Agronomic Performance and Grain Yield Stability of Elite Field Pea (*Pisum Sativum* L.) Genotypes Tested at Various Potential Growing Environments in Ethiopia

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Abstract: Field pea is a multipurpose crop. Despite its diverse benefits, its production and productivity in Ethiopia has remained low compared to its potential due to several biotic and abiotic constraints. Hence, this experiment was carried out with the objective to select best field pea genotypes in terms of yield potential, stability, pest resistance and other desirable agronomic traits for high potential production areas of the country. A total of 17 field pea genotypes including two standard checks, Burkitu and Bursa were arranged in a randomized complete block design with four replications over nine locations in 2019 and 2020 main cropping seasons. The computed analysis of variance showed highly significant differences (p < 0.01) among the genotypes for all studied agronomic traits. One field pea genotype, GPHA-38 found better having 4 and 5% grain yield advantage over the two checks, Bursa and Burkitu, respectively. Additionally, GPHA-38 had comparable performance on the other agronomic traits with standard checks. Moreover, this genotype was found stable in grain yield among the test entries based on GGE biplot stability analysis. However, this genotype may not fulfill the criteria to present as candidate for variety verification trial due to low grain yield advantage and other agronomic traits compared with the checks. Therefore, considering its consistent performance and relatively better yielding capacity, the line GPHA-38 can alternatively be used as a trait donor parent in the pre-breeding programs.

Keywords: Checks, Field pea, Grain yield, GGE biplot, Stable.

INTRODUCTION

Field pea (*Pisum sativum* L.) was a model organism used to discover the laws of inheritance in Mendel's experiment, making the foundation of modern plant genetics (Smýkal *et al.*, 2012). It is belongs to the Leguminosae family, Genus; Pisum, subfamily; Faboideae, tribe; Fabeae. The area of origin and initial domestication of the crop were in the Mediterranean region, particularly in the Middle East (Hagedorn, 1984). In Ethiopia, two botanical cultivars are known to grow, namely P. sativum var Sativum and the native P. sativum var Abyssinicum, (Westphal, 1974). The country has a wide range of field pea germplasm as a result considered as one of the secondary centers of genetic diversity for this crop (Gemechu *et al.*, 2012).

Field pea is an ancient pulse crop grown mainly for human food in Ethiopia (Kefyalew *et al.*, 2017). It is called as "hunger break" crop in highlands of Ethiopia (Asfaw *et al.*, 1997). Also it plays important economic and ecological roles for sustainability of the farming system. It has double advantage in terms of fixing atmospheric nitrogen and a "break crop" to diseases and pests when rotated with cereals and other crops where mono cropping is dominantly practiced (Gemechu *et al.*, 2016). Therefore, the role of pulses in general and field pea in particular as soil fertility restoration in maintaining the sustainability of the farming system is enormous and cost-effective given the alarming price of commercial fertilizers in Ethiopia.

In Ethiopia, the current annual national production of field pea is estimated to 223,657 hectares with a total production of 390,564 tons and average productivity of 1.7 tons per hectare and sharing 14% and 13% in area coverage and production of the total pulses, respectively (CSA, 2019/20). Ethiopia is one of leading producer of field pea in Africa as dry seed, while Canada and China are the largest producers in the world (FAOSTAT, 2017). However, the productivity of the crop is far below its potential due several yield limiting factors.

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Since the beginning of formal research, the national field pea improvement program has made enormous efforts in terms of varietal development using genetic materials of different sources mainly from collections, introductions and hybridization. So far, the program has made list of major achievements and released19improved varieties with their full production packages. The national and regional field pea variety trials were implemented in the breeding program in the national research system since the establishment of formal research system in Ethiopia. However, due to the existing biotic and abiotic constraints, there is an increasing demand for more improved varieties adaptable to the challenging growing conditions. In addition to that, many of so far released cultivars are becoming obsolete and gradually being out of production. The variety development process needs to continue with novel approaches of the modern genomic tools. Hence, in the course of new variety development, important attention should be given to the key economic traits like increased grain yield, large seed size, resistant to major diseases (Ascochyta blight and powdery mildew) and insect pests (field and storage). To this effect, identifying best performing and stable genotypes in grain yield and other important agronomic traits isa prerequisite to develop adaptive field pea genotypes for wider environmental conditions. Therefore, this experiment were conducted with the objective to select field pea genotypes combining desirable agronomic traits (high yield and disease resistance) for potential growing areas of the Ethiopia.

