVA) using the MSTATC software computer package to assess the difference among the tested genotypes. Mean separation was carried out using Duncan's Multiple Range Test (DMRT). Genotypic and phenotypic coefficient of variations was calculated by the formula suggested by Ral et al. (2013). Broad sense heritability was estimated following the formula described by Hasan et al. (2012a, b). The expected genetic advance for different characters under selection was estimated using the formula of Rahman et al. (2007). Genetic advance in percentage of mean was calculated from the formula given by Azam et al. (2014).

RESULTS AND DISCUSSION

Analysis of variance

The significance of mean squares due to different sources of variability for studied characters combined is summarized in Table 2. Results revealed that the studied genotypes differed significantly for all the characters in combined analyses except the days to 90% maturity and plant height, indicating the presence of sufficient

variability in the materials. This result confirmed with the results reported by several authors (Eman et al., 2017; Abbas et al., 2012; Talaat and Abdallah, 2008), who found a wide diversity among the Egyptian faba bean genotypes in yield and yield component traits. Also, the

results showed that the mean square of environments (seasons) x genotypes interaction was significant for all characters measured except the plant height and number of pods per plant, and number of seeds per pod were not significant.

Table 2. Mean squares of seed yield ($t\ ha^{-1}$) and some yield components for 11 faba bean genotypes grown during two winter seasons 2020/21 and 2021/22 at Dongola.

Characters	Season (d.f = 1)	Genotype (d.f = 10)	Seas. X geno. (d.f = 10)
Days to 50% flowering	276.545***	4.575*	5.170**
Days to 90% maturity	575.284***	11.795n.s	24.509*
Plant height (cm)	4050.102**	85.409n.s	101.977n.s
No. of pods /plant	929.500*	95.059**	18.550n.s
No. of seeds /pod	0.920*	0.367**	0.106n.s
100-seed weight (g)	530.182***	1530.607***	154.907**
Seed yield ($t\ ha^{-1}$)	0.230n.s	1.413***	0.652***

*, ** and *** Significant at 0.05, 0.01 and 0.001 levels of probability, respectively. n.s = non - significant difference at 0.05 probability level.

Mean performance of growth, yield and yield component characters

The mean performances for different characters of 11 faba bean genotypes are given in Table 3. Data revealed that there is a wide range of variability observed for most of the studied characters. The genotypes no. 7 and 2 possessed the earliest flowering (32 and 33 days respectively). On the other hand, genotype no. 1 and the two checks Shendi and Turkey had the latest days to flowering. The genotype no. 2 and the check Basabeer were the earliest to maturity as they need 105 days to reach maturity. On the other hand, the genotypes no. 10 and 11 were the latest as they required 109 days to mature. The two genotypes no. 5 and 1 possessed the tallest plants, whereas the genotypes no. 4, 10 and 11 exhibited the shortest plants (Table 3). Results showed that the number of pods per plant ranged from 23 to 11, with a mean of 18. The maximum number of pods per plant was obtained from check Shendi, whereas check Turkey produced minimum number of pods per plant (Table 3). The values for the number of seeds per pod for genotypes varied from 2.62 (genotype no. 10) to 1.96 (genotype no. 3) with a mean value of 2.26. This character clearly shows that sufficient variability is present in the genotypes. For 100-seed weight (g), the genotypes no. 5, 9, 2, 10 and 7 possessed the heaviest seed weight among the eleven genotypes tested. While the two checks Basabeer and Shendi recorded the lowest value (54 g). Genotypes no. 5 and 2 recorded significantly higher seed weights than the two checks, Basabeer and Shendi. On average over the two seasons, the highest mean seed yield was obtained by genotype no. 1, followed by genotypes no. 2, 10 and

check Basabeer. The lowest seed yield was obtained by genotype no. 3. These three genotypes out-yielded all the checks, in particular, the check Turkey by 22.0, 20.7 and 20.7%, respectively (Table 3). The same genotypes surpassed the third check Shendi by 9.3, 8.8 and 8.8%, respectively. Genotype no.3 showed a lower seed yield than all genotypes represented in the current study. Six of the tested genotypes had yield exceeding the overall mean of the trial.

Genetic parameters

Genetic variability and heritability for all characters of eleven faba bean genotypes are shown in Table 4. In all studied characters except the plant height and number of pods per plant, less difference between the phenotypic and genotypic coefficient of variations was observed. The low difference between the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for most studied characters indicates the negligible environmental effect on these characters. The narrow gap between PCV and GCV variation in faba bean has been observed in studies before. This narrow gap between PCV and GCV indicated that the variability between genotypes due to the genetic constitution of the genotypes was higher than the variability due to environmental factors (Hamza et al., 2017). The magnitude of the PCV was higher than the corresponding GCV for all the characters studied, indicating more or less equal genetic effect on the character. This result was similar to that reported by Ahmad (2016) and Amit et al. (2020). Heritability (H^2) in broad sense estimates were generally moderate for most studied characters, which

Table 3. Average performance for some vegetative characters, its primary components and seed yield ($t\ ha^{-1}$) of 11 faba bean genotypes, combined over two winter seasons.

