Research Article *Open Access*

Journal of Geoscience and Eco Agricultural Studies

ISSN: 3067-7297

***DOI:** doi.org/10.63721/25JGEAS0119*

Assessment of Genotype x Environment Interactions and Stability for Seed Yield of Selected Faba Bean (Vicia faba L.) Genotypes across Five Environments of Sudan

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Citation: Fatih Elalim A Hamza, Rasha M O Mahagoub, Elkhazin A Yousef, Nazar B Hussein (2025) Assessment of Genotype x Environment Interactions and Stability for Seed Yield of Selected Faba Bean (Vicia faba L.) Genotypes across Five Environments of Sudan. J. of Geo Eco Agr Studies 2(4): 1-13. WMJ/JGEAS-119

Abstract

In this study, eight faba bean genotypes were tested against three checks (Basabeer, Shandi and Turkey) across five environments during two winter seasons (2020/2021 and 2021/2022). The main objectives of this study were to estimate G x E interactions and identify the highest yielding and stable genotypes under different environments. A randomized complete block design with four replicates was used. Data were collected on days to 50% flowering, days to 90% maturity, plant height (cm), number of pods per plant, 100-seed weight (g) and seed yield (t ha-1). A wide range of genetic variability was observed among the genotypes for most of the studied traits. Combined analyses of variance revealed highly significant environment, genotype and genotype x environment (GE) component of interaction and indicated wide differences among the environments and differential genotypic behavior to the tested environments. Results indicated that the genotype G1 (C.2/2) ranked the best with yield increment of 15.8% and 9.8%, respectively over the two standard checks, Shandi and Turkey. The genotypes G4 (C.5), G2 (Elarkey 82), G10 (Gelass 36) and G11 (Gelass 2) out - yielded the two standard checks Shandi and Turkey in seed yield with average yield advantage over the check Turkey amounting to more than 10%. The heaviest seed weight (79 g) was obtained by the genotypes Elarkey 82 and check Turkey, followed by Gelass 35 (72 g) and Gelass 36 (66 g). Results of additive main effect and multiplicative interaction (AMMI) analysis showed that genotypes (G), environments (E), and genotype x environment interaction (GEI) had highly significantly ($P \leq 0.01$) affected seed yield. From the total sum of squares due to treatments (G + E + GEI), E attributed the highest proportion of the variation (73.83%), followed by GEI (16.63%) and G (9.54%). The partitioning of the GxE by AMMI analysis showed that two of the Interaction Principal Component Axes (IPCAs) were highly significant ($P \leq 0.001$). AMMI and GGE biplot analyses result identified that genotypes, C.5, Elarkey 82 and Gelass 36 were declared as widely adapted genotypes with likewise recorded higher seed yield of 3.36 t ha-1, 3.23 t ha-1 and 3.21 t ha-1, respectively. Therefore, the three promising faba bean genotypes C.2/2, Elarkey 82 and Gelass 36 were release in 22 June 2025 for commercial production under the names, Hudeiba 2025, Elwafer and Mahira, respectively to be grown in River Nile and Northern States as well as similar agro-ecologies of Sudan.

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Submitted: 16.10.2025 **Accepted:** 27.10.2025 **Published:** 20.12.2025

Keywords: Vegetation Degradation, Environment, Forest Ecosystem Services, Sudan

Introduction

Faba bean (Vicia faba L.) is a diploid legume plant with a chromosome number of 2n=2x=12 and one of the largest genomes among crops, with a genome size of 13,000 Mb [1]. Faba beans are a nutritious crop that is high in carbohydrates, protein, minerals, and bioactive compounds [2].

Faba bean is grown as a winter crop under irrigation mainly in the Northern State in about 70% of the total cultivated area and the River Nile State in about 30% of the total cultivated area in the Sudan. It is also grown to a limited extent in Khartoum State and Jabel Marra in Western Sudan due to the suitability of the environmental conditions [3]. Lately, it was introduced to the larger irrigated schemes of Gezeira, Rahad and New Halfa.

