



Full Length Article

AMMI Analysis to Assess Genotype-by-environment Interaction, Adaptability and Stability of Potato (*Solanum tuberosum*) Genotypes for Tuber Yield and Disease Tolerance in Northern-Pakistan

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Abstract

Genotype × environment interaction is a crucial aspect of identifying and selecting adaptable, stable, and high-yielding potato genotypes that exhibit lower incidence of late blight disease. Twenty-eight potato genotypes, five parents and a check hybrid were tested using randomized complete block design with three replications under three different environments. Analysis of variance revealed significant differences in the studied traits, indicating substantial genetic variability among the genotypes. According to the Eberhart and Russell Stability method, G10, G17 and G21 were identified as adaptable and stable genotypes. The PC1 of the AMMI bi-plot indicated that genotypes G10, G17 and G21 were high-yielding and exhibited lower incidence of late blight disease. Additionally, PC2 suggested that G8, G10 and G12 were consistent in tuber yield, while G10, G11, G17 and G23 were found to be stable against late blight. It was concluded from the study that the G23 produced the highest (38.376 tons ha⁻¹) tuber yield coupled with highest percentage (80.3%) of disease tolerance. In addition, G17 also performed exceptionally with yield potential (38.15 tons ha⁻¹) and disease tolerance (76.7%). Overall, these two genotypes were declared as the most adaptable and stable. Higher tuber production with lower incidence to disease percentage was found in Battakundi environment. Therefore, assessment of such potato hybrids in various environments can exploit more potential for yield and yield attributing traits in upcoming breeding strategies. These useful strategies will be helpful in identifying and choosing the most favorable environments for potato production, not only to contend with original requirements but also to support the large-scale food availability and sustainability.

Keywords: Eberhart and Russell stability; Genotype × environment interaction; AMMI; PC1; PC2; Battakundi

Introduction

Potatoes (*Solanum tuberosum* L.), a member of nightshade family has attracted much attention for playing a very comprehensive role to fulfill food demand. It belongs to family *Solanaceae* (Britannica 2023). Potatoes are enriched with folate, vitamin C, potassium, and iron (Luitel *et al.* 2020). Potato cultivation is highly influenced by number of factors like climate, different soil factors, management practices and particularly, variety selection. Recently, 376 million tons of potatoes were produced from an area of almost 18.1 million hectares, worldwide (FAOSTAT 2023). Meanwhile, record production of potato was noted in

Pakistan with 8319 thousand tons from an area of 341 thousand hectares (PBS 2023).

The central aim of a potato breeding program is to harness and improve genetic variation under diverse environmental conditions. Adaptability and stability under diverse environments, along with maximum production and low disease percentage, are the key goals of local breeding strategies. Adaptability is the superior performance of hybrids across diverse geographic locations, while stability refers to the regularity of a genotype's performance and its ability to withstand the fluctuations in yield across different climatic conditions (Cedarsa *et al.* 2022). Genotype × environment interaction (GEI) is the response of different

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genotypes to varying environmental conditions, leading to variations in phenotypic outcomes. Therefore, assessing stability and genotype $\times$ environment interaction across diverse environments is crucial before the approval, release, and dissemination of a variety/ hybrid for different attributes. Genotype $\times$ Environment Interaction is a complex phenomenon involving climatic, agro-ecological, agronomic, physiological, soil, and genetic factors that affect the development and growth of a crop (Aboughadareh *et al.* 2022). Several techniques have been employed to quantify the effects of GEI across different environments. Among these, the Genotype Main Effects and Genotype $\times$ Environment Interaction (GGE) model (Gauch 2006) and the Additive Main Effects and Multiplicative Interaction (AMMI) model (Zobel *et al.* 1988) are the two most widely used for bi-plot analysis (Flis *et al.* 2014) across different environments. AMMI bi-plot analysis is a dominant means used for selection of adaptable and stable genotypes in GEI, globally (Byarugaba *et al.* 2018). It is particularly important and widely utilized in potato breeding for evaluating and selecting genotypes based on tuber yield and disease resistance across diverse environments (Flis *et al.* 2014).

Generally, three potato crops are grown in Pakistan, ranging from plains to hilly areas, with diverse regional climates (Majeed and Muhammad 2018). In Pakistan, factors limiting potato yield include drought, salinity, temperature fluctuations, inadequate fertilization, irrigation challenges, soil quality and climatic changes compounded by soil-borne issues such as nutrient deficiencies, including nitrogen and others (Majeed and Muhammad 2018). Additionally, biological constraints such as poor seeds, low yield, and diseases caused by bacteria, viruses, and fungi significantly reduce potato growth and production (Majeed *et al.* 2017). The diverse and favorable environmental conditions in Pakistan offer significant opportunities for increasing potato yield. Growth and local environmental conditions play a role in mitigating the unfavorable effect of abiotic and biotic stresses, such as plant diseases. Meanwhile, modifications in potato cultivation and production are required to adapt to the diverse environmental conditions across Pakistan (Majeed and Muhammad 2018). Therefore, the current field study was designed to evaluate potato genotypes for identifying and selecting adaptable and stable varieties in terms of high yield and disease resistance across different environments in northern Pakistan. Additionally, AMMI bi-plot analysis was also used to identify the most suitable and reliable environments for large-scale potato cultivation, growth management, and production, with the goal of meeting domestic food requirements and ensuring future food security.

