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Evaluation of genetic variability, heritability and trait interrelationships in Potato (*Solanum tuberosum* L.) genotypes for yield and nutritional quality through planting at two environmental conditions in Northern India

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Abstract

This study was conducted during the Rabi season of 2024–25 in Northern India to evaluate the genetic variability, heritability, and trait interrelationships among five potato genotypes (*Solanum tuberosum* L.) evaluated under two planting dates (25 September 2024 and 10th October 2024). Analysis of variance revealed highly significant differences among the treatment combinations for all yield and nutritional quality traits. Higher yield values were generally observed under the second planting date (10th October 2024), with Kufri Kiran recording the highest total tuber yield (26.5 t/ha) and superior carotenoid content. High genotypic (GCV) and phenotypic (PCV) coefficients of variation were observed for anthocyanin, total flavonoid, and carotenoid contents, indicating substantial genetic variability for antioxidant-related traits. Uniformly high broad-sense heritability ($H^2 > 93\%$) was recorded for all traits, while high genetic advance as percent of mean (GAM) was particularly evident for anthocyanin (99.23%) and total flavonoid content (86.72%), suggesting the predominance of additive gene action and a good response to selection. Pearson correlation and Principal Component Analysis (PCA) demonstrated strong positive associations among yield-related traits and among antioxidant compounds, whereas sugar-related traits exhibited negative correlations with several yield and biochemical attributes. These findings identify Kufri Kiran and Kufri Surya as promising genotypes for the simultaneous improvement of yield and nutritional quality under North Indian conditions.

Keywords: *Solanum tuberosum* L., genetic variability, heritability, genetic advance, antioxidant activity, planting date, tuber yield

Introduction

Potato (*Solanum tuberosum* L.) is one of the most important food crops globally and ranks as a major staple in India which account for a substantial share of national production (Pandey *et al.*, 2020) ^[1]; (Singh *et al.*, 2024) ^[2]. It is the food and vegetable crop that is considered one of the most promising crops for alleviating inadequate and unbalanced nutrition crisis because of its high yield potential and large production area (Aksoy *et al.*, 202) ^[3]; (Zhou *et al.*, 2023) ^[4]. Beyond its contribution to food security, potato is recognized for its high nutritional value, serving as an excellent source of carbohydrates, high-quality protein, dietary fiber, vitamin C, vitamin B6, potassium and several essential minerals (Devaux *et al.*, 2021) ^[5]. As malnutrition and micronutrient deficiencies remain serious public health concerns, particularly in developing countries, strengthening the nutritional profile of widely consumed crops like potato is considered a practical and sustainable strategy to combat hidden hunger (WHO, 2024) ^[6]. Consequently, modern potato improvement programmes increasingly emphasize the simultaneous enhancement of yield and nutritional quality to ensure both food and nutrition security (Devaux *et al.*, 2021) ^[5].

In Northern India, potato cultivation forms a major component of the cropping system; however, productivity is often influenced by varietal performance, environmental fluctuations and

planting time (Pandey *et al.*, 2020) ^[1] Yield gaps persist due to limited availability of high-yielding, stress-tolerant and nutritionally enhanced cultivars adapted to variable planting dates (Singh *et al.*, 2024) ^[2]. Although breeding programmes in India have traditionally focused on improving yield potential and disease resistance, comparatively less emphasis has been placed on enhancing nutritional and biochemical quality traits alongside productivity (Sood *et al.*, 2025) ^[7]. The growing demand for nutritionally enriched food products necessitates the development of potato genotypes combining superior yield performance with enhanced levels of dry matter, vitamins, minerals and antioxidant compounds (Aishwarya *et al.*, 2024) ^[8]. Understanding the extent of genetic variability among genotypes, estimating heritability of key traits and studying correlations among yield and nutritional attributes are essential prerequisites for designing effective selection strategies in crop improvement programmes (Johnson *et al.*, 1955) ^[9]; (Panse & Sukhatme, 1985) ^[10].

