# GENETIC VARIABILITY AND AMMI BIPLOT ANALYSIS FOR GENOTYPE × ENVIRONMENT INTERACTION AMONG POTATO GENOTYPES EVALUATED IN NORTHERN PAKISTAN

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## ABSTRACT

Among major food crops, potato (*Solanum tuberosum* L.) holds a prominent position because of its nutritional importance, broad genetic diversity, and capacity to adapt to a wide range of growing environments. Genetic variability and genotype × environment interactions (GEI) are crucial components of potato breeding programs, enabling breeders for developing high-yielding, stable, and disease-resistant cultivars. In this study, thirty-four potato genotypes were evaluated in a randomized complete block design with three replications across three contrasting environments (Abbottabad, Battakundi, and Kaghan) during the 2021–2023 growing seasons. Additive Main Effects and Multiplicative Interaction (AMMI) analysis of variance revealed highly significant ($p \leq 0.001$) effects of genotype, environment, and GEI for all evaluated characters, signifying considerable genetic diversity. Broad-sense heritability (49.17–95.49%) and genetic advance (13.40–331.82%) suggested the predominance of additive gene action, while phenotypic coefficients of variation consistently exceeded genotypic coefficients for all traits. AMMI biplot analysis identified genotypes G17, G18, and G23 as superior performers, combining high tuber yield with low late blight incidence. Stability analysis further recognized G10, G12, G17, G18, and G23 as consistently stable for tuber yield and late blight resistance. Battakundi emerged as the most favorable environment for potato production, with most genotypes showing superior adaptation. Among the evaluated materials at Abbottabad, Battakundi and Kaghan, G23 (TPSSMC61) and G17 (TPSSMR11) recorded the highest tuber yields (37.2, 45.4, 42.5 t $ha^{-1}$ and 35.7, 45.5, 42.7 t $ha^{-1}$, respectively) and strong resistance to late blight (89.7, 89.5, 89.7% and 90.0, 89.9, 89.8%), respectively. These elite genotypes represent promising candidates for commercial cultivation and valuable parental lines for future potato breeding aimed at improving yield stability, disease resistance, and broad environmental adaptability.

**Keywords:** Genetic Variability; Genotype × Environment Interaction; Additive Main Effects and Multiplicative Interaction; Additive Gene Action; Battakundi

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## INTRODUCTION

Rapid population growth is placing increasing pressure on global food systems, making it essential to develop sustainable agricultural strategies that can support greater crop productivity while maintaining long-term food and nutritional security. Among the world's major food crops, potato (*Solanum tuberosum* L.), a member of the Solanaceae, holds particular importance due to its substantial contribution to human food supply and nutrition. Consequently, potato improvement has received increasing attention as a potential means of strengthening global food and nutritional security under changing production conditions (Khan *et al.*, 2026). Historically, breeding potato cultivars primarily paid attention on improving varieties with enhanced tuber yield, improved tuber superiority, and resistance to major diseases. However, current agricultural production systems still face considerable difficulty in satisfying the growing demand for nutritious

food because of various biotic, a-biotic, and production-related limitations (Wu *et al.*, 2018). Potato remains one of the major crops contributing to the global food supply. Approximately, 376 million tons of potatoes were produced worldwide from about 16.9 million hectares (FAOSTAT, 2024), and nearly 8.43 million tons, harvested from an area of approximately 341 thousand hectares, in Pakistan (PBS, 2024).

The success of crop improvement largely depends on the extent of heritable variation present within a breeding population. Adequate genetic diversity allows breeders to select genotypes possessing favorable attributes and to combine useful traits through hybridization and selection. Such variation is particularly important for improving yield potential, tolerance or resistance to biotic and abiotic stresses, and important quality traits (Sun *et al.*, 2024). In potato breeding, several quantitative genetic i.e. genotypic, environmental, and phenotypic variances, genotypic and phenotypic coefficients of variation, broad-sense heritability, and genetic advance are commonly used to characterize the extent and nature of variability within evaluated germplasm. Their combined interpretation can therefore assist breeders in identifying promising genotypes and designing more efficient selection strategies (Gebrehanna *et al.*, 2022; Kumar *et al.*, 2023). The performance of a potato genotype, however, may vary considerably when it is grown under different environmental conditions. GEI is particularly important for considering the consistency and adaptability of promising hybrids. Assessment of GEI helps breeders recognize genotypes that maintain desirable performance over a range of agro-ecological conditions, as well as those specifically suited to particular environments (Cadersa *et al.*, 2022). A range of analytical techniques has been developed to characterize GEI and facilitate the interpretation of multi-environment trial data. The AMMI model (Zobel *et al.*, 1988) and the Genotype plus Genotype × Environment (GGE) biplot (Gauch, 2006) approach focuses on genotype and GEI effects and provides a graphical means of comparing genotypes, environments, and their relationships (Gauch, 2006). Both approaches have been extensively applied to identify stable, widely adapted, and specifically adapted genotypes in multi-environment crop evaluation studies (Flis *et al.*, 2014).

Potato cultivation in Pakistan extends across diverse agro-climatic regions, from the irrigated plains of Punjab to the temperate highlands of Khyber Pakhtunkhwa and Gilgit-Baltistan, indicating its wide adaptableness and production potential (Hussain *et al.*, 2024). Recently, the True Potato Seed (TPS) breeding has emerged as a optional alternative to conventional clonal propagation, particularly for high-altitude potato production systems (Khan *et al.*, 2026). However, information on the genetic variability and GEI of TPS-derived potato hybrids across high-altitude environments in Pakistan remains limited. This study is novel in integrating genetic variability parameters with AMMI analysis to identify stable, high-yielding, and late blight-resistant potato genotypes. We hypothesized that TPS-derived hybrids possess sufficient genetic variability and that AMMI analysis would effectively identify widely adapted, superior genotypes. Therefore, the present study was conducted under the high-altitude agro-ecological conditions of the Hazara Division, Khyber Pakhtunkhwa, Pakistan with the aimto select TPS-derived potato hybrids with enhanced yield, stability, and disease resistance across diverse environments of northern Pakistan.

## MATERIALS AND METHODS

**Study site:** The study was carried out in three different agro-ecological environments namely, Abbottabad (34°12′22.8″ N, 73°14′24.0″ E), Battakundi (34°55′53.8″ N, 73°46′27.5″ E) and Kaghan (34°46′34.2″ N, 73°31′28.8″ E), Northern Pakistan. The experimental trials were established at Hazara Agriculture Research Station, Abbottabad (February–May 2021), the Summer Agriculture Research Station, Kaghan (May–August 2022) and the Seed Potato Research and Multiplication Farm, Battakundi (June–October 2023).

**Description of experimental material:** A total of thirty-four potato genotypes, comprising 28 hybrid clones, five parental cultivars, and one commercial check, were obtained from the Seed Potato Research and Multiplication Farm, Battakundi, and the Hazara Agricultural Research Station, Abbottabad, Khyber Pakhtunkhwa, Pakistan (Table 1). The hybridization program involved five parental cultivars, namely Sarpomira, Roko, Cardinal, Kuroda, and Burna. The cultivars were selected for their favorable agronomic and quality characteristics, particularly yield performance, tuber quality, and adaptation to local growing conditions. These characteristics made them suitable parental material for developing potato hybrids with improved performance and greater potential for commercial production (Biwas *et al.*, 2005).

**Field layout and design:** The experiment was conducted using a randomized complete block design (RCBD) with three replications. In each replication, 34 plots were prepared, with a plot size of 3.0 m × 1.5 m, giving a total area of 4.5 m² per plot. Twenty-four seed tubers were planted in two rows within each plot, maintaining 75 cm and 25 cm distance between rows and tubers planted, respectively. Fertilizers were applied according to the recommendations for potato production in the study area. The fertilizer rates were 220 kg $ha^{-1}$ of diammonium phosphate (DAP), 260 kg $ha^{-1}$ of sulphate of potash (SOP), and 180 kg $ha^{-1}$ of urea. No fungicide was applied during the crop-growing period so that late blight could develop naturally and disease incidence could be evaluated under field conditions. All experimental plots received similar crop management. Uniform agronomic management practices including land preparation, planting,

fertilizer application, irrigation, earthing-up, manual weed removal, and harvesting were performed manually according to the recommended agronomic practices followed at the respective experimental locations. These practices were applied uniformly to all experimental plots to minimize variation arising from differences in field management and operations.

