Evaluation of AdvancedFaba Bean (*Viciafaba* L.) Genotypes for Yield and Yield Related Traits underHigh Potential Environments.

Abstract

~~We~~ evaluated Twenty two (22) advanced F~~f~~aba bean genotypes included two standard checks were evaluated using RCBD design with two replicationsat four testing locationswith the objectives of to evaluate genetic variability, assess associations of characters,~~and to~~ estimate the effects of genotype, environment, and genotype x environment interaction on grain yield.The ANOVA result showed highly significant ($p<0.01$*) differences were recorded among genotypes and location for days to flowering, days to maturity, plant height, number of pods per plant,~~and~~ disease data and grain yiled.~~Grain yield only showedhighly significant (p<0.01) variations among testing locations, indicating that diverse responses of genotypes across locations.~~From AMMI analysis, environment, genotype and their interaction had about 59%, 4.1% and 11.4% contributions of the total sum of squares respectively.Result indicated that the environments were diverse and causing most of the variation in genotypes.Genotypic coefficient of variation were recorded from the lowest to medium GCV for days to maturity and thousand seed weight respectively. Higher heritability values were estimated from days to flowering, plant height, number of pod per plant and thousands seed weight, indicating that the direct selection of this traits can be practiced in the evaluation of advanced F~~f~~aba bean genotypes. Grain yield showed highly significant (*$p<0.01$*) and positive associations with traits of number of pods per plant this indicates that direct effects of traits on grain yield. According to AMMI2 biplot, the first two IPCA cumulatively accounted about 87.4% of the total genotype environment interactions, the first IPCA1 and second IPCA2 described about 53% and about 34.3% of the total sum square of genotype × environment interaction. Based on ASV scores the genotypes *G_8, G_5 *and* G_{19}*had the lowest ASV score, thus which were the most widely stable genotypes across environments.*

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Key words:genotypic variance, heritability, genetic advance, variability, Interaction, AMMI, IPC, ASV

1. Introduction

Fababean (*Viciafaba* L.) is the most important pulse crops widely grown in Ethiopia,usually under rain fed conditions. Ethiopia is the first faba bean growers in Africa and the second most faba bean producer in the world next to China (FAO, 2019). The crop grows widely with an altitude of from 1800 to 3000 meter above sea level and annual rainfall of 700 to 1100 mm.In Ethiopia, F~~f~~aba bean land coverage and production were about 30% and 35% of the total pulse area and total production respectively (CSA, 2020).Faba bean have a majorrole in the community of the country as a source good protein, starch, and minerals for human beings (Hacıseferoğulları*et al*., (2003).

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In recent year, F~~f~~aba bean production and productivity had substantially increaseddue to superiorattentions on varietal release and developments with high grain yield, large seed size,and resistance to both biotic and abiotic constraint (Keneni*et al*., 2016). Butits productivityis mostlylimited by different production factors including use of less productive varieties, acidity, drought, chocolate spot, rust and the absence of genetic diversity on gene pools for improvement in the breeding programs. In addition, Ethiopia have diverse agro ecological conditionhence, the absence of F~~f~~aba bean genotypeswhich perform stable across environments and growing season is the main concern and problems for production.

Genotypic improvement of F~~f~~aba bean varieties through hybridization across environment and seasons is the basic strategy for breeders to the increment of grain yield. The more the diverse parents, the more the chance of improving the traits under consideration.Hence, selection of better crossing materials from the gene pool is crucial, so the presence of sufficient and desirable genotypic variability among genotypes and heritable traits must be exist (Holeme*et al*., 2019). In agreement to this different researcher in their study reported the presence of highly significant genotypic difference among evaluated F~~f~~aba bean genotypes (Temesgen*et al.*, 2023, Hiywotu*et al.*, (2022), Beyene*et al.*, 2018, Takele*et al.*, (2024)). In view of this, the current researchexperiment was conducted with the objective of studying genetic variability, character relations of traitsand estimate the effects of genotype, environment, and genotype x environment interaction on grain yield.

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2. Materials and Methods

2.1. Description of the study area

The field experiments were conducted at four testing locations namelyKulumsa, Bekoji, Asasa and Kofele during 2018/19 main cropping seasons (June-August). A detail information about the locations was described in Table 1 below.

Table 1:Full descriptions of the experimental locations

Location	**Latitude**	**Longitude**	**Altitude**	**Mean annual rainfall**	**T^0**		**Soil type**
					Min	Max	
Kulumsa	0801'10"N	3909'11"E	2200	820	10.5	22.8	clay
Bekoji	0732'37"N	3915'21"E	2780	1020	7.9	18.6	clay
Asasa	0707'09"N	3911'56"E	2340	620	5.8	23.6	clay loam
Kofele	0704'28"N	3847'11"E	2660	1211	7.1	18	Heavy clay

Min =minimum, Max= maximum

2.2. Experimental materials

A total of twenty two advancedF~~f~~aba bean genotypes including two standard check (Gora and Tumsa)wereused for this ~~experiment~~ trail. List of genotypes were presented in Table 2.

