

Research Article

Field Pea (*Pisum sativum* L.) Variety Development for Moisture Deficit Areas of Eastern Amhara, Ethiopia

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Twelve field pea genotypes were evaluated in seven environments in Eastern Amhara in main production season (2010-2012). The objective of this trial was to identify stable and high yielding field pea genotype for production in Eastern Amhara. The trial was conducted using randomized complete block design with three replications. Combined analysis of variance for grain yield revealed that genotypes, environments, and genotype by environment interaction effect were highly significant ($P \leq 0.01$). The environments, GEI, and genotypes were accounted for 77.47%, 13.83%, and 4.37%, of the total sum squares, respectively, indicating that field pea grain yield was significantly affected by the changes in the environment, followed by GEI and genotypic effect. The candidate genotype, EH-03-002, showed 14.42% and 44.87% yield advantage over the standard and local checks, respectively. Considering the seven environments data and field performance evaluation during the variety verification trial, the National Variety Releasing Committee has approved the official release of EH-03-002 with the vernacular name of “Yewaginesh” for moisture deficit areas of Wag Lasta and similar agroecologies.

1. Introduction

Field pea (*Pisum sativum* L.) is one self-pollinated diploid ($2n=14$) annual of the most important annual cool season pulse crop and is valued as high protein food [1]. It is widely grown in the cooler temperate zones and in the highlands of tropical regions of the world. The crop is cultivated in a wide range of soil types from light sandy loams to heavy clays but it does not tolerate to saline and waterlogged soil conditions [2]. The soil pH optimum is 5.5-6.5. Field pea is one of the most important pulse crops in Ethiopia which is produced for a long time in high- and mid-altitude areas by smallholder farmers. It covers an area of about 25147.69 hectares with an annual production volume of 21406364 kg [3]. Field pea is nutritious food staff when fully matures and they are valuable food legume, often being ground into flour and used extensively in the manufacture of soups. Fresh green peas are almost universally accepted as a nutritious vegetable [4].

Nutritionally, field peas contain all the essential amino acids and are rich in high-quality vegetable protein [5]. Therefore, this crop can substitute high protein containing animal meat products in the developing countries including Ethiopia. The crop has an important role in the highlands of Ethiopia by playing a significant role in soil fertility improvement occupying a unique position in cereal-based cropping systems [6]; the crop is considered environmentally friendly and economical feasible from soil improvement point of view. Despite its importance, the average national productivity (0.85 tha^{-1}) is very low [3]. It is below the potential as compared to the research findings that ranged from 0.82 tha^{-1} to 4.6 tha^{-1} in Ethiopia [7] and the higher yield reported about 7 tha^{-1} to 8 tha^{-1} in Europe (England and France) [8]. The major yield-limiting constraints in field pea production in Ethiopia are aphids, low yielding local varieties, lodging, diseases (ascochyta blight, powdery mildew), and

TABLE 1: Description of the test environment.

Location	Years	Environment Code	Altitude (m.a.s.l)	Annual rain fall	Soil Type
Aybera	2010, 2011, 2012 & 2013	E1, E2, E3 & E4	1850	789	vertisol and red sandy soil
Lalibela	2010, 2011 & 2012	E5, E6 & E7	2400	940	Black (vertisol) soil

pod shattering [9] (Yayis *et al.*, 2014). Ethiopian field pea landraces showed lack of resistance gene for two major field pea insect pests, namely, pea aphid and pea weevil (Melaku *et al.*, 2003). Kemal (2002) identified options for the control of field pea pests such as the use of mixed cropping, time of planting and fertilizer application, cultural control, and biological control. On the other hand, several studies revealed that there is valuable genetic variability in field pea collections for yield and yield-related traits [9, 10] which is a good opportunity for Ethiopian field pea researchers to exploit the genetic potential of the crop by integrating conventional with molecular techniques. In general, we believe that the current field pea research should be assisted by more efficient molecular tools to develop varieties that are resistant or tolerant to field pea insect pest.

