



RESEARCH ARTICLE

# Characterisation and evaluation of *Solanum andigena* genotypes for yield, maturity and processing quality under the Indo-Gangetic Plain

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## Abstract

Analysis of the relationships between yield and its component characters provides valuable insights for formulating effective selection strategies, thereby increasing the efficiency of crop improvement programs. An investigation involving 18 potato (*Solanum andigena*) genotypes was undertaken to assess the relationships among eight morphological and four biochemical traits to quantify their direct and indirect contributions to tuber yield in potato. The present study was conducted at the Potato Research Farm, Tirhut College of Agriculture, Dholi, Bihar, during the rabi seasons of 2023 and 2024. The pooled data across two crop seasons were subjected to analysis of variance (ANOVA), which revealed significant variation among the studied traits. The correlation coefficient analyses demonstrated that tuber weight per plant, the principal yield attribute, exhibited strong and positive associations with number of tubers per plant ( $r_g = 0.517^{**}$ ), tuber dry matter content ( $r_g = 0.513^{**}$ ), number of compound leaves ( $r_g = 0.4448^{**}$ ), plant height ( $r_g = 0.5867^{**}$ ) and plant emergence ( $r_g = 0.4058^{**}$ ), thereby confirming their critical role in yield determination under Indo-Gangetic Plain conditions. Path analysis further revealed that number of tubers per plant and number of compound leaves exerted the highest positive direct effects on tuber weight per plant, along with substantial favourable indirect effects via plant height, tuber dry matter and plant emergence, indicating their importance in yield enhancement in potato. Diversity analysis identified seven clusters where Cluster III genotypes JEXA75, JEXA456, JEXA52, JEXA132, JEXA805, Kufri Girdhari, Kufri Jyoti represent promising parental material for breeding programs aimed at enhancing productivity and processing traits. Cluster V genotypes JEXA30, JEXA1181 used for early maturing varieties breeding program.

**Keywords:** correlation analysis; diversity analysis; path coefficient analysis; potato processing quality; *Solanum andigena*; yield components

## Introduction

Potato (*Solanum andigena*), often referred to as the "King of Vegetables," is the world's most important non-cereal food crop, playing a pivotal role in global food and nutritional security (1). *Solanum andigena* is an important cultivate potato taxon belonging to the family Solanaceae and represents one of the primary Andean potato groups. It originated in the high-altitude regions of the Andes, particularly in Peru, Bolivia and Ecuador, where it has been traditionally cultivated under cool tropical environments (2). *Solanum andigena* is referred to as the Andigenum group of

cultivated potato (*Solanum tuberosum* L.), characterised by substantial genetic and phenotypic diversity. In the present study, the term Andigenum group is therefore used to reflect its current taxonomic treatment and to distinguish it from the Tuberosum group of cultivated potato. *Solanum andigena* exhibits a high degree of genetic diversity, reflecting long-term farmer selection and adaptation to heterogeneous agro-ecological conditions (3).

*Solanum andigena* is characterised by its strong short-day photoperiod sensitivity for tuberisation, which restricts its direct cultivation in long-day temperate regions (4). From a breeding

standpoint, *S. andigena* represents an important genetic reservoir, possessing natural resistance to a wide range of biotic stresses and tolerance to abiotic stresses such as cold temperatures and nutrient-poor or marginal soils (5). Consequently, *S. andigena* has been extensively used in pre-breeding and introgression programs aimed at broadening the genetic base of cultivated potato and improving yield stability (6). Owing to its favourable agronomic and adaptive traits, *S. andigena* continues to be an indispensable genetic resource for potato improvement, particularly in the Indo-Gangetic Plain, where potato constitutes a high-calorie staple food and an essential source of livelihood for smallholder farming communities (7). However, achieving sustainable yield increases in this region is increasingly challenging due to fluctuating environmental conditions, shrinking natural resources and the complex polygenic nature of tuberyield (8).

Yield is a complex quantitative trait influenced by multiple morpho-physiological and biochemical characters and their interaction with the environment. Although several studies have investigated correlation, path coefficient and genetic diversity in *S. tuberosum*, information on these relationships but in exotic germplasm particularly *S. andigena* remains scarce. Hence, comprehensive evaluation of *S. andigena* genotypes is necessary to facilitate their effective utilisation in potato breeding programmes (9). Selection based purely on yield is often misleading because yield is characterised by low heritability and is subject to high environmental variance (10). Therefore, a comprehensive understanding of the relationship between yield and its component traits such as plant height, number of stems per hill, leaf area index and tuber dry matter is essential for the systematic improvement of the crop (11).

Correlation analysis provides a measure of the degree of association between yield and its components, helping breeders identify traits that can serve as reliable indirect selection criteria (12). While simple correlation coefficients indicate the statistical relationship between two variables, they do not account for the complex web of interrelationships existing among various traits. To overcome this limitation, path coefficient analysis is employed to partition the correlation into direct and indirect effects (13). Path analysis allows more granular view of how a specific trait influences yield, either directly or through its influence on other traits (14). Despite numerous studies, the correlation patterns of emerging genotypes under the specific agro-climatic conditions of the

Indo-Gangetic Plain remain insufficiently documented. An essential goal of many breeding programs is to create heterosis. By analysing genetic diversity, breeders can identify parents that are genetically distinct from one another. Crossing these diverse parents often results in offspring that are stronger, faster-growing and higher-yielding than either parent (15).

This study was therefore undertaken to estimate the correlation and path coefficients for various morpho-physiological traits among diverse andigena genotypes. Genetic diversity analysis ensures efficient utilisation of genetic resources and plays a key role in crop improvement and breeding programs. The findings aim to provide a roadmap for breeders to prioritise specific traits in selection programs, ultimately leading to enhanced productivity and food security in the Indo-Gangetic Plain.

## Materials and Methods

### Experimental materials and site

The study was conducted during the two rabi seasons of 2023–2024 and 2024–2025 at the Potato Research Farm, Dr. Rajendra Prasad Agricultural University, Pusa, Tirhut College of Agriculture (TCA), Dholi, Bihar. The farm is situated between 25.99° N, 85.59° E. The trial site is 52.12 m above mean sea level, located in Bihar's first agro-climatic zone. The meteorological data recorded during the crop growing seasons, including maximum and minimum temperature, rainfall and relative humidity, have presented in Fig. 1.

A total of 18 genotypes namely JEXA102, JEXA456, JEXA1160, JEXA132, JEXA805, JEXA135, JEXA314, JEXA1181, JEXA30, JEXA148, JEXA444, JEXA633, JEXA52, JEXA457, JEXA75, JEXA319, Kufri Girdhari and Kufri Jyothi were evaluated in a randomised block design (RBD) with 3 replications. Planting was carried out in 10 November 2023 and 2024 using treated seed tubers placed on ridges at a spacing of 60 × 20 cm. Irrigation was applied as per crop requirement throughout the growing season to maintain optimum soil moisture. Each genotype was grown in plots measuring 2.0 × 1.8 m, comprising five rows, with six plants per row, accommodating 30 plants per plot. Standard agronomic practices were followed throughout the crop period. Earthing up was performed manually at 30 days after planting (DAP) and fertilisers were applied at the recommended dose of 180 : 80 : 100 kg nitrogen : phosphorus pentoxide : potassium oxide per hectare (N : P<sub>2</sub>O<sub>5</sub> : K<sub>2</sub>O ha<sup>-1</sup>).

