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Research Article

Revelation of Genotype × Environment Interaction in Linseed (*Linum usitatissimum* L.) Under Conventional and Natural Farming Production Systems in the North-Western Himalayas

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The development of superior genotypes for use in plant breeding programmes is significantly influenced by the genotype in environment (G × E) interaction. The effects of G × E complicate the improvement of linseed as an important oilseed crop. The present study aimed at assessing the G × E interaction of 30 linseed genotypes for seed yield traits and oil content under conventional and zero-budget natural farming conditions across four locations for two consecutive years (16 different environments) in the North-Western Himalayan region. The AMMI model was used to estimate G × E interaction in the present study. The highest contribution to the total variance belonged to G × E interaction (34.75%), followed by genotype main effects (34.28%). Based on the IPCA1 scores, the most stable genotypes identified with high mean performance for oil content were KL-257 and Nagarkot, and for seed yield, Giza-7 was the most promising genotype. However, genotypes KL-280, KL-285, and Giza-8 showed specific adaptation to the natural production system environments in both years for oil content at locations of Palampur, Bajaura, and Kangra, respectively. Therefore, these genotypes could be recommended specifically under the natural production system in the respective locations. However, the genotypes with stable oil content did not have stable seed yields as well. None of the genotypes that exhibited high oil content stability also exhibited good seed yield stability. In terms of the environment, Palampur was recognised as a favourable location for oil content based on the above average performance, whereas Kangra and Dhaula Kuan were found to be unfavourable locations. In terms of discriminating ability, the natural production system at Palampur showed the highest discrimination, whereas Dhaula Kuan was revealed as the least discriminating environment. These stable and high oil-yielding genotypes are valuable genetic resources for linseed breeding programs for reduced input conditions and marginal environments.

1. Introduction

Flax or linseed (*Linum usitatissimum* L.) is a member of the genus *Linum* and family Linaceae [1]. The name "*Linum*" originated from the Celtic word "lin" or thread and "*usitatissimum*" is Latin for "most useful" [2]. Linseed is among the oldest crop plants cultivated for its dual purpose of oil and fibre. Though linseed is a minor crop, it is grown in a variety of locations and climates, and for a variety of purposes, which could be attributed to its ability to adapt well to various climatic conditions [3]. It is a widely cultivated and economically significant oil seed crop for use in industry [4]. Though India imports edible oil worth more than 80,000 crores every year, linseed oil is mostly used in the paints and varnish industry. Also, the residue cake remaining after oil extraction is a very rich source of polyphenol compounds, including benzoic and cinnamylic acids, coumarin, flavonoids, and others that act as

antioxidants [5] for livestock and quick growth of animals. However, in the last two decades, flaxseed has gained popularity and has become the centre of high interest in the area of diet and disease research due to its unique nutrient profile, mainly omega-3 and omega-6 fatty acids present in its oil [6]. Linseed oil is one of the richest sources of polyunsaturated essential fatty acids. Its oil contains three times as much omega-3 fatty acid as omega-6, representing up to 57% of the total fatty acid composition. These unsaturated fatty acids are well-known for their use in functional foods to control blood pressure, boost cognition, and lower cholesterol [7, 8]. Therefore, demand for linseed is increasing due to its numerous health benefits and nonedible purposes, mostly in the form of oil, and there is a need for stable cultivars with high oil content.

The northwestern himalayan region of Himachal Pradesh is traditionally suited for linseed cultivation. The state is situated between 320 22′40–330° 12′40 north latitude and 750 47′55–790 04′22 east longitude in altitudes ranging from 350 m to 6,975 m above the mean sea level and temperature varies according to the elevation. The state offers great potential for high production and linseed is either sown on poor marginal land, *viz.,* under a low-input production system, or broadcasted in standing paddy crops 15–20 days before its harvest, popularly known as the "utera" or "paira" system. It is mostly grown under conserved moisture and limited nutrient conditions with poor management practises [9]. Most of the linseed production on such lands is based on crop varieties that were bred in the conventional high-input sector, which is one of the major reasons for their poor performance under a low-input production system. Zero budget refers to the zero net cost of production [10]. The importance of zero budget and organic agriculture is gaining impetus due to health and environmental concerns across the globe. Therefore, there is a need to explore and develop more linseed genotypes for realising the productivity potential of the zero-budget production systems across the northwestern himalayan region and elsewhere as well. Zero-budget natural farming (ZBNF) conditions in Himachal Pradesh offer a good opportunity for linseed genotype evaluation under low input and natural farming systems. Himachal Pradesh is one of the first states in India to adopt ZBNF. ZBNF is the practice of advocating the natural growth of crops without adding fertilisers and pesticides or any other external elements. It seeks to delink farmers from external inputs and credit markets to foster autonomy through a policy of never purchasing from outside parties, particularly corporations [11]. This would help farmers get rid of their debts and would also improve soil fertility, yield, and quality of products obtained for healthy living and preserve the natural ecosystem. For all of the chosen crops, ZBNF procedures use between 50 and 60 percent less water and electricity than non-ZBNF processes. Through multiple aerations, ZBNF greatly lowers methane emissions. Mulching techniques may also help prevent residue burning. Therefore, ZBNF is undoubtedly an economically, socially, biologically, and physiologically viable and profound technique [12]. The State government has also been encouraging zero-budget natural farming under the specific program known as *Paramparagat Krishi Vikas Yojana*, a traditional agricultural development scheme.

The requirement for stable genotypes that perform well over a wide range of environments becomes increasingly important as farmers need reliable production quantities [13]. Instability of a genotype across environments/locations arises due to genotype × environment interaction (G × E). It complicates the process of selecting a genotype and achieving superior performance [14]. Its knowledge has been instrumental in improving the sustainability of agricultural production because interactions may involve changes in rank order for genotypes between environments [15]*viz.,*the performance of one genotype that is superior in one environment might be inferior in another environment. Several statistical procedures can be used for measuring crop yield stability and to predicting phenotypic responses to environmental changes. The first of methods used to measure stability were based on the analysis of variance. Fisher was the first scientist who created the statistical methods such as the analysis of variance, the design of experiments, and statistical significance testing to deal with the interaction of nature with nurture. The second of the methods is based on linear regression analysis also known as the univariate method of stability analysis. The basic idea behind regression analysis is regressing the genotypes' performances on the environmental mean yields, expressed by an environmental index, through a linear or a nonlinear model in the parameters [16]. However, in the present study, analysis was performed by using the additive main effects and multiplicative interaction model (AMMI) which belongs to the multivariate group. Multivariate statistical approaches explored the multidirectional aspects of GE interaction and attempted to extract more information from GE interaction components [17]. They are based on singular value decomposition (SVD) and biplot concept [18]. Among the multivariate methods, the AMMI model [19, 20] and genotype (G) main effect plus genotype by environment interaction (GGE) [21] biplot analysis are the most well-known and appealing methods for analysing the GE interaction data [22]. As proposed by Gauch [20], AMMI analysis uses ANOVA and PCA in a joint approach that can be used to analyse multiple yield trials and is hence more suitable for characterizing the G × E interaction [23].

In view of the above, the current investigation was conducted to identify stable and high oil-yielding linseed genotypes with better and wider adaptability under natural and conventional farming systems across 4 diverse locations. This would help in popularizing and increasing linseed production even under low-input natural farming systems in order to achieve multiple goals of enhanced productivity, health and environmental safety, and agricultural sustainability.

2. Materials and Methods

2.1. Germplasm and Study Sites. The experimental material comprised of 30 linseed genotypes (13 released elite varieties, 14 advanced breeding lines, and 3 exotic varieties and KL-241 (Him Palam Alsi-1), KL-263 (Him Palam Alsi-2),

and Him Alsi-2 as standard checks) (Table 1). Four different locations having varying altitudes in Himachal Pradesh were selected for the study (Table 2) *viz.,* Palampur, Bajaura, Kangra, and Dhaula Kuan with two production systems *viz.,*conventional and ZBNF at each location repeated over two years *viz.,* during *rabi* 2019-20 and *rabi* 2020-21. Therefore, the stability analysis for oil content was analysed over a total of 16 environments (production systems-sites-years). A description of the sixteen environments is given in Table 2.

2.2. Trial Design and Management. In all sixteen environments' trials, the experiment was arranged as a randomized complete block design (RCBD) with three replications. The plot consisted of three rows with row spacing of 25 cm and plant spacing of 5 cm. The experimental field under the conventional system was well prepared and recommended doses of fertilisers were applied at 50 kg N, 40 kg P_2O_5, and 20 kg K_2O per hectare. Half the dose of N and the full dose of P_2O_5 and K_2O were applied as basal and the remaining half of nitrogen was top dressed after 45 days of sowing. Post-emergence herbicide 'Vesta' was applied as a measure of weed control followed by regular weeding to keep the experimental field weed-free.