Table 2: Lists of evaluated experimental materials (genotypes)

Entry	**Variety name**	**~~Remark~~**	**Entry**	**Variety name**	**~~Remark~~**
G_1	Gora	~~Check~~	G_{12}	EH 06027-2	~~candidate~~
G_2	EK 05024-3	~~candidate~~	G_{13}	EH 06007-2	~~candidate~~
G_3	EK 05006-3	~~candidate~~	G_{14}	EH 06084-5	~~candidate~~
G_4	EK 05023-1	~~candidate~~	G_{15}	EH 06088-6	~~candidate~~
G_5	EK 05001-1	~~candidate~~	G_{16}	EH 07015-7	~~candidate~~
G_6	EK 05035-3	~~candidate~~	G_{17}	EH 06070-3	~~candidate~~
G_7	EK 05037-4	~~candidate~~	G_{18}	EH 07023-3	~~candidate~~
G_8	EK 05037-5	~~candidate~~	G_{19}	EH 06006-6	~~candidate~~
G_9	EH 06031-3	~~candidate~~	G_{20}	EH 06025-2	~~candidate~~
G_{10}	EH 06007-4	~~candidate~~	G_{21}	EH 06029-1	~~candidate~~
G_{11}	EH 07023-6	~~candidate~~	G_{22}	TUMSA	~~Check~~

G= genotypes

2.3. The experimental designs and field trial Management

~~The experiment was done in main cropping season of mid-June to Novemberat 2018/19.~~ The trials was conducted using randomized completed block design (RCBD) with two replications. The plot size have 4m length and 0.8m in width, which is 3.2m^{2}area. The spacing between rows and plants were 0.4m and 0.1m respectively. Each experimental plots have 2 rows and the spacing between plots are 0.6m in order to separate twogenotypes and for trial management.Row planting was done by drilling the seeds at randomly allocated plots at each locations and 121 kg ha-1 rates of NPS fertilizer was applied. All agronomic practices was uniformly applied at each treatment, replications and locations.

2.4. Data collected

Data was collected from the whole experimental plot and from five randomly selected F~~f~~aba bean plants.

2.4.1. Data collected from the whole experimental plot basis

Days to 50% flowering (FLD), days to 90% physiological maturity (MTD), grain yield in hectare (GYH), chokolate spot (CHS), root rot (RR) and rust

2.4.2. Data collected on sample plant basis

Thousand seed weight (TSW), number of pods per plant (NPP),plant height (PLH),

2.5. Data analysis

2.5.1. Statistical analysis

The statistical analysis of variance (ANOVA) for combined data over location were calculated using R software version 4.4.0 with packages “*agricolae*” and “*metan*”. The following RCBD models were used for combined analysis.

$$Yij = \mu + Gi + Ej + GEij + \beta(E)jk + \varepsilon ijk$$

Where; Y_{ij} is the grain yield of the ith genotype in the jth environment, μ = the grand mean, G_i = the effect of the ithgenotype, E_j = the effect of the jth environment, GE_{ij} = the interaction of the ith genotype with the jthenvironment, (E) = the effect of the kth replication in the jth environment, and ε_{ijk} = the error.

2.5.2. Estimation of genetic parameters

The genetic parameters (genotypic variance, phenotypic variance, H^{2}b,GCV, PCV, GA and GAM) were estimated using the following equations;

$$\sigma^2 g = \frac{MSg - MSg*l}{rl},\ \sigma^2 g*l = \frac{MSg*l - MSe}{r},\ \sigma^2 p = \sigma^2 g + \frac{\sigma 2p}{rl} + \frac{\sigma 2g*l}{l},$$

$$PCV = \frac{\sqrt{\sigma 2p}}{\ddot{X}} * 100, GCV = \frac{\sqrt{\sigma 2g}}{\ddot{X}} * 100, H^2b = \frac{\sigma 2g}{\sigma 2p} * 100,$$

$$GA = K*\sqrt{\sigma 2p} *H^2b,\ GAM = \frac{GA}{\ddot{X}}*100$$

*Where, σ^2g =genotypic variance, σ^2e =environmental variance, σ^2p = phenotypic variance, MSg =mean square due to genotypes, MSe =error mean square, r =number of replication, MSg*l =mean square due* *to genotypes X location, l =number of environment, PCV =phenotypic coefficient of variation, GCV =genotypic coefficient of variation,* H^2b *= heritability in broad sense, GA =genetic advance, K=Selection differential at 5 % selection intensity which accounts to a constant value 2.063, GAM =genetic advance as percent of mean, Ẍ =population Mean.*

2.5.3. Estimation of genotypic and phenotypic correlation coefficient

The phenotypic and genotypic associations of grain yield per hectare with other agronomic traits were estimated using the following function of R software using the “stats” package;

Phenotypiccorrelationcoefficient (rpxy)= $\frac{Pcovxy}{\sqrt{(\sigma 2px)(\sigma 2py)}}$

Genotypiccorrelationcoefficient(rgxy)= $\frac{Pcovxy}{\sqrt{(\sigma 2px)(\sigma 2py)}}$

2.5.4. AMMI Model Analysis

The Additive main effects and multiplicative interaction (AMMI) model was performed the following models (Gauch, 1992).

$$Y_{ij} + \mu + G_i + E_j + \left(\sum_{k=1}^{n} \lambda_k \alpha_{ik} \gamma_{jk}\right) + \varepsilon_{ij}$$

where Y_{ij} *= is the yield of the* i^{th} *genotype in the* j^{th} *environment; μ = is the grand mean;* G_i*and* E_j*are the genotype and environment deviations from the grand mean, respectively;* λ_k *= is the eigenvalue of the PCA analysis axis k;* α_{ik} *and* $\boldsymbol{\gamma}_{ik}$ *= are the genotype and environment principal component scores for axis k; n is the number of principal components retained in the model, and* e_{ij} *is the error term.*

AMMI Stability Value (ASV) which is the distance from the coordinate point to the origin in a two-dimensional of IPCA1 score against IPCA2 scores wereestimated as using the following formula (Purchase *et al.*, 2000).

$$ASV = \sqrt{\left[\frac{IPCA1\ sumsquares}{IPCA2\ \ sumsquares}(IPCA1score)\right]^2 + \left[\ IPCA2score\right]^2}$$

Where: IPCA1 = interaction principal component axis 1, IPCA2 = interaction principal component axis 2.