Thus, multi-environment trials are essential in the selection cycle of variety development programs to identify superior and stable genotypes through estimating genotype by environment interaction (GEI) effect [4]. Genotype by environment interaction (GEI) refers to the inconsistent performance (differential response) of different genotypes for measured trait across different environmental conditions. Even though the existence of GEI challenges breeders for selection of superior and wide adaptable varieties, the study of genotype by environment interaction (GEI) is very important for crop improvements and it is necessary to understand the pattern of GEI and performance stability across environments especially at the final stage of variety development [5,6].

Statistical analysis of yield trials can help agronomists, breeders, and other agricultural researchers to make faster progress [7]. Hence stability analysis provides a general summary of the response patterns of genotypes to change environments or the interaction of genotypes with locations and other agro-ecological conditions that help in getting information on adaptability and stability of performance of genotypes [8].

There are advanced statistical tools such as Additive main effects and multiplicative interaction (AMMI) and genotype main effect and genotype by environment interaction (GGE) biplot models that will enable breeders for analyzing GEI and to visualize the phenotypic stability of genotypes over environments from multi-environmental trial data and to easily identify superior genotypes within a given environment [9].

Therefore, the major objectives of the present research were to estimate G x E interactions of faba bean genotypes grown under different environments and the stability for seed yield.

Materials and Methods

Experimental Area

Multi-environment trials were conducted during the two winter seasons 2020/21 and 2021/22 at three locations. The experimental environments were selected to covering the main production areas of faba bean in Sudan. The locations were distributed as follow; the two locations in the River Nile state: Hudeiba, Shendi and one location in the Northern state: Dongola

Genetic Material

The genetic materials used in this study consisted of 8 genotypes of faba bean. In addition, three faba bean released cultivars namely; Basabeer, Shandi and Turkey were included as checks. Among eight genotypes, three genotypes were chosen from the Hudeiba faba bean breeding program, while the other five faba bean landraces were chosen from the Merowe faba bean breeding program. The pedigrees of the genotypes used in this study are presented in Table (1).

Experimental Design and Agronomic Practices

The experiments were conducted using a randomized complete block design (RCBD) with four replications.

Soil preparation included plowing with a disc plow, Subsequently, the soil was harrowed, leveled, and lastly plots were ridged at a spacing of 60 cm between rows. Each genotype was manually sown in plots consisting of five rows of 5 meters in length, with a 20 cm spacing between planting holes and two seeds per hole. Irrigation was applied every 12-14 days throughout the crop cycle, totaling nine irrigations. Nitrogen was supplied during the third irrigation, using urea at a rate of 43 kg (N ha-1). Weed control was carried out manually within the first month after sowing. Harvesting was performed manually when the plants reached 90% physiological maturity, with pods being dried, threshed, cleaned, and weighed to determine the final seed yield. Yield data were collected from an area of 8.28 m2 (the inner three rows and the inner 4.6meter ridge length) for each experimental plot.

Data Collection and Evaluated Traits

During both seasons, five plants were randomly selected from each experimental plot for data collection on the following traits:

Seed Yield (t ha-1): Determined after harvesting, threshing, and manually cleaning the seeds, later converted to tons per hectare (t ha-1).

Days to 50% Flowering: Number of days from sowing until 50% of the plants had at least one open flower.

Days to 90% Maturity: Number of days from sowing until 90% of the plants reached physiological maturity.

Plant Height (cm): Measured from the base to the apex of the mature plant.

Number of pods per plant: Count of the total number of mature pods containing seeds, obtained from the five sampled plants per plot.

100-Seed weight (g): Measured by weighing 100 randomly selected seeds from each plot using a precision balance.

Statistical Analysis

Statistical analysis of the collected data was done using the GenStat 12th edition statistical analysis package for windows [10]. Individual analyses of variance for each experiment in each location and season were analyzed followed by the combined analysis for seed yield of overall testing environments. The analysis of variance (ANOVA) for all measured characters was carried out according to the procedure described by [11].

