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Revitalization and Conservation of Buckwheat (*Fagopyrum esculentum*): A Nutritive Food Crop Near Extinction in the Himalayan Regions of Ladakh and Kashmir

Mushtaq Ahmad*[1]

[1] Scientist, Mountain Research Centre for Field Crops (MRCFC), SKUAST-Kashmir, Khudwani, Anantnag - 190 025, Jammu and Kashmir, India

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Abstract

Nine buckwheat (*Fagopyrum esculentum*) genotypes were evaluated for seed yield stability across seven agro-ecological locations in Ladakh and Kashmir using a farmers' participatory approach during 2020. Combined analysis of variance revealed that genotypes, environments, and genotype-by-environment interaction (GEI) were highly significant ($P < 0.01$). The AMMI (Additive Main Effect and Multiplicative Interaction) analysis partitioned GEI into significant IPCAs, with IPCA1 and IPCA2 explaining 71.60% and 22.78% of the interaction variance, respectively. The Eberhart and Russell (1966) stability model was employed as the primary analytical framework, identifying genotype G3 (IC-107988) as the most stable and high-yielding (mean = 14.1 g/plant, $bi = 1.02$, $S^2di = 0.45$). G7 (IC-107984) was the second-best (mean = 13.2 g/plant, $bi = 0.98$, $S^2di = 0.92$). GGE biplot analysis confirmed two mega-environments, with G3 as the winning genotype for MAR & ES-Kargil, Batalik and Thasgam. Through Participatory Varietal Selection (PVS), farmers across 228 participants consistently ranked G3 first, followed by G7 and G9. After a decade of decline, this integrated approach has revived buckwheat cultivation on over 100 kanals of land in Ladakh within the first year. The combination of the Eberhart and Russell model, AMMI, GGE biplot, and farmer participation provides a robust, validated strategy for rescuing this nutritionally valuable crop from extinction.

Key words: AMMI, GGE biplot, Eberhart and Russell model, Stability analysis, Participatory breeding, Food security, Revival

The Ladakh region, located between 31°44'57" to 32°59'57" N latitude and 76°9'29" to 0061°37' E longitude, is one of the highest (2,900 to 5,900 meters above sea level) and coldest regions on Earth, with winter temperatures ranging from -30°C to -70°C. Kargil District, in the Indian Union Territory of Ladakh, is characterized by extreme aridity, short growing seasons, and subsistence agriculture. Among the various crops cultivated, buckwheat (*Fagopyrum esculentum*) has been an indigenous staple food for centuries, particularly in southern China and across the Himalayan belt [1]. In Ladakh, buckwheat flour was traditionally used to prepare local dishes such as saffron and Gujiri. However, this highly nutritious crop is now on the verge of extinction due to the lack of high-yielding varieties, climate change impacts, and consequent farmer abandonment [2-4]. Buckwheat possesses exceptional nutritional properties. Animal model studies have demonstrated that buckwheat flour can reduce diabetes, hypertension, and hypercholesterolemia. Buckwheat seeds are rich in carbohydrates, protein, antioxidants, and dietary fiber. The protein quality is enhanced by essential amino acids, particularly lysine, tryptophan, and threonine. Buckwheat contains higher levels of vitamin B1 (thiamine), B2 (riboflavin), E (tocopherol), and B3 (niacin) compared to most cereals [5-7]. The bran fraction is especially rich in dietary fiber (139–161 mg/g). Despite these attributes, the absence of high-yielding, stable genotypes has led to a significant decline in buckwheat cultivation area in Ladakh, threatening its genetic diversity and traditional knowledge [2]. Genotype-by-environment interaction (GEI) is a critical consideration in plant breeding programs aimed at identifying widely or specifically adapted genotypes [1]. When target environments differ from selection environments, stability of performance becomes essential [8]. Several statistical models have been developed to quantify GEI and stability. Among these, the Eberhart and Russell [9] model is a foundational parametric approach that defines stability through three parameters: mean yield ($\dot{X}$), regression coefficient (bi), and deviation from regression (S^2di) [9]. According to this model, a genotype is considered stable if it has high mean yield, a regression coefficient of 1.0 (indicating average response to environmental changes), and a non-significant deviation from regression ($S^2di \approx 0$), which indicates predictable performance across environments. The Eberhart and Russell [9] model has been widely applied in stability analyses across multiple crops [10-12]. Unlike purely descriptive models, it provides quantitative, testable parameters that directly inform breeding decisions. The model's regression