3. Results and Discussions

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3.1. Analysis of variance (ANOVA)

~~The combined analysis of variance (ANOVA) results were presented in Table 3 below.~~The result showed that highly significant ($p \leq 0.01$) and significant ($p \leq 0.05$) variations were recorded for flowering day, days to maturity, plant height, pods per plant, thousand seed weight, chocolate spot, root rot and rust while,grain yield does not showed variation among the F~~f~~aba bean genotypes. These significant differences of traits on genotypes indicated that the presence of wide genetic variability among genotypes.The presence of variability in the genotypes have opportunity to researchers in improvement of grain yield and its component traits through selection and hybridization.Significant ($p<0.05$) and highly significant ($p<0.01$) variations were previously reported by Temesgen*et al.*, (2023) for grain yield, thousand seed weight, pods per

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plant, plant height, days to flowering and 90% physiological maturity. Similar results were also presented by Hiywotu*et al.*, (2022) for days to flowering, days to 90% physiological maturity, plant height, thousand seed weight and number of pods per plant. Keneni~~&~~andJarso (2009) also reported the presence of highly significant genotypic variability for grain yield and thousand seed weight.Beyene*et al.*, (2018) reported significant differences of chocolate spot disease reactions on F~~f~~aba bean genotypes.

Table 3:ANOVA mean square of~~nine~~F~~f~~aba bean traits for combined locations.

Source of variation	Genotype	Location	Location : Replication	Genotype: Location	Residuals
Traits	Df=21	Df=3	Df=4	Df=63	Df=84
FLD	55.41***	410.9***	2.2^{ns}	2.5***	1.0
MTD	92.60*	20276.3***	22.7^{ns}	45.4^{ns}	45.9
PLH	323.19***	2814.4***	134.2^{ns}	81.8^{ns}	81.3
PPL	29.2***	239.2***	12.3^{ns}	6.8^{ns}	9.3
TSW	113440.4***	312530.1***	243.8^{ns}	5548.4^{ns}	4307
GYH	1089833^{ns}	110355979***	1597664^{ns}	1011132^{ns}	868070
CHS	1.82***	25.7***	1.1*	0.6^{ns}	0.4
RR	0.34*	4.0***	0.2^{ns}	0.2^{ns}	0.2
Rust	1.27***	43.4***	6.4***	0.4^{ns}	0.3

FLD= days to flowering, MTD= days to 90% physiological maturity, PLH= plant height, PPL= number of pods per plant, TSW= thousand seed weight, GYH= grain yield, CHS= chocolate spot, RR= root rot, Df = degree of freedom, ***= highly significant, *=significant difference, ns= non-significant difference

Testing locations also revealed highly significant differences(p<0.01) for all evaluated traits, this indicates that the differences of phenotypic performance across the four environments.The interaction effects of genotypes × locations showed that a highly significant (P<0.05) effects on the performances of F~~f~~aba bean genotypes for all observed traits (Table 3). This result implies that the diverse responses of genotypes for those traits at each testing environments. In agreement to this finding,Temesgen*et al.*, (2023) reported significant genotype × location interaction for grain yield, thousand seed weight, plant height, pods per plant, and days to 90% physiological maturity and days to flowering.

3.2. Range and mean performances of genotypes

~~The range and mean performances of 22 genotypes for nine traits were presented in Table 4 below.~~The result showed that significant variations among the genotypes for grain yield, combined mean grain yield were ranged from 4,503 kg ha^{-1} to 6,207 kg ha^{-1}. The maximum mean grain yield were recorded from G_9(6,207 kg ha^{-1}) followed by G_4 (6,064 kg ha-1), G_1 (5,820kh ha-1), G_5 (5,618 kg ha-1) and G_{13} (5,569 kg ha-1).Only two genotypes G_9 (6,207 kg ha-1) and G_4(6,064 kg ha-1) which showed better mean grain yield performance than standard check Gora (5,820 kg ha-1) and Tumsa (5,147 kg ha-1). ~~It~~ This implies that the presence of promising advanced F~~f~~aba bean genotypes which release as variety for commercial production. Days to 50% flowering was also ranged from 48 days (G_{11}) to 57 days (G_{21}) after dates of sowing with a mean of 52 days. The 22 genotypes days to 90% physiological maturity were

Comment [E5]: Please white full name ranging from 143 days to 155 days after days of planting. Genotypes G_{21}, G_{10}, G_{13}, G_{15} and G_{14} have a physiological maturity of 152 days and above starting from sowing time, while G_9, G_4, G_3, G_{18} and G_{11} have physiological maturity of below 145 days from days to planting.

