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Performance Evaluation and Stability Study of Field Pea (*Pisum sativum* L.) Genotypes for Potential Production Areas in the Highlands of Ethiopia

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Abstarct

Field pea is an important crop for Ethiopian farmers, but its national average yield of 1.7 t ha^{-1} is much lower than its potential, primarily due to the low yield of local cultivars and their vulnerability to various stresses. This study aimed to identify high-yielding, stable genotypes with disease resistance and other desirable traits. Fifteen genotypes, including two standard checks (Bursa and Jeldu), were evaluated across ten environments during the 2021 and 2022 growing seasons using a randomized complete block (RCB) design with four replications. Significant differences ($P \leq 0.01$) were found for genotype, environment, and their interaction for most traits. The best-performing genotype, G7 (EH014011-4), showed an 8% to 17% increase in seed weight and a 19% to 35% yield advantage over the standard checks. The second-best genotype, G14 (EH014007-1), exhibited a 10% increase in seed weight and an 11% to 28% yield advantage. Both genotypes were stable across environments, as shown by the genotype-by-environment (GGE) biplot analysis. Based on these results, G7 and G14 were recommended for further variety verification and evaluation, alongside the standard checks, for potential release as high-yielding, stable varieties in Ethiopia. The variety EH014011-4 outperformed all tested genotypes, including standard checks, in yield, stability, and showed moderate resistance to Ascochyta blight and powdery mildew. Farmers also favored this variety for its overall performance and market suitability. As a result, field pea variety EH014011-4 was approved for national release in 2024 for use in the tested areas and similar agro-ecological zones.

Keyword: Biotic stresses, field pea, genotype-by-environment , yield , stability,

Introduction

Field pea (*Pisum sativum* L., 2n = 14) is a crucial annual legume crop, originally domesticated in the Mediterranean region, particularly in the Middle East (Smýkal *et al*., 2012). Ethiopia is considered the center of diversity for this crop, with wild and primitive forms found in its highland regions. Field pea is grown across various Ethiopian regions at altitudes ranging from 1,800 to 3,000 masl with annual rainfall between 700 -1,000 mm. It is the fourth most important legume in the country, following faba bean, common bean, and chickpea, covering 219,927.59 ha and producing 376,236.9 tons (CSA, 2021).

The crop offers significant economic and ecological benefits to Ethiopian farming communities. It provides a valuable source of food and feed, offering an affordable protein source, and plays a vital role in restoring soil fertility through nitrogen fixation. Additionally, field pea serves as a cash crop, contributing to foreign currency generation for the country. However, the national average yield remains low at around 1.7 t ha^{-1}, far below its potential, with research indicating yields ranging from 2.5 to 3.5 t ha^{-1} in Ethiopia (Mussa *et al*., 2006) and 7 to 8 t ha^{-1} in countries like England and France (Smykal *et al*., 2012). Yield constraints include the low productivity of local cultivars, susceptibility to biotic stresses (e.g., *Ascochyta blight*, powdery mildew), and abiotic stresses (e.g., frost, moisture stress, poor soil fertility). Poor cultural practices, including marginal land use, inadequate tillage, and lack of fertilization, also contribute to low yields.

Addressing these challenges requires robust breeding programs to develop varieties with improved yield potential, resistance to biotic and abiotic stresses, and suitability for different agro-ecologies. Over the past decades, Ethiopia's National Highland Pulse Breeding Program has released more than 18 superior field pea varieties for various environments. Given the high genotype-environment interaction (GEI), it is crucial to conduct multi-location trials to identify genotypes with broad or specific adaptability, stability, and high yield potential. This experiment aimed to select and release high-yielding, stable, and disease-resistant field pea genotypes with desirable agronomic traits for the highlands of Ethiopia.

Materials and Methods

National varity trials

Fifteen field pea genotypes, including two standard checks (Bursa and Jeldu), were evaluated across ten environments (Asassa 2021, Asassa 2022, Areka 2021, Bekoji 2022, Dabat 2021, Holetta 2021, Holetta 2022, Haramaya 2021, Jeldu 2021, and Sinana 2022) for seed yield and other agronomic traits during the 2021 and 2022 Meher growing seasons (Table 1). The experiment was arranged in a randomized complete block (RCB) design with four replications, consisting of four rows (4 m long) with 0.2 m spacing between rows and 5 cm between plants (80 seeds/row). There was a 1.0 m distance between adjacent plots. NPS fertilizer was applied at a rate of 121 kg ha^{-1} at planting. Weeding and other management practices were conducted according to standard research recommendations, uniformly across all treatments.

