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Mean Performance of Field pea (Pisum sativum L) Advanced Genotypes for Yield and Yield-related Traits in Arsi Zone, Ethiopia

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ABSTRACT

Pea (Pisum sativum L.) is the second most important cool-season food legume in Ethiopia after faba bean, both in terms of production area and annual yield. The study comprises 13 advanced field pea genotypes that were evaluated in a randomized complete block design with four replications across four different environments during two consecutive main cropping seasons (2020–2021). The primary objectives were to identify a field pea genotype with a reliable, high grain yield that could be subsequently released as a new cultivar for farmers in specific areas of Ethiopia. A combined analysis of field pea grain yield revealed a significant difference ($P < 0.01$) between genotypes and environments, suggesting that the genetic composition of the genotypes varied and the environments were distinct. The average grain yield ranged from 1614 kg/ha to 2412 kg/ha, with a mean of 2032.69 kg/ha. Genotype G13 had the highest average grain yield (2412 kg/ha) compared to the standard check varieties Bilalo (2190 kg/ha) and Bursa (2100 kg/ha), indicating its potential for developing adaptable varieties suited to specific environments. This outcome may aid breeders in choosing the most appropriate cultivars for particular environments, resulting in higher field pea yields and productivity. Nonetheless, the research also indicates that to create broadly adaptable and climate-resilient varieties, it is crucial to carry out trials in various locations and across multiple years.

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Introduction

Field pea (Pisum sativum L.) is a diploid (2n=14) annual plant that undergoes self-pollination (Gurmu et al., 2022) and (Kindie et al., 2019). It is considered one of the most significant cool season pulse crops and is highly considered for its high protein content. This crop is extensively cultivated in cooler temperate zones as well as in the highlands of tropical regions across the globe. While it can thrive in various soil types, ranging from light sandy loams to heavy clays, it is unable to withstand saline and waterlogged soil conditions. The crop covers 219,927.59 ha, ranking fourth in pulse crops production in Ethiopia after faba bean, haricot bean, and chickpea. The average yield productivity is 1.71 t/ha (Kebede et al., 2023).

The yield of field pea production varies from location to location due to the differences in the environment and the lack of suitable field pea varieties that can adapt to a broader range of environments (Yihunie and Gessese, 2018). Farmers produce various types of varieties that differ from one place to another. They have also developed local cultivars and somewhat improved ones that show instability in their performance. (Tadele et al., 2017). Therefore, it is necessary to test selected materials across various sites and years to ensure that new varieties exhibit consistent performance in different environments. The traditional approach of dividing the total variation into different components such as genotype, environment, and GEI provides limited insight into the specific response patterns of individuals (Tadele et al., 2017). Additionally, using stability measures can help to identify varieties that are adaptable to a wide range of conditions or specific environments, which is important for large-scale production.

The term stability in agriculture is commonly used to evaluate how consistent certain characteristics are over time or in different locations. Specifically, it refers to the capacity of agricultural outputs, such as yield, to remain consistent over a long period or in diverse spatial settings. In recent years, the importance of yield stability analysis has increased due to the effect of climate variability on crop yield stability.

Selection progress can be limited by significant G x E interaction for quantitative traits like grain yield due to climate change and ecological variations. According to predictions, by 2050 we can expect significant impacts such as higher temperatures, more frequent droughts caused by increased evaporation and changes in rainfall patterns, and increased levels of CO2 due to greenhouse and agricultural gas emissions (Andrews and Hodge, 2010). It is predicted that current levels of agricultural production and field crop productivity in different ecologies and regions will be significantly impacted. It is predicted that people in developing countries who rely mostly on vegetarian diets will face a major challenge in accessing legumes by the year 2050. To address this issue, it is important to develop an efficient agronomic production system, introduce widely adopted resistant and high-yielding cultivars, and utilize diverse genetic sources to improve new varieties that can thrive in different ecologies and regions.