Materials and Methods

Experimental sites

The current investigation was carried out in three diverse

sites namely Abbottabad, Battakundi, and Kaghan, Khyber Pakhtunkhwa, Northern Pakistan. The experimental trials were conducted under diverse environmental conditions at the Hazara Agricultural Research Station, Abbottabad; the Seed Potato Research and Multiplication Farm, Battakundi; and the Summer Agricultural Research Farm, Kaghan, during the years 2021-2023. Details about the geography of the studied environments are provided in Table 1.

Germplasm

In the beginning 2020-21, hybridization (crosses) among different potato parents were conducted in order to transfer desirable traits with genetic variations at Battakundi. On harvest of successful crosses, true potato seed (TPS) were extracted from the collected berries and seedlings were produced in nurseries under green-house controlled environments. The selected plantlets with mini tubers were grown in field for tuber production with desirable agronomic traits, to identify potato varieties or hybrids. The details of experimental material used in the present study are presented in Table 2.

Field layout

All the experiments were grown using randomized complete block (RCB) design in three replications. Row-to-row and tuber-to-tuber distance was maintained at 0.75 m and 0.25 m, respectively. The single plot size was 4.5 m², where two rows per plot were sown having 24 tubers.

Agronomic practices

Research blocks were prepared following plough and soil preparation. Seed tubers were planted manually. Fertilizers like diammonium phosphate (DAP), sulphate of potash (SOP) and urea were applied at standard rates, respectively. Other cultural practices like weeding, hoeing and roughing were also applied during the study. No fungicide was applied during the experiments to assess disease incidence, specifically for late blight (*Phytophthora infestans*). By not applying fungicide, the study gives a clearer understanding of how *late blight* behaves in diverse environments without external control factors.

Data collection

Data were collected for tuber yield plot⁻¹ and incidence of disease plot⁻¹, according to described data protocols.

Tuber yield plot⁻¹ (tons ha⁻¹)

The tubers were collected and weighed, and the tuber yield was then converted into tons ha⁻¹ by using the formula (Vandamme *et al.* 2023).

$$\text{Tuber Yield} \left(\frac{\text{Tons}}{\text{ha}} \right) = \frac{\text{Plot Yield (kg)}}{\text{Plot Area (m}^2\text{)}} \times 10 \quad (1)$$

Table 1: Details of geography of Abbottabad, Battakundi and Kaghan environments

Components	Abbottabad	Battakundi	Kaghan
Latitude	34°10'7.5036"N	34°56'0"N	34°32'30"N
Longitude	73°13'17.3892"E	37°46'0"E	73°21'0"E
Altitude (masl.)	1256	2812	2510
pH	6.3	5.0	5.3
Annual Rainfall (mm)	1532	1500	1489
Annual Temperature (°C)	15.9	3.9	4.3
Soil type	Loam to clay loam	Sandy loam	Sandy loam

*Source: Hazara Agriculture Research Station, Abbottabad, Pakistan

Table 2: Potato genotypes evaluated under multiple environments for their means and stability analysis

Genotypes	Hybrid Codes	Genotypes	Hybrid Codes	Genotypes	Hybrid Codes
G1	<i>Sarpomira</i>	G12	<i>TPSCLB43</i>	G23	<i>TPSSMC61</i>
G2	<i>Burna</i>	G13	<i>TPSCR51</i>	G24	<i>TPSSMC62</i>
G3	<i>Coroda</i>	G14	<i>TPSCR52</i>	G25	<i>TPSSMC63</i>
G4	<i>Rocco</i>	G15	<i>TPSCR53</i>	G26	<i>TPSRSM71</i>
G5	<i>Cardinal</i>	G16	<i>TPSCR54</i>	G27	<i>TPSRSM72</i>
G6	<i>TPSCB31</i>	G17	<i>TPSSMR11</i>	G28	<i>TPSRSM73</i>
G7	<i>TPSCB32</i>	G18	<i>TPSSMR12</i>	G29	<i>TPSRSM74</i>
G8	<i>TPSCB33</i>	G19	<i>TPSCLR21</i>	G30	<i>TPSCSM81</i>
G9	<i>TPSCB34</i>	G20	<i>TPSCLR22</i>	G31	<i>TPSCSM82</i>
G10	<i>TPSCLB41</i>	G21	<i>TPSCLR23</i>	G32	<i>TPSCSM83</i>
G11	<i>TPSCLB42</i>	G22	<i>TPSCLR24</i>	G33	<i>TPSCSM84</i>