Table 1: Description of the test genotypes

Genotype code	Genotype name	Flower color	Seed shape	Type	Pedigree	
					Female	Male
G1	EH 014005-4	purple	Dented	Shiro	Burkitu	IFPI 5136
G2	EH 014007-3	purple	*Dented*	Shiro	Bilallo	IFPI 3208
G3	EH 014011-3	purple	Dented	Shiro	Letu	IFPI 5136
G4	EH 014007-4	White	Round	Kik	Bilallo	IFPI 3208
G5	Jeldu	White	Round	Kik	EH099003-8	IFPI 5136
G6	EH 014006-4	Purple	Dented	Shiro	Bilallo	Cooke
G7	EH 014011-4	Purple	Dented	Shiro	Letu	IFPI 5136
G8	EH 014008-2	Purple	Dented	Shiro	Bilallo	IFPI 5136
G9	EH 014006-5	Purple	Dented	Shiro	Bilallo	Cooke
G10	EH 014006-2	White	Round	Kik	Bilallo	Cooke
G11	EH 014004-5	White	Round	Kik	Burkitu	IFPI 3208
G12	Bursa	Purple	Dented	Shiro	EH04053	EH04051
G13	EH 015001	White	Round	Kik	EH014001	EH014002
G14	EH 014007-1	Purple	Dented	Shiro	Bilallo	IFPI 3208
G15	EH 014010-1	Purple	Dented	Shiro	Letu	IFPI 3208

Data collection and analysis

Data on phenological, disease, grain yield, and yield-related traits were collected. The grain yield from each plot was harvested, cleaned, dried, measured, and then converted to kilograms per hectare for analysis. A combined analysis of variance across environments was conducted to assess differences between genotypes, among environments, and their interaction effects, using the following statistical model:

$$Yij = \mu + Gi + Bj + eij \text{ and } Yijk = \mu + Gi + Ej + GEij + Bk(j) + eijk.$$

Where, Yij = observed value of genotype i in block j, Yijk = observed value of genotype i in block k of environment j, µ = grand mean of the experiment, Gi = the effect of genotype i, Bj = the effect of block j, Bk(j) = the effect of block k in environment j, eij = error effect of genotype i in block j , Ej = environment effect, GEij = the interaction effect of genotype i with environment j, eijk = error (residual) effect of genotype i in block k of environment j.

The analysis of variance and adjusted means were calculated using R software version 4.2.2 (R Core Team, 2022). GGE Biplot analysis was performed to evaluate the stability and performance of the tested entries across years and locations. The GGE Biplot model (Yan *et al.*, 2007; Yan and Hunt, 2001; Yan and Kang, 2002) was implemented using the GGE Biplot graphical user interface package in R (R Core Team, 2022).

Varitye verification trial

From the national varity trials field pea candidate genotypes (EH 014011-4 and EH 014007-1) were selected for variety verification trial. In 2023, varity verification trial was conducted at four locations in Ethiopia (Holeta, Bekoji, Dabat, and Areka) and the two candidate varities were evaluated with Bursa (Standared check), and Mieso (regionally recently registered) checks. On a single plot of 10 m x 10 m at each research sites on - station and replicated in two on farmers' fields. All agronomic practices were applied at all trial sites according to recommendations, and necessary data, including farmers' assessments, were collected. The candidate varieties were evaluated by the National Variety Releasing Committee at the twelve field sites.

Results and Discussions

The combined analysis of variance indicated significant differences for genotype, environment, and genotype by environment interaction for most of the traits (P≤0.01). The results showed that genotypes responded differently to grain yield across various environments, highlighting the importance of multi-location trials to assess the specific or broader adaptability of genotypes (Table 2).

Effect of Genotypes

Genotypes showed significant differences for several traits, including days to flowering, days to maturity, aschochyta blight, plant height, pods per plant, seeds per pod, thousand seed weight, and grain yield. However, there were no significant differences for powdery mildew (Table 2). The significant genotype effects indicated notable variability among the tested genotypes.