Materials and Methods

Descriptions of Experimental Locations

The field experiment was carried out in four Kulumsa Agricultural Research sub-stations, each situated in the South-Eastern region of Ethiopia and characterized by a unique set of climatic and soil conditions that influence the growth of cool-season legumes, including field peas. The experiment, which spanned over two cropping years, from 2020 to 2021, was meticulously designed to investigate the impact of various environmental factors on the yield of these legumes.

Design and Experimental Materials

Thirteen advanced field pea genotypes were tested against two standard checks (Bursa and Bilalo) in the main growing season of 2020-2021, under rain-fed conditions, across four environments (Table 2). A randomized complete block design was utilized across all testing sites, with four replications. The plots were all the same size, measuring 4 meters in length and 0.8 meters in width. The distances between the replications, plots, rows, and plants were carefully maintained at 1.5 meters, 1 meter, and 20 centimeters between rows, respectively. The recommended amount of bulked fertilizer (NPS) used was 100 kg/ha, and hand weeding was carried out three to four weeks after emergence.

Data Collection

Data on yield and yield component traits were collected from each experimental unit on both plot and plant basis. Phenology data, such as the date of flowering and maturity, were recorded when each plot attained 50% of the plant starting to flower and 90% of the pod changed to black or physiological maturity, respectively in plot bases. Thousand seed weight was determined by measuring the weight of 1000 randomly selected seeds from each plot. Plant height (in cm), number of pods per plant, and number of seeds per pod were measured by randomly selecting five sample plants from each plot. The average measurements of these five sample plants were then used for analysis. The grain yields in grams of each plot were measured on clean, dried seed, and the measured grain yield was adjusted to 10% grain moisture content and converted to kg ha^{-1} for analysis.

The severity of Ascochyta blight and powdery mildew diseases was measured using a scale ranging from 1 to 9. A score of 1 meant there were no visible disease symptoms, indicating immunity. A score of 3 indicated a few disease symptoms, meaning resistance. A score of 5 meant there were some coalesced lesions with some defoliation, indicating moderate resistance. A score of 7 meant large coalesced sporulation lesions, and 50% defoliation of some dead plants, indicating susceptibility. A score of 9 meant extensive, heavy sporulation, stem girdling, blackening, and death of more than 80% of plants, indicating heavy susceptibility (Tadele et al., 2021).

Data Analyses

The collected data were analyzed using the R software version 4.3.2 with Metan and other appropriate packages. The analysis of variance was performed on data from both individuals and combined environments. The significance of the main effect and interactions related to the measured parameters were determined using a randomized complete block design (RCBD) for each environment and across four environments. A combined ANOVA was conducted using combined ANOVA a model in which the genotype was fixed, environment and interactions were random. The year factor was considered a separate environment.

The model: RiJкr = M + Gi+ Lj + r (L) + (G×L)iJ + eijkr. Where M = grand mean; G = genotype; L = location; and (G×L)iJ = genotype by location interaction; r (L) = replication within the location; and eijkr = random error. A statistical analysis was performed using Duncan's Multiple Range Test (DMRT) to determine the significant differences between the means of various genotypes and environments.

Table 1 Description of the experiment area soil physical with chemical property and climate data

Location	Altitude (m)	Latitude	Longitude	%Clay	%Silt	% Sand	Soil type	Soil pH	%TN	%OC	Av.P (ppm)
Assasa	2372	07007'04.3''	039011'50.4"	39.375	23.125	37.5	Clay-loam	6.25	0.12	2.26	34.22
Bekoji	2811	07032'32.7"	039015'18.6"	61.875	30.625	7.5	Clay-soil	5.48	0.19	2.44	4.72

climate data

	Year- 2020 Temperature			Year-2021 Temperature		
Location	MAX	MIN	Rainfall	MAX	MIN	Representing Agro-ecology
Assasa	19.3	8.1	539.6	21.9	5.7	Terminal drought prone
Bekoji	20.7	4.8	876.1	22	4.6	Highland and high rainfall