*G34 = Check (UOH100)

Incidence of late blight disease (%)

Incidence of late blight disease was observed in each experimental plot at the initial appearance of disease, almost 45 days after planting. Disease data were collected on seven randomly selected plants with ten-day intervals. A disease scale ranging from 1 to 10 was used, as described by Monjil and Ulfat (2020). Meanwhile, the following formula was used to measure the Incidence of late blight disease percentage (Teshome *et al.* 2022).

$$\text{DiseaseIncidence(\%)} = \frac{\text{Number of Infected Plants}}{\text{Total Number of Observed Plants}} \times 10 \quad (2)$$

Statistical analysis

Analysis of variance (ANOVA) was applied using analytical software Statistics 8.1 (1985-2003) followed by the least significant difference test (LSD) Fisher ($P \leq 0.05$) test to observe treatment means differences.

Stability analysis

Eberhart and Russell's (1966) joint regression model was used to study stability of different genotypes. The behavior of the genotypes was assessed using the following model.

$$Y_{ij} = m_i + b_i I_j + d_{ij} \quad (3)$$

Where, Y_{ij} = the mean performance of the i th genotype in the j th environment; m_i = the grand mean of the i th genotype over all the environments; b_i = the regression coefficient which measures the response of the i th genotype on the environmental index; I_j = the environmental index obtained by the difference between the mean of each environment and the grand mean, and d_{ij} = the deviation from the regression of the i th variety in the j th environment.

Genotype x environment interaction analysis

AMMI bi-plot model was used to analyze and evaluate the interaction for tuber yield plot⁻¹ and incidence to late blight% through principal components analysis components *i.e.*, PC1 and PC2, derived using environment-centered average data.

AMMI bi-plot model was used as proposed by Gauch (2006).

$$Y_{ij} = \mu + G_i + E_j + \sum_{k=1} \lambda_k \alpha_{ik} \gamma_{jk} + e_{ij} \quad (4)$$

Where, Y_{ij} is the observed mean yield of the i th genotype in the j th environment; μ is the general mean; G_i and E_j represent the effects of the genotype and environment; λ_k is the singular value of the k th axis in the principal component analysis; α_{ik} is the eigenvector of the i th genotype for the k th axis; γ_{jk} is the eigenvector of the j th environment for the k th axis; n is the number of principal components in the model, and e_{ij} is the average of the corresponding random errors.

Results

Analysis of variance

The genotypes and environments have shown highly significant ($P < 0.001$) effects on both tuber yield and incidence of late blight disease, respectively. The interaction between genotype and environment exhibited very highly significant ($P < 0.001$) effects on tuber yield, and highly significant ($P < 0.01$) effects on late blight disease incidence (Table 3).

Wide ranges of mean performance were observed under the agro-climatic conditions of diverse environments,

Table 3: AMMI – Analysis of variance for Tuber yield (tons ha⁻¹) and Incidence to late blight (%) disease across three diverse environments

Traits	Source	DF	SS	MS	F Value	Pr (> F)	Sign
Tuber Yield (Tons ha ⁻¹)	G	33	2184.9	66.21	7.29	< 2e – 16	***
	R	2	44.3	22.16	2.44	0.08	
	E	2	5226.9	2613.45	287.96	< 2e – 16	***
	G × E	66	3074.4	46.58	5.13	< 2e – 16	***
Incidence of late blight disease (%)	G	33	34412	1042.8	4.24	7.159e – 11	***
	R	2	73	36.6	0.14	0.86	
	E	2	11577	5788.6	23.57	6.267e – 10	***
	G × E	66	28312	429.0	1.74	0.001	**

G = Genotype; R = Replication; E = Environment; G × E = Genotype by environment; SS = Sum of square; MS = Mean square; Pr = Probability value; > F = Less than F value; *** = Very highly Significant; ** = Significant

Table 4: Mean and stability analysis for tuber yield (tons ha⁻¹) among potato genotypes based on Eberhart and Russell method

