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SHORT RESEARCH ARTICLE

AMMI and GGE analyses of linseed (*Linum usitatissimum* L.) genotypes for stability in the north-west Himalayan region of India

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Abstract

Thirty linseed genotypes were assessed across 3 locations during 2019-20 using AMMI and GGE models. AMMI revealed significant effects for genotype (16.16%), environment (57.39%), and G × E interaction (26.05%). GGE identified Palampur and Kangra as ideal mega-environments, with Dhaulakuan as a representative testing environment. KL-322, JRF-4, KL-325, KL-314, and Ayogi were identified as stable genotypes based on AMMI stability parameters, while KL-315 and Nagarkot exhibited high yield according to GGE. These promising genotypes warrant further testing and potential release as stable varieties for targeted agricultural regions.

Keywords: Linseed, stability, AMMI, GGE

Linseed (*Linum usitatissimum* L.), crucial for oil, seed, and fiber in India, faces challenges in Himachal Pradesh, with meager cultivation statistics contrasting the national average. For this, identifying stable linseed genotypes across diverse environments is vital. Understanding G × E interactions aids efficient evaluation, minimizing unnecessary testing sites. The intricate interplay between genotype and environment impacts trait expression, reducing selection efficiency. Plant breeders recognize the significance of integrating G and GE, especially in prominent G × E interactions (Yadawad et al. 2023). Various methods, categorized into univariate and multivariate stability statistics, exist for G ± E interaction analysis. This study employs joint regression for simplicity and AMMI model, presenting data in a biplot for visualizing genotype-environment relationships. GGE biplot analysis provides a comprehensive visual assessment, identifying mega-environments. Utilizing both AMMI and GGE biplot models, the goal is to identify the most stable linseed genotype with wide and specific adaptation. Insights gained can guide plant breeders in selecting genotypes for enhanced linseed cultivation and productivity across diverse environments.

Thirty linseed genotypes, including checks, Nagarkot and Him Palam Alsi-2 having anthocyanin pigmentation, were assessed for their stability in rabi 2019-2020 using RBD with three replications. Each genotype was grown in two rows of 1m length with 30 × 10 cm spacing, following recommended practices. The seasonal requirements of seed-type linseed vary from 10-38°C temperature, well-drained loamy soils and ready to harvest in around 90 to 140 days. The type of soil and climate that prevailed at the site of the experiment is described in Table 1. The pedigree and other characteristic features of the genotypes are given in Table 2.

Data for 12 traits, namely, plant and technical height, number of primary and secondary branches, number of capsules, number of seeds per capsule, aerial biomass, seed yield, harvest index, and 1000-seed weight, were recorded on five competitively selected plants for each genotype across replications. Flowering and maturity days were recorded on plot basis. The data obtained was further subjected to 'R' software version 4.1.2 for the AMMI and GGE biplot analyses.

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Table 1. Site description for G × E interactions

S. no.	Location	Latitude and longitude	Elevation (m amsl)	Annualrainfall (mm)	Agro-climate Zone of Himachal Pradesh	Soil texture and pH
E1	Hill Agricultural Research and Extension Centre, Dhaulakuan	30°4′ N, and 77°5′ E	468	1100	Zone I, sub-tropical, sub montane & low hilly area	Sandy loam
E2	Shivalik Agricultural Research and Extension Centre, Kangra	32°09′N and 76°22′E	700	1849	Zone I, Dhauladhar range of western Himalayas in the North	Clayloam
E3	Chaudhary Sarwan Kumar Himachal Pradesh Krishi Vishvavidyalaya, Palampur	32°09′ N and 76°55′ E	1290.80	1500–2500	Zone II, mid hill, humid sub-temperate climate	Acidic, silty clay loam

* m amsl= meters above mean sea level; mm=milli meters

AMMI analysis of variance

In AMMI model, PCA is based on the matrix of deviation from additivity or residual and the genotypes and environments are grouped based on their similar responses. AMMI analysis for seed yield revealed 16.16% of the significant sum of squares attributed to genotype, 57.39% to the environment, and 26.05% to G×E interaction effects (Table 3). PC1 and PC2 explained 55.50 and 44.50%, with the environment making a substantial contribution to seed yield variation. The AMMI biplot, incorporating PC1 axis and mean yield, displayed genotypes and environments dispersed around the center, indicating significant variability.

Environmental effect scores were comparatively more scattered than genotypic effect scores, emphasizing greater variability due to the environment. These findings align with previous studies by Berti et al. (2010), Jacobsz et al. (2015), and Kumar et al. (2020).