Note: Av.ppm = available phosphors in parts per million, %OC = Organic carbon in

Table 2. Descriptions of Plant Materials

Code	Genotypes	Sources
G1	EH 012014-4	Hybrid
G2	EH0120206-6	Hybrid
G3	Bursa	Released variety
G4	EH012026-3	Hybrid
G5	EH012002-1	Hybrid
G6	EH012020-5	Hybrid
G7	EH012002-2	Hybrid
V2	EH012024-5	Hybrid
G9	Bilalo	Released variety
G10	EH012026-6	Hybrid
G11	EH012024-3	Hybrid
G12	EH012003-3	Hybrid
G13	EH012026-7	Hybrid

Note: G1, G2, G3…G13 are Genotype one up to Genotype thirteen and V1 and V2 variety one, variety two

Table 3. Combined Analysis of Variance (ANOVA) for nine traits of 13 Field pea Genotypes evaluated at 4 environments (2020-2021)

TR	Source of variations					
	Genotype (df = 12)			Location (df =3)		
	S	M	P	S	M	P
DF	987.36	82.28	0.000	7086.63	2362.21	0.000
DM	118.77	9.90	0.001	41861.17	13953.72	0.000
PH	4941.55	411.80	0.482	281554.77	93851.59	0.000
PPL	119.73	9.98	0.298	2484.36	828.12	0.000
SPP	7.14	0.60	0.260	238.96	79.65	0.000
TSW	26885.62	2240.47	0.000	95532.99	31844.33	0.000
AB	7.48	0.62	0.076	38.36	12.79	0.000
PM	22.89	1.91	0.000	42.48	14.16	0.000
YLD	14936615.7	1244718.0	0.000	414548046.0	138182682.0	0.000

TR	Source of variations							
	Genotype × Loc (df= 36)			Rep(Loc) df= 12			Error (df=144)	
	S	M	P	S	M	P	S	M
DF	459.18	12.76	0.000	58.52	4.88	0.000	218.23	1.52
DM	193.08	5.36	0.038	108.04	9.00	0.004	498.46	3.46
PH	14198.61	394.41	0.591	5162.23	430.19	0.441	61242.77	425.30
PPL	290.51	8.07	0.540	178.56	14.88	0.058	1210.44	8.41
SPP	10.74	0.30	0.951	11.38	0.95	0.030	68.96	0.48
TSW	12891.13	358.09	0.361	7662.45	638.54	0.035	47633.72	330.79
AB	12.33	0.34	0.594	18.98	1.58	0.000	53.27	0.37
PM	25.14	0.70	0.008	39.19	3.27	0.000	55.81	0.39
YLD	11739331.2	326092.5	0.263	2178966.0	181580.5	0.8	40345726.0	280178.7

Note: TR: Traits; S: Sum sq.; M: Mean sq.; P: $P<0.05$.; DF = Number of days to 50% flower, DM = Number of days to Mature, PH = Plant height, PPL = Number of pods per plant, SPP = Number of seeds per pod, TSW = 1000 seeds weight, AB = Ascochyta blight, PM = Powdery mildew and YLD = grain yield

Results and Discussion

Analysis of Variance for Yield and Other Component Traits

The study found significant differences ($P < 0.01$) in grain yield and seed weight among different genotypes and locations. However, the genotype by environmental interactions showed non-significance ($P < 0.05$) for both traits (Table 3). The results of this study align with the findings of (Argaye et al., 2023), (Kindle et al., 2019) and (Girma Mangistu et al., 2011) significant variations were reported. indicating that the yield component traits, namely Number of pods per plant (PPL), number of seeds per pod (SPP), and plant height (PLH) did not exhibit significant differences ($P< 0.05$) between genotypes or genotype by environment interactions. These results suggest that the thirteen genotypes studied demonstrated uniform responses for yield-related traits across varied locations, as evidenced by the data presented in Table 3.