Genotypes	Mean	Sd	CV (%)	Bi	S2di	Genotypes	Mean	Sd	CV (%)	Bi	S2di
UOHSMP1	35.45	4.54	12.80	0.60	19.81	TPSSMR12	37.65	3.73	9.92	0.64	3.82
UOHPBP2	29.94	3.07	10.26	0.46	4.98	TPSCLR21	36.82	6.48	17.62	0.90	39.09
UOHCP3	25.73	2.69	10.47	0.44	1.73	TPSCLR22	34.45	6.86	19.90	0.91	48.13
UOHRP4	32	3.05	9.55	0.45	5.34	TPSCLR23	35.15	6.88	19.58	1.06	34.43
UOHCLP5	31.07	4.87	15.68	0.42	35.41	TPSCLR24	35.38	6.56	18.55	0.92	39.29
TPSCB31	36.86	1.37	3.73	0.04	0.98	TPSSMC61	38.76	7.57	19.54	1.42	7.58
TPSCB32	34.82	5.34	15.33	1.03	-0.30	TPSSMC62	34.28	9.18	26.77	1.56	40.95
TPSCB33	35.27	6.77	19.19	1.27	6.06	TPSSMC63	36.48	5.55	15.21	0.54	43.59
TPSCB34	34	4.48	13.19	0.88	-2.54	TPSRSM71	33.36	5.10	15.31	0.92	5.78
TPSCLB41	36.06	8.15	22.60	1.44	23.30	TPSRSM72	36.03	6.23	17.29	0.91	31.84
TPSCLB42	35.36	9.79	27.68	1.91	1.89	TPSRSM73	36.01	8.48	23.56	1.65	0.75
TPSCLB43	36.12	7.30	20.21	1.38	6.18	TPSRSM74	36.03	4.45	12.34	0.73	9.54
TPSCR51	31.77	8.40	26.44	1.65	-1.79	TPSCSM81	33.84	3.76	11.12	0.71	-0.56
TPSCR52	30.73	10.35	33.69	2.03	-1.07	TPSCSM82	33.18	3.44	10.37	0.64	-0.44
TPSCR53	33.08	8.07	24.38	1.56	1.54	TPSCSM83	31.9	4.88	15.31	0.96	-2.29
TPSCR54	32.24	10.65	33.05	1.91	37.11	TPSCSM84	33.06	4.69	14.20	0.23	38.55
TPSSMR11	38.15	5.80	15.21	1.07	5.46	UOHC100	30.28	3.97	13.11	0.59	10.55

Sd = Standard deviation; CV = Coefficient of variation; bi = Regression coefficient; S2di = Standard deviation from linearity of Regression

which further reinforce the findings of ANOVA analysis and provide additional insight into the variability of performance across different conditions, as presented in Table 4-5 and Fig. 1A and B, respectively.

Stability analysis

According to Eberhart and Russell (1966) method, a potato genotype is considered stable and productive if the regression coefficient is equal to 1, the deviation from regression (S^2d_i) is minimal, and a high mean performance for specific trait across different environmental conditions. In the present study, the genotypes identified for adaptability to tuber yield plot⁻¹ were TPSCLB42, TPSCR51, TPSCR52, TPSCR53 and TPSRSM73 (Fig. 2B). Similarly, the potato genotypes recognized for adaptability to late blight incidence were TPSCB34, TPSCR53 and TPSSMC62, respectively (Fig. 3A). In the case of genotypes stability, UOHSMP1, TPSCLB41, TPSCR54, TPSSMR11 and TPSRSM71 have demonstrated stability for resistance to late blight disease across different environments, making them highly promising for disease management in potato cultivation (Fig. 3A).

The CV is an important statistical tool that helps to assess the degree of variation relative to the mean, and has been widely used to evaluate both tuber yield and resistance to late blight disease across different environments.

Results for coefficient of variation determined that only 8 genotypes produced the highest tuber yield per plot (Fig. 2A) indicates that these genotypes were high-yielding per plot and have exhibited less variability in yield across different environments while 9 genotypes were found to be less susceptible to late blight disease (Fig. 3B).