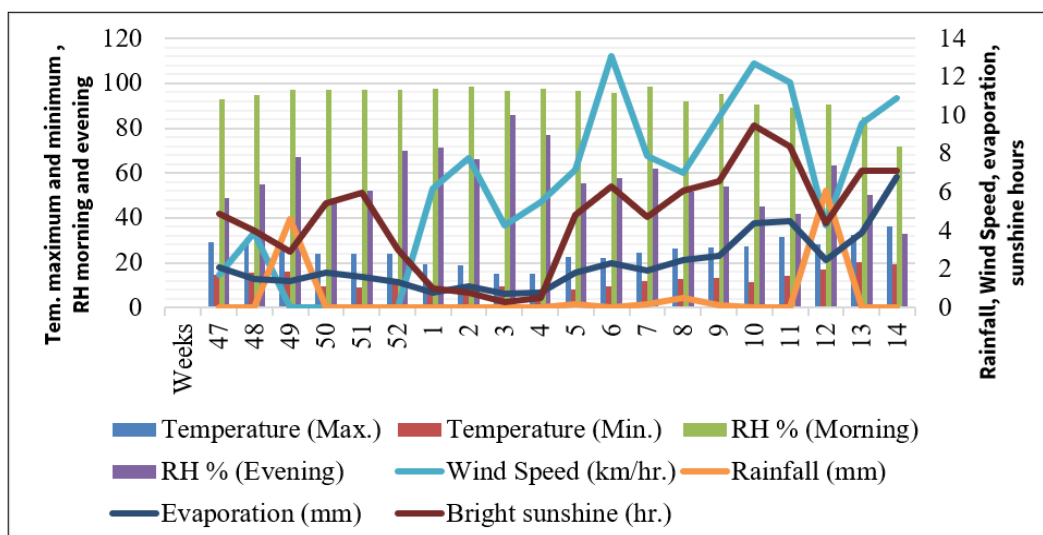


Fig. 1. Weather data of rabi season 2023–2024.

## Morphological and biochemical parameters

Data were collected for eight agro-morphological and four biochemical traits. In each plot, five plants were selected at random for measurement, with their mean values used for subsequent statistical analysis. The variables recorded were plant height (PH) (cm), plant emergence (GP) (%), number of shoots per plant (NSP), number of compound leaves per plant (NCL), number of tubers per plant (NTP), days to maturity (DTM), harvest index (HI) (%), tuber dry matter content (DM), specific gravity of tuber (SG) ( $\text{g cm}^{-3}$ ), reducing sugar (RS) ( $\text{mg } 100 \text{ g}^{-1}$ ), non-reducing sugar (NRS) ( $\text{mg } 100 \text{ g}^{-1}$ ) and tuber yield per plant (TWPP) (kg). The biochemical traits, namely dry matter, specific gravity, reducing sugar and non-reducing sugar, were selected because they are widely recognised as key indicators of potato processing quality. Dry matter and specific gravity are closely associated with starch content and processing recovery, whereas reducing and non-reducing sugars influence frying quality, chip colour and the development of undesirable browning during processing (16).

### Plant emergence 20 days after planting (DAP)

The germination percent was recorded at 20 DAP after planting from each genotype in each replication.

Plant emergence 20 days after planting =

$$\frac{\text{Number of plants emerged}}{\text{Total number of planted tubers}} \times 100$$

### Harvest index (%)

The following equation is used to calculate the harvest index.

$$\text{Harvest index} = \frac{\text{Economical yield}}{\text{Biological yield}} \times 100$$

### Tuber dry matter content (%)

Total tuber dry matter content was determined by taking 100 g of tuber tissue cut and dehydrated it using a hot air oven at 55 to 60 °C for 48 hr until the water present in the tuber was evaporated. Following equation was used to determine total dry matter content of tuber.

$$\text{Dry matter} = \frac{\text{Dry weight of tuber}}{\text{Fresh weight of tuber}} \times 100$$

### Specific gravity of tuber

This parameter was determined by the following formula:

Specific gravity of tuber =

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

## Sugars

Non-reducing sugar (sucrose) content was estimated using the anthrone method and reducing sugar content was estimated using the Nelson-Somogyi method as described by previous researchers (16–19).

### Statistical analysis

The path coefficient analysis was conducted to determine the direct and indirect contributions of component traits to tuber yield per plant, using the procedure outlined in previous research (20). The correlation coefficients were also calculated according to previous research (21). The genetic diversity or degree of divergence among the cultivars was computed using  $D^2$  statistics had been suggested by Mahalanobis (22). The analysis carried out using R software version 4.4.3.

## Results and Discussion

### Analysis of variance

The pooled analysis of variance (ANOVA) under the randomised complete block design (RCBD), revealed significant higher amount of variability among the genotypes for all the characters studied (Table 1). The pooled mean data for the 12 studied traits are presented in Table 2.

### Trait correlation among the yield attributing traits of andigena genotypes

#### Plant height (PH)

Plant height showed significant positive associations with number of tubers per plant, tuber dry matter and tuber weight per plant, while positive relationships were also observed with other growth traits (23). Taller plants generally develop a larger photosynthetic canopy, enhancing light interception and carbohydrate production. The increased assimilate supply enhances source-sink translocation, thereby promoting tuber initiation and starch accumulation, ultimately resulting in higher tuber yield (Fig. 2 and 3) (24).

#### Plant emergence (GP)

The present investigation unveiled that trait plant emergence had a positive and significant association with tuber weight per plant (0.4058\*\*), number of compound leaves (0.3162\*) and days to maturity (0.3116\*) as shown in Fig. 2 (25). Early and uniform emergence promotes rapid canopy establishment and efficient resource utilisation, thereby enhancing photosynthetic activity.

#### Number of shoots per plant (NSP)

Number of shoots per plant exhibited a negative and non-significant

**Table 1.** Analysis of variance for 12 yield contributing traits of andigena genotypes

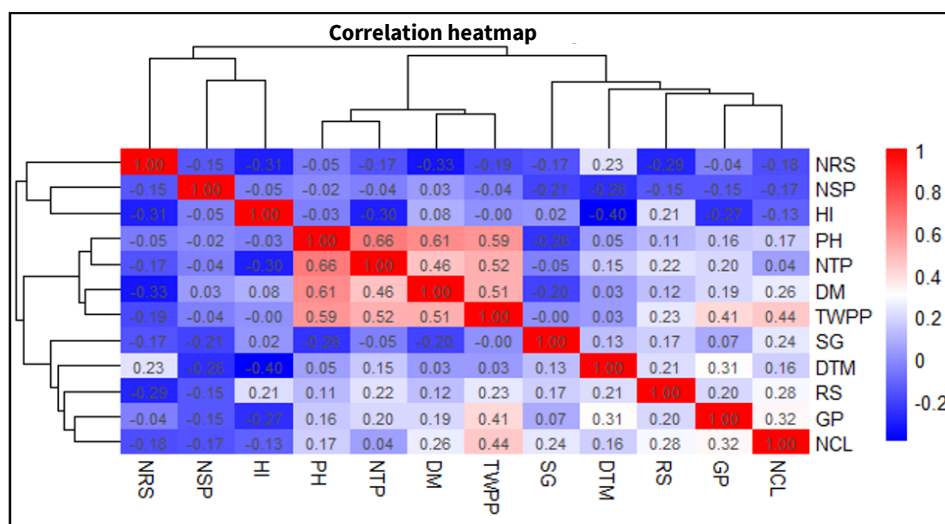
| Characters                                       | Mean sum of squares  |                     |                 |
|--------------------------------------------------|----------------------|---------------------|-----------------|
|                                                  | Replication (df = 2) | Genotypes (df = 17) | Error (df = 34) |
| Plant height (cm)                                | 1.66                 | 131.54**            | 15.11           |
| Plant emergence (%)                              | 8.48                 | 89.92**             | 22.94           |
| Number of shoots per plant                       | 0.0027               | 2.264**             | 0.064           |
| Number of compound leaves per plant              | 15.08                | 130.69**            | 13.69           |
| Number of tubers per plant                       | 0.0039               | 4.59**              | 0.27            |
| Days to maturity                                 | 90.31                | 107.21**            | 32.19           |
| Harvest index (%)                                | 18.07                | 63.96**             | 18.89           |
| Tuber dry matter                                 | 0.11                 | 5.04**              | 2.05            |
| Specific gravity of tuber ( $\text{g cm}^{-3}$ ) | 0.0018               | 0.013**             | 0.0037          |
| Reducing sugar ( $\text{mg}/100 \text{ g}$ )     | 116.61               | 1911.26**           | 360.96          |
| Non-reducing sugar ( $\text{mg}/100 \text{ g}$ ) | 394                  | 5735.8**            | 1214.6          |
| Tuber yield per plant (kg)                       | 0.00054              | 0.0064**            | 0.00068         |

\*Significant at  $\alpha = 0.05$ ; \*\*Significant at  $\alpha = 0.01$ ; df: degrees of freedom.