The earliest genotype to flower was G1, taking 70 days, while G7 took 79 days. The earliest maturity was observed in G4, which matured in 136 days, while G1 matured in 140 days. The lowest aschochyta blight score (3.38) was recorded for G8, while G4, G11, and G13 had the highest score (4.12). For powdery mildew, G8 had the lowest score (2.4), while G10 and G12 recorded the highest (3.3). The highest plant height (164-170 cm) was found in G3, G7, and G14, while the lowest (146.2 cm) was recorded in G5. The highest number of pods per plant (11.56-12.45) was observed in G4, G5, G6, G11, G12, and G13, while G7 had the lowest (10.25) (Table 3). Early maturing genotypes may help escape drought stress, especially in regions with limited rainfall or terminal moisture stress. These genotypes are also less likely to be affected by aschochyta blight, powdery mildew, and aphids, which typically emerge later in the season. Significant variation for flowering, maturity, pods per plant, seeds per pod, and plant height across locations and years has also been reported (Fikere *et al.*, 2010; Argaye *et al*., 2023).

The lowest thousand seed weight was 193 grams for G4, while the highest was 236 grams for G7, with an average of 217 grams. The most promising genotype, G7 (EH 014011-4), showed an 8% to 17% advantage in thousand seed weight and a 19% to 35% yield advantage over the standard checks, Jeldu and Bursa (Table 3). Genotype G14 (EH 014007-1) also demonstrated a 10% advantage in thousand seed weight and a yield advantage of 11% to 28% over Jeldu and Bursa. Significant variation for grain yield was also observed across locations and years (Fikere *et al*., 2010; Argaye *et al*., 2023). Focusing on yield in breeding programs is crucial to developing varieties that support sustainable agricultural productivity, farmer livelihoods, and food security. According to Yang (2022), comprehensive cross-breeding efforts that incorporate key traits for abiotic stress tolerance will facilitate the evaluation of genotypes, enhancing yield testing.

Table 2.. Combined analysis of variance showing mostly significant main effects (genotype environment and interaction terms in 15 field pea genotypes evaluated across 10 environments

Mean square[1]					
characters[1]	Geno	Env	Geno:Env	Env:Rep	Residuals
DF	355***	4178***	24***	13***	4
DM	57***	6650***	11**	22***	7
AB	0.91*	133.86ns	0.61ns	1.70**	0.51
PM	0.99ns	82.23***	0.69ns	0.56ns	0.67
PLH	2103***	34934***	377**	582**	253
PPL	28***	597***	9ns	25***	9
SPP	1.4***	14.1***	0.5ns	0.5ns	0.4
TSW	5109***	55156***	567**	479ns	388
GYLD	4032149***	12714112***	1175777***	474464*	277952

Where: DF = number of days to 50% flowering, DM = number of days to 90% maturity, PHT = plant height (cm), PPP = number of pods per plant, SPP = number of seeds per pod, AB = aschochyta blight (in 1-9 scale), PM = powdery mildew diseases (in 1-9 scale), TSW=thousand seeds weight (g), GYLD = grain yield (Kg ha-1) ** = highly significant (P 0.05).

Effect of environment

Significant differences were observed across most locations for traits such as days to flowering, days to maturity, *Aschochyta blight*, plant height, pods per plant, seeds per pod, thousand seed weight, and grain yield. However, no significant differences were found for *Aschochyta blight* (Table 2). The overall means for the combined environments are presented in Table 3. In terms of grain yield, genotypes G7 and G14 significantly outperformed the best check, Bursa, while nine genotypes (G4, G6, G7, G9, G10, G11, G13, G14, and G15) showed significantly higher yields than the second check, Jeldu (Table 3). For thousand seed weight, genotypes G1, G7, G9, and G11 had significantly higher mean values compared to the two standard checks.