Simultaneous improvement of tuber yield and nutritional quality can be challenging due to the complex inheritance patterns and environmental sensitivity of quantitative traits (Falconer and Mackay, 1996) ^[11]. In Northern India, variation in planting dates leads to differences in temperature regimes and crop phenology, which may alter the expression of yield and quality traits and influence genetic parameter estimates. Heritability and genetic advance are critical parameters for understanding the inheritance pattern of quantitative traits and predicting the efficiency of selection (Johnson *et al.*, 1955) ^[9]; Panse and Sukhatme, 1985) ^[10]. Moreover, correlation and path coefficient analyses help elucidate the interrelationships among yield and its component traits, enabling breeders to identify key attributes influencing overall productivity (Dewey and Lu, 1959) ^[12]. Nevertheless, comprehensive information on genetic variability, heritability and the association between tuber yield and nutritional traits under multiple planting dates is still limited. Therefore, the present investigation was undertaken to (i) assess the extent of genetic variability and heritability among potato genotypes evaluated under two planting dates in Northern India (ii) analyze the interrelationships between tuber yield and nutritional quality traits to facilitate the development of high-yielding and nutritionally enriched cultivars adapted to North Indian conditions.

Materials and Methods

Planting materials, experimental site and design

Five potato genotypes were used in this study namely Kufri Lima, Kufri Kiran, Kufri Bahar, Kufri Pukhraj and Kufri Surya procured from the Department of Vegetable Science, CCS Haryana Agricultural University, Hisar (Haryana). The present investigation was conducted during the Rabi season of 2024–25 at the Research Farm of the Department of Vegetable Science, CCS Haryana Agricultural University, Hisar, Haryana, India during the main cropping season of 2024 at 29°10' N, 75°46' E; 215.2 m amsl altitude. The experiment was laid out in a factorial randomized block design (RBD) with three replications. The treatments consisted of five potato genotypes and two planting dates, viz. 25 September 2024 and 10 October 2024, resulting in ten treatment combinations. Each plot measured 3.0 × 2.4 m², with a planting geometry of 60 cm × 20 cm.

Data Collection

Yield and Yield Components

Total number of tubers /plot

This metric was calculated by counting the number of tubers

from each of the randomly selected plants at the time of harvest from each plot and taking their average.

Total weight of tubers (kg/plot)

Total yield of potato was obtained from each plot and was expressed in kg.

Marketable tuber yield (kg/plot and t/ha)

Marketable tuber yield for each plot was calculated by subtracting the yield of tubers less than 25g in weight from total tuber yield obtained in kilogram per plot and then, the values were converted to tonnes per hectare.

Total tuber yield (kg/plot and t/ha)

The total tuber yield obtained from each plot was noted in kilogram per plot, and then, converted into tons per hectare.

Nutritional Traits

Carotenoid content, total phenolic content, total flavonoid content, anthocyanin content, total soluble sugar, total reducing sugar and anti-oxidant activity were determined using the following methods:

Carotenoid content (mg/g)

To measure carotenoid content, the protocol by (Hiscox and Israelstam 1979) ^[13] was followed. 50mg of finely chopped fresh leaves were ground with 5ml of 80% acetone and kept in the dark overnight. The supernatant was collected, and the process was repeated until the residue becomes colorless. The absorbance of the resulting solution was measured at 480nm, 645nm, and 663nm against an 80% acetone blank. Carotenoid content was calculated using the following equation:

$$\text{Carotenoid} = [A_{480} + (0.114(A_{663}) - (0.638 - A_{645}))] \times V/1000 \times W$$

Where;

V- Volume of 80% acetone solution.

W- Weight of leaf tissue in milligrams.

Total phenolic content

Total phenolic content was estimated using the method of Bray and Thorpe (1954) ^[14]. Sample was homogenized with 10ml of 80% methanol and centrifuged at 2000 rpm for 20 minutes. The supernatant was collected, and the residue was re-extracted with 80% methanol. This process was repeated 2 to 3 times collecting the supernatant each time. In a test tube, 1 ml of supernatant was mixed with 1 ml of Folin Ciocalteu reagent and 2 ml of 20% sodium carbonate. This solution was then placed in a water bath for 5 minutes, and absorbance was measured at 650 nm, using catechol as the standard.