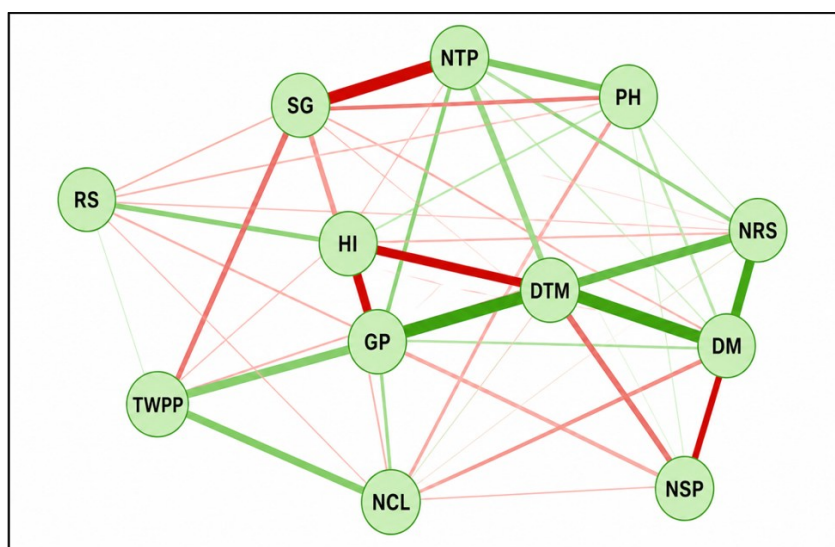
**Table 2.** Mean performance of andigena genotypes for 12 traits

| Sl. No               | Genotypes   | PH (cm)      | PE (%)       | NSP         | NCL          | NTP         | DTM          | HI (%)      | DM (%)       | SG (g cm <sup>-3</sup> ) | RS (mg/100g)  | NRS (mg/100g) | TWPP (kg)    |
|----------------------|-------------|--------------|--------------|-------------|--------------|-------------|--------------|-------------|--------------|--------------------------|---------------|---------------|--------------|
| 1                    | JEXA 52     | 50.81        | 92.22        | 5.82        | 44.02        | 6.93        | 88.27        | 64.07       | 21.37        | 1.06                     | 183.53        | 254.42        | 0.19         |
| 2                    | JEXA457     | 40.05        | 95.55        | 3.87        | 33.85        | 5.74        | 92.73        | 65.27       | 20.53        | 1.04                     | 172.68        | 335.51        | 0.16         |
| 3                    | JEXA75      | 42.22        | 92.22        | 3.92        | 26.78        | 8.04        | 92.33        | 70.40       | 21.16        | 1.03                     | 188.95        | 332.85        | 0.16         |
| 4                    | JEXA319     | 43.35        | 95.00        | 3.79        | 46.99        | 7.18        | 95.73        | 66.87       | 19.72        | 1.14                     | 169.63        | 395.74        | 0.15         |
| 5                    | JEXA102     | 45.98        | 87.22        | 3.54        | 28.48        | 8.21        | 93.60        | 74.13       | 19.35        | 1.04                     | 176.32        | 383.30        | 0.14         |
| 6                    | JEXA456     | 41.85        | 87.78        | 3.88        | 36.38        | 7.18        | 88.47        | 72.47       | 22.37        | 1.04                     | 183.50        | 332.25        | 0.15         |
| 7                    | JEXA1160    | 29.50        | 90.00        | 3.97        | 33.11        | 7.63        | 85.60        | 74.53       | 20.93        | 1.09                     | 172.09        | 249.45        | 0.14         |
| 8                    | JEXA 132    | 52.12        | 92.22        | 4.36        | 34.94        | 5.70        | 89.80        | 73.33       | 21.22        | 1.08                     | 214.80        | 280.00        | 0.21         |
| 9                    | JEXA 805    | 53.71        | 88.89        | 6.23        | 36.51        | 6.15        | 81.93        | 70.33       | 22.76        | 1.11                     | 162.83        | 224.64        | 0.27         |
| 10                   | JEXA 135    | 35.90        | 90.56        | 3.87        | 29.53        | 5.50        | 81.67        | 73.00       | 18.74        | 1.16                     | 173.55        | 269.23        | 0.10         |
| 11                   | JEXA314     | 30.34        | 88.33        | 4.32        | 34.46        | 6.48        | 93.01        | 67.00       | 19.72        | 1.15                     | 160.60        | 367.20        | 0.11         |
| 12                   | JEXA1181    | 34.29        | 74.46        | 3.93        | 32.76        | 6.20        | 77.27        | 79.67       | 18.54        | 1.08                     | 182.95        | 334.21        | 0.10         |
| 13                   | JEXA 30     | 45.73        | 83.90        | 4.36        | 38.78        | 4.76        | 82.13        | 80.20       | 21.49        | 1.16                     | 187.21        | 271.75        | 0.16         |
| 14                   | JEXA 148    | 34.26        | 85.56        | 3.69        | 29.58        | 5.25        | 92.87        | 72.27       | 19.72        | 1.20                     | 167.12        | 295.61        | 0.12         |
| 15                   | JEXA 444    | 42.56        | 82.21        | 4.57        | 28.83        | 5.86        | 92.47        | 64.97       | 19.06        | 1.14                     | 165.30        | 325.35        | 0.12         |
| 16                   | JEXA633     | 36.73        | 87.78        | 3.61        | 26.30        | 6.11        | 92.53        | 71.87       | 18.31        | 1.16                     | 211.61        | 357.82        | 0.10         |
| 17                   | K. Girdhari | 42.8         | 96.1         | 3.6         | 40.65        | 5.08        | 105.25       | 75.45       | 20.12        | 1.20                     | 247.38        | 275.01        | 0.205        |
| 18                   | K. Jyoti    | 43.26        | 95.55        | 4.6         | 48.14        | 5.28        | 101.52       | 71.18       | 21.68        | 1.19                     | 259.51        | 249.03        | 0.21         |
| <b>Mean</b>          |             | <b>41.15</b> | <b>89.19</b> | <b>4.29</b> | <b>35.03</b> | <b>6.41</b> | <b>88.67</b> | <b>71.5</b> | <b>20.35</b> | <b>1.12</b>              | <b>186.36</b> | <b>315.76</b> | <b>0.155</b> |
| <b>CD (p = 0.05)</b> |             | <b>3.004</b> | <b>3.88</b>  | <b>0.31</b> | <b>2.43</b>  | <b>0.49</b> | <b>6.64</b>  | <b>4.44</b> | <b>0.64</b>  | <b>0.07</b>              | <b>12.58</b>  | <b>21.90</b>  | <b>0.014</b> |

PH: plant height; PE: plant emergence; NSP: no. of shoots per plant; NCL: no. of compound leaves per plant; NTP: no. of tubers per plant; DTM: days to maturity; HI: harvest index; DM: dry matter; SG: specific gravity; RS: reducing sugar; NRS: non reducing sugar; TWPP: tuber weight per plant; K. Jyoti: Kufri Jyoti; K. Girdhari: Kufri Girdhari.

**Fig. 2.** Correlation coefficients amongst eight morphological and four biochemical characteristics under study.

PH: plant height; PE: plant emergence; NSP: no. of shoots per plant; NCL: no. of compound leaves per plant; NTP: no. of tubers per plant; DTM: days to maturity; HI: harvest index; DM: dry matter; SG: specific gravity; RS: reducing sugar; NRS: non reducing sugar; TWPP: tuber weight per plant.

**Fig. 3.** Genotypic network among the yield attributing traits of andigena genotypes.

PH: plant height; PE: plant emergence; NSP: no. of shoots per plant; NCL: no. of compound leaves per plant; NTP: no. of tubers per plant; DTM: days to maturity; HI: harvest index; DM: dry matter; SG: specific gravity; RS: reducing sugar; NRS: non reducing sugar; TWPP: tuber weight per plant.

association with days to maturity (-0.2611), specific gravity (-0.2062), number of compound leaves (-0.1712) (26), reducing sugar (-0.1542), non-reducing sugar (-0.1536), harvest index (-0.0458), tuber weight per plant (-0.0446) and number of tubers per plant (-0.0427) (27).

#### Number of compound leaves per plant (NCL)

The study revealed that trait NCL had a positive and significant relationship with tuber weight per plant (0.4448\*\*), plant emergence (0.3162\*) and reducing sugar (0.2779\*). Greater leaf number increases the photosynthetically active area, improving carbohydrate synthesis and translocation to developing tubers (Fig. 2 and 3) (28, 29).