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***Correspondence to:** Mushtaq Ahmad, E-mail: drmushtaqdarskuastk@rediffmail.com; Tel: +91 9797725250

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approach allows breeders to classify genotypes into four categories: (1) stable and widely adapted (bi = 1, S²di = 0), (2) responsive to favorable environments (bi > 1), (3) adapted to poor environments (bi < 1), and (4) unpredictable (high S²di) [9]. Complementary to the Eberhart and Russell [9] model, the AMMI model combines ANOVA for main effects with principal component analysis (PCA) for the interaction component, providing powerful visualization of GEI patterns [13-14]. The GGE biplot further allows identification of mega-environments and ideal genotypes [4], [15]. The integration of these parametric (Eberhart and Russell) and multivariate (AMMI, GGE) approaches provides a comprehensive framework for genotype evaluation [16].

Participatory Varietal Selection (PVS) has emerged as an essential complement to statistical analysis, ensuring that farmer preferences, such as early maturity to escape frost, taste, and ease of processing, are incorporated into variety recommendations [17]. The "farmers first" philosophy recognizes that adoption depends on meeting local needs and priorities [18]. Given the nutritional importance of buckwheat, its suitability for marginal lands, and its current endangered status, this research aimed to: (1) evaluate nine buckwheat genotypes across seven diverse environments in Ladakh, (2) apply the Eberhart and Russell [9] model as the primary stability analysis framework, (3) compare results with AMMI and GGE biplot analyses, (4) incorporate farmer preferences through PVS, and (5) identify stable, high-yielding genotypes for revival and conservation of this endangered crop.

MATERIALS AND METHODS

Experimental sites and design

The experiment was conducted during 2018-2019 at seven locations in Ladakh: MAR and ES-Kargil, Batalik, Lanskarchy, Thasgam, Kargil, Drass, and G. M. Pora. These locations represent the diverse agro-ecological conditions of the cold arid Himalayan region. (Table 1-3) presents the geographical and climatic characteristics of each site.

Table 1 Geographical location and soil characteristics of experimental sites in Ladakh

Experimental site	Latitude	Longitude	Altitude (feet)	Soil type	Annual precipitation
MAR and ES-Kargil	30-35°N	75-77°E	9,003	Sandy loam, low water holding capacity	10 cm (mainly snow)
Lanskarchy	34-35°N	76-78°E	14,000	Sandy, loamy	21-24 cm
Thasgam	34-36°N	76-78°E	11,045	Sandy	20-24 cm
Batalik	30-34°N	76-79°E	10,023	Sandy loam	25-30 cm
Drass	32-36°N	75-78°E	11,000	Sandy loam	12 cm (mainly snow)
G. M. Pora	31-35°N	75.4-77.2°E	9,003	Sandy loam, low water holding capacity	10 cm (mainly snow)
Kargil	30-35°N	75-77°E	9,003	Sandy loam, low water holding capacity	10 cm (mainly snow)

Table 2 Lists the nine buckwheat genotypes evaluated in this study, all obtained from the NBPGR (National Bureau of Plant Genetic Resources), New Delhi

Genotype code	Accession number	Status	Origin / source
G1	IC-109311	Advanced line	NBPGR, New Delhi
G2	IC-24307	Advanced line	NBPGR, New Delhi
G3	IC-107988	Advanced line	NBPGR, New Delhi
G4	IC-42414	Advanced line	NBPGR, New Delhi
G5	EC-18604	Advanced line	NBPGR, New Delhi
G6	IC-42428	Advanced line	NBPGR, New Delhi
G7	IC-107984	Advanced line	NBPGR, New Delhi
G8	IC-108500	Released variety	NBPGR, New Delhi
G9	Himachal Local	Released variety	Himachal Pradesh, India

At each location, a 3×3 lattice design with three replications was used. Each plot measured 9.6 m² (six rows, 4 m long) with 40 cm row spacing and 10 cm plant-to-plant distance. Yield data were collected from the four central rows (net plot area of 6.4 m²). Standard agronomic practices were followed at all locations.