Total flavonoid content

Fresh leaf samples (200 mg) were extracted in 5 ml of 80% acetone and then the extracts were centrifuged. To 1.5 ml of methanolic extract, add 1.5 ml of 2% AlCl₃ solution. The samples were incubated for an hour at room temperature. The absorbance was determined using spectrophotometer at 415 nm using blank without methanolic extract. The same procedure was repeated for the standard solution of Quercetin and the calibration line was construed. The content of flavonoids in extracts was expressed in terms of Quercetin Equivalent (QE).

Anthocyanin content

Total anthocyanin content was recorded with the method as

described by Hodges and Nozzolillo (1996)^[15]. Fresh leaves (0.1 g) were crushed in 2 mL of acidified methanol (methanol+1% HCl) by using the mortar and pestle. The homogenized material shifted to the test tube and boiled at 100°C for half an hour in the water bath. Centrifuge the material at 12000 rpm for 15 minutes. The absorbance was recorded at 530 nm and 600 nm with the help of the spectrophotometer (GENESYS 180UV-Visible Spectrophotometer). The anthocyanin content of the sample was expressed by cyaniding-3- glucoside (CGE) and calculated by using the following equation:

$$\text{Carotenoid} = [A_{530} + (0.114(A_{535}) - (0.638 - A_{645}))] \times V / 1000 \times W$$

Where,

$A_{530\text{nm}}$ and $A_{600\text{nm}}$ are the absorbance at 530 and 600 nm, respectively;

V is the total volume of extract;

Mw is the relative molecular weight of CGE (449.4);

ϵ is the molar extinction coefficient (29,600 M⁻¹ cm⁻¹);

m is the mass of the sample.

Total soluble sugar (mg/g)

For estimation, the method given by (Dubois *et al.*, 1956)^[16] was used. To extract total sugars from tubers, 100mg of crushed sample was taken and 10ml of 80% (v/v) methanol was added. The mixture was kept in water bath for one hour at 80°C with intermittent shaking. After cooling the homogenate was centrifuged at 4000 rpm for 20 minutes. The supernatant obtained after centrifugation was collected in separate tube and the residue left was heated again with 10ml of 80% (v/v) methanol at 80°C for one hour. Homogenate was centrifuged at 4000 rpm for 20 minutes. Supernatant thus obtained as pooled into the supernatant obtained earlier. This procedure is repeated thrice. The pooled was then concentrated by drying at 400 °C under water bath and 50% methanol was added to make the volume to 5ml. An aliquot of 0.5ml of above solution was taken in a test tube and 2ml of 2% (w/v) phenol and 5ml of concentrated H₂SO₄ added. The resultant mixture was cooled to room temperature and shaken using a vortex. The resultant colour was read by using spectrophotometer at 490 nm against blank reagent. The standard curve prepared using dextrose (50-300 µg/ml) was used to determine the amount of sugar in sample.

Total reducing sugar(mg/g)

It was estimated through method suggested by (Hulme and Narain, 1996)^[17]. The measurement was performed according to the procedure of Krivorotova and Sereikaite with slight modification. DNSA reagent was prepared by dissolving 1g of DNSA and 30g of sodium-potassium tartaric acid in 80mL of 0.5N NaOH at 45°C. After dissolution, the solution was cooled down to room temperature and diluted to 100mL with the help of distilled water. For the measurement, 2mL of DNSA reagent was pipetted into a test tube containing 1mL of plant extract (1mg/mL) and kept at 95°C for 5 minutes. After cooling, 7mL of distilled water was added to the solution and the absorbance of the resulting solution was measured at 510nm using a spectrophotometer. The reducing sugar content was calculated from the calibration curve of standard D-glucose (200-1000mg/L), and the results were expressed as mg D-glucose equivalent (GE) per gram dry extract weight.