MATERIALS AND METHODS

Planting Materials and Testing Locations

A total of 17 field pea genotypes involving both *kik* and *shiro* types were evaluated along with two standard checks, Burkitu and Bursa (Table 1). The genotypes were evaluated across nine locations Viz. Adet, Areka, Asasa, Bekoji, Dabat, Holetta, Jeldu, Kulumsa and Sinana for two consecutive years during 2019 and 2020 main cropping seasons.

Table 1: Description of 17 field pea genotypes used in the study

No.	Genotype	Code	Status	Type	Source
1	EH 09029-3	G1	Pipeline	*Kiki*	Hybridization
2	GPHA-5	G2	Pipeline	*Kiki*	Gene pool
3	EH 011019-1	G3	Pipeline	*Shiro*	Hybridization
4	GPHA-13	G4	Pipeline	*Kiki*	Gene pool
5	Burkitu*	G5	Released (2008[1])	*Kiki*	Hybridization
6	EH 011028-1	G6	Pipeline	*Kiki*	Hybridization
7	EH 011025-3	G7	Pipeline	*Shiro*	Hybridization
8	GPHA-2	G8	Pipeline	*Kiki*	Gene pool
9	EH 011027-5	G9	Pipeline	*Shiro*	Hybridization
10	GPHA-22	G10	Pipeline	*Kiki*	Gene pool
11	EH 09016-1	G11	Pipeline	*Shiro*	Hybridization
12	EH 011027-4	G12	Pipeline	*Shiro*	Hybridization
13	GPHA-20	G13	Pipeline	*Kiki*	Gene pool
14	GPHA-41	G14	Pipeline	*Shiro*	Gene pool
15	Bursa*	G15	Released (2015[2])	*Shiro*	Hybridization
16	GPHA-38	G16	Pipeline	*Kiki*	Gene pool
17	EH 011020-2	G17	Pipeline	*Kiki*	Hybridization

*, Standard checks;[1, 2]Year of release

Experimental Layout and Design

The genotypes were arranged in a randomized complete block design (RCBD) with four replications. Each genotype was planted in 4 rows of 4 m plot length with inter and intra row spacing of 20 and5 cm, respectively. A recommended rate of NPS fertilizer (121 kgha[-1]) was applied during planting. Weeding and other management practices were carried out as per the national recommendations for field pea uniformly to all plots.

Data Collection and Analysis

Data for all agronomic traits were recorded on plot and plant base from 5 (five) randomly sampled plants. Accordingly, days to 50% flowering, days to 90% physiological maturity, Disease (Ascochyta blight and powdery mildew) scoring (1-9 scale) and grain yield were taken from the entire plot. Traits like plant height, number of pods per plant and number of seeds per pod were recorded on plant basis. Thousand seeds weight was measured from randomly selected 1000 seeds from each plot. Grain yield data adjustments were made by weighing the oven drying and adjusting to a constant moisture level of pulses (10%). For statistical analysis, the average of five sample plants were used and grain yield recorded on a plot basis was converted to kg ha^{-1}.

Data of all traits were subjected to analysis of variance for RCBD as per the procedure of Gomez and Gomez (1984) using SAS software version 9.3 statistical software package (SAS Institute, 2012). For combined analysis of variance, variance homogeneity test was done

using SAS the PROC GLM (General Linear Model) procedure to partition the total variation into components due to genotype (G), environment (E) and G × E interaction effects. Mean separation at 5% probability level was done using least significant difference (LSD), based on significant genotype differences. The total variability for the traits was quantified using pooled analyses of variance across environments using the following model:

$$Y_{ijk} = \mu + G_i + E_j + GE_{ij} + B_{k(j)} + \epsilon_{ijk}$$

Where Y_{ijk} is an observed value of genotype $_i$ in block $_k$ of environment $_j$; μ is a grand mean; G_i is effect of genotype $_i$; E_j is an environmental effect; GE_{ij} is the interaction effect of genotype $_i$ with environment $_j$; $B_{k(j)}$ is the effect of block $_k$ in environment $_j$; ϵ_{ijk} is an error effect of genotype $_i$ in block $_k$ of environment $_j$.