IPCA scores, AMMI stability values and mean yields

DK (E1) and Plmpr (E3) had more genotypes above the 3.16 g grand mean for seed yield/plant. Kan (E2) recorded the lowest mean seed yield of 2.48 g. Mean grain yield across environments ranged from 1.90 to 5.11 g (Fig. 1). Across environments, Nagarkot (DK) was the highest yielder (5.11 g), followed by KL-316 (5.06 g). Genotypes KL-313 (Kan) and KL-318 (Plmpr) had the lowest yields (1.90 and 1.92 g). 25 genotypes yielded above the grand mean, while 5 were below. Genotypes KL-311 (G7), KL-314 (G10), KL-320 (G16), JRF-4 (G27), KL-325 (G21), Ayogi (G28), KL-313 (G9), KL-309 (G5), and KL-322 (G18) exhibited the most stability across environments, as indicated by their lowest IPCA1 values near the biplot origin (Fig. 2a). Among these, KL-322 (G18), JRF-4 (G27), KL-325 (G21), KL-314 (G10), and Ayogi (G28) were not only stable but also demonstrated high seed yield (>grand mean 3.16 g). In contrast, genotypes KL-315 (G11), KL-314 (G10), KL-318 (G14), K1 Raja (G26), Nagarkot (G29), and Him Palam Alsi-2 (G30) exhibited specific adaptations, being more distant from the biplot origin.

GGE biplot analysis

Yan et al. (2000) combined genotype main effects (G) and genotype-by-environment interactions (GE) into GGE, emphasizing their joint importance in evaluating genotypes, especially when GE interaction is repeatable. The GGE biplot, a powerful visualization tool, displays G×E interactions, aiding in mega-environment identification and genotype evaluation as mentioned below. In this investigation, the first two principal components explained 76.08% of total GGE variation, facilitating analysis of genotype performance across diverse environments.

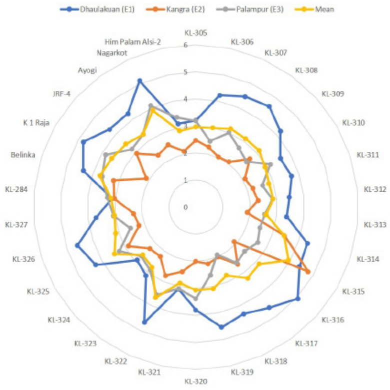

Fig. 1. Radar depicting mean seed yield performance of genotypes over three locations

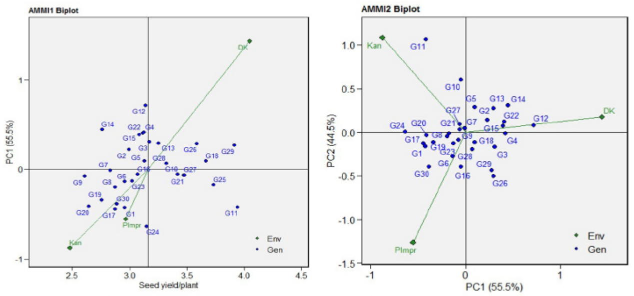

Fig. 2. **(a):** AMMI1 biplot showing the IPCA1 vs. means for seed yield of 30 genotypes evaluated in three environments (b): AMMI2 biplot showing the first two principal axes of interaction (IPCA2 vs. IPCA1) for seed yield of 30 genotypes evaluated in three environments

