



Biochemical profiling of tetraploid potato (*Solanum tuberosum*) genotypes

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ABSTRACT

An experiment was conducted out during winter (*rabi*) seasons of 2021–22 and 2022–23 at Litchi and Mango Research Station (Dr. Y S Parmar University of Horticulture and Forestry, Solan, Himachal Pradesh), Nagrota Bagwan, Kangra, Himachal Pradesh to study the biochemical profiling of tetraploid potato (*Solanum tuberosum* L.) genotypes. The experiment comprises of 357 genotypes including varieties, advanced breeding lines and exotic germplasm belonging to the tetraploid group of potato were evaluated in augmented block design. Data were recorded on different biochemical attributes. Adjusted mean values indicated that CP 3145 (10.15°Brix) for total soluble solids, CP 1689 (36.89 mg/g) for total polyphenols, CP 1302 (28.68 mg/100 g) for ascorbic acid, CP 3891 (24.41 µg/g) for total carotenoids content, CP 1667 (0.21%), for total sugars, CP 1667 (0.10%) for reducing sugars and CP 1884 (0.06%) for non-reducing sugars were the top ranked genotypes. High PCV and GCV were observed for total polyphenols and total carotenoids content. High heritability coupled with high genetic advance was recorded for total polyphenols, ascorbic acid content, starch content, total carotenoids content and reducing sugars. Principal component analysis indicated the three most informative principal components with more than one eigen value, accounting for 57.40% of the total variance for all traits.

Keywords: GCV, Genetic advance, Genotypes, Heritability, PCV, Traits

Potato (*Solanum tuberosum* L.) is one of the most significant and calorie-dense vegetable crops, has the ability to feed the world's expanding population. Its consumption is increasing day by day, as a result of its high nutritional content and wide range of adaptation (Pradhan *et al.* 2015). During the growing season, the potato thrives mostly in regions with fairly chilly temperatures during the day with bright sunshine, as well as cool nights (Das *et al.* 2014). In order to combat poverty and malnutrition, it is thus a crucial crop for providing food and nutritional security (Singh *et al.* 2021). Potatoes have a number of biochemical components that are extremely desirable in the diet, including starch content, ascorbic acid, reducing sugars, non-reducing sugars, total sugars, phenolic content and carotenoids. The development of analytical methods has allowed for the identification of the roles played by different biochemical and antioxidant characteristics of potato tubers (Brar *et al.*

2017). To introduce desired genes from variable germplasm into the current genetic foundation require knowledge about levels and patterns of genetic variability. This suggests that the degree of genetic variety in the germplasm is roughly inversely correlated with a crop's capacity for development and offers a chance to improve yield and quality through a deliberate breeding effort. From breeding point of view, the main emphasis is on heritable characters and genetic parameters (Sekhon and Sharma 2019). The heritability estimates forecast the consistency of phenotypic values in trait expression (Unche *et al.* 2008). Genetic variation is a highly important aspect for the success of a breeding programme (Singh *et al.* 2024). Several scientists have emphasized the significance of genetic diversity in the selection of optimal genotypes for hybridization. The development of cutting-edge biometrical techniques has made it feasible to model the genotypes in a desired genetic architecture (Pradhan *et al.* 2015). In order to maximize the nutritional content in potato, special attention must be paid to use the genetically diverse parents. Hence an experiment was planned to study the biochemical profiling of tetraploid potato.

MATERIALS AND METHODS

The present experiment was conducted during winter (*rabi*) seasons of 2021–22 and 2022–23 at the Litchi and

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Mango Research Station (Dr. Y S Parmar University of Horticulture and Forestry, Solan, Himachal Pradesh), Nagrota Bagwan, Kangra, Himachal Pradesh. Experimental site is located in mid hill zone of Himachal Pradesh with humid sub subtropical climate. During the growing seasons average values for mean maximum temperature was 27.68°C and 26.33°C, mean minimum temperature was 8.94°C and 11.43°C, average relative humidity was 75.46% and 73.48%, average rainfall was 13.60 mm and 14.38 mm; respectively (Chaudhary Sarwan Kumar Himachal Pradesh Krishi Vishvavidyalaya, Palampur). The experimental material comprised of 357 potatoes (Supplementary Table 1) genotypes obtained from ICAR-Central Potato Research Institute, Shimla, Himachal Pradesh. Experiment was laid out in augmented block design on 28th December, 2021 during 1st year planting and 21th December, 2022 during 2nd year planting with six blocks and in each block 59 genotypes along with three standard checks (Kufri Girdhari, Kufri Himalini and Kufri Jyoti) were planted. The package of practices to raise the healthy crop were followed as per the recommendations by ICAR-Central Potato Research Institute, Shimla, Himachal Pradesh.