**Table 1. Potato parental cultivars and their hybrids tested under different environmental sites for their genetic variability and stability analysis**

| Code | Hybrids | Parents ♀ | ♂ | Code | Hybrids | Parents ♀ | ♂ | Source of Germplasm |
|---|---|---|---|---|---|---|---|---|
| G1 | *Sarpomira* | | | | | | | *HARS ATD* |
| G2 | *Burna* | | | | | | | *HARS ATD* |
| G3 | *Coroda* | | | | | | | *HARS ATD* |
| G4 | *Rocco* | | | | | | | *HARS ATD* |
| G5 | *Cardinal* | | | | | | | *HARS ATD* |
| G6 | *TPSCB31* | *C3* × | *B1* | G21 | *TPSCLR23* | *CL2* × | *R3* | *SPR&MF BK* |
| G7 | *TPSCB32* | *C3* × | *B2* | G22 | *TPSCLR24* | *CL2* × | *R4* | *SPR&MF BK* |
| G8 | *TPSCB33* | *C3* × | *B3* | G23 | *TPSSMC61* | *SM6* × | *C1* | *SPR&MF BK* |
| G9 | *TPSCB34* | *C3* × | *B4* | G24 | *TPSSMC62* | *SM6* × | *C2* | *SPR&MF BK* |
| G10 | *TPSCLB41* | *CL4* × | *B1* | G25 | *TPSSMC63* | *SM6* × | *C3* | *SPR&MF BK* |
| G11 | *TPSCLB42* | *CL4* × | *B2* | G26 | *TPSRSM71* | *R7* × | *SM1* | *SPR&MF BK* |
| G12 | *TPSCLB43* | *CL4* × | *B3* | G27 | *TPSRSM72* | *R7* × | *SM2* | *SPR&MF BK* |
| G13 | *TPSCR51* | *C5* × | *R1* | G28 | *TPSRSM73* | *R7* × | *SM3* | *SPR&MF BK* |
| G14 | *TPSCR52* | *C5* × | *R2* | G29 | *TPSRSM74* | *R7* × | *SM4* | *SPR&MF BK* |
| G15 | *TPSCR53* | *C5* × | *R3* | G30 | *TPSCSM81* | *C8* × | *SM1* | *SPR&MF BK* |
| G16 | *TPSCR54* | *C5* × | *R4* | G31 | *TPSCSM82* | *C8* × | *SM2* | *SPR&MF BK* |
| G17 | *TPSSMR11* | *SM1* × | *R1* | G32 | *TPSCSM83* | *C8* × | *SM3* | *SPR&MF BK* |
| G18 | *TPSSMR12* | *SM1* × | *R2* | G33 | *TPSCSM84* | *C8* × | *SM4* | *SPR&MF BK* |
| G19 | *TPSCLR21* | *CL2* × | *R1* | G34 | ***Check**** | | | *SPR&MF BK* |
| G20 | *TPSCLR22* | *CL2* × | *R2* | | | | | *SPR&MF BK* |

*Check* = UOHSM; HARS ATD = Hazara Agriculture Research Station Abbottabad; SPR&MF BK = Seed Potato Research and Multiplication Farm Battakundi*

**Data collection:** Data were recorded for plant height (cm), total number of tubers per plot, total tuber weight per plot (kg), tuber yield (t $ha^{-1}$), and late blight disease incidence (%) following the standard evaluation procedures described by Cabello *et al.* (2020). Plant height was determined for eight differently selected plants (from ground surface to apical tip) at 60–70 days after planting, corresponding approximately to the 50% flowering stage (Asnake *et al.*, 2023). At harvest, all tubers from each plot, irrespective of size (small, medium, and large), were counted to determine the total tubers number per plot (Asnake *et al.*, 2025). The harvested tubers were subsequently weighed to obtain the total tuber weight per plot, which was converted into tuber yield (t $ha^{-1}$) using the appropriate conversion formula (Tessema *et al.*, 2020). Late blight disease incidence was assessed on eight plants per plot at weekly intervals, repeatedly, throughout the growing season under natural field conditions to evaluate the resistance or susceptibility of the tested potato hybrids. Disease incidence was determined by calculating the proportion of diseased plants within each. plot and expressing the value as a percentage, following the method of Mohsin *et al.* (2016). Tuber yield and late blight incidence were subsequently estimated using the equations given below.

$$\text{Yield}\left(\frac{\text{Tons}}{\text{ha}}\right) = [(\text{total Tubers Weight} \times 9880/\text{Plot Area} \times 100)/1000] \quad 1$$

$$\text{Disease Incidence \%} = \text{No. of Infected Plants} / \text{No. of Total Plants Planted} \times 100 \quad 2$$

Data were also collected for humidity (%), temperature (˚C), and rainfall (mm), to check their effects on tuber yield and related attributes (Figure 1).

**Genetic variability, heritability and genetic advance:** The magnitude of genetic variability among potato genotypes can be accessed through quantitative genetic parameters including phenotypic variance (Vp) , genotypic variance (Vg), environmental variance (Ve), phenotypic coefficient of variation (PCV), and genotypic coefficient of variation (GCV), which provide valuable information regarding genetic potential and selection efficiency in breeding programs (Singh and Chaudhary, 1985).

PCV = ($^{\delta}$p/x) $x$ 100 3
GCV= ($^{\delta}$g/x) $x$ 100 4

Broad-sense heritability ($H^2_{BS}$) was estimated as the proportion of genotypic variance relative to the total phenotypic variance among the evaluated potato genotypes (Allard, 1999; Wricke and Weber, 1986).

$H^2_{(BS)}$ = Vg/ Vp $x$ 100 5
Where;
Vg = MSG-MSE / r Vp = MSG / r Ve = MSE / r

Where;
MSG = Mean square for genotype, MSE = Mean square for error, r = Number of replications

Genetic advance (GA) was calculated to determine the expected improvement in quantitative traits under applied selection pressure. This parameter provides an indication of the selection effectiveness by estimating the gain that can be achieved in subsequent generations and was computed (Shukla *et al.*, 2006).
EGA = isph 6
GA % = GA/ $x$ 100 7

**Genotype × environment interaction (GEI):** The AMMI model was used to check the effects of GEI. Two principal components (PC1 and PC2) analysis was used to recognize highly adaptable and stable potato genotypes in different environments by partitioning the interaction effects and evaluating genotype adaptability.

$$Yij = \mu + G_i + E_j + \sum_{k=1}^{n} \lambda_k \alpha_{ik} \gamma_{jk} + e_{ij} \quad 8$$

Where;

*Yij* is the observed mean yield of the *ith* genotype in the *jth* environment,
μ is the general mean,
*Gi* and *Ej* represent the effects of the genotype and environment, respectively
l*k* is the singular value of the *kth* axis in the principal component analysis;
a*ik* is the eigenvector of the *ith* genotype for the *kth* axis.
g*jk* is the eigenvector of the *jth* environment for the *kth* axis;
*n* is the number of principal components in the model;
*eij* is the average of the corresponding random errors.

**Statistical analysis:** Analysis of variance (ANOVA) was performed separately for each environment and subsequently on the pooled data across environments using Statistix 8.1.Fisher's least significant difference (LSD) test ($p \leq 0.05$) was used to observe significant differences. Furthermore, GEI analysis, biplot visualization, and correlation analysis among the studied traits were performed using Origin Pro 2023b software to evaluate genotype stability, trait associations, and overall performance patterns.