The study found significant differences ($P<0.01$) among genotypes, location, and genotype by location interaction in the phonological traits of days to 50% flower and days to mature. The results suggest that the genotypes were genetically diverse and that location had varying effects on these traits. Moreover, the significant effects of genotype by location interaction indicate that different genotypes exhibited different flowering and maturing patterns in different locations (Table 3).

The study investigated the reactions of different genotypes to the major field pea disease; Aschochyta blight (AB) and Powdery mildew (PM).

Table 4. Combined Mean performance of 13 field pea genotypes for the nine traits conducted in 2020 - 2021 main cropping seasons

Genotype	Entry	DF	DM	PH	PPP	SPP	TSW	Yldkg/ha	AB	PM
EH 012014-4	G1	74^{ef}	140^{b-d}	172^{abc}	10^{abc}	4^{bc}	223^{a}	2269^{abc}	5^{a}	4^{ab}
EH0120206-6	G2	77^{b}	140^{b-d}	165^{abc}	10^{abc}	4^{abc}	218^{a}	2360^{ab}	5^{a}	4^{ab}
Bursa	G3	71^{g}	140^{b-d}	164^{bc}	11^{a}	4^{abc}	179^{d}	2100^{a-d}	5^{a}	5^{a}
EH012026-3	G4	74^{ef}	139^{de}	171^{abc}	10^{abc}	4^{c}	216^{a}	1642^{f}	5^{a}	4^{ab}
EH012002-1	G5	74^{de}	140^{b-d}	178^{ab}	10^{abc}	4^{abc}	202^{bc}	1820^{def}	5^{a}	4^{ab}
EH012020-5	G6	76^{bc}	140^{abc}	169^{abc}	10^{abc}	4^{c}	195^{c}	2038^{b-e}	5^{a}	4^{ab}
EH012002-2	G7	76^{c}	140^{bcd}	174^{abc}	$9b^{c}$	4^{abc}	203^{bc}	1614^{f}	5^{a}	4^{ab}
EH012024-5	G8	78^{a}	141^{a}	178^{a}	9^{abc}	4^{abc}	201^{bc}	1945^{c-f}	5^{a}	4^{ab}
Bilalo	G9	76^{b}	141^{ab}	169^{abc}	8^{c}	5^{a}	213^{ab}	2190^{abc}	5^{a}	4^{ab}
EH012026-6	G10	75^{cd}	139^{cde}	165^{abc}	10^{abc}	4^{abc}	203^{bc}	1722^{ef}	5^{a}	4^{ab}
EH012024-3	G11	77^{b}	140^{abc}	163^{c}	9^{abc}	4^{abc}	201^{bc}	1946^{c-}f	5^{a}	4^{ab}
EH012003-3	G12	70^{g}	140^{abc}	169^{abc}	11^{a}	5^{ab}	194^{c}	2369^{ab}	5^{a}	4^{ab}
EH012026-7	G13	73^{f}	138^{e}	174^{abc}	11^{ab}	4^{abc}	195^{c}	2412^{a}	5^{a}	4^{ab}
	Mean	74.70	139.80	170.02	9.85	4.31	203.41	2032.69	5	3.95
	CV	1.65	1.33	12.13	29.43	16.07	8.94	26.04	12.04	15.75
	LSD	0.86	1.30	14.41	2.03	0.48	12.71	369.90	0.43	0.44

Table 5. Within Environment mean grain yield (kgha^{-1}) performance of 13 field pea genotypes conducted across two years (2020 - 2021)