Thousand seed weight showed a highly significant variation and ranged from 658 g to 1,077 g with a mean of 867 g. Three genotypes, G_{18}, G_{14} and G_{13} have scored ~~more~~ highthousand seed weight with a value of 997 g, 1,001 g and 1,077 g respectively. Genotype G_5, G_8, G_{22}, and G_3 have relatively small seed weight and have less than 740 grams.More than 50% of the evaluated genotypes has scored better seed weight than standard check Gora and Tumsa. Number of pods per plant also ranged from 10 pods to 14 pods with an average of 14 pods. Three genotypes namely G_5, G_4 and G_2 have the maximum number of pods per plant as compared to other evaluated genotypes, while minimum number of pods per plant were recorded from G_{13}, G_{17} and G_{14} and scored less than 11 pods per plant. This traits have a great and significant role on the selection of best yielding F~~f~~aba bean genotypes thus special focus should giveat times selection and hybridization. Plant height ranged from 127 cm to 151 cm with a mean of 139 cm. The highest was recorded from G_{21} (151 cm) followed by G_3 (150 cm) and G_5 (148 cm).

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Table 4: Combined mean performances of 22 F~~f~~aba bean genotypes over locations

Entry	FLD	MTD	PLH(cm)	PPL	TSW(g)	CHS	Rust	RR	GYH(Kg/ha)
G_1	55.1^{c}	148.8^{a-g}	141^{b-f}	14.9^{ag}	877ef	3.6^{def}	3^{c-g}	1.4^{a-d}	5820^{abc}
G_2	51.5^{fgh}	147.4^{b-g}	135^{d-h}	16.9^{a}	771g	4.6^{ab}	3.9^{a}	1.5^{abc}	5493^{abc}
G_3	51.6^{fgh}	143.9^{efg}	149.8^{ab}	15.1^{af}	740gh	3.9^{cde}	3.4^{ad}	1.4^{a-d}	5485^{abc}
G_4	50.1^{ij}	143.5^{fg}	142.5^{af}	16.3^{ab}	768^{g}	4.1^{bcd}	3.5^{abc}	1.3^{bcd}	6064^{ab}
G_5	49.5^{j}	148.4^{a-g}	147^{a-c}	16.1^{a-c}	658^{i}	4.1^{bcd}	3^{c-g}	1.4^{a-d}	5618^{abc}
G_6	51.4^{fgh}	149.6^{a-f}	139^{c-g}	13.1^{c-j}	772^{g}	4.1^{bcd}	3.4^{a-d}	1^{d}	4969^{cd}
G_7	51.5^{fgh}	148.4^{a-g}	144^{a-d}	15.6^{a-d}	775^{g}	4.3^{bc}	3.6^{ab}	1.4^{a-d}	5282^{a-d}
G_8	49.5^{j}	146^{c-g}	139^{c-g}	15.6^{ad}	675^{hi}	5^{a}	3.6^{ab}	1.5^{abc}	5193^{bcd}
G_9	51.1^{gh}	142.8^{g}	132^{gh}	15.4^{ae}	767^{g}	3.5^{ef}	3^{c-g}	1.4^{a-d}	6207^{a}
G_{10}	55.5^{bc}	152.1^{abc}	135^{e-f}	12.8^{d-j}	946^{bcd}	3.6^{def}	2.5^{gh}	1.1^{cd}	5430^{abc}
G_{11}	47.8^{k}	144.8^{d-g}	130.9^{gh}	13.6^{b-i}	844^{f}	4.6^{ab}	3.1^{b-f}	1.75^{a}	5226^{bcd}
G_{12}	53.9^{d}	150.1^{a-f}	142^{a-f}	14.3^{ah}	920^{de}	3.5^{ef}	2.6^{fgh}	1.1^{cd}	5186^{bcd}
G_{13}	53.9^{d}	152.9^{ab}	134^{f-h}	10.4^{j}	1077^{a}	3.5^{ef}	2.5^{gh}	1.1^{cd}	5569^{abc}
G_{14}	52.3^{ef}	154.4^{a}	127.3^{h}	11.1^{ij}	1001^{b}	3.6^{def}	2.8^{e-h}	1^{d}	5393^{a-d}
G_{15}	51^{hi}	153.8^{ab}	131.1^{gh}	12.1^{f-j}	966^{bcd}	3.9^{cde}	3^{c-g}	1.4^{a-d}	5556^{abc}
G_{16}	51.3^{gh}	151^{a-d}	143^{a-e}	13.5^{bi}	958^{bcd}	3.9^{cde}	3.3^{b-e}	1.3^{bcd}	5490^{abc}
G_{17}	52.8^{e}	149.6^{a-f}	138^{d-g}	11^{ij}	934^{cde}	3.4^{ef}	2.8^{e-h}	1.1^{cd}	5558^{abc}
G_{18}	48.1^{k}	144.4^{d-g}	137^{d-g}	12^{g-j}	997^{bc}	4.1^{bcd}	3^{c-g}	1.6^{ab}	5471^{abc}
G_{19}	52^{efg}	150^{a-f}	136^{d-h}	12.5^{e-j}	961^{bcd}	3.5^{ef}	3.3^{be}	1.1^{cd}	5610^{abc}
G_{20}	56.3^{b}	151^{a-d}	132^{gh}	11.8^{h-j}	957^{bcd}	3.3^{f}	2.4^{h}	1^{d}	4942^{cd}
G_{21}	57^{a}	151.5^{abc}	151a	12.3^{f-j}	962^{bcd}	3.1^{f}	2.9^{d-h}	1.1^{cd}	4503^{d}
G_{22}	56^{ab}	150.5^{a-e}	144a-d	14.9^{ag}	737^{gh}	3.6^{def}	2.9^{d-h}	1.1^{cd}	5147^{bcd}
LSD	**0.99**	**6.74**	**8.97**	**3.02**	**65.3**	**0.62**	**0.54**	**0.41**	**926.4**