Anti-oxidant activity (µmole/g)

The antioxidant activity was calculated using DPPH method by

the procedure reported by Apak *et al.*, (2016)^[18]. By dissolving 0.025g of DPPH in 1L of 70% methanol the standard DPPH solution was prepared. This solution is stored in dark conditions until use (absorbance value of 0.8±0.02 at 517 nm). The working solution was made by mixing 3.9ml of DPPH solution followed by addition of 0.1ml of potato leaf sample extract and left for 30 min to react. The absorbance values were read at 517nm, by using a UV- visible spectrophotometer. High percent inhibition values indicate the high antioxidant activity. DPPH activity can be measured using the following formulae:

$$\text{Anthocyanin (mg } \epsilon^{-1}\text{FW)} = (A_{530\text{nm}} - A_{600\text{nm}}) \times \frac{V \times M_w}{\epsilon \times m}$$

Data analysis

- The data obtained were subjected to ANOVA using OPSTAT software. The traits that exhibited significant mean squares in general ANOVA was further subjected to genetic analyses using the software R version 4.3.2 (R Core Team, 2024)^[19].

Phenotypic and genotypic variance

The phenotypic and genotypic variance and coefficients of variance of each trait were calculated using the formula suggested by (Singh and Chaudhary, 1996)^[20] as follows.

Genotypic variance (σ^2_g) = $MS_g - MSe / r$, where σ^2_g = genotypic variance, MS_g = mean square of genotypes, MSe = mean square of experimental error, r = number of replications, and environmental variance (σ^2_e) = mean square of error.

Phenotypic variance (σ^2_p) = $\sigma^2_g + \sigma^2_e$, where σ^2_p , σ^2_g and σ^2_e = phenotypic, genotypic, and environmental variance, respectively.

$$PCV = (\sqrt{\sigma^2_p} / \bar{X}) * 100 \text{ and } GCV = (\sqrt{\sigma^2_g} / \bar{X}) * 100$$

where PCV and GCV = phenotypic and genotypic coefficient of variation, respectively, and $\bar{X}$ = grand mean of the character evaluated.

Heritability

Broad-sense heritability (H^2) is the proportion of phenotypic variance (σ^2_p) and genotypic variance

(σ^2_g) using the formula suggested by (Falconer and Mackay, 1996)^[11]. as follows:

$$H^2 = (\sigma^2_g / \sigma^2_p) * 100$$

Expected genetic advance under selection (GA) and as percent of mean (GAM)

Genetic advance in absolute unit (GA) and percent of the mean (GAM), assuming selection of the superior 5% of the genotypes, were calculated using the methods illustrated by (Johnson *et al.*, 1955)^[9]; as follows:

$GA = K * SD_p \times H^2$ where, GA = genetic advance, SD_p = phenotypic standard deviation on mean basis, H^2 = broad-sense heritability, and K = standardized selection differential at 5% selection intensity ($K = 2.063$).

$GAM = GA / \bar{X} * 100$, where GAM = genetic advance as percent of mean, GA = genetic advance, and $\bar{X}$ = grand mean of the character evaluated.

Pearson correlation and principal component analysis

Pearson correlation and principal component analysis were performed by the variability package of the software R version 4.3.2 (R Core Team, 2024)^[19].

Results and Discussion
Analysis of variance, mean performance of tuber yield and nutritional quality traits
The analysis of variance revealed highly significant ($p \leq 0.01$)

differences among the ten treatment combinations comprising five potato genotypes evaluated under two planting dates for yield and nutritional quality traits (Table 1).

