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# Genotype × Environment Interaction and Stability of Field Pea (*Pisum sativum* L.) Genotypes for Seed Yield in Northwestern Ethiopia

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## Abstract

Field pea (*Pisum sativum* L.) is a self-pollinated diploid (2n=14) annual cool-season pulse crop. It is a major food legume with a valuable and cheap source of plant protein having essential amino acids that have high nutritional value for resource-poor households. Biotic stress such as weed and insect pests and abiotic stresses like water logging, soil acidity, and low soil fertility are the major constraints to field pea production and productivity. Fourteen field pea genotypes, obtained from Holeta Agricultural Research Center, were evaluated in eight environments in Northwestern Ethiopia in the main production season (2018-2019) to identify stable and high-yielding field pea genotypes. The trial was laid out using a randomized complete block design and replicated three times. Combined analysis of variance for seed yield revealed that genotype, environments, and genotype-by-environment interaction effects were significant ($P < 0.05$). The lowest hundred seed weight value (12.83 g) was manifested by the local check, while the highest value (20.73 g) was revealed by EH 07007-3 genotype from the overall mean of location. The highest mean grain yield of 2400 kg.ha$^{-1}$ was obtained from the EH08003-2 genotype, while the lowest yield 1660 kg.ha$^{-1}$ was obtained from EH 08041-3. The maximum grain yield of 4140 kg.ha$^{-1}$ was recorded from Debark by EH 09015-3 genotype, while the minimum grain yield of 560 kg.ha$^{-1}$ was revealed by EH 08041-3. The environments, GxE, and genotypes accounted for 74.8%, 16.3%, and 7.0% of the total sum squares, respectively, indicating that field pea seed yield was significantly affected by the changes in the environment, followed by GxE interaction and genotypic effect. The candidate genotype, EH08003-2, was the most stable genotype followed by EH 09068-2 and EH 08042-2 having an IPCA score closer to zero with a yield advantage of 26.3% and 36.4% over the standard and local checks, respectively. Considering the eight environments' data and field performance evaluation during the variety verification trial, the National Variety Releasing Committee has approved the official release of EH08003-2 for *kik* seed utilization class with a vernacular name of *Hasset* for high potential areas of Northwestern Ethiopia and similar agro-ecologies.

Keywords: GxE Interaction, GGE-biplot, grain yield, yield attributes

## Introduction

Field pea (*Pisum sativum* L.) is a self-pollinated diploid (2n=14) annual cool-season pulse crop. It is among the major cool-season pulse crops grown in the world (Cherinet and Tazebachew, 2015; Muoni et al., 2019). It is also a major food legume with a valuable and cheap source of protein (23%-25%) having essential amino acids that have high nutritional value for resource-poor households (Getachew, 2019). 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 loam to heavy clay but does not tolerate saline and waterlogged soil conditions (Endres et al., 2016). The crop has the potential of growing in variable ranges of altitude from 1450-3200 meter above the sea level where the annual rainfall is in the range of 400-1000 mm.

Field pea is one of the most important pulse crops next to faba bean, haricot bean, and chickpea in area coverage (219,927.59 ha) with an average seed yield productivity of 1710 kg.ha$^{-1}$ in Ethiopia (CSA, 2021). The crop has ecological and economic importance in Ethiopian highlands as it plays a significant role in

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soil fertility amendment and as a breaking crop. It is suitable for rotation systems to minimize the negative impacts of cereal-based mono-cropping (Muoni et al., 2019).

Despite its importance, biotic stress such as weed and insect pests and abiotic stresses like water logging, soil acidity, lack of emphasis, and low soil fertility are the major constraints to field pea production and productivity, owing to these production constraints and less improved varieties available are widely adopted, the average national productivity of field pea is very low (1700 kg.ha$^{-1}$) (CSA, 2021) as compared to its genetic potential (3560 kg.ha$^{-1}$) and (4170 kg.ha$^{-1}$) research finding in Ethiopia reported by Tolasa et al. (2013) and Mogiso (2017) respectively. Field pea seed quality, as well as how and when the crop is marketed, and high yielder are essential factors in variety development. The development of cultivars, which are adapted to a wide range of diversified environments, is the aim of plant breeders in a crop improvement program (Muhammad et al., 2003). The adaptability of a variety over diverse environments is commonly evaluated by the degree of its interaction with the different environments in which it is grown. A variety is more stable if it has a high mean yield but a low degree of fluctuation in yielding ability when planted over diverse environments (Purchase, 1997).