CV	**1.95**	**4.5**	**6.51**	**20.93**	**7.41**	**16.3**	**18.02**	**32.23**	**17.19**
Mean	**52**	**149**	**139**	**14**	**867**	**4**	**3**	**1**	**5419**

FLD= days to flowering, MTD= days to maturity, PLH= plant height, PPL= number of pods per plant, TSW= thousand seed weight, GYH= grain yield, CHS= chocolate spot, RR= root rot, CV= coefficient of variation, LSD= least significant difference

~~The individual mean grain yieldperformances of 22 advanced faba bean genotypes across four location was presented in Table 5 below.~~From individual location analysis, highest mean grain yield was recorded from Bekoji location with a mean grain yield of 6,951 kg ha-1. These results indicated that Bekoji was the most favorable and ideal testing environments for the evaluation and estimation of advanced genotypes genetic potentials.On the other hand, Kulumsa (6,581 kg ha-1) was the next best favorable environments for the production of F~~f~~aba bean.~~next to Asasa (4,383 kg ha-1) and Kofele(3,760 kg ha-1)~~ (Table 5). The highest grain yield were recorded from G_{12}(8,238 kg ha-1) and G_9 (8,198 kg ha-1) at Bekoji and Kulumsa respectively. From the four locations, Kofele was recorded the minimum mean grain yield of F~~f~~aba bean genotypes with a value mean of 2,404.3 kg ha-1.All minimum yielder genotypes namely G_{21}, G_{12}, G_{16}, G_{14} and G_{10} were recorded from Kofele (Table 5).

Table 5: Mean grain yield (Kg/ha) performance of 22 F~~f~~aba bean genotypes at four locations in 2014.

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Genotypes	Asasa	Bekoji	Kofele	Kulumsa	Mean
G_1	5072	7588	4351	6271	5820
G_2	5195	5665	4218	6895	5493
G_3	4387	6563	3632	7357	5485
G_4	4236	6854	5281	7884	6064
G_5	4608	7310	4202	6351	5618
G_6	4723	5426	3541	6187	4969
G_7	5513	5445	3268	6904	5282
G_8	4433	6678	3051	6609	5193
G_9	5208	7238	4186	8198	6207
G_{10}	3632	7227	4106	6757	5430
G_{11}	5151	7094	3166	5494	5226
G_{12}	3298	8238	3115	6095	5186
G_{13}	3814	8056	3852	6555	5569
G_{14}	3615	7534	3716	6707	5393
G_{15}	4156	6848	3810	7412	5556
G_{16}	3324	7291	4655	6690	5490
G_{17}	3959	7653	3330	7291	5558
G_{18}	5601	6727	3981	5574	5471

G_{19}	4442	6878	3932	7191	5611
G_{20}	4049	7257	3358	5103	4942
G_{21}	3295	6579	2627	5505	4502
G_{22}	4723	6784	3331	5750	5147
Mean	**4383**	**6951**	**3760**	**6581**	**5419**

G= genotype

When ~~we~~ compared the mean performances of advanced genotypes with standard check Gora and Tumsa; five genotypes G_{11}, G_2, G_9, G_7 and G_{18} scored higher grain yield than the standard check Gora at Asasa. At Bokoji only three genotypes namely G_{17}, G_{13} and G_{12} recorded better yield performance than the standard check Gora. Two candidate genotypes G_{16} and G_4 have better yield advantage than the standard check Gora at Kofele. Averagely more than 60% of candidate's genotypes have better yield performance than the standard check Gora at Kulumsa. The mean performance result showed that three promised advanced genotypes namely G_{21}, G_{20} and G_6 which scored maximum grain yield performance that the standard checks Tumsa. In general the result showed that the presence of promising advanced F~~f~~aba bean genotypes for the release/registration of new improved variety for production and cultivation.

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3.3. Estimation of Genetic Parameters

3.3.1. Phenotypic and genotypic coefficient of variation

~~The genotypic and phenotypic coefficient of variation are presented in Table 6 below~~. In this study the phenotypic variance were higher than the genotypic variance implies that the environmental effects and other uncontrolled errors on the phenotypic performance of genotypes. Relatively higher genotypic variances were observed from thousand seed weight and grain yield while minimum value of genotypic variance were observed from disease data (CHS, Rust and RR) and stand counts.

In the present study, genotypic coefficient of variation was ranged from 1.63% for days to maturity to 13.4% for thousand seed weight. Genotypic and phenotypic coefficient of variation values which score more than 20% are considered as high, between 10 and 20 % as moderate and less that 10% scores are low (Deshmukh*et al.*, 1986).According to thiscategories, moderate genotypic coefficient of variation (GCV) were observed from pods per plant, thousand seed weight, grain yield, chocolate spot, rust and root rot.Tadele*et al.*, (2021) reported the same result for number of pods per plant. While lowest genotypic coefficient of variation were recorded from days to flowering, plant height and days to maturity(Table 6). The presence of genotypic coefficient of variation indicated that the presence of genotypic variation among testing genotypes for the selection of F~~f~~aba bean genotypes.In ~~our~~ previous study, lower estimate of genotypic coefficient of variation were recorded for days to maturity and plant height (Kebede*et al.* 2022).