Table 1: Expected mean squares of yield and nutritional quality traits of potato genotypes

Analysis of variance	df	Mean sum of square										AA
		TNT	TWT	MTY	TTY	Car	TPC	TFC	Anth	TSS	TRS	
Replication	2	52.50	0.013	2.663	0.013	0.001	0	0.02	0	0.175	0.082	0.073
Treatment	9	8,453.33**	16.285**	16.285**	16.285**	0.419**	1.738**	1.91**	0.005**	26.068**	0.613**	297.096**
Error	18	21.944	0.121	0.121	0.121	0.005	0.001	0.003	0	0.086	0.004	0.51

TNT – Total number of tubers per plot; TWT – Total weight of tubers per plot (kg); NDT – Number of deformed tubers; WDT – Weight of deformed tubers per plot (kg); MTY – Marketable tuber yield (t ha⁻¹); TTY – Total tuber yield (t ha⁻¹) Car – Carotenoid content (mg g⁻¹ FW; TPC – Total phenolic content (mg g⁻¹ FW); TFC – Total flavonoid content (mg g⁻¹ FW); Anth – Anthocyanin content (mg g⁻¹ FW); TSS – Total soluble sugars (mg g⁻¹ FW); TRS – Total reducing sugars (mg g⁻¹ FW); AA – Antioxidant activity(μmol/g)

The performance of five potato genotypes evaluated under two planting dates (D₁ and D₂) revealed substantial variation for yield and nutritional quality traits (Table 2). Total number of tubers (TNT) ranged from 185 to 240 under D₁ and 290 to 325 under D₂, with Kufri Kiran recording the highest values at both dates, whereas Kufri Bahar showed the lowest. Total tuber weight (TWT) varied from 11.8 to 16.8 kg/plot under D₁ and 13.7 to 19.1 kg/plot under D₂. Marketable tuber yield (MTY) ranged from 13.6 to 20.6 t/ha (D₁) and 16.3 to 23.8 t/ha (D₂), while total tuber yield (TTY) varied from 16.4 to 23.3 t/ha under D₁ and 19.1 to 26.5 t/ha under D₂. In general, higher yield values were observed under D₂, indicating the influence of planting date on yield expression, as also reported under North Indian conditions (Singh *et al.*, 2024)^[2].

Quality traits also exhibited marked variability. Carotenoid content ranged from 0.11 to 0.43 mg/g (D₁) and 0.16 to 0.48 mg/g (D₂), with Kufri Kiran showing the highest values. Total phenolic content (TPC) ranged from 1.40 to 3.38 mg/g under D₁ and 0.95 to 2.30 mg/g under D₂, while total flavonoid content (TFC) varied from 1.16 to 3.32 mg/g (D₁) and 0.81 to 2.15 mg/g (D₂). Anthocyanin content ranged from 0.03 to 0.12 mg/g under D₁ and 0.04 to 0.15 mg/g under D₂. Total soluble sugars (TSS) ranged from 17.2 to 25.5 mg/g (D₁) and 16.8 to 24.1 mg/g (D₂), whereas total reducing sugars (TRS) varied from 1.8 to 2.9 mg/g (D₁) and 1.4 to 2.6 mg/g (D₂). Antioxidant activity (AA) ranged from 30.7 to 53.5% under D₁ and 22.7 to 41.2% under D₂, with Kufri Kiran and Kufri Surya exhibiting comparatively higher antioxidant potential. The observed genotypic differences suggest the presence of exploitable genetic variability for simultaneous improvement of yield and nutritional quality traits (Devaux *et al.*, 2021)^[5]; Sood *et al.*, 2025)^[7].

Genetic Parameters

The estimates of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad-sense heritability (H²), genetic advance (GA), and genetic advance as percent of mean (GAM) are presented in (table 3) For all the traits, PCV values were slightly higher than their corresponding GCV values, indicating limited environmental influence and a predominant genetic control over trait expression. The narrow PCV–GCV differences suggest that phenotypic performance reliably reflects genotypic potential, thereby improving the efficiency of selection. Similar observations have been reported in recent potato studies under controlled field conditions (Alam *et al.*, 2023)^[21]; (Reddy *et al.*, 2024)^[22].