The individual environment mean performances for thousand seed weight and grain yield are presented in Tables 4 and 5. The highest grain yields were recorded in Holeta (2021 and 2022), Jeldu 2021, Areka 2021, and Haramaya 2021 (Table 5), and the highest thousand seed weights were observed in the same environments (Tables 4 and 5). These results suggest that these locations are potentially suitable for field pea production, with favorable agro-ecological, edaphic, and climatic conditions that support the expression of the genetic potential of different genotypes. Conversely, lower grain yields were recorded in Asassa (2021 and 2022), Bekoji (2022), Dabat (2021), and Sinana (2022). Specifically, Asassa showed consistently poor grain yields over the two seasons, which may indicate that the environment was not ideal for field pea production, or that genotype responses varied. Further research is needed to explore these results.

Genotype by location interaction effects were significant for traits such as days to flowering, days to maturity, plant height, thousand seed weight, and grain yield, but non-significant for *Aschochyta blight*, powdery mildew, pods per plant, and seeds per plant. The high genotype-by-location interaction (G×E) effects for several traits are expected, as the study involved diverse genotypes from different eco-geographical origins evaluated in distinct environments. High G×E interaction typically calls for breeding efforts focused on specific adaptation rather than broad adaptation. However, non-significant G×E interactions for certain traits suggest that some genotypes may perform consistently well across diverse environments. Genotypes with low G×E interaction tend to exhibit stable performance, making them reliable for breeding programs and beneficial for farmers in various locations.

Table 3. Over environments combined mean performances of nine traits tested in field pea national varieties trail conducted at 10 environments in 2021 and 2022

Geno	DF	DM	AB	PM	PLH	PPP	SPP	TSW	GYLD
G1	70h	140a	3.6bcd	3.1ab	162.2bcd	9.8d	4.7abc	230.ab	2754ef
G2	72fg	139.4a-d	3.6bcd	2.9abc	164.4abc	10.7cd	4.5b-f	219cde	2702f
G3	79a	139.9abc	3.7a-d	2.8abc	170.6a	10.5cd	4.75ab	217de	2771ef
G4	69i	135.7f	4.1ab	2.6bc	155.4d	11.7abc	4.5b-f	193f	2968cde
G5	72g	137.04e	3.7a-d	2.9abc	146.2e	12.01ab	4.2fg	216e	2455g
G6	73ef	138.9cd	3.8a-d	2.8abc	164.8abc	11.6abc	4.6a-d	218de	2826def
G7	78ab	138.5d	3.7a-d	3.1ab	168.2ab	10.3d	4.7ab	236a	3769a
G8	75d	139.9abc	3.4d	2.4c	164.8abc	10.5cd	4.4d-g	217de	2683fg
G9	75d	139.5a-d	3.5cd	2.8abc	164.7abc	10.9bcd	4.5bc-f	224bcd	30631c
G10	77c	139.9abc	3.9abc	3.3a	155.7d	10.9bcd	4.3efg	223bcde	2900c-f
G11	74e	139.03bcd	4.12a	3.2ab	147.7e	12.5a	4.2g	227bc	2957cde
G12	73ef	138.4d	3.7a-d	3.3a	165.9abc	11.7abc	4.6a-e	195f	3038cd
G13	70h	138.8cd	3.6cd	2.8abc	159.8cd	12.7a	4.4c-g	215e	2766ef
G14	70hi	139.9abc	3.8a-d	2.9abc	164.3abc	10.7cd	4.8a	217de	3419b
G15	77bc	140.2ab	4.1ab	3abc	167.9ab	10.7cd	4.4c-g	216de	2883c-f
Mean	74	139	4	3	162	11	5	217	2930
CV	3	2	19	28	10	26	15	9	18
LSD	0.95	1.22	0.5	0.57	6.99	1.28	0.3	8.66	231.7

Where: DF = number of days to 50% flowering, DM = number of days to 90% maturity, PHT = plant height (cm), PPP = number of pods per plant, SPP = number of seeds per pod, AB = aschochyta blight (in 1-9 scale), PM = powdery mildew diseases (in 1-9 scale), TSW=thousand seeds weight (g), GYLD = grain yield (Kg ha^{-}1) ** = highly significant (P 0.05).