Many researchers and breeders have investigated and reported grain yield stability using a variety of genotypes in various agro-climatic zones (Samyuktha et al., 2020; Mwiinga et al., 2020; Happ et al., 2021), which are useful for evaluating crop yield stability across varied environmental circumstances and determining acceptable habitats for all genotypes studied. Many stability methods, such as regression, have been devised to uncover the genotype by environment interaction (GxE) pattern (Eberhart and Russell, 1966), but Additive main effect and multiplicative interactions (AMMI) and the genotype and genotype by environmental interaction effect (GGE) were by far providing the better interpretation of GEI data and widely used than the rest of stability procedures (Khan et al., 2021). The AMMI technique combines analysis of variance (ANOVA) and principal component analysis with a biplot displaying the genotype means and their relationship to the first PCA as a key output (Bocianowski et al., 2019). The GGE biplot will aid researchers in better understanding complicated GxEs in multi environment breeding line trials and agronomic investigations (Luo et al., 2015). Phenotypic selection, one of the most critical processes in genetic improvement, is the foundation of traditional field pea breeding. According to Mederos-Ramirez et al. (2021), GxEI in improvement programs has a determining influence on the new cultivar obtained and more stable and adapted genotypes.

The AMMI, the genotype and genotype X environmental interaction effect (GGE) model, can detect GEIs in terms of crossover effects due to significant changes in ranking, therefore, it is widely used. In addition, AMMI and GGE have proven to be particularly useful in visualizing GxE effects in graphical representations. The knowledge and extent of the GxEI provided by this study would aid breeders in allocating limited resources to the appropriate varietal development cycle, as the phenotype combines genotype (G) and environment (E) components, as well as a GxEI. Plant breeders conduct multi environment experiments (MET) to examine the yield stability performance of genetic resources under diverse environmental circumstances (Mwiinga et al., 2020).

This experiment was intended to determine G-x-E interaction and identify superior and stable genotypes for different environmental conditions to attain high seed yield, resistance to both biotic and abiotic stresses, and suitable under different agroecology and cropping systems. The newly developed variety has characteristics of wider adaptation, the most stable, high yield potential, and resistant to powdery mildew disease with growth habit between determinate and indeterminate and bushy stems.

## Materials and Methods

### *The Study Area*

Field experiments were conducted at Adet, Mota, Debark, and Debre Tabor), during the 2018-2019 main cropping season. Descriptions of the geographical coordinates, climate, and soil types of the testing locations are shown in Table 1.

### *Planting Materials and Trial Management*

Fourteen crossing genotypes, obtained from Holeta Agricultural Research Center (HARC), were evaluated along with one recently released variety as a standard check (Teshale), and one local variety which was popularly grown by farmers at each testing site. The genotypes were evaluated in a Randomized Complete Block Design (RCBD) with three replications in a plot size of 4 m by 0.8m (3.2 m$^2$), 4 rows of 4 m length and 0.2 m apart). NPS (38% P, 19% N, and 7% S) were applied at a rate of 121 kg.ha$^{-1}$. All NPS was applied at planting time. Seed at a rate of 150 kg.ha$^{-1}$ was used and planted with an intra- and inter-row spacing of 0.05 m and 0.2 m, respectively. Other agronomic practices such as land preparation, planting, and weeding were applied uniformly to all treatments as

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Table 1. Description of the study site of Adet, Mota, Debark and Debre Tabor

| Location | Latitude (N) | Longitude (E) | Altitude (m) | Soil type | Temperature (°C) | | Annual rainfall (mm) | |
|---|---|---|---|---|---|---|---|---|
| | | | | | 2018 | 2019 | 2018 | 2019 |
| Adet | 11°16’ | 37°29’ | 2216.0 | Nitosol | 18.2 | 18.7 | 1431.8 | 1591. |
| Debark | 13°08′ | 37°54′ | 2850.0 | Cambisol | 19.72 | | 850.14 | |
| DebreTabor | 11°51′ | 38°10′ | 2630.0 | Luvisol | 15.67 | 15.43 | 1609.5 | 1926.1 |
| Mota | 11°50′ | 37°60′ | 2470.0 | Nitosol | 17.15 | 17.75 | 1334.1 | 1457.8 |

Source: Ethiopian Meteorological station at each location in 2018 and 2019

per the recommendation. At all locations, the land was plowed three times by oxen and no irrigation supplement was implemented.

