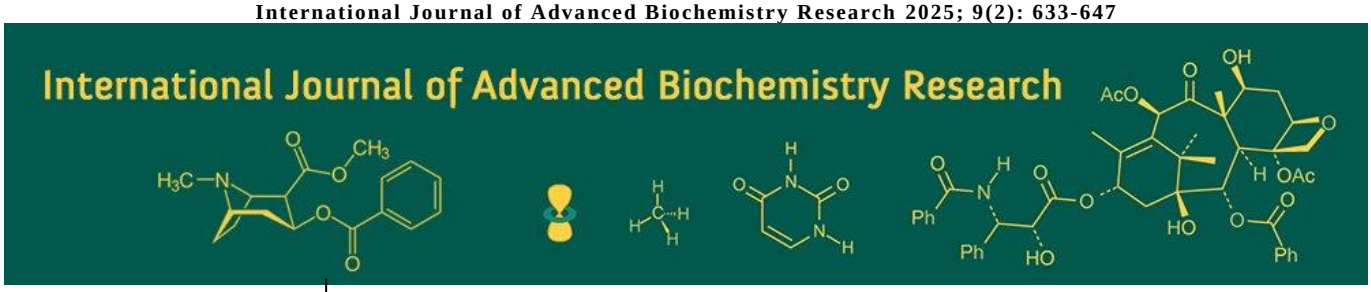

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K Hanume Gowda
College of Horticulture, Bangalore, UHS, Bagalkot, Karnataka, India

H Amarananjundeswara
College of Horticulture, Sirsi, UHS, Bagalkot, Karnataka, India

B Fakrudin
College of Horticultural Engineering and Food Technology, Devihosur, UHS, Bagalkot, Karnataka, India

KR Vasudeva
College of Horticulture, Bangalore, UHS, Bagalkot, Karnataka, India

Jyoti Kattegoudar
College of Horticulture, Kolar, UHS, Bagalkot, Karnataka, India

B Doddabasappa
Regional Horticulture Research and Extension Centre, Bangalore, UHS, Bagalkot, Karnataka, India

Corresponding Author:
K Hanume Gowda
College of Horticulture, Bangalore, UHS, Bagalkot, Karnataka, India

Genetic variability, heritability and divergence analysis for growth, yield and nutritional quality parameters in potato (*Solanum tuberosum* L)

K Hanume Gowda, H Amarananjundeswara, B Fakrudin, KR Vasudeva, Jyoti Kattegoudar and B Doddabasappa

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Abstract
Potato is a globally significant food crop and a vital source of nutrition, plays a crucial role in food security due to its high productivity, nutritional value and adaptability to diverse agro-climatic conditions. This study was conducted at Horticulture Research and Extension Centre, Haasan during kharif and rabi season of 2021-22, aimed to investigates genetic variability, heritability and divergence analysis for growth, yield and nutritional traits in potato genotypes. The pooled analysis of variance revealed significant differences among potato genotypes for growth, yield and biochemical traits, with stable genotypic effects for agronomic traits and notable genotype × environment interactions for specific biochemical parameters. The study revealed significant genetic variability for growth, yield and biochemical traits of potato genotypes, with high heritability and genetic advance for traits like tuber yield, number of tubers, carbohydrates and micronutrient content, indicating strong additive gene action. Moderate heritability with moderate genetic advance was observed for traits like haulm yield and titratable acidity, suggesting a mixed influence of genetic and environmental factors. These findings highlight the potential for direct selection to enhance yield, quality, and nutritional traits in potato breeding programs. Genetic divergence analysis grouped them into eight distinct clusters with tuber size, protein content, and tuber length contributed the most to genetic divergence. The highest genetic distance was observed between Clusters VI and VIII, suggesting potential for heterotic hybridization. Cluster VIII showed superior vegetative growth, while Cluster VI excelled in tuber yield, emphasizing the scope for selecting diverse parental lines for targeted trait improvement in potato breeding programs. This study underscores the significant genetic variability among potato genotypes, with high heritability and genetic advance for yield and nutritional traits, making them ideal for direct selection and offering potential for heterotic hybridization and trait improvement in potato breeding programs.

Keywords: Genetic divergence, genetic variability, heritability, potato breeding, tuber yield, yield components

1. Introductions
Potato (*Solanum tuberosum* L.) is the third most important food crop worldwide after rice and wheat, playing a crucial role in global food security. It is a staple for over a billion people, providing essential carbohydrates, proteins, vitamins, and minerals (Anon, 2020a) [1]. As a highly productive crop with a short growth cycle, potato cultivation is expanding rapidly, particularly in developing countries, where it serves as a critical component in alleviating hunger and malnutrition (Hijmans, 2001) [13]. In India, potato is widely cultivated, with major producing states including Uttar Pradesh, West Bengal, Gujarat, Madhya Pradesh, Punjab, Assam, and Karnataka, contributing significantly to the national and global supply (Anon, 2020b) [2].
Understanding genetic variability is fundamental to any crop improvement program. It provides a basis for selection and breeding strategies aimed at enhancing growth, yield, and nutritional quality traits (Haydar *et al*., 2007) [11]. In potato, genetic variability is often constrained due to the narrow genetic base of cultivated varieties, making it essential to explore and utilize diverse germplasm for breeding high-yielding and nutritionally superior genotypes (Shekhawat, 2001) [30].

Heritability and genetic advance estimates further aid in identifying traits that can be effectively passed on to subsequent generations, facilitating targeted genetic improvements (Hornokova *et al*., 2003) [14].

Divergence analysis plays a crucial role in understanding genetic diversity and identifying potential parental combinations for hybridization. High genetic divergence among genotypes suggests a greater possibility of obtaining heterotic hybrids, which is particularly important for potato, an outbreeding species exhibiting heterosis (Tarn and Tai, 1977) [35]. Multivariate statistical tools such as Principal Component Analysis (PCA), hierarchical clustering, and genetic distance measures allow for the efficient classification of genotypes based on their morphological, biochemical, and molecular attributes (Rao, 2004) [26]. These techniques help breeders in selecting genotypes with desirable growth, yield, and quality traits for further improvement programs.

Nutritional composition is an essential aspect of potato breeding, as consumer demand for nutritionally rich food crops continues to rise. Key biochemical traits such as carbohydrate content, protein levels, minerals (Fe, Zn, Mn, Cu), and vitamins (B1, B2, B6, C) are critical determinants of nutritional quality. Understanding the variability of these parameters among potato genotypes can aid in the identification of nutrient-dense cultivars suitable for both commercial production and biofortification programs (Reed *et al*., 2004) [27].

Given these considerations, the present study aims to assess genetic variability, heritability, and genetic divergence among potato genotypes for growth, yield, and nutritional traits. The findings will contribute to the identification of promising genotypes for breeding programs aimed at improving yield potential and nutritional quality, ultimately supporting sustainable potato production and food security initiatives.

2. Materials and Methods

2.1. Plant materials

Forty genotypes of potato were selected for the study. These genotypes were chosen from All India coordinated research project (AICRP) centre of Horticulture Research and Extension Centre (HREC), Somanahallikaval, Hasssan of University of Horticultural Sciences (UHS), Bagalkot, Karnataka. The list of potato genotypes used for the experiment along with their characters were given in Table 1.

2.2. Experimental site and design

The field experiments were conducted at HREC, Somanahallikaval, Hasssan for 2 consecutive seasons of *kharif* and *rabi* for the year 2021-22. The study followed a randomized complete block design (RCBD) with two replications to minimize experimental error and ensure uniformity in treatment application.

2.3. Planting material and experimental details

A total of 40 potato genotypes were evaluated for growth, yield, and nutritional composition. The experimental plot consisted of five rows per genotype, with a row length of 3 meters, maintaining a spacing of 60 cm × 20 cm between rows and plants, respectively. Standard agronomic practices were followed for crop management. The manual weeding, fertilizer application and earthing up were carried out as and when necessary. The growth, yield and yield component characters were recorded. The harvesting was done during in the month of Sept-2021 for kharif and Feb-2022 for rabi season experiments.

2.4. Growth parameters

2.4.1 percent emergence

Per cent emergence was calculated as the percentage of tubers that successfully germinated 30 days after planting, using the formula.

$$\text{Emergence (\%)} = \frac{\text{Total number of tubers germinated}}{\text{Total number of tubers planted}} \times 100$$

2.4.2 Plant height (cm)

Plant height was measured at 30, 60 and 75 days after planting, from the ground to the tip of the longest aerial leaf. An average height of five randomly selected plants per treatment was calculated.

2.4.3 Number of branches per plant

The number of branches per plant was recorded at 30, 60 and 75 days after planting and the mean for each treatment was determined from five randomly selected plants.

2.4.4 Number of leaves per plant

The number of fully grown, green and functional compound leaves per plant was recorded at 30, 60 and 75 days after planting. An average number of compound leaves per plant was calculated from five randomly selected plants.

2.4.5 Leaf area (cm^2)

Leaf area was measured by using a leaf area meter (LAM 211) from the leaves of five selected plants per treatment. The leaf area was expressed in cm^2 per plant at 30, 60 and 75 DAP.