AMMI Bi-plot analysis

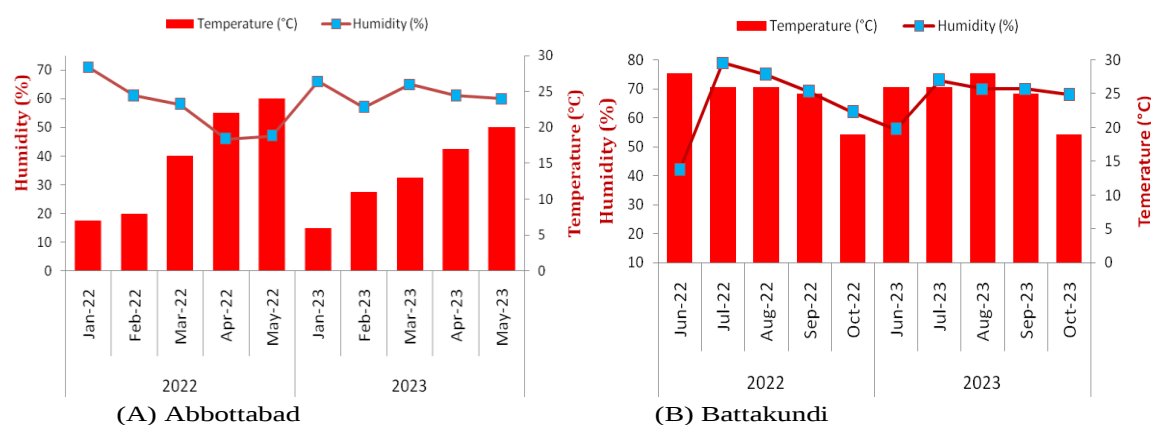
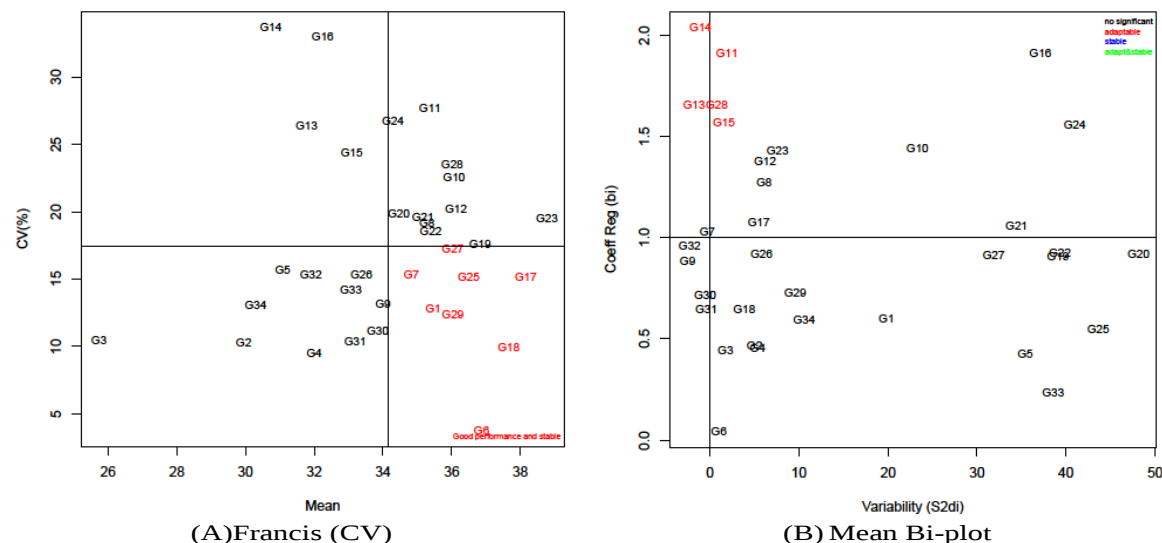
AMMibi-plot analysis effectively splits the variation into additive main effects and multiplicative interaction effects, and PC1 and PC2 represented the principal axes of the interaction component. However, the results presented here were according to the findings of Worku *et al.* (2018). In this approach, the center of origin can be interpreted as a baseline or reference point, against which the performance of other genotypes is compared within each specific environment.

The AMMI bi-plot with PC1 and PC2 was used effectively to analyze and judge the performance and stability of potato genotypes for both tuber yield per plot and late blight resistance, respectively. PC1 refers to either high or low yielding genotypes and it helps in identifying genotypes with high potential yield. Similarly, PC2 displays either stability or instability of the genotypes. It also provides insight into how stable those genotypes are across different environmental conditions, including the presence of disease.

Table 5: Mean and stability analysis for Incidence of late blight disease% among potato genotypes based on Eberhart and Russell method