Entry no.	DF	DM	PH	NPP	NSPO	HSW	SY
1	35 ^a	107 ^a	98 ^a	18 ^{ab}	2.40 ^{ab}	54 ^c	4.18 ^a
2	33 ^{ab}	105 ^a	95 ^a	16 ^{ab}	2.16 ^{ab}	78 ^b	4.11 ^a
3	35 ^a	108 ^a	97 ^a	20 ^a	1.96 ^b	55 ^c	2.89 ^c
4	34 ^{ab}	108 ^a	91 ^a	19 ^{ab}	2.28 ^{ab}	56 ^c	3.88 ^{ab}
5	34 ^{ab}	108 ^a	102 ^a	16 ^{ab}	2.10 ^{ab}	92 ^a	3.66 ^{ab}
6	34 ^{ab}	105 ^a	96 ^a	21 ^a	2.48 ^{ab}	54 ^c	4.09 ^a
7	32 ^b	108 ^a	93 ^a	16 ^{ab}	2.11 ^{ab}	61 ^c	3.54 ^{abc}
8	35 ^{ab}	107 ^a	97 ^a	23 ^a	2.25 ^{ab}	54 ^c	3.79 ^{ab}
9	35 ^{ab}	108 ^a	96 ^a	11 ^b	2.01 ^b	85 ^{ab}	3.26 ^{bc}
10	34 ^{ab}	109 ^a	92 ^a	18 ^{ab}	2.62 ^a	63 ^c	4.11 ^a
11	34 ^{ab}	109 ^a	92 ^a	21 ^a	2.47 ^{ab}	58 ^c	3.35 ^{bc}
Mean	34	107	95	18	2.26	64	3.72
S.E ±	0.485	1.112	3.032	1.881	0.125	2.653	0.150
C.V (%)	3.9	2.9	8.9	28.6	15.6	11.5	11.4

DF: Days to 50 % flowering, DM: Days to 90 % maturity and PH: Plant height (cm), NPP: Number of pods per plant, NSPO: Number of seeds per pod, HSW: Hundred seed weight (g) and SY: Seed yield ($t\ ha^{-1}$).

According to Duncan's Multiple Range Test then it should be (DMRT) the data in the same column that had the same letter were not significant.

Table 4. Genetic parameters for some characteristics in 11 faba bean genotypes grown during two winter seasons 2020/21 and 2021/22.

Characters	δ^2_g	δ^2_{ph}	GCV (%)	PCV (%)	H ² (%)	GA	GAM (%)
Days to 50% flowering	0.605	2.726	7.07	15.00	22.19	0.75	2.20
Days to 90% maturity	0.297	5.278	4.95	20.88	5.62	0.12	0.11
Plant height (cm)	0.290	200.438	4.89	128.70	0.14	0.04	0.04
No. of pods /plant	0.839	136.006	8.32	106.01	0.61	0.14	0.77
No. of seeds /pod	0.728	0.918	7.75	8.71	79.30	0.75	33.18
100-seed weight (g)	5.996	25.36	22.26	45.78	23.64	2.45	3.82
Seed yield ($t\ ha^{-1}$)	1.962	3.221	12.73	16.31	60.91	2.25	60.48

δ^2_g = Genotypic variance, δ^2_{ph} = Phenotypic variance, GCV = Genotypic coefficient of variation, PCV = Phenotypic coefficient of variation, H² (%) = Broad sense heritability, GA = Genetic advance and GAM = Genetic advance as percent of mean.

ranged from 0.14% for plant height to 79.30 for the number of seeds per pod. The highest estimates of broad sense heritability (H²) were recorded as 79.30, 60.91, 23.64 and 22.19% for number of seeds per pod, seed yield ($t\ ha^{-1}$), 100-seed weight and days to 50% flowering, respectively (Table 4). This high heritability signifies the effectiveness of these characters through selection for the crop improvement, as fewer environmental effects will be utilized in future breeding programs. Moreover, the value is low for the rest of the characters, including the plant height, number of pods per plant and days to 90% maturity, indicating the limited possibility of improvement of these characters through selection. The results were similar to the findings of Toker (2004), who recorded high to moderate heritability for characters containing days to 50% flowering and low heritability for the number of pods per plant. In this study, genetic advance as a percent of means ranged from 0.04% for plant height to 60.48% for seed yield ($t\ ha^{-1}$). High expected genetic advance as percent of mean for seed yield ($t\ ha^{-1}$) and number of seeds per pod indicated that these characters are

controlled more by additive genes.

CONCLUSION

The results clearly showed the presence of considerable variations among genotypes for all characters measured except the days to 90% maturity and plant height. This indicated the possibility of conducting a further study on these genotypes to exploit the existing variability in the faba bean improvement program.

The ranges of the mean values for the most of characters were high, showing the existence of variation among the tested genotypes.

Genotypes no. 1, 2 and 10 recorded the highest yield among the genotypes tested. They out-yielded the three checks. These promising genotypes with desirable characters could be recommended to produce new varieties or use as parental lines for future breeding programs.

The phenotypic coefficient of variation (PVC) was found

to be higher than the genotypic coefficient of variation (GCV) for all the characters. The two values deferred somewhat indicating less influence of the environmental factors.

High heritability values were obtained for number of seeds per pod (79.30%) followed by seed yield (t ha⁻¹) (60.91%), 100-seed weight (23.64%) and days to 50% flowering (22.19%).

The results of genetic advancement as a percent of means increased from 0.04% to 60.48% magnitude made by selection.

High estimates of heritability accompanied by high genetic advance as percent of mean for number of seeds per pod and seed yield indicated that additive gene effects are important in determining these characters. Crop improvement for these two characters is assumed to be possible by simple selection.

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