Pooled data were analyzed for phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) and heritability (h^2) in broad sense and were calculated as per Burton and De Vane (1953). GA (Genetic advance) was estimated according to the procedure of Johnson *et al.* (1955). The procedure as described by Pardo *et al.* (2000) was used to determine the total soluble solids (°Brix) of the fresh potato tubers using a hand refractometer, total polyphenols (mg/g) were determined as per the method described by Makkar *et al.* (2003), ascorbic acid content (mg/100 g) was estimated according to Ranganna (1979), starch content (%) was calculated as suggested by Hedge

and Hofreiter (1962), with D-glucose serving as the standard, total carotenoids content (µg/g) was determined (absorbance = µg carotene/100 g flesh weight) by following the protocol described by Thomas and Joshi (1997), total sugars were estimated by following the procedure of DuBois *et al.* (1956) and reducing sugars were calculated according to Miller (1972) while non-reducing sugar content was determined by deducting the reducing sugar content from total sugars.

Statistical analysis: Various packages of R programming were used to analyze the data. PAST 4.13 software was used for principal component analysis (PCA) to determine the appropriate associations among different traits.

RESULTS AND DISCUSSION

Genetic variability studies: The perusal of the adjusted mean values for different genotypes revealed significant variations for different biochemical parameters. This suggests that genotypes have a wide range of genetic variability, which would provide tremendous prospects for genetic improvement in potato. The total soluble solids (TSS) ranged from 4.83 (CP 4798)–10.15°Brix (CP 3145) during 2021–22, 4.55 (KCM)–10.20°Brix (CP 2390) during 2022–23 and 5.14 (CP 4798)–10.15°Brix (CP 3145) in pooled years (Table 1). In pooled over years, 102 genotypes performed statistically at par with the top ranked genotype i.e. CP 3145 (10.15°Brix). TSS, which is composed of fructose, glucose, and sucrose that were converted from starch, grew as ambient storage time increased, firstly it increased slowly but subsequently, it increased rapidly (Mostofa *et al.* 2019). Datta *et al.* (2015) also reported a wide range of variations for TSS in their breeding material. The most prevalent antioxidants in human diets are a class of secondary metabolites called polyphenols, which have drawn increased attention from food marketers, manufacturers and

Table 1 Mean, range and coefficient of variation for 357 genotypes of potato for different biochemical traits during 2021–22, 2022–23 and pooled over years

Trait	Mean			Range			CV		
	2021–22	2022–23	Pooled	2021–22	2022–23	Pooled	2021–22	2022–23	Pooled
Total soluble solids (°Brix)	7.54	7.13	7.54	4.83- 10.15	4.55- 10.20	5.14- 10.15	7.78	8.06	7.75
Total polyphenols (mg/g)	18.4	22.96	18.41	8.96- 39.24	12.18- 39.52	9.95- 36.89	10.48	14.67	11.76
Ascorbic acid content (mg/100 g)	18.53	20.67	19.04	11.25- 30.65	11.24- 31.19	11.50- 28.68	7.64	7.01	6.69
Starch content (%)	15.95	17	15.97	9.55- 26.35	9.37- 26.29	10.34- 24.41	8.15	11.98	9.25
Total carotenoids content (µg/g)	1.23	1.28	1.23	0.28- 2.70	0.52- 2.57	0.40- 2.60	14.97	12.80	12.27
Total sugars (%)	0.34	0.34	0.34	0.18- 0.60	0.21- 0.54	0.21- 0.59	8.88	13.12	10.01
Reducing sugars (%)	0.22	0.23	0.22	0.10- 0.40	0.10- 0.39	0.10- 0.36	8.65	16.25	11.72
Non-reducing sugars (%)	0.12	0.11	0.12	0.03- 0.28	0.02- 0.30	0.06- 0.30	23.38	28.33	16.15