Genotypes	Code	E 1	E2	E3	E4
EH 012014-4	G-1	3232.03^{ab}	4166.87^{ab}	1098.04^{abc}	577.52^{ab}
EH0120206-6	G-2	3336.34^{a}	4520.91^{ab}	941.4^{bcde}	640.45^{ab}
Bursa	G-3	2933.59^{abcd}	4321.32^{ab}	722.79^{def}	421.48^{b}
EH012026-3	G-4	1901.55^{cd}	3753.67^{abc}	662.93^{ef}	251.16^{b}
EH012002-1	G-5	2188.86^{bcd}	3985.36^{ab}	899.61^{bcdef}	270.44^{b}
EH012020-5	G-6	2742.5^{abcd}	4148.09^{ab}	642.85^{f}	616.72^{ab}
EH012002-2	G-7	2094.21^{cd}	3091.85^{c}	834.96^{cdef}	435.08^{b}
EH012024-5	G-8	2803.62^{abcd}	3698.85^{bc}	858.95^{cdef}	481.94^{b}
Bilalo	G-9	2511.41^{abcd}	4559.91^{a}	1174.69^{ab}	513.05^{b}
EH012026-6	G-10	1883.24^{d}	3682.54^{bc}	735.99^{def}	585.68^{ab}
EH012024-3	G-11	2870.85^{abcd}	3686.74^{bc}	682.3^{ef}	543.5^{b}
EH012003-3	G-12	3023.27^{abc}	4437.73^{ab}	1006.93^{abcd}	1006.48^{a}
EH012026-7	G-13	3541.65^{a}	4209.53^{ab}	1240.79^{a}	656.45^{ab}
	Mean	2697.2	4020.3	884.8	538.5
	CV	29.2	14.2	23.2	28.8
	LSD	1133.1	845	295.5	454.8

Note: G1, G2, up to G13 Number of Genotypes, E1, E2, E3, E4 Number of Environments

The study found that there was no significant difference ($P<0.05$) between genotypes and the genotype by location interaction for Aschochyta blight disease. However, Powdery mildew disease showed a highly significant difference among genotypes, location, and genotype by location interaction. Interestingly, none of the tested genotypes showed different reactions to Aschochyta blight disease. However, the study revealed that different genotypes showed distinct reactions to the powdery mildew disease at different locations and genotype-by-location interaction. These findings are important for plant breeders and growers as they help them select the best genotypes that can resist the powdery mildew disease, which is a major threat to field pea production in Ethiopia.

Mean Performance of Grain Yield and Other Related Traits

The mean grain yield of 13 different field pea genotypes was analyzed, and it ranged from 1614kgha^{-1} to 2412kgha^{-1}, with a grand mean of 2032.69 kg/ha^{-1}. Five of the genotypes produced a higher yield than the control varieties, Bursa and Bilalo, as shown in (Table 4). The findings of similar advanced field pea research have been documented by previous researchers (Haile and Tesfaye, 2024; Zeleke et al., 2024; Tolessa et al., 2013). Genotype G13 had the highest mean grain yield amongst all the genotypes, relative to the two standard check varieties. This suggests that there is potential for better genetic gain from the field pea breeding program. This finding is consistent with the study conducted by (Yang et al. 2023) and (Vasileva et al., 2021) which also reported significant differences among the advanced field pea genotypes compared to the control varieties.

There were genetic differences among the field pea genotypes for days to 50% flowering. The genotype G12 had the shortest time to reach 50% flowering compared to other genotypes. On the other hand, the genotype G8 was delayed in flowering. The findings of (Tadele et al., 2021) support this result, demonstrating significant variations in both yield and yield component traits in faba bean mean performance trials. When it comes to days to maturity, genotype G13 matured the earliest, while G8 was the latest. G13 was a relatively early-maturing genotype that had a high number of pods per plant and produced the highest yield. The mean disease score for AB was found to be consistently similar across all tested genotypes, while PM showed no significant differences, except for the control variety Bursa i.e. susceptible. These results strongly suggest that breeding strategies for field peas must prioritize disease resistance to ensure better crop yield and robustness.

The experiment evaluated the performance of 13 different genotypes of field peas in different environments. The data collected from the study showed that the highest mean yield was obtained from genotype G-13, followed by G-2, at Environment E1. In contrast, the lowest yield was recorded from G-10, indicating significant differences in the performance of the genotypes under varying environmental conditions. Further analysis of the data showed that at Environment E2, the highest mean yield was obtained from genotype G-9, with an average grain yield of 4209.53 kg/ha. Considering the environmental mean performance, it was observed that the highest yield was obtained from Environment E-2, while the lowest yield was recorded from Environment E4.