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Phenotypic coefficient of variation were ranged from 2.29% for days to maturity to 16.22% for root rot. Moderate phenotypic coefficient of variation were observed from traits of number of pods per plant, thousand seed weight, chocolate spot, rust and root rot. Other traits showed lower phenotypic coefficient of variation.

3.3.2. Estimation of Heritability and Genetic advance

Heritability values were ranged from 7% for grain yield to 96% for days to flowering. Estimates of heritability in broad sense was categorized as high (>70%), moderate (50 – 70%) and low (<50%) as suggested by Robinson (1966). According to this estimation higher estimates of heritability were estimated from days to flowering, plant height, number of pod per plant and thousands seed weight.Similar results were reported by Chaudhary *et al.*, (2018) for thousand seed weight. Moderate estimates of heritability were recorded from traits of days to maturity, chocolate spot and rust, while the remaining three traits grain yield, stand count and root rot showed the lowest estimates of heritability (Table 6). Similar finding were reported by Hiywotu*et al.*, (2022) and Mulualem (2013) for days to flowering and thousand seed weight. The higher heritability estimates from days to flowering and thousand seed weight showed that direct selection of this traits can be practiced at the phenotypic levels in the selection and evaluation of genotypes.

Genetic advance as percent of mean (GAM) were ranged from 1.01% for grain yield to 26.96% for thousand seed weight. Genetic advance as percent of mean (GAM) was classified as high (>20%), moderate (10 – 20%) and low (<10%) according to Johansen *et al*. (1955). Based on this classification number of pod per plant and thousand seed weight were recorded as higher genetic advance as percent of mean (Table 6). The result implies that we can improvethe genotypes with simple selection of number of pod per plant and thousand seed weight because the traits are controlled by genetic factors.Abo-Hegazy (2022) also reported higher genetic advance result for number of pod per plant. Moderate GAM result were observed from disease data (chokolate spot, root rot and rust). Lower genetic advance as percent of mean were also estimated from days to flowering, days to maturity, plant height and grain yield (Table 6). This result showed that simple selection will not make any improvement for those traits on the performance of this faba bean genotypes. In agreement with this finding, Tadele*et al.*, (2021) reported lower GAM values for days to flowering, days to maturity and plant height.

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Table 6: Estimates of genetic parameters for nine traits

Traits	GV	PV	H	GA	GAM	GCV	PCV
FLD	6.62	6.93	0.96	5.19	9.92	4.92	5.04
MTD	5.90	11.58	0.51	3.58	2.40	1.63	2.29
PLH	30.17	40.40	0.75	9.79	7.07	3.96	4.59
PPL	2.63	3.65	0.72	2.84	20.72	11.84	13.97
TSW	13486	14180	0.95	233.64	26.96	13.40	13.74
GYH	9839	136230	0.07	54.99	1.01	1.83	6.81
CHS	0.16	0.23	0.68	0.67	17.43	10.23	12.38
Rust	0.10	0.16	0.65	0.54	17.61	10.55	13.04
RR	0.02	0.04	0.41	0.17	13.67	10.37	16.22

GV= genotypic variance, PV= phenotypic variance, H= heritability, GA= genetic advance, GAM= genetic advance as percent of mean, GCV/PCV = genotypic and phenotypic coefficient of variance

3.4. Association of characters

3.4.1. Genotypic correlation coefficient

~~The genotypic correlation coefficient of 9 traits was presented in Table 7 below.~~The results of indicated that grain yield showed positive and significant ($p<0.05$) genotypic associations with number of pod per plant, chocolate spot and root rot. This indicates that the improvement through indirect selection of one traits can also result on the increment of grain yield.Temesgen*et al* (2023) reported a significant positive genotypic association of grain yield with number of pods per plant. Negative and highly significant ($p<0.01$) association of grain yield with days to flowering, days to90% physiological maturity and plant height. This negative association of traits with grain yield indicates that an increase in days to maturity, days to flowering, root rot and plant height could result in the decrease of grain yield.

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Table 7: Genotypic associations of F~~f~~aba bean genotypes for nine traits

Traits	FLD	MTD	PLH	PPL	TSW	GYH	CHS	RR	Rust
FLD	1	0.81***	0.19	-0.33	0.33	-0.86***	-0.83***	-0.97***	-0.63**
MTD	0.81	1	-0.42	-0.87***	0.83***	-0.89***	-0.64**	-0.90	-0.83***
PLH	0.17	-0.42	1	0.60**	-0.54**	-0.99***	0.030	0.003	0.378
PPL	-0.33	-0.87	0.60	1	-0.95***	0.57**	0.750	0.79***	0.86***
TSW	0.33	0.83	-0.54	-0.95	1	-0.397	-0.65***	-0.491*	-0.725
GYH	-0.86	-0.89	-0.99	0.57	-0.39	1	0.50*	0.90***	0.282
CHS	-0.83	-0.64	0.03	0.75	-0.65	0.50	1	0.99***	0.90***
RR	-0.97	-0.90	0.003	0.9	-0.49	0.90	0.995	1	0.81***
Rust	-0.63	-0.83	0.38	0.86	-0.73	0.28	0.900	0.812	1