On the other hand, under the ZBNF farming system, the seeds were treated with *beejamrit* @10 ml per kg of the seed which was freshly prepared. It comprised of cow dung, cow urine, and lime. It is considered as a preventive measure against insect-pest infestation. *Ghanjeevamrit* (microbial mix) was applied @ 250 kg/ha at the time of sowing and its liquid form *i.e., jeevamrit* (10%) was sprayed during the crop period with the first spray at 21 days after sowing and the rest at an interval of 15 days till harvesting. Ghanjeevamrit is a dry form of jeevamrit whereas jeevamrit is a microbial culture that has been fermented using soil, jaggery, pulse flour, and cow manure and urine [11]. No farm yard manure and recommended chemicals were applied. Furthermore, mulching was performed to control weeds. Each genotype was harvested separately on a plot basis. The harvested seeds of each genotype from each environment were stored separately in seed envelopes at room temperature before processing.

2.3. Oil Content Estimation. Oil content was estimated using the Soxhlet extraction method [24] in the biochemistry laboratory at ICAR-National Bureau of Plant Genetic Resources (ICAR-NBPGR), New Delhi. The principle of the method is based on the extraction of oil using nonpolar solvent petroleum ether (40–60°C). It involves repeated extraction of oil. The solvent is then distilled off completely. The oil is dried and weighed, and the percentage of oil is calculated.

2.4. Data Analysis. In the present investigation, stability assessment of thirty genotypes for oil content over sixteen environments (production systems-sites-years) was computed using the AMMI model (multivariate approach) [20].

2.4.1. Analysis of Variance. Data was statistically analysed using 'R' software version 4.1.2 and package "metan" [25]. The analysis of variance was based on the model given in the following equation:

$$Y_{ij} = \mu + g_i + r_j + e_{ij}, \quad (1)$$

where Y_{ij} is the phenotypic effect of the i^{th} genotype in the j^{th} replication, μ is the general population mean, g_i is the effect of i^{th} genotype, r_j is the effect of j^{th} replication, and e_{ij} is the random error associated with i^{th} genotype in j^{th} replication.

2.4.2. Additive Main Effects and Multiplicative Interaction (AMMI) Analysis. AMMI is a hybrid model involving both additive and multiplicative components of a two-way data structure. The AMMI model separates the additive variance from the multiplicative variance and then applies principal component analysis (PCA) to the interaction portion to obtain a new set of coordinate axes that explain the interaction pattern in greater detail [26]. The main effects of the model are estimated using the additive two-way analysis of variance (ANOVA) by least squares. Then, the singular value decomposition (SVD) is applied to the residuals from the ANOVA, *viz.,* to the interaction and to obtain the estimates for the multiplicative terms of the AMMI model [27]. An F-test which uses the ratio between the mean square for the axis against an estimate of the error term is used for determining the number of multiplicative terms to be retained in the multiplicative model [28]. The model used is given in equation (3).

$$Y_{ij} = \mu + \alpha_i + \beta_j + \sum_n \lambda_n \delta_{in} \gamma_{jn} + P_{ij} e_{ij}, \quad (2)$$

where Y_{ij} is the observed mean yield of the i^{th} genotype in the j^{th} environment, μ is the additive components (the grand mean), α_i is the i^{th} genotype effect and β_j is the j^{th} environment effect, λ_n is the singular value, δ_{in} is the ith genotype principal component scores for axis n, γ_{jn} is the jth environment principal component scores for axis n, and P_{ij} is the AMMI residuals and e_{ij} is the error term.

Furthermore, biplots of a number of genotypes vs mean oil content across the environments were plotted using the same software.

To assess model diagnosis and to identify the mega-environments, AMMISOFT software version 1.0 was used in the AMMI model for the analysis of yield trial data. Model selection is one of the most important steps in AMMI analysis because the selection of the best AMMI model will increase predictive accuracy [29]. AMMI constitutes a model family, with AMMI0 having no IPC, AMMI1 having 1 IPC, AMMI2 having 2 IPC, and so on up to AMMIF (residual discarded). The ratio of yield for AMMI "winners" within each environment (identified in the first column of AMMI ranks) was calculated by dividing the yield for the overall winner [30]. According to Gauch [30], a ratio of 1 represents a "winning" genotype across environments. This ratio is an assessment of the importance of narrow adaptation due to GEI effects, with a ratio of ≥1.10 as an indicative of narrow adaptation.

Table 1: Experimental linseed elite lines and checks evaluated in sixteen environments.

Code	Genotype	Source/pedigree	Flower colour
G1	KL-311	Giza-6 × Nagarkot	Blue
G2	KL-315	TL-27 × Flak-1	White
G3	KL-309	Canada × Nagarkot	Blue
G4	KL-314	Belinka 60 × Nagarkot	White
G5	KL-317	Him Alsi-1 × Binwa	White
G6	KL-236	Jeevan × Janki	Blue
G7	KL-241(Him Palam Alsi-1)*	Giza-7 × KLS-1	Blue
G8	KL-244	(RLC 29 × Jeevan) × RLC-29	Blue
G9	KL-257	LC-2323 × KLS-1	Blue
G10	KL-263 (Him Palam Alsi-2)*	KL-223 × KL-224	Blue
G11	KL-269	EC-21741 × LC-216	Blue
G12	KL-278	Giza-5 × Aayogi	Blue
G13	KL-279	Mariena × Giza-5	Blue
G14	KL-280	Giza-7 × Belinka	Blue
G15	KL-284	Rajeena × Him Alsi-2	White
G16	KL-285	Binwa × Him Alsi-2	White
G17	Giza-8	Exotic collection	Blue
G18	Giza-7	Exotic collection	Blue
G19	Him Alsi-2*	EC-21741 × LC-216	Blue
G20	Nagarkot	New river × LC-216	Blue
G21	Himani	DPL-20 × KLS-1	Blue
G22	Jeewan	Sumit × LC-216	Blue
G23	Baner	EC-21741 × LC-214	White
G24	Bhagsu	RL-50-3 × Surbhi	Blue
G25	Himalini	K2 × Kangra local	White
G26	Him Alsi-1	K2 × TLP-1	White
G27	Janki	Palampur	Blue
G28	Surbhi	LC-216 × LC-185	White
G29	Canada	Exotic collection	Blue
G30	Binwa	Flak-1 × SPS 47/7-10-3	Blue

*refers to the check varieties.

Table 2: Description of sixteen sites used for evaluation in Himachal Pradesh, India.

S. no.	Location	Sowing time		Altitude (m)	Latitude	Longitude	Annual rainfall (mm)
		Rabi 2019-20	Rabi 2020-21				
1	Palampur	(i) Conventional (E1) (ii) ZBNF (E2)	(i) Conventional (E9) (ii) ZBNF (E10)	1290	32°8′	76°3′	2500
2	Bajaura	(i) Conventional (E3) (ii) ZBNF (E4)	(i) Conventional (E11) (ii) ZBNF (E12)	1090	31°8′N	77°E	975
3	Kangra	(i) Conventional (E5) (ii) ZBNF (E6)	(i) Conventional (E13) (ii) ZBNF (E14)	700	32°09′N	76°22′E	1539
4	Dhaula Kuan	(i) Conventional (E7) (ii) ZBNF (E8)	(i) Conventional (E15) (ii) ZBNF (E16)	468	30°4′N	77°5′E	1250

The AMMI model equation is represented as

$$\mathrm{Yge}_{\mathrm{ge}} = \mu + \alpha_g + \beta_e + \sum n\lambda_n\gamma_{\mathrm{gn}}\delta_{\mathrm{en}} + \rho_{\mathrm{ge}}, \quad (3)$$

where Y_{ge} is the yield of genotype g in environment e, μ is the grand mean, α_g is the genotype deviation from the grand mean, β_e is the environment deviation, λ_n is the singular value for IPC n and correspondingly λ_n^2 is its eigenvalue, γ_{gn} is the eigenvector value for genotype g and component n, δ_{en} is the eigenvector value for environment e and component n, with both eigenvectors scaled as a unit vector, and ρ_{ge} is the residual. The cross-validation techniques were applied for predictive assessment. It was estimated as the differences between the prediction values (model's fitted values) and validation observations first squared and summed over all genotypes and environments and divided by the number of validation observations, and then its squared root was taken to compute the root mean square of the predictive difference (RMS PD). Smaller values of RMS PD indicate good predictive success.

3. Results

3.1. Meteorology Data. The weekly data recorded on weather parameters viz. temperature (maximum and minimum), rainfall, and relative humidity for all the four diverse locations was averaged to form the monthly data as presented

in the Figures 1–4. In the early stages of crop growth and development, low rainfall conditions could be observed for locations Palampur, Bajaura, and Kangra. On the other hand, Dhaula Kuan experienced relatively more rainfall with low relative humidity. By and large, all the four locations experienced high temperatures and limited rainfall during the time of maturity. The warmest summer, nevertheless, was experienced in Dhaula Kuan followed by Kangra, Bajaura, and Palampur. Bajaura experienced the coldest winters with subzero temperatures in the month of December followed by Palampur, Dhaula Kuan, and Kangra. Relative humidity was highest at Bajaura almost throughout the growing period followed by Kangra, Palampur and Dhaula Kuan. However, overall meteorological data was averaged over all four locations as presented in Figure 5 which revealed December and January as the coldest months across all four locations. March was observed as the wettest month. While high relative humidity was observed during the early months of the crop season, the lowest relative humidity was observed in February across all locations.