consumers due to their potential health advantages (Mahdavi *et al.* 2010). Considerable variation for phenol content was recorded ranging from 8.96 (CP 3632) – 39.24 mg/g (CP 1689) during 2021–22, 12.18 (JEX/A 498)–39.52 mg/g (CP 4175) during 2022–23 and 9.95 (CP 3588)–36.89 mg/g (CP 1689) in pooled years (Table 1). Marwaha *et al.* (2010) and Dalamu *et al.* (2015) also reported significant differences for total polyphenols in potato genotypes. Ascorbic acid is a phytonutrient that is necessary for living cells' metabolism and is found in varying amounts in natural foods. It is also regarded as the main dietary antioxidant (Mahdavi *et al.* 2010). Ascorbic acid content for different genotypes ranged from 11.25 (JEX/A 45)–30.65 mg/100 g (CP 1302) during 2021–22, 11.24 (CP 1330)–31.19 mg/100 g (CP 1688) in 2022–23 and 11.50 (CP 3608)–28.68 mg/100 g (CP 1302) in pooled years with population mean of 18.53 mg/100 g, 20.67 mg/100 g and 18.58 mg/100 g in the respective years. Dalamu *et al.* (2015) and Andre *et al.* (2017) also observed sufficient variations for ascorbic acid in different genotypes. Granules of starch make up the majority of a potato tuber's dry mass. The tuber's reserve ingredient for respiration and sprouting is starch. For the potato starch industry, the chemical makeup of the potato is crucial (Grommers and Van der Krogt 2009). In case of starch content, 98 genotypes, in pooled over years, were statistically at par with the top ranked genotype CP 3891 (24.41%) while the standard check i.e. Kufri Girdhari was significantly superior than 240, 111 and 201 genotypes during 2021–22, 2022–23 and pooled over years, respectively. Kaur and Aggarwal (2014) also reported variations for starch content. In the potato tuber flesh, carotenoids generally present as the yellow-pigment which protects against various diseases and infections. The concentration of carotenoids in potato is generally governed by the genetic material as well as environmental factors. The highest carotenoid content was observed for CP 3091 (2.70 µg/g, 2.57 µg/g and 2.60 µg/g) as compared to population means of 1.23 µg/g, 1.28 µg/g and 1.23 µg/g during 2021–22, 2022–23 and pooled years, respectively.

Andre *et al.* (2017) also reported significant variations for total carotenoids content.

Potato tubers also contain a small fraction of sugars, viz. sucrose, glucose and fructose and their concentration is generally effected by the genotype as well as the environmental conditions. The lowest value for total sugar content was observed in genotype CP 1667 (0.18%, 0.21%, 0.21%) with the population mean of 0.34%, 0.35% and 0.34% in respective years. Further, critical evaluation of data indicated that Kufri Girdhari was significantly superior to 84, 55 and 90 genotypes during 2021–22, 2022–23 and pooled over years, respectively. Reducing sugar content is an important quality criterion for processing purpose. Higher sugar content in potato tubers affects the quality of potato chips and even changes the colour of chips from yellow to dark brown. In pooled over years, 143 genotypes were statistically at par with the top ranking genotype CP 1667 (0.10%) having lowest reducing sugar content. Choi *et al.* (2020) also observed similar variations for reducing sugars in their breeding material. The lowest value of non-reducing sugars was observed in CP 1884 (0.06%), statistically at par with all the genotypes except 24 genotypes.

The choice of superior/desirable genotypes often depends on the phenotypic characteristics that occur from interactions between the genotype and the environment. Combining genetic advance and heritability is more helpful in determining the genuine effects of selection. (Johnson *et al.* 1955). As a result, the genetic advance has an advantage over heritability and breeders may use it as a guide throughout the selection process. A critical evaluation of the results revealed that all the biochemical characteristics showed either high or medium magnitude of genotypic coefficient of variation for all the traits irrespective of years and pooled over years indicating the presence of broad genetic base. High PCV and GCV were observed for total polyphenols and total carotenoids irrespective of years. Besides, starch content also showed high PCV estimates during both the years as well as in pooled over

Table 2 Estimates of parameters of variability for different traits in potato during 2021–22, 2022–23 and pooled over years