High GCV and PCV were observed for anthocyanin content (49.73% and 51.34%), total flavonoid content (42.20% and 42.30%), carotenoid content (40.12% and 40.45%), and total phenolic content (37.05% and 37.07%), indicating substantial genetic variability for antioxidant-related traits. Moderate variability was recorded for total number of tubers, total reducing sugars, and antioxidant activity, while comparatively lower values were noted for total tuber weight, total tuber yield, and total soluble sugars. Traits exhibiting moderate to high GCV are considered amenable to improvement through direct selection. Comparable results for yield and biochemical traits have been documented in recent germplasm evaluations of potato (Verma *et al.*, 2024)^[23]; (Khan *et al.*, 2025)^[24].

Heritability estimates were uniformly high, ranging from 93.83% (anthocyanin content) to 99.87% (total phenolic content). High heritability coupled with high GAM was particularly evident for anthocyanin (99.23%), total flavonoid content (86.72%), carotenoid content (81.95%), total phenolic content (76.26%), and total reducing sugars (43.89%), indicating predominance of additive gene effects and good response to selection. Yield traits exhibited high heritability with moderate GAM, suggesting involvement of both additive and non-additive gene action. Similar trends have been reported in recent potato breeding studies (Sharma *et al.*, 2023)^[25]; Gupta *et al.*, 2025)^[29]. Overall, the results demonstrate substantial exploitable genetic variability for simultaneous yield and nutritional improvement.

Table 2: Mean Performance of tuber yield and yield components and nutritional traits of potato genotypes

Genotypes	Mean sum of square																				AA (μmol/g)	
	TNT		TWT (kg/plot)		MTY(t/ha)		TTY (t/ha)		Car(mg/g)		TPC (mg/g)		TFC (mg/g)		Anth (mg/g)		TSS (mg/g)		TRS (mg/g)			
	D1	D2	D1	D2	D1	D2	D1	D2	D1	D2	D1	D2	D1	D2	D1	D2	D1	D2	D1	D2		
Kufri Lima	215	305	15.6	18.6	18.9	23.0	21.6	25.8	0.29	0.36	2.50	1.70	2.17	1.50	0.07	0.09	17.2	16.8	1.8	1.4	42.0	33.2
Kufri Kiran	240	325	16.8	19.1	20.6	23.8	23.3	26.5	0.43	0.48	3.38	2.30	3.32	2.15	0.12	0.15	19.3	17.9	2.3	1.6	53.5	41.2
Kufri Bahar	185	290	11.8	13.7	13.6	16.3	16.4	19.1	0.11	0.16	1.40	0.95	1.16	0.81	0.03	0.04	21.0	19.8	2.1	1.9	30.7	22.7
Kufri Pukhraj	200	300	13.0	14.3	15.3	17.1	18.1	19.9	0.21	0.25	1.90	1.35	1.70	1.21	0.05	0.06	25.5	24.1	2.9	2.6	32.7	25.9
Kufri Surya	205	305	14.6	15.7	17.5	19.0	20.3	21.8	0.38	0.43	3.01	2.05	2.98	1.90	0.08	0.12	22.8	21.7	2.4	2.2	50.2	38.0
Mean	209	305	14.4	16.3	17.2	19.8	19.9	22.6	0.28	0.34	2.44	1.67	2.27	1.51	0.07	0.09	21.2	20	2.3	1.9	41.8	32.2

Table 3: Estimates of variability components for yield and nutritional traits of potato genotypes

S. No.	Character	Heritability (%)	GCV (%)	PCV (%)	GA	Genetic Advance as% of mean (GAM) (5%)
1	TNT	99.23	20.63	20.71	108.79	42.33
2	TWT	97.80	15.15	15.32	4.73	30.86
3	MTY	97.80	17.42	17.62	4.73	35.49
4	TTY	97.80	15.15	15.32	4.73	30.86
5	Car	98.36	40.12	40.45	0.25	81.95
6	TPC	99.87	37.05	37.07	1.57	76.26
7	TFC	99.52	42.20	42.30	1.64	86.72
8	Anth	93.83	49.73	51.34	0.08	99.23
9	TSS	99.01	14.29	14.36	6.03	29.28
10	TRS	97.98	21.52	21.74	0.92	43.89
11	AA	99.49	26.87	26.94	20.43	10.82