Upon closer examination, it was found that the low performance of the genotypes at Environment E4 could be attributed to the terminal moisture deficit during the podding and seed seating stages, as well as the irregular rainfall distribution during that particular growing season. These factors limited the growth and development of the plants, leading to reduced yield. In conclusion, the study highlights the importance of selecting the appropriate genotype for different environments to maximize yield. It also underscores the need for adequate moisture management to ensure optimal growth and development of plants, especially during critical growth stages.

Several genotypes exhibited consistent incremental or decremented performance across the target population environments. Notably, genotype G-13 demonstrated superiority in environment E1 and exhibited a consistent increase in yield across all other environments, as indicated in (Table 5). Although there were differences in yield across environments, G-13 did not experience any rank changes or cross-over interactions, but only magnitude changes. This result is supported by the previous researchers According to (Atlin et al., 2011) trial-to-trial variation within the target population environment exists at all times, even in highly uniform regions due to annual variations in rainfall, disease pressure, planting dates, and so on.

Consequently, both genotypes G-13 and G-2 exhibited superior mean grain yield performance, as illustrated in Table 3, and were relatively stable across all environments. These results suggest that the novel hybrid field pea genotypes exhibit superior performance for grain yield when compared to the two control varieties, Bursa and Bilalo. Therefore, identifying and releasing better-adapted field pea varieties for commercial production in our target environment is highly probable.

Conclusion

This study has provided valuable insights into the performance of different field pea genotypes across various environments, which can guide breeders in selecting cultivars for specific target environments. While there were differences in the performance of genotypes compared to standard check varieties, the study found that genotype by environment interaction did not significantly impact the grain yield performance of the 13 field pea genotypes tested. This means that breeders can confidently select cultivars based on their mean yield and adaptation without considering the influence of genotype by environment interactions.

However, the study also suggests that to develop widely adaptable varieties, it is important to conduct experiments in multiple locations and over several years. By doing so, breeders can identify genotypes that perform consistently well across different environments using appropriate stability analysis tools. Overall, the study found that the hybrid field pea genotypes G-13 and G12 performed exceptionally well in terms of mean grain yield across different environments and these could be strong candidates for developing environment-specific adaptable varieties. This information can assist breeders in selecting the most suitable cultivars for specific environments, ultimately leading to increased field pea yields and productivity.

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References

Andrews, M., and Hodge, S. (2010). Climate Change, a Challenge for Cool Season Grain Legume Crop Production. Climate Change and Management of Cool Season Grain Legume Crops, 1–9. https://doi.org/10.1007/978-90-481-3709-1_1

Argaye, S., Tadele, M., & Tilahun, N. (2023). Agronomic Performance and Grain Yield Stability of Elite Field Pea (Pisum Sativum L.) Genotypes Tested at Various Potential Growing Environments in Ethiopia. Middle East Research Journal of Biological Sciences, 3(03), 96–104. https://doi.org/10.36348/merjbs.2023.v03i03.010

Atlin, G. N., Kleinknecht, K., Singh, K. P., & Piepho, H. P. (2011). Managing genotype x environment interaction in plant breeding programs: a selection theory approach. Journal of the Indian Agricultural Society of Statistics 65(2), 237-247

Gurmu, G. N., Mulisa, T. B., Gemechu, A. L., Amena, K. G., & Terfa, G. N. (2022). Evaluation of Field Pea (Pisum sativum L.) Varieties for Yield and Yield-Related Traits. Sarhad Journal of Agriculture, 38(4). https://doi.org/10.17582/journal.sja/2022/38.4.1219.1227

Haile, G. A., & Tesfaye, D. (2024). Response of field pea (Pisum sativum L.) genotypes for grain yield in a multi-environment trial in Southeastern Ethiopia. Heliyon, 10(15), e35233. https://doi.org/10.1016/j.heliyon.2024.e35233