RESULTS AND DISCUSSION
Agronomic Performances

The combined analysis of variance for grain yield of the 17 field pea genotypes tested across 14 environments is presented in Table 2 and other agronomic traits in Table 3. The overall analysis of variance for 9 traits across14 environments showed a highly significant (p ≤ 0.01) variation among the 17tested genotypes for all evaluated traits (DTF, DTM, PHT, PPP, SPP, AB, PM, TSW and GYLD) across locations and year (Tables 2and 3) indicating that the environmental factors were highly contributed for the variation. Similarly, significant variation forDTF, DTM, PPP, SPP and PHT were reported across locations and years (Mulusew *et al.*, 2010).

The mean grain yield of genotypes across environments ranged from 2160kg ha⁻¹ for genotype EH011025-3 to 3109kg ha⁻¹for GPHA-38 followed by 2973 and 2962 kg ha⁻¹ for the standard checks Bursa and Burkitu, respectively. The mean grain yields of

environments were ranged from lowest 1546 kg ha⁻¹ at Asasa 2020 to the highest 4582 kg ha⁻¹ at Sinana 2020 with an overall genotype and environmental mean of 2718kg ha⁻¹ (Table 3). The maximum grain yield 5621 kg ha⁻¹ were recorded for genotype GPHA-38 followed by 5610 kg ha⁻¹ for GPHA-13 at Sinana 2020whereas the minimum grain yield recorded from 1018 kg ha⁻¹for genotype EH011025-3at Adet 2019 (Table 3). Likewise, Sinana was reported as the best yielding environment for field pea (Mulusew *et al.*, 2010).The smallest yield range was obtained from EH011025-3 (2530 kg ha⁻¹) followed by GPHA-20 (2538 kg ha⁻¹) indicating their consistently low grain yield performance across the 14 test environments (Table 3).The standard check Burkitu ranked first in four of the 14 environments (Areka 2019, Asasa 2020, Dabat 2019 and Kulumsa 2019) and Bursa ranked first at three environments (Areka 2020, Dabat 2020 and Sinana 2019). Likewise, one best-performing pipeline genotypeGPHA-38 ranked first at Jeldu 2019 and Sinana 2019. GPHA-38 had the top grain yield of 5621 kg ha⁻¹at Sinana 2020(the highest yielding environment); whereas the standard check Burkitu gave the highest yield of 2279 kg ha⁻¹in the least-yielding environment (Asasa 2020) (Table 3). The ranks order of genotypes changed across the test environments. Previously Tamene *et al.*, (2015) stated the differential rank order change of genotypes in different environments implied the genotype × environment interaction effect was of the crossover type.

Overall, among the 15 field pea pipelines genotypes, GPHA-38 showed better performance having grain yield advantage of 4% and 5% over Bursa and Burkitu, respectively. Additionally, this genotype recorded about 4% more TSW advantage than Bursa and comparable with Burkitu. On the other hand, more than 50% of the tested genotypes were performed better than the grand mean value on major economic traits (GYLD and TSW) across locations and over seasons (Tables 2 and 3).

Table 2: Combined mean performance of agronomic traits of 17 field pea genotypes tested across 14 environments in the national variety trial during 2019 to 2020 main crop seasons