#### Number of tubers per plant (NTP)

The present investigation unveiled that trait number of tubers per plant had a positive and significant association with tuber weight per plant (0.517\*\*) and tuber dry matter (0.4593 \*\*), which is in agreement with previous reports in potato (30).

#### Days to maturity (DTM)

The traits plant emergence (0.3116\*) showed a positive and significant association with days to maturity (Fig. 2 and 3). Longer growth duration prolongs photosynthetic activity and carbohydrate accumulation, allowing sustained tuber bulking (31).

#### Harvest index (HI)

Harvest index showed a positive but non-significant correlation with reducing sugar (0.2057), tuber dry matter (0.0829) and specific gravity (0.0211), indicate that greater assimilate partitioning towards tubers was accompanied by modest variation in tuber biochemical composition. Whereas the correlation with tuber weight per plant was weakly negative (-0.0034) (32).

#### Tuber dry matter (DM)

The present investigation unveiled that trait tuber dry matter had a positive and significant association with tuber weight per plant (0.5132\*\*) and number of tubers per plant (0.4593\*\*), in conformity with earlier studies emphasising the role of dry matter in yield improvement (Fig. 2) (33). Higher dry matter indicates efficient conversion of sucrose into starch through enhanced carbohydrate metabolism.

#### Reducing sugar (RS)

The trait reducing sugar exhibited a positive and significant association with number of compound leaves (0.2779). Soluble

sugars act as intermediate products in carbohydrate metabolism and provide substrates for starch biosynthesis during tuber development. Their balance influences both tuber quality and dry matter accumulation (34).

#### Non reducing sugar (NRS)

For the trait non reducing sugar genotypic correlation was positive and non-significant for days to maturity (0.229) (Fig. 3), which is in consistent with previous reports (35). Elevated non-reducing sugar levels may indicate reduced conversion of sucrose into storage starch, thereby limiting dry matter accumulation.

#### Tuber weight per plant (TWPP)

The traits number of tubers per plant (0.517\*\*), tuber dry matter (0.5132\*\*), number of compound leaves (0.4448\*\*) and plant emergence (0.4058\*\*) showed a positive and significant association with tuber weight per plant (Fig. 2 and 3) (36).

#### Path coefficient analysis of andigena genotypes for yield attributing traits

Tuber yield was considered the dependent variable and was influenced both directly and indirectly by eight agro-morphological traits along with four biochemical traits

#### Plant height (PH)

There was a positive and significant relationship between plant height and tuber weight per plant ( $r = 0.5867^{**}$ ). Path coefficient analysis revealed that plant height exerted a positive direct effect (0.2088) on tuber weight per plant, indicating its importance as a selection criterion for yield improvement (37).

#### Plant emergence (GP)

The correlation coefficient between plant emergence and tuber weight per plant was positive and significant (at 1 % level of significance) with correlation value ( $r = 0.4058^{**}$ ). Plant emergence exhibited a positive direct effect (0.2794) on tuber weight per plant, suggesting its direct contribution towards yield (Table 3) (38).

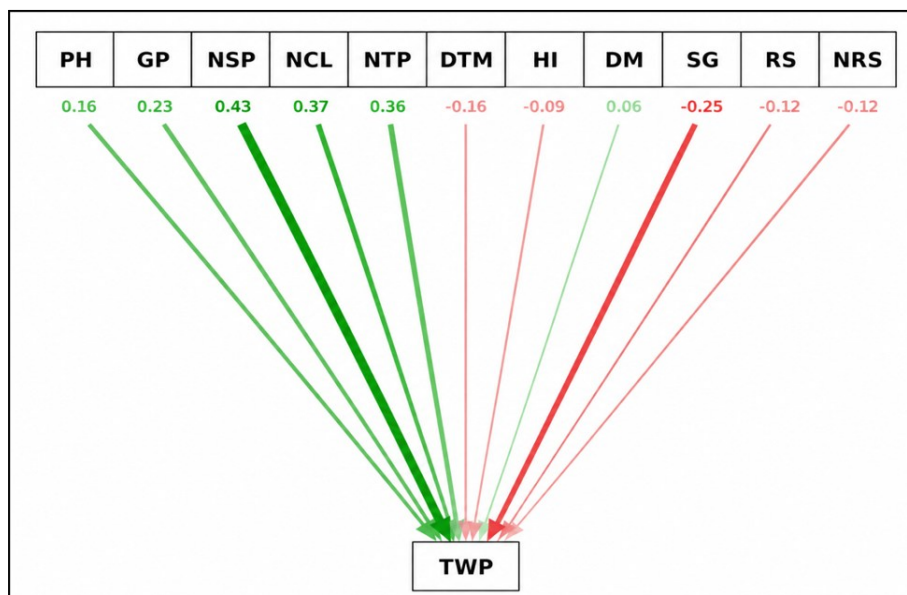
#### Number of shoots per plant (NSP)

Negative and non-significant correlation was observed between number of shoots per plant and tuber weight per plant ( $r = -0.0446$ ) (Fig. 4). The direct effect of number of shoots per plant was positive (0.07806). Number of shoots per plant exerted positive indirect effects on tuber weight per plant through days to maturity (0.02284), reducing sugar (0.00549) and tuber dry matter (0.00252) (39).

**Table 3.** Path analysis showing direct and indirect effects of traits on tuber yield

|            | PH            | GP            | NSP           | NCL           | NTP           | DTM            | HI            | DM            | SG            | RS             | NRS           | TWPP     |
|------------|---------------|---------------|---------------|---------------|---------------|----------------|---------------|---------------|---------------|----------------|---------------|----------|
| <b>PH</b>  | <b>0.2088</b> | 0.0439        | -0.0015       | 0.0611        | 0.2516        | -0.0043        | -0.0081       | 0.0503        | -0.0069       | -0.0038        | -0.0044       | 0.5867** |
| <b>GP</b>  | 0.0328        | <b>0.2794</b> | -0.0117       | 0.1139        | 0.0752        | -0.0273        | -0.0638       | 0.0157        | 0.0018        | -0.007         | -0.0031       | 0.4058** |
| <b>NSP</b> | -0.0041       | -0.0418       | <b>0.0781</b> | -0.0617       | -0.0163       | 0.0228         | -0.0108       | 0.0025        | -0.0055       | 0.0055         | -0.0132       | -0.0446  |
| <b>NCL</b> | 0.0354        | 0.0883        | -0.0134       | <b>0.3603</b> | 0.0171        | -0.0143        | -0.0304       | 0.021         | 0.0064        | -0.0099        | -0.0158       | 0.4448** |
| <b>NTP</b> | 0.1373        | 0.0549        | -0.0033       | 0.0161        | <b>0.3825</b> | -0.0129        | -0.0715       | 0.0376        | -0.0013       | -0.0079        | -0.0145       | 0.517**  |
| <b>DTM</b> | 0.0102        | 0.087         | -0.0204       | 0.0589        | 0.0566        | <b>-0.0875</b> | -0.0939       | 0.0024        | 0.0034        | -0.0075        | 0.0196        | 0.029    |
| <b>HI</b>  | -0.0071       | -0.0754       | -0.0036       | -0.0463       | -0.1156       | 0.0347         | <b>0.2365</b> | 0.0068        | 0.0006        | -0.0073        | -0.0266       | -0.0034  |
| <b>DM</b>  | 0.1284        | 0.0535        | 0.0024        | 0.0926        | 0.1757        | -0.0026        | 0.0196        | <b>0.0818</b> | -0.0055       | -0.0043        | -0.0283       | 0.5132** |
| <b>SG</b>  | -0.0534       | 0.0184        | -0.0161       | 0.0859        | -0.0179       | -0.0111        | 0.005         | -0.0167       | <b>0.0268</b> | -0.0061        | -0.0148       | 0.0023   |
| <b>RS</b>  | 0.0225        | 0.055         | -0.012        | 0.1001        | 0.0844        | -0.0184        | 0.0486        | 0.01          | 0.0046        | <b>-0.0356</b> | -0.0251       | 0.2341   |
| <b>NRS</b> | -0.0107       | -0.0101       | -0.012        | -0.0665       | -0.065        | -0.02          | -0.0735       | -0.0271       | -0.0046       | 0.0104         | <b>0.0856</b> | -0.1934  |

Residual value is 0.395. PH: plant height; PE: plant emergence; NSP: no. of shoots per plant; NCL: no. of compound leaves per plant; NTP: no. of tubers per plant; DTM: days to maturity; HI: harvest index; DM: dry matter; SG: specific gravity; RS: reducing sugar; NRS: non reducing sugar; TWPP: tuber weight per plant.