Kebede, B., Bobo, T., Korji, D., & Amare, G. (2023). Pre Extension Demonstration of Improved Desho Grasses at Highland Districts of Guji Zone, Southern Oromia, Ethiopia. American Journal of Agriculture and Forestry. https://doi.org/10.11648/j.ajaf.20231101.14

Kindie, Y., Bezabih, A., Beshir, W., Nigusie, Z., Asemamaw, Z., Adem, A., Tebabele, B., Kebede, G., Alemayehu, T., & Assres, F. (2019). Field Pea (Pisum sativum L.) Variety Development for Moisture Deficit Areas of Eastern Amhara, Ethiopia. Advances in Agriculture, 2019, 1–6. https://doi.org/10.1155/2019/1398612

Reckling, M., Ahrends, H., Chen, T.-W., Eugster, W., Hadasch, S., Knapp, S., Laidig, F., Linstädter, A., Macholdt, J., Piepho, H.-P., Schiffers, K., & Döring, T. F. (2021). Methods of yield stability analysis in long-term field experiments. A review. Agronomy for Sustainable Development, 41(2). https://doi.org/10.1007/s13593-021-00681-4

Tadele Tadesse, Gashaw Sefera, Behailu Mulugeta, Amanuel Tekalign (2017). Interaction of Field Pea Genotypes with Environment for Grain Yield in the Highland of Bale Zone, Southeastern Ethiopia. Journal Plant Vol. 5 (1), 18-22 doi: 10.11648/j.plant.20170501.14

Tadele, M., Jarso, M., Argaye, S., Tekalign, A., Tilahun, N., Mulugeta, W., Robsa, A., Tesfaye, D., Yimam, K., Silesh, Y., Yirga, M., Merga, B., Basa, D., & Esmael, J. (2021). Performance of Large Seeded Faba Bean Genotypes for Yield and Related Agronomic Traits in Different Parts of Ethiopia. East African Journal of Agriculture and Biotechnology, 4(1), 1–11. https://doi.org/10.37284/eajab.4.1.486

Tolessa, T. T., Keneni, G., Sefera, T., Jarso, M., & Bekele, Y. (2013). Genotype× environment interaction and performance stability for grain yield in field pea (Pisum sativum L.) genotypes. *International Journal of plant breeding*, *7*(2), 116-123.

Vasileva, V. M., & Kosev, V. I. (2021). Genotype Environment Interaction and Stability of Quantitative Traits in Pea (Pisum sativum L.) Varieties. Journal of Agricultural Sciences – Sri Lanka, 16(2), 317–326. https://doi.org/10.4038/jas.v16i2.9337

Yang, X., Soliman, A. A., Hu, C., Yang, F., Lv, M., Yu, H., Wang, Y., Zheng, A., Dai, Z., Li, Q., Tang, Y., Yang, J., Zhang, Y., Niu, W., Wang, L., & He, Y. (2023). Yield Adaptability and Stability in Field Pea Genotypes Using AMMI, GGE, and GYT Biplot Analyses. Agriculture, 13(10), 1962. https://doi.org/10.3390/agriculture13101962

Yihunie, T. A., and Gesesse, C. A. (2018). GGE Biplot Analysis of Genotype by Environment Interaction in Field Pea (Pisum sativum L.) Genotypes in Northwestern Ethiopia. Journal of Crop Science and Biotechnology, 21(1), 67–74. https://doi.org/10.1007/s12892-017-0099-0

Zeleke, B., Esimeal, J., Amogne, K., Mengie, Y., Sendekie, F., Hailu, A., & Taye, Y. (2024). Genotype × Environment Interaction and Stability of Field Pea (Pisum sativum L.) Genotypes for Seed Yield in Northwestern Ethiopia. Journal of Tropical Crop Science, 11(02), 155–164. https://doi.org/10.29244/jtcs.11.02.155-164