Genotypes	Mean	Sd	CV (%)	Bi	S2di	Genotypes	Mean	Sd	CV (%)	Bi	S2di
UOHSMP1	1.11	1.92	173.20	0.23	-80.72	TPSSMR12	22.22	11.70	52.67	1.52	-73.57
UOHBP2	30.00	12.01	40.06	1.20	40.90	TPSCLR21	37.77	23.41	61.97	1.52	751.3
UOHCP3	45.55	6.93	15.23	0.90	-78.67	TPSCLR22	34.44	9.62	27.93	1.04	-19.89
UOHRP4	64.44	6.93	10.76	0.85	-69.08	TPSCLR23	43.33	18.55	42.82	1.36	396.3
UOHCLP5	48.88	6.93	14.19	0.72	-44.67	TPSCLR24	43.33	21.85	50.44	1.54	602.2
TPSCB31	34.44	29.12	84.55	2.90	655.08	TPSSMC61	19.70	5.77	19.24	0.07	-15.92
TPSCB32	24.44	19.24	78.72	2.32	46.46	TPSSMC62	27.77	20.09	72.33	2.61	-53.21
TPSCB33	24.44	16.44	67.26	2.06	-25.88	TPSSMC63	28.88	10.71	37.09	1.27	-36.47
TPSCB34	30.00	26.03	87.78	3.22	91.13	TPSRSM71	21.11	5.09	24.11	0.67	-81.52
TPSCLB41	27.77	11.70	42.14	1.55	-81.96	TPSRSM72	27.77	5.09	18.33	-0.64	-77.93
TPSCLB42	31.11	18.35	59.09	1.85	203.4	TPSRSM73	24.44	6.93	48.03	-0.90	-78.67
TPSCLB43	18.88	7.69	40.75	0.83	-42.25	TPSRSM74	27.77	7.69	27.71	0.92	-61.45
TPSCR51	32.22	5.09	15.80	0.28	-39.06	TPSCSM81	32.22	9.62	29.86	-0.12	101.5
TPSCR52	26.66	8.81	33.07	1.06	-55.26	TPSCSM82	33.33	11.54	34.64	0.14	182.3
TPSCR53	34.44	19.53	56.70	2.50	-32.32	TPSCSM83	32.22	5.09	15.80	0.28	-39.06
TPSCR54	26.66	10	37.5	1.32	-80.24	TPSCSM84	24.44	1.92	7.87	-0.02	-74.66
TPSSMR11	23.33	6.66	28.57	0.88	-81.22	UOHC100	25.55	21.43	83.85	-2.03	366.6

Sd = Standard deviation; CV = Coefficient of variation; bi = Regression coefficient; S2di = Standard deviation from Linearity of Regression

**Fig. 1:** Average temperature (°C) and humidity (%) for months/years*Source: www.climate-data.org**Fig. 2:** Stability analysis for potato genotypes (A) Francis (CV) vs. (B) Mean bi-plot for tuber yield Eberhart and Russell (bi, S2di) bi-plot for tuber yield

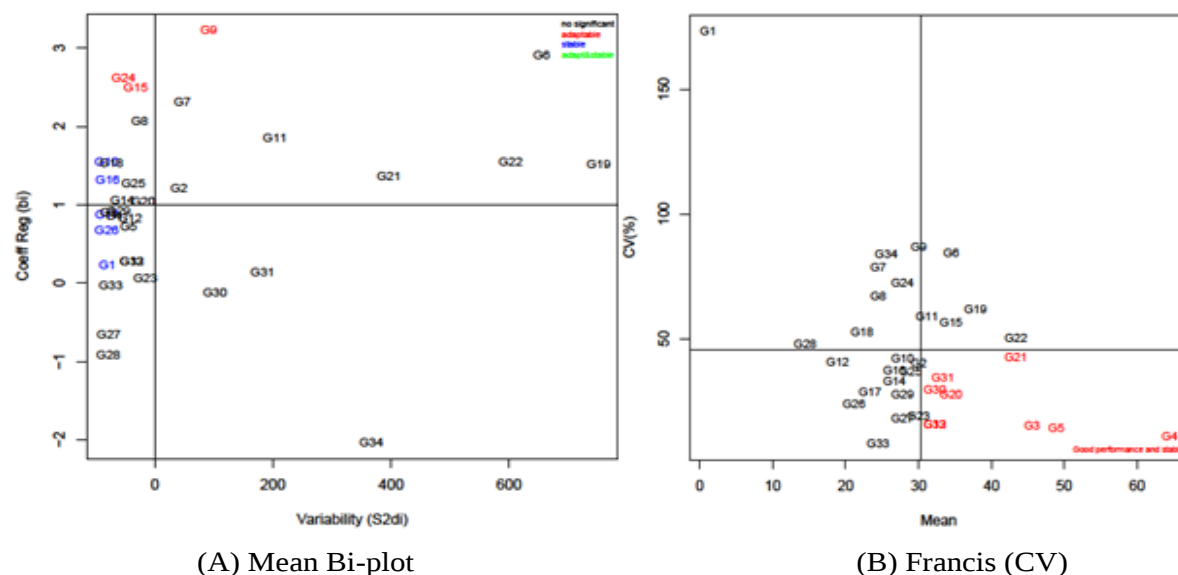


Fig. 3: Stability analysis for potato genotypes (A) Mean bi-plot vs. (B) Francis (CV) For Incidence of late blight disease% Eberhart and Russell (bi, S2di) bi-plot for Incidence of late blight disease%

A PC1 value > 0 indicates that the genotypes are high-yielding. These genotypes perform better in terms of yield potential across the environments under study and vice versa. Similarly, a PC2 value < 0 indicates that genotypes with low PC2 values tend to perform consistently across various environments, maintaining stability in both tuber yield and late blight resistance, regardless of environmental fluctuations. Same interpretation pattern has been applied for Incidence of late blight disease percentage.