2.4.6 Leaf area index

Leaf area index (LAI) was calculated using the formula suggested by Sestak *et al*. (1971) [29].

$$\text{LAI} = \frac{\text{Leaf area}}{\text{Ground area covered by plant or spacing}} \times 100$$

2.4.7 Number of internodes

An average number of internodes per plant was calculated by dividing the total number of internodes by the total number of plants counted and assessed at 80 days after planting.

2.4.8 Internodal length (cm)

An internodal length was determined by measuring the height of each tagged plant from the base to the top and dividing by the number of internodes per plant. An average length was calculated for each replication.

2.4.9 Number of days to flowering

The total number of days taken for flower initiation of plants was counted from the date of planting to flower initiation.

2.4.10 Days taken for physiological maturity

The number of days taken for each variety when the haulms of 50 percent of the plant population per plot turned yellowish or showed senescence to reach physiological

maturity from the date of planting was recorded.

2.4.11 Plant spread (cm^2)
Plant spread was measured from both North to South and East to West direction from five randomly selected plants at 60 days after planting. An average plant spread was calculated in square centimeters.

2.5 Yield and yield components
2.5.1 Tuber length (cm)
The length of five randomly selected tubers per genotype was measured and an average length was calculated and expressed in centimeters.

2.5.2 Tuber diameter (cm)
The diameter of the same five selected tubers per genotype was measured and an average diameter was calculated in centimeters.

2.5.3 Tuber size (cm^2)
Tuber size was measured by determining the length and width between the two polar ends using Vernier calipers. The mean tuber size was calculated by multiplying the length and breadth values, expressed in square centimeters.

2.5.4 Number of tubers per plant and plot (kg)
After harvest, the number of tubers per plant and plot were counted and recorded.

2.5.5 Grade-wise number and weight of tubers per plant and plot
The harvested tubers were graded based on their size categories (< 25 g, 25-50 g, 50-75 g, > 75 g). The number and weight of tubers in each grade were recorded per plant and plot.

2.5.6 Marketable tuber yield per plant and plot (kg)
From the harvested tubers, those categorized as marketable (excluding small tubers < 25 g) were weighed to determine the marketable tuber yield per plant and plot.

2.5.7 Un-marketable tuber yield per plant and plot (kg)
The weight of tubers categorized as un-marketable (small tubers < 25 g) was recorded per plant and plot.

2.5.8 Tuber yield per plant (g) and plot (kg)
The total weight of tubers harvested per plant was measured and this data was used to calculate the tuber yield per plot in kilograms.

2.5.9 Average tuber weight (g)
An average weight of five randomly selected tubers per genotype was calculated.

2.5.10 Haulm yield of fresh and dry weight basis (kg/ha)
Haulm yield was determined by weighing five randomly selected plants at the beginning of senescence for fresh weight and after air drying for one week for dry weight. The dry weight was further determined by oven-drying at 75 °C for 72 hours. Using this data, haulm yield per hectare was calculated.

2.5.11 Total tuber yield (t/ha)
The total tuber yield from each plot was used to calculate the yield in tones per hectare using the formula

$$\text{Total tuber yield (t/ha)} = \frac{\text{Area of 1 ha X tuber yield (kg/plot)}}{\text{Plot size X 1000}} \text{ x } 100$$

2.5.12 Total tuber per square meter (kg)
The total tuber yield per square meter was calculated using the formula

$$\text{Total tuber yield (kg/m}^2\text{)} = \frac{\text{Total tuber yield (kg/plot)}}{\text{Plot area (m}^2\text{)}}$$

2.5.13 Harvest Index
The harvest index was calculated by using the formula

$$\text{Harvest Index (HI)} = \frac{\text{Economic yield (tuber yield)}}{\text{Biological yield (total above ground biomass + tuber yield)}} \text{ x } 100$$

Where:
Economic yield is the tuber yield (the weight of harvested tubers).
Biological Yield is the total weight of the above-ground biomass plus the tuber yield.

2.6. Sample collection and estimation of nutritional quality parameters
Tubers of all the genotypes were collected, properly washed, cleaned and chopped in small pieces. The small pieces of tubers were kept in an oven at 60 °C for 12 hours for drying and fine powder were prepared after grinding for nutritional analysis. Nutritional composition such as pH, moisture content, TSS, specific gravity, dry matter, carbohydrates, protein, ascorbic acid, titratable acidity, total sugar, reducing sugar, non-reducing, crude fiber, fat, ash content, non-enzymatic browning, Fe, Cu, Zn and Mn were estimated. The nutritional compositions of potato genotypes were estimated at Department of Post-Harvest Technology, College of Horticulture, Bangalore. The details procedure and methods for estimation for all the nutritional composition were mentioned below.

2.6.1 Moisture content (%): Moisture content was determined using an electronic moisture analyzer (Sartorius MA 35) and reported as a percentage

2.6.2 pH: The pH was measured using a digital pH meter under constant temperature conditions.

2.6.3 Total soluble solids (ºB): TSS was measured using a refractometer and expressed in °Brix (Ranganna, 2008) [24].

2.6.4 Specific gravity in volume (g/cm^3)
The specific gravity of potato tubers was measured using the air weight and water displacement method, following the procedure described by Birhman *et al*. (1988) [6]. It was calculated using the formula.

$$\text{Specific gravity} = \frac{\text{Weight of tuber in air}}{\text{Weight of tuber in air-Weight of tuber in water}}$$

2.6.5 Total protein (%): The protein content was calculated using the absorbance value and specific constants. The total protein content was determined using the Lowry method. The potato samples (0.5 g) were soaked overnight in distilled water and the volume was adjusted to 20 ml the following day. A 1 ml aliquot of the extract was combined with 5 ml of reagent C (prepared by mixing reagent A and reagent B in a 50:1 ratio) and 0.5 ml of Folin-Ciocalteu reagent, diluted 1:1 with water

The mixture was thoroughly blended and incubated in the dark for 30 minutes, after which the absorbance was measured at 660 nm.

Reagent A: 50 ml of 2 percent Na_2CO_3 in 0.1N NaOH + 1 ml $CuSO_4$

Reagent B: 50 mg $CuSO_4 \cdot {}_5H_2O$ in 10 ml of 1 percent Sodium Potassium Tartrate

$$\text{Total protein (\%)} = \frac{\text{OD 660} \times \text{Std. value (mg)} \times \text{Total vol. of extract}}{\text{Assay volume} \times \text{wt. of the sample (g)} \times 1000} \times 100$$

Where OD represents the optical density measurement.

2.6.6 Ascorbic acid (mg/100 g): Ascorbic acid content was determined using one gram of tuber sample. The sample was mixed with 4 percent oxalic acid and diluted to 50 ml in a volumetric flask. The solution was filtered using Whatman No. 4 filter paper and 25 ml of the filtrate was titrated with 2,6-dichlorophenol-indophenol dye until a light pink colour appeared. The dye solution was prepared by dissolving 50 mg of the sodium salt of 2,6-dichlorophenol-indophenol in approximately 200 ml of double-distilled water containing 4.2 mg of sodium bicarbonate. The dye was used for both titration and the standardization of ascorbic acid, following the method described by Ranganna (1986) [23]. The dye concentration was adjusted and used a pH meter to confirm the endpoint during the titration process. The increased dye concentration helps to minimize interference from the natural pigments in red or pink-skinned potato tubers, allowing for clearer detection of the colour change. Additionally, the pH meter provides precise measurements, ensuring the accuracy of the endpoint determination and confirming the ascorbic acid content without relying solely on visual inspection. This adjustment helps in accurately determining the ascorbic acid content despite the challenges posed by the tuber's natural colour.

The ascorbic acid content (mg/100 g) was calculated using the formula

$$\text{Ascorbic acid (mg/100 g)} = \frac{\text{Titre value x Dye factor x Volume made up}}{\text{Aliquot of extraction x Volume of sample taken}} \text{X } 100$$

2.6.7 Titratable acidity (%): The acidity was determined by titrating a potato sample solution against 0.1 N NaOH using phenolphthalein as an indicator, with the acidity expressed as a percentage of citric acid equivalent (AOAC, 1995) [4].

2.6.8 Crude fiber (%): Crude fiber content was measured using the double digestion technique described by Sadasivam and Manickam (1996), which involved sequential boiling with sulfuric acid and sodium hydroxide, followed by filtration, drying and ignition. The fiber content was calculated based on weight differences.

2.6.9 Ash content (%): Ash content was determined by placing a known weight of potato tuber samples in crucibles, drying in a muffle furnace at 525 °C and weighing the residual ash.

2.6.10 Fat (%): Fat content was measured by extracting the fat from potato samples using petroleum ether and calculating the fat percentage based on weight differences before and after extraction.

2.6.11 Dry matter content (%): Dry matter content was calculated by drying fresh potato slices at 65 °C for 72 hours and measuring the oven-dry weight as a percentage of the fresh weight.

2.6.12 Total carbohydrates (g/100 g): Total carbohydrates were quantified using the phenol-sulfuric acid method. The absorbance of the prepared sample was measured at 490 nm. The filtered extract was incubated overnight at room temperature for complete dissolution and stabilization of sugars, further reducing variability due to interfering compounds, this measure collectively ensure that the total carbohydrate content is accurately estimated with minimal interference from other biochemical constituents.

2.6.13 Total sugars (%): Total sugars were estimated using a modified Lane and Eynon method. The sample was hydrolyzed, neutralized and titrated against Fehling's solution with methylene blue as an indicator to calculate the sugar content (Ranganna, 1977) [22].