3.5. AMMI analysis

The analysis of variance for additive and multiplicative interaction effect on grain yield showed that significant variation among environments, while non-significant variation were observed among the genotypes and genotype × environment interactions. The result indicated that there is different performance of genotypes over the testing environments. The effect of environment, genotype and genotype × environment interaction accounted about59%, 4.1% and 11.4% of the total sum of squares respectively (Table 8). From the analysis of AMMI result we observed that environment was great source of variation in grain yield but genotype and their interactions effects have little contributions for the observed variation.The same result of high environment contribution for the total variation were reported by Takele*et al.*, (2024) and Achenef and Alemu (2020).

Table 8: AMMI analysis table

Source of variation	Degree of freedom	Sum Square	Mean Square	Proportion
ENV	3	3.31E+08	1.1E+08	
REP(ENV)	4	6390658	1597664	
GEN	21	22886498	1089833	
GEN:ENV	63	63701319	1011132	
PC1	23	33789500	1469109	53%
PC2	21	21873505	1041596	34.3%
PC3	19	8038314	423069.2	12.6%
Residuals	84	72917877	868070	
Total	238	5.61E+08	2355738	

ENV = environment, REP = replication, GEN = genotype, PC = principal component 1,2&3.

3.5.1. AMMI2 biplot

The AMMI2 analysis result showed that the first two IPCA cumulatively accounted about 87.4% of the total genotype × environment interactions. The first IPCA1 explained about 53% of variation and the second IPCA2 explained about 34.3% of the total sum square of genotype × environment interaction. Different scholars ~~faba bean researchers~~Tekalign*et al.*, (2017), Temesgen*et al.*, (2015)and Takele*et al.*, (2024) they reported about 82.6%, 78.89%and 75% of the first two IPCAs contribution of the total genotype × environment interactions respectively. Testing environment Asasa, Bekoji andKulumsa were the most discriminating environment by its long distance from the center origin of the axis, however Kofele had low discriminating environment of genotypes.

Most genotypes were relatively located near to the origin and they are confirmedas low interactions effects or stable over the environments, but G18, G7, G12, G2 are relatively far away from the center of the bi-plot as compared to other genotypes and they are considered as unstableor the presence of strong interactionsp to the differences of testing environments.

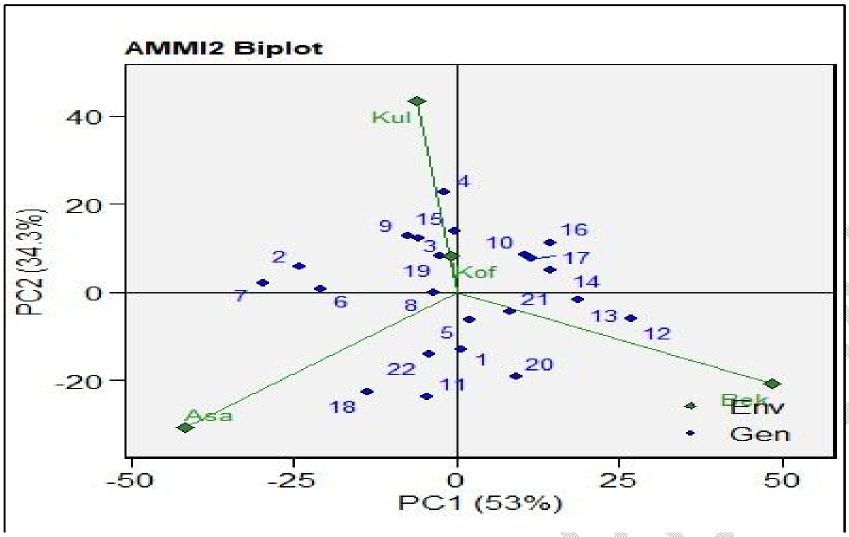

Figure 1: AMMI2

3.5.2. AMMI1 bi-plot analysis

Genotypes which placed on the right side of the midpoint axis have higher yield than genotypes which located on the left sides of the mid line. From the AMMI1 bi-plot figure, theeleven genotypes namely G2, G18, G19, G9, G4, G1, G3, G5, G13, G16 and G17 were recorded as relatively higher grain yield than the other Ffaba bean genotypes which are located on the right side of the grand mean (figure 1). While the other remaining seven genotypes were located on the left side of the grand mean and scored the lowest grain yield.

