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Assessment of genotypic and phenotypic variability, heritability and genetic advance for seed yield and related agronomic traits in faba bean (*Vicia faba* L.) genotypes in the Northern State, Sudan

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ABSTRACT

A study was conducted at Merowe Research Station Farm, Northern state of Sudan, during two successive winter seasons 2010/11 and 2011/2012. Genotypic and phenotypic coefficient of variation, heritability and genetic advance were determined for yield and its contributing parameters in 12 faba bean genotypes. Data were gathered on the seed yield (kg ha^{-1}) and some yield related traits: days to 50% flowering, days to 90% maturity, plant height (cm), number of pods/plant, number of seeds/pod and 100-seed weight (g). Analysis of variance for traits studied showed significant differences among genotypes, seasons and their interaction ($P \leq 0.01$) for most of the studied traits. High phenotypic coefficient of variation (PCV) was observed for number of pods/plant and 100 – seed weight. Medium PCV was observed for plant height and days to 50% flowering. High genotypic coefficients of variation (GCV) were observed for plant height and 100 - seed weight. Moderate genotypic coefficients of variation were estimated for days to 50% flowering and number of pods/plant. Phenotypic coefficient of variation values for most characters was closer to the corresponding genotypic coefficient of variation values showing little environment effect on the expression of these characters. The estimated values of broad-sense heritability were found to be between 57.97% for 100 – seed weight and 1.87% for number of pods per plant. High heritability indicated that selection based on mean would be successful in improving these traits. Genetic grains that expected from selecting the top 5% of the genotypes, as a present of mean were varied from 0.65% for plant height to 8.45% for 100 – seed weight.

Keywords: Faba bean, variability, heritability, genetic advance, seed yield.

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INTRODUCTION

Faba bean (*Vicia faba* L.) is a significant crop worldwide, ranking fourth important grain pulse after dry beans, dry peas and chickpeas (Hawtin and Stewart, 1979) and second popular food legume in Europe (Picard et al., 1988). The bean is a common breakfast meal in the Mediterranean region, Central and East Asia, and Ethiopia, and a familiar crop in the Americas and Oceania (Bond et al., 1985). Broad beans are the most favored food legume in Sudan (Salih and Ali, 1989).

World production has varied during the past 10 years ranging from a low of 3.58 million tons in 997/98 to a high of 4.85 million tons in 2002/03, trending upward (FAO, 2004).

Faba bean is the most important food legume in Sudan

(Osman et al., 2010a, b). It is the main staple food and the main source of protein for millions of people. Its nutritional importance is even greater as many people have limited access to animal food protein. Its consumption increased among the middle and low income strata of the population, being the traditional dish for breakfast and supper. Further demand has, however, increased over time in the whole country to magnitudes that increasing productivity would be essential to satisfy local needs.

Faba beans are traditionally grown in the fertile (Gureir) soils, which are silty loams deposited in a narrow strip along the banks of the Nile and on isolated islands. Due to the scarcity of fertile soil and the high demand for Faba bean coupled with the ever increasing prices, non-traditional lands of inferior quality such as 'karu' and 'high terrace' soils are coming up into production.

Selection of superior genotypes based on the yield alone is less efficient due to the complexity of the yield and its dependence on its components (Sindhu et al., 1985). Direct selection was also ineffective due to the large genotype - environment interaction (Yassin, 1973). For a breeding program to be successful there must be genetic differences among the individual plants of the breeder's collection of material. Then the breeder will be able to select the desirable combination of genes. Most desirable traits such as yield, protein content and quality are under the control of many genes and environmental factors. The environment affects the expression of the character and there will be no discrete classes of phenotype and there are continuous variations of this character. Such variations need statistical techniques for their evaluation. This type of character is known as the quantitative character. The situation is different from the character considered by Mendel, the qualitative character. Observed phenotypes can be measured and assessed while the genotypes can be inferred from the phenotype data.

In faba bean, a self pollinated crop, the analyses of variance method can be used to estimate the heritability. The observed mean square will be equated to the expected mean square and the value of phenotypic variance, σ^2p, and genotypic variance, σ^2g, will be obtained from the analyses of variance table. The genetic advance achieved in each breeding cycle depends on how the additive gene effect is beneficial (Hassan, 1991).

The present study aimed to estimate the variability, heritability and genetic advance for yield and yield components of twelve faba bean genotypes.

MATERIALS AND METHODS

Experimental site

The data of this research experiment were collected from a study conducted over two consecutive winter seasons (2010/11 and 2011/12), at Merowe (The Experimental Farm of Merowe Research Station of Northern state), which is located at Latitude: 18° 27' 0" N, Longitude: 31° 49' 59" E, Elevation: 258 m.