2.6.14 Reducing sugars (%): Reducing sugars were estimated by titrating the sample filtrate against Fehling's solution with methylene blue as an indicator, calculating the percentage based on titrate value and weight.

2.6.15 Non-reducing sugars (%): Non-reducing sugars were determined by subtracting the percentage of reducing sugars from the total sugars (Ranganna, 1986) [23].

2.6.16 Minerals: The mineral content (iron, copper, zinc and manganese) was determined by wet digestion of samples with a diacid mixture and subsequent analysis using an Atomic Absorption Spectrophotometer.

2.6.17 Non-enzymatic browning reaction (OD value): Non-enzymatic browning was assessed by soaking the sample in alcohol, filtering and measuring the absorbance at 440 nm, expressed as optical density (OD) (Srivastava and Sanjeevkumar, 2002) [34].

2.7. Statistical analysis

2.7.1. Combined analysis of variance

A combined ANOVA for biochemical parameters was calculated to estimate treatment effects and interactions among various sources of variation.

2.7.2 Estimation of genetic parameters

2.7.2.1 Genotypic and phenotypic co-efficient of variation

The genotypic and phenotypic co-efficient of variation were calculated using the formulas recommended by Cockerham (1963) [8].

Genotypic co-efficient of variation (GCV)

$$GCV\ (\%) = \frac{бg}{\overline{X}} \times 100$$

Phenotypic co-efficient of variation (PCV)

$$PCV\ (\%) = \frac{бp}{\overline{X}} \times 100$$

Where,
$\overline{X}$ = General mean
r = Number of replications
σg = Genotypic standard deviation
σp = Phenotypic standard deviation

GCV and PCV values were categorized as follows based on the classification by Burton and Devane (1953) [7]:
0-10 percent: Low
10-20 percent: Moderate
20 percent and above: High

2.7.2.2 Heritability

The Broad-sense heritability (h^2) was estimated using the method proposed by Webber and Moorthy (1952) [37]. The formula is as follows:

$$h^2 = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Where,
h^2 (%) = Heritability (Broad sense)
$\sigma^2 g$ = Genotypic variance
$\sigma^2 p$ = Phenotypic variance

The heritability was classified according to the criteria suggested by Robinson *et al*. (1949) [28]:
0-30 percent = Low
30-60 percent = Moderate
60 percent and above = High

2.7.2.3 Expected genetic advance

The expected genetic advance for each trait was calculated using the formula provided by Johnson *et al*. (1955) [16]:

$$GA = h^2 \times \sigma_p \times k$$

Where
k = selection differential (2.06) at 5 percent selection intensity
h^2 = Heritability in broad sense
σ_p = Phenotypic standard deviation

2.7.2.4 Genetic advance over percent of mean (GAM)

The genetic advance as a percentage of the mean was calculated using the method suggested by Johnson *et al*. (1955) [16]:

Genetic advance over percent of mean (GAM) = $\frac{GA}{\overline{X}} \times 100$

Where
GA = Genetic advance
X = General mean
The categories for genetic advance as a percentage of the mean, as proposed by Johnson *et al*. (1955) [16], are:
0-10 percent: Low,
11-20 percent: Moderate
21 percent and above: High

2.7.3 Genetic divergence

The genetic divergence between different populations was analyzed using Mahalanobis' D^2 statistic (Mahalanobis, 1928) [17]. This analysis was performed on the recorded germplasm data. The generalized distance (D^2) between any two populations is calculated using the following formula.

$$D^2 = \Sigma \lambda^{ij} \sigma^i \sigma^j$$

Where,
D^2 = Square of generalized distance
λ^{ij} = Reciprocal of the common dispersal index
σ^i = μi1-μi2
σ^j = μj1-μj2
μ = General mean

To simplify the computation, which involves inverting higher-order determinants, the original correlated, unstandardized character means (Xs) were transformed into standardized, uncorrelated variables (Ys). The D^2 values were then derived using these uncorrelated (Ys) values for any two genotypes as outlined by Rao (1952) [25].

2.7.3.1 Clustering D^2 values

All the n (n-1)/2 values were clustered using Tocher's method (Rao, 1952) [25].

2.7.3.2 Intra and inter-cluster distance

The intra and inter cluster distances were computed using the formula provided by Singh and Choudhary (1977) [32].

$$\text{Square of intra cluster distance} = \frac{\sum Di^2}{N}$$

Where,
$\sum Di^2$= Sum of distances between all possible combinations ($n_i n_j$) of the entries within the cluster.
ni = Number of entries in the cluster i
nj = Number of entries in the cluster j

2.8. Data analysis

The analysis of data was done in R statistical package version 4.3.2.

3. Results

3.1 Pooled analysis of variance (ANOVA)

The pooled analysis of variance for growth parameters in potato (Table 2) revealed significant variability across genotypes and environmental effects. Genotypic effects were highly significant ($p = 0.01$) for traits like percent emergence, plant height, number of branches, leaves, leaf area, and phenological traits such as days to flowering and maturity. The nonsignificant genotype × environment (G × E) interaction for these traits suggests stability across environments.

For yield traits (Table 3), significant effects of genotype, environment, and G × E interaction were observed for tuber length, tuber diameter, and tuber size. The total tuber yield per plant and plot showed significant effects of genotype and environment, with no significant G × E interaction, indicating stable performance. Marketable tuber yield was significantly influenced by genotype and environment, while unmarketable yield showed a significant G × E interaction. Haulm yield (fresh and dry weight) exhibited significant genotype and environment effects but no significant G × E interaction, suggesting consistent performance.

Biochemical traits (Table 4) displayed strong genotypic influences, with significant G × E interactions for total soluble solids, ascorbic acid, ash content, tuber firmness, dry matter, total carbohydrates, iron, color, taste, texture, and overall acceptability. Traits like protein, specific gravity, total sugar, reducing sugar, crude fiber, and fat content were mainly controlled by genotype, with minimal environmental influence. Skin and flesh color parameters showed significant genotypic effects, with G × E interactions observed for some skin color attributes.

The study underscores the importance of genetic selection for stable potato genotypes, particularly for traits such as yield, dry matter, protein, total sugar, and mineral content, which exhibited strong genotypic control with minimal environmental influence.

3.2 Genetic parameters

The estimates of mean, range, components of variance, heritability and genetic advance for growth parameters in potato for pooled data of both seasons are presented in Table 5. The pooled analysis of growth parameters in potato genotypes demonstrated significant genetic variation. High genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for traits such as the number of branches per plant at different growth stages (30, 60, and 75 DAP), number of leaves per plant, leaf area, leaf area index, internodal length, and plant spread. These traits also exhibited high heritability (>90%) and high genetic advance as a percentage of the mean (GAM), suggesting a strong influence of additive gene action, making them ideal for direct selection in breeding programs.

Moderate heritability with moderate GAM was recorded for plant height at different growth stages and the number of internodes, indicating a balanced influence of both genetic and environmental factors. Traits like days to flowering and days to physiological maturity showed moderate heritability with low GAM, suggesting a higher contribution of non-additive gene action and environmental influences.

The estimates of mean, range, components of variance, heritability and genetic advance for yield parameters in potato for pooled data of both seasons are presented in Table 6. The mean tuber length was 6.73 cm, with a range of 4.11 to 8.82 cm. The GCV and PCV were 14.81 and 15.08 percent, respectively. Heritability was 97 percent, with a GAM of 29.98 percent. The mean tuber diameter was 5.66 cm, with a range of 3.86 to 7.11 cm. The GCV and PCV were 10.93 and 11.19 percent, respectively, with a heritability of 96 percent and the GAM was 22.01 percent.

Tuber size had a mean of 38.45 cm^2, ranging from 15.89 to 54.84 cm^2, with GCV and PCV values of 22.07 and 22.42 percent, respectively. Heritability was 97 percent, with a GAM of 44.76 percent. The total number of tubers per plant had a mean of 7.15, ranging from 4.2 to 9.5, with GCV and PCV values of 21.51 and 21.64 percent, respectively. Heritability was 99 percent, with a GAM of 44.08 percent. The total number of tubers per plot had a mean of 428.78, ranging from 221.5 to 625, with GCV and PCV values of 24.41 and 24.70 percent, respectively. Heritability was 97 percent and a GAM of 49.71 percent.

The mean grade wise number of tubers per plant <25 g was 1.26, with a range of 0.8 to 2.1. The GCV and PCV of 25.89 and 27.08 percent, respectively, with a heritability of 91 percent and the GAM was 50.83 percent.

The pooled analysis of yield and yield component traits in potato genotypes revealed significant genetic variation. High genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for total tuber yield per plant, marketable tuber yield per plant, number of tubers per plant, and grade-wise tuber numbers (50-75 g category). These traits also exhibited high heritability (>95%) and high genetic advance as a percentage of the mean (GAM), indicating a strong influence of additive gene action, making them ideal for direct selection in breeding programs.

Moderate heritability with moderate GAM was recorded for haulm yield and harvest index, suggesting a balanced influence of both genetic and environmental factors. Traits such as total tuber yield per hectare and marketable tuber yield per hectare showed high heritability but moderate GAM, implying that while selection may be effective, environmental factors also play a role.