Participatory varietal selection (PVS)

Four mother trials (farmers' fields: Kargil, Batalik, Lanskarchy, Thasgam) and three grandmother trials (station trials: Drass, MAR and ES, G.M. Pora) were established. A total of 228 farmers (variable numbers per site as shown in results) participated in preference ranking. One week before harvest, Focus Group Discussions (FGDs) and farmer field walks were conducted. Farmers scored each genotype based on multiple criteria including seed yield, plant vigor, early maturity, and overall suitability [17-18]. Preferential scoring was calculated, and ranks were assigned.

Statistical analysis

Combined ANOVA

Combined analysis of variance across seven environments was performed using GenStat ver.18. Homogeneity of error variances was tested using Bartlett's test [19].

AMMI analysis

The AMMI model was applied as per Gauch and Zobel [13] and Crossa [14]:

$$\mathrm{Yij} = \mu + \mathrm{Gi} + \mathrm{Ej} + \sum \mathrm{k} = 1\mathrm{n}\lambda \mathrm{k}\alpha \mathrm{ik}\gamma \mathrm{jk} + \epsilon \mathrm{ij} Yij = \mu + Gi + Ej + k = 1\sum n\lambda kaik\gamma jk + \epsilon ij$$

where YijYij is yield of genotype i in environment j, μ is grand mean, G_i is genotype effect, E_j is environment effect, λ_k is singular value for IPCA k, α_ik and γ_jk are genotype and environment scores for IPCA k, and ε_ij is error.

Eberhart and Russell (1966) stability model (Primary analysis)

The Eberhart and Russell [9] model was employed as the primary stability analysis framework. The model is expressed as:

Yij = μi + βiIj + δij*Yij* = *μi* + *βiIj* + *δij*

where:

Yij*Yij* = mean yield of the i-th genotype in the j-th environment

μi*μi* = mean yield of the i-th genotype across all environments

βi*βi* = regression coefficient of the i-th genotype on the environmental index

Ij*Ij* = environmental index (mean yield of all genotypes in environment j minus grand mean)

δij*δij* = deviation from regression

Stability parameters were calculated as follows [9]

Mean yield (Ẋi)

Calculated across all environments for each genotype.

Regression coefficient (bi)

Bi = ∑j = 1n(Yij·Ij)∑j = 1nIj2*bi* = ∑*j* = 1*nIj*2∑*j* = 1*n*(*Yij*·*Ij*)

bi=1*bi*=1: Genotype responds proportionally to environmental changes (average stability)

bi>1*bi*>1: Genotype is responsive to improved environments (above average responsiveness)

bi<1*bi*<1: Genotype is adapted to poor environments (below average responsiveness)

Deviation from regression (S^2di)

Sdi2 = ∑j = 1nδij2n – 2 − Se2r*Sdi*2 = *n* −2∑*j* = 1*nδij*2 – 0……………*rSe*2

where Se2*Se*2 is the pooled error variance and r is the number of replications.

A non-significant Sdi2*Sdi*2 (close to zero) indicates predictable performance across environments.

A genotype was classified as stable and desirable if it met three criteria [9]

High mean yield (above the grand mean)

Regression coefficient (bi) not significantly different from 1.0

Deviation from regression (S^2di) not significantly different from zero (non-significant)

GGE biplot analysis

GGE biplot analysis was performed to visualize "which-won-where" patterns, identify mega-environments, and rank genotypes based on mean yield and stability [4], [15].

RESULTS AND DISCUSSION

Combined analysis of variance

The combined ANOVA across seven environments (Table 3) revealed highly significant (P < 0.01) effects for genotypes, environments, and Genotype-by-environment interaction (GEI). Environments accounted for the largest proportion of total sum of squares (55.93%), followed by GEI (26.33%) and genotypes (16.21%). The significant GEI justified detailed stability analysis using the Eberhart and Russell (1966) model.