### *Data Collection and Growth Measurement*

Data were collected on plot basis and plant basis from the central rows. Days to flowering (FD) were taken from planting to 50% of the plot exerted flowers. Days to maturity (DM) were taken from planting to 90% of the pod’s reached physiological maturity. Seed yield (kg.ha$^{-1}$) was measured from the harvestable central rows. Finally, the yield per plot was converted to a per hectare basis and the average yield was recorded in kg.ha$^{-1}$. The seed yield was measured at 12% moisture content and the moisture content of all genotypes was adjusted to 12% moisture content. Hundred Seed Weight: Random samples of 100 seeds were counted from the harvested plot yields immediately after grain moisture determination and were weighed in grams.

The number of seeds per pod data were taken from five pods that were randomly taken per plant from each of the ten plants after counting the number of seeds per pod was determined by the average of pods. The number of pods per plant were calculated from five plants that were randomly taken per plot and from each of the five plants after counting; the number of pods per plant was determined by the average of pods. Plant height (cm) was measured from five plants that were randomly taken per plot and from each of the five plants after measuring the height (cm) per plot was determined by the average height.

Improving of a field pea cultivar with high yielder, resistant or tolerant to major diseases such as Ascokyta blight (*Mycosphaerella pinodes*) and powdery mildew (*Erysiphe polygoni*) are among the major objectives of the national field pea improvement program. Ascokyta blight and powdery mildew were very serious problems for field pea crops. The values recorded for both diseases was based on (1-9) scale, which then were converted to pre-transformed percentage values. The percentage values were used to determine the reaction of the released variety ‘Hasset’ to these diseases.

### *Statistical Analysis*

The analysis of variance (ANOVA) for each location and combined analysis of variance over locations and over seasons were performed following the standard procedure given by Gomez and Gomez (1984) using the SAS program Version, 9.4 (SAS, 2013). GGE biplot analysis was carried out using Genstat (2015) software. The homogeneity of error variance was tested using the F-max test method of Hartley (1950) prior to pooled analysis over locations. The F-test was used to detect a significant effect while the mean separation was done using the Least Significant Difference (LSD) at 5% probability level.

## Results and Discussion

### *Analysis of Variance (ANOVA)*

Combined analysis of variance over location and season was carried out for all traits. The combined analysis of variance over the four locations revealed significant differences in yield, thousand seed weight, and plant height among the tested varieties (Table 2). This may be due to the genetic composition of the tested genotypes. The analysis of variance also manifested significant differences among the tested genotypes, locations, and genotype X environmental interactions. This indicates that the tested locations have different potential for field pea crop production due to their agroecological differences (Table 1). Since yield is determined by many factors such as soil, climate, and agronomic conditions (Din et al., 2019).

These results agree with previous findings of Tolesa et al. (2013) and Rezene et al. (2014) which reported that genotype, environments, and genotype by environmental interaction were significantly different for seed yield in field pea. In line with this, Tadele

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et al. (2018) reported a highly significant variation of year, environment, genotypes, and genotype by environmental interaction for mean seed yield of combined data analysis of common bean genotypes. Similarly, Mogiso (2017) reported a significant difference among the tested improved varieties of field pea that were tested over the years. The performance of a given variety depends upon its genetic potential and the environment where it is grown (Mangistu et al., 2011). Kindie et al. (2019) reported significant differences among the tested field pea genotypes across the tested environments for grain yield and other yield-related traits.

Table 2. Combined mean analysis of variance (ANOVA) of 16 field pea genotypes combined locations (Adet, Mota, Debark, and Debre-Tabore) and season (2018 and 2019) as per AMMI model

| Source variation | DF | SS | M S | F Value | P-value |
|---|---|---|---|---|---|
| Total | 383 | 223.12 | 0.583 | | |
| Treatments | 127 | 218.81 | 1.723 | 99.04 | <0.001 |
| Genotypes | 15 | 15.47 | 1.032 | 59.30 | <0.001 |
| Environments | 7 | 166.94 | 23.849 | 2826.76 | <0.001 |
| Block | 16 | 0.13 | 0.008 | 0.49 | 0.9530 |
| G x E | 105 | 36.39 | 0.347 | 19.93 | <0.001 |
| IPCA 1 | 21 | 14.16 | 0.674 | 38.77 | <0.001 |
| IPCA 2 | 19 | 7.06 | 0.372 | 21.36 | <0.001 |
| Residuals | 65 | 15.17 | 0.233 | 13.42 | <0.001 |
| Error | 240 | 4.17 | 0.017 | | |