To determine the performance, stability and genotypic superiority across environments or at specific environment, additive main effect and multiplicative interaction (AMMI) model was used [12]. AMMI stability value (ASV) was calculated for each genotype according to the relative contribution of IPCA1 and IPCA2 to the interaction sum square (SS) following the method proposed by [13]. According to ASV, genotype with lower ASV score is regarded as more stable.

Table 1: Faba bean genotype, Pedigree, collection/released year and seed sources used in multi-environment trials during two winter seasons (2020/2021 and 2021/2022).

No.	Cultivar/genotype	Pedigree	Collection/Released year	Seed sources
G1	C.2/2	H.93 x Wahab	-	Hudeiba station
G2	Elarkey 82	Single plant selection 82-2016, landrace	2016	Merowe station
G3	C.3/3	W.Habashi x Egy53	-	Hudeiba station
G4	C.5	BB.7 x Egy53	-	Hudeiba station
G5	Gelass 35	Single plant selection 35-2016, landrace	2016	Merowe station
G6	Basabeer (check)	Released variety	1993	Hudeiba station
G7	Elarkey 48	Single plant selection 48-2016, landrace	2016	Merowe station
G8	Shendi (check)	Released variety	2013	Hudeiba station
G9	Turkey (check)	Released variety	2017	Merowe station
G10	Gelass 36	Single plant selection 36-2016, landrace	2016	Merowe station
G11	Gelass 2	Single plant selection 2-2016, landrace	2016	Merowe station

Results and Discussion

Multi- Location Trials for Seed Yield and Yield Related Traits

Seed Yield (t ha-1)

The analysis of variance revealed significant variation ($P \leq 0.001$) in seed yield of the tested genotypes among the five environments and for their average (Table 2). This result was conformity with the results reported by many authors [14,15]. The highest mean seed yield across the five environments was recorded by the cultivar Basabeer (check) (3.39 t ha-1) followed by G1 (C.2/2) (3.36 t ha-1), G4 (C.5) (3.24 t ha-1), G2 (Elarkey 82) (3.23 t ha-1) and G10 (Gelass 36) (3.21 t ha-1). While, the seed yield of cultivar Shandi (check) was 3.03 t ha-1 and for cultivar Turkey (check) was 2.83 t ha-1.

In the Dongla 2021/22 site, three faba bean genotypes were superior to the check Basabeer with G2, G1 and G10 as the top yielders having an increment over the check by 15.6, 14.3 and 8.2%, respectively. While in Shendi 2021/22 site, the highest yield was achieved by five genotypes. These genotypes are G1, G4, G2, G10 and G11 which out-yielded the check Turkey by 15.7, 12.6, 12.3, 11.8 and 10.1%, respectively.

Across the five environments the percent increase in seed yield of G1 over the two checks (Turkey and Shandi) was 15.8% and 9.8%, respectively (Table 4). On the other hand, the respective increases in seed yield of G4 over the two checks (Turkey and Shandi) were 12.6% and 6.5%, respectively. G2 out-yielded the two checks (Turkey and Shandi) by about 12.4% and 6.2%, respectively. Also, G10 was more the two checks (Turkey) and Shandi) by 11.8 % and 5.6%, respectively (Table 3). As well, the G11 recorded high yield and out–yield the two standard checks (Turkey) and Shandi) by about 10.8% and 3.8%, respectively.

Days to 50% Flowering

The genotypes showed significant differences in days to 50% flowering at the four tested environments (Table 4). Similar results were reported in previous studies by who found that, the highly significant differences among faba bean genotypes for days to flowering. The overall average for days to 50% flowering was 37 with a range of 35 – 39 days (Table 4) [16]. The earliest genotype (36 days) was G2, followed by G5, G6, G7, G9 and G10, whereas the latest genotype was G1 (39 days). Days to 50% flowering for the two checks (Turkey) and Shandi) was 43 and 41 respectively.