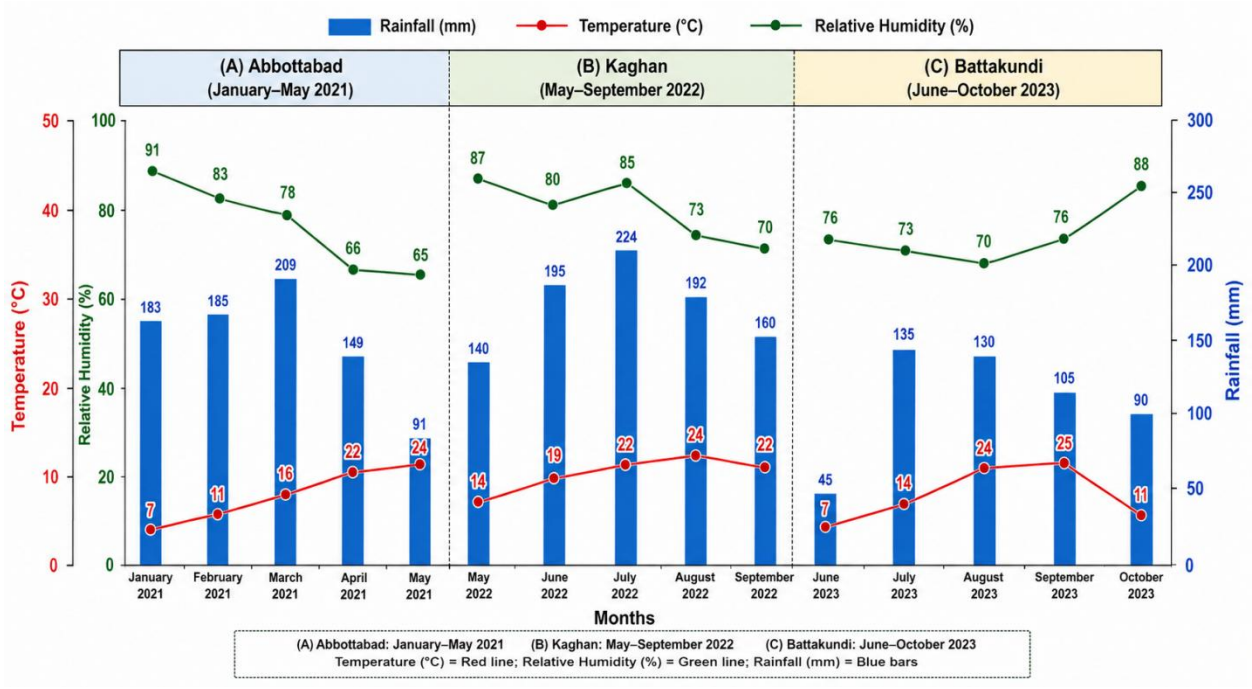


**Fig. 1. Weather data - temperature (°C), rainfall (mm) and humidity% of studied environments.** (*Source:* www.climate-data.org)

## RESULTS

**Analysis of variance:** The AMMI analysis indicated significant variation among genotypes and environments, as well as their GEI interaction, for all the traits examined. These traits included plant height, number of tubers per plot, total tuber weight per plot, tuber yield per plot, and late blight incidence. (Table 2). The significance levels ($p \leq 0.001$, 0.005) varied among studied genotypes indicating substantial genetic variability and differential responses of genotypes across environments.

**Table 2. AMMI analysis of variance for tuber yield and yield contributing traits of 34potato genotypes cultivated at three different environments**

| Traits | Plant Height (cm) | | | No. of Total Tubers Plot$^{-1}$ | | | Total Tubers Weight (kg plot$^{-1}$) | | |
|---|---|---|---|---|---|---|---|---|---|
| **Source** | **G** | **E** | **G × E** | **G** | **E** | **G × E** | **G** | **E** | **G × E** |
| **DF** | 33 | 2 | 66 | 33 | 2 | 66 | 33 | 2 | 66 |
| **Sum of Squares** | 7701 | 252 | 4871.2 | 101.2 | 19069 | 12086 | 441.9 | 1058 | 623.3 |
| **Mean Squares** | 233.4 | 126 | 73.81 | 3068 | 9534 | 1831 | 13.39 | 529.0 | 9.44 |
| **F Value** | 25.3 | 137 | 8.02 | 10.63 | 330.3 | 6.34 | 7.31 | 288.4 | 5.15 |
| **p ≦ 0.001** | *** | *** | *** | *** | *** | *** | *** | *** | *** |

| Traits | Tuber Yield Plot$^{-1}$ (t ha$^{-1}$) | | | Incidence to Late Blight Disease Plot$^{-1}$ (%) | | |
|---|---|---|---|---|---|---|
| **Source** | **G** | **E** | **G × E** | **G** | **E** | **G × E** |
| **DF** | 33 | 2 | 66 | 33 | 2 | 66 |
| **Sum of Squares** | 218 | 5226.9 | 3074.4 | 3441 | 1157 | 28312 |
| **Mean Squares** | 66.2 | 2613.5 | 46.58 | 1042 | 5789 | 429 |
| **F Value** | 2.44 | 287.9 | 5.13 | 4.24 | 23.5 | 1.74 |
| **p ≦ 0.001** | *** | *** | *** | *** | *** | ** |

*G = Genotype; E = Environment; G x E = Genotype x Environment; DF = Degree of freedom; P = Probability; ** = Highly significant; No. = Number*

Significant variation was revealed among the evaluated potato genotypes for plant height, number of total tubers per plot, and weight of total tubers per plot. Plant height ranged from 37.7 cm (TSPCLR21) to 67.1 cm (TPSSMR11), total tubers per plot from 139.6 (TPSCR51) to 315.6 (TPSSMR11), and total tuber weight per plot from 8.7 kg (TPSCR52) to 20.5 kg (TPSSMR11), for studied potato genotypes (Table 3). The coefficients of variation (CV) for the studied traits ranged from 4.97% to 10.69%, indicating good experimental precision and reliability of the recorded data among the TPS-derived hybrid population. Notably, genotype TPSSMR11 consistently exhibited superior performance for plant height, tuber number, and tuber weight, highlighting its potential as a promising breeding line. Overall, the observed variability provides a strong basis for the selection of high-performing potato hybrids for further evaluation and advancement in the breeding program.

**Table 3. Mean performance for plant height (cm), number of total tubers plot$^{-1}$and weight of total tubers (kg plot$^{-1}$) of potato hybrids cultivated at three different environments**