No	Genotype	Traits							
		DTF	DTM	PHT(cm)	PPP	SPP	AB (1-9)	PM(1-9)	TSW(g)
1	EH 09029-3	67ᵈᵉ	134ᵈᵉ	161ᵇᶜ	11.5ᵃᵇ	3.7ᵈ⁻ᵍ	4.5ᵇᶜᵈ	5.1ᵃᵇᶜ	193ᶠᵍ
2	GPHA-5	65ᵍʰ	131ⁱ	153ᵈᵉ	11.4ᵃᵇᶜ	4.0ᵃᵇᶜ	4.7ᵇᶜᵈ	4.5ᵈ	198ᵉᶠ
3	EH 011019-1	68ᵈ	133ᵈᵉᶠ	154ᶜᵈᵉ	10.3ᶜᵈ	3.8ᵇ⁻ᶠ	4.9ᵃᵇ	5.1ᵃᵇᶜ	208ᵈ
4	GPHA-13	66ᶠᵍ	132ʰⁱ	150ᵉ	11.5ᵃᵇ	3.8ᵇ⁻ᶠ	4.6ᵇᶜᵈ	4.5ᵈ	187ᵍʰ
5	Burkitu	66ᵉᶠ	132ʰⁱ	142ᶠ	10.9ᵃ⁻ᵈ	3.9ᵃ⁻ᵈ	4.4ᵈ	4.7ᶜᵈ	196ᵉᶠ
6	EH 011028-1	68ᵈ	135ᵇᶜ	157ᵇ⁻ᵉ	11.2ᵃ⁻ᵈ	3.6ᶠᵍ	4.4ᵈ	5.1ᵃᵇᶜ	212ᶜᵈ
7	EH 011025-3	73ᵃ	136ᵃ	162ᵇ	10.1ᵈ	3.8ᵇ⁻ᶠ	4.6ᵇᶜᵈ	5.3ᵃᵇ	220ᵇ
8	GPHA-2	67ᵈᵉ	132ᵍʰ	153ᵈᵉ	10.7ᵇ⁻ᵈ	3.6ᵉᶠᵍ	4.7ᵃ⁻ᵈ	4.4ᵈ	195ᵉᶠ
9	EH 011027-5	68ᵈ	133ᵈᵉ	161ᵇᶜ	11.2ᵃ⁻ᵈ	3.9ᵃ⁻ᵈ	4.7ᵃ⁻ᵈ	4.6ᶜᵈ	178ⁱ
10	GPHA-22	66ᶠᵍ	132ᶠᵍʰ	157ᵇ⁻ᵉ	11.4ᵃᵇᶜ	3.8ᵇ⁻ᶠ	4.5ᵇᶜᵈ	4.5ᵈ	218ᵇᶜ
11	EH 09016-1	73ᵃ	134ᵇ⁻ᵉ	162ᵇ	11.3ᵃ⁻ᵈ	4.0ᵃᵇᶜ	4.4ᵈ	5.1ᵃᵇᶜ	162ʲ
12	EH 011027-4	71ᵇ	133ᵈᵉᶠ	161ᵇᶜ	10.8ᵃ⁻ᵈ	4.2ᵃ	4.7ᵃ⁻ᵈ	4.9ᵃ⁻ᵈ	201ᵉ
13	GPHA-20	68ᵈ	134ᵇᶜᵈ	162ᵇ	11.3ᵃᵇᶜ	3.5ᵍ	4.6ᵇᶜᵈ	4.9ᵇᶜᵈ	247ᵃ
14	GPHA-41	67ᵈᵉ	135ᵇ	170ᵃ	10.3ᶜᵈ	4.0ᵃᵇ	4.5ᶜᵈ	4.8ᶜᵈ	175ⁱ

No	Genotype	Traits							
		DTF	**DTM**	**PHT(cm)**	**PPP**	**SPP**	**AB (1-9)**	**PM(1-9)**	**TSW(g)**
15	Bursa	64[h]	133[efg]	158[bcd]	11.7[ab]	3.8[c-f]	5.1[a]	5.4[a]	186[h]
16	GPHA-38	67[de]	132[hi]	156[b-e]	10.8[b-d]	3.8[b-f]	4.8[abc]	4.6[cd]	194[fg]
17	EH 011020-2	69[c]	133[ef]	159[bcd]	11.9[a]	3.9[b-e]	4.5[bcd]	4.7[cd]	194[fg]
	Mean	68	133	157	11	3.8	4.6	4.8	198
	CV (%)	4.3	2.2	12.2	27.7	17.8	18.0	17.2	8.4
	LSD (5%)	1.1	1.2	7.8	1.2	0.25	0.4	0.5	7.2

DTF (days to 50% flowering), DTM (days to 90% physiological maturity), AB (Ascochyta blight), PM (powdery mildew), PHT (plant height), PPP (number of pod per plant), SPP (number of seeds per pod), TSW (thousand seeds weight), LSD (least significant difference at $P = 0.05$).

Table 3: Mean grain yield (kg ha^{-1}) of 17 field pea genotypes tested across 14 environments in the national variety trial during 2019 to 2020 main crop season

Environment	Genotype	EH 09029-3	GPHA-5	EH 011019-1	GPHA-13	Burkitu	EH 011028-1
E1	Adet 2019	1886	2557	1680	1771	1973	2293
E2	Adet 2020	2512	2141	2174	2232	2273	2556
E3	Areka 2019	1953	2209	1747	2472	2643	1728
E4	Areka 2020	3732	3213	2597	3341	3215	2960
E5	Asasa 2020	1660	1423	1251	1461	2279	1743
E6	Bekoji 2019	3104	3054	2840	2279	3179	2698
E7	Dabat 2019	3865	3922	3937	4138	4833	4455
E8	Dabat 2020	1976	2601	2239	2483	3069	2862
E9	Holetta 2020	1643	1457	1976	1713	2246	2559
E10	Jeldu 2019	2666	2691	1927	1993	2349	2997
E11	Jeldu 2020	1624	1656	2417	1418	1415	1399
E12	Kulumsa 2019	1621	2414	1842	2453	2764	1975
E13	Sinana 2019	4184	3643	3366	3528	4293	3765
E14	Sinana 2020	4428	5423	3485	5610	4934	3695
	Mean GYLD	2632[f]	2743[def]	2391[g]	2635[f]	2962[b]	2692[ef]