3.2. Combined Analysis of Variance as per the AMMI Model for Seed Yield per Plant. For seed yield per plant, highly significant differences were observed for environments, genotypes, and GE interactions (Table 3). The environmental sum of squares made the largest contribution to the overall variation (89.74%), followed by the GE interaction component (8.08%). The genotype sum of squares revealed a small contribution of 0.81%. All the differences were found significant at a 1% level of significance. IPCA1 accounted for 39.1% of the total GEI contribution, while IPCA2, IPCA3, IPCA4, and IPCA5 explained 28%, 18.4%, 4.8%, and 3.7% of the total contribution, respectively. 67.2% of the total GEI was captured by the first two IPCAs combined whereas the first three IPCAs' captured more than 70% (85.5%) of the total GEI.

3.3. Genotype by Environment Interaction and Genotype Performance for Seed Yield per Plant. The abscissa of the biplot represents the main effects, while its ordinates represent the IPCA1 scores showing the GE of the genotypes and environments. Environments and genotypes with IPCA1 scores close to or equal to zero contribute greatly to the stability of environments and genotypes whilst providing little contribution to interactions. The mean performance of the environments and genotypes on the left side of the origin was lower than the grand mean, whereas those on the right side of the origin were higher. For seed yield, IPCA 1 scores (Figure 6) indicated that Palampur (E9) and Kangra (E13) both under conventional production systems were the main contributors to the stability of genotypes in terms of seed yield per plant. However, the highest interaction was observed for locations Dhaula Kuan and Kangra. The highest mean performances were also favoured in these locations. The highest mean performance was observed in Dhaula Kuan under the conventional production system (E7) in the first year. However, the lowest was observed in Bajaura under a natural system of production (E12).

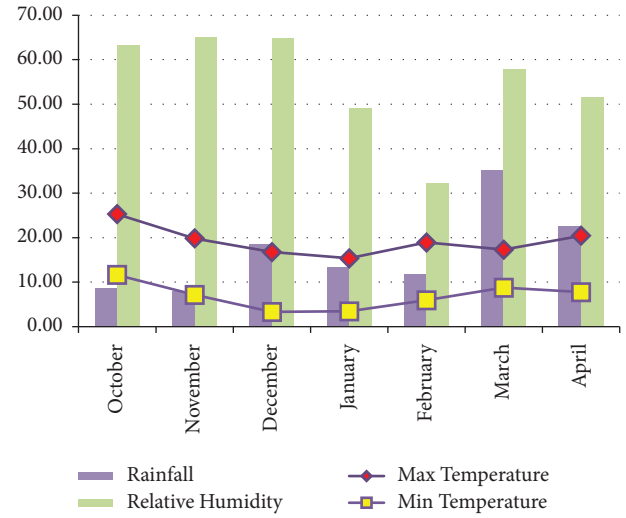

Figure 1: Weather data for Palampur location averaged over two years.

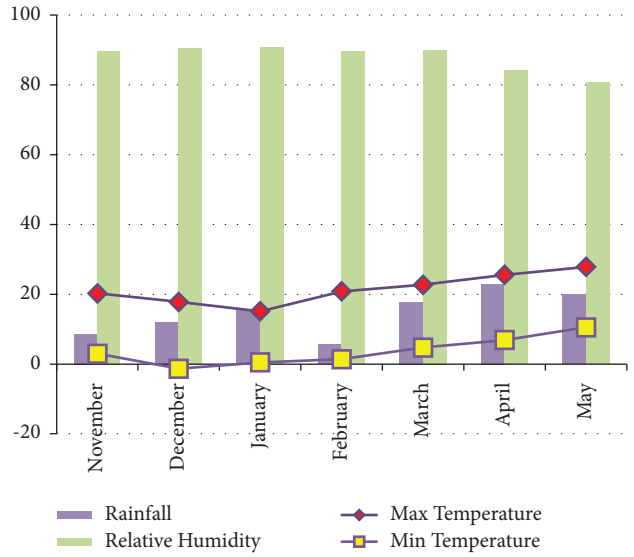

Figure 2: Weather data for Bajaura location averaged over two years.

As per the AMMI2 biplots (Figure 7), environments with low IPCA1 and IPCA2 scores that are close to the origin have a high contribution to the stability of genotypes and a low contribution to GE interaction. In the present study environment E13, i.e., the conventional production system at Kangra was placed closest to the origin with the lowest IPCA1 and IPCA2 values. A positive correlation was observed among all test environments belonging to all the locations in the second year whereas, in the first year the test environments differed in their correlation and interaction effects. In the second year, all the locations were equally informative in genotype evaluation but the test environments did not show any correlation with one another in the first year.

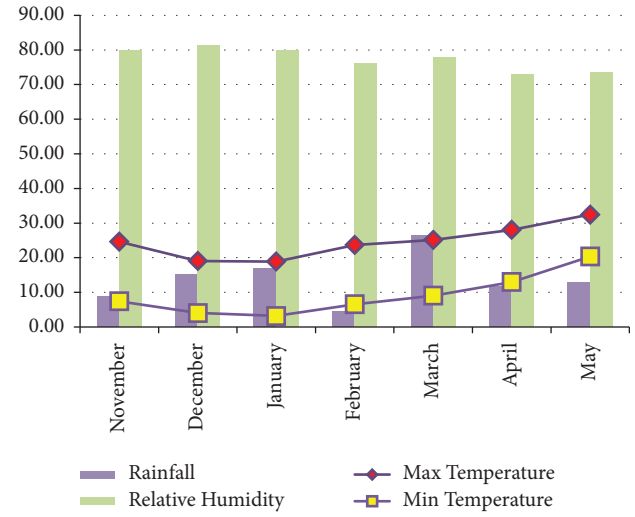

Figure 3: Weather data for Kangra location averaged over two years.

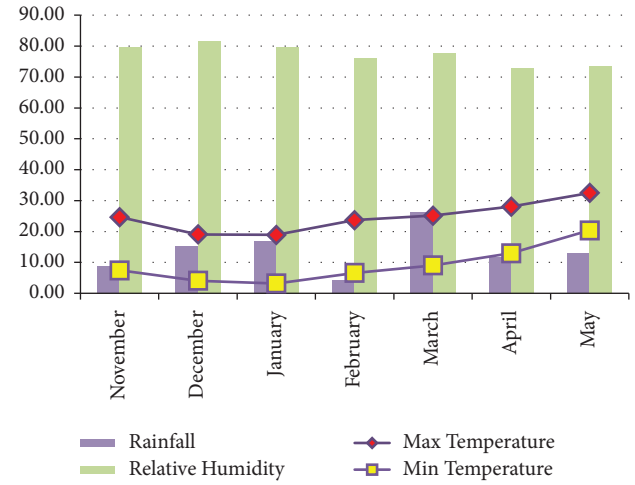

Figure 4: Weather data for Dhaula Kuan location averaged over two years.

As per the genotypes performance, the most stable genotypes for seed yield as per IPCA1 scores were G13 (5.07), G19 (5.15), G27 (5.09), G12 (5.31), and G18 (5.62). Among them, the most desirable genotype is G18 due to its high mean performance and high stability. G12 (5.31) and G19 (5.15) were average in performance but stable whereas, G13 (5.07) and G27 (5.09) were below average in seed yield but close to average. The most unstable genotypes were G2 (6.00), G6 (5.91), G30 (4.88), and G11 (4.06) as they had the highest PC scores. The genotype performance was consistently poor under ZBNF across years as well as locations (Table 4) for all genotypes with few exceptions at location Kangra where the two systems were at par with each other for the respective genotypes.

Among the stable genotypes identified for seed yield, genotypes Janki and Him Alsi-2 were also high in oil content (Table 4). However, these genotypes did not show stability in oil content across environments. The genotype stable for

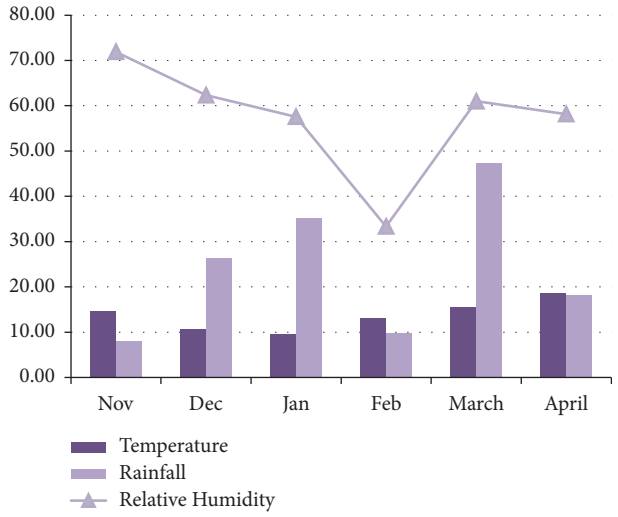

Figure 5: Average weather data over four locations.

both seed yield and oil content was KL-279, however, the mean performance for both the traits was below average. Genotype Nagarkot was the only genotype that showed above-average oil content and also high seed yield. However, it showed stability only for oil content. None of the genotypes showing high seed yield stability were also stable for high oil content.