Days to 90% Maturity

Across all environments, the statistical analysis of variance showed that there was no significant different for this character between the eleven faba bean genotypes used in this study. The range of days to 90% maturity at four environments was (98 – 100 days) for Shendi 2020/2021, (93 – 96 days) for Shendi 2021/2022, (105 - 108 days) for Hudeiba 2020/2021, (105 – 114 days) for Dongola 2021/2022 and (101 – 103 days) for the average of environments (Table 5). Generally, the G2 was the earliest to reach 90% maturity as compared with the two checks (Turkey) and Shandi).

Plant Height (cm)

The plant height of tested genotypes across three environments was no significant Table (6). At Dongla 2021/2022, the G5 was the tallest (110 cm), while G11 was the shortest (82 cm) (Table 6). At Shendi 2021/2022 the tallest plant height (135 cm) was G1 (C.2/2), where the shortest one (105 cm) was G11. At Hudeiba 2020/21, it was ranged from 68 cm for G7 to 84 cm for Basabeer
(Check).

Number of Pods Per Plant

The significant differences between the genotypes for number of pods per plant were only found in Dongla 2021/22 environment (Table 7). The number of pods per plant is an important selection criterion for the development of high yielding genotypes and is strongly influenced by the environment in faba bean [17]. The number of pods per plant ranged from 13 - 27 at Dongla 2021/22, from 25 – 44 at Hudeiba 2020/21 and from 28 – 43 at Shendi 2021/22. Over all environments, G6, G8 and G1 gave the highest number of pods per plant. The lowest number of pods per plant was recorded by the check Turkey and G7.

100 - Seed Weight (g)

Highly significant differences ($P \leq 0.001$) among genotypes were found in 100 – seed weight across the five environments (Table 8). These results are in agreement with those of [18]. The genotype G2 and the check Turkey recorded the heaviest 100 - seeds weight (79 g). On the other hand, the G3 and G4 gave the lowest value of 54 g. The genotypes; G2, G7, G10 and G9 (Turkey) recorded high seed weight at all sites (Table 8).

AMMI Model and the AMMI Stability Value (ASV)
The AMMI analysis of variance of seed yield (t ha-1) of 11 faba bean genotypes evaluated in 5 environments is presented in Table 9. Highly significant effects of the environment (E), GxE interaction, and genotypes (G) had been observed by AMMI analysis. Environment explained significantly 73.83% and genotypes contributed only 9.54%of the total sum of squares. The GxE interaction accounted for 16.63% indicated that the best genotype in one environment is not necessarily the best in another. Therefore, while recommending promising genotypes to an environment we need to consider their adaptability and stability into account. To further partition the multiplicative variance of the genotype sum of squares caused by GEI, interaction principal component analysis (IPCA) was employed. The first two multiplicative terms explained 85.47% of GxE interaction (Table 9). These are in agreement with the recommendation of who recommended that the most accurate model for AMMI can be predicted using the first principal components (IPCAs) [19].

AMMI stability values (ASV) revealed variations in yield stability among the eleven faba bean genotypes (Table 10). According to, a stable variety is defined as one with ASV value close to zero. Consequently, the G4 with ASV value of 0.943 was the most stable after the G8 (Shandi check) with ASV value of 0.247, while the other genotypes G1, G11 and G9 (Turkey check) were the least stable (Table 10) [20].

The best four genotypes in each environment for seed yield according to AMMI selections showed that the genotypes G1, G11 and G4 were best adapted at three environments. Whereas, the genotypes G2 and G10 were best adapted at two environments (Table 11).

AMMI Biplot Model

According to AMMI1 biplot model, the genotypes with PC1 scores close to zero expressed general adaptation whereas the larger scores are for more specific adaptation to particular environments [21]. The AMMI1 biplot model that shows both main and interaction effects clustered the testing environments into four groups. Dongla 2021 and Hudeiba 2020 environments clustered as one group positioned on the up-right side of the graph indicating they are favorable environments. Similarly, the Dongla 2020 demon strated as favorable environment located in down-right side of the graph. Shendi 2020 and Shendi 2021 were identified as low yielding environments with different IPCA score (Figure 1).