In Ethiopia, in order to increase field pea productivity, more than 30 improved varieties have been developed and released by national and regional Agricultural Research Center of the country. Most of them are targeted to favourable and wide environments but they are not suited for diverse and challenging environments. In general genotype by environment (GxE) interaction affects the efficiency of crop improvement programs that may lead to complicates recommendation of varieties across divers' environments. Therefore, information on the structure and nature of GxE interaction is particularly useful to breeders (Bridges, 1989; Yayis *et al.*, 2014). However, there is limited information on the extent of GEI in Eastern Amhara in general and in Waghimra in particular. Hence, this trial was initiated with the following objectives:

- (1) To determine and understand the effect of genotype, environment, and their interaction on grain yield of field pea.
- (2) To identify and release stable and high yielding field pea genotype for Wag Lasta and similar agroecologies of the country.

2. Materials and Methods

2.1. Genotypes, Testing Sites, and Experimental Design. Twelve field pea genotypes advanced from observation nursery and preliminary variety trials, together with local check and standard check (Agrit), were evaluated during the main cropping season for four consecutive years (2010 to 2012) in two sites and each site and year were treated as a single environment. The trial was conducted using a randomized complete block design with 3 replications throughout the testing sites. Description of the testing sites is presented in Table 1. The trial was conducted on the plot size of 4m*0.8m with four rows per plot throughout all trial sites and 1.5m

between replication, 1m between plot, 20cm between rows, and 5cm between plant distances were maintained. A variety verification trial was conducted at both Lalibela and Aybera on the trial station and in seven farmers' field during 2016/17 main production season.

2.2. Data Collection. Data on grain yield and yield-related traits were collected on plot and plant basis from each plot, respectively. Date of flowering and maturity were taken when each plot attained 50% flowering and 90% of the pod's physiological maturity, respectively, and days were calculated beginning from the date of sowing. Data for plant height (cm), number of pods per plant, and number of seeds per pod were collected on the basis of five sample plants which were randomly taken from each plot and the average of five sample plants was used for analysis. Hundred seed weight (g) and grain yield (g) of each plot were measured on clean, dried seed and the measured grain yield value (g) has converted to kilogram per hectare for analysis. All agronomic practices were done as per the recommendation for field pea.

2.3. Data Analysis and Analysis of Variances. Data from individual environments and combined over seven locations were analyzed by using SAS (2009) software. The analysis of variance for grain yield and yield-related traits for each environment and over seven environments was analyzed by using randomized complete block design. The combined analysis of variance across the environment was done in order to determine the differences between genotypes across environments, among environments and their interaction. Bartlett's test was used to assess the homogeneity of error variances prior to doing combine analysis over environments. Mean comparison using Duncan's Multiple Range Test (DMRT) was performed to explain the significant differences among means of genotypes and environments.

The combined analysis of variance across environments was done in order to determine differences between field pea genotypes across the environment, among the environment, and also to determine their interaction effect by using the following statistical model:

$$Y_{ij} = \mu + E_j + R(E) + G_i + GE_{ij} + e_{ij} \quad (1)$$

where Y_{ij} is observed mean of the i^{th} genotype (G_i) at the j^{th} environments (E_j), μ is the general mean, G_i , E_j , and GE_{ij} represent the effects of the genotype, environment, and genotype by environment interaction, respectively, $R(E)$ is the effect of replications within environments, and e_{ij} is the average random error associated with the i^{th} plot that receives the i^{th} genotype in the j^{th} environment.

TABLE 2: Mean grain yield (Kg ha⁻¹) of twelve field pea genotypes over seven environments (i.e., across two locations and four years).