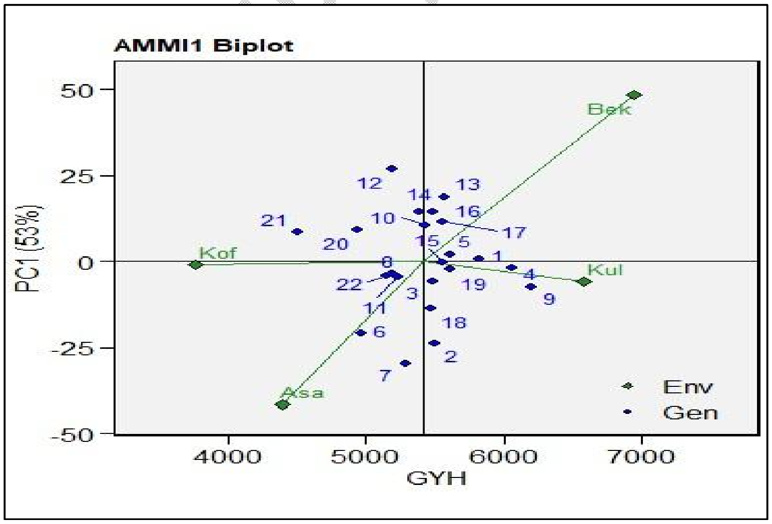

Figure 2: AMMI1 biplot

A high absolute IPC1 score of the genotype far from the origin showed variable performance of the genotype across the environment and they are unstable across environments. In this result G12, G2, G6, G7, G13, G14 and G18 have large magnitude of IPCA1 score that showed high interaction and they are unstable genotypes, while the list magnitude IPCA1 scores recorded from G1, G15, G5, G4 and G19 and they areless interaction effects across environments,theyare more stable genotypes.Asasa and Bekoji scored the highest magnitude of IPC1 value associated with a high mean grain yield indicating that their higher contributions to the genotype × environment andgreat discriminating power of genotypes. The other locations (Kofele and Kulumsa) on the other hand scored lower IPC1 values and have little contribution to the interactions of genotype × environment.

3.5.3. AMMI stability value (ASV)

AMMI stability value (ASV) is the distance from the coordinate point to the origin in a two dimensional scatter diagram of IPC1 scores against IPC2 scores.There for based on ASV scores the genotypes G8, G5 and G19 had the lowest ASV score, thus which were the most widely stable genotypes across environments.However, other remaining nineteen genotypes which scores relatively highest ASV value considered as unstable genotypes across environments (Table 9).

Table 9:Grain yield, ranks by grain yield, AMMI Stability Value (ASV), yield stability index (YSI), ranks by ASV and IPCA1 scores of 22F~~f~~aba bean genotypes tested at four environments

No-	Type	Code	Y	PC1	ASV	YSI	rASV	rYSI
1	GEN	1	5820	0.86	13.04	7	4	3
2	GEN	10	5430	10.52	18.28	23	10	13
3	GEN	11	5226	-4.39	24.63	31	15	16
4	GEN	12	5186	26.98	42.11	39	21	18
5	GEN	13	5569	18.80	29.09	23	17	6
6	GEN	14	5393	14.47	22.90	26	12	14
7	GEN	15	5556	-0.14	13.76	14	6	8
8	GEN	16	5490	14.37	24.91	26	16	10
9	GEN	17	5558	11.62	19.55	18	11	7
10	GEN	18	5471	-13.55	30.71	30	18	12
11	GEN	19	5611	-2.38	9.10	8	3	5
12	GEN	2	5493	-23.92	37.41	29	20	9
13	GEN	20	4942	9.20	23.86	35	14	21
14	GEN	21	4502	8.42	13.74	27	5	22
15	GEN	22	5147	-4.11	15.38	27	8	19
16	GEN	3	5485	-5.71	15.09	18	7	11
17	GEN	4	6064	-1.87	22.96	15	13	2
18	GEN	5	5618	2.18	7.10	6	2	4

19	GEN	6	4969	-20.79	32.12	39	19	20
20	GEN	7	5282	-29.54	45.69	37	22	15
21	GEN	8	5193	-3.61	5.58	18	1	17
22	GEN	9	6207	-7.41	17.15	10	9	1
23	ENV	Asasa	4383.35	-41.59				
24	ENV	Bekoji	6951.43	48.42				
25	ENV	Kofele	3759.59	-0.87				
26	ENV	Kulumsa	6580.78	-5.95				

GEN = Genotypes, ENV = Environments, Y = Yield mean, PC = principal component 1, 2& 3, Y = mean grain yield, ASV = AMMI Stability Value, YSI = yield stability index, r = rank

4. Conclusion

Twenty-twoF~~f~~aba bean genotypes were evaluated at four locations in main cropping season using randomized complete block design to estimate genetic variability, assess associations of traits and to estimate the effects of genotype, environment, and genotype x environment interaction on grain yield. The ANOVA result showed non-significant ($p<0.05$) variations among genotypes.However highly significant ($p<0.01$) variations of environments; thus genotypes had different performances across growing environments. In this study genotypes were better performed at Bekoji and Kulumsa. Maximum grain yield were recorded from genotype G_{12}(8,238 kg ha-1) and G_9 (8,198 kg ha-1) at Bekoji and Kulumsa respectively.

The presence of genotypic and phenotypic coefficient of variation in F~~f~~aba bean breeding have great opportunity in the selection of best performed genotypes, hence the evaluated materials were scored from lowest to medium genotypic coefficient of variation. Highly significant genotypic correlations of grain yield with thousand seed weight were recorded in this study. ~~You~~ should focus special attentions on traits that have significant effects on the improvement of grain yield. The AMMI analysis result showed highly significant environmental effects on the total sum squares of grain yield.AMMI2 biplot showed the first two IPCA cumulatively accounted about 87.4% of the total genotype × location interactions. Most of the genotypes were not stable across the environments. This implies that the differential responses of each genotypes across the four environments.In general ~~we~~ recommended the individual testing of genotypes across locationand growing seasons for better estimation of genotypes performance and stability analysis.

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