The AMMI1 biplot graph displayed the superior and high yielding genotypes C.2/2, (Elarkey 82 and Gelass 36 on the up-right side of the graph. Also, the high yielding genotypes Basabeer (check), C.5 and Gelass 2 were situated in down-right side of the environment Dongla 2020. The genotypes; Shandi (check), C.3/3), Gelass 35 and Elarkey 48 were stable as it revealed low PC1 score (Figure 1).

Using the test for angles between location vectors AMMI2 graph, three groups of the four environments were formed. It was found that the first group had a minimal angle between Dongla 2020 and Hudeiba 2020. The second group was formed between Dongla 2021 and Shendi 2021. Shendi 2020 was clustered individually (Figure 2). According to AMMI2 model; the genotypes C.2/2 and Gelass 36 showed general adaptability to Dongla 2020, Hudeiba 2020 and Dongla 2021. The genotype Elarkey 82 was specific adaptation with the environment Dongla 2020. The genotypes Basabeer (check), C.5, Gelass 2 and Turkey (check) explained general adaptability to Dongla 2020, Hudeiba 2020 and Shendi 2020 (Figure 1).

Conclusions

Based on the results obtained in this study, the following conclusions could be drawn:-

- A wide range of variability in performance was observed among the tested faba bean genotypes in this study.
- The significant environments, genotypes and genotypes x environment interaction indicated wide differences between environments and differential genotypic behavior under the test environments.
- Genotype and environment main effects and genotype by environment interaction effects were significant for seed yield of the eleven faba bean genotypes evaluated in this study.
- The four genotypes no. 1, 4, 2 and 10 were performed better than the standard check Turkey with seed yield advantage of 15.7%, 12.6%, 12.3% and 11.8% respectively.
- The two genotypes no. 2 and 10 gave significantly heavier seed weight than the two standard checks, Basabeer and Shandi.
- Both AMMI and GGE-biplot analyses showed that G1, G2 and G10 as the higher yielding and stable over most of the environments covered by the current study. These three genotypes were released in 22 June 2025 for commercial production under winter irrigated conditions in the River Nile and Northern States of the Sudan.

Table 2: Mean of seed yield (t ha-1) of eleven faba bean genotypes tested across five different environments.

Genotype	Dongla 2020/21	Shendi 2020/21	Hudeiba 2020/21	Dongla 2021/22	Shendi 2021/22	Combined
C.2/2	3.85	2.3	4.31	4.53	1.8	3.36
Elarkey 82	3.62	2.58	3.48	4.6	1.85	3.23
C.3/3	2.5	2.28	2.56	3.28	1.73	2.47
C.5	4	3.45	3.24	3.75	1.75	3.24
Gelass 35	3.52	2.55	2.52	3.8	1.6	2.8
Basabeer (check)	4.3	3.78	3.45	3.88	1.53	3.39
Elarkey 48	3.4	2.5	2.66	3.68	1.4	2.73
Shandi (check)	3.82	2.7	3.37	3.73	1.53	3.03
Turkey (check)	3.52	3.25	2.93	3	1.45	2.83
Gelass 36	4	2.45	3.83	4.23	1.53	3.21
Gelass 2	3.75	3.7	3.72	2.95	1.63	3.15
Mean	3.66	2.87	3.28	3.76	1.62	3.04
S.E ±	0.267***	0.244***	0.292***	0.330***	0.083**	0.303*
C.V (%)	10.3	12.1	12.6	12.4	7.3	31.6

*, ** and *** Significant at 0.05, 0.01 and 0.001 levels of probability, respectively.

Table 3: Percentage increase in seed yield of the newly five promising faba bean genotypes over the two standard checks across the five environments.

Genotype	S.Y (t ha-1)	Increase over the two checks	
		Turkey	Shendi
G1 (C.2/2)	3.36	15.8	9.8
G4 (C.5)	3.24	12.6	6.5
G2 (Elarkey 82)	3.23	12.4	6.2
G10 (Gelass 36)	3.21	11.8	5.6
G11 (Gelass 2)	3.15	10.2	3.8
G9 (Turkey check)	2.83		
G8 (Shandi check)	3.03		

Table 4: Mean of days to 50% flowering of eleven faba bean genotypes evaluated in Hudeiba location during season 2020/21 and over two locations Dongla and Shendi during season 2021/22.