Genotypes	Gen. Code	Environment Code							Gen. mean
		E1	E2	E3	E4	E5	E6	E7	
IFPII2712	G1	1941	1081	2273	2882	2115	1459	1351	1872
EH-03-001	G2	1483	976	2565	3125	1999	1475	825	1778
COLL-24/002-1	G3	2263	877	2703	3347	1966	950	1365	1924
EH-03-002	G4	2045	1183	2527	3361	2446	2082	2400	2292
EH-03-010	G5	1408	867	2597	3484	2757	1487	1220	1974
COLL-217/99-5	G6	1971	741	2329	2696	2633	1260	1263	1842
EH-99-009-8	G7	1317	621	2527	3120	2307	1443	1885	1889
IPF-4021	G8	1894	869	2267	2448	2409	1178	2230	1899
EH-03-018	G9	1751	791	2161	2830	1967	1778	1650	1847
EH-99-020-3	G10	1995	823	2446	2629	2545	1455	1243	1877
Agrit (ch)	G11	1487	1140	2580	3017	2218	1377	2202	2003
Local (ch)	G12	2037	623	1923	2855	2135	385	1120	1582
Env. Mean		1799	883	2408	2983	2291	1361	1563	1898
CV%		11.6	8.8	8.0	6.0	6.4	12.5	11.7	9.7
Duncan 5%		**	*	**	**	**	**	**	**

** = significant at 1% probability level, * = significant at 5% probability level, CV = coefficient of variation (%), Env. mean = environmental mean, Gen. Code = genotype code, and Gen. mean = genotypic mean.

ANOVA from Additive Main Effect and Multiplicative Interaction (AMMI) [11] was computed for grain yield by using Gen Stat software (16th edition) that exhibited significant mean squares for genotype and genotype by environment interaction.

3. Results and Discussion

3.1. Analysis of Variance and Mean Performance of 12 Field Pea Genotypes. Analysis of variance for each environment showed a highly significant ($p \leq 0.01$) variation for grain yield and yield-related traits among the tested field pea genotypes (Table 2). This indicated the presence of performance variation among the tested field pea genotypes for grain yield and yield-related traits across the testing environments. Likewise, Mulusew *et al.* [12] and Tamene *et al.* [7] in field pea and Mulusew *et al.* [13] in faba bean had reported significant variation for grain yield and most of the yield-related traits among the tested genotypes across testing environments.

As indicated in Table 2, the average environmental grain yield across genotypes varied from the lowest 621 kg ha⁻¹ at E2 (Aybera in 2011) to the highest at 3484 kg ha⁻¹ in E4 (Aybera in 2012). The highest yielding environment (E4) had 57.16% yield advantage over the environmental gran mean. Environments, E3 and E5, were the second and the third highest yielding environments with mean grain yield of 2408 and 2291 kg ha⁻¹, respectively.

The mean grain yield of field pea genotypes across seven environments ranged from 1582 kg ha⁻¹ for the local check to 2292 kg ha⁻¹ for G4 (EH-03-002) (Table 2). Moreover, performances of genotypes were not consistent across seven environments. For instance, at E2 (Aybera 2011) genotype EH-03-002, at E3 (Aybera in 2012) genotype COLL-24/002-1, at E4 (Aybera in 2013) genotype EH-03-010, and at E6

(Lalibela 2011) genotype EH-03-002 were the top ranking genotypes with the mean grain yield of 1183 kg ha⁻¹, 2703 kg ha⁻¹, 3484 kg ha⁻¹, and 2082 kg ha⁻¹, respectively. Thus, such inconsistent yield ranking from the environment to environment indicated the presence of possible cross over GEI as described by Ermiyas [14] and Matova and Gasura [15].

3.2. Combined Analysis of Variance and Mean Performance of Genotypes over Seven Environments. The combined analysis of variance for grain yield and yield-related traits of twelve field pea genotypes tested in seven environments had performed on the original (untransformed) data (Table 3). The analysis showed that field pea grain yield was significantly ($p \leq 0.01$) affected by environment, genotype, and genotype by environment interaction. The significance of GEI indicated that the relative performances of the genotypes were not consistent across the test environments and the environments had different effects on the yield potential of the genotypes. This, in turn, suggested the need to conduct further analysis on genotype by environment interaction to understand the nature of the interaction. These results agreed with previous findings of Tamene *et al.* [7] which reported that genotypes, environments, and GxE interaction were significantly different for grain yield of field pea. Likewise, other authors also documented a significant GxE interaction for grain yield in field pea [12] and in faba bean [13]. Similarly, analysis of variance indicated a significant effect of genotypes for all collected yield-related traits and significant environmental effect for days to flowering, number of pods per plant, number of seeds per pod, and hundred seeds weight while tested genotypes showed significant variation in days to flowering, number of seeds per pod, and hundred seed weight due to the G X E interaction effect.