**Fig. 4.** Path diagram for tuber weight per plant.

PH: plant height; PE: plant emergence; NSP: no. of shoots per plant; NCL: no. of compound leaves per plant; NTP: no. of tubers per plant; DTM: days to maturity; HI: harvest index; DM: dry matter; SG: specific gravity; RS: reducing sugar; NRS: non reducing sugar; TWPP: tuber weight per plant.

#### Number of compound leaves (NCL)

A positive and significant association was observed between the number of compound leaves and tuber weight per plant ( $r = 0.4448^{**}$ ). Path coefficient analysis indicated that this trait exerted a positive direct effect (0.3603) on tuber weight per plant (40). Conversely, negative indirect effects were recorded through number of shoots per plant (-0.01336), days to maturity (-0.01431), non-reducing sugar content (-0.01580) and harvest index (-0.03039), indicating compensatory interactions among vegetative growth, maturity and yield components (41).

#### Number of tubers per plant (NTP)

The correlation coefficient between number of tubers per plant and tuber weight per plant was positive and significant with correlation value ( $r = 0.517$ ) (Fig. 4). Number of tubers per plant had a positive direct effect on tuber weight per plant (0.3825) (42). The indirect effect of this trait was positive via plant height (0.13735), plant emergence (0.05492), tuber dry matter (0.03756) and number of compound leaves (0.01607) (Table 3).

#### Days to maturity (DTM)

A positive but non-significant correlation was observed between days to maturity and tuber weight per plant ( $r = 0.029$ ). However, path coefficient analysis revealed a negative direct effect (-0.0875), indicating that the positive association was mainly due to indirect effects through other traits (43).

#### Harvest index (HI)

There was a negative and non-significant relationship between harvest index and tuber weight per plant ( $r = -0.0034$ ). Path coefficient analysis revealed a positive direct effect (0.2365) on tuber weight per plant, although the overall correlation remained negative due to indirect effects through other traits (41).

#### Tuber dry matter (DM)

The correlation coefficient between tuber dry matter and tuber weight per plant was positive and significant ( $r = 0.5132^{**}$ ). Path coefficient analysis revealed a positive direct effect (0.0818) on tuber weight per plant, indicating its contribution to yield improvement (Table 3) (44).

#### Reducing sugar (RS)

There was a positive but non-significant relationship between reducing sugar and tuber weight per plant ( $r = 0.2341$ ). However, path coefficient analysis showed a negative direct effect (-0.0356), indicating that its positive association with yield was mainly due to indirect effects through other traits (45).

#### Non reducing sugar (NRS)

The correlation coefficient between non-reducing sugar and tuber weight per plant was negative and non-significant ( $r = -0.1934$ ). Negative correlation can occur when the trait has a positive direct effect on yield but its indirect effects through other traits are sufficiently negative to outweigh that direct contribution. Path coefficient analysis revealed a positive direct effect (0.0856) on tuber weight per plant, suggesting that its overall negative association resulted from indirect effects through other traits (Table 3) (46).

#### Diversity analysis

In order to maximise heterosis, outstanding and diverse genotypes are chosen as parents for hybridisation with the use of genetic diversity analysis (47). Clustering was done by using hierarchical clustering method suitable for multivariate assessment of genetic diversity in crop germplasm, for the eighteen genotypes of potato in to seven clusters (Table 4).

**Table 4.** Cluster groups from andigena genotypes

| Clusters    | No. of genotypes | Genotypes                                                        |
|-------------|------------------|------------------------------------------------------------------|
| Cluster I   | 1                | JEXA102                                                          |
| Cluster II  | 2                | JEXA457, JEXA319                                                 |
| Cluster III | 5                | JEXA75, JEXA456, JEXA52, JEXA132, JEXA805, K. Girdhari, K. Jyoti |
| Cluster IV  | 2                | JEXA 1160, JEXA135                                               |
| Cluster V   | 2                | JEXA30, JEXA1181                                                 |
| Cluster VI  | 2                | JEXA314, JEXA444                                                 |
| Cluster VII | 2                | JEXA148, JEXA633                                                 |

K. Jyoti: Kufri Jyoti; K. Girdhari: Kufri Girdhari.

## Cluster analysis of andigena genotypes

The cluster analysis grouped the andigena genotypes into seven distinct clusters as shown in Fig. 5, indicating considerable genetic diversity. Cluster I included genotypes such as JEXA102, showing close genetic similarity among its members. Cluster II comprised JEXA457 and JEXA319, indicating moderate divergence. Cluster III included JEXA75, JEXA456, JEXA52, JEXA132, JEXA805, Kufri girdhari and Kufri Jyoti reflecting moderate variability within the group. Cluster IV contained JEXA1160 and JEXA135, while Cluster V included JEXA30 and JEXA1181, both showing intermediate diversity. Cluster VI consisted of JEXA314 and JEXA444, indicating high divergence from other clusters. Cluster VII included JEXA148 and JEXA633 (Table 4). Overall, the presence of diverse clusters suggests wide genetic variability and crossing genotypes from distant clusters, particularly Cluster VI with others, can help exploit heterosis and develop superior genotypes. Overall, the results reveal wide variability and crossing genotypes from distant clusters may help develop superior recombinants and heterotic hybrids for effective breeding programs (48).

## Average inter- and intra-cluster distances among seven clusters of andigena types

The Mahalanobis  $D^2$  analysis revealed considerable genetic divergence among the seven clusters of andigena genotypes. Intra-cluster distances were relatively low, indicating homogeneity within clusters. Cluster II (41.92) and Cluster III (51.64) showed moderate variability, while Cluster I exhibited minimum internal variation (Table 5). Inter-cluster distances were much higher, reflecting substantial divergence among clusters. The maximum distance was observed between Cluster VI and Cluster VII (447.82), followed by Cluster IV and Cluster VII (380.94), indicating highly divergent groups (Table 5). The minimum distance between Cluster I and Cluster V (119.68) showed closer similarity. Crossing distant clusters can enhance heterosis and yield improvement. The large inter-cluster distances indicate maximum genetic divergence, which is essential for obtaining transgressive segregants (49). Hybridisation among these clusters can combine desirable traits from diverse genetic backgrounds, enhancing yield, quality and stress tolerance. Such

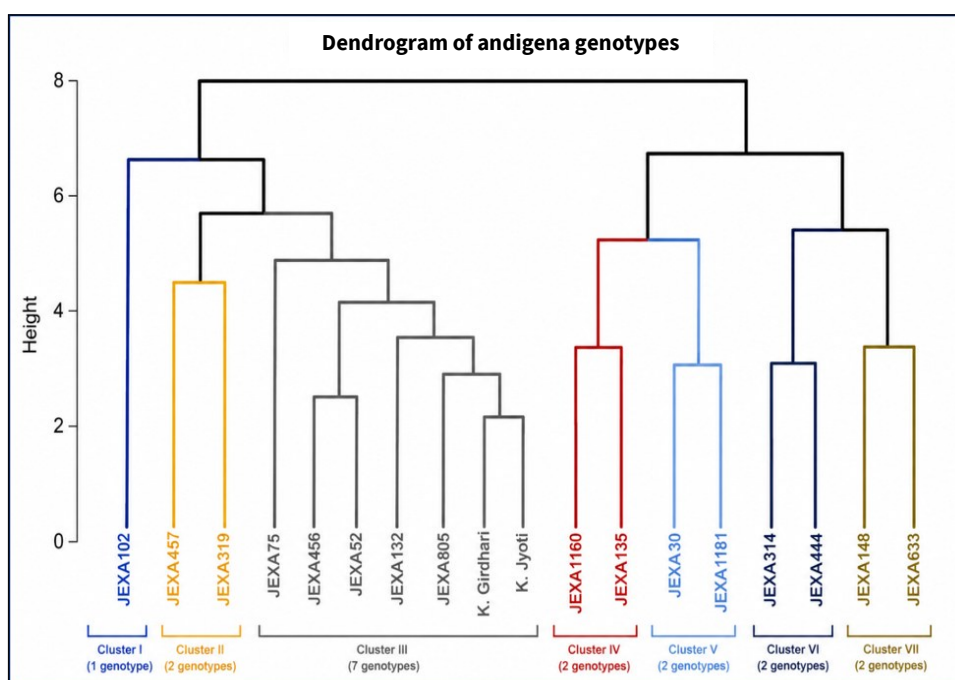
crosses are likely to produce broad variability in segregating generations, providing better opportunities for selection (50). Therefore, these divergent clusters should be prioritised in breeding programs aimed at genetic improvement and varietal development (51).