Note: SV- source of variation; DF=degree of freedom, MS=mean of squares, SS=Sum of squares, IPCA = Interaction Principal Component Axes

### *Mean Performance of the Genotypes*

#### *Seed yield*

The mean grain yield of the evaluated field pea genotypes across the four locations ranged from 1660 kg.ha$^{-1}$ (EH 08041-3) to 2400 kg.ha$^{-1}$ (EH08003-2) (Table 3). Moreover, the performance of the genotypes was not consistent across the eight environments. This may be due to environmental variations and the genotype-by-environment interaction (GEI) that causes variation in seed yield and phenotypic traits of specific genotypes. Niedbała et al. (2019) and Niazian and Niedbała (2020) explained environmental variations and genotype by environment interaction (GEI) that causes variation in seed yield and phenotypic traits. For combined data analysis, genotype EH08003-2 revealed the highest mean grain yield over the eight environments, followed by EH 09068-2, EH 05048-3, while EH 08041-3 manifested the lowest seed yields. Significant yield variations between Debark and Adet were observed, indicating considerable environmental differences between them. Debark was more favorable for field pea production, whereas Adet recorded low seed yield. It also indicated that the varieties responded differently at different locations because of genotype X environment interaction.

Grain yield may be the result of many plant characteristics which interact with numerous external factors during the life of the plant. The ranking of genotypes based on grain yield may be considered a reliable measure of genotypic performance (Niazian and Niedbała, 2020). The mean yield obtained showed a statistically significant difference among the tested genotypes for grain yield at a 5% significance level. The highest mean grain yield of 2400 kg.ha$^{-1}$ was obtained from the EH08003-2 genotype, while the lowest yield 1660 kg.ha$^{-1}$ was obtained from EH 08041-3 (Table 3). The maximum grain yield of 4140 kg.ha$^{-1}$ was recorded from Debark by EH 09015-3 genotype, while the minimum grain yield of 560 kg.ha$^{-1}$ was revealed by EH 08041-3. On another hand, all tested genotypes performed well at Debark whereas relatively low yield was obtained from Adet environment. But Ceyhan and Avci (2015) reported that the observed differences in grain weight among varieties might be due to inherent genetic differences among the varieties.

#### *One hundred seed weight*

Even though a hundred seed weight is one of the seed yield-determining traits, in the present study, the maximum hundred seed weight was not revealed for the maximum seed yield genotypes. This may be because of genotype and its interaction with the

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environment. Habtamu and Million (2013) reported a negative association between hundred seed weight and seed yield. In the present study, a hundred seed weights showed statistically significant differences among the tested genotypes. The lowest hundred seed weight value (12.83 g) was manifested by the local check, while the highest value (20.73 g) was revealed by EH 07007-3 genotype from the overall mean of location (Table 3). The obtained value for hundred seed weights varied among locations within the same genotype, this is due to the existence of genotypes in environmental interaction.

The maximum hundred seed weight (20.73 g) was recorded by EH 07007-3 genotype for the combined data analysis, while the minimum hundred seed weight (12.83 g) was shown by local check. Bolded seeded field pea has high market preference whereas smaller seed size is preferred by women farmers since small seed size variety is mainly used for local *shiro* preparation.

*Number of pods per plant*

The number of pods per plant, number of seeds per plant, plant height, biological yield, and harvest index were the most important factors in determining seed yield, indicating that selection for any one of them may permit an improvement in seed yield in the field pea program (Yasin and Mathewos, 2014). The combined data analysis for the number of pods per plant revealed non-significant differences among the tested genotypes (Table 3). In this study, the number of pods per plant is one of the most important components for seed yield, but the number of pods per plant was non-significant. Higher numbers of pods per plant were desired for getting higher seed yield per plant. The relationship of yield per plant with the number of pods per plant had a significant role for desirable seed yield improvement.

*Number of seeds per pod*

The number of seeds per pod is the most important component for seed yield and their higher values are desired in seed yield. The relationship of yield per plant with the number of seeds per pod has a significant role for desirable seed yield improvement. The maximum number of seeds per pod was 5, registered for local check, while the other 15 genotypes have 4 numbers of seeds per pod of each genotype locations (Table 3).