Correlation

Pearson correlation analysis among the studied traits revealed that total tuber yield (TTY) showed a strong and positive correlation with marketable tuber yield (MTY), indicating the importance of these traits for improving overall tuber productivity in potato. (Fig.1). Positive correlations were also observed among yield-related traits such as total number of tubers (TNT) and tuber weight (TWT) with MTY and TTY, suggesting that these traits play a significant role in determining tuber yield. Similar positive associations among yield components in potato were reported by Luthra *et al.* (2018) [26], who observed a strong relationship between marketable tuber yield and total tuber yield. Furthermore, biochemical traits including total phenolic content (TPC), total flavonoid content (TFC), and anthocyanin (Anth) showed positive correlations with each other, indicating a close association among antioxidant compounds. Comparable relationships among antioxidant compounds in potato tubers were also reported by Navarre *et al.*, (2011) [27] and Tsao *et al.*, (2006) [28]. However, sugar-related traits such as total soluble sugars (TSS) and total reducing sugars (TRS) exhibited negative correlations with several yield and biochemical traits, suggesting a possible trade-off between sugar accumulation and yield performance.

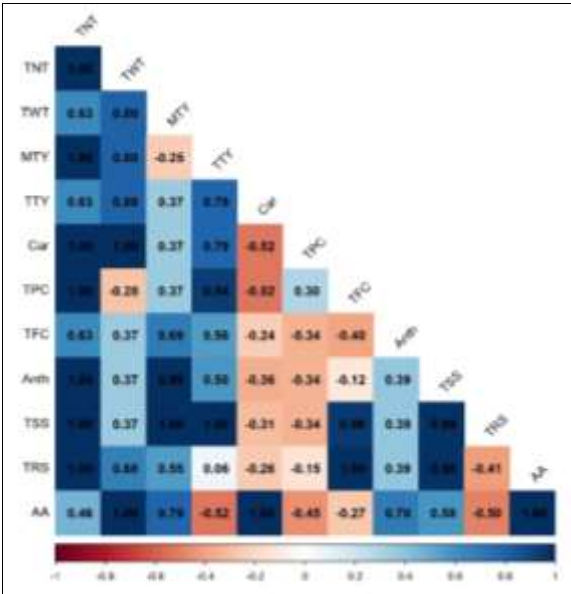


Fig1: Pearson phenotypic correlation heatmap showing the relationships among yield and biochemical traits of potato (*Solanum tuberosum* L.) genotypes. TNT = Total number of tubers, TWT = Tuber weight, MTY = Marketable tuber yield, TTY = Total tuber yield, Car = Carotenoid content, TPC = Total phenolic content, TFC = Total flavonoid content, Anth = Anthocyanin content, TSS = Total soluble sugars, TRS = Total reducing sugars, and AA = Anti-oxidant activity

Principal Component Analysis

Principal component analysis (PCA) revealed that the first two principal components explained a large proportion of the total variation among the studied traits. The first principal component (Dim1) accounted for 78.7% of the total variability, while the second component (Dim2) explained 17.6%, together contributing 96.3% of the cumulative variation. Yield-related traits including total number of tubers (TNT), tuber weight (TWT), marketable tuber yield (MTY), and total tuber yield (TTY) across both planting dates were closely grouped and oriented in a similar direction, indicating strong positive associations among these traits. Similarly, biochemical traits such as total phenolic content (TPC), total flavonoid content (TFC), and anthocyanin (Anth) formed a distinct cluster, suggesting a strong relationship among antioxidant compounds. In contrast, sugar-related traits including total soluble sugars (TSS) and total reducing sugars (TRS) were positioned in a different direction, indicating weaker associations with several yield traits. Similar patterns of trait contribution and variability using PCA in potato genotypes have been reported by (Sood *et al.*, 2025) [7].