Genotype	Shendi 2020/21	Hudeiba 2020/21	Dongla 2021/22	Shendi 2021/22	Combined
C.2/2	41	40	38	39	39
Elarkey 82	38	38	35	35	36
C.3/3	40	38	38	37	38
C.5	43	38	36	37	38
Gelass 35	43	36	35	36	37
Basabeer (check)	39	37	36	37	37
Elarkey 48	43	36	33	36	37
Shandi (check)	41	39	38	36	39
Turkey (check)	43	36	37	36	38
Gelass 36	40	37	36	35	37
Gelass 2	41	42	37	36	39
Mean	41	38	36	36	38
S.E ±	1.636*	1.192***	0.888***	0.361***	0.988*
C.V (%)	5.6	4.4	3.5	1.4	7.3

*, *** Significant at 0.05 and 0.001 levels of probability, respectively.

Table 5: Mean of days to 90% maturity of eleven faba bean genotypes evaluated in Hudeiba location during season 2020/21 and over two locations Dongla and Shendi during season 2021/22.

Genotype	Shendi 2020/21	Hudeiba 2020/21	Dongla 2021/22	Shendi 2021/22	Combined
C.2/2	99	108	111	96	103
Elarkey 82	102	106	105	94	101
C.3/3	102	105	111	95	103
C.5	101	105	113	95	104
Gelass 35	98	106	111	93	102
Basabeer (check)	101	107	106	95	102
Elarkey 48	98	106	114	94	103
Shandi (check)	99	109	105	95	102
Turkey (check)	100	107	111	95	103
Gelass 36	99	107	113	95	103
Gelass 2	100	105	113	95	103
Mean	100	106	110	94	103
S.E ±	1.260*	0.815***	2.030***	0.478***	2.379 n.s
C.V (%)	1.8	1.1	2.6	0.7	6.5

*, *** Significant at 0.05 and 0.001 levels of probability, respectively.
n.s: not significant at 0.05 level of probability.

Table 6: Mean of plant height (cm) of eleven faba bean genotypes evaluated in Hudeiba location during season 2020/21 and over two locations Dongla and Shendi during season 2021/22.

Genotype	Hudeiba 2020/21	Dongla 2021/22	Shendi 2021/22	Combined
C.2/2	82	93	135	103
Elarkey 82	76	89	129	98
C.3/3	75	93	125	97
C.5	75	83	124	94
Gelass 35	79	100	116	98
Basabeer (check)	84	96	126	102
Elarkey 48	68	86	111	88
Shandi (check)	81	86	130	99
Turkey (check)	72	83	107	87
Gelass 36	77	88	121	95
Gelass 2	78	82	105	88
Mean	77	89	121	96
S.E ±	3.430**	5.16*	3.613***	8.49 n.s
C.V (%)	6.3	8.2	4.2	21.7

*, ** and ***Significant at 0.05, 0.01 and 0.001 levels of probability, respectively.
n.s: not significant at 0.05 level of probability.

Table 7: Mean of number of pods per plant of eleven faba bean genotypes tested across five different environments.

Genotype	Dongla 2020/21	Shendi 2020/21	Hudeiba 2020/21	Dongla 2021/22	Shendi 2021/22	Combined
C.2/2	13	29	44	23	43	30
Elarkey 82	16	24	28	17	39	25
C.3/3	14	23	30	27	36	26
C.5	16	25	33	21	28	25
Gelass 35	11	27	25	20	39	24
Basabeer (check)	19	21	43	24	43	30
Elarkey 48	13	29	23	20	30	23
Shandi (check)	20	24	41	26	41	30
Turkey (check)	8	28	29	13	35	23
Gelass 36	15	23	36	21	28	25
Gelass 2	19	29	34	23	37	28
Mean	15	25	33	21	36	26
S.E ±	2.316***	2.349*	7.44*	4.79 n.s	3.960**	3.417 n.s
C.V (%)	21.4	12.8	31.2	31.1	15.3	40.5

*, ** and *** Significant at 0.05, 0.01 and 0.001 levels of probability, respectively.
n.s: not significant at 0.05 level of probability.