| Genotypes | Parents & Hybrids | Plant height (cm) | | | No. of total tubers plot$^{-1}$ | | | Weight of total tubers (kg plot$^{-1}$) | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | ATD | BK | ATD | ATD | ATD | KN | ATD | BK | KN |
| G1 | Sarpomira | 38.4$^{a-d}$ | 40.2$^{ab}$ | 49.8$^{ab}$ | 202.3$^{a}$ | 244.3$^{a}$ | 236.6$^{ab}$ | 13.8$^{ab}$ | 16.2$^{a}$ | 17.8$^{a}$ |
| G2 | Burna | 42.6$^{a-d}$ | 39.2$^{ab}$ | 41.6$^{ab}$ | 188.6$^{a-h}$ | 187.6$^{a}$ | 199$^{ab}$ | 11.9$^{a}$ | 13.8$^{ab}$ | 14.6$^{a}$ |
| G3 | Coroda | 35.6$^{b}$ | 39.9$^{a-c}$ | 44.1$^{a-c}$ | 155.3$^{ab}$ | 193$^{ab}$ | 191.3$^{ab}$ | 10.2$^{a}$ | 12.5$^{ab}$ | 12.4$^{ab}$ |
| G4 | Rocco | 32.4$^{b-c}$ | 43.9$^{a-c}$ | 48.3$^{a-d}$ | 172.6$^{ab}$ | 240.6$^{ab}$ | 212.3$^{ac}$ | 12.9$^{ac}$ | 14.7$^{ab}$ | 15.5$^{ac}$ |
| G5 | Cardinal | 32.6$^{c-d}$ | 47.1$^{abc}$ | 45.6$^{a-d}$ | 167.3$^{ab}$ | 188.6$^{a-c}$ | 199.6$^{ac}$ | 12.3$^{ac}$ | 13.5$^{ab}$ | 16.5$^{ab}$ |
| G6 | TPSCB31 | 61.2$^{a}$ | 52.8$^{a-d}$ | 55.3$^{a-e}$ | 214$^{a}$ | 210.3$^{a-d}$ | 207.3$^{ac}$ | 16.7 $^{a-c}$ | 17.1$^{a-c}$ | 15.9$^{a-c}$ |
| G7 | TPSCB32 | 60.3$^{e}$ | 58.1$^{a-d}$ | 56.6$^{a-e}$ | 198.3$^{a-e}$ | 241$^{a-d}$ | 216.6$^{ab}$ | 13.4$^{a-c}$ | 18.2$^{a-c}$ | 15.4$^{a-c}$ |
| G8 | TPSCB33 | 63.3$^{g}$ | 61.5$^{a-d}$ | 54.8$^{a-c}$ | 190.3$^{a-h}$ | 263.3$^{a-c}$ | 217.3$^{a-f}$ | 13.$^{2a-d}$ | 19.2$^{ab}$ | 15.5$^{a-e}$ |
| G9 | TPSCB34 | 62.8$^{b-j}$ | 66.7$^{ac}$ | 57.6$^{a-c}$ | 191.3$^{a-g}$ | 239.3$^{a-e}$ | 236$^{a-f}$ | 13.2$^{a-d}$ | 17.2$^{a-d}$ | 15.4$^{a-e}$ |
| G10 | TPSCLB41 | 50.9$^{b-j}$ | 51.9$^{ac}$ | 50.6$^{a-c}$ | 161.6$^{b-d}$ | 273$^{a-e}$ | 202.6$^{a-d}$ | 13.5$^{a-d}$ | 20.4$^{a-d}$ | 14.8$^{a-c}$ |
| G11 | TPSCLB42 | 49.7$^{a-c}$ | 53.9$^{ae}$ | 50$^{a-f}$ | 143$^{b-d}$ | 275$^{a-e}$ | 213.6$^{a-e}$ | 11.6$^{a-e}$ | 19.7$^{e-f}$ | 15.7$^{a-c}$ |
| G12 | TPSCLB43 | 47.6$^{a-d}$ | 56.1$^{ae}$ | 47.3$^{a-f}$ | 149.3$^{a-d}$ | 264.6$^{a-c}$ | 203.6$^{a-e}$ | 13.5$^{a-e}$ | 19.8$^{d-f}$ | 15.5$^{a-c}$ |
| G13 | TPSCR51 | 46.8$^{e-f}$ | 59.2$^{bc}$ | 46.9$^{a-f}$ | 139.6$^{a-d}$ | 256.6$^{a-c}$ | 216.6$^{a-e}$ | 10.5$^{ab}$ | 17.6$^{a-e}$ | 15.3$^{a-f}$ |
| G14 | TPSCR52 | 48$^{g}$ | 61.7$^{bc}$ | 54.7$^{gh}$ | 144.6$^{a-d}$ | 260.6$^{a-c}$ | 205.3$^{a-b}$ | 8.7$^{ab}$ | 17.8$^{a-e}$ | 14.9$^{a-f}$ |
| G15 | TPSCR53 | 44.2$^{h}$ | 60$^{de}$ | 48.5$^{gh}$ | 157$^{a-d}$ | 260.6$^{a-f}$ | 209.3$^{a-f}$ | 11.4$^{ab}$ | 18.6$^{a-f}$ | 14.6$^{a-g}$ |
| G16 | TPSCR54 | 46.7$^{i-J}$ | 58.7$^{de}$ | 59.6$^{gh}$ | 150.3$^{a-d}$ | 249$^{a-f}$ | 184.3$^{a-f}$ | 10.8$^{ac}$ | 19.9$^{f-h}$ | 12.7$^{a-g}$ |
| G17 | TPSSMR11 | 63.4$^{b-h}$ | 67.1$^{d-f}$ | 59.7$^{g-i}$ | 211.7$^{ab}$ | 315.6$^{a-l}$ | 270.6$^{a-f}$ | 15.9$^{ab}$ | 20.5$^{f-h}$ | 19.9$^{a-g}$ |
| G18 | TPSSMR12 | 45.8$^{a-d}$ | 52.7$^{d-f}$ | 52.7$^{a-e}$ | 207.3$^{a-c}$ | 278$^{a-l}$ | 243$^{a-e}$ | 15.7 $^{a-c}$ | 18.8$^{h-j}$ | 16.2$^{e-h}$ |
| G19 | TPSCLR21 | 37.7$^{a-d}$ | 56.5$^{e-j}$ | 52.4$^{a-d}$ | 201.6$^{ab}$ | 280.3$^{a-j}$ | 205.3$^{a-e}$ | 15.3 $^{a-c}$ | 19.9$^{h-j}$ | 14.5$^{e-h}$ |
| G20 | TPSCLR22 | 39.4$^{a-d}$ | 56.6$^{e-j}$ | 53.1$^{a-d}$ | 196.6$^{a-f}$ | 274.6$^{b-f}$ | 205.6$^{a-c}$ | 14.3 $^{a-c}$ | 19$^{c-i}$ | 13.5$^{c-f}$ |
| G21 | TPSCLR23 | 43.1$^{a-d}$ | 59.6$^{b-f}$ | 52.3$^{a-e}$ | 181.6$^{a-e}$ | 261.6$^{b-f}$ | 207$^{a-c}$ | 14.6$^{a-e}$ | 19.4$^{c-i}$ | 13.9$^{a-e}$ |
| G22 | TPSCLR24 | 39.1$^{b-f}$ | 51.6$^{a-c}$ | 57.9$^{f-i}$ | 189.3$^{b-j}$ | 252.6$^{b-f}$ | 212$^{a-c}$ | 14.6$^{a-e}$ | 19.3$^{c-e}$ | 13.8$^{a-e}$ |
| G23 | TPSSMC61 | 58.1$^{b-f}$ | 59.3$^{a-c}$ | 56.4$^{f-i}$ | 202.6$^{a-e}$ | 298.3$^{a-e}$ | 261$^{a-c}$ | 16.7$^{a-f}$ | 20.4$^{a-d}$ | 19.7$^{a-c}$ |
| G24 | TPSSMC62 | 45.7$^{c-e}$ | 45.6$^{a-e}$ | 53$^{a-e}$ | 165.6$^{a-c}$ | 206.3$^{a-e}$ | 283$^{a-h}$ | 10.7$^{a-f}$ | 17.3$^{a-d}$ | 18.3$^{a-c}$ |
| G25 | TPSSMC63 | 43.3$^{a-c}$ | 44.2$^{a-e}$ | 51$^{a-e}$ | 173.3$^{a-c}$ | 201$^{ab}$ | 248.3$^{a-h}$ | 14.1$^{a-f}$ | 16.1$^{e-g}$ | 19.5$^{ac}$ |
| G26 | TPSRSM71 | 45.4$^{a-c}$ | 50.6$^{i-f}$ | 49.4$^{bc}$ | 182.6$^{b-j}$ | 201$^{ab}$ | 217$^{a-h}$ | 12.5$^{a-f}$ | 16.3$^{f-j}$ | 16.5$^{ac}$ |
| G27 | TPSRSM72 | 41.1$^{ab}$ | 52.4$^{f-h}$ | 53.1$^{b-d}$ | 177.6$^{a-c}$ | 215.3$^{ab}$ | 225.6$^{a-h}$ | 13.1 $^{a-c}$ | 16.8$^{h-l}$ | 18.6$^{a-d}$ |
| G28 | TPSRSM73 | 43.4$^{ab}$ | 58.4$^{f-h}$ | 50.4$^{a-f}$ | 175.3$^{a-c}$ | 219.3$^{ab}$ | 218.3$^{de}$ | 11.9 $^{a-c}$ | 19.3$^{h-l}$ | 17.5$^{e-h}$ |
| G29 | TPSRSM74 | 42.3$^{c-f}$ | 57.1$^{d-g}$ | 57.6$^{a-f}$ | 187.$^{3a-h}$ | 229$^{a-c}$ | 204$^{d-f}$ | 14.9$^{a-c}$ | 18.5$^{kl}$ | 15.1$^{e-i}$ |
| G30 | TPSCSM81 | 42.4$^{c-j}$ | 46.3$^{d-g}$ | 54.4$^{a-f}$ | 169.3$^{a-e}$ | 202.3$^{a-c}$ | 218$^{d-f}$ | 13.3$^{a-h}$ | 16.4$^{kl}$ | 15.9$^{e-i}$ |
| G31 | TPSCSM82 | 45.4$^{b-j}$ | 46.3$^{c-i}$ | 55.3$^{a-g}$ | 164$^{a-e}$ | 198$^{a-i}$ | 200.6$^{d-f}$ | 13.6$^{a-h}$ | 15.9$^{a-c}$ | 15.6$^{d-h}$ |
| G32 | TPSCSM83 | 50.3$^{b-j}$ | 47$^{c-i}$ | 52.2$^{a-g}$ | 186$^{a-i}$ | 206$^{a-i}$ | 196$^{dc}$ | 12.1$^{a-h}$ | 16.5$^{ac}$ | 14.4$^{d-h}$ |
| G33 | TPSCSM84 | 48.2$^{b-j}$ | 45.7$^{c-i}$ | 52.8$^{a-g}$ | 172.6$^{a-i}$ | 198.6$^{ab}$ | 212.3$^{d-h}$ | 13.5$^{a-h}$ | 13.9$^{a-e}$ | 17.3$^{g-i}$ |
| G34 | Check* | 48.9$^{a-e}$ | 47.2$^{a-c}$ | 48.6$^{a-g}$ | 168$^{a-e}$ | 182.3$^{a-c}$ | 197.6$^{d-h}$ | 11.6$^{a-h}$ | 14.1$^{b-f}$ | 15.1$^{g-i}$ |
| LSD @ 0.05 | | **4.67** | **5.81** | **4.19** | **29.08** | **27.50** | **21.69** | **2.49** | **1.88** | **1.83** |
| CV (%) | | 5.01 | 6.10 | 4.97 | 10.69 | 6.10 | 6.15 | 8.54 | 5.80 | 7.28 |

*Means sharing same letters, within a column, are statistically at par at p≤0.05*

*Check* = UOHSM; ATD = Abbottabad; BK = Battakundi; KN = Kaghan; cm = centimeter; kg = kilogram; LSD = Least significant difference; CV = Coefficient of variation; p ≤ 0.05, No. = Number*

The newly developed and evaluated potato genotypes exhibited substantial variation, with tuber yield ranging from 19.4 to 45.50 t ha$^{-1}$ and late blight resistance ranging from 59.3% to 90.0%, among the evaluated environments (Table 4). Most of the TPS-derived hybrids performed well for both tuber yield and late blight resistance across the evaluated environments.