Environment	Genotype	EH 011025-3	GPHA-2	EH 011027-5	GPHA-22	EH 09016-1	EH 011027-4	GPHA-20	GPHA-41	Bursa	GPHA-38
E1	Adet 2019	1018	1461	2078	2094	1836	1608	1641	1773	2407	2207
E2	Adet 2020	1406	1778	2189	2411	1727	2348	2012	2055	2357	2416
E3	Areka 2019	1223	2092	1992	2222	1398	1564	1951	1364	2133	2088
E4	Areka 2020	1973	2624	3595	3883	3659	3318	3171	3016	4375	3792
E5	Asasa 2020	1322	1024	1468	1434	1500	2092	1129	1511	1306	1807
E6	Bekoji 2019	2764	2100	4019	3493	3434	2978	2578	3191	3385	3782
E7	Dabat 2019	3548	3917	3897	2916	4275	4287	3230	4740	4112	4722
E8	Dabat 2020	2647	2300	2403	2071	3061	2838	2286	3233	3874	3052
E9	Holetta 2020	2408	1437	2691	1396	3489	2017	2134	1898	1282	1478
E10	Jeldu 2019	2418	2268	2929	3336	2984	3447	3627	3836	3097	3777
E11	Jeldu 2020	1470	1723	2039	1607	1991	2793	2061	1719	1928	1720
E12	Kulumsa 2019	1758	2342	2149	2009	1709	1868	1675	2628	2056	2521
E13	Sinana 2019	3415	3432	4813	3853	4093	4656	2803	4586	4704	4544
E14	Sinana 2020	2876	4387	5049	5277	4016	4949	3667	5022	4607	5621
	Mean GYLD	2160^h	2349^g	2951^b	2714^{ef}	2798^{cde}	2911^{bc}	2426^g	2898^{bcd}	2973^b	3109^a

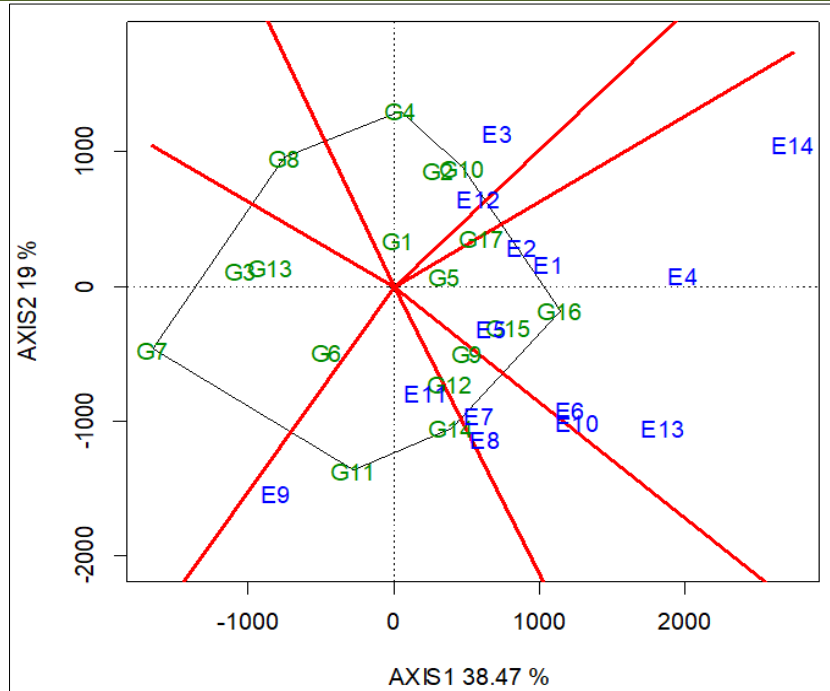| Environment															
Genotype	E1 Adet 2019	E2 Adet 2020	E3 Areka 2019	E4 Areka 2020	E5 Asasa 2020	E6 Bekoji 2019	E7 Dabat 2019	E8 Dabat 2020	E9 Holetta 2020	E10 Jeldu 2019	E11 Jeldu 2020	E12 Kulumsa 2019	E13 Sinana 2019	E14 Sinana 2020	Mean GYLD
EH 011020-2	2014	2729	2174	4267	1877	2824	3134	2040	1704	3655	2197	2156	4543	4853	2869[bcd]
Mean	1900	2195	1938	3337	1546	3041	3996	2649	1972	2941	1887	2061	4012	4582	2718
CV (%)	9.3	9.8	9.7	13.2	22.6	4.5	3.2	15.6	13.9	4.5	16.0	7.8	3.6	18.6	13.1
LSD (5%)	251.3	304.9	268.3	628.3	497.8	196.5	180.8	587.7	390.9	187.8	430.1	227.2	205.8	1209.0	131.8