In case of PC1 > 0 , genotypes with PC1 > 0 such as TPSCLB41, TPSCB31, TPSSMR11, TPSSMR12 and TPSSMC61 were found to be high yielding as these genotypes were in the positive PC1 region (Fig. 4A). Genotypes with low late blight incidence include TPSCLB41, TPSCLB42, TPSCR54, TPSSMR11, TPSSMR12, TPSSMC62, TPSSMC63, TPSRSM71 and TPSRSM73, which suggests that these genotypes exhibited low Incidence of late blight disease (Fig. 4B).

In terms of PC2 < 0 , lower values for TPSCB33, TPSCLB41, and TPSCLB43 confirmed that genotypes were highly stable in terms of tuber yield plot⁻¹ (Fig. 4A). These genotypes (TPSCB33, TPSCLB41, TPSCLB43) would be located in the low PC2 region (*i.e.*, closer to the origin or negative side of the PC2 axis), signifying that they exhibited stable tuber yields across the different environments. The genotypes such as TPSCLB41, TPSCLB42, TPSCR54, TPSSMR11, TPSSMR12 and TPSSMC63 have been found to be highly stable in terms of low late blight incidence due to their low PC2 values (Fig. 4B).

Discussion

In potato breeding, selecting for adaptability and stability

across varying environmental conditions is crucial for developing high-yielding and disease-resistant genotypes. Achieving high tuber yield in potatoes while maintaining good agronomic traits and balancing the selection of genotypes and environments, is certainly complicated by the effects of viral infections and genotype $\times$ environment interactions. Viral diseases can drastically reduce both the yield and quality of potatoes, while GEI can make it difficult to identify consistently high-performing varieties across diverse environments (Malik *et al.* 2021). However, through advances in breeding and genetics research, seed production practices, and modern breeding techniques, such as MAS, multi-location trials, and hybridization, breeders continue to make progress in overcoming these challenges. The need for stable genotypes performing best under different environments is becoming increasingly critical, especially as farmers face a variety of factors like climatic issues, soil conditions and disease/pest occurrence (Tatarowska *et al.* 2024).

The results from statistical analysis indicated that there was significant differentiation in studied variables across the three environments, signifying that the tested genotypes exhibited variable performance in each of the environments. This highlighted the significance of considering both factors *i.e.*, genetic and environmental when evaluating potato cultivars for yield and disease performance. The study suggested significant ($P < 0.001, 0.01$) variability due to genotypes, environments, and their interaction (GEI) across the three different environments. The current findings underscore the importance of genotype $\times$ environment interaction and environmental factors in shaping potato yield variability. By incorporating GEI into breeding programs, breeders can increase selection efficiency, ensuring the identification of high-yielding, disease-resistant cultivars that

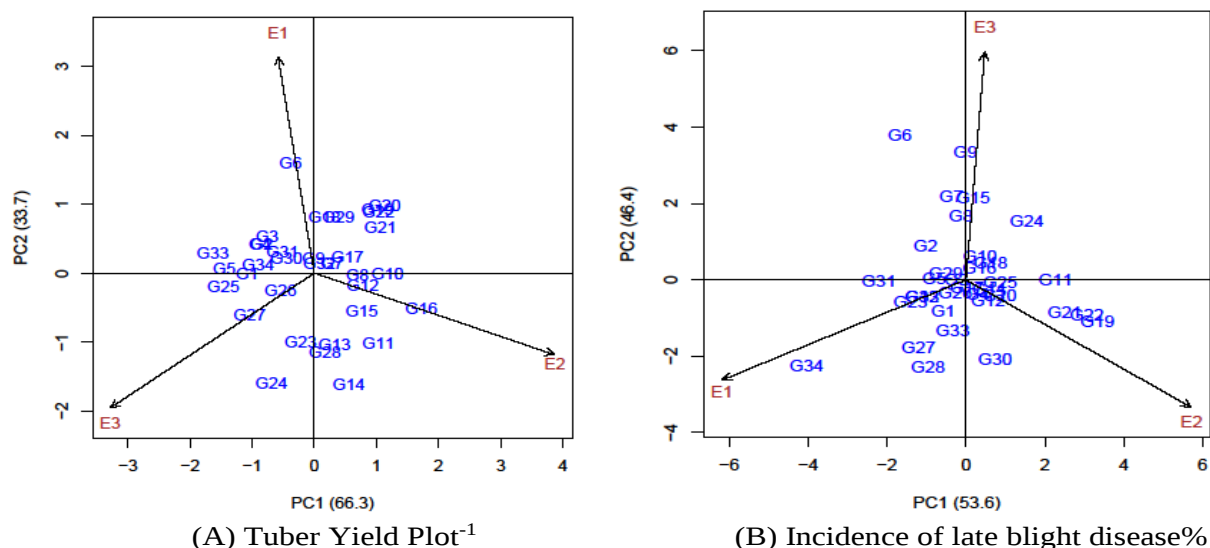


Fig. 4: AMMI bi-plot analysis (A) Tuber yield plot⁻¹ (B) Incidence to late blight disease% for Representativeness of potato genotypes with their environments

are adaptable to a variety of environmental conditions. Kim *et al.* (2018) and Tatarowska *et al.* (2024) have also presented similar findings and acknowledged the importance of GEI in assessing cultivar performance particularly in potato under varying environmental conditions.