3.4. Model Diagnosis and Mega-Environment Delineation for Seed Yield and Oil Content. For seed yield, G × E noise and signal were 32.41% and 67.39%, respectively. According to the root mean square prediction differences (RMSPD) based on 1000 runs and 446000 validations, AMMI3 with a value of 4.85 was the most accurate for mega-environment delineation. AMMI1 delineated the sixteen environments into 3 mega-environments, with G20 as the winner in 11 environments and G30 in 3 environments and G20 in 2 environments (Table 5). AMMI3 delineated the sixteen environments into 6 mega-environments. In AMMI3, G30 won in 7 environments, followed by G20 in 4 environments, and G9 in 1 environment. The three mega-environments as per AMMI1 comprised environments E7 and E5 as the first mega-environment, E1, E4, E6, E8, E9, E10, E11, E12, E13, and E14 as the second mega-environment, and E2, E3, and E15 as the third mega-environment (Table 5). The second mega-environment comprised of 10 environments and was the largest of all three. G2 ranked first in the first mega-environment whereas G30 and G20 ranked first in the second and third mega-environments, respectively. G2 and G30 ranked second in the second mega-environment, whereas, G20 ranked second in the third mega-environment.

For oil content, the results indicated that the GEI captured 10.20% as noise and 89.80% as a signal. Results from model diagnosis (Table 6) identified a model family from AMMI0 to AMMIF, with AMMI0 having one winner genotype in one mega-environment whereas AMMIF consisted of 3 winner genotypes in 3 mega-environments. On the basis of RMSPD value with 1000 runs and 446000

Table 3: Pooled analysis of variance over environments as per the AMMI model for seed yield and oil content.

Source	DF	Seed yield/plant		Oil content	
		MSS (mean sum of squares)	% explained	MSS	% explained
Trials	479				
Environments	15	2972.35**	89.74	85.09**	30.69
Replications × environments	32	21.11**	1.36	0.36*	0.28
Genotypes	29	13.98**	0.81	49.17**	34.28
Genotype × environment	435	9.22**	8.08	3.32**	34.75
PC1	43	36.51**	39.1	9.24**	27.50
PC2	41	27.46**	28	7.37**	20.90
PC3	39	18.89**	18.4	5.12**	13.80
PC4	37	5.16**	4.8	4.91**	12.60
PC5	35	4.29**	3.7	2.99**	7.2
PC6	33	—	—	2.45**	5.6
PC7	31	—	—	1.48**	3.4
PC8	29	—	—	1.38**	3.1
PC9	27	—	—	1.28**	2.8
PC10	25	—	—	0.94**	2.4
Residuals	928	2.99	5.6	0.33	7.54
Noise		1301.18**	32.41	147.48**	10.20
Signal		2713.88**	67.59	1297.85	89.80
Total	1874				

*refers to "significance at 5% level" and **refers to "significance at 1% level."

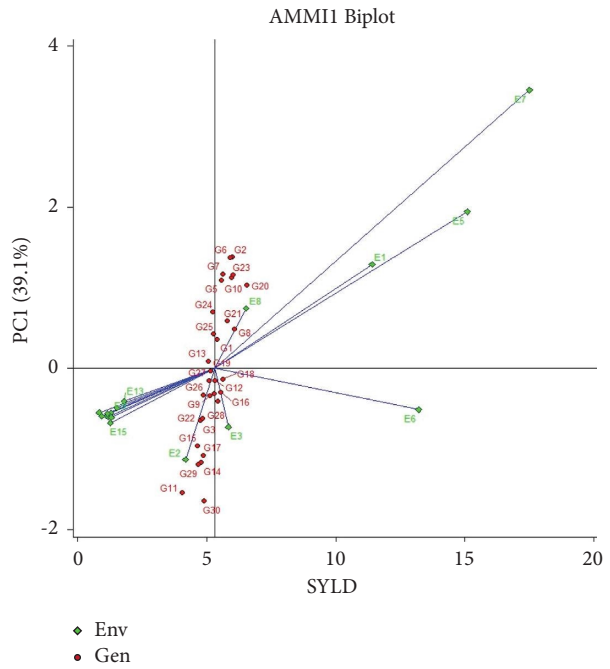

Figure 6: AMMI1 biplot display (IPCA1 vs mean) of linseed genotypes for seed yield in sixteen environments.

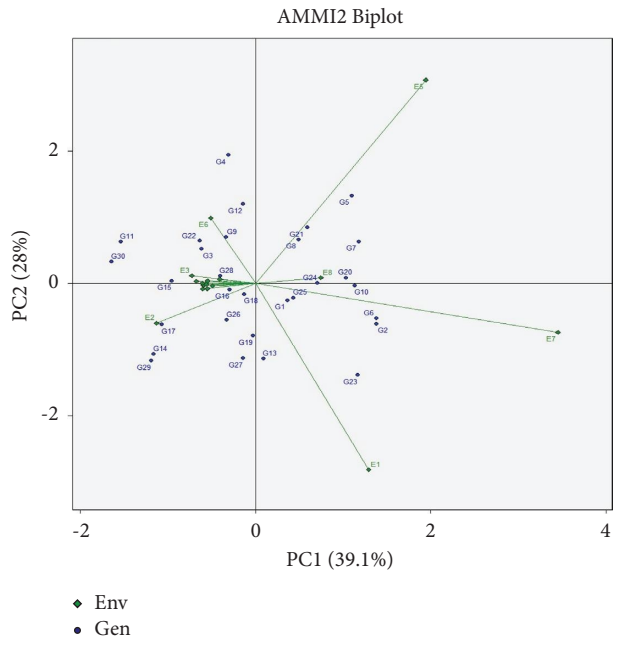

Figure 7: AMMI2 biplot display (IPCA1 vs IPCA2) of linseed genotypes for seed yield in sixteen environments.

validations, AMMI6 with a value of 26.37 may be considered the best model as per the model diagnosis for the given dataset. The results indicated that 26 genotypes never win for oil content. As per AMMI1, genotype 30 won in all sixteen environments with the highest mean performance across environments. G19 and G20 were second in number whereas, as per AMMI6 and AMMI7 models, G19 won in one environment, G30 in fourteen environments, and G24 in one environment. The mega-environment delineation was based on the different genotype winners in different environments. Accordingly, AMMI1 identified only a single mega-environment with G30 as the winner whereas AMMI6 identified 3 mega-environments with three different genotype winners (G30, G19, and G20). The first mega-environment was the largest, which comprised of fourteen environments (E1, E2, E3, E4, E5, E7, E8, E9, E10, E11, E12, E13, E15, and E16), the second mega-environment comprised of 6 environments, and third mega-environment comprised of 14 environments (Table 6).

Table 4: (a–d) Percent difference in the mean performance of the genotypes under conventional and ZBNF farming systems for seed yield and oil content.