E (Environment), GYLD: grain yield (kg ha^{-1}), LSD (least significant difference at *P* = 0.05)

Grain Yield Stability

A polygon view of the GGE Biplot resulted vertex genotypes that have either positive or negative grain yield. Accordingly, seven vertex genotypes were identified with both positive and high yielding (G4, G10, G14 and G16) and negative or low yielding (G7, G8 and G11) genotypes based on PCA1 scores. Vertex genotypes perform either the best or the poorest in one or more environments (Figure1). As stated by Asnakech *et al.,* (2017) the best genotype at one environment may not perform best at another environment if the environments fell in different sectors of the polygon. Likewise, the environments fell in four different sectors of the polygon view.The genotypes G4, G10, G11, G14 and G16 were the best performers in environments with that sectors where as G7 and G8 fell in sectors with no environment markers. The genotype G16 (GPHA-38) performed best in most of the test environments (Figure 1). Furthermore, genotypes fell within the polygon were less responsive than the vertex genotypes for the interaction. PC1 and PC2 accounted 57.47% of the total PCs variation of grain yield over 14 environments showing that it was not sufficiently explained the GGE (Figure 1). According to Yan *et al*., (2010) if the GGE is sufficiently approximated by PC1 and PC2, genotypes at the apex of each sector performs best at environments included in that sector. Accordingly, the performance of vertex genotypes may not be best in the environments they fell. Therefore, genotypes with environmental markers can be recommended for those specific environments. However, stability of the genotypes across environments should first be considered as wider adaptable genotypes are preferred in crop breeding than specifically adapted once.

According to Yan (2001), environments with large PC1 scores have better discriminative power among the genotypes, and those with PC2 scores near zero are more representative of an average environment. Accordingly, E4, E13 and E14 had larger PC1 scores and well discriminated the genotypes and E4 found as an ideal environment. Genotypes G15 and G16 were high yielding genotypes with high PC1 while genotypes G3, G7, G8 and G13 were with large negative PC1 scores and they were low yielding genotypes. Pipeline genotypes with relatively low PC2 scores and above average grain yield such as G16 and G17showed relatively better stability, and can thus be considered for wider adaptability in the potential growing environments (Figure 1).

Figure 1: GGE-Biplot showing environments (E1–E14 indicated in Table 3), and their respective field pea genotypes (G1-G17 indicated in Table 1)

The GGE biplot compares the 'ideal genotype' with 15 other field pea genotypes shown in Figure 2. The small circle located on the average environment coordinate (AEC) abscissa and with an arrow pointing to it, represents the ideal genotype. The ideal genotype has the highest yield of the entire dataset and is the most stable (Yan and Kang, 2002). Accordingly, genotypes G15 and G16 were closest to the hypothetical ideal genotype and they are the most desirable of all genotypes. Since G15 (Bursa) is a standard check, it can be considered as an ideal genotype to which other test genotypes compared.
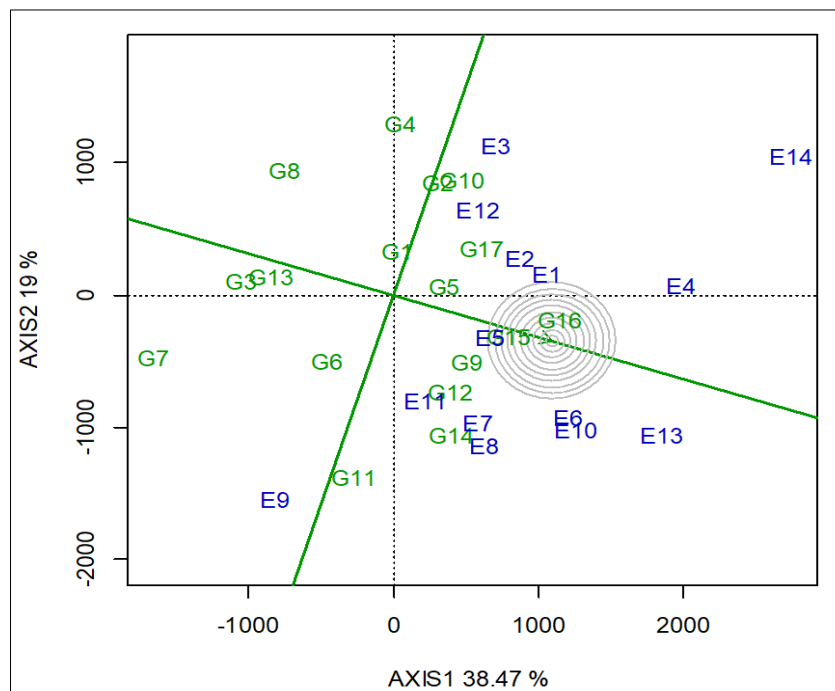