Mega-environment analysis

The GGE biplot's compelling feature lies in displaying the

Table 2. A list of plant material used in the study

Code	Genotypes	Pedigree/Source	Flower color	Seed color	Types
G1	KL-305	TL-27 × Nagarkot (ABL)	Blue	Light brown	Seed type
G2	KL-306	Nagarkot × T-397 (ABL)	Blue	Dark brown	Seed type
G3	KL-307	Him Alsi-2 × Nagarkot (ABL)	White	Brown	Seed type
G4	KL-308	TL-397 × Nagarkot (ABL)	Blue	Brown	Seed type
G5	KL-309	Canada × Nagarkot (ABL)	Blue	Brown	Seed type
G6	KL-310	Giza-8 × Nagarkot (ABL)	Blue	Dark brown	Seed type
G7	KL-311	Giza-6 × Nagarkot (ABL)	Blue	Dark brown	Seed type
G8	KL-312	Giza -7 × Nagarkot (ABL)	Blue	Brown	Seed type
G9	KL-313	Faiking × Nagarkot (ABL)	Blue	Brown	Seed type
G10	KL-314	Belinka 60 × Nagarkot (ABL)	White	Brown	Seed type
G11	KL-315	TL-27 × Flak-1 (ABL)	White	Brown	Seed type
G12	KL-316	Him Alsi-2 × Binwa (ABL)	Blue	Brown	Seed type
G13	KL-317	Him Alsi-1 × Binwa (ABL)	White	Dark brown	Seed type
G14	KL-318	Him Alsi-2 × TL-11 (ABL)	Blue	Brown	Seed type
G15	KL-319	(KL-243× Janki) × KL-243 (ABL)	Violet	Brown	Seed type
G16	KL-320	(Gaurav × Nagarkot) × Nagarkot (ABL)	Blue	Brown	Seed type
G17	KL-321	TL-43 × Binwa (ABL)	Blue	Brown	Fibre type
G18	KL-322	(TL-43× Binwa) × TL-43 (ABL)	Blue	Dark brown	Seed type
G19	KL-323	(KL-178× Ariane) × KL-178 (ABL)	White	Yellow	Seed type
G20	KL-324	TL-11 × Him Alsi-2 (ABL)	Blue	Brown	Seed type
G21	KL-325	TL-37-2 × Him Alsi-2 (ABL)	Blue	Light brown	Seed type
G22	KL-326	Binwa × Him Alsi-2 (ABL)	White	Brown	Seed type
G23	KL-327	(Janki × TL- 43) × Janki (ABL)	Blue	Brown	Seed type
G24	KL-284	Rajeena × Him-Alsi-2 (ABL)	White	Light brown	Dual purpose
G25	Belinka	Exotic collection	White	Light brown	Fibre type
G26	K 1 Raja	CSIRO, Canberra, Australia	Blue	Brown	Fibre type
G27	JRF-4	CRIJAF, Barrackpore	White	Brown	Fibre type
G28	Ayogi	Exotic collection	Blue	Brown	Fibre type
G29	Nagarkot (check)	New River × LC-216 (Released)	Blue	Brown	Dual purpose
G30	Him Palam Alsi-2 (check)	KL-223 × KL-224 (Released)	Blue	Brown	Seed type

CSIRO: Commonwealth Scientific and Industrial Research Organization, CRIJAF = Central Research Institute for Jute and Allied Fibres
Flower color and seed color mentioned are as per the descriptors by AICRP 1991 and $ABL = Advanced Breeding Line

Table 3. AMMI ANOVA for seed yield of 30 linseed genotypes grown over 3 locations

Source	df	Sum Square	Mean Square	F value	P(>F)	%Explained
ENV	2	116.194	58.097**	428.485	3.36097E-07	57.39
REP(ENV)	6	0.8135	0.1355**	0.876	0.513301581	0.40
GEN	29	32.710	1.127**	7.292	5.85946E-18	16.16
GEN × ENV	58	52.746	0.909**	5.879	5.24908E-20	26.05
PC1	30	29.298	0.976	6.310	0	55.50
PC2	28	23.448	0.837	5.410	0	44.50
Residuals	174	26.912	0.1546			
Total	327	282.123	0.8627			