The performance of a genotype in crop production is in fact influenced by genotypic, environmental and their interaction effects, which play an important role in developing breeding strategies to develop genotypes with high-yielding, stable and adaptable across various environmental conditions (Tatarowska *et al.* 2024). The work of Mijic *et al.* (2019) highlighted the importance of quantifying genotype stability by different statistical tests. Among the various statistical models used to analyze genotype $\times$ environment interactions, the Additive Main Effects and Multiplicative Interaction (AMMI) model has emerged as one of the most effective and competent methods for stability analysis and interpretation (Worku *et al.* 2018; Cedarsa *et al.* 2022; Scavo *et al.* 2022). AMMI is one of the most important techniques for breeders seeking to understand genotype $\times$ environment interactions and improve genotype stability in crops like potatoes (Mustamo *et al.* 2018). By applying this model, breeders can select genotypes that will perform reliably under various environmental conditions, thereby advancing crop breeding strategies for sustainable agricultural production.

An ideal genotype in agricultural breeding, including potato breeding, is one that demonstrates high performance (e.g., high yield, disease resistance) coupled with high stability across diverse environments (Cedarsa *et al.* 2022; Tatarowska *et al.* 2024). This concept is foundational to breeding programs, particularly those aiming for consistent crop production under variable environmental conditions. The present study clearly identified TPSSMC61 and

TPSSMR11 as highly promising potato genotypes and considered as ideal for the commercial cultivation across varied regions and multiple environments, particularly in Northern Pakistan. The use of AMMI analysis has proven to be an effective tool for evaluating tuber yield and disease incidence across different environments, allowing us to identify the best genotypes like G23 (TPSSMC61) and G17 (TPSSMR11), which have also been highlighted by (Adebola *et al.* 2013; Worku *et al.* 2018; Cedarsa *et al.* 2022; Tatarowska *et al.* 2024). These genotypes are not only appropriate for immediate promotion in areas/regions with high late blight pressure but also hold promise for long-term breeding efforts to enhance disease resistance, yield stability, and environmental adaptability. Selecting local genotypes for breeding programs can be a key strategy in improving tuber yield, reducing disease incidence, and enhancing stability across diverse environments (Pinto *et al.* 2010).

In the present study, Battakundi's conditions were found to be most favorable for expressing the genetic potential of potato genotypes, highlights the importance of local environmental factors in maximizing crop performance. The specific climatic conditions in Battakundi including high altitude, long sunny days, and cooler temperatures can create an environment that favors high potato yields while minimizing the impact of late blight. These factors make it a promising location for potato cultivation and productions, ensuring that genetically superior potato varieties can thrive, achieve higher production, better quality, and potentially reduced disease incidence. The genetic factors are the primary drivers of trait expression in the context of potato breeding, with lower environmental influences. This finding is important to expand new potato genotypes, in determining desirable yield and yield attributing characters. The selection of potato

genotypes based on adaptability and stability in relation to tuber yield and disease resistance is a powerful strategy for improving potato production, and guaranteeing food security. This approach will take part in meeting domestic food requirements and contributing to global food security, ensuring that potatoes continue to be a reliable and sustainable food source in the future.

Conclusion

Significant genetic variability and diversity among potato genotypes across different environments were observed, indicating a broader range of genetic traits that respond to varying conditions. The study concluded that G23 (TPSSMC61) and G17 (TPSSMR11) were found to be excellent hybrids and could thus be selected as new potato hybrids. Additionally, Battakundi was identified as an appropriate site for potato cultivation, offering maximum production and supporting the continuation of breeding strategies. AMMI has proven to be an effective method for selecting adaptable and stable genotypes in specific environments, facilitating potato breeding and the introduction of new potato genotypes locally. This, in turn, could help smallholder farmers to address global challenges related to malnutrition and food security.

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Authors' Contributions

The primary author arranged, wrote and edited the manuscript. All other authors equally contributed through distinct areas of their research expertise.

Conflict of Interest

The authors declare no conflict of interest.

Data Availability

Data will be available on request from author.

Ethics Approval

This study does not require human or animal ethical approval; however, all authors declare their informed consent to be part of this manuscript. All information contained in this manuscript is properly cited following standard procedures.

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