Table 4. Mean thousand seed weight (gm) performance of 15 field pea genotypes tested in NVT at 10 environments in 2021 and 2022

Geno	AA21	AA22	AR21	BE22	DA21	HL21	HL22	HU21	JL21	SN22	Mean
G1	201	190	303	243	229	240	219	229	251	200	230
G2	187	179	278	256	208	227	218	211	212	214	219
G3	181	173	293	233	217	228	213	178	254	198	217
G4	176	174	254	196	175	192	187	201	210	160	193
G5	184	180	302	214	220	234	217	185	229	192	216
G6	194	182	265	232	221	220	217	202	244	201	218
G7	204	193	307	254	244	230	233	221	257	215	236
G8	174	177	285	237	223	224	214	193	242	201	217
G9	183	173	299	240	228	233	219	202	269	201	224
G10	187	186	305	242	230	227	224	202	234	191	223
G11	203	199	298	226	223	228	228	218	239	204	227
G12	236	143	258	202	177	191	192	192	199	164	195
G13	182	182	277	214	208	222	218	223	222	199	215
G14	183	182	302	231	209	217	211	228	231	182	217
G15	189	182	295	233	228	219	207	197	222	192	216

Where: AA21(Asassa 2021), AA22(Asassa 2022), AR21(Areka 2021), BE22(Bekoji 2022), DA21(Dabat 2021), HL21(Holetta 2021), HL22(Holetta 2022), HU21(Haramaya 2021), JL21(Jeldu 2021) and SN22(Sinana 2022)

Table 5: Mean grain yield (Kg ha^{-1}) performance of field pea varieties tested in NVT at 10 environments 2021 and 2022

Geno	AA21	AA22	AR21	BE22	DA21	HL21	HL22	HU21	JL21	SN22	Mean
G1	1745	1561	3180	3525	2157	3417	3768	3073	2831	2281	2754
G2	2132	2848	3091	2168	1975	2867	3377	2543	3342	2676	2702
G3	2106	2355	3235	1470	2446	3322	3613	2907	3824	2429	2771
G4	2998	4187	3225	858	2406	2588	3216	4590	2331	3280	2968
G5	2428	2130	2870	1119	2671	2848	3023	2698	2519	2242	2455
G6	2812	2378	2789	1229	2503	2731	3509	3313	4121	2876	2826
G7	3163	3063	3798	3812	3581	3781	5306	3177	4406	3608	3769
G8	2215	1707	3520	1542	2468	3171	3722	2629	3156	2702	2683
G9	2077	1672	3263	3962	2392	3230	4107	3403	3983	2538	3063
G10	2476	2358	2986	2627	3403	3420	3161	2457	3550	2565	2900
G11	2961	2931	2843	2825	2178	2984	3957	3655	2854	2377	2957
G12	2409	2512	3116	2687	2502	2721	4360	3018	3727	3323	3037
G13	1732	2650	2883	3084	2074	2276	3520	3556	3107	2781	2766
G14	3279	4099	3761	3555	2771	2975	4587	3568	3413	2184	3419
G15	1976	2322	2975	2882	2303	2978	3609	2790	4539	2455	2883

Where: AA21(Asassa 2021), AA22(Asassa 2022), AR21(Areka 2021), BE22(Bekoji 2022), DA21(Dabat 2021), HL21(Holetta 2021), HL22(Holetta 2022), HU21(Haramaya 2021), JL21(Jeldu 2021) and SN22(Sinana 2022)

Grain yield stability

The GGE Biplot and AMMI analysis

The AMMI variance analysis revealed significant differences ($p < 0.01$) among genotypes, environments, and their interactions. The GGE biplot indicated that some genotypes exhibited either broad or specific adaptability to different environments. Among them, EH 014011-4 and EH014007-1 stood out as the most stable and ideal genotype across all tested environments.

In the AMMI1 biplot model, the abscissa represents the main effects and its ordinate represents IPC1 scores. Genotypes and environments on the right side of the midpoint (abscissa) of the perpendicular line have higher yields than those on the left side. As a result, genotypes, G7, G14, G9, G12, G4, G11, G10, G15 were generally high yielding. In contrast, genotypes, G5, G8, G2, G1, G13, G3, G6 were generally low yielding genotypes. Environments HL, JL, AR, HU were on the right-hand side of the midpoint of the main effect axis, seemed to be potential environments, while BE, AA, SN and DA were poor environments. Genotypes with IPC1 scores close to zero expressed general adaptation whereas the larger scores depicts more specific adaptation to environments with IPC1 scores of the same sign (Ebdon and Gauch, 2002). Accordingly, genotypes G7, G14, G9, G12, and G11 with mean yields greater than the overall mean and low IPC1 scores had a combination of high yield and stability performance. Environments, AR and HL were poor and were the most stable environment due to low IPC1 score, while the remaining environments had the highest interaction with genotypes because they had higher IPCA scores (Figure 1).