Genotypes	Seed yield (g)		Difference in seed yield	% difference	Oil content (%)		Difference in oil content	% difference
	Conventional	ZBNF			Conventional	ZBNF		
(a)	*Location Palampur*							
KL-311	6.23	4.62	1.61	29.76	38.82	39.51	−0.69	−1.75
KL-315	7.35	3.48	3.86	71.33	39.3	41.48	−2.18	−5.41
KL-309	4.48	2.67	1.81	50.67	40.55	41.46	−0.91	−2.22
KL-314	3.49	2.04	1.45	52.45	41.22	41.65	−0.43	−1.04
KL-317	5.28	2.21	3.07	81.92	38.83	40.5	−1.67	−4.22
KL-236	8.85	1.64	7.21	137.6	40.71	41.41	−0.7	−1.7
KL-241	5.76	1.46	4.29	118.94	38.9	39.74	−0.84	−2.14
KL-244	6.5	3.92	2.58	49.45	36.9	40.46	−3.56	−9.2
KL-257	6.31	1.39	4.92	127.96	40.98	42.26	−1.28	−3.07
KL-263	8.11	2.65	5.45	101.34	40.13	38.28	1.84	4.7
KL-269	2.71	3.6	−0.89	−28.2	39.51	39.44	0.06	0.16
KL-278	4.23	2.93	1.3	36.35	39.33	40.53	−1.19	−2.99
KL-279	8.52	2.31	6.22	114.84	39.9	38.46	1.44	3.68
KL-280	7.42	3.83	3.59	63.78	38.67	41.41	−2.74	−6.83
KL-284	4.55	2.3	2.25	65.63	39.02	39.5	−0.48	−1.22
KL-285	7.33	2.43	4.9	100.4	39.36	41.63	−2.27	−5.59
Giza-8	6.72	2.73	3.99	84.42	40.42	39.69	0.73	1.84
Giza-7	8.36	2.17	6.19	117.66	38.82	40.16	−1.35	−3.41
Him Alsi-2	7.07	1.93	5.14	114.38	40.7	43.62	−2.93	−6.94
Nagarkot	8.5	3.38	5.12	86.29	40.58	42.53	−1.95	−4.69
Himani	7.08	1.95	5.13	113.56	40.65	40.29	0.35	0.88
Jeewan	4.24	1.98	2.26	72.75	38.49	39.25	−0.76	−1.95
Baner	9.09	2.48	6.6	114.16	41.4	40.73	0.68	1.65
Bhagsu	5.86	1.77	4.09	107.22	41.81	39.25	2.56	6.32
Himalini	7.08	2.59	4.49	92.77	38.88	41.29	−2.41	−6.01
Him Alsi-1	6.09	3.47	2.62	54.81	38.53	40.27	−1.75	−4.44
Janki	7.61	3.53	4.08	73.34	40.67	38.73	1.94	4.88
Surbhi	7.19	2.33	4.86	102.02	39.33	42.29	−2.96	−7.25
Canada	7.25	4.4	2.85	48.86	39.05	38.67	0.38	0.97
Binwa	4.78	4.1	0.68	15.28	43.95	44.14	−0.19	−0.44
Mean	6.47	2.74	3.72	80.88	39.85	40.62	−0.77	−1.92
(b)	*Location Bajaura*							
KL-311	3.54	0.69	2.85	134.63	41.12	38.64	2.49	6.24
KL-315	3.55	0.96	2.58	114.66	40.23	37.2	3.03	7.81
KL-309	2.8	1.34	1.46	70.46	41.31	40.5	0.81	1.99
KL-314	2.73	1.57	1.16	54.24	41.33	39.72	1.61	3.97
KL-317	3.12	0.92	2.2	108.99	38.65	36.78	1.88	4.97
KL-236	3.26	0.89	2.37	114.48	42.14	37.77	4.37	10.94
KL-241	3.41	1.09	2.32	102.87	37.14	37.05	0.09	0.23
KL-244	3.76	0.89	2.86	123.26	39.17	39.01	0.16	0.41
KL-257	3.04	0.84	2.2	113.22	39.65	38.45	1.2	3.08
KL-263	3.57	0.71	2.87	133.95	41.6	40.31	1.29	3.15
KL-269	3.13	1.03	2.1	101.04	40.28	36.6	3.68	9.57
KL-278	2.53	0.95	1.58	90.96	39.59	36.51	3.08	8.1
KL-279	3.29	0.94	2.36	111.42	40.75	39.17	1.58	3.94
KL-280	2.85	1.15	1.7	84.85	37.65	37.01	0.63	1.7
KL-284	3.57	1.33	2.24	91.68	37.81	36.6	1.21	3.25
KL-285	2.87	1.13	1.75	87.45	43.05	40.15	2.9	6.98
Giza-8	4.19	1.25	2.94	107.98	38.4	37.22	1.18	3.13
Giza-7	2.8	0.93	1.87	100.23	40.05	38.66	1.39	3.52
Him Alsi-2	4.04	0.73	3.31	138.98	42.62	40.06	2.56	6.19
Nagarkot	4.04	1.47	2.57	93.18	41.98	39.53	2.44	6
Himani	3.14	0.8	2.33	118.55	39.26	38.65	0.61	1.57
Jeewan	3.57	1.36	2.21	89.62	40.99	39.45	1.54	3.82
Baner	3.32	1.07	2.25	102.66	41.5	39.23	2.26	5.6

Table 4: Continued.

Genotypes	Seed yield (g)		Difference in seed yield	% difference	Oil content (%)		Difference in oil content	% difference
	Conventional	ZBNF			Conventional	ZBNF		
Bhagsu	2.32	0.87	1.46	91.29	40.86	38.76	2.1	5.28
Himalini	3.95	1.33	2.63	99.48	40.78	39.53	1.25	3.11
Him Alsi-1	3.92	1.11	2.81	111.79	40.76	39.34	1.42	3.55
Janki	3.53	1.66	1.87	72.11	41.72	39.14	2.58	6.39
Surbhi	4.44	1.51	2.93	98.56	41.22	39	2.22	5.53
Canada	3.52	0.6	2.92	141.98	38.84	36.77	2.07	5.47
Binwa	4.22	1.05	3.18	120.48	44.1	42.56	1.54	3.56
Mean	3.4	1.07	2.33	104.17	40.48	38.65	1.84	4.65
(c)	*Location Kangra*							
KL-311	8.6	5	3.6	52.98	38.23	36.61	1.61	4.31
KL-315	8.42	6.51	1.91	25.6	39.29	37.52	1.77	4.6
KL-309	7.97	6.98	0.99	13.32	38.83	37.41	1.42	3.72
KL-314	10.57	9.19	1.38	14	40	36.63	3.37	8.8
KL-317	12.4	6.11	6.29	68	37.85	38.71	−0.87	−2.26
KL-236	9.11	7.79	1.32	15.63	40.14	37.17	2.98	7.7
KL-241	10.8	6.13	4.67	55.15	37.98	35.99	1.99	5.37
KL-244	10.77	8.81	1.96	20.03	36.94	36.16	0.78	2.14
KL-257	9.62	9.16	0.46	4.86	39.49	36.79	2.7	7.08
KL-263	9.76	7.51	2.25	26.07	40.38	38.76	1.62	4.11
KL-269	6.96	5.5	1.46	23.42	39.28	37.75	1.53	3.97
KL-278	9.98	7.89	2.09	23.36	38.22	38.3	−0.09	−0.22
KL-279	6.33	6.98	−0.64	−9.64	38.3	35.39	2.9	7.88
KL-280	6.25	7.02	−0.77	−11.53	37.63	36.56	1.07	2.89
KL-284	6.39	7.86	−1.47	−20.67	37.97	36.88	1.09	2.91
KL-285	8.29	9.51	−1.22	−13.69	38.72	37.01	1.7	4.5
Giza-8	6.59	7.54	−0.95	−13.44	39.31	38.09	1.22	3.14
Giza-7	9.14	8.54	0.59	6.69	38.18	37.44	0.74	1.95
Him Alsi-2	6.45	6.54	−0.09	−1.36	40.32	39.48	0.84	2.11
Nagarkot	10.99	8.35	2.65	27.35	40.04	39.29	0.75	1.88
Himani	11.55	8.07	3.48	35.5	39.49	38.68	0.81	2.08
Jeewan	7.8	7.08	0.73	9.75	39.84	39	0.84	2.14
Baner	7.54	7.86	−0.32	−4.11	39.52	38.47	1.04	2.67
Bhagsu	8.45	5.56	2.89	41.3	41.57	39.68	1.89	4.64
Himalini	9.01	5.13	3.88	54.85	39.32	36.48	2.84	7.5
Him Alsi-1	6.41	5.91	0.51	8.23	39.26	37.51	1.75	4.55
Janki	6.33	4.91	1.42	25.18	41.04	39.13	1.91	4.76
Surbhi	8.54	8.52	0.02	0.23	38.63	38.46	0.17	0.44
Canada	5.44	6.62	−1.18	−19.48	39.83	37.63	2.2	5.67
Binwa	7.02	7.16	−0.14	−2	42.26	38.45	3.8	9.43
Mean	8.45	7.19	1.26	16.1	39.26	37.71	1.55	4.02
(d)	*Location Dhaula Kuan*							
KL-311	10.14	4.51	5.63	76.81	37.9	39.46	−1.56	−4.03
KL-315	12.78	5.61	7.17	77.92	38.39	39.09	−0.7	−1.81
KL-309	8.32	3.55	4.77	80.44	38.41	39.45	−1.04	−2.67
KL-314	8.28	3.72	4.56	75.92	38.61	39.04	−0.43	−1.1
KL-317	10.38	4.57	5.81	77.68	36.24	37.03	−0.8	−2.17
KL-236	12.17	3.81	8.36	104.69	38.28	40.25	−1.98	−5.04
KL-241	11.55	4.83	6.72	82.05	37.43	36.65	0.77	2.09
KL-244	10.32	3.75	6.56	93.28	37.52	39.48	−1.96	−5.08
KL-257	7.57	3.13	4.45	83.07	39.7	39.17	0.53	1.35
KL-263	11.61	3.82	7.78	100.91	39.35	39.53	−0.18	−0.46
KL-269	6.98	2.71	4.27	88.06	38.14	40.49	−2.35	−5.98
KL-278	9.21	3.65	5.56	86.44	37.99	36.89	1.1	2.94
KL-279	9.22	3.11	6.1	99.03	38.36	38.04	0.31	0.82
KL-280	7.2	3.18	4.02	77.39	37.49	38.49	−1	−2.64
KL-284	8.27	2.98	5.29	93.97	37.35	38.4	−1.05	−2.77
KL-285	8.71	4.23	4.48	69.2	38.83	38.19	0.64	1.67

Table 4: Continued.