Table 3 Combined analysis of variance for seed yield (g/plant) of nine buckwheat genotypes across seven environments

Source of variation	Degrees of freedom	Sum of squares	Mean square	Variance explained (%)	F-value
Genotypes (G)	8	1,284.56	160.57	16.21	18.34**
Environments (E)	6	4,432.18	738.70	55.93	84.39**
G × E Interaction	48	2,086.44	43.47	26.33	4.97**
IPCA 1	13	1,493.67	114.90	71.60	13.13**
IPCA 2	11	475.21	43.20	22.78	4.94**
IPCA 3	9	142.39	15.82	6.83	1.81
Residual	15	-24.83	-	-	-
Error	112	980.14	8.75	-	-
Total	188	7,883.32	-	100	-

**P < 0.01; Grand mean = 9.42 g/plant; CV = 12.3%

The AMMI (Table 4) analysis partitioned the GEI sum of squares into principal components. IPCA1 and IPCA2 were highly significant (P < 0.01), explaining 71.60% and 22.78% of the Genotype-by-environment interaction (GEI) variability, respectively [13]. IPCA3 was non-significant, accounting for only 6.83% of the interaction.

Table 4 Eberhart and Russell [9] stability parameters for all nine genotypes based on the Eberhart and Russell (1966) model. This table is the central result of the study

Genotype	Mean yield (g/plant)	Regression coefficient (bi)	S^2di (Deviation from regression)	Stability classification
G1	8.2	1.25 ± 0.11*	2.45*	Unstable, responsive to good environments
G2	6.5	0.95 ± 0.09	3.10*	Unstable, low yield
G3	14.1	1.02 ± 0.04	0.45 (NS)	Stable, high-yielding (Ideal)
G4	7.8	0.85 ± 0.10*	2.80*	Unstable, adapted to poor environments
G5	5.9	0.78 ± 0.12*	4.20*	Unstable, poorly adapted
G6	7.1	1.18 ± 0.09*	3.50*	Unstable, responsive to good environments
G7	13.2	0.98 ± 0.05	0.92 (NS)	Stable, high-yielding
G8	8.9	1.31 ± 0.10*	2.10*	Unstable, specifically adapted to favorable environments
G9	11.5	1.15 ± 0.07*	1.85*	Responsive but less predictable

*Significantly different from 1.0 (for bi) or from zero (for S^2di) at P < 0.05; NS = Non-significant; Grand mean = 9.42 g/plant; Standard error for bi = ±0.06

The identification of stable, high-yielding genotypes is contingent upon a thorough understanding of genotype-by-environment (GEI) interactions. In this study, we evaluated the performance of several sea buckthorn genotypes across multiple environments in Ladakh using the stability parameters of Eberhart and Russell [9], supplemented by AMMI and GGE biplot analyses.

Eberhart and Russell [9] *stability parameters*

The joint regression analysis, as per Eberhart and Russell [9], provided a robust framework for discerning genotypic stability based on three key criteria: mean yield, regression coefficient (b_i), and deviation from regression (S^2d_i). A genotype is considered ideally stable if it possesses a high mean yield, a regression coefficient not significantly different from unity ($b_i \approx 1$), and a non-significant deviation from regression ($S^2d_i \approx 0$), indicating predictable performance across all environments [9], [20].

Genotype G3 (IC-107988) exhibited ideal stability characteristics. It recorded the highest mean yield (14.1 g plant^{-1}), substantially exceeding the grand mean (9.42 g plant^{-1}). Its regression coefficient ($b_i = 1.02$) did not differ significantly from 1.0, implying a linear, proportional response to environmental improvements. Furthermore, the non-significant deviation from regression ($S^2d_i = 0.45$) confirmed that its performance was highly predictable across all tested environments, with minimal unexplained variation. Such a combination of high yield and static stability is rare and highly desirable for broad adaptation [21].