**Table 4. Mean performance for total tuber yield(tons ha$^{-1}$) and incidence to late blight disease per plot (%) of potato hybrids cultivated at three different environments**

| Genotypes | Parents & Hybrids | Total Tubers Yield (tons ha$^{-1}$) | | | Incidence to Late Blight Disease Plot$^{-1}$ (%) | | |
|---|---|---|---|---|---|---|---|
| | | ATD | BK | KN | ATD | BK | KN |
| G1 | Sarpomira | 30.6$^{a}$ | 36$^{a}$ | 39.7$^{a}$ | 0.0$^{a}$ | 0.0$^{a}$ | 0.06$^{a}$ |
| G2 | Burna | 26.5$^{ab}$ | 30.8$^{ab}$ | 32.5$^{bc}$ | 20.1$^{a}$ | 10.9$^{a}$ | 30.4$^{ab}$ |
| G3 | Coroda | 22.6$^{ab}$ | 26.8$^{ab}$ | 27.7$^{bc}$ | 10.6$^{a}$ | 10.4$^{ab}$ | 10.5$^{ab}$ |
| G4 | Rocco | 28.6$^{a-c}$ | 32.7$^{a-c}$ | 34.5$^{bc}$ | 10.5$^{ab}$ | 10.6$^{ab}$ | 10.7$^{a-c}$ |
| G5 | Cardinal | 26.7$^{a-c}$ | 30.5$^{a-c}$ | 36.3$^{a-c}$ | 20.2$^{ab}$ | 20.4$^{ab}$ | 20.5$^{a-c}$ |
| G6 | TPSCB31 | 37.2$^{ac}$ | 38$^{a-c}$ | 35.3$^{a-e}$ | 20.9$^{ab}$ | 20.1$^{ab}$ | 10.6$^{ab}$ |
| G7 | TPSCB32 | 29.7$^{ac}$ | 40.4$^{a-d}$ | 34.2$^{a-e}$ | 30.5$^{a-c}$ | 30.1$^{a-c}$ | 30.4$^{cd}$ |
| G8 | TPSCB33 | 29.4$^{a-d}$ | 42.6$^{a-d}$ | 33.7$^{a-e}$ | 40.4$^{a-c}$ | 30.1$^{a-c}$ | 20.4$^{cd}$ |
| G9 | TPSCB34 | 29.4$^{a-d}$ | 38.3$^{b-d}$ | 34.2$^{b-d}$ | 30.7$^{a-c}$ | 20.1$^{a-c}$ | 20.6$^{cd}$ |
| G10 | TPSCLB41 | 30$^{b-f}$ | 45.3b$^{cd}$ | 32.8$^{b-d}$ | 40.5$^{b-d}$ | 20.2$^{c-e}$ | 20.4$^{d-f}$ |
| G11 | TPSCLB42 | 25.8$^{bc}$ | 43.9$^{be}$ | 34.8$^{b-d}$ | 40.5$^{b-d}$ | 30.4$^{c-e}$ | 40.4$^{d-f}$ |
| G12 | TPSCLB43 | 29.7$^{b-g}$ | 44.5$^{be}$ | 34.5$^{b-d}$ | 30.5$^{d-g}$ | 20.2$^{d-f}$ | 30.2$^{d-g}$ |
| G13 | TPSCR51 | 22.5$^{c-g}$ | 39.1$^{c-e}$ | 33.6$^{e-g}$ | 40.5$^{d-g}$ | 20.2$^{ef}$ | 30.3$^{d-g}$ |
| G14 | TPSCR52 | 19.4$^{c-g}$ | 39.7$^{c-e}$ | 33.1$^{e-g}$ | 30.5$^{d-g}$ | 20.3$^{ef}$ | 20.3$^{d-g}$ |
| G15 | TPSCR53 | 25.3$^{c-g}$ | 41.5$^{c-f}$ | 32.4$^{f-i}$ | 30.9$^{d-g}$ | 20.2$^{ef}$ | 30.5$^{d-f}$ |
| G16 | TPSCR54 | 24.5$^{d-h}$ | 44.2$^{c-f}$ | 28.3$^{f-i}$ | 30.6$^{e-g}$ | 30.2$^{e-g}$ | 40.3$^{d-f}$ |
| G17 | TPSSMR11 | 35.7$^{d-h}$ | 45.5$^{d-f}$ | 42.7$^{f-i}$ | 10.0$^{e-g}$ | 10.1$^{e-g}$ | 10.2$^{c-e}$ |
| G18 | TPSSMR12 | 35.5$^{d-i}$ | 41.9$^{d-f}$ | 36$^{j-l}$ | 10.7$^{e-g}$ | 10.7$^{b-d}$ | 10.8$^{ac}$ |
| G19 | TPSCLR21 | 34.5$^{e-h}$ | 44.2$^{d-g}$ | 32.1$^{j-l}$ | 30.6$^{c-e}$ | 30.1$^{b-d}$ | 20.4$^{ac}$ |
| G20 | TPSCLR22 | 31.8$^{e-h}$ | 42.2$^{e-g}$ | 29.2$^{j-l}$ | 40.5$^{c-e}$ | 30.2$^{ac}$ | 30.4$^{b-d}$ |
| G21 | TPSCLR23 | 31.4$^{d-i}$ | 43.1$^{e-g}$ | 30.8$^{kl}$ | 40.7$^{a-c}$ | 40.1$^{a-d}$ | 40.4$^{b-d}$ |
| G22 | TPSCLR24 | 32.5$^{g-i}$ | 42.8$^{e-h}$ | 30.7$^{d-f}$ | 40.4$^{a-d}$ | 30.3$^{a-d}$ | 30.4$^{fg}$ |
| G23 | TPSSMC61 | 37.2$^{kl}$ | 45.4$^{g-i}$ | 42.5$^{d-f}$ | 10.3$^{a-d}$ | 10.5$^{a-d}$ | 10.3$^{fg}$ |
| G24 | TPSSMC62 | 23.7$^{kl}$ | 38.4$^{g-i}$ | 40.6$^{g-j}$ | 10.8$^{a-d}$ | 10.7$^{a-d}$ | 10.3$^{d-f}$ |
| G25 | TPSSMC63 | 31.3$^{g-l}$ | 35.7$^{h-j}$ | 42.3$^{g-j}$ | 20.4$^{a-d}$ | 20.1$^{b-d}$ | 20.3$^{d-f}$ |
| G26 | TPSRSM71 | 27.4$^{g-m}$ | 36.2$^{h-j}$ | 36.3$^{g-j}$ | 40.5$^{e-g}$ | 20.2$^{b-d}$ | 30.2$^{c-g}$ |
| G27 | TPSRSM72 | 29.2$^{g-m}$ | 37.4$^{j-l}$ | 41.4$^{e-g}$ | 30.9$^{e-g}$ | 20.2$^{b-d}$ | 20.2$^{c-g}$ |
| G28 | TPSRSM73 | 26.5$^{g-l}$ | 42.8$^{j-l}$ | 38.5$^{e-g}$ | 40.1$^{a-c}$ | 20.1$^{ef}$ | 20.6$^{ef}$ |
| G29 | TPSRSM74 | 33.2$^{d-h}$ | 41.1$^{j-l}$ | 33.6 $^{e-g}$ | 40.7$^{a-c}$ | 30.2$^{e-g}$ | 30.3$^{ef}$ |
| G30 | TPSCSM81 | 29.5$^{d-h}$ | 36.5$^{kl}$ | 35.8 $^{e-g}$ | 30.4$^{ac}$ | 20.4$^{fg}$ | 20.2$^{fg}$ |
| G31 | TPSCSM82 | 29.5$^{d-i}$ | 35.4$^{kl}$ | 34.8$^{fg}$ | 40.1$^{ac}$ | 30.2$^{fg}$ | 30.4$^{d-g}$ |
| G32 | TPSCSM83 | 26.9$^{d-i}$ | 36.7$^{d-h}$ | 32$^{fg}$ | 40.1$^{de}$ | 20.2$^{g}$ | 20.3$^{fg}$ |
| G33 | TPSCSM84 | 29.7$^{d-i}$ | 31.0$^{d-h}$ | 38.4$^{fg}$ | 30.1$^{gh}$ | 20.2$^{fg}$ | 30.2$^{g}$ |
| G34 | Check* | 25.9$^{a-d}$ | 31.3$^{a-d}$ | 33.6$^{g}$ | 30.5$^{g}$ | 40.1$^{g}$ | 30.1$^{g}$ |
| LSD @ 0.05 | | **5.55** | **4.18** | **4.07** | **0.18** | **0.24** | **0.33** |
| CV (%) | | 8.54 | 5.80 | 7.28 | 21.52 | 23.93 | 29.59 |