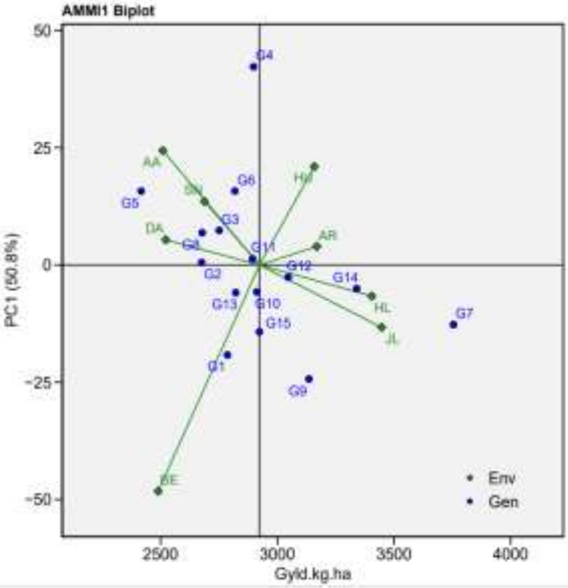

Figure 1. AMMI1 biplot showing the mean (main effect) vs. stability (IPCA1) view of both genotype and environment on grain yield.

GGE Biplot analysis

Which-Won-Where Pattern and Mega Environments

The GGE biplot polygon for the "which-won-where" pattern is created by connecting the markers of the genotypes that are located furthest from the biplot origin, ensuring that all other genotypes are enclosed within the polygon (Cravero *et al.*, 2010). The GGE biplot illustrates the “Which-Won-Where” pattern for seed yield among 15 genotypes across ten environments, identifying the best-performing genotypes for each environment. PC1 and PC2 accounted for 39.86% and 27.66% of the total variation in seed yield, respectively, together explaining 62.52% of the overall variation (Figure 2). The polygon view of the biplot offers a clear visualization of genotype-environment interactions. It is created by connecting the genotype markers located farthest from the origin, forming a convex polygon that contains all other genotype markers within it. Environments located in different sectors correspond to different winning genotypes. The "Which-Won-Where" biplot showed distinct winning genotypes in different environments (Gasura *et al*., 2015).

The mega-environment concept requires multi-year data. In this study, four mega-environments were identified (Figure 3). Specifically, environments HL22, JL21, AR21, HU21, SN21, DA21, and AA21 formed one mega-environment, while AA22, BE22, and HL21 formed another split mega-environment. Genotypes located at the corners of the polygon performed best in each respective environment sector defined by the broken lines. Based on the analysis, vertex genotypes G1, G9, G7, G14, G4, and G5 performed best in their respective environments. Genotypes G7, G14, G9, and G12 were the vertex genotypes in the mega-environment formed by HL22, JL21, AR21, HU21, SN21, DA21, and AA21, showing broad adaptation. On the other hand, G12 demonstrated specific adaptation to E4. Environments E3, E5, E2, E6, and E1 shared the same sector, indicating the same winning genotypes, while environments in other sectors had different top-performing genotypes. Seven other genotypes fell into sectors without any environment markers. Similar observation was reported from the study by Yihunie and Gesesse (2018).