Genotypes	Seed yield (g)		Difference in seed yield	% difference	Oil content (%)		Difference in oil content	% difference
	Conventional	ZBNF			Conventional	ZBNF		
Giza-8	7.25	3.15	4.1	78.92	38.45	37.48	0.97	2.54
Giza-7	8.19	4.71	3.49	54.05	37.49	38	−0.51	−1.35
Him Alsi-2	9.93	4.33	5.6	78.62	39.51	39.87	−0.35	−0.89
Nagarkot	11.18	5.75	5.43	64.2	39.66	39.24	0.42	1.07
Himani	9.8	3.47	6.33	95.39	39.61	37.9	1.72	4.43
Jeewan	7.85	3.89	3.96	67.41	38.12	37.57	0.54	1.44
Baner	12.86	4.23	8.64	101.08	39.26	38.64	0.62	1.59
Bhagsu	10.94	4.64	6.3	80.88	42.52	37.82	4.7	11.69
Himalini	9.91	3.68	6.23	91.67	39.84	40.71	−0.87	−2.16
Him Alsi-1	8.84	4.77	4.07	59.77	37.87	37.27	0.6	1.6
Janki	9.85	2.97	6.87	107.21	39.61	40.53	−0.91	−2.28
Surbhi	8.76	2.41	6.35	113.74	38.38	41.45	−3.07	−7.69
Canada	7	2.41	4.59	97.57	37.8	38.02	−0.22	−0.58
Binwa	6.44	3.7	2.74	53.99	43.17	41.64	1.53	3.6
Mean	9.38	3.84	5.54	83.78	38.71	38.86	−0.15	−0.39

The negative values indicate high mean performance under the ZBNF system.

Table 5: Winner genotypes in the AMMI model families for seed yield and oil content.

Genotype			AMMI model family								
			0	1	2	3	4	5	6	7	F
Seed yield	2	GEN2		2	1	2	2	2	2	2	2
	23	GE23			1	1	1	1	1	1	1
	5	GEN5			1	1	1	1	1	1	1
	20	GE20	16	11	9	4	3	3	2	4	
	21	GE21									1
	8	GEN8									1
	1	GEN1					1	1	1	1	1
	19	GE19					1	1	2	2	1
	18	GE18							1		1
	27	GE27						2	2	1	1
	16	GE16						1	1	1	1
	4	GEN4			1						1
	9	GEN9				1	1				
	28	GE28						1			1
	15	GE15					1				
	14	GE14			1					1	
	11	GE11									1
	30	GE30		3	2	7	5	3	3	2	2
Mega-environments			1	3	7	6	9	10	10	10	14
Oil content	28	GE28				2					
	19	GE19				2	2	1	1	1	
	30	GE30	16	16	16	12	14	14	14	14	14
	24	GE24				2			1	1	1
Mega-environments			1	1	1	3	2	2	3	3	3

3.5. Combined Analysis of Variance as per the AMMI Model for Oil Content. For oil content, all the components of variation, *viz.,* environments, genotypes, and G ∗ E interactions, showed significant differences (Table 3). Environments' main effects contributed to 30.69% of the variation. The GE interaction showed a maximum contribution of 34.75%, followed by genotypes' main effects (34.28%). The genotype × environment interaction (GEI) and genotype components were almost equal in their contribution to total variation. The GEI was further partitioned into five principal components. All ten PCs were significant in explaining their contribution. IPCA1 explained maximum GEI with a proportion of 27.5%, while IPCA2, IPCA3, IPCA4, and IPCA5 explained 20.9%, 13.80%, 12.60, and 7.2% of total GEI, respectively. The first two components cumulatively contributed 48.4% to the total GEI. However, more than 70% of the variation was explained by the first four components cumulatively. However, the first 10 principal components showed a 100% contribution to the total GEI.

Table 6: Ranking genotypes in environments for AMMI1 and AMMIF of 30 linseed genotypes in sixteen environments for seed yield and oil content.

Environment			Ratio	AMMI1 ranks					AMMIF ranks				
				1	2	3	4	5	1	2	3	4	5
Seed yield	7	ENV7	1.03	2	6	20	23	10	2	23	6	7	10
	5	ENV5	1.01	2	6	20	23	10	5	21	4	8	20
	1	ENV1	1.00	20	2	6	23	10	23	6	13	18	20
	8	ENV8	1.00	20	2	6	23	10	2	20	7	26	24
	13	EN13	1.00	20	8	16	18	28	21	14	20	7	9
	9	ENV9	1.00	20	8	16	30	18	27	21	28	19	30
	6	ENV6	1.00	20	8	30	16	18	16	4	9	8	28
	12	EN12	1.00	20	8	30	16	18	4	27	20	26	23
	10	EN10	1.00	20	8	30	16	18	8	14	20	27	13
	16	EN16	1.00	20	30	8	16	18	18	20	11	19	9
	11	EN11	1.00	20	30	8	16	18	30	8	28	19	17
	14	EN14	1.00	20	30	8	16	18	19	3	18	24	16
	4	ENV4	1.00	20	30	8	16	18	28	22	15	27	14
	15	EN15	1.07	30	20	16	8	18	11	30	28	16	14
	3	ENV3	1.04	30	20	16	28	8	30	27	22	19	28
	2	ENV2	1.32	30	14	17	29	16	1	29	30	8	26
Oil content	10	EN10	1.0000	30	19	28	16	25	30	19	20	28	9
	2	ENV2	1.0000	30	19	28	20	16	30	19	20	9	28
	16	EN16	1.0000	30	19	28	20	16	30	28	27	25	11
	8	ENV8	1.0000	30	19	28	20	16	30	28	25	11	19
	11	EN11	1.0000	30	19	28	20	16	30	16	19	20	6
	4	ENV4	1.0000	30	19	28	20	3	30	16	10	19	3
	12	EN12	1.0000	30	19	20	28	3	30	3	23	25	20
	3	ENV3	1.0000	30	19	20	28	3	30	16	19	6	27
	9	ENV9	1.0000	30	24	19	27	20	30	24	27	6	23
	15	EN15	1.0000	30	24	19	27	20	30	24	20	9	25
	7	ENV7	1.0000	30	24	27	19	20	30	24	21	25	27
	13	EN13	1.0000	30	24	27	19	10	30	24	27	20	19
	5	ENV5	1.0000	30	24	27	10	19	30	24	27	10	6
	1	ENV1	1.0000	30	24	27	10	19	30	21	23	4	9
	6	ENV6	1.0000	30	24	27	10	19	19	24	22	27	20
	14	EN14	1.0000	30	24	27	10	19	24	20	19	27	21

3.6. AMMI Biplots. There are two basic AMMI biplots, the AMMI1 biplot, where the main effects (genotype mean and environment mean) and IPCA1 scores for both genotypes and environments are plotted against each other. It enables a simultaneous view of the mean performance and the stability of genotypes and environments [31]. As per the AMMI1 biplot, displacements along the abscissa indicate differences in main (additive) effects, whereas displacements along the ordinate indicate differences in interaction effects. The second biplot is AMMI2, where scores for IPCA1 and IPCA2 are plotted. The genotypes and environments that have the same sign on the PCA axis show positive interaction and hence are positioned close to each other on the biplot. No correlation was observed when environment and genotype formed a right angle, while the severe and nearer angles between them indicate a negative and positive correlation, respectively.

3.6.1. AMMI1 Biplot and IPCA Scores

(1) Performance of the Environments. Genotypes were distributed below and above the mean oil content between IPCA1 values of −1.10 to +1.74. The mean oil content of the environments and genotypes on the left side of the origin was lower than the grand mean, whereas those on the right side of the origin were higher. For location Palampur, as per the AMMI1 biplot (Figure 8) analysis greater variation in the interaction effects was observed as compared to the main effects among the test environments (E1, E2, E9, and E10) (Figure 8). Interaction effects were greater across production systems for both years *viz.,* between E1 and E2 and E9 and E10 whereas less variation was observed for the same production system across years *viz.,* between E1and E9 and E2 and E10. E1 and E9 showed positive PC scores, whereas, E2 and E10 showed high negative PC scores. However, the mean performances were above average in both environments across years and were also similar in magnitude. The lowest mean performance was observed in E1, whereas, the highest was observed in E10. The natural production system showed comparatively higher means than the conventional system under the Palampur location. With respect to site Bajaura (Figure 8), the four test environments (E3, E4, E11, and E12) varied more for the main effects than the interaction effects. It was observed that natural production system environments (E4 and E12) showed consistently below-average oil content, whereas, conventional system

environments (E3 and E11) showed consistently above-average performance. In the case of Kangra (Figure 8), very little variation was observed for interaction and main effects among the test environments (E5, E6, E13, and E14). E6 and E14 were the same in their interactions as well as their main effects *viz.,* interaction effects, and the mean performance was stable under the natural production system across years. However, for conventional systems, variation was observed for both interaction and main effects but it was very low. The mean performance was close to average under conventional systems (E5 and E13) and below average under natural systems (E6 and E14). For site Dhaula Kuan, AMMI1 biplot analysis revealed that the test environments varied more for their interaction effects more than the main effects (Figure 8). E7 and E15 showed positive PC scores with less variation between them, whereas E8 and E16 showed negative PC scores with less variation. However, the mean performances in both production systems were similar in magnitude.