*Plant height*

Plant height ranged from 121.48 cm to 140.18 cm, where EH008029-3 cm exhibited the highest while EH 04052-1 cm were the lowest (Table 3).

*GGE Biplot Analysis*

GGE Biplot can be used to evaluate the average yield and stability of a genotype as compared with others in the trial rank environments based on the ability to differentiate genotype performance, distinguish a genotype having the best performance in a particular environment, and identify mega-environments within a target region based on the specifically adapted genotypes (Esan et al., 2023). A line that passes through the biplot origin and the average environment, referred to as the “average environment coordination” (AEC); a small circle indicating the position of the average environment, which is defined by the average PC1 and PC2 scores across all environments. This average environment can be regarded as an ideal environment; a thick line that passes through the biplot origin and the average environment, referred to as the average- environment Coordination (AEC); a green arrow pointing to the average environment from the biplot origin; a thick green line that passes through the biplot origin and is perpendicular to the AEC. The blue line separates entries with below-average means from those with above-average means (figure 1). In GGE, genotypes that fall in the central (concentric) circle are considered stable genotypes. Therefore, genotype EH08003-2 fell in the central circle indicating its high yield potential and relative stability compared to the rest of the genotypes.

*Genotype and Stability*

The vector length of the average environment (the distance from biplot origin and the average environment marker), relative to the biplot size, is a measure of the relative importance of the genotype main effect (G) vs. the genotype by environment interaction (GE). The longer it is, the more important G is and the more meaningful the selection based on the mean performance. At extremes, a zero average environment vector means G = 0 and therefore the selection based on mean performance is meaningless. Based on their mean performance across all environments, the genotypes are ranked along the AEC, with the arrow pointing to a greater value. The closer an environment is placed to this ‘ideal” genotype, the more desirable it is judged on both mean performance and stability.

The Interaction Principal Component Axe (IPCA) scores of a genotype in the AMMI analysis indicate the stability of a genotype across environments. The closer the IPCA scores to zero, the more stable the genotypes are across their testing environments

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Table 3. Combined mean grain yield and other important agronomic characters of 16 field pea genotypes in the field pea regional variety trial (2018 and 2019)

| Code | GENOTYPE | PH | DF | DM | PPP | SPP | HSW | GY (kg.ha$^{-1}$) |
|---|---|---|---|---|---|---|---|---|
| 1 | EH 05048-3 | 131.64 | 65.13 | 119.71 | 8.58 | 4.14 | 18.61 | 2280 |
| 2 | EH08003-2 | 123.73 | 67.92 | 120.38 | 9.13 | 4.31 | 18.21 | 2400 |
| 3 | EH 08042-2 | 135.59 | 68.13 | 121.58 | 8.82 | 4.21 | 17.52 | 2170 |
| 4 | EH 09068-2 | 133.40 | 65.42 | 120.04 | 8.67 | 4.38 | 16.75 | 2170 |
| 5 | EH0 08029-3 | 140.18 | 65.17 | 121.58 | 8.66 | 4.27 | 19.00 | 2100 |
| 6 | EH 09005-3 | 128.72 | 66.42 | 120.25 | 8.28 | 4.08 | 18.56 | 1990 |
| 7 | EH 09015-3 | 127.34 | 66.48 | 119.30 | 8.23 | 4.13 | 18.92 | 2140 |
| 8 | EH08037-1 | 133.13 | 65.63 | 119.67 | 8.22 | 4.15 | 18.37 | 1780 |
| 9 | EH 08041-3 | 135.82 | 65.83 | 122.00 | 8.78 | 3.86 | 17.37 | 1660 |
| 10 | EH09009-2 | 128.56 | 69.08 | 121.13 | 8.29 | 4.40 | 19.14 | 2100 |
| 11 | EH 04052-1 | 121.48 | 64.58 | 117.96 | 8.05 | 3.99 | 20.14 | 2130 |
| 12 | EH 09029-2 | 124.45 | 64.13 | 117.67 | 8.63 | 4.37 | 17.44 | 2040 |
| 13 | EH 09017-1 | 128.25 | 65.67 | 118.96 | 8.37 | 4.25 | 18.61 | 1820 |
| 14 | EH 07007-3 | 128.43 | 65.96 | 120.00 | 8.68 | 3.77 | 20.73 | 1810 |
| 15 | Teshale | 123.35 | 65.21 | 118.75 | 8.90 | 3.96 | 18.27 | 1900 |
| 16 | Local variety (control) | 129.20 | 67.38 | 119.79 | 8.88 | 4.63 | 12.83 | 1760 |
| | Means | 129.58 | 66.13 | 119.92 | 8.57 | 4.18 | 18.15 | 2010 |
| | CV | 13.8 | 14.3 | 8.69 | 23.02 | 16.3 | 10.27 | 19.57 |
| | Genotype | * | ns | ns | ns | ** | ** | ** |
| | Environment | ** | ** | ** | ** | ** | * * | ** |
| | G x E | ns | ns | ns | ns | ns | * | ** |