**significance at 1% level of significance

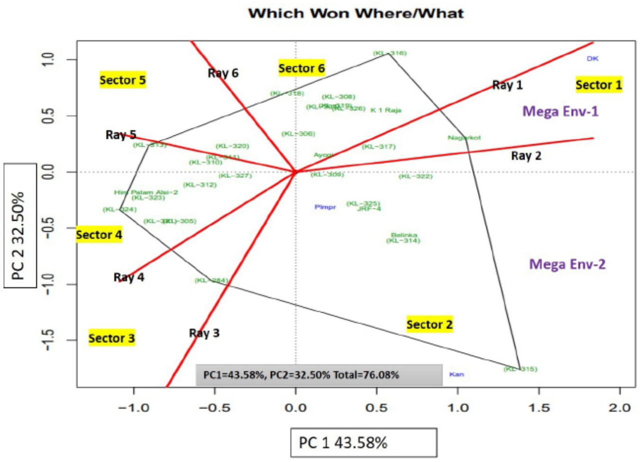

Fig. 3. Polygon views of the GGE-biplot depicting the which-won-where

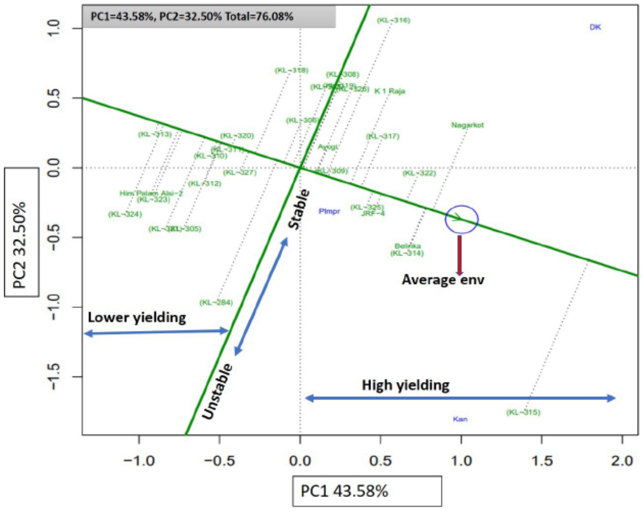

Fig. 4. Depiction of AEC based on means performance and stability of genotypes

"which-won-where" pattern in a genotype-by-environment dataset. Mega-environment analysis involves visualizing this pattern through an irregular polygon, its vertices representing genotypes farthest from the biplot origin. Rays, perpendicular to polygon sides, facilitate visual comparisons between neighboring genotypes. In Fig. 3, six rays divide the biplot into sectors, with each sector encompassing three environments. The vertex genotype in each sector consistently outperforms others in all environments within that sector. This characteristic enhances the GGE biplot's utility in identifying genotypes with broad and specific adaptability across diverse environments (Yan 1 and Tinker 2006). Two environments, Kan and Plmpr, falling into sector 2 with vertex genotype KL-315, suggest it as a high-yielding genotype for both.

Dhaulakuan, in sector 1 with vertex genotype Nagarkot, forms a distinct mega-environment. This pattern implies the potential for simplifying stability and adaptability evaluation by considering a single mega-environment, optimizing cost and cultivar selection. The Average Environment Coordination (AEC) method assesses yield performance and genotype stability (Yan, 2002 and Kaya et al. 2006). Average PC1 and PC2 scores across all environments define the average environment (Fig. 4). The AEC abscissa, drawn through this average environment and the biplot origin, points to greater genotype main effects. In contrast, the AEC ordinate, perpendicular to the abscissa, represents greater GEI and reduced stability, indicated by double arrows.

The AEC ordinate aids in categorizing genotypes with below and above-average means. Genotypes with above-average means include KL-308, KL-326, Ayogi, KL-316 to Belinka, Nagarkot, and KL-315, while those with below-average means are from KL-319, KL-306, KL-318 to Him Palam Alsi-2, KL-324, and KL-313. The distance from the biplot origin to the average environment marker in Fig 4 measures the length of the average environment vector, indicating the relative importance of the genotype main effect *vs* the genotype-environment interaction effect. A longer vector signifies greater importance of genotype main effect and more meaningful selection based on mean performance. Select genotypes KL-308 to KL-315 for above-average mean yield. Prioritize genotypic stability; longer projections on AEC ordinate (Fig. 4) indicate variable nature and less stability. Stable and high-yielding genotypes: KL-314, KL-322, KL-325, JRF-4, Belinka; in contrast to Nagarkot, K1 Raja and KL-316 which were more variable and high yielding.

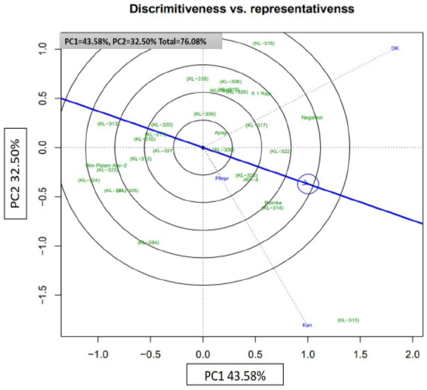

Fig. 5. The 'discriminativeness vs. representativeness' view of the GGE biplot where scaling =0 i.e., data is not scaled

An ideal test environment should effectively discriminate superior genotypes and be representative of all test environments. Palampur and Kangra were chosen as the most ideal testing environments, close to the ideal representation (Fig. 5). Unscaled data show environment vector length proportional to genotypic standard deviation, indicating discriminating power. DK has the longest vector, suggesting high genotype discrimination. Plmpr's short vector near the origin implies genotype similarity, providing little information. GGE biplot's discriminativeness vs.

representativeness graph aids in identifying crucial, and a few discriminating and representative environments in QTL mapping studies. Seed yield, a complex quantitative trait, is influenced by various components and environmental factors, emphasizing the need for stability and adaptability analysis. AMMI and GGE models reveal diverse environments' significant impact on variation. Genotypes KL-322, JRF-4, KL-325, KL-314, and Ayogi exhibit stability. GGE identifies Palampur and Kangra as ideal environments, optimizing multi-environment trials. KL-315 and Nagarkot, high-yielding in GGE, are potential stable varieties for targeted regions.

Authors' contribution

Conceptualization of research (RT, SP); Designing of the experiments (RT, SP); Contribution of experimental materials (SP); Execution of field/lab experiments and data collection (RT, SP, GT, VC, GS); Analysis of data and interpretation (GT, RT); Preparation of manuscript (RT).

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