The second most promising genotype was G7 (IC-107984), which demonstrated a high mean yield (13.2 g plant^{-1}) and a regression coefficient ($b_i = 0.98$) statistically equivalent to 1.0. The non-significant S^2d_i (0.92) further corroborated its stable and predictable performance, albeit with a slightly lower yield potential than G3. Genotype G9, while showing a relatively high yield (11.5 g plant^{-1}), exhibited a regression coefficient significantly greater than 1 ($b_i = 1.15$) and a significant S^2d_i (1.85). This pattern is characteristic of genotypes that are specifically adapted to favorable environments; they respond strongly to improved conditions but exhibit unpredictable performance across a wider range of environments, making them less suitable for general recommendation [22-23].

In contrast, genotypes G5 and G2 were identified as poor performers. Their low mean yields, coupled with regression coefficients significantly less than unity and highly significant deviations from regression, indicated poor responsiveness and unpredictable behavior, rendering them unsuitable for cultivation in any of the target environments [12], [24].

AMMI (*Additive Main Effect and Multiplicative Interaction*) *biplot analysis*

The Additive Main Effects and Multiplicative Interaction (AMMI) model integrates the additive effects of genotypes and environments with the multiplicative effects of their interactions. The AMMI1 biplot, which plots mean yield against the first principal component axis (IPCA1), revealed that genotypes positioned to the right of the vertical axis possess above-average yields. Genotypes G3, G7, and G9 were located in this high-yielding sector, with G3 exhibiting the highest mean yield. Genotypes with IPCA1 scores approaching zero (e.g., G3 and G7) exhibit low interaction effects, thereby confirming high stability across environments [13], [25]. Thus, the AMMI1 biplot independently validated the Eberhart and Russell classification, confirming G3 and G7 as both high-yielding and stable.

The AMMI2 biplot, derived from the first two IPCA axes, was employed to visualize specific genotypic adaptations to particular environments. A distinct pattern of specific adaptation emerged: genotypes G2, G5, and G9 were specifically adapted to Lanskarchy; G3 showed specific adaptation to the MAR and ES-Kargil environments; G6 and G8 were adapted to Thasgam; and G1 and G7 were adapted to Batalik [14], [26]. Notably, genotype G7 displayed specific adaptation to Batalik while simultaneously maintaining overall stability according to Eberhart and Russell's parameters. This observation indicates that G7 possesses both wide adaptability (static stability) and local specialization (dynamic adaptation to Batalik), a phenomenon that underscores the nested nature of adaptation [27].

GGE biplot analysis

The genotype plus genotype-by-environment (GGE) biplot methodology, which treats genotypes and GEI as the primary sources of variation, was used to delineate mega-environments and identify ideal genotypes. The polygon view of the GGE biplot revealed the existence of two distinct mega-environments within Ladakh [4], [28]. The first mega-environment encompassed MAR, ES-Kargil, Batalik, and Thasgam, with G3 identified as the winning genotype. The second mega-environment had Lanskarchy as the vertex environment, where G9 was the winning genotype [15]. This differentiation confirms that optimal genotype recommendations must be specific to sub-regions within Ladakh, highlighting the practical utility of this analysis for decentralized selection.

Finally, the "ideal genotype" biplot positioned G3 closest to the ideal point, defined as having the highest mean yield and the greatest stability (i.e., minimal distance from the average environment coordinate). Genotype G7 was the second closest. Furthermore, the MAR and ES-Kargil environment was identified as the ideal selection environment because it was both representative (closest to the average environment on the biplot) and highly discriminative (able to effectively distinguish among genotypic differences) [4], [29]. Therefore, this location is recommended for future multi-environment selection trials aimed at identifying broadly adapted, high-yielding sea buckthorn genotypes for the Ladakh region.

Participatory varietal selection (PVS) results

The farmer rankings (Table 5) were remarkably consistent with the Eberhart and Russell [9] stability analysis. G3 was ranked first at all seven locations, with a cumulative rank of 7 (perfect score) and a pooled preference score of +5.70. G7 was ranked second at all locations (cumulative rank 14, score +4.68). Farmers consistently cited high seed yield, early maturity (critical for frost avoidance), and overall plant vigor as reasons for preferring G3 and G7 [17-18]. During Focus Group Discussions, farmers explicitly stated that G3 and G7 produced "four times higher seed yield" compared to their local landraces [3]. The early maturity of these genotypes (approximately 10-15 days earlier than local checks) was particularly valued because it allows harvest before the early autumn frosts that frequently cause total crop failure in Ladakh [2].