Table 8: Mean of 100 – seed weight (g) of eleven faba bean genotypes tested across five different environments.

Genotype	Dongla 2020/21	Shendi 2020/21	Hudeiba 2020/21	Dongla 2021/22	Shendi 2021/22	Combined
C.2/2	53	55	62	54	53	56
Elarkey 82	83	82	84	77	71	79
C.3/3	52	59	54	58	48	54
C.5	57	55	53	54	51	54
Gelass 35	99	56	75	86	47	72
Basabeer (check)	52	71	54	57	49	56
Elarkey 48	63	54	59	58	67	60
Shandi (check)	53	61	54	56	49	55
Turkey (check)	97	53	114	74	58	79
Gelass 36	65	82	72	62	51	66
Gelass 2	62	58	61	53	57	58
Mean	67	62	67	63	54	63
S.E ±	4.206***	4.617***	5.04***	5.61***	2.257***	3.785***
C.V (%)	8.8	10.4	10.5	12.6	5.8	18.9

*** Significant at 0.001 level of probability.

Table 9: ANOVA of additive main effects and multiplicative interaction (AMMI) on seed yield ($t\ ha^{-1}$) of eleven faba bean genotypes grown across five environments.

Source of variation	DF	Sum of Squares (SS)	Mean of Squares (MS)	Percent explained
Total	219	208.70	208.70	
Treatments	54	180.42	3.341***	
Genotypes	10	17.21	1.721***	9.54
Environments	4	133.21	33.303***	73.83
Block	15	8.30	0.554***	
Interactions	40	30.00	0.750***	16.63
IPCA 1	13	19.00	1.462***	63.64
IPCA 2	11	6.64	0.604***	22.13
Residuals	16	4.36	0.272***	2.42
Error	150	19.98	0.133	

* * * significant at 0.001 levels of probability.

Table 10: Estimates of stability parameters for yield (t ha-1) of eleven faba bean genotypes tested across five environments.

Genotype	Mean	Rank (RSY)*	IPCA		ASV	
			IPCA1	IPCA2	Value	Rank (RASV)
C.2/2	3.36	2	0.73315	-0.47209	2.151	11
Elarkey 82	3.23	4	0.53721	0.17169	1.547	8
C.3/3	2.47	11	0.09524	0.59304	0.653	4
C.5	3.24	3	-0.32839	0.07319	0.943	5
Gelass 35	2.80	9	0.08748	0.47131	0.534	3
Basabeer (check)	3.39	1	-0.44488	-0.17347	1.285	6
Elarkey 48	2.73	10	0.08069	0.27912	0.362	2
Shandi (check)	3.03	7	0.06360	-0.16698	0.247	1
Turkey (check)	2.83	8	-0.55677	0.02462	1.594	9
Gelass 36	3.21	5	0.44712	-0.40208	1.341	7
Gelass 2	3.15	6	-0.71446	-0.39835	2.083	10

Rank (RSY)* = rank in seed yield, IPCA 1 and IPCA 2 = interaction principal component axis 1 and 2, ASV = AMMI stability value, RASV = rank of AMMI stability value.

Table 11: The best four genotypes in each environment for seed yield according to AMMI selections.

No.	Environments	Estimated yield (t ha^{-1})	Score	Best four genotypes			
				1st	2nd	3rd	4th
1	Dongla 2020	3.66	-0.1697	G6	G11	G1	G4
2	Hudeiba 2020	3.28	0.2839	G1	G10	G6	G11
3	Shendi 2020	2.87	-1.1063	G11	G6	G4	G9
4	Dongla 2021	3.76	0.9168	G1	G2	G10	G8
5	Shendi 2021	1.62	0.0753	G2	G4	G6	G5