Figure 2: GGE biplot ranking of 17 field pea genotypes with ideal genotype, Bursa; G1-G17 islists of genotypes indicated in Table 1; E1-E14 is list of environments indicated in Table 3

Genotypes with short vector length from the horizontal line were stable and with long vector length in the contrasting direction. Accordingly, G5, G15, G16 and G9 proved as stable genotypes (Figure 3). Likewise,

earlier reports indicated that genotypes with greater absolute length projection are less stable and those with shorter absolute length are more stable (Fekadu *et al.,* 2012; Asnakech *et al*., 2017). The A line separates genotypes with grain yield below and above the mean. Those genotypes to the right of this line were high yielders while those to the left were low yielders. The single-arrow on the horizontal line (AEC) points to higher mean yield indicating G16 had the highest yield while G7 is the poorest genotype for grain yield (Figure 3).
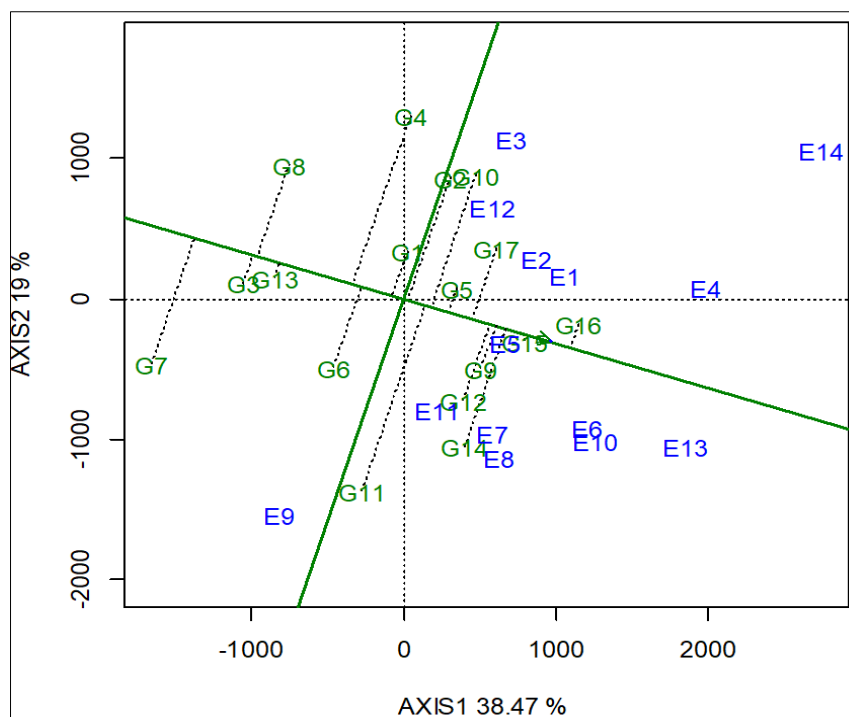
Figure 3: Mean yield performance and stability of genotypes (G1–G17 listed in Table 1) over environments (E1–E14 listed in Table 3)

CONCLUSIONS

The evaluation made from the breeding materials are either directly used for development of new varieties or utilized as parent materials to transfer their valuable genetic attributes in the locally adapted field pea varieties via crossing. In the present study, one genotype GPHA-38 recorded significantly better grain yield and comparable thousand seeds weight as compared to the two standard checks, Burkitu and Bursa. Additionally, this genotype showed more stable response based on the GGE biplot analysis. Hence, with its better overall agronomical performance and grain yield stability, GPHA-38 can be used as trait donor parent for grain yield improvement in the future breeding program.