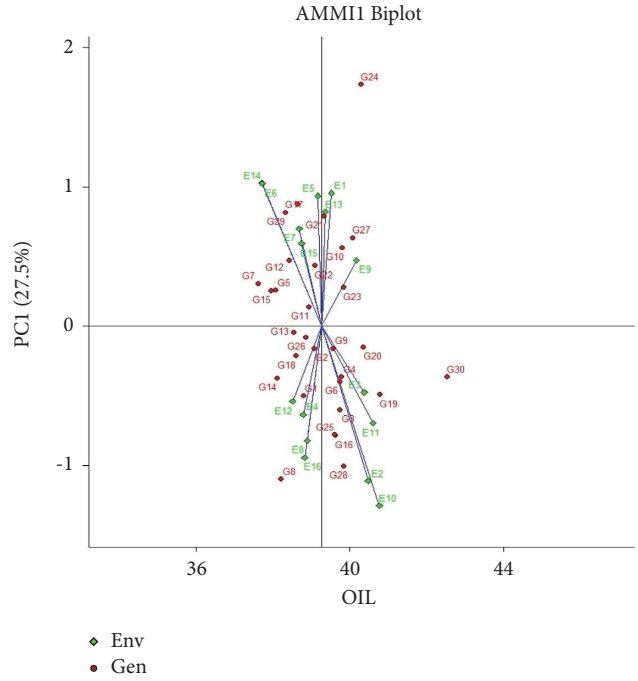

Figure 8: AMMI1 biplot display (IPCA1 vs mean) of linseed genotypes for oil content in sixteen environments.

(2) Performance of the Genotypes. Genotypes differed in their interactions and main effects (Figure 8). Among all the genotypes evaluated, genotypes G11 (38.94%), G13 (38.54%), G26 (38.85%), G9 (39.56%), and G20 (40.35%) were the most stable in performance across all the environments, with PC scores close to zero (Table 7). Among them, G9 (39.56%) and G20 (40.35%) had oil content above average whereas G11 (38.94%), G13 (38.54%), and G26 (38.85%) showed below average performance. The genotype with the highest oil content was G30 (42.53%), which was moderately stable. G24 (40.28%) and G8 (38.20%) were the most unstable genotypes because of their high positive and negative PC scores, respectively. A higher oil content under ZBNF than that of the conventional system was observed at Palampur and Dhaula Kuan (Table 4). However, the difference was not more than 10 percent. A decrease in oil content under ZBNF was observed at locations in Kangra and Bajaura. However, the largest difference of 11.69 percent was observed for genotype Bhagsu at Dhaula Kuan.

3.6.2. AMMI2 Biplot

(1) Performance of the Environments. For site Palampur, AMMI2 and biplot analysis (Figure 9) revealed that the two production systems showed a negative correlation with one another for both years, *viz.,* between E1 and E2 and E9 and E10. However, a positive correlation was observed across years for the same production systems *viz.,* between E1 and E9 and E2 and E10. A very close association was found between E2 and E10, both showing high interaction. E1 and E9, although positively correlated, did not show a very high correlation. The natural production system was constant in its discriminating ability across years; hence, it could be regarded as more informative than the conventional system. However, with respect to site Bajaura all four test environments (E3, E4, E11, and E12) showed high interaction and were also closely associated with one another (Figure 9). Among the genotypes evaluated, none of the genotypes showed specific adaptation under conventional systems (E3 and E11) (Figure 9). For site Kangra (Figure 9) as well, all the four test environments (E5, E6, E13, and E14) showed a positive correlation with one another. However, a very close association was observed between test environments of natural production systems across years, *viz.,* between E6 and E14. E5 and E13 were also positively correlated. E14 was observed as the most discriminating and E13 was the least discriminating as depicted by the spoke length. With respect to location, Dhaula Kuan AMMI2 biplot analysis (Figure 9) clearly revealed that the two production systems were two important test environments, as a negative correlation existed between them in both years, *viz.,* between E7 and E8 and E15 and E16. However, a very close association was observed for the same production system across years *viz.,* between E7 and E15 and E8 and E16.

Overall, all four locations were not closely related to one another hence, all four locations are important test environments. However, Kangra and Dhaula Kuan were the most similar in providing genotype performances with respect to oil content. E2 and E10 were the most discriminating environments among all and belonged to the natural production system of Palampur. None of the environments showed a lower level of discrimination, indicating that all the environments were informative in nature.

(2) Specific Adaptation of Genotypes as per the AMMI Model. For site Palampur, among all the genotypes evaluated, G14 (KL-280) showed specific adaptation to natural production systems (E2 and E10) (Figure 9). However, for conventional systems, G17 (Giza-8) was the winner in the first year (E1) and G23 (Baner) in the second year (E9). While at site

Table 7: Genotypes stable for seed yield and oil content along with their PC scores and mean performances.

Genotypes stable for seed yield	IPCAg1	Mean seed yield performance (g)	Oil content (%)	Genotypes stable for oil content	IPCAg1	Mean seed yield performance (g)	Oil content (%)
KL-279	0.08	5.07	38.54	KL-269	0.14	4.06	38.94
Him Alsi-2	−0.03	5.15	40.72	KL-279	−0.05	5.07	38.54
Janki	−0.15	5.09	40.07	Him Alsi-1	−0.08	4.88	38.85
KL-278	−0.14	5.31	38.42	KL-257	−0.16	4.06	39.56
Giza-7	−0.13	5.62	38.60	Nagarkot	−0.15	6.57*	40.35*

IPCAg1, first interaction principal component axis scores for genotype. *refers to "significance at 5% level."

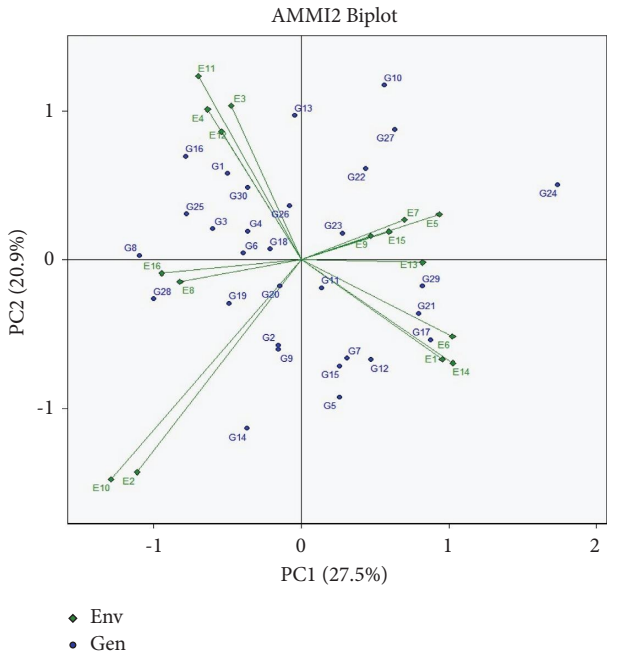

Figure 9: AMMI2 biplot display (IPCA1 vs IPCA2) of linseed genotypes for oil content in sixteen environments.

Bajaura, none of the genotypes showed specific adaptation under the conventional system (E3 and E11) (Figure 9), and G16 (KL-285) and G1 (KL-311) genotypes were found to be the most responsive under the natural system of production (E4 and E12). With respect to location Kangra, G17 (Giza-8) was most responsive under natural conditions for both years (E6 and E14) whereas G21 (Himani) was the most responsive in the first year (E6) (Figure 9). However, for conventional conditions, none of the genotypes showed specific adaptation in the first year (E5), whereas G29 (Canada) was found to be the most responsive in the second year (E13) under the same production system. However, for site Dhaula Kuan, the AMMI2 biplot analysis (Figure 9) revealed that none of the genotypes showed specific adaptation under conventional systems (E7 and E15) whereas under natural conditions the winner in the first year (E8) was genotype G28 (Surbhi) and G8 (KL-244) in the second year (E16).