*Means sharing same letters, within a column, are statistically at par at p≤0.05*

*Check* = UOHSM; ATD = Abbottabad; BK = Battakundi; KN = Kaghan; t ha$^{-1}$ = Tons per hectare; LSD = Least significant difference; CV = Coefficient of variation; p 0.05*

Among the estimated variance components, the total tubers number exhibited the highest genotypic variance (Vg = 1167.3), phenotypic variance (Vp = 1262.23), and environmental variance (Ve = 94.88) under the Battakundi environment (Figure 2).

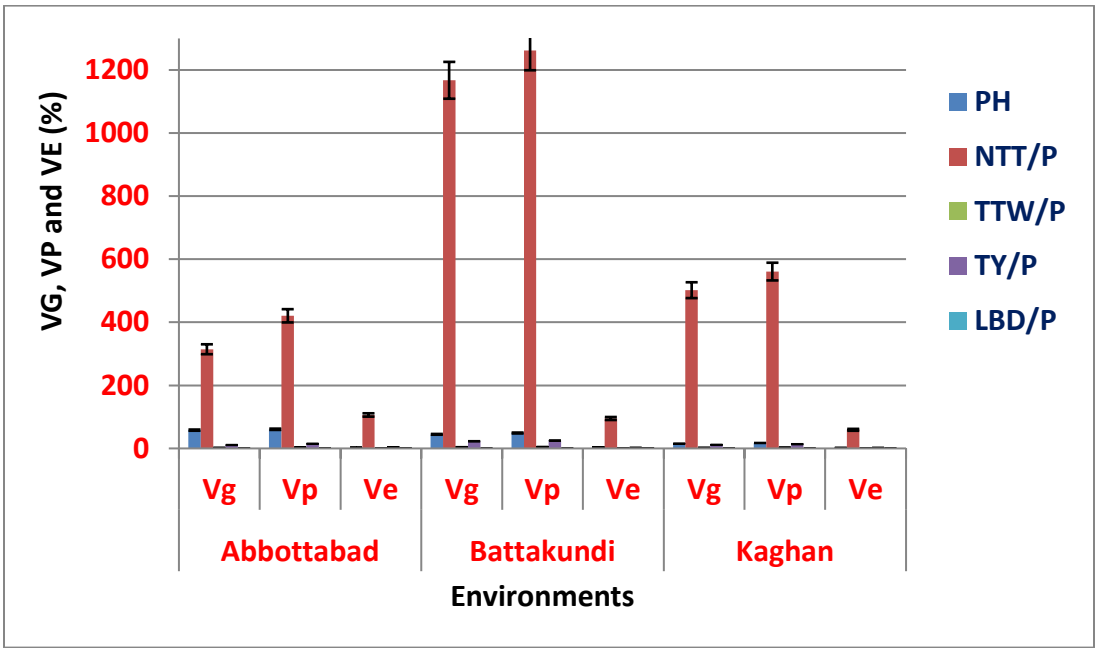


**Fig. 2. Genotypic variance, phenotypic variance and environmental variancefor different yield and yield morpho-traits in Abbottabad, Battakundi and Kaghan**

*Vg = Genotypic variance, Vp = Phenotypic variance, Ve = Environmental variance,*
*PH = Plant height, NTT/P = Number of total tubers plot$^{-1}$, TTW/P = Tubers weight plot$^{-1}$, TY/P = Tubers yield plot$^{-1}$ and LBD/P = Late blight disease plot$^{-1}$*

**Heritability and genetic advance:** Heritability and genetic advance are important genetic parameters for predicting selection efficiency and identifying superior hybrids based on their phenotypic performance. In the present study, moderate to high broad-sense heritability and genetic advance were noted for the evaluated characters across different environments (Figure 3). Highest estimates of heritability were observed for plant height (95.49, 91.34, and 87.26%), total number of tubers per plot (92.48, 89.47, and 74.77%), total tuber weight per plot (91.19, 84.58, and 73.80%), and tuber yield per plot (91.19, 84.59, and 73.80%) across the tested locations. Similarly, moderate to high genetic advance values were observed for plant height (13.40–25.32%), total number of tubers per plot (17.81–28.33%), total tuber weight per plot (18.38–23.94%), and tuber yield per plot (18.39–23.95%). Late blight disease incidence exhibited comparatively higher genetic advance values, ranging from 48.76 to 331.82%, along with moderate to high heritability estimates (49.17–93.26%) across different environments.

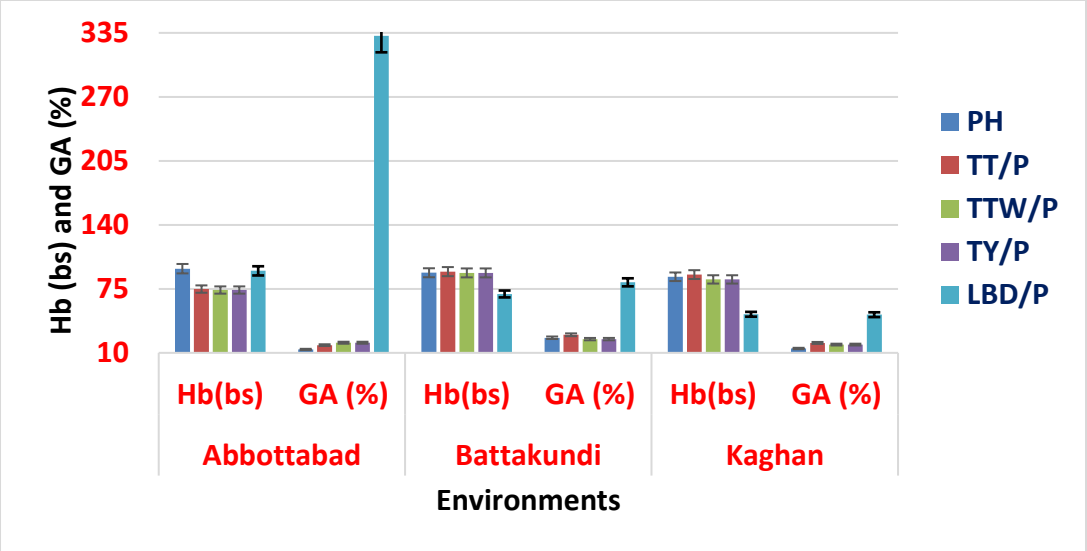


**Fig. 3. Broad sense heritability and genetic advance mean (%) for tuber yield andyield related traits of 34 potato genotypes in Abbottabad, Battakundi and Kaghan sites**

*$H^2$(bs) = Broad sense heritability, GA = Genetic advance, PH = Plant height, NTT/P = Number of total tubers plot$^{-1}$, TTW/P = Tubers weight plot$^{-1}$, TY/P = Tubers yield plot$^{-1}$ and LBD/P = Late blight disease plot$^{-1}$*

**Phenotypic and genotypic coefficient of variation**: Phenotypic and genotypic coefficient of variations are the key indicators to assess the extent of genetic variability and the relative effects of environments (Zeleke *et al.*, 2021). In the present study, all the evaluated traits revealed higher PCV, signifying the contribution of environmental effects to phenotypic appearance. Late blight disease incidence exhibited the highest variability, with PCV values ranging from 48.13 to 172.71% and GCV values from 33.81 to 166.66%. Tuber yield per plot showed moderate variation, with PCV ranging from 10.56 to 13.34% and GCV from 9.71 to 12.26%. Plant height exhibited low to moderate variability, with PCV and GCV values ranging from 8.00 to 16.97% and 7.47 to 16.59%, respectively. Similarly, total number of tubers per plot recorded moderate PCV (10.88–14.97%) and GCV (10.00–14.39%), while total tuber weight per plot showed moderate PCV (10.55–13.33%) and low to moderate GCV (9.70–12.25%) values (Figure 4).