Conflicts of Interest: The authors declare that there is no conflict of interest.

REFERENCES
- Asfaw, N., Abdissa, G., Tesfaye, K., & Gemechu, G. (1997). Agro ecological and socio-economic circumstances of farmers in eastWolloga zone of Oromiya region. Research report, 32. *Institute ofAgriculture Research* (IAR). Addis Ababa.
- CSA (Central Statistical Agency of Ethiopia). 2019/20. Report on Area and Production of Major Crops (Private peasant holdings, meher season). Statistical Bulletin, *Addis Ababa, Ethiopia, 1*(587), 9-17.
- FAOSTAT. (2017). Food and Agriculture Organization of the United Nations. Available online at http://www.fao.org/faostat/en/#data/QC/visualize.
- Fikere, M., Tadesse, T., Gebeyehu, S., & Hundie, B. (2010). Agronomic performances, disease reaction and yield stability of field pea (Pisum sativum L.) genotypes in Bale Highlands, Ethiopia. *Australian Journal of Crop Science*, *4*(4), 238-246.
- Gomez, K. A., & Gomez, A. A. (1984). *Statistical procedures for agricultural research*. John wiley & sons.
- Gurmu, F., Lire, E., Asfaw, A., Alemayehu, F., Rezene, Y., & Ambachew, D. (2012). GGE-biplot analysis of grain yield of faba bean genotypes in

southern Ethiopia. *Electronic Journal of Plant Breeding*, *3*(3), 898-907.

- Hagedorn, D. J. (1984). Compendium of pea diseases. University of WisconsinMadison.

- Keneni, G., Bekele, E., Assefa, F., Imtiaz, M., Debele, T., Dagne, K., & Getu, E. (2012). Phenotypic diversity for symbio-agronomic characters in Ethiopian chickpea (Cicer arietinum L.) germplasm accessions. *African Journal of Biotechnology*, *11*(63), 12634-12651.

- Keneni, G., Fikre, A., & Eshete, M. (2016). Reflections on highland pulses improvement research in Ethiopia. *Ethiopian Journal of Agricultural Sciences Special*, (17-50).

- Negisho, K., Teshome, A., & Keneni, G. (2017). Genetic diversity in Ethiopian field pea (Pisum sativum L.) germplasm collections as revealed by SSR markers. *Ethiopian Journal of Agricultural Sciences*, *27*(3), 33-47.

- SAS Institute. 2012. SAS proprietary software. Release 9.3 SAS Inst., Cary, NC, USA.

- Smýkal, P., Aubert, G., Burstin, J., Coyne, C. J., Ellis, N. T. H., Flavell, A. J., Ford, R., Hýbl, M., Macas, J., Neumann, P., McPhee, K. E., Redden, R. J., Rubiales, D., Weller, J. L., & Warkentin, T. D.

- (2012). Pea (Pisum sativum L.) in the Genomic Era. *Agronomy, 2*, 74115.

- Tekalign, A., Sibiya, J., Derera, J., & Fikre, A. (2017). Analysis of genotype× environment interaction and stability for grain yield and chocolate spot ('Botrytis fabae') disease resistance in faba bean ('Vicia faba'). *Australian journal of crop science*, *11*(10).

- Temesgen, T., Keneni, G., Sefera, T., & Jarso, M. (2015). Yield stability and relationships among stability parameters in faba bean (Vicia faba L.) genotypes. *The crop journal*, *3*(3), 258-268.

- Westphal, E. (1974). Pulses in Ethiopia. Wageningen: Centre for AgriculturalPublishing and Documentation.

- Yan, W. (2001). GGEbiplot—A Windows application for graphical analysis of multienvironment trial data and other types of two-way data. *Agronomy journal*, *93*(5), 1111-1118.

- Yan, W., & Kang, M. S. (2002). A graphical tool for breeders, geneticists, and agronomists. *CRC Press, UK*.

- Yan, W., Frégeau-Reid, J., Pageau, D., Martin, R., Mitchell-Fetch, J., Etienne, M., ... & Sparry, E. (2010). Identifying essential test locations for oat breeding in eastern Canada. *Crop Science*, *50*(2), 504-515.