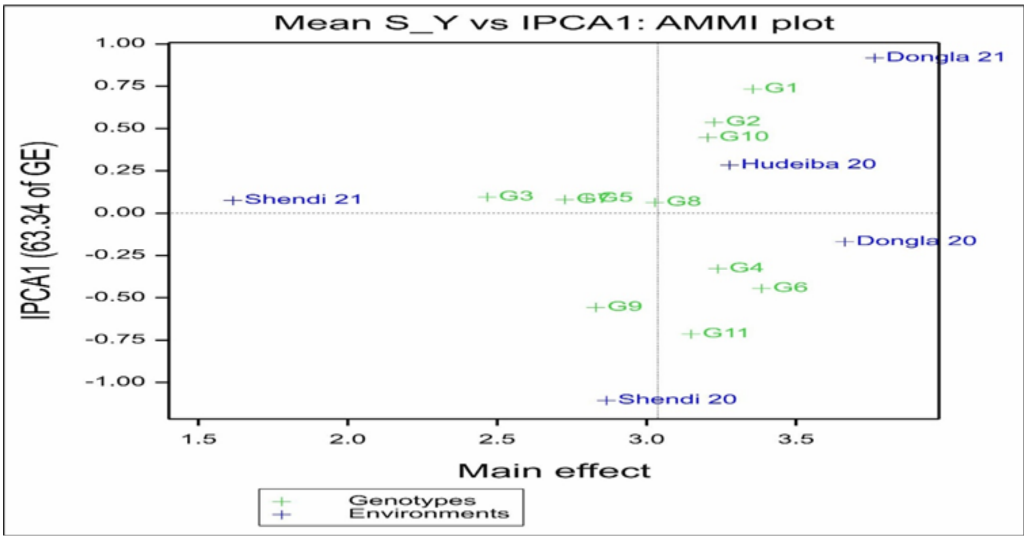

Figure 1: AMMI1 graph of the first interaction principal component axis (IPCA1) for mean seed yield (t ha^{-1}).

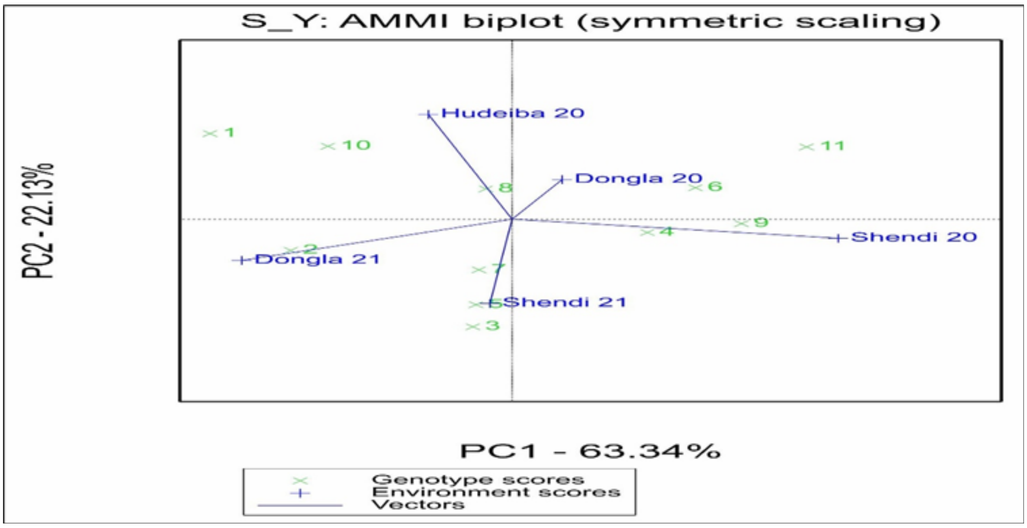

Figure 2: AMMI2 graph of the first interaction principal component axis (IPCA1) versus the second interaction principal component axis (IPCA2) for seed yield (t ha-1).

Acknowledgement

The authors are thankful to our collaborators at a number of research stations including Hudeiba, Dongola and Shendi. We are also thankful to the supporting staff at all research station where these experiments were executed.

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