Genetic material

The genetic material used in this study comprised a total of 12 genotypes of faba bean (*Vicia faba* L.), which were selected from the national legume breeding program of the Agricultural Research Corporation (ARC), Sudan. Ten genotypes are advanced breeding lines and two released faba bean varieties; Basabeer and Hudeiba 93 were included as checks. Code number and name of the faba bean studied genotypes are given in Table 1.

Cultural practices

Land preparation

The field prepared by disk ploughing, harrowing and leveling. After two days from leveling, the land was ridged.

Sowing

The seeds were sown manually on both sides of the ridge in rows, at the rate of two seeds per hole. The plot size was consisted of 5 ridges, 5 m long spaced 0.6 m. The sowing dates of the two seasons were usually within the third week of November. The plants were irrigated equally at 10 to 12 days interval. The crop took a total of 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 and weeds populations were kept to a minimum by hand removal during the first month from sowing. In the first and second season, plants were sprayed with (2-dimethoxyphosphorylsulfanyl-N-methylacetamide) against the aphid (*Aphis fabae* sp.), when it appeared in the field.

Experimental layout

The experiments were arranged in a randomized complete block design with three replications.

Observations and measurements

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

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 centimetres (cm).

Reproductive characters

(i) Number of pods per plant: pods of 5 randomly taken plants were counted to estimate number of pods per plant.

Table 1. Faba bean genotypes used in the study.

Entry no.	Cultivar / line
1	C.98/02
2	C.98/8
3	C.1/02
4	C.4/02
5	C.8/02
6	C.9/02
7	C.14/02
8	C.15/02
9	C.19/02
10	C.28/02
11	BB-7 (check)
12	H.93 (check)

(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 per plant.

(iii) 100 - seed weight (g)

Hundred seeds were taken randomly from each plot and weighed using a sensitive balance namely, Sartorius (made in Germany).

(iv) Seed yield (kg ha^{-1})

At maturity, plots were harvested by hand and seed yield kg ha^{-1} was determined.

Statistical analysis

Analysis of variance was performed separately for each season before running the combined analysis. The mean separation was done using Duncan's Multiple Range Test (DMRT) for the different characters. Statistical analysis was carried out using MSTATC program.

Genetic parameters estimates

Heritability in broad sense (H^2) was estimated according to Falconer (1989) using Equation 1:

$$\text{Heritability } (H^2) = (\sigma^2 g / \delta^2 ph) \times 100 \qquad (1)$$

H^2: Heritability; $\delta^2 g$: genotypic variance and $\delta^2 ph$: phenotypic variance. Genotypic ($\delta^2 g$) and phenotypic variances ($\delta^2 ph$) were obtained from the analysis of variance table according to Comstock and Robinson (1952) using Equations 2 and 3:

$$\delta^2 g = (MS1 - MS2) / r \times s \qquad (2)$$

$$\delta^2 ph = (MS1) / r \times s \qquad (3)$$

Where r: replication, s: season MS1: Mean square for cultivar, MS2: Mean square for genotype × season.

The mean values were used for genetic analyses to determine Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV), according to Singh and Chaudhury (1985) using Equations 4 and 5:

$$\text{Phenotypic coefficient of variation (PCV)} = (\sqrt{\delta^2 g} / \bar{x}) \times 100 \qquad (4)$$

$$\text{Genotypic coefficient of variation (GCV)} = (\sqrt{\delta^2 ph} / \bar{x}) \times 100 \qquad (5)$$

Where:
$\delta^2 g$ = genotypic variance
$\delta^2 ph$ = phenotypic variance
$\bar{x}$ = sample mean

Genetic advance (GA) was calculated with the method suggested by Allard (1960) and Singh and Chaudhury (1985) using Equation 6:

$$GA = K.\ \sigma ph.\ H^2 \qquad (6)$$

Where:
GA: genetic advance
K: constant = 2.06 at 5% selection intensity
σph: square root of phenotypic variance
H^2: Heritability
GA as % of mean (GAM) = (GA / mean value) × 100

RESULTS AND DISCUSSION

Mean squares of 7 traits of the twelve faba bean genotypes in the two environments (seasons) are shown in Table 2. There were significant differences among genotypes, seasons and their interaction ($P \leq 0.01$) for most of the studied traits.

Estimates of phenotypic and genotypic variances, phenotypic coefficient of variance (PCV), genotypic coefficient of variance (GCV), genetic advance (GA), genetic advance as percent of mean (GAM) and broad sense heritability are presented in Table 3. The phenotypic coefficient of variation (PCV) was high for the number of pods per plant (33.85%) followed by 100 – seed weight (27.08%). The estimates of PCV were low for days to 90% maturity (9.42%), days to 50% flowering (8.66%) and number of seeds per pod (2.03%). The genotypic coefficient of variation (GCV) was high for the traits for the plant height (39.48%) followed by 100 – seed weight (20.58%). High GCV value of characters suggested the possibility of improving these traits through selection. Similarly, El-Hosary and Nawar (1984) estimated different levels of GCV in faba bean. Moreover, the difference between PCV and GCV for all traits was small and PCV value was greater than GCV for all the characters indicating that these characters were less influenced by environment. A similar result was reported by Ahmad, (2016). High PCV and GCV values were recorded for the trait 100 – seed weight. The estimates of GCV were low for days to 50% flowering (6.40%), followed by number of pods per plant (4.63%) and number of seeds per pod (1.17%). High heritability with moderate GA and high GCV was recorded for the characters seed yield per plot and 100 – seed weight.