The pooled analysis of biochemical parameters in potato genotypes revealed significant genetic variation. High genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for zinc, manganese, iron, total carbohydrates, protein content, and reducing sugar. These traits also exhibited high heritability (>95%) and high genetic advance as a percentage of the mean (GAM), indicating strong additive gene action, making them suitable for direct selection in breeding programs.

Moderate heritability with moderate GAM was recorded for titratable acidity, total sugar, crude fiber, ash content, and chlorophyll b, suggesting a balanced influence of both genetic and environmental factors. Traits such as moisture content, pH, and tuber firmness showed moderate heritability with low GAM, implying a greater contribution of non-additive gene action and environmental effects.

The high heritability coupled with high GAM in key traits highlights their potential for genetic improvement through selection, particularly for enhancing nutritional quality and processing attributes in potato breeding programs.

3.3 Genetic divergence

Forty genotypes of potato were assessed for 18 characters and data obtained was subjected to D^2 statistics to assess the genetic diversity. Eight clusters were constructed using Tocher's method.

3.3.1 Relative contribution of different characters towards divergence

The relative contribution of different characters for genetic divergence is given in table 8. The divergence analysis of potato genotypes revealed that tuber size (22.25%) contributed the most to total genetic divergence, followed by protein content (19.21%) and tuber length (12.45%). Growth traits such as the number of leaves per plant (11.59%) and plant height (4.35%) also played a significant role. Yield-related traits, including tuber yield per plant (4.23%) and per hectare (3.69%), showed moderate contributions. In contrast, traits like days to physiological maturity (0.49%) and percent emergence (0.12%) had minimal influence. These findings indicate that tuber size, protein content, and tuber length are key traits for genetic differentiation and should be prioritized in breeding programs.

3.3.2 Classification of potato genotypes

The 40 potato genotypes were grouped into eight distinct clusters based on Mahalanobis' D^2 statistics (Table 8). Cluster I was the largest, comprising 19 genotypes (C-24, P-16, P-24, P-43, P-45, P-48, P-53, P-62, P-63, P-65, P-69, P-71, P-72, P-73, P-74, P-75, P-77, P-82, P-9), indicating considerable genetic similarity among these genotypes. Cluster II included four genotypes (P-46, P-51, P-54, P-60), while Cluster III contained five (C-15, C-17, P-68, P-78, P-79). Clusters IV, V, and VI comprised four (P-42, P-57, P-67, P-81), two (P-58, P-85), and two (C-20, P-55) genotypes, respectively. Cluster VII included three genotypes (C-13, P-83, RH-2), whereas Cluster VIII was the smallest, with only one genotype (P-64). The observed clustering pattern highlights the genetic diversity among the studied genotypes, providing insights for parental selection in breeding programs.

The average intra-and inter-cluster D^2 values among the eight clusters of potato genotypes are presented in Table 9. The intra-cluster distances ranged from 1179.02 (Cluster V) to 1761.77 (Cluster I), indicating varying levels of genetic homogeneity within clusters. The highest inter-cluster distance was observed between Clusters VI and VIII (14454.85), suggesting maximum genetic divergence, while the lowest was between Clusters I and III (2802.66). Notably, Clusters II and VI (10547.08) and Clusters VII and VIII (11185.25) also exhibited substantial divergence, indicating the potential for heterotic hybridization. The clustering pattern and genetic distances provide valuable insights for selecting diverse parental lines in breeding programs.

3.3.3 Cluster means

The mean performance of different clusters for yield and related traits in potato genotypes is presented in Table 10. Cluster VIII exhibited the highest percent emergence (84.00%), plant height at 75 DAP (77.63 cm), number of leaves per plant (44.70), haulm dry weight (1.10 t/ha), and haulm fresh weight (9.72 t/ha), suggesting superior vegetative growth. Cluster VI recorded the highest average tuber weight (72.11 g), tuber yield per hectare (21.59 t/ha), and tuber yield per plant (432.77 g), highlighting its potential for yield improvement. Cluster V showed the highest total soluble solids (7.97 °Brix), whereas Cluster II exhibited the highest carbohydrate content (19.12 g/100 g FW). Protein content was highest in Cluster III (6.82%), followed by Cluster VIII (6.15%). The substantial variability observed across clusters suggests opportunities for targeted breeding strategies to enhance specific traits, particularly tuber yield, quality parameters, and plant vigor.

4. Discussion

The pooled analysis of variance revealed significant genetic variability for growth, yield, and biochemical traits in potato genotypes, indicating substantial scope for selection and genetic improvement. Growth traits such as percent emergence, plant height, number of branches, number of leaves, and leaf area exhibited highly significant genotypic effects, with minimal G × E interaction, suggesting that these traits are stable across environments and primarily controlled by genetic factors. The stability of these traits makes them reliable selection criteria for breeding programs aiming to enhance plant vigour and productivity. Similar findings have been reported in potato genotypes, where strong genetic control was observed for growth-related traits. For yield-related traits, significant G × E interactions were observed for tuber length, tuber diameter, and tuber size, indicating that these traits are influenced by environmental conditions. However, total tuber yield per plant and plot showed significant genotype and environment effects with no significant G × E interaction, implying stable performance across different environments. These findings are consistent with previous research in potato (Muthoni *et al*., 2015; Maulana *et al*., 2024) [19, 18] and in sweet potato by Gowda *et al*., 2024.

The pooled analysis of growth parameters in potato genotypes revealed substantial genetic variation, as indicated by the significant estimates of variance components. High GCV and PCV were observed for traits such as the number of branches per plant at different growth stages (30, 60, and 75 DAP), number of leaves per plant, leaf area, leaf area index, internodal length, and plant spread. These findings align with previous studies in potato by Tessemma *et al*., 2022; Zeleke *et al*., 2021; Asefa *et al*., 2016) [36, 38, 39, 5].

The high heritability (>95%) and high GAM was observed for traits such as tuber size, number of tubers per plant and marketable tuber yield suggest strong additive genetic control, making them suitable for direct selection. Previous studies have highlighted the importance of selecting genotypes with high heritability and genetic advance to improve tuber yield and quality traits in potato breeding programs (Ramachandra and Srinivasa, 2017 and Singh *et al*., 2024) [21, 31].

Biochemical parameters exhibited strong genotypic influences, with significant G × E interactions observed for total soluble solids, ascorbic acid, ash content, tuber firmness, dry matter, total carbohydrates, iron, color, taste, texture, and overall acceptability. High heritability coupled with high GAM was observed for total carbohydrates, protein content, reducing sugars, and micronutrients such as zinc, manganese, and iron, indicating their suitability for genetic improvement. These findings are consistent with previous reports suggesting that selection for high-nutrient

potato genotypes can be effectively carried out based on genetic variation in biochemical traits. These findings are consistent with previous research in potato (Zhou *et al*., 2015; Das *et al*., 2024; Singh *et al*., 2023) [40, 9, 33].

The results underscore the potential for improving potato genotypes for yield, quality, and stress tolerance through targeted selection. Traits exhibiting high heritability and genetic advance, such as tuber size, number of tubers per plant, and carbohydrate content, can be effectively utilized in breeding programs to develop high-yielding and nutritionally rich genotypes. Furthermore, moderate heritability with moderate GAM for traits such as haulm yield and harvest index suggests the need for recurrent selection or hybridization to improve these traits. The presence of significant G × E interactions for certain traits highlights the importance of multi-environment testing to identify stable genotypes with superior agronomic and biochemical attributes.

The study emphasizes the role of genetic selection in enhancing potato productivity and quality. The identification of high-yielding, nutritionally superior, and environmentally stable genotypes provides valuable insights for breeding programs focused on developing climate-resilient and high-quality potato cultivars.

The genetic divergence analysis revealed grouped potato genotypes into eight distinct clusters. The largest cluster (Cluster I) contained 19 genotypes, indicating a high degree of genetic similarity, while Cluster VIII, with a single genotype, exhibited maximum distinctiveness. The high inter-cluster distances, particularly between Clusters VI and VIII, suggest a strong potential for heterotic hybridization, which could be exploited in breeding programs to enhance yield and quality traits. Previous studies have highlighted the importance of selecting genotypes with more diverse to improve tuber yield and quality traits in potato breeding programs (Zeleke 2021, and Anoumaa *et al*., 2023) [38, 39, 3].