Note: DF=days to flowering, DM=days to maturity, PH=plant height, PPP=pod per plant, SPP=seed per pod, HSW=hundred seed weight, GY= Grain yield, ** significant at p<0.01, * significant at p<0.05, and ns is not significant

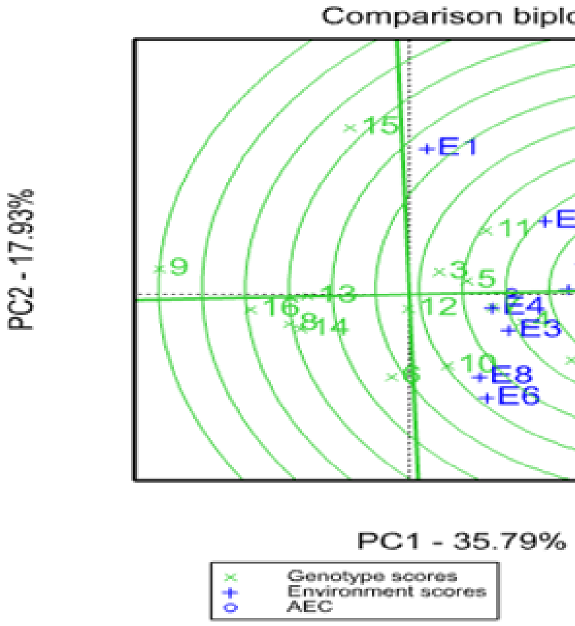

Figure 1. GGE-biplot based on genotype-focused scaling for comparison the genotypes with the ideal genotype. X followed by number and + followed by E (E1= Adet 2018, E2= Adet 2019, E3=Mota 2018, E4=Mota 2019, E5= Debre Tabor 2018, E6= Debre Tabor2019, E7= Debark 2018 and E4= Debark 2019) stand for genotypes and environments, respectively.

(Carbonell et al., 2004).

A longer projection of the blue line, regardless of the direction, represents a greater tendency of the genotype by environment interaction for the genotype, which means more variable and less stable across environments (Figure 2). High stability means performing consistently well when associated with high mean performance and consistently poorly when associated with low mean performance, like genotype 2 which performs constantly with high seed yield (Figure 2). The ranking of the genotypes from figure 2 is: genotype2 > genotype 1 > genotype 3 > genotype 4 > genotype 7 > genotype 10 > genotype 11…> genotype 9.

are characterized by the similar performance of all genotypes; hence they provide little information about the genotypic differences. The GGE biplot provides us with significant visualization of the data by creating a biplot that represents the mean performance and stability as well (Esan et al*.,* 2023). Therefore, these four locations can be efficiently used for field pea multi-environment yield trials across years for cultivar recommendation. However, identification and removal of non-informative test locations, as well as identification of test locations for yield evaluation trials, requires multiyear data (Esan et al., 2023).

The GGE biplot result revealed that EH08003-2 was the most stable and high yielding genotype compared to other genotypes and standard checks. The utilization of this variety is Kik type (the Kik type of field pea has white flower color and white creamy seed color, larger seed size and mostly produced for export). The passport data of “Hasset” is indicated in Table 4.