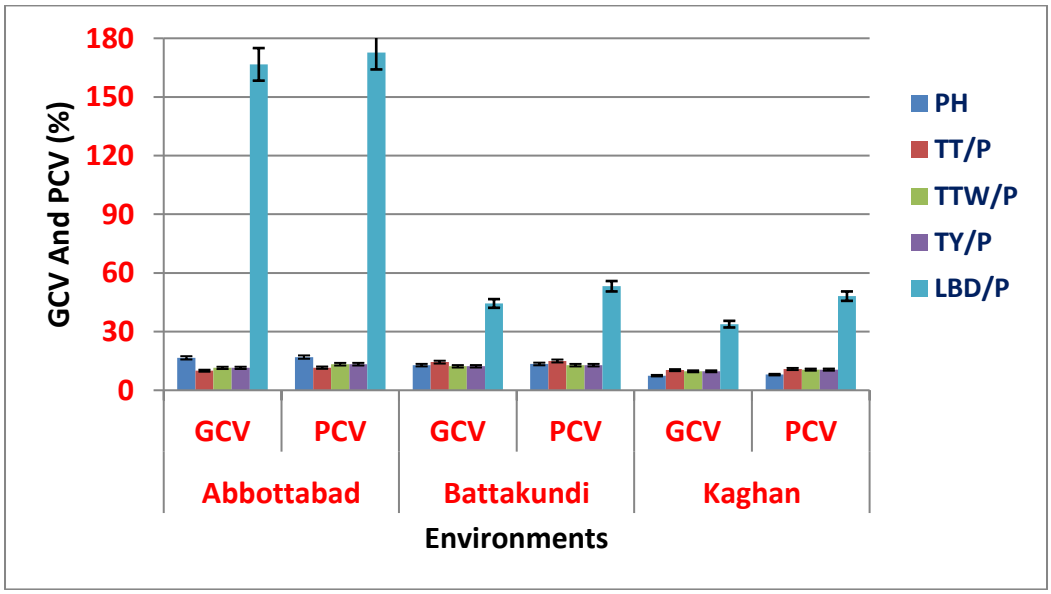


**Fig. 4. Phenotypic and genotypic coefficient of variations for studied characters in 34 potato genotypes across three diverse environments**

*GCV = Genotypic coefficient of variation, PCV – Phenotypic coefficient of variation, PH = Plant height; NTT/P =Number of total tubers plot$^{-1}$; TTW/P = Tubers weight plot$^{-1}$; TY/P = Tubers yield plot$^{-1}$; LBD/P = Late blight disease plot$^{-1}$*

**AMMI Bi-plot analysis:** The AMMI stability was employed to partition GEI effects into principal components (PC1 and PC2) for evaluating potato performance and stability across environments. The interpretation of AMMI bi-plot results was followed as results declared from Worku *et al.* (2018), where relative position of genotypes and environments in the bi-plot provides valuable information regarding genotype adaptability and performance under specific environmental conditions. In the present study, PC1 primarily explained the magnitude of genotype performance, where positive PC1 scores represented superior-performing genotypes, while negative values indicated comparatively lower performance. In contrast, PC2 was used to assess the stability of genotypes across the tested environments. Genotypes showing smaller absolute PC2 scores were regarded as relatively more stable. This criterion was used consistently for the evaluation of all traits included in the study.

The AMMI analysis indicated that the first principal component (PC1) contributed 63.02% of the total GEI, while the second component (PC2) explained a further 19.99% (Figure 5). For tuber yield, genotypes G23, G17, G18, G6, G19, and G12 showed favorable PC1 scores. In terms of late blight response, G12, G26, G17, G18, and G28 were associated with lower disease incidence. The PC2 results indicated greater yield stability for G12, G17, G18, and G19, whereas G26, G10, G11, G16, G17, and G18 showed relatively stable responses for late blight incidence across the test environments. For the remaining traits, G9 showed favorable performance for plant height, while G17 and G23 were superior for total tuber number and total tuber weight per plot, respectively. Based on the stability estimates, G18 and G29 were relatively stable for plant height; G11, G12, G23, and G25 for total tuber number; and G17, G18, G23, and G24 for total tuber weight per plot. These results demonstrate substantial differences among genotypes in their responses to environmental conditions. On the basis of their overall performance, G23 (TPSSMC61) and G17 (TPSSMR11) emerged as the most promising genotypes, combining high tuber yield with comparatively stable performance and lower late blight incidence. These two genotypes therefore warrant further multi-environment testing and consideration in subsequent stages of potato varietal development (Figure 5).

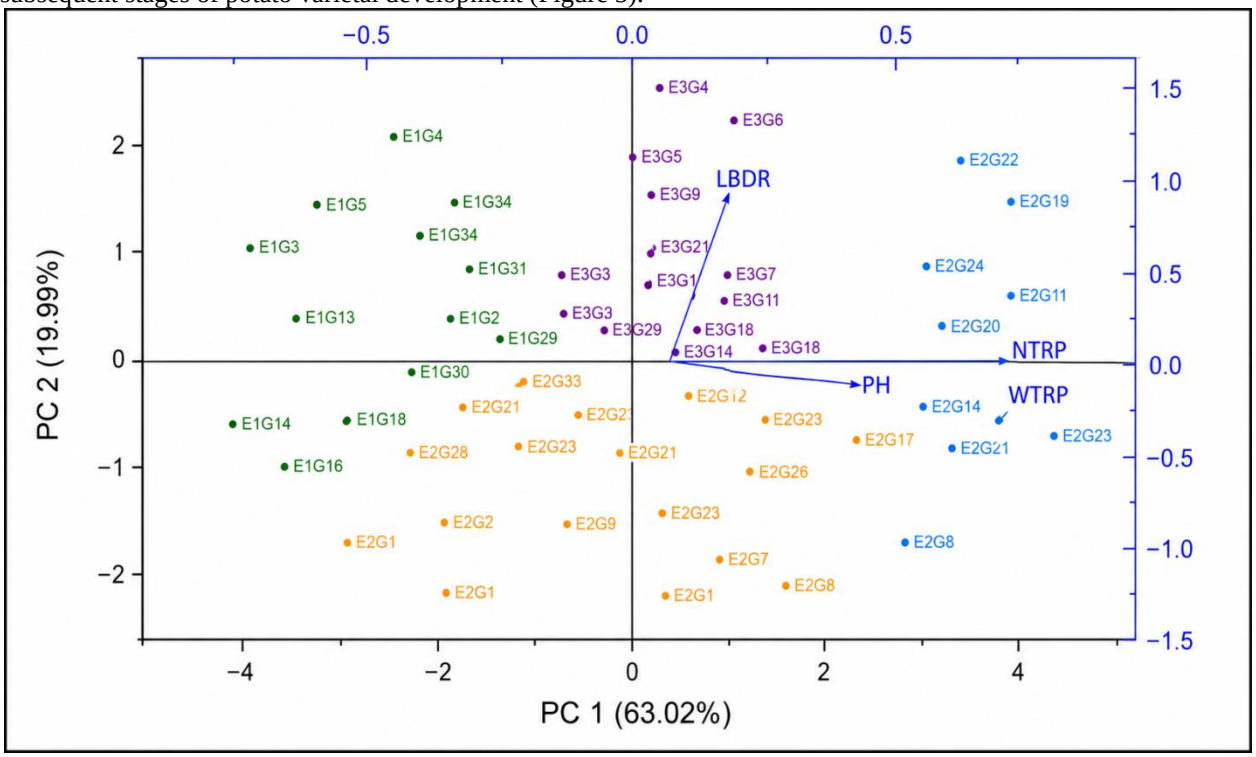


**Fig. 5. AMMI Bi-plot for yield and yield contributing traits of 34 potato genotypes across three different diverse environments**

**E1 = Abbottabad; E2 = Battakundi; E3 = Kaghan**

**Correlation:** Correlation analysis was performed in order to determine the strength and direction of relationships among the traits under evaluation. The strength of relationships between variables was represented by the size of the correlation circles, where larger circles indicated stronger associations. Tuber yield exhibited significant positive associations ($p \leq 0.001$ and $p \leq 0.05$) with key yield-contributing traits (Figure 6).