Table 1: List of potato genotypes used in the study and their characteristics

Sl. No.	Genotypes	TS	TSC	TST	TFC	UTS	TED	NET	DTE	TDD
1	P-9	LO	Brown	Smooth	LY	Low	Medium	Im	PA	Absent
2	P-16	SO	Brown	Rough	Cream	Low	Shallow	Im	ED	Absent
3	P-24	SO	Brown	Smooth	LY	Medium	Medium	Few	ED	Absent
4	P-42	Oval	WC	Smooth	White	Medium	Medium	Im	ED	Absent
5	P-43	Round	WC	Smooth	White	Low	Deep	Im	ED	Absent
6	P-45	SO	DP	Smooth	White	Medium	Medium	Im	PA	Absent
7	P-46	Round	Pink	Smooth	LY	Medium	Medium	Im	PA	Absent
8	P-48	SO	Yellow	Smooth	Yellow	Low	Medium	Im	ED	Absent
9	P-51	LO	WC	Smooth	White	Medium	Medium	Im	ED	Absent
10	P-53	Com	Red	Smooth	White	Medium	Deep	Im	PA	Absent
11	P-54	Oval	Brown	Rough	Yellow	Low	Shallow	Im	PA	Absent
12	P-55	SO	WC	Smooth	Cream	Medium	Shallow	Im	PA	Absent
13	P-57	Round	Brown	Rough	Cream	Low	Deep	Im	PA	Absent
14	P-58	Round	Yellow	Smooth	White	Medium	Shallow	Im	PA	Absent
15	P-60	LO	Yellow	Smooth	LY	Medium	VS	Im	ED	Absent
16	P-62	Oval	WC	Smooth	Yellow	Low	Medium	Im	ED	Absent
17	P-63	LO	Pink	Smooth	LY	Medium	Shallow	Im	PA	Absent
18	P-64	Round	Yellow	Smooth	White	Low	DPA	Im	PA	Absent
19	P-65	SO	Pink	Smooth	LY	Medium	Deep	Im	ED	Absent
20	P-67	Round	Yellow	Smooth	Cream	Medium	Medium	Im	ED	Absent
21	P-68	Round	WC	Smooth	White	Medium	Medium	Im	ED	Absent
22	P-69	LO	Brown	Smooth	Cream	Medium	Deep	Im	ED	Absent
23	P-71	Oval	Brown	Smooth	Cream	Medium	Medium	Im	ED	Absent
24	P-72	Round	Brown	Rough	Cream	Medium	Medium	Im	ED	Absent
25	P-73	LO	Pink	Smooth	LY	Medium	Shallow	Im	PA	Absent
26	P-74	SO	WC	Smooth	Cream	Low	Deep	Im	ED	Absent
27	P-75	Oval	WC	Smooth	LY	Low	Medium	Im	PA	Absent
28	P-77	Round	Brown	Rough	LY	Low	Medium	Im	PA	Absent
29	P-78	Round	WC	Smooth	Cream	Medium	Shallow	Im	ED	Absent
30	P-79	Round	WC	Smooth	White	Medium	Shallow	Few	PA	Absent
31	P-81	SO	PB	Rough	DP	Medium	Medium	Im	ED	Absent
32	P-82	Oval	Black	Rough	LP	Medium	Deep	Im	PA	Absent
33	P-83	SO	Brown	Rough	Cream	Low	Shallow	Few	ED	Absent
34	P-85	Round	Yellow	Smooth	White	Low	Medium	Im	ED	Absent
35	RH-2	SO	Brown	Smooth	Yellow	Low	Medium	Im	PA	Absent
36	C-13	SO	WC	Smooth	White	Medium	Shallow	Im	ED	Absent
37	C-15	SO	WC	Smooth	White	Medium	Deep	Im	ED	Absent
38	C-17	SO	Yellow	Smooth	White	Medium	Medium	Im	ED	Absent
39	C-20	Long	Brown	Rough	Yellow	Medium	Medium	Im	PA	Absent
40	C-24	Oval	Brown	Rough	White	Low	Deep	Im	ED	Absent

TS: Tuber shape, TSC Tuber skin colour, TST: Tuber skin texture, TFC: Tuber flesh colour, UTS: Uniformity of tuber size, TED: Tuber eye depth, NET: Number of eyes per tuber, DTE: Distribution of tuber eyes, TDD: Tuber defects and disorders LO: Long oval, SO: Short oval, WC: White cream, PB: Purple black, LY: Light yellow, Dp: Dark purple, VS: Very shallow, DPA: Deep predominantly aside, Im: Intermediate, PA: Predominantly apical, ED: Evenly distributed,

Table 2: Pooled analysis of variance (mean sum of squares) for growth parameters in potato.

Sl. No.	Source of variation/Characters	ENV	REP(ENV)	GEN	GEN:ENV	Residuals	CV (%)	OV mean
	Df	1	2	39	39	78		
1	Per cent emergence	22.49*	20.41*	135.67**	9.16ns	7.06	3.4	78.16
2	Plant height at 30 DAP (cm)	56.69**	14.37**	63.45**	0.59ns	2.79	5.65	29.56
3	Plant height at 60 DAP (cm)	118.78**	13.59*	370.13**	2.96ns	3.28	3.14	57.66
4	Plant height at 75 DAP (cm)	64.19**	13.93*	363.17**	2.61ns	3.16	2.83	62.84
5	Number of branches per plant at 30 DAP	0.21**	0.02ns	0.89**	0.04*	0.02	7.37	2.00
6	Number of branches per plant at 60 DAP	1.89**	0.03ns	3.80**	0.03ns	0.05	5.06	4.25
7	Number of branches per plant at 75 DAP	0.87**	0.15ns	5.43**	0.05ns	0.06	5.04	4.96
8	Number of leaves per plant at 30 DAP	32.76**	4.46*	37.43**	057ns	1.41	7.27	16.32
9	Number of leaves per plant at 60 DAP	48.18**	5.54*	103.71**	0.46ns	2.50	5.06	31.22
10	Number of leaves per plant at 75 DAP	58.80**	8.21*	126.44**	0.36ns	2561	4.38	36.56
11	Leaf area at 30 DAP (cm^2)	3623**	474*	4531**	63ns	155	7.26	171.51
12	Leaf area at 60 DAP (cm^2)	5294.6**	604.2ns	12654.9**	48.5ns	282.4	5.12	327.99
13	Leaf area at 75 DAP (cm^2)	6471.9**	881.6*	15927.6**	38.7ns	283.2	4.38	384.09
14	Leaf area index at 30 DAP	0.003**	0.003*	0.003**	0.004ns	0.008	7.26	0.14
15	Leaf area index at 60 DAP	0.004**	0.004ns	0.009**	0.003ns	0.002	5.12	0.27
16	Leaf area index at 75 DAP	0.005**	0.006*	0.01**	0.002ns	0.003	4.38	0.32
17	Number of internodes	94.86**	11**	133.03**	3.78**	0.92	3.46	27.69
18	Internodal length (cm)	0.14**	0.03*	4.345**	0.01*	0.01	2.60	3.87
19	Days to flowering	4.10*	3.93ns	23.50**	0.55ns	4.28	4.55	45.44
20	Days to physiological maturity	30.98*	10.68ns	49.41**	3.73ns	4.59	2.26	94.98
21	Plant spread (cm^2)	185536**	9375ns	1606338**	2049ns	12531	4.47	2501.55

*: Significant at 5 percent level (p = 0.05), **: Significant at 1 percent level (p = 0.01), DAP: days after planting, ENV: Environment, REP: Replication, GEN: Genotype, ns: non-significant, Df: Degrees of freedom, OV mean: Overall mean, CV: Coefficient of variation

Table 3: Pooled analysis of variance (mean sum of squares) for yield and yield component characters in potato

Sl. No.	Source of variation/Characters	ENV	REP(ENV)	GEN	GEN:ENV	Residuals	CV (%)	OV mean
	Df	1	2	39	39	78		
1	Tuber length (cm)	0.081**	0.036*	4.05**	0.072**	0.009	1.44	6.73
2	Tuber diameter (cm)	0.048**	0.003ns	1.58**	0.04**	0.001	0.59	5.66
3	Tuber size (cm^2)	7.63**	1.55ns	294.67**	4.89**	0.36	1.55	38.43
4	Total number of tubers per plant	10.06**	3.82**	9.56**	0.05ns	0.13	4.98	7.15
5	Total number of tubers per plot	43659**	9044**	44356**	519*	298	4.03	428.78
6	Grade wise number per plant <25 g	0.012ns	0.17**	0.45**	0.02ns	0.034	14.55	1.26
7	Grade wise number per plant 25-50 g	0.072ns	0.18**	0.47**	0.009ns	0.033	12.93	1.41
8	Grade wise number per plant 50-75 g	0.46**	0.26**	1.15**	0.016ns	0.024	8.04	1.94
9	Grade wise number per plant >75 g	0.09ns	0.38**	1.51**	0.016ns	0.04	7.86	2.54
10	Grade wise number per plot <25 g	697.2**	333.1**	1783.8**	40ns	44.5	8.87	75.21
11	Grade wise number per plot 25-50 g	1677**	366.5**	1955.5**	29.7ns	42.8	7.75	84.46
12	Grade wise number per plot 50-75 g	5417.3**	682.7**	5165.2**	82.2ns	62.2	6.75	116.94
13	Grade wise number per plot >75 g	4622.5**	1047.2**	6630.1**	76.6ns	131.1	7.53	152.16
14	Grade wise weight of tuber per plant <25 g	48.36**	17.96**	190.58**	3.81ns	3.01	6.89	25.19
15	Grade wise weight of tuber per plant 25-50 g	288.9**	30.3ns	649.7**	13.8ns	30.7	11.45	48.39
16	Grade wise weight of tuber per plant 50-75 g	1737.9**	598.8**	2754.4**	70.1ns	54.7	7.87	93.98
17	Grade wise weight of tuber per plant >75 g	747**	1105**	8057**	165*	86	5.44	170.48
18	Grade wise weight of tuber per plot <25 g	0.19**	0.14**	0.73**	0.03**	0.01	7.20	1.48
19	Grade wise weight of tuber per plot 25-50 g	1.26**	0.34**	1.45**	0.12**	0.04	8.80	2.38
20	Grade wise weight of tuber per plot 50-75 g	3.40**	0.54**	4.80**	0.16**	0.05	5.85	4.07
21	Grade wise weight of tuber per plot >75 g	5.40**	1.43**	7.44**	0.40*	0.22	6.06	7.72
22	Marketable tuber yield per plant (g)	7219**	3102**	22750**	242ns	152	3.94	312.77
23	Marketable tuber yield per plot (kg)	10.86**	5.96**	27.88**	0.49ns	0.44	4.70	14.15
24	Unmarketable tuber yield per plant (g)	48.36**	17.96**	190.58**	3.81ns	3.01	6.89	25.19
25	Unmarketable tuber yield per plot (kg)	0.03ns	0.16**	0.78**	0.0007ns	0.01	6.66	1.50
26	Total tuber yield per plant (g)	8449**	3592**	25858**	242ns	161	3.75	337.95
27	Total tuber yield per plot (kg)	12.07**	8.06**	34.97**	0.50ns	0.44	4.25	15.65
28	Average weight of the tubers (g)	488.60**	42.53**	715.78**	8.98**	2.12	2.58	56.51
29	Tuber yield per meter square (kg)	0.15**	0.08**	0.43**	0.006ns	0.008	5.42	1.74
30	Tuber yield per hectare (t)	14.90**	8.17**	43.17**	0.62ns	0.89	5.42	17.39
31	Haulm yield on fresh weight basis (t/ha)	1.38**	0.41**	2.67**	0.06**	0.01	1.39	7.51
32	Haulm yield on dry weight basis (t/ha)	0.04**	0.017**	0.06**	0.001ns	0.002	6.14	0.78
33	Harvest index	1.11ns	2.35ns	33.08**	1.60ns	1.35	1.67	69.49