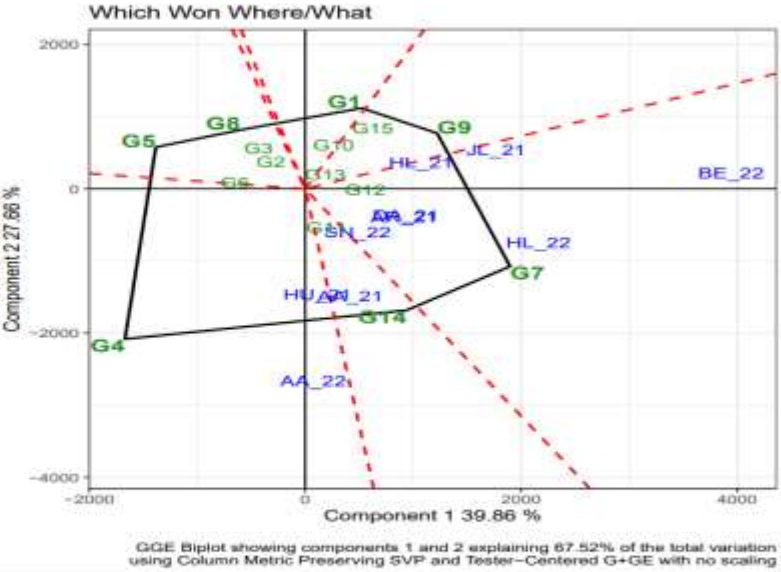

Figure 2. Polygon view of GGE (genotype plus genotype by environment interaction) bi-plot for the “whichwon where” pattern of 15 field pea genotypes tested in ten environments.

Rank of genotypes

The Average Environment Coordination (AEC) view of the GGE biplot ranks genotypes based on their performance relative to an ideal genotype. The ranking shows that genotypes G7 and G14 are closest to the ideal genotype, indicating their superior performance. In contrast, the standard check variety G5 and candidate variety G4 are positioned farther from the center of the concentric circles, suggesting lower performance. In the biplot, genotypes positioned at the center of the circles are considered the most ideal, while those further away are regarded as poorer performers that do not align with the characteristics of an ideal genotype. Therefore, the positions of G5 and G4, farther from the center, highlight their inferior performance compared to the superior genotypes G7 and G14 (Figure 3).

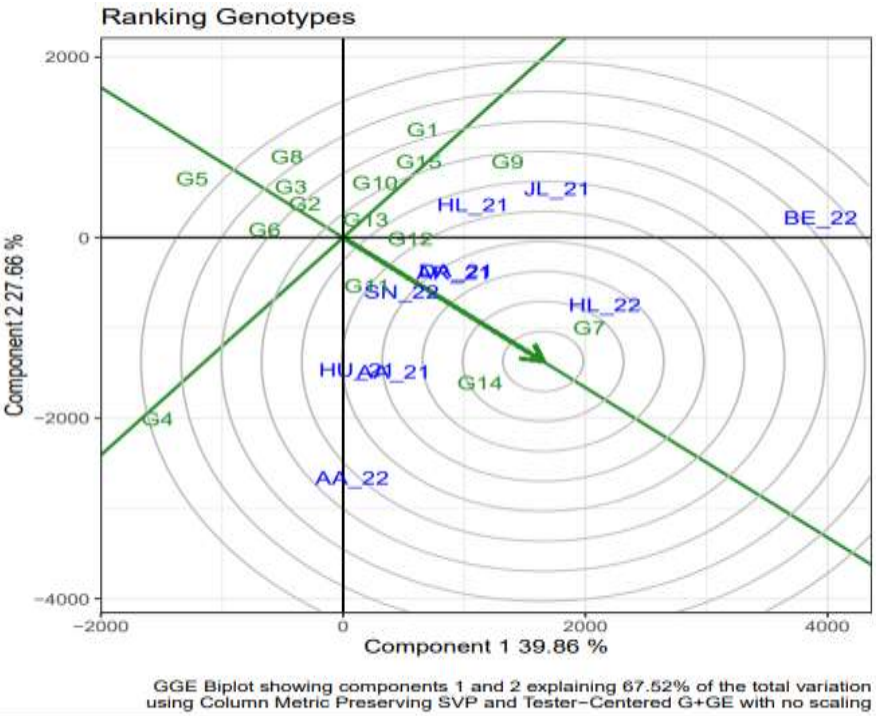

Fig 3. The average environment coordination (AEC) view of ranking of 15 field pea genotypes relative to an ideal genotype (center of the concentric circle).

Result of Varity verification trials (VVT)

The field pea candidate varieties EH 014011-4 and EH 014007-1 were developed through crosses involving large seed size gene donor parents from ICARD. EH 014011-4 is a cross between the released variety *Letu* and IFPI 5136, while EH 014007-1 is a cross between the released variety *Bilallo* and IFPI 3208, both of which were introduced from ICARD. These candidate varieties were evaluated in a variety testing trial (VVT) alongside with the recently nationaly and regionaly released standard checks *Bursa* and *Mieso* respectively.