4. Discussion

In the present investigation, the performance stability of the genotypes could be examined and identified for the traits, *viz.,* oil content and seed yield. The AMMI biplot model provided a clear distinction among the genotypes with respect to their oil content and stability, along with an understanding of the environments. As per the AMMI model for oil content, the maximum contribution of GEI to the total variation (34.75%) and the presence of different winning genotypes across the environments indicated the presence of a crossover type of GEI also reported by Satasiya and Paul [32]. On the contrary, Kumar et al. [33] reported genotype to be the highest contributor to the total variation for oil content in linseed. According to the AMMI biplot analysis, the genotypes varied in their response and stability for various traits in the two different production systems, *viz.,* the conventional system and the natural farming system. The response also varied from year-to-year, as could be seen from the change in ranks of the genotypes across years as well as across production systems, as was also observed by Kindeya and coworkers [34] in sesame, Tadesse et al. [35] in mustard genotypes, and Agahi et al. [29] in rapeseed. Different responses of the same genotype when subjected to different environments (production systems-sites-years) detected the presence of G × E interactions. The underlying causes of the G × E interaction could be due to the genetic differences among the genotypes and the difference in the environments under which the genotypes were tested [36]. The two production systems differed in the magnitude of their genotype and environment interaction and main effects for different traits. This could be attributed to differences in the production systems in which they were grown as well as the fact that they were grown at different altitudes with distinct weather circumstances. Variation among the genotypes' performance across years was also observed. This could be due to the fact that weather conditions vary from year-to-year, affecting the crop's level of stress [37], which may alter the genotype response, leading to varying phenotypes. However, few genotypes were found to be stable in their response to oil content across all sixteen environments, whereas, few showed specific adaptation to specific production systems at one particular location for a particular year, and few were specifically adapted to one location for both production systems across both years.

AMMI is not a single model, rather, it constitutes a model family from AMMI0 to AMMIF. AMMI0 captures no GEI_{noise} and GEI_{signal} whereas AMMIF, the full model, equals the actual data, so it has no residual and captures all GEIN and GEIS. Therefore, model selection is one of the most important steps in AMMI analysis. Model diagnosis provides cues for selecting the best model family for a given dataset [30]. As a result of the present study, the AMMI

model family 3 for seed yield and AMMI6 for oil content have the maximum predictive accuracy. For seed yield, GEIN was 32.41% and GEIS was 67.39% whereas, for oil content, GEIN and GEIS were 10.20% and 89.80%, respectively. For seed yield, three mega-environments could be observed as per the mega-environment delineation analysis. The first mega-environment comprised of environments E7 and E5, which belonged to locations Kangra and Dhaula Kuan under the conventional production system from the first year. In relation to the meteorological data, these locations were comparatively warmer and showed higher temperatures and longer growing seasons. These environments also belonged to conventional production systems. These variations in climatic conditions and production systems could contribute to total GEI interactions whereas the second mega-environment was the largest of all, comprising of 11 environments out of 16. It comprised of mostly the environments from the second year across locations and production systems whereas the third mega-environment comprised of environments from locations Dhaula Kuan, Bajaura, and Kangra. Variation in the ranks of the genotypes among the mega-environments could be observed. This could be attributed to the variation in temperature, rainfall, and humidity across years and also across locations over the different growth stages of the crop. From the warmest summers in Dhaula Kuan to subzero temperatures in Bajaura were observed over the growing period until maturity. However, for oil content, AMMI1 identified only a single mega-environment with G30 as the winner. This meant that genotype 30 was the best-performing in all the locations for two years and also across production systems. The effect of environment could not be observed for the change in the first rank of the genotype. However, variation in the ranks from 2 to 5 could be observed for oil content whereas AMMI6 as the best predictive family model identified 3 mega-environments with three different genotype winners (G30, G19, and G20).

Looking at the AMMI1 biplot, genotypes or an environment with a PCA score of nearly zero indicated small interaction effects and hence was more stable [19]. The most stable genotype for seed yield with above average performance identified was G18, and for oil content, KL-257 and Nagarkot. These genotypes could be a potential source of stability alleles and could be utilized in breeding programs for trait improvement. The most unstable genotypes identified using the AMMI stability model for oil content were Bhagsu and Surbhi although both showed above-average oil content.

Regarding the overall environments, the four locations differed in their interaction and main effects, but greater variation was observed for interaction effects than main effects for oil content. It was also observed that the variation in the oil content under conventional and natural production systems was not very large, however, at two locations *viz.,* Bajaura and Kangra natural production systems showed performance below that of conventional systems. At location Palampur, the natural production system was better performing whereas no effect of production system was observed on oil content at location Dhaula Kuan. For seed yield, the ZBNF system was identified as a poor yielder at all locations. However, it is suggested that the environments be evaluated for a greater number of years to have a better validation of the most representative environment and a clear understanding of the grouping of environments into different mega-environments with respect to the trait seed yield per plant. On the basis of the repeatability of the results across years and across production systems, the important test environments for oil content were also identified. For site Palampur, the two production systems were identified as important test environments for evaluating genotypes for oil content, but year-to-year evaluation was not required. Test environments of natural production systems (E2 and E10) showed the highest discriminating ability. For Bajaura, any one of the test environments would be equally helpful in providing the same amount of information on genotype performances. All the test environments showed high discriminating ability. Hence, the location of Bajaura could be considered an important representative environment for genotype evaluation of the trait oil content. With respect to location, Kangra, natural production system and conventional production system were consistent in their ability to provide information on genotype performance across years; therefore, year-to-year evaluation under these systems is not required, whereas at Dhaula Kuan, year-to-year evaluation of genotypes on the same production system was not required. Also, the natural production system was found to be more discriminative than the conventional production system in both the years, and hence, it was more informative. Palampur was also recognised as a favourable environment based on above-average performance, whereas, Kangra and Dhaula Kuan had lower oil concentrations than the average. As per the performance across production systems, not very large variations in mean performance were observed. Only at location Palampur, the natural production system was better performing than the conventional production system. However, no effect of the production system was observed at location Dhaula Kuan.

The close positioning between the genotype and the environment indicates that the genotype has a positive response to that environment [31]. Lines KL-280, KL-285, and genotype Giza-8 showed interactive action with natural production environments during both the years, at locations Palampur, Bajaura, and Kangra, respectively. Therefore, these genotypes could be recommended specifically under the natural production system in these subtemperate locations. However, further studies are required over more years to confirm these findings and assess the repeatability of the detected GEI. In accordance with our findings, Berti et al. [38], Lirie et al. [39], and Kumar et al. [33] also identified widely adapted linseed genotypes for oil content. Also, in the present investigation, as per the AMMI analysis, the variation explained by the first two PC's was below 50 percent for oil content and below 70 per cent for seed yield. This would mean that the rest of the variation is probably concealed in other principal components or other dimensions, and this would require more than three PC's to explain a significant amount of variation. Low contributions attributed by the first two PCAs to total GEI were also

reported by Balestre et al. [40] and Alwala et al. [41] in maize. This is usually the case when high-dimensional data, *viz.*, large number of genotypes as well as environments, are involved [42].This questions the reliability of the biplots. However, as per Yang et al. [31] in case of the agricultural literature so far, there is no guidance concerning how much of the total variability accounted for the first two PCs should be considered adequate.

5. Conclusions

Genotype × environment interaction was shown to be the most significant contributor to total variation for oil content in the study, whereas for seed yield, it was the environment. Crossover GEI was present, and as a result, genotypes ranked differently, which justified the need for stability analysis [43]. For oil content, strong interactive forces were observed for the test environments of Palampur belonging to the natural production systems indicating their strong discriminating ability; however, the test environments of Dhaula Kaun showed the least discrimination among all the environments studied. This revealed Dhaula Kuan as a poor discriminating environment for trait oil content. However, for seed yield, three mega-environments were identified which stipulated the importance of specific adaptation and for oil content, only one mega-environment was identified. For seed yield, genotype Nagarkot was identified as the most stable with a high yield. Genotypes KL-257 and Nagarkot were identified as the most stable as per the IPCA1 scores with high oil content, whereas genotype Giza-7 was stable and high yielding was evaluated across sixteen environments and therefore, it could be used in future breeding programmes as a source of high oil content, high seed yield, and stability genes. There were no genotypes that showed stability in both seed yield and oil content along with high mean performances. However, genotypes KL-280, KL-285, and Giza-8 showed specific adaptation under natural production systems of Palampur, Bajaura, and Kangra, respectively, for the trait oil content. As a result, it is suggested that they can be used as breeding resources for particular adaptations in the respective test environments.

Data Availability

The data used to support the findings of the study are included within the article.

Conflicts of Interest

The authors declare that they have no conflicts of interest.

Authors' Contributions

GT was responsible for conceptualization, methodology, investigation, analysis, software, and writing the original draft. SP was responsible for conceptualization, methodology, funding acquisition, supervision, and project administration. RKG was responsible for supervision, project administration, and editing and improving the original draft. SL was responsible for analytical experimentation, data curation, supervision, and writing the original draft.

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