*: Significant at 5 percent level (p = 0.05), **: Significant at 1 percent level (p = 0.01), ENV: Environment, REP: Replication, GEN: Genotype, ns: non-significant, OV mean: Overall mean

Table 3: Pooled analysis of variance (mean sum of squares) for biochemical parameters in potato

Sl. No.	Source of variation/Characters	ENV	REP(ENV)	GEN	GEN:ENV	Residuals	CV (%)	OV mean
	Df	1	2	39	39	78		
1	Moisture (%)	3.16ns	8.22ns	33.58**	1.62ns	5.92	3.03	80.44
2	pH	0.013ns	0.0201ns	0.2289**	0.0108ns	0.0147	1.96	6.17
3	Total soluble solids (°Brix)	0.0023ns	0.0006ns	5.87**	0.083**	0.013	2.27	5.06
4	Specific gravity (g/cm^3)	0.006*	0.0012ns	0.011**	0.002ns	0.0016	3.71	1.08
5	Protein content (%)	0.86**	0.009ns	12.01**	0.0348ns	0.099	8.08	3.91
6	Ascorbic acid (mg/100g fresh weight)	3.78**	0.143ns	9.499**	0.676**	0.124	4.26	8.26
7	Titratable acidity (%)	0.003ns	0.0011ns	0.0099**	0.0009ns	0.00086	9.413	0.312
8	Total sugar (%)	0.008ns	0.0016ns	0.0184**	0.00107ns	0.00157	6.50	0.61
9	Reducing sugar (%)	0.003ns	0.0033*	0.020**	0.00082ns	0.00095	9.291	0.333
10	Non reducing sugar (%)	0.009ns	0.007ns	0.00098*	0.00039ns	0.0011	12.081	0.277
11	Crude fibre (%)	0.004ns	0.0056ns	0.206**	0.0039ns	0.00415	3.78	1.71
12	Ash content (%)	0.0015ns	0.0069ns	0.472**	0.04.**	0.016	4.078	0.988
13	Total fat (%)	0.002ns	0.001ns	0.0088**	0.0064ns	0.0049	10.281	0.216
14	Tuber firmness (kg/cm^2)	0.16ns	0.14ns	0.64**	0.167*	0.089	3.43	8.72
15	Dry matter (%)	0.13ns	1.60ns	23.32**	2.86**	0.80	4.59	19.48
16	Total carbohydrates (g/100g fresh weight)	17.86**	0.124ns	69.62**	0.679**	0.279	4.28	12.33
17	Copper (ppm)	1.72*	0.07ns	5.26**	0.29ns	0.31	7.20	7.78
18	Zinc (ppm)	2.02ns	0.017ns	283.8**	0.78ns	0.90	7.20	13.21
19	Manganese (ppm)	1.81*	0.07ns	57.73**	0.537ns	0.322	7.56	7.50
20	Iron (ppm)	3.65ns	18.38ns	5329.9**	67.49**	24.55	5.04	98.40
21	Colour	0.10ns	0.09ns	1.33**	0.20**	0.09	4.37	7.08
22	Taste	0.68**	0.02ns	1.44**	0.14**	0.06	3.86	6.41
23	Flavour	0.23ns	0.03ns	1.69**	0.08ns	0.07	4.15	6.44
24	Texture	0.04ns	0.02ns	2.02**	0.09**	0.02	2.32	6.67
25	Overall acceptability	0.43**	0.05ns	2.77**	0.19**	0.03	2.62	6.60
26	Browning reaction	0.007*	0.006ns	0.007**	0.004ns	0.0011	10.907	0.316
27	Skin colour L values	10.60**	2.32ns	166.12**	4.56**	0.82	1.61	56.31
28	Skin colour a values	1.23**	0.34ns	68.33**	0.26*	0.13	4.97	7.37
29	Skin colour b values	7.85ns	2.41ns	159.46**	1.63ns	2.55	7.36	21.69
30	Flesh colour L values	6.32ns	14.06ns	325.27**	8.47ns	13.82	5.47	67.97
31	Flesh colour a values	0.24ns	0.05ns	36.30**	0.09ns	0.08	-14.0	-1.98
32	Flesh colour b values	3.97ns	2.23ns	363.47**	2.21ns	2.91	8.45	20.20
33	Chlorophyll ‘a’ (mg/g)	0.002ns	0.002ns	0.03**	0.001ns	0.003	6.84	0.82
34	Chlorophyll ‘b’ (mg/g)	0.003ns	0.001ns	0.01**	0.001ns	0.001	10.41	0.37
35	Total chlorophyll (mg/g)	0.01ns	0.003ns	0.05**	0.001ns	0.004	5.69	1.20

*: Significant at 5 percent level (p = 0.05), **: Significant at 1 percent level (p = 0.01), ENV: Environment, REP: Replication, GEN: Genotype, ns: non-significant, CV: Coefficient of variation, OV mean: Overall mean

Table 4: Estimate of mean, range, components of variance, heritability and genetic advance for growth parameters in potato genotypes (Pooled data of both seasons)

Sl. No	Characters	Mean±S.Em	Range	GCV (%)	PCV (%)	h^2 (%)	GA	GAM (%)
1	Percent emergence	78.16±1.51	70.67-93.33	7.20	7.7	87.30	10.82	13.84
2	Plant height at 30 DAP (cm)	28.72±0.46	23.54-37.53	12.94	13.13	97.00	7.54	26.27
3	Plant height at 60 DAP (cm)	57.66±0.86	39.25-78.00	16.61	16.75	98.00	19.58	33.95
4	Plant height at 75 DAP (cm^2)	62.84±0.81	45.34-83.05	15.10	15.22	98.00	19.42	30.90
5	Number of branches per plant at 30 DAP	2.00±0.09	1.0-3.0	23.11	24.07	92.00	0.91	45.77
6	Number of branches per plant at 60 DAP	4.25±0.08	1.7-5.5	22.81	22.98	98.00	1.98	46.63
7	Number of branches per plant at 75 DAP	4.96±0.11	1.8-6.4	23.35	23.56	98.00	2.36	47.67
8	Number of leaves per plant at 30 DAP	16.32±0.37	10.3-24.20	18.60	18.90	97.00	6.16	37.73
9	Number of leaves per plant at 60 DAP	31.22±0.34	21.4-40.30	16.27	16.35	99.00	10.42	33.67
10	Number of leaves per plant at 75 DAP	36.56±0.30	25.5-47.7	15.35	15.40	99.00	11.53	31.54
11	Leaf area at 30 DAP (cm^2)	1372.07±31.75	844.00-2046.00	19.49	19.76	97.00	543.21	39.60
12	Leaf area at 60 DAP (cm^2)	3279.88±34.83	2200.00-4389.00	17.12	17.18	99.00	1152.04	35.12
13	Leaf area at 75 DAP (cm^2)	3840.90±31.09	2615.0-5164.50	16.41	16.45	99.00	1295.1	33.72
14	Leaf area index at 30 DAP	1.14±0.03	0.70-1.71	19.49	19.76	97.00	0.45	39.60
15	Leaf area index at 60 DAP	2.73±0.03	1.83-3.66	17.12	17.18	99.00	0.96	35.12
16	Leaf area index at 75 DAP	3.20±0.03	2.18-4.30	16.41	16.45	99.00	1.08	33.72
17	Number of internodes	27.69±0.97	12.4-40.80	20.53	21.12	95.00	11.39	41.11
18	Internodal length (cm)	3.87±0.06	2.11-7.39	26.89	26.99	99.00	2.14	55.22
19	Days to flowering	45.44±0.37	40.50-50.50	5.27	5.39	95.00	4.82	10.61
20	Days to physiological maturity	94.99±0.97	83.5-100.5	3.56	3.84	86.00	6.46	6.80
21	Plant spread (cm^2)	2501.55±22.63	1086.11-3673.4	25.32	25.35	99.00	13.02	52.06