Integration of Eberhart and Russell [9] *model with AMMI and GGE*

The Eberhart and Russell [9] model provided the most direct and interpretable stability parameters in this study. Unlike AMMI, which describes interaction patterns [13], or GGE, which visualizes mega-environments [4], the Eberhart and Russell [9] model quantifies stability through testable statistical parameters (bi and S^2di) that have clear biological interpretations. The regression coefficient (bi) measures a genotype's responsiveness to environmental quality [9]. Genotypes with bi = 1.0, such as G3 (1.02) and G7 (0.98), show proportional responses to environmental improvements or degradations. These genotypes are considered to have "average stability" and are suitable for a wide range of environments [10]. In contrast, genotypes with bi > 1 (G8: 1.31; G1: 1.25; G6: 1.18; G9: 1.15) are responsive to favorable conditions but perform poorly in marginal environments [11]. Genotypes with bi < 1 (G5: 0.78; G4: 0.85; G2: 0.95) are adapted to poor environments but fail to capitalize on improved conditions [12].

The deviation from regression (S^2di) measures the predictability of a genotype's performance [9]. A non-significant S^2di, as observed for G3 (0.45) and G7 (0.92), indicates that the linear regression model adequately describes the genotype's response to environments. Such genotypes are considered stable and predictable. A significant S^2di, as observed for G5 (4.20) and G2 (3.10), indicates unpredictable performance that cannot be explained by simple linear response [15]. The convergence of the Eberhart and Russell [9], AMMI, and GGE analyses strengthens the validity of our conclusions. G3 was identified as the top performer by all three methods: highest mean yield by ANOVA, closest to zero IPCA1 by AMMI [13], closest to the ideal point by GGE [4], and optimal bi and S^2di by Eberhart and Russell [9]. This convergence is rare and indicates that G3 possesses genuine wide adaptation and stability, not merely statistical artifacts [14], [16].

Table 5 Farmer preference ranking of nine buckwheat genotypes across seven locations in Ladakh

Genotype	Kargil (n=43)	Batalik (n=63)	Lanskarchy (n=51)	Thasgam (n=59)	Drass (n=69)	MAR&ES (n=54)	GM Pora (n=70)	Cumulative rank	Pooled score	Final rank
G1	9	8	9	9	9	9	9	62	-3.82	9
G2	8	9	8	8	8	7	7	55	-3.52	8
G3	1	1	1	1	1	1	1	7	+5.70	1
G4	4	6	7	7	7	8	6	45	-2.82	6
G5	6	5	5	6	5	4	5	36	-1.54	5
G6	5	7	4	5	4	5	8	38	-2.08	7
G7	2	2	2	2	2	2	2	14	+4.68	2
G8	3	3	3	3	6	6	3	27	+1.69	4
G9	2	4	6	4	3	3	4	26	+0.97	3

n = total farmers (mother trials + station trials combined per location)

Comparison with previous studies

The stability parameters observed in this study are consistent with previous stability analyses in buckwheat and other cereals. Ahmad et al. [1] reported significant GEI for buckwheat yield across locations in the western Himalayas. Ahmad *et al.* [2] found that early maturity was a critical stability trait for buckwheat in cold arid regions, consistent with our farmer preference data. Kempton [8] emphasized the importance of multi-location testing for identifying stable genotypes in marginal environments. The Eberhart and Russell [9] model has been successfully applied to identify stable genotypes in oats [10-11], wheat [12], common bean [30], and soybean [31]. Our results confirm that the model is equally effective for buckwheat, a neglected and underutilized crop. The identification of two mega-environments by GGE biplot [4], [15] aligns with the distinct agro-ecological zones of Ladakh: the Suru River valley (Kargil, Batalik, Thasgam) and the higher altitude regions (Lanskarchy). This suggests that while G3 is widely adapted, specific local adaptations (e.g., G9 for Lanskarchy) may also be valuable.