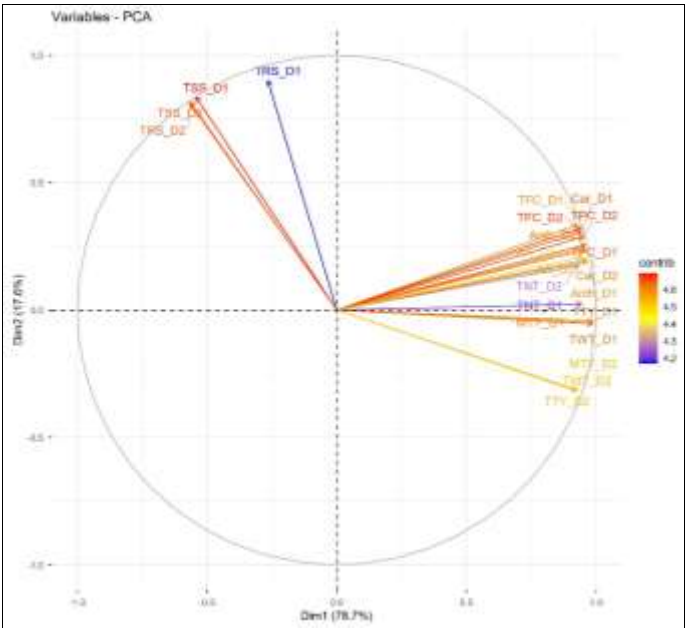


Fig 2: Principal component analysis (PCA) variable plot showing the relationships among yield and biochemical traits of potato (*Solanum tuberosum* L.) genotypes evaluated across two planting dates. TNT = Total number of tubers, TWT = Tuber weight, MTY = Marketable tuber yield, TTY = Total tuber yield, Car = Carotenoid content, TPC = Total phenolic content, TFC = Total flavonoid content, Anth = Anthocyanin content, TSS = Total soluble sugars, TRS = Total reducing sugars, and AA = Anti-oxidant activity

Conclusion

The present investigation highlights the significant impact of both genotype and planting date on the productivity and nutritional profile of potato in Northern India. The second planting date proved more conducive for maximizing tuber yield, with Kufri Kiran and Kufri Surya emerging as the most high-yielding and nutritionally sound genotypes. The study revealed high broad-sense heritability coupled with high genetic advance for most antioxidant-related traits, suggesting that direct selection for these characters would be highly effective for crop improvement. Furthermore, the strong positive correlation among yield components and the distinct clustering of biochemical traits in PCA provide a clear roadmap for breeders to select for multiple traits simultaneously. However, the negative relationship observed between sugar accumulation and yield suggests that a balanced selection strategy is necessary to maintain productivity while enhancing quality. Overall, these results provide a robust genetic basis for developing superior potato cultivars that cater to both food security and the growing demand for nutritionally enriched produce.

Acknowledgments

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Author Contributions

Garima Kanyal: Investigation, Data curation, Writing - original draft, Writing - review & editing, Data interpretation. Davinder Singh: Conceptualization, Investigation, Methodology, Writing - original draft, Writing - review & editing, Data interpretation, Supervision. Surender Kumar Dhankhar: Writing - original draft, Writing - review & editing, Methodology, Data interpretation. Arusha Sharma: Writing - review & editing, Data interpretation. Makhan Lal: Methodology, Writing - review & editing; Kuldeep Kumar: Conceptualization; Methodology, Writing - review & editing; Vikash Kumar: Methodology, Writing - review & editing.

Statements and Declarations

Data Availability

The data and materials of this study are presented in the manuscript; further inquiries can be directed to the corresponding author.

Conflict of Interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Ethics Approval and Consent to Participate

All authors provided consent for their participation in this research. The study did not involve any research on animals or experiments on humans that would require approval from an Ethics Committee or an Ethical Clearance Number.

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