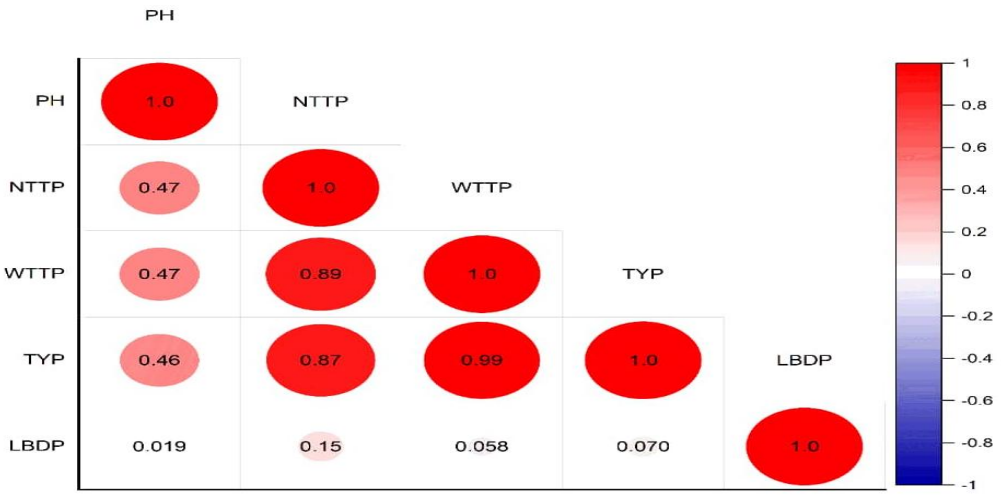


**Fig. 6. Correlations matrix showing relationship between tuber yield and yield-contributing traits of potato genotypes**

## DISCUSSION

The analysis of variance revealed that genotype, environment, and GEI significantly influenced tuber yield and most yield-related traits, indicating that both genetic and environmental conditions played important roles in determining potato genotypes performance. The significant genotypic effects confirm the presence of substantial genetic variability among the evaluated TPS-derived potato genotypes, providing a broad genetic base for effective selection. A diverse genetic base is essential for effective crop breeding, as it provides the variation needed to select desirable traits and combine favorable characteristics through breeding. Such diversity enables breeders to identify promising genetic resources and use them in the development of improved cultivars with better agronomic performance and other target attributes (Bonierbale *et al.*, 2020).

The strong environmental effects observed in the study can be related to the substantial differences in elevation and weather conditions among the experimental sites. Battakundi and Kaghan, being located at higher altitudes, generally had cooler growing conditions, with mean temperatures of about 3–10 °C, along with greater relative humidity and more frequent rainfall than Abbottabad. Such conditions may have favored potato growth by reducing heat stress, maintaining soil moisture, and allowing greater canopy development and a longer crop growth period. These environmental advantages were reflected in the comparatively higher yield of several genotypes at the high-altitude sites. This variation was useful for distinguishing genotypes according to their level of resistance or susceptibility. The highly significant GEI further confirmed that the performance of the tested genotypes was not consistent across all locations. Genotypes better suited to cooler temperatures, sufficient moisture, and longer growing periods performed particularly well at Battakundi and Kaghan, whereas some genotypes responded more favorably to the comparatively warmer conditions at Abbottabad. The changes in genotype ranking among locations indicate a crossover type of interaction, in which temperature, rainfall, relative humidity, and elevation collectively influenced genotype performance. Thus, a genotype showing superior performance at one site could not necessarily be expected to perform similarly under different environmental conditions. These findings support the importance of evaluating potato hybrids across multiple environments before selecting them for wider cultivation, particularly when the objective is to identify genotypes with stable performance across diverse agro-ecological conditions (Cadersa *et al.*, 2022; Muhammadania *et al.*,2021).

The observed variability among genotypes was further supported by estimates of genetic parameters. In clonally propagated crops such as potato, broad-sense heritability is particularly relevant because it incorporates additive, dominance, and epistatic genetic effects that are largely preserved during vegetative propagation (Fekadu *et al.*, 2013; Zeleke *et al.*, 2021). During this study, several economically important traits exhibited high broad-sense heritability accompanied by high genetic advance, suggesting effectiveness of phenotypic selection of superior clones (Ortiz *et al.*, 2021; Nagumma *et al.*, 2020; Benavides *et al.*,2017). High heritability together with high genetic advance also confirm the role of additive gene action, making them more responsive to direct selection. Consequently, traits like tuber yield and other highly heritable yield components can be effectively improved through conventional breeding approaches. Conversely, traits with comparatively lower genetic advance despite moderate or high heritability may involve non-additive gene action or greater environmental influence, lowering simple phenotypic selection role. The magnitude of the PCV surpassed that of GCV for traits under study, indicating the contribution of environmental factors to the observed

phenotypic variation in addition to genetic differences (Subedi *et al.,* 2021; Zeleke *et al.,*2021). However, the PCV and GCV values for late blight were found higher only at Abbottabad, which could be due to presence of favorable environmental conditions prevailing at Abbottabad i.e. moderate temperature (15–20ºC), high humidity and prolonged wetness, which are congenial for disease development. This higher disease pressure allowed clear differentiation of resistant and susceptible genotypes, resulting in higher genetic variability. Moderate heritability observed for late blight disease incidence indicates that resistance was controlled by environmental and genetic effects. The moderate heritability observed therefore, exhibits that improvement of late blight resistance should rely on repeated multi-environment evaluations to accurately identify stable resistant genotypes, also reported by Sood *et al.* (2020).

To further investigate GEI and identify stable genotypes, the AMMI model was employed because it effectively partitions additive genotype and environment effects from multiplicative interaction effects through the integration of ANOVA and principal component analysis for identifying both high-performing and stable genotypes than conventional mean comparisons alone (Scavo *et al.,* 2022; Cadersa *et al.,* 2022). Among the evaluated environments, Battakundi consistently provided the most favorable conditions for potato production. Its high altitude, cooler temperatures, and extended growing period likely promoted greater photosynthetic efficiency, prolonged tuber bulking, and reduced disease pressure, resulting in higher tuber yield and lower late blight incidence compared with the other test locations, highlighting the previous studies (Worku *et al.,* 2018; Cadersa *et al.,* 2022).

AMMI stability analysis highlighted G23 (TPSSMC61) and G17 (TPSSMR11) as particularly promising TPS-derived genotypes. Both entries combined high tuber yield with comparatively low late blight incidence and showed satisfactory performance across the tested environments. Their consistent response under different growing conditions suggests that they may have useful adaptation beyond a single test location. Therefore, these genotypes can be considered for further yield evaluation and subsequent stages of cultivar development (Fantaw, 2023; Khan *et al.,* 2025). The results of the present study confirmed appreciable genetic differences among the TPS-derived genotypes, while the significant environmental effects demonstrated that trait expression was also influenced by growing conditions. Combining genetic parameter estimates with AMMI analysis allowed promising entries to be distinguished on the basis of yield, late blight response, and performance consistency. Nevertheless, the identified genotypes should be tested over additional seasons and locations before any recommendation for commercial production is made. Further evaluation will also determine their suitability for use as potential parents in subsequent potato breeding work.

**Conclusions:** The study demonstrated that AMMI analysis was useful for identifying potato genotypes with high yield, late blight resistance, and stable performance across environments. High heritability and genetic advance indicated good potential for selection-based improvement. G23 (TPSSMC61) and G17 (TPSSMR11) were the most promising genotypes, combining higher yield, lower late blight incidence, and stable performance. Battakundi (E2) was the most favorable environment for potato evaluation and breeding. Further multi-location and multi-year testing is recommended before cultivar release.

**Authors' contributions:** Bilal Ahmed Khan, the first author, organized, drafted, and revised the manuscript. The remaining authors contributed equally according to their respective areas of research expertise.

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**Research content:** The research content of manuscript is original and has not been published elsewhere.

**Consent to publish:** All authors agree to publish the paper in Journal of Animal and Plant Sciences.

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