Heritability (H^2) in broad sense estimates were varied from 1.87% for number of pods per plant to 57.97% for 100 – seed weight. In earlier studies, high heritability estimates for seed weight (Shukla and Sharma, 1978) were reported. This finding is thus in agreement with the

Table 2. Mean squares of yield and some yield components for 12 faba bean genotypes grown during two seasons 2010/11 and 2011/12.

Traits	Season (d.f = 2)	Genotype (d.f = 11)	Seas. x genotype (d.f = 22)	Pooled error (d.f = 66)
Days to flowering	41.194***	6.667***	1.316**	0.544
Days to maturity	83.676**	4.138 ns	4.969*	3.283
Plant height (cm)	3283.968***	61.109*	49.561 ns	41.911
No. of pods/plant	2113.001***	43.611*	40.749*	23.507
No. of seeds/pod	0.526*	0.303**	0.098ns	0.100
100-seed weight	15.509 ns	65.201***	9.934 ns	10.288
Seed yield	10514492.565***	344371.976*	166309.000 ns	187605.497

*, ** and *** Significant at 0.05, 0.01 and 0.001 levels of probability, respectively. ns= non-significant.

Table 3. Estimation of genetic parameters for different quantitative traits in faba bean genotypes grown during two seasons 2010/11 and 2011/2012.

Traits	δ^2ph	δ^2g	GCV (%)	PCV (%)	H^2 (%)	GA	GAM (%)
Flowering	1.08	0.59	6.40	8.66	54.60	1.19	3.21
Maturity	-	-	-	-	-	-	-
Plant height	22.45	1.28	39.48	9.42	5.70	0.55	0.65
Pods / plant	16.50	0.31	4.63	33.85	1.87	0.15	0.76
Seeds / pod	0.06	0.02	1.17	2.03	33.33	0.16	6.95
100-seed weight	10.59	6.14	20.58	27.08	57.97	3.89	8.45
Seed yield	96066.15	19784.77	1172.15	2582.87	20.59	7.79	0.20

δ^2g = Genotypic variance, δ2ph = Phenotypic variance, PCV = Phenotypic coefficient of variance, GCV = Genotypic coefficient of variance, H^2 = Broad sense heritability, GA = Genetic advance, GAM= Genetic advance as percent of mean.

results obtained in the present investigation. The highest estimate of broad sense heritability (H^2) was followed by days to 50% flowering (54.60%) and number of seeds per pod (33.33%). Accordingly Bond et al. (1985) confirmed that faba bean genotype determines the number of seeds per plant. Nevertheless (Daur, et al., 2010) found no significant variability of number of seeds per pod between twelve studied faba bean genotypes. On the other hand the low heritability estimates were established for the traits plant height (5.70%) and number of pods per plant (1.87%).

Generally, heritability determines the effectiveness of selection. The effectiveness of selection for a trait depends on the relative importance of the genetic and environmental factors in the expression of phenotypic differences among genotypes in a population (Singh, 1990). The components of yield that were most heritable in this faba bean population were 100 – seed weight and number of seeds per pod. Therefore, the simultaneous selection for these traits could lead to an increase in seed yield. No trait recorded high GAM. The moderate GAM was recorded by 100 – seed weight (8.45%) and number of seeds per pod (6.95%). All other traits recorded the lowest genetic advance as per cent of mean. These results indicated that the environmental factors had a small effect on the inheritance of such traits.

The moderate heritability and the low genetic advance obtained in this study for the seed yield is probably due the epistemic gene action (Kalia and Sood, 2004) so the mass selection may be ineffective in improving the seed yield in these four genotypes.

CONCLUSION

The mean squares due to seasons were significant for all the traits except 100 – seed weight. The mean squares due to genotypes were highly significant for seed yield, indicating the existence of the sufficient genetic variability for seed yield. Narrow range of variability was detected in the days to 50% flowering, number of pods per plant and number of seeds per pod in the twelve faba bean genotypes evaluated in the study. Whereas the high genetic coefficient of variation was observed for plant height (cm) followed by 100 – seed weight (g).Heritability of large number of traits was high and moderate. High estimates of heritability indicated that selection based on mean would be successful in improving these traits. High heritability indicate an additive gene action and, hence, possible trait improvement through selection.

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