## Cluster means for 12 yield contributing traits in andigena potato genotypes

The cluster means for twelve yield-contributing traits revealed substantial variability among the andigena potato genotypes. Cluster III recorded higher values for number of tubers per plant (7.08), dry matter (21.5) and reducing sugars (200.92), indicating its potential for yield and processing traits (Table 6). Cluster VII exhibited maximum plant emergence (95.55 %), number of compound leaves (48.14), days to maturity (101.58), specific gravity (1.21) and tuber weight per plant (0.23), suggesting superiority for growth and yield attributes. Cluster II showed high emergence and non-reducing sugars (342.11), while Cluster I had higher harvest index (74.31) (Table 6). Cluster V and VI showed moderate performance, whereas Cluster IV had lower values for several traits.

## Percentage contribution of various yield attributing characters towards genetic diversity

The analysis of percentage contribution revealed that different traits contributed unequally to the total genetic divergence among the andigena genotypes (52). The circular representation of percentage contribution revealed that reducing sugar (RS) contributed the highest (14 %) towards total genetic divergence, followed by tuber yield per plant (11 %) and number of compound leaves (10 %) (Fig. 6). The relatively high contribution of reducing sugar to genetic divergence indicates substantial variability among genotypes for this quality trait (Fig. 7). Traits such as specific gravity and plant height showed moderate contributions (9 %), whereas days to maturity (4 %) contributed the least. The results indicate that sugar-related and yield-associated traits play a major role in genetic diversity and should be prioritised in selection strategies. Overall, yield-related traits, especially tuber and compound leaves played a dominant role in genetic divergence and should be prioritised in selection and breeding programs (53).



**Fig. 5.** Hierarchical clustering of andigena genotypes.

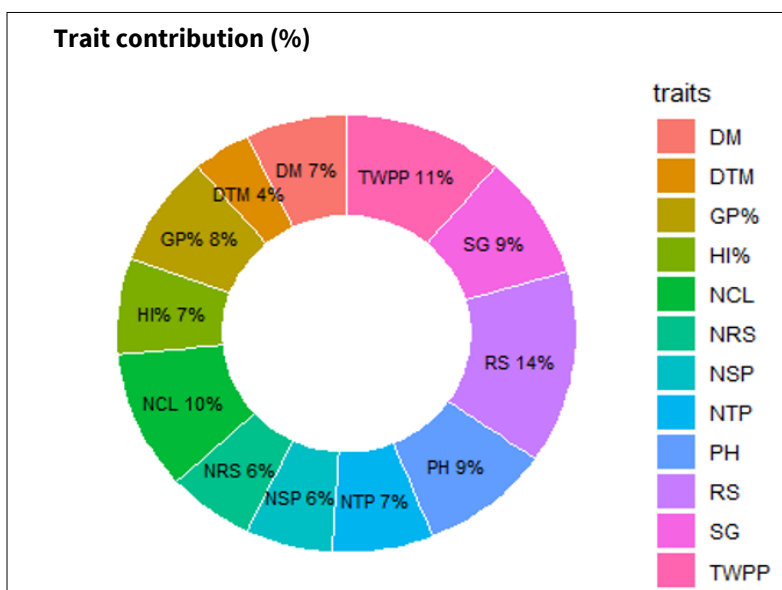
**Table 5.** Average inter- and intra-cluster distances among seven clusters of andigena types

|             | Cluster I | Cluster II | Cluster III | Cluster IV | Cluster V | Cluster VI | Cluster VII |
|-------------|-----------|------------|-------------|------------|-----------|------------|-------------|
| Cluster I   | 0         | 132.72     | 173.04      | 188.51     | 119.68    | 123.81     | 287.47      |
| Cluster II  |           | 41.92      | 159.11      | 141.09     | 255.14    | 261.58     | 164.42      |
| Cluster III |           |            | 51.64       | 165.42     | 351.5     | 109.84     | 234.92      |
| Cluster IV  |           |            |             | 53.403     | 362.72    | 164.16     | 380.94      |
| Cluster V   |           |            |             |            | 79.07     | 270.87     | 335.52      |
| Cluster VI  |           |            |             |            |           | 54.87      | 447.82      |
| Cluster VII |           |            |             |            |           |            | 48.68       |

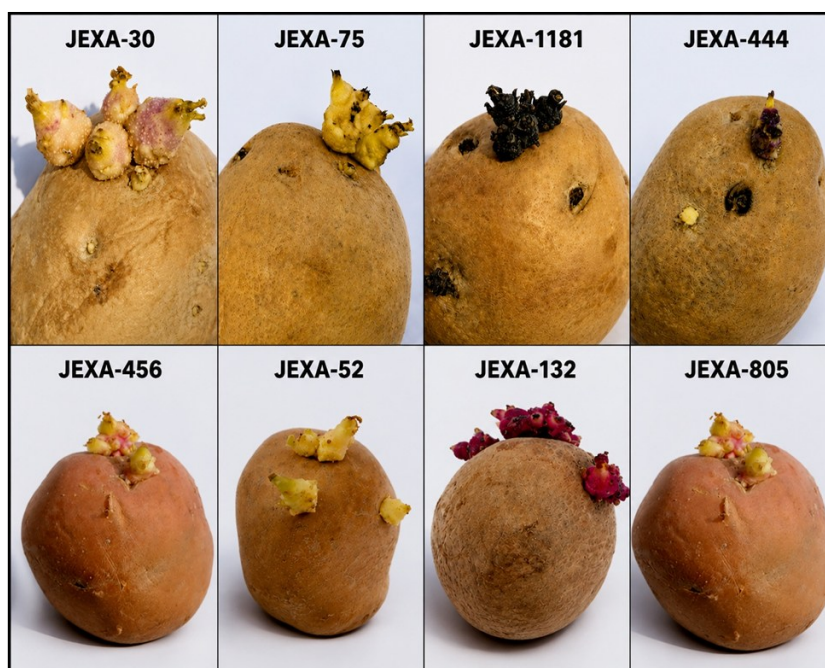
**Table 6.** Cluster means for twelve yield contributing traits in andigena potato genotypes

| Trait       | PH    | PE    | NSP  | NCL   | NTP  | DTM   | HI    | DM    | SG   | RS     | NRS    | TWPP |
|-------------|-------|-------|------|-------|------|-------|-------|-------|------|--------|--------|------|
| Cluster I   | 58.87 | 87.22 | 4.60 | 24.13 | 9.20 | 93.60 | 74.13 | 23.53 | 1.04 | 167.69 | 425.32 | 0.11 |
| Cluster II  | 30.80 | 95.28 | 3.33 | 42.37 | 6.37 | 94.23 | 66.07 | 22.88 | 1.09 | 159.49 | 395.21 | 0.14 |
| Cluster III | 33.43 | 90.67 | 4.89 | 35.20 | 6.92 | 88.16 | 70.12 | 21.13 | 1.06 | 184.18 | 291.61 | 0.20 |
| Cluster IV  | 41.17 | 90.28 | 5.23 | 28.47 | 6.54 | 83.63 | 73.77 | 20.64 | 1.12 | 162.13 | 214.08 | 0.07 |
| Cluster V   | 31.20 | 79.18 | 4.80 | 35.27 | 4.78 | 79.70 | 79.93 | 21.23 | 1.12 | 181.57 | 288.45 | 0.09 |
| Cluster VI  | 34.53 | 85.27 | 5.87 | 28.97 | 5.90 | 92.74 | 65.99 | 21.96 | 1.14 | 146.47 | 362.24 | 0.06 |
| Cluster VII | 30.63 | 86.67 | 3.47 | 23.30 | 5.10 | 92.70 | 72.07 | 21.48 | 1.18 | 188.37 | 328.90 | 0.05 |

PH: plant height; PE: plant emergence; NSP: no. of shoots per plant; NCL: no. of compound leaves per plant; NTP: no. of tubers per plant; DTM: days to maturity; HI: harvest index; DM: dry matter; SG: specific gravity; RS: reducing sugar; NRS: non reducing sugar; TWPP: tuber weight per plant.