Trait	GCV			PCV			h ² _{bs}			GAM (%)		
	2021–22	2022–23	Pooled	2021–22	2022–23	Pooled	2021–22	2022–23	Pooled	2021–22	2022–23	Pooled
Total soluble solids (°Brix)	13.01	12.90	11.57	15.15	15.21	13.92	73.71	71.90	69.1	23.04	22.56	19.85
Total polyphenols (mg/g)	32.61	20.21	25.38	34.23	24.92	27.94	90.76	65.74	82.5	64.08	33.80	47.56
Ascorbic acid content (mg/100 g)	25.85	17.83	20.56	26.94	19.13	21.6	92.07	86.87	90.58	51.17	34.29	40.36
Starch content (%)	23.99	17.55	20.5	25.36	21.29	22.52	89.50	67.98	82.91	46.83	29.85	38.52
Total carotenoids content (µg/g)	38.84	32.95	36.16	41.67	35.37	38.21	86.87	86.78	89.55	74.69	63.32	70.6
Total sugars (%)	23.27	12.96	18.02	24.91	18.47	20.63	87.25	49.25	76.31	44.84	18.77	32.48
Reducing sugars (%)	24.13	15.53	19.72	25.65	22.52	22.97	88.52	47.54	73.74	46.84	22.08	34.94
Non-reducing sugars (%)	27.86	15.13	12.39	36.30	32.18	28.9	58.89	22.10	18.38	44.10	14.67	10.96

PCV, Phenotypic coefficient of variation; GCV, Genotypic coefficient of variation; h²_{bs}, Heritability in broad sense; GAM, Genetic advance over mean (%).

Table 3 Principal component analysis for different biochemical traits in potato in pooled over years

Trait	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
Total soluble solids (°Brix)	0.04	0.64	-0.15	0.05	0.05	0.75	-0.10	-0.04
Total polyphenols (mg/g)	-0.02	0.16	0.70	0.24	-0.66	0.04	0.05	0.01
Ascorbic acid content (mg/100 g)	-0.14	0.28	-0.44	0.74	-0.15	-0.35	0.10	-0.01
Starch content (%)	-0.02	-0.56	0.17	0.57	0.29	0.47	0.13	0.02
Total carotenoids content (µg/g)	0.01	0.40	0.51	0.15	0.68	-0.30	0.00	0.01
Total sugars (%)	0.65	-0.03	-0.01	0.10	-0.02	-0.06	-0.05	-0.75
Reducing sugars (%)	0.56	-0.04	-0.02	0.16	-0.03	-0.05	-0.60	0.55
Non-reducing sugars (%)	0.50	0.10	-0.05	-0.07	-0.01	0.01	0.77	0.37
Eigen values	2.33	1.19	1.07	0.94	0.92	0.86	0.67	0.02
Variability (%)	29.10	14.90	13.30	11.70	11.50	10.80	8.40	0.20
Cumulative (%)	29.10	44.00	57.40	69.10	80.70	91.40	99.80	100.00

years. In addition, total sugars during 2021–22, ascorbic acid content in pooled over years also showed high GCV estimates (Table 2). Earlier research workers have also observed high or medium magnitude of PCV and GCV for starch content (Tessema *et al.* 2022 and Zeleke *et al.* 2021) and total soluble solids (Zeleke *et al.* 2021). The heritability estimates were high for total polyphenols, ascorbic acid content, starch content and total carotenoids content during 2021–22, 2022–23 and pooled over years. Seid *et al.* (2023) also reported high heritability estimates in their breeding material. High heritability along with high genetic advance was reported for total polyphenols, ascorbic acid content, starch content, total carotenoids content and reducing sugar content during both the years in addition to total soluble solids during 2021–22, total sugars during 2021–22 and pooled over years, thereby indicating the importance of additive gene action for the inheritance of these traits and

improvement can be possible through phenotypic selection for these traits. Similar results were found by Zeleke *et al.* (2021) and Tessema *et al.* (2022) in their respective breeding material.

Principal component analysis: According to principal component analysis (PCA), each axis of differentiation has a significant large contribution to the overall variance (Sharma 1998). On the basis of eigen values greater than one, principal components were selected. The PCA (Table 3) for different attributes revealed the three most valuable principal components with eigen values 2.33, 1.19 and 1.07, respectively accounting for 57.40% of the total variance for all the attributes. PC1 imitates that total sugars, reducing sugars and non-reducing sugars had comparatively more significant contributions to the total biochemical variability. The results of PCA are like those of Tessema *et al.* (2022). Seid *et al.* (2023) also recorded similar results