TABLE 3: Combined means of grain yield and yield-related traits of 12 field pea genotypes grown at seven environments.

Genotypes	DF	DM	PP	SP	PH	HSW	GY
IFPII2712	50	93	7	5	127	16	1872
EH-03-001	53	95	8	5	131	17	1778
COLL-24/002-1	53	93	7	6	111	13	1924
EH-03-002	53	93	7	6	135	18	2292
EH-03-010	53	94	7	6	120	16	1974
COLL-217/99-5	54	95	8	5	126	16	1842
EH-99-009-8	55	98	8	5	126	18	1889
IPF-4021	53	96	7	5	133	18	1899
EH-03-018	53	95	8	6	131	17	1847
EH-99-020-3	53	94	7	5	124	15	1877
Agrit (ch)	50	92	8	5	129	21	2003
Local (ch)	53	95	7	6	130	12	1582
Mean	53	95	7	5	127	16	1898
Cv %	4.22	2.66	23.98	13.48	11.44	7.28	9.66
Genotype	**	**	**	**	**	**	**
Environment	**	Ns	*	**	Ns	**	**
GxE interaction	**	Ns	Ns	**	Ns	**	**

Ns, *, and ** = nonsignificant, significant at $p < 0.05$, and significant at $p < 0.01$, respectively, DF = days to flowering, DM = days to maturity, PP = pods/plant, SP = seeds/pod, HSW = 100 seed weight (g), GY = grain yield (kg/ha), and CV = coefficient of variation (%).

Among the tested genotypes, EH-03-002 was the highest yielder genotype with the mean grain yield of 2292 kg/ha followed by standard check Agrit (2003 kg ha⁻¹) and genotype, EH-03-010 (1974 kg ha⁻¹), respectively, whereas the lowest mean grain yield (1582 kg ha⁻¹) was registered from a local check (Table 2). As indicated in the same Table 3, five genotypes scored highest grain yield over the grand mean (i.e., 1898 kg ha⁻¹) but only one candidate genotype scored mean grain yield above the standard check Agrit. The candidate genotype, G4 (EH-03-002), was statistically high yielder (2292 kg ha⁻¹) than the other genotypes and showed 14.42% and 44.87% yield advantage over the standard check: Agrit (2003 kg ha⁻¹) and local check (1582 kg ha⁻¹), respectively. This genotype has been verified in 2017 and visited by the national variety releasing technical committee. Accordingly, genotype EH-03-002 has been officially released for its high yielding, deep white grain colour, and high adaptability in the moisture deficit areas of Wag Lasta.

3.3. Additive Main Effects and Multiplicative Interaction Analysis for Grain Yield. The additive main effects and multiplicative interaction (AMMI) analysis for grain yield showed highly significant ($p \leq 0.01$) effect of environment, genotype, and genotype by environment interaction. The effects of environment, genotype, and genotype by environment interaction accounted for 77.47%, 13.83%, and 4.38% of the total sum of squares, respectively (Table 4). A large sum of squares for environments indicated that the environment was diverse, with large differences among environmental means causing most of the variation in grain yield. This also designated the reliability of the multi-environment experiments. The variation in soil type, soil fertility, and moisture availability might be the main reasons for the presence of variation

among environment. In line to this Ermiyas [14] has reported the highest contribution (51.6%) of environmental effect for total variance of soybean grain yield. Similarly, Massaine et al. [16] in cowpea and Tadesse et al. [17] in common bean noticed the highest variation explained by the environmental effect.

AMMI analysis (Table 4) also showed that the first interaction principal component axis (IPCA1), the second interaction principal component axis (IPCA2), and the third interaction principal component axis (IPCA3) of the interaction explained 37.86%, 27.97%, and 14.75% of the interaction sum of squares, respectively. The mean squares for the IPCA1 and IPCA2 were Significant at $P \leq 0.01$ and cumulatively contributed to 65.83% of the total GxE interaction. The third interaction principal component axis (IPCA 3) was also significant ($p \leq 0.05$). For the validation of the variation explained by GEI, the first two multiplicative component axes are adequate because of notable reduction of dimensionality and graphical visualization for the stability patterns of genotypes [18]. According to Yan et al. [19] and Annicchiarico (2002), the AMMI model can be predicted by using the first two IPCAs. Numerous authors utilized the first two IPCAs for AMMI analysis in different crops: for faba bean [13], for field pea (Tamene et al., 2008), for finger millet [20], and for triticale [21]. Thus, the interaction of the 12 field pea genotypes with seven environments was best predicted by the first two principal components of genotypes and environments.