The evaluations took place at 12 field sites, including Holeta, Bekoji, Dabat, Areka, and twelve farmers' fields, where the performance of the candidates was compared to the checks. Both candidate varieties were assessed for important agronomic traits and disease resistance. The overall performance of the varieties was ranked by a technical committee, researchers, and farmers. The results, summarized in Table 6, indicate that the candidate varieties performed better than the checks at all evaluation sites.

Table 6: The on-station and on-farm agronomic performance of the candidate genotypes in 2023

Field pea	**Grain yield kilogram per hectare**		
Genotype	**On-station**	**On-farm**	
Candidate (Released)	EH014011-4	2440	1800
Candidate (Rejected)	EH014007-1	2010	1680
Standard check	Meiso	1420	1200
Standard check	Bursa	1970	1625

The field evaluation results demonstrated that the candidate varieties consistently outperformed in terms of stand and pod loading (Table 7). EH 014011-4 and EH 014007-1 were particularly well-adopted and showed superior overall performance compared to the standard checks. Based on the results from both the NVT and VVT field evaluations, the candidate varieties were uniform, stable, and adaptable to the tested environments. Notably, the candidate variety EH 014011-4 exhibited a higher number of pods per plant, moderate tolerance to *Ascochyta blight* and *Powdery mildew*, and yielded 3,769 kg ha^{-1} superior to all other materials tested. This variety also featured larger seeds, making it more desirable for the local market. Considering the importance of incorporating farmers' preferred traits and desirable characteristics into breeding programs for better adoption of new varieties (Sheikh et al., 2017), farmers' selection criteria were assessed. As a result, farmers expressed a strong preference for EH 014011-4 due to its exceptional performance compared to the standard checks. This highlights the significance of farmers' preferences in variety selection. Consequently, the committee approved the national release of the candidate variety EH 014011-4 for use in the tested areas and other similar agro-ecological zones.

Table 7: Agronomic performance and disease reaction of Field pea varieties evaluated by technical commeette, breeders and farmers in 2023

No	Variety	Agronomic Characters							Disease (0-5)		Overall performance/Ranking		
		Uniformity	PHT(cm)	Maturity	No of pods/plant	No of seeds/pod	TSW(gm)	Seed color	Powdery mildew(PM)	Ascochyta blight(AB)	Technical Committee	Breeder	Farmer
1	Bursa	1	165	**	33.7	5	187	Light brown	3.6	3.9	3	3	2
2	EH014011-4	1	164	**	47.8	5	224	Pale green	3.3	3.6	1	1	1
3	EH014007-1	1	163	*	44.1	5	202	Pale green	3.4	3.9	2	2	3
4	Mieso	3	131	***	27.9	4.2	153	Dark gray	4.1	4	4	4	4

Where: 1= Excellent; 2=V.good; 3=Good; 4= Poor; *** Early; **Medium; * Late

Conclusion and Recommendations

Genotype-by-environment interaction (GEI) is a critical factor in crop variety development, often complicating the release of varieties across diverse and challenging environments. The ANOVA results indicated significant differences among genotypes, environments, and their GEI effects on grain yield and most other traits studied. In this research, two promising genotypes, EH 014011-4 (G7) and EH 014007-1 (G14), showed significantly higher grain yields and comparable thousand seed weights compared to the standard checks Bursa and Jeldu during the national variety trial, and Bursa and Mieso during the variety verification trial. These genotypes also demonstrated more stable performance, as evidenced by GGE biplot analysis and positive evaluations from both farmers and researchers during field trials. Based on their high yield and stability, these genotypes are recommended for further evaluation and potential commercial release for growers. The candidate variety EH 014011-4 showed a higher number of pods per plant, moderate tolerance to Ascochyta blight and powdery mildew, and a yield of 3,769 kg ha $^{-1}$ surpassing all other tested varieties. It also produced larger seeds, increasing its appeal to the local market. Farmers favored EH 014011-4 for its exceptional performance compared to the checks. Consequently, in 2024, the national varitiy releasing committee approved the candidate varity EH 014011-4 for its national release and recommended it for use in the tested areas and other similar agro-ecological zones.

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