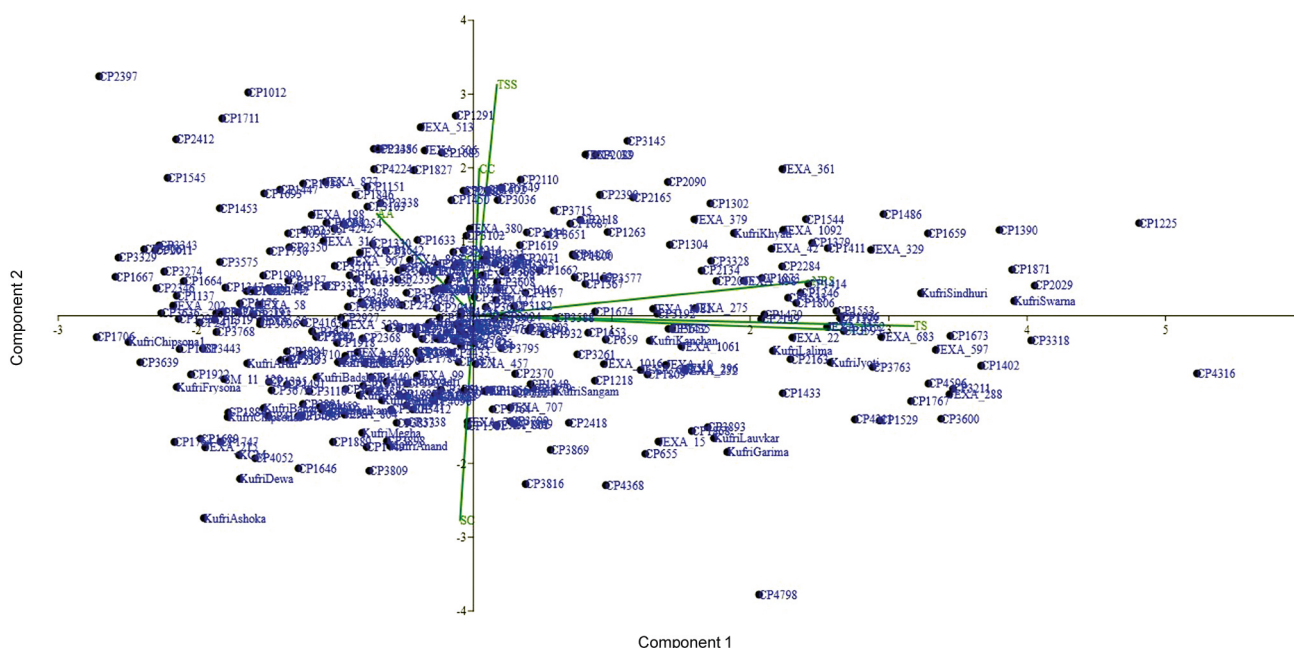


Fig. 1 Biplot among first two PCs representing genetic diversity in pooled over years.