**Fig. 6.** Percentage contribution of various yield attributing characters towards genetic diversity.

PH: plant height; PE: plant emergence; NSP: no. of shoots per plant; NCL: no. of compound leaves per plant; NTP: no. of tubers per plant; DTM: days to maturity; HI: harvest index; DM: dry matter; SG: specific gravity; RS: reducing sugar; NRS: non reducing sugar; TWPP: tuber weight per plant.

**Fig. 7.** Variation among the genotypes.

## Conclusion

The correlation and path analyses demonstrated that tuber weight per plant showed strong and positive associations with number of tubers per plant, tuber dry matter content, number of compound leaves, plant height and plant emergence, confirming their key role in yield determination under Indo-Gangetic Plains (IGP) conditions. The integrated correlation and path approach suggests that simultaneous selection for higher tuber number, increased dry matter content, improved foliage development, adequate plant height and early uniform emergence would be the most effective breeding strategy for enhancing potato productivity across the diverse agro-ecological environments of the Indo-Gangetic Plain. Reducing sugar content should be considered an important quality trait when selecting potato genotypes for processing purposes. The present study was limited to a relatively small set of genotypes evaluated at a single location and molecular characterisation was beyond its scope. Therefore, multi-location and multi-season validation using a broader germplasm collection, together with molecular characterisation, is recommended to confirm the stability and wider applicability of the identified promising genotypes. Cluster analysis revealed that Cluster V genotypes (JEXA30 and JEXA1181), which exhibit fewer days to maturity, can be used in breeding programs targeting early maturity. The genotypes JEXA75, JEXA456, JEXA52, JEXA132 and JEXA805, which belonged to Cluster III, were utilised as parents for yield improvement. Overall, Cluster III were superior for key yield and quality traits. Therefore, the genotypes JEXA75, JEXA456, JEXA52, JEXA132, JEXA805, Kufri Girdhari and Kufri Jyoti from these clusters can be effectively utilised in breeding programmes to improve yield, quality and processing characteristics.

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## Authors' contributions

KPR was responsible for conceptualisation, methodology, investigation, formal analysis and writing-original draft. AT handled resources, formal analysis, validation and supervision. MKS undertook visualisation and writing-review and editing. ALC and DKM performed formal analysis and writing-review and editing. KPR, PJ and SB undertook writing-review and editing. KPR, GB and MG performed data analysis and reviewing. All authors have read and approved the final manuscript.

## Compliance with ethical standards

**Conflict of interest:** Authors do not have any conflict of interests to declare.

**Ethical issues:** None

## Declaration of generative AI and AI-assisted technologies in the writing process

During the preparation of this work the authors used Grammarly in order to checking grammar and sentence structure during the preparation of this manuscript. After using this tool, the authors

reviewed and edited the content as needed and take full responsibility for the content of the publication.

## References

- Bradshaw JE. Potato-breeding strategy. In: Potato biology and biotechnology. Elsevier Science BV; 2007. p. 157–77. <https://doi.org/10.1016/B978-044451018-1/50050-6>
- Hijmans RJ. Global distribution of the potato crop. *Am J Potato Res.* 2001;78(6):403–12. <https://doi.org/10.1007/BF02896371>
- Hawkes JG. The potato: evolution, biodiversity and genetic resources. 1990. p. viii–259. <https://doi.org/10.1007/BF03044023>
- Ewing EE, Struik PC. Tuber formation in potato: induction, initiation and growth. *Hortic Rev.* 1992;14:89–198. <https://doi.org/10.1002/9780470650523.ch3>
- Scott GJ, Suarez V. The rise of Asia as the centre of global potato production and some implications for industry. *Potato J.* 2012;39(1):1–22.
- Bradshaw JE, Ramsay G. Utilisation of the Commonwealth Potato Collection in potato breeding. *Euphytica.* 2005;146(1):9–19. <https://doi.org/10.1007/s10681-005-3881-4>
- de Haan S, Rodriguez F. Potato origin and production. In: Advances in potato chemistry and technology. Academic Press; 2016. p. 1–32. <https://doi.org/10.1016/B978-0-12-800002-1.00001-7>
- Kumar SN. Assessment of impact of climate change on potato and potential adaptation gains in the Indo-Gangetic Plains of India. *Int J Plant Prod.* 2015.
- Raju KP, Soniya K, Tigga A, Uday K, Balraj G, Suresh K, et al. Correlation and path analysis of potato genotypes for morphophysiological traits under Indo-Gangetic plain. *Plant Arch.* 2025;25(1). <https://doi.org/10.51470/PLANTARCHIVES.2025.v25.no.1.412>
- Gopal J, Gaur PC, Rana MS. Heritability and intra- and inter-generation associations between tuber yield and its components in potato (*Solanum tuberosum* L.). *Plant Breed.* 1994;112(1):80–3. <https://doi.org/10.1111/j.1439-0523.1994.tb01280.x>
- Shubha K, Singh D. Selection of yield-associated morphological and biochemical traits using correlation and path coefficient analysis in potato (*Solanum tuberosum* L.) in the foothills of North-Western Himalayas. *Potato Res.* 2018;61(3):273–81. <https://doi.org/10.1007/s11540-018-9376-1>
- Zelege AA, Getahun BB. Association and path coefficient analysis studies in potato (*Solanum tuberosum* L.) genotypes at Adet, northwestern Ethiopia. *Int J Bio-resour Stress Manag.* 2024;15(6):1–14. <https://doi.org/10.23910/1.2024.5335a>
- Tai GC, Levy D, Coleman WK. Path analysis of genotype-environment interactions of potatoes exposed to increasing warm-climate constraints. *Euphytica.* 1994;75(1):49–61. <https://doi.org/10.1007/BF00024531>
- Urbany C, Stich B, Schmidt L, Simon L, Berding H, Junghans H, et al. Association genetics in *Solanum tuberosum* provides new insights into potato tuber bruising and enzymatic tissue discoloration. *BMC Genomics.* 2011;12(1):7. <https://doi.org/10.1186/1471-2164-12-7>
- Lavanya KS, Srinivasa V, Ali S, Devaraju, Lakshmana D, Kadian MS. Correlation and path analysis for yield and yield-related traits of potato (*Solanum tuberosum* L.) in Karnataka. *Natl Acad Sci Lett.* 2020;43(2):137–40. <https://doi.org/10.1007/s40009-019-00831-z>
- Yemm EW, Willis A. The estimation of carbohydrates in plant extracts by anthrone. *Biochem J.* 1954;57(3):508. <https://doi.org/10.1042/bj0570508>
- Sadasivam S. Biochemical methods. New Age International; 1996.
- Nelson N. A photometric adaptation of the Somogyi method for the determination of glucose. *J Biol Chem.* 1944;153(2):375–80. [https://doi.org/10.1016/S0021-9258\(18\)71980-7](https://doi.org/10.1016/S0021-9258(18)71980-7)