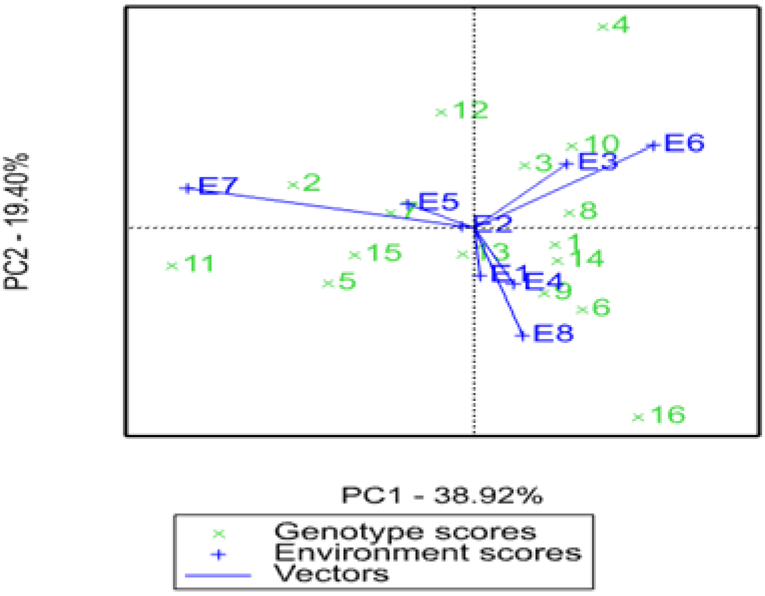

Figure 2. GGE- biplot based on Environment -focused scaling for comparison of genotypes with the ideal genotype. X followed by number and + followed by E stand for genotype and environments, respectively.

The discriminating power of environments vs the representativeness of the mega-environment view of the biplot is indicated in Figure 2. From this GGE biplot view, the discriminating power of the environment is proportional to the length of an environment vector. Accordingly, the test environment E7, E6, and E8 show long vectors, Hence, Debark is a more discriminating environment than others and could be a potential environment to screen early generation field pea genotypes. Moreover, E7, E6, and E8 exhibited smaller angles with the average environment coordination (AEC), implying debark is not only a discriminating but also a representative environment of field pea growing areas of Northwestern Ethiopia. Thus, future field pea screening should be conducted at Debark to identify superior field pea genotypes that could do well in field pea growing areas of Northwestern Ethiopia. Environments E2, closer to the biplot origin,

### *Reaction to Major Diseases*

Improving of a field pea cultivar with high yielder, resistant or tolerant to major diseases such as powdery mildew (*Erysiphe polygoni*) and for wider adaptation areas are among the major objectives of the national field pea breeding program. Powdery mildew disease is a very serious problem for field pea crops. The value recorded for this disease based on the (1-9) scale was converted to the pre-transformed percentage values, which were then

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Table 4. Morpho-agronomic description of "Hasset" variety released in 2021.

| Characteristic parameter | Description of agronomic/morphological characteristics |
|---|---|
| Variety name | Hasset (EH08003-2) |
| Adaptation area | Adet, Mota, Debre Tabor, Debark, and similar agroecology in Ethiopia. |
| Seed rate (kg.ha$^{-1)}$ | 150 (spacing: 20 cm between rows and 5 cm between plants) |
| Planting date: | Mid-June to early July depending on the onset of rainfall |
| Fertilizer rate (kg.ha$^{-1}$) | 121 NPS |
| Days to flowering | 61-76 |
| Days to maturity | 117-152 |
| Plant height (cm) | 123 |
| 100 seed weight (g) | 20.5 |
| Seed characters | Spherical |
| Seed color | Variegated (yellow) |
| Flower color | White |
| Growth habit | Indeterminate and bushy |
| Pod character | Full |
| Crop pest rection | Moderately resistant to powdery mildew and rust |
| Seed yield (kg.ha$^{-1}$) | Research field = 2300–3340, and Farmers' field = 1800–2700 |
| Breeder/maintainer | Adet Agricultural Research Center |

used to determine the reaction of the released variety 'Hasset' to major diseases (Little and Hills, 1978). Consequently, the released variety 'Hasset' showed moderately resistant to powdery mildew disease.

## Conclusions

Based on genotype means and stability analysis and mean separation result analysis, the genotypes EH08003-2, EH 09068-2, EH 08042-2, and EH0 08029-3 were high yielding and have wide adaptability. adapted. Whereas EH08003-2 was the most stable genotype followed by EH 09068-2 and EH 08042-2 having IPCA score closer to zero. The GGE biplot result revealed that EH08003-2 was the most stable and high yielding genotype, as a result, the candidate genotype; EH08003-2 had 26.3% yield advantage over the standard check and 36.4% over the local check. Considering the eight environments' data and field performance evaluation during the variety verification trial, the National Variety Releasing Committee has approved the official release of EH08003-2 with the local name of "Hasset" for potential areas of northwestern Ethiopia and similar agro-ecologies.

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