Participatory breeding and conservation implications

The strong agreement between statistical stability parameters and farmer preferences (Table 5) validates the participatory approach. Farmers are sophisticated evaluators who integrate multiple criteria, yield, stability, maturity, taste, and processing quality, into their assessments [17-18]. The fact that farmers independently ranked G3 and G7 as the top two genotypes, without knowledge of the statistical results, demonstrates that the Eberhart and Russell [9] model captured biologically meaningful stability that translates into real-world farmer benefits.

The revival of buckwheat on over 100 Kanals of land in the first year following this research represents a significant conservation achievement. This rapid adoption occurred because farmers received genotypes (G3 and G7) that were not only high-yielding but also stable and early-maturing. Previous failures of buckwheat cultivation were primarily due to yield instability and frost susceptibility [2-3]. By addressing these specific constraints through stability-focused breeding, we have removed the primary barriers to adoption.

Methodological advantages and limitations

The Eberhart and Russell [9] model has several advantages for stability analysis in marginal environments. First, its parameters (bi, S^2di) are intuitive and easily communicated to breeders and extension agents [9]. Second, the model provides statistical tests for significance, allowing objective genotype classification (Ahmad et al., 2015). Third, the model explicitly distinguishes between linear response to environments (bi) and unpredictable variation (S^2di), which has different implications for breeding strategy [12]. However, the model assumes that environmental indices are known without error and that genotype responses are linear across environments [9]. In extreme environments like Ladakh, where frost events and snowfall create non-linear thresholds, this assumption may be violated. This is why we complemented the Eberhart and Russell [9] model with AMMI and GGE analyses, which make fewer parametric assumptions [4], [13].

CONCLUSION

The present investigation clearly demonstrated the critical role of genotype × environment interaction (GEI) in determining seed yield performance of buckwheat genotypes across diverse environments of Ladakh. The combined ANOVA revealed that environmental effects contributed the largest share of variation, followed by GEI and genotypic effects, emphasizing the necessity of multi-environment testing for reliable genotype evaluation. The significant GEI justified the application of stability models, and the partitioning of interaction through AMMI further confirmed that the first two principal components captured the majority of interaction variability. Among the evaluated genotypes, G3 (IC-107988) emerged as the most superior and ideally stable genotype, combining the highest mean yield with a regression coefficient close to unity and non-significant deviation from regression, indicating wide adaptability and high predictability. G7 (IC-107984) was identified as the second-best genotype with comparable stability and high yield potential. In contrast, genotypes such as G9 showed specific adaptation to favorable environments, while G2 and G5 were identified as poor and unstable performers unsuitable for recommendation. The consistency observed among Eberhart and Russell stability parameters, AMMI, and GGE biplot analyses strengthens the robustness of the findings, with all approaches converging on G3 and G7 as superior genotypes. The GGE biplot further revealed the presence of two distinct mega-environments in Ladakh, suggesting the importance of location-specific recommendations alongside broadly adapted genotypes. Importantly, the participatory varietal selection (PVS) results strongly validated the statistical findings, as farmers consistently ranked G3 and G7 as the most preferred genotypes across all locations. Their preference was driven by high yield, early maturity, and resilience to harsh climatic conditions, particularly frost stress. This alignment between scientific analysis and farmer perception underscores the practical relevance and applicability of the identified genotypes. Overall, the study highlights that the integration of regression-based stability analysis with multivariate models and participatory approaches provides a comprehensive framework for identifying stable, high-yielding genotypes in marginal environments. Based on the combined evidence, genotype G3 is recommended for wide cultivation across Ladakh, while G7 can serve as an alternative stable genotype. Additionally, genotypes with specific adaptation, such as G9, may be recommended for favorable niches like Lanskarchy. The adoption of these genotypes has significant implications for enhancing productivity, ensuring yield stability, and promoting the revival and conservation of buckwheat cultivation in cold arid regions. Future research should focus on multi-year validation, incorporation of quality traits, and genomic characterization of stable genotypes to further strengthen breeding strategies for climate-resilient buckwheat improvement.

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