19. Somogyi M. A new reagent for the determination of sugars. *J Biol Chem.* 1945;160:61–8. [https://doi.org/10.1016/S0021-9258\(18\)43097-9](https://doi.org/10.1016/S0021-9258(18)43097-9)
20. Dewey DR, Lu KH. A correlation and path-coefficient analysis of components of crested wheatgrass seed production. *Agron J.* 1959;51(9):515–8. <https://doi.org/10.2134/agronj1959.00021962005100090002x>
21. Al-Jibouri A, Miller PA, Robinson HF. Genotype and environmental variation and correlation in an upland cotton crop of the interspecific origin. *Agron J.* 1958;50(10):626–36.
22. Mahalanobis PC. On the generalized distance in statistics. *Sankhyā: The Indian Journal of Statistics, Series A* (2008-). 2018;80:S1–7.
23. Zhang D, Cervantes J, Huamán Z, Carey E, Ghislain M. Assessing genetic diversity of sweet potato (*Ipomoea batatas* (L.) Lam.) cultivars from tropical America using AFLP. *Genet Resour Crop Evol.* 2000;47(6):659–65. <https://doi.org/10.1023/A:1026520507223>
24. Singh Yadav SP, Bhandari S, Ghimire NP, Mehata DK, Majhi SK, Bhattarai S, et al. Genetic variability, character association, path coefficient and diversity analysis of rice (*Oryza sativa* L.) genotypes based on agro-morphological traits. *Int J Agron.* 2024;2024(1):9946332. <https://doi.org/10.1155/2024/9946332>
25. Regassa D, Basavaraja N. Correlation and path analysis in potato (*Solanum tuberosum* L.). *Potato J.* 2013;32(3–4).
26. Kaur RP, Chaudhary B, Alam W. Associations among yield and yield contributing traits of potato (*Solanum tuberosum*) in north-western plains of India. *Indian J Agric Sci.* 2017;87(10):1409–11. <https://doi.org/10.56093/ijas.v87i10.75060>
27. Sucar S, Carboni MF, Rey Burusco MF, Castellote MA, Massa GA, Monte MN, et al. Assessment of genetic diversity and relatedness in an Andean potato collection from Argentina by high-density genotyping. *Horticulturae.* 2022;8(1):54. <https://doi.org/10.3390/horticulturae8010054>
28. Felenji H, Aharizad S, Afsharmanesh GR, Ahmadzadeh M. Evaluating correlation and factor analysis of morphological traits in potato cultivars in fall cultivation of Jiroft area. *Am Eurasian J Agric Environ Sci.* 2011;11(5):679–84.
29. Kolbe H, Stephan-Beckmann S. Development, growth and chemical composition of the potato crop (*Solanum tuberosum* L.). II. Tuber and whole plant. *Potato Res.* 1997;40(2):135–53. <https://doi.org/10.1007/BF02358240>
30. Ghislain M, Andrade D, Rodríguez F, Hijmans RJ, Spooner DM. Genetic analysis of the cultivated potato *Solanum tuberosum* L. Phureja Group using RAPDs and nuclear SSRs. *Theor Appl Genet.* 2006;113(8):1515–27. <https://doi.org/10.1007/s00122-006-0399-7>
31. Osundahunsi OF, Fagbemi TN, Kesselman E, Shimoni E. Comparison of the physicochemical properties and pasting characteristics of flour and starch from red and white sweet potato cultivars. *J Agric Food Chem.* 2003;51(8):2232–6. <https://doi.org/10.1021/jf0260139>
32. Fekadu A, Petros Y, Zelleke H. Genetic variability and association between agronomic characters in some potato (*Solanum tuberosum* L.) genotypes in SNNPRS, Ethiopia. *Int J Biodivers Conserv.* 2013;5(8):523–8.
33. Mohanty P, Ashok P, Sasikala K, Swami DV. Character association and path analyses in sweet potato. *Int J Veg Sci.* 2016;22(6):541–54. <https://doi.org/10.1080/19315260.2015.1084968>
34. Mazza G. Correlations between quality parameters of potatoes during growth and long-term storage. *Am Potato J.* 1983;60(3):145–59. <https://doi.org/10.1007/BF02853948>
35. Birhman RK, Singh BP. Path-coefficient analyses and genetic parameters of the components of field resistance of potatoes to late blight. *Ann Appl Biol.* 1995;127(2):353–62. <https://doi.org/10.1111/j.1744-7348.1995.tb06679.x>
36. Asghari-Zakaria R, Fathi M, Hasan-Panah D. Sequential path analysis of yield components in potato. *Potato Res.* 2006;49(4):273–9. <https://doi.org/10.1007/s11540-007-9022-9>
37. Srivastava A, Bhardwaj V, Singh BP, Khurana SP. Potato diversity and its genetic enhancement. In: *Gene pool diversity and crop improvement: volume 1.* Cham: Springer International Publishing; 2016. p. 187–226. [https://doi.org/10.1007/978-3-319-27096-8\\_6](https://doi.org/10.1007/978-3-319-27096-8_6)
38. Rajkumar, Kang GS. Path coefficient and stability analysis studies in Andigena potato. *Indian J Agric Sci.* 2000;70:158–62.
39. Dash SP, Singh J, Panigrahi T, Thakur P. Correlation and path analysis in sweet potato (*Ipomoea batatas* (L.) Lam.). *Plant Arch.* 2015;15(2):695–99.
40. Desai NC, Jaimini SN. Correlation and path analysis of some economic characters in potato. *J Indian Potato Assoc.* 1998;25(1–2):25–9.
41. Hunde NF, Galalcha DT, Limeneh DF. Correlation and path coefficient analyses of tuber yield and yield components among potato (*Solanum tuberosum* L.) genotypes at Bekoji, Southeastern Ethiopia. *Int J Agric Res Innov Technol.* 2022;12(2):144–54. <https://doi.org/10.3329/ijarit.v12i2.64102>
42. Lynch DR, Tai GCC. Yield and yield component response of eight potato genotypes to water stress. *Crop Sci.* 1989;29(5):1207–11. <https://doi.org/10.2135/cropsci1989.0011183X002900050024x>
43. Verma VS, Jha VB. Correlation and path analysis for quality traits in potato (*Solanum tuberosum* L.). *J Indian Potato Assoc.* 1990;17:169–72.
44. Wan X, Wang X, Xiao Q. Comparative metabolomic analysis of the nutrient composition of different varieties of sweet potato. *Molecules.* 2024;29(22):5395. <https://doi.org/10.3390/molecules29225395>
45. Zia MAB, Demirel U, Nadeem MA, Caliskan ME. Genome-wide association study identifies various loci underlying agronomic and morphological traits in diversified potato panel. *Physiol Mol Biol Plants.* 2020;26(5):1003–20. PMID:32377049. <https://doi.org/10.1007/s12298-020-00785-3>
46. Andre CM, Ghislain M, Bertin P, Oufir M, del Rosario Herrera M, Hoffmann L, et al. Andean potato cultivars (*Solanum tuberosum* L.) as a source of antioxidant and mineral micronutrients. *J Agric Food Chem.* 2007;55(2):366–78. <https://doi.org/10.1021/jf062740i>
47. Kamsali Pruthvi Raju, Roy A, Tigga A, Balraj G, Govindu M, Maneesha M. Genetic diversity analysis among *Solanum tuberosum* genotypes of potato under Indo-Gangetic plain. *Int J Adv Biochem Res.* 2026;10(1S):31–3. <https://doi.org/10.33545/26174693.2026.v10.i1Sa.6877>
48. Wang F, Li F, Wang J, Zhou Y, Sun H. Genetic diversity of the selected 64 potato germplasms revealed by AFLP markers. *Mol Plant Breed.* 2011;2(4). <https://doi.org/10.5376/mpb.2011.02.0004>
49. Monte MN, Rey Burusco MF, Carboni MF, Castellote MA, Sucar S, Norero NS, et al. Genetic diversity in Argentine Andean potatoes by means of functional markers. *Am J Potato Res.* 2018;95(3):286–300. <https://doi.org/10.1007/s12230-018-9630-8>
50. Wang Y, Rashid MAR, Li X, Yao C, Lu L, Bai J, et al. Collection and evaluation of genetic diversity and population structure of potato landraces and varieties in China. *Front Plant Sci.* 2019;10:139. <https://doi.org/10.3389/fpls.2019.00139>
51. Rasheed H, Ahmad D, Bao J. Genetic diversity and health properties of polyphenols in potato. *Antioxidants.* 2022;11(4):603. <https://doi.org/10.3390/antiox11040603>
52. Demeke T, Lynch DR, Kawchuk LM, Kozub GC, Armstrong JD. Genetic diversity of potato determined by random amplified polymorphic DNA analysis. *Plant Cell Rep.* 1996;15(9):662–7. <https://doi.org/10.1007/BF00231920>
53. Carputo D, Alioto D, Aversano R, Garramone R, Miraglia V, Villano C, et al. Genetic diversity among potato species as revealed by phenotypic resistances and SSR markers. *Plant Genet Resour.* 2013;11(2):131–9. <https://doi.org/10.1017/S1479262112000500>

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