GCV: Genotypic co-efficient of variation, h^2: Heritability (broad sense), PCV: Phenotypic co-efficient of variation, DAP: Days after planting, GA: Genetic advance, GAM: Genetic advance over percent mean

Table 5: Estimate of mean, range, components of variance, heritability and genetic advance for yield and yield component characters of potato genotypes (Pooled data of both seasons)

Sl. No	Characters	Mean±S.Em	Range	GCV (%)	PCV (%)	h^2 (%)	GA	GAM (%)
1	Tuber length (cm)	6.73±0.13	4.11-8.82	14.81	15.08	97.00	2.02	29.98
2	Tuber diameter (cm)	5.66±0.09	3.86-7.11	10.93	11.19	96.00	1.25	22.01
3	Tuber size (cm^2)	38.45±1.08	15.89-54.84	22.07	22.42	97.00	17.21	44.76
4	Total number of tubers per plant	7.15±0.12	4.2-9.5	21.51	21.64	99.00	3.15	44.08
5	Total number of tubers per plot	428.78±17.45	221.5-625	24.41	24.70	97.00	213.17	49.71
6	Grade wise number of tubers per plant <25 g	1.26±0.10	0.8-2.1	25.89	27.08	91.00	0.64	50.83
7	Grade wise number of tubers per plant 25-50 g	1.41±0.05	0.80-2.1	24.13	24.65	96.00	0.69	48.62
8	Grade wise number of tubers per plant 50-75 g	1.94±0.06	1.0-3.0	27.35	27.74	97.00	1.07	55.6
9	Grade wise number of tubers per plant >75 g	2.53±0.06	1.4-3.8	24.13	24.39	98.00	1.24	49.23
10	Grade wise number of tubers per plot <25 g	75.21±3.16	43.0-126.0	27.76	28.39	95.00	42.05	55.91
11	Grade wise number of tubers per plot 25-50 g	84.46±2.73	44.0-134.0	25.97	26.37	97.00	44.51	52.70
12	Grade wise number of tubers per plot 50-75 g	116.94±4.53	53.0-187.5	30.48	30.97	96.00	72.29	61.82
13	Grade wise number of tubers per plot >75 g	152.16±4.37	74.0-230.0	26.60	26.91	97.00	82.41	54.16
14	Grade wise weight of tubers per plant <25 g	25.18±0.98	14.4-41.85	27.13	27.68	96.00	13.80	54.80
15	Grade wise weight of tubers per plant 25-50 g	48. 39±1.86	26.45-80.40	26.05	26.61	95.00	25.41	52.52
16	Grade wise weight of tubers per plant 50-75 g	93.97±4.18	48.7-147.25	27.56	28.27	95.00	52.00	55.33
17	Grade wise weight of tubers per plant >75 g	170.48±6.42	67.35-241.85	26.05	26.59	96.00	89.65	52.59
18	Grade wise weight of tuber per plot <25 g	1.48±0.08	0.82-2.42	28.25	29.35	93.00	0.83	56.09
19	Grade wise weight of tuber per plot 25-50 g	2.39±0.16	1.19-4.26	23.42	25.32	86.00	1.07	44.73
20	Grade wise weight of tuber per plot 50-75 g	4.07±0.20	1.77-5.86	26.43	27.34	94.00	2.14	52.67
21	Grade wise weight of tuber per plot >75 g	7.72±0.32	4.42-11.76	17.17	18.12	90.00	2.58	33.52
22	Marketable tuber yield per plant (g)	312.84±7.77	155.73-424.3	23.97	24.23	98.00	152.88	48.86
23	Marketable tuber yield per plot (kg)	14.18±0.34	9.45-20.09	18.52	18.83	97.00	5.32	37.55
24	Unmarketable tuber yield per plant (g)	25.18±0.98	14.4-41.85	27.13	27.68	96.00	13.80	54.79
25	Unmarketable tuber yield per plot (kg)	1.48±0.08	0.82-2.42	28.25	29.35	93.00	0.83	56.09
26	Total tuber yield per plant (g)	338.03±7.77	174.31-449.8	22.25	29.79	98.00	163.22	48.28
27	Total tuber yield per plot (kg)	15.66±0.35	10.75-21.54	18.66	18.92	97.00	5.93	37.89
28	Average weight of the tubers (g)	56.01±1.49	32.5-80.60	22.30	22.61	97.00	25.36	45.27
29	Tuber yield per meter square (kg)	1.74±0.04	1.19-2.39	18.61	18.87	97.00	0.66	37.90
30	Tuber yield per hectare (t)	17.40±0.39	11.94-23.93	18.66	18.93	97.00	6.59	37.90
31	Haulm yield on fresh weight basis (kg/ha)	7.50±0.13	5.86-9.80	10.74	10.99	95.00	1.62	21.59
32	Haulm yield on dry weight basis (kg/ha)	0.78±0.01	0.6-1.16	15.17	15.27	99.00	0.25	31.41
33	Harvest index (%)	69.63±0.60	61.55-75.52	4.56	4.72	93.00	6.32	9.07

GCV: Genotypic co-efficient of variation, h^2: Heritability (broad sense), PCV: Phenotypic co-efficient of variation, DAP: Days after planting, GA: Genetic advance, GAM: Genetic advance over percent mean

Table 6: Estimate of mean, range, components of variance, heritability and genetic advance for biochemical parameters in potato genotypes (Pooled data of both seasons)

Sl. No	Characters	Mean ± S.Em	Range	GCV (%)	PCV (%)	h^2 (%)	GA	GAM (%)
1	Moisture (%)	80.44±0.63	76.31-86.95	3.51	3.69	91.00	5.55	6.89
2	pH	6.17±0.05	5.72-7.19	3.79	3.97	91.00	0.46	7.43
3	Total soluble solids (°Brix)	5.06±0.14	3.4-10.2	23.77	24.11	97.00	2.44	48.26
4	Specific gravity(g/cm^3)	1.08±0.02	0.98-1.25	4.13	5.06	78.00	0.09	8.13
5	Protein content (%)	3.91±0.09	1.27-7.9	44.26	44.39	99.00	3.55	90.89
6	Ascorbic acid (mg/100g fresh weight)	8.26±0.41	6.15-12.42	17.98	19.31	87.00	2.85	34.48
7	Titratable acidity (%)	0.31±0.01	0.21-0.42	14.33	17.56	75.00	0.09	27.24
8	Total sugar (%)	0.61±0.01	0.43-0.74	10.37	11.59	87.00	0.13	20.82
9	Reducing sugar (%)	0.33±0.01	0.2-0.48	21.13	21.23	97.00	0.14	42.34
10	Non reducing sugar (%)	0.28±0.01	0.18-0.37	16.14	19.77	78.00	0.09	31.77
11	Crude fiber (%)	1.71±0.03	1.3-2.12	13.24	13.49	96.00	0.45	26.61
12	Ash content (%)	0.99±0.03	0.74-1.18	10.60	11.53	82.00	0.19	19.41
13	Total fat (%)	0.22±0.001	0.15-0.34	20.70	20.70	99.00	0.09	43.52
14	Tuber firmness (kg/cm2)	8.72±0.20	7.57-9.67	3.94	5.16	59.00	0.54	6.23
15	Dry matter (%)	19.48±0.84	12.88-23.25	11.61	13.13	78.00	4.12	21.13
16	Total carbohydrates (g/100g fresh weight)	12.33±0.41	7.14-23.55	33.67	34.001	98.00	8.47	68.71
17	Copper (ppm)	7.78±0.27	5.0-11.26	14.32	15.16	89.00	2.17	27.89
18	Zinc (ppm)	13.21±0.44	0.49-34.4	63.69	63.86	99.00	17.27	130.77
19	Manganese (ppm)	7.50±0.36	0.95-24.67	50.42	50.89	98.00	7.72	102.95
20	Iron (ppm)	98.4±4.10	44.25-208.33	36.86	37.33	98.00	73.78	74.98
21	Colour	7.08±0.23	6.00-8.00	7.49	8.76	73.00	0.93	13.19
22	Taste	6.41±0.19	5.00-7.50	8.88	9.85	81.00	1.06	16.50
23	Flavour	6.44±0.15	6.00-8.00	9.82	10.35	90.00	1.24	19.21
24	Texture	6.67±0.15	5.00-8.00	10.43	10.91	91.00	1.37	20.53
25	Overall acceptability	6.60±0.22	4.00-8.00	12.15	13.06	86.00	1.54	23.28
26	Browning reaction	0.32±0.01	0.21-0.41	14.15	14.15	92.5	0.09	26.89
27	Skin colour L values	56.31±1.07	36.75-67.65	11.29	11.60	94.00	12.74	22.62
28	Skin colour a values	7.37±0.25	1.55-19.55	55.98	56.19	99.00	8.47	114.89
29	Skin colour b values	21.69±0.64	1.35-31.25	28.96	29.26	97.00	12.81	59.06
30	Flesh colour L values	67.97±1.45	26.25-80.40	13.09	13.44	94.00	17.86	26.28
31	Flesh colour a values	-1.98±0.15	-4.35-10.75	-151.87	-152.23	99.00	6.18	-312.05
32	Flesh colour b values	20.30±0.74	-9.30-35.20	47.05	47.34	98.00	19.46	96.34
33	Chlorophyll a (mg/g)	0.80±0.02	0.70-1.00	9.77	10.20	91.00	0.16	19.26
34	Chlorophyll b (mg/g)	0.37±0.02	0.25-0.45	13.65	15.09	82.00	0.09	25.45
35	Total chlorophyll (mg/g)	1.20±0.02	0.99-1.42	9.43	9.66	95.00	0.23	18.97