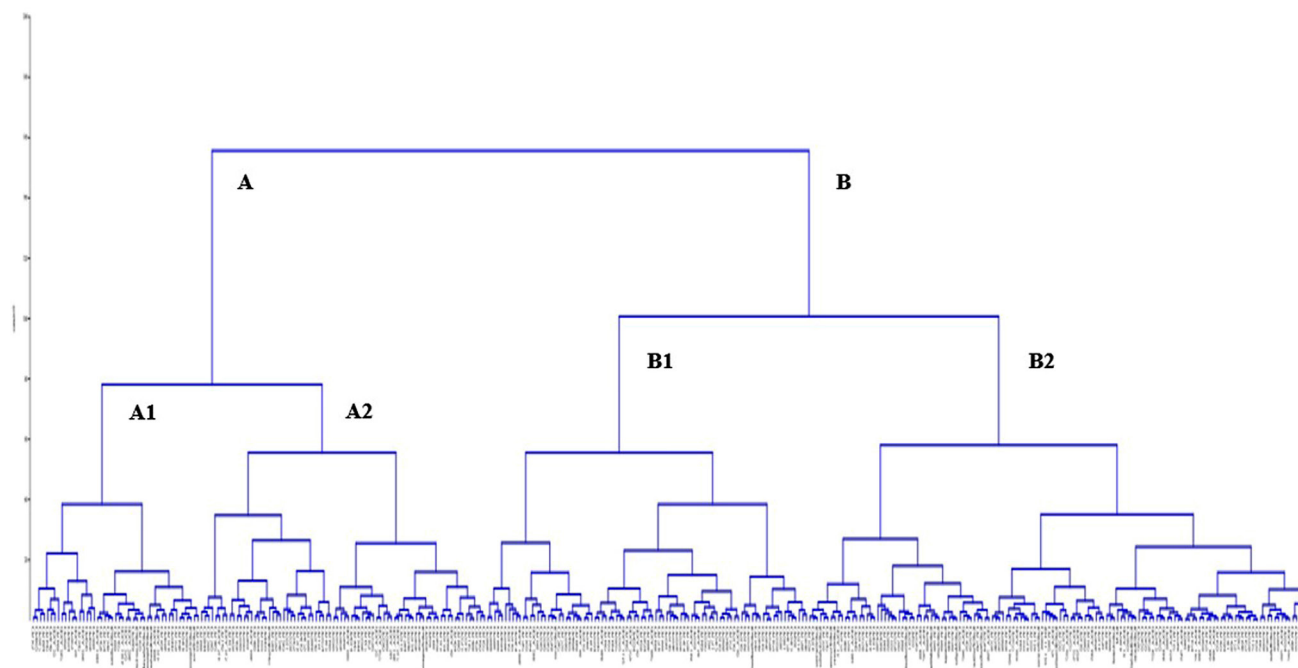


Fig. 2 Dendrogram showing grouping of 357 genotypes of potato in pooled over years generated using Ward's method.

while evaluating 45 potato genotypes. Besides, TSS, starch content and total carotenoids content had maximum loading in PC2. Similarly, total polyphenols, ascorbic acid content and total carotenoids showed maximum loadings in PC3. Principal component analysis showed the significance of PC1 and PC2, accounting for 44% of the total variance with respective loading of 29.10 and 14.90%. The biplot of the first two principal components together with the loadings of various traits and genotype distributions has been displayed in Fig. 1. On the biplot, genotypes that were close to one another were meant to be similar when scored on specific attributes (Fig. 1). However, genotypes that were far from their origin are expected to be very different from other genotypes.

Cluster analysis: The hierarchical cluster analysis arranged 357 genotypes into two major clusters (A and B) with two sub clusters (A1, A2 and B1, B2) for all the biochemical traits in pooled over years presented through dendrogram using Ward's method (Ward 1963) (Fig. 2). The diverse clustering patterns showed how significant an environment is in the development of different characters under a variety of climatic circumstances. Seid *et al.* (2023) have also observed variable clustering patterns in potato genotypes. However, various genotypes showed inconsistent clustering behaviour in the respective years and this kind of clustering behaviour have also reported by Luthra *et al.* (2005). Cluster A was divided into two sub clusters i.e A1 with 47 genotypes and A2 with 80 genotypes. Similarly, cluster B was also divided into 2 sub-clusters with 90 genotypes in sub-cluster B1 and 140 genotypes in sub-cluster B2 (Fig. 2). Maximum inter cluster distance between cluster A and cluster B was observed for CP 1971 and CP 1700 while intra cluster distance in cluster A was maximum for CP 1971 and CP 1827. Similarly, maximum

intra cluster distance in cluster B was reported for CP 3096 and CP 1700. Selection of genotypes on the basis of inter cluster distances for hybridization programme from various clusters rather than inside the clusters would be a paying preposition. As genotypes with the same geographic distribution were divided into various clusters, the genetic makeup of the genotypes had an impact on the clustering patterns. Thus, it suggests that the genetic diversity will not always linked to the geographical diversity (Sattar *et al.* 2011, Datta *et al.* 2015).

Genotypes, viz. CP 3145 and CP 1235 for TSS; CP 1689 and CP 1685 for total polyphenols; CP 1302 and CP 2412 for ascorbic acid content; CP 3091 and CP 1827 for total carotenoids content; CP1667, CP 2346 and CP 2397 for total sugars; CP 1667 and CP 1689 for reducing sugars; CP 1684 and CP 2397 for non-reducing sugars were desirable for selection. High PCV and GCV was observed for total polyphenols and total carotenoids, irrespective of years. High heritability coupled with high genetic advance was observed for total polyphenols, ascorbic acid content, starch content, total carotenoids content and reducing sugars, during both the years indicating the importance of additive gene action for inheritance of these traits. It would be advantageous to select the genotypes from diverged clusters to increase the biochemical characteristics of potato, as evidenced by the genotypes grouped in distinct clusters with substantial inter-cluster distance. Thus, identified superior genotypes represents the untapped potential to increase the nutritional content and can be used as parental material for the improvement of potato varieties.

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