4. Conclusion and Recommendation

Genotype by environment interaction has a key effect on crop variety development by complicating the release of varieties across challenging environments. Analysis of variance for every seven locations and combined over seven

TABLE 4: Additive main effects and multiplicative interaction (AMMI) analysis of variance for grain yield (Kg ha⁻¹) of field pea genotypes across seven environments.

Source	Df	SS	MS	% Total	Sum of square Explained	
					%G X E	% Cumulative Interaction
Total	251	140958296	561587			
Genotypes	11	6169770	560888**	4.38		
Environments	6	109198668	18199778**	77.47		
Block	14	914635	65331	0.65		
Interactions	66	19493498	295356**	13.83		
IPCA1	16	7380110	461257**	5.24	37.86	37.86
IPCA2	14	5451738	389410**	3.87	27.97	65.83
IPCA3	12	2876239	239687*	2.04	14.75	80.58
Residuals	24	3785411	157725			
Error	154	5181726	33648			
Grand Mean (kg/ha) =1897.60			CV(%) = 13.49		R-Square = 0.93	

** = highly significant at the 0.01 probability level, * = significant at the 0.05 probability level, Df = degree of freedom, and IPCA: principal component axis for interaction.

locations showed significant differences among genotypes, environments, and genotypes x environments interaction (GEI) for grain yield and most of the yield-related traits. The significant genotypes x environments interaction effects indicated the inconsistent performance of genotypes across the tested environments. Among the tested genotypes, EH-03-002, Agrit, EH-03-010, COLL-24/002-1, and IPF-4021 had mean grain yield above the overall mean grain yield of genotypes. Only the candidate genotype EH-03-002 had mean grain yield above the standard check Agrit.

Additive main effects and multiplicative interactions (AMMI) model was used to partition the G x E interaction of grain yield of field pea. The results indicated that the environments, GEI, and genotypes were accounted for 77.47%, 13.83%, and 4.37%, of the total sum squares, respectively, indicating that field pea grain yield was significantly affected by the changes in the environment, followed by GEI and genotypic effect.

Considering the seven environments data and field performance evaluation during the variety verification trial, the national variety releasing committee has approved the official release of candidate genotype, EH-03-002, with the vernacular name of “Yewaginesh” for moisture deficit areas of Wag Lasta and similar agroecologies.

Data Availability

The data used to support the findings of this study are available from the corresponding author upon request.

Conflicts of Interest

The authors declare that they have no conflicts of interest.

Acknowledgments

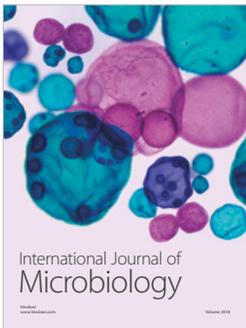
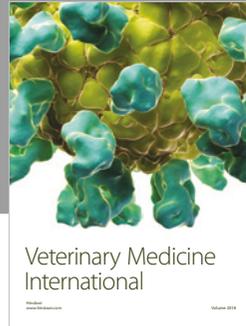
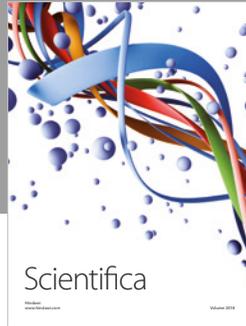
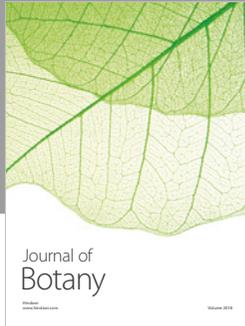
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