GCV: Genotypic co-efficient of variation, h^2: Heritability (broad sense), PCV: Phenotypic co-efficient of variation, DAP: Days after planting, GA: Genetic advance, GAM: Genetic advance over percent mean

Table 7: percent contribution of seventeen characters towards total divergence in potato genotypes

Sl. No.	Traits	Proportion	Cumulative proportion
1	Tuber size (cm^2)	22.25	22.25
2	Protein content (%)	19.21	41.47
3	Tuber length (cm)	12.45	53.92
4	Number of leaves per plant at 75 DAP	11.59	65.50
5	Total carbohydrates (g/100g of fresh weight)	4.75	70.25
6	Plant height at 75 DAP (cm)	4.35	74.61
7	Tuber yield per plant (g)	4.23	78.84
8	Tuber yield per hectare (t)	3.69	82.52
9	Number of branches per plant at 75 DAP	3.58	86.11
10	Tuber diameter (cm)	3.28	89.38
11	Total soluble solids (^{0}Brix)	2.28	91.67
12	Haulm yield on fresh weight basis (t/ha)	2.16	93.83
13	Days to flowering	2.01	95.84
14	Average weight of tuber (g)	1.94	97.77
15	Number of tubers per plant	1.06	98.84
16	Haulm yield on dry weight basis (t/ha)	0.55	99.39
17	Days to physiological maturity	0.49	99.88
18	Per cent emergence	0.12	100.00

Table 8: Classification of potato genotypes into different clusters based on D^2 statistics

Cluster	Number of genotypes	Genotypes included in the cluster
I	19	C-24, P-16, P-24, P-43, P-45, P-48, P-53, P-62, P-63, P-65, P-69, P-71, P-72, P-73, P-74, P-75, P-77, P-82, P-9
II	4	P-46, P-51, P-54, P-60
III	5	C-15, C-17, P-68, P-78, P-79
IV	4	P-42, P-57, P-67, P-81
V	2	P-58, P-85
VI	2	C-20, P-55
VII	3	C-13, P-83, RH-2
VIII	1	P-64

Table 9: Average intra-cluster (diagonal) and inter-cluster D^2 value in potato genotypes

Clusters	I	II	III	IV	V	VI	VII	VIII
I	1761.77	3539.43	2802.66	3674.92	3980.84	4429.36	3184.53	5923.25
II		1596.69	5881.99	7142.65	4527.37	10547.08	6678.79	3861.76
III			1674.25	3337.98	4810.42	4237.92	5339.20	5330.35
IV				1474.99	3132.73	3212.39	5361.24	9354.49
V					1179.02	7343.67	6825.87	6277.33
VI						1566.09	3616.56	14454.85
VII							2096.92	11185.25
VIII								0.00

Table 10: Cluster mean values for yield and its components in potato genotypes

Sl. No.	Character	Cluster mean							
		I	II	III	IV	V	VI	VII	VIII
1	PE	81.75	76.17	74.92	75.67	80.67	82.33	76.75	84.00
2	PH 75DAP	71.60	66.81	60.86	51.68	52.31	71.31	60.83	77.63
3	NOB 75DAP	2.95	5.70	5.30	3.90	6.00	4.82	5.16	6.23
4	NOL 75DAP	31.34	35.20	35.65	28.03	32.20	44.41	37.08	44.70
5	DTF	44.75	48.50	43.94	43.88	44.83	46.40	45.79	41.75
6	DTPM	93.50	98.38	98.00	96.25	94.83	93.60	94.93	88.00
7	TL	7.62	8.01	5.49	5.71	6.27	7.62	6.67	5.65
8	TD	5.69	6.41	4.71	6.14	5.31	6.01	5.70	5.50
9	TS	43.78	51.26	26.19	34.91	33.18	45.71	38.16	31.02
10	NOTPL	8.65	8.48	5.16	8.33	6.75	8.98	6.50	8.60
11	AWT	61.65	60.15	54.18	55.60	51.30	72.11	50.92	63.60
12	YHA	21.37	18.99	13.39	18.57	17.00	21.59	15.88	21.28
13	HFW	8.06	7.80	6.69	7.83	7.17	8.61	7.15	9.72
14	DHY	0.85	0.77	0.70	0.76	0.76	0.97	0.72	1.10
15	TSS	4.50	5.35	4.75	4.75	7.97	4.50	4.93	5.30
16	CHO	13.23	19.12	9.22	10.09	16.67	15.04	11.17	7.55
17	PR	3.78	2.28	6.82	5.53	2.01	3.33	3.66	6.15
18	YPP	413.97	397.51	226.99	403.64	318.15	432.77	307.42	395.93

PE: Percent emergence, PH 75DAP: Plant height at 75 DAP (cm), NOB 75DAP: Number of branches per plant at 75 DAP, NOL 75DAP: Number of leaves per plant at 75 DAP, DTF: Days to flowering, DTPM: Days to physiological maturity, TL: Tuber length (cm), TD: Tuber diameter (cm), TS: Tuber size (cm^2), NOTPL: Number of tubers per plant, AWT: Average weight of tuber (g), YHA: Tuber yield per hectare(t), HFW: Haulm yield on fresh weight basis (t/ha), DHY: Haulm yield on dry weight basis (t/ha), TSS: Total soluble solids (^{0}Brix), CHO: Carbohydrates (g/100g of fresh weight), PR: Protein content (%), YPP: Tuber yield per plant (g), DAP: Days after planting

The relative contribution of traits to genetic divergence highlighted tuber size, protein content, and tuber length as the most influential, suggesting that these traits play a key role in genetic differentiation. This aligns with previous studies that emphasize tuber-related traits as major contributors to variability in potato breeding populations. Growth parameters such as the number of leaves per plant and plant height also contributed significantly, underscoring their role in genetic diversity. The cluster mean analysis revealed significant trait variation, with Cluster VIII exhibiting superior vegetative growth, Cluster VI excelling in tuber yield, and Cluster V displaying the highest total soluble solids. These findings suggest that different clusters harbor unique trait advantages, which can be strategically utilized for trait-specific breeding. The presence of high-yielding genotypes in diverse clusters highlights the potential for selecting genetically distant parents to develop superior hybrids with improved yield and quality attributes. These findings are consistent with previous research in potato (Hossain *et al*., 2023; Prabha *et al*., 2019) [15, 20].

The study underscores the importance of genetic divergence analysis in guiding parental selection for breeding programs. The identification of highly diverse genotypes offers opportunities for hybridization to develop improved potato varieties with enhanced productivity, nutritional quality, and stress resilience.

5. Conclusion

The study revealed significant genetic variability among potato genotypes for growth, yield, and biochemical traits, with stable genotypic effects observed for growth traits, making them reliable for selection. High heritability and

genetic advance for yield-related traits such as tuber size, number of tubers per plant, and marketable tuber yield suggest strong additive genetic control, making them suitable for direct selection. Genetic divergence analysis grouped the genotypes into eight clusters, with tuber size, protein content, and tuber length contributing most to divergence, highlighting their importance in genetic differentiation. High inter-cluster distances, particularly between Clusters VI and VIII, indicate the potential for heterotic hybridization to enhance yield and quality traits. Cluster mean analysis identified clusters with superior vegetative growth, yield potential, and quality attributes, providing insights for parental selection. These findings underscore the importance of multi-trait selection and genetic divergence analysis in potato breeding programs, facilitating the development of high-yielding, nutritionally rich, and climate-resilient cultivars. Future research should focus on integrating molecular and genomic approaches to accelerate genetic improvement and ensure sustainable potato production.

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7. Credit authorship contribution statement
K. Hanume Gowda: Methodology, Conceptualization, Investigation, Writing-original draft, Data curation, Formal analysis, Software, H. Amarananjundeswara: Conceptualization, Investigation, Resources, Supervision, B. Fakrudin: Methodology, Resources, Supervision, K.R. Vasudeva: Methodology, Conceptualization, Supervision, Resources, J. Kattegoudar: Supervision, Resources, Review & editing, B. Doddabasappa: Supervision, Resources, Review & editing.

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9. Declaration of interest statement
The authors declare that there is no conflict of interest regarding the publication of this manuscript.

10. Availability of data and materials
The datasets underpinning the findings presented in this article are accessible upon request.

11. Authors' contributions
KHG has designed the experiment, performed the experiments, carried out statistical analysis and wrote the manuscript. HA, BF, KRV, BD and JK have assisted in methodology, conceptualization, supervision, resources, validation, review and editing. All authors have read and approved the manuscript for publication.

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