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Genetic Studies of Variability, Correlation and Path Analysis in Potato (*Solanum tuberosum* L.) Genotypes for Yield and Yield Attributing Traits

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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Abstract

Potato (*Solanum tuberosum* L.) breeding requires quantitative information on variation and relationships among traits associated with tuber yield. A field study was conducted at Assam Agricultural University, Jorhat, Assam, during the rabi season of 2021–2022 to evaluate 33 potato genotypes in a randomised block design with three replications. Seventeen traits related to plant growth, tuber characteristics and yield were measured. Analysis of variance indicated significant genotypic differences for all traits. The phenotypic coefficient of variation exceeded the corresponding genotypic coefficient for each trait. Tuber volume had the highest

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genotypic and phenotypic coefficients of variation (46.69% and 49.63%, respectively). Broad-sense heritability was highest for non-marketable yield per hectare (97.70%), followed by leaf area index (93.00%), whereas the number of stems per hill had the lowest value (31.10%). Genetic advance as a percentage of the mean was also highest for non-marketable yield per hectare (92.98%). Total yield per hectare showed positive associations with marketable yield, tuber yield per plant and average tuber weight at both the genotypic and phenotypic levels. Path analysis identified marketable yield per hectare as having the largest positive direct effect on total yield. Mahalanobis D^2 analysis grouped the genotypes into three clusters containing 22, 10 and one genotype, respectively. These findings identify variation and trait associations that may inform selection and parental choice within the evaluated material.

Keywords: Solanum tuberosum L.; genetic variability; heritability; potato.

1. Introduction

Potato (*Solanum tuberosum* L.) is one of the most important staple vegetable crops and is utilised throughout the year in India. The history of potato cultivation demonstrates its importance for food security during periods of food-grain scarcity. Owing to its utility, potato occupies a prominent position among crops and is recognised as the "king of vegetables". Potato (*Solanum tuberosum* L.) belongs to the family Solanaceae and the genus *Solanum*. Cultivated potato species have 2n = 48 chromosomes (autotetraploid). Approximately 74% of tuber-bearing species are diploid (2n = 24) and the remaining 26% are polyploid, specifically tetraploid (2n = 48), pentaploid (2n = 60) and hexaploid (2n = 72). Worldwide, the commercial cultivation of *Solanum tuberosum* and *Solanum andigenum* is practised. Potato is an essential crop and has attracted considerable attention, because it is well suited to multiple-cropping and intercropping systems. Given the importance of the crop, there is a need to improve its yield. Trait-based selection during the early generations of potato clonal breeding has been used to identify material for further yield evaluation (Yadav, 2026). Quantitative-genetic analyses of tetraploid potato have also examined genetic variability in yield- and quality-related traits (Yousaf *et al*., 2025).

India's potato production faces challenges such as biotic and abiotic stresses. The low potato yield in India especially in north-eastern India can be attributed to several factors, including inadequate crop management practices, high incidence of diseases and pests, utilisation of low-quality seeds, and a lack of disease-free seed tubers. While some potato genotypes well suited for the north-eastern region are available, limited information exists regarding the genetic factors influencing various economically important traits. Therefore, it is essential to identify potato varieties with high yield potential, adaptability, and consistent performance across diverse agro-climatic conditions. This approach can significantly contribute to increasing potato production in India. By focusing on varieties that exhibit favourable traits and resilience to local challenges, farmers can enhance their crop yield and overcome the limitations imposed by the region's specific agricultural conditions. The use of low-quality seed tubers infected with viruses, pests and other diseases, a shortage of improved varieties and poor crop management have contributed to low yield of potato in India. Addressing this situation requires the development of high-yielding varieties with consistent performance and adaptability to diverse agro-climatic situations and preferred by both growers and consumers. This, in turn, requires information on the nature and magnitude of genetic variability in the existing plant material. Estimation of variability for a given character is essential for effective screening of superior genotypes. The GCV and PCV parameters (genotypic and phenotypic coefficients of variation) can be used to measure the degree of genetic variability among the available genotypes. Broad-sense heritability and genetic advance assist in identifying the influence of the environment on trait expression and the potential for improvement after selection (Robinson *et al*., 1949). Associations among traits are important for yield improvement, and correlations among traits can be used to select better plant types. Path coefficient analysis further partitions correlation coefficients into direct and indirect effects, facilitating the identification of important traits. Genetic divergence analysis estimates the extent of diversity among the selected genotypes. Potato exhibits considerable variation for several traits, which provides greater scope for improving this crop through selection. Genetic variability, heritability, correlation and path coefficient analyses have been used to assess yield-associated traits in cultivated potato (Singh *et al*., 2024). A study of potato accessions in Uttarakhand likewise identified tuber number and average tuber weight as relevant characters in correlation and path analyses of yield (Aishwarya *et al*., 2024). Multivariate approaches have also been applied to examine genetic diversity in relation to yield and quality characters among potato genotypes (Thakur *et al*., 2026). However, the joint evaluation of genetic variability, trait associations, direct and indirect effects, and genetic divergence remained necessary for the specific set of potato genotypes assessed under the conditions of Jorhat, Assam.

Therefore, this study was conducted to determine the nature and magnitude of variability in selected potato genotypes for yield and yield-attributing traits by estimating phenotypic and genotypic coefficients of variation, heritability and genetic advance. Genetic diversity among the genotypes was also analysed using D^2 statistics.

2. Materials and Methods

The field experiment was conducted at the Instructional-cum-Research Farm of Assam Agricultural University, Jorhat, Assam during the *Rabi* season of 2021–2022. A set of 33 potato genotypes was used in the present investigation. These comprised 33 potato genotypes, including 11 genotypes from the International Potato Research Centre (CIP), Lima, Peru, 16 from the Central Potato Research Institute (CPRI), Shimla, four local genotypes of Assam and two released high-yielding varieties (Table 1). The experiment was laid out in a randomised block design (RBD) with three replications and a plot size of $4m^2$. The seed tubers were planted on ridges spaced at 60 cm and intra-row spacing of 20 cm. The recommended package of practices was followed to raise the crop. The crop was harvested at maturity and observations were recorded on five randomly selected competitive plants for each genotype in each replication and the means were calculated. Observations were recorded for plant height, number of stems/ hill, number of branches/plant, stem diameter, shoot dry weight(g/plant), leaf area index, NDVI values, number of tubers/plant, average tuber weight, number of eyes/tuber, total soluble solids, tuber dry matter content, tuber volume, tuber yield/plant, marketable yield/ha, non-marketable yield/ha and total yield/ ha. Mean values for all the designated characters were worked out in each genotype. All data were subjected to analysis of variance (ANOVA) following the procedure described by Gomez and Gomez

(1984). The genotypic and phenotypic coefficients of variation were estimated using the procedure described by Burton and Devane (1953); heritability was calculated following Singh and Chaudhary (1985) and genetic advance was calculated using the procedure described by Allard (1999). Correlation analysis was conducted following the procedure described by Singh and Chaudhary (1979) and path coefficients were estimated following Dewey and Lu (1959). The Mahalanobis D^2 method (Mahalanobis, 1936) was used to analyse the genetic divergence based on morphological characters among the selected genotypes.

Table 1. List of experimental materials used in the study

Sl. No.	Accession name	Sl. No.	Accession name
1	4609	18	MP/19-4
2	4610	19	MP/20-6
3	4611	20	MP/20-12
4	4614	21	MP/20-16
5	4615	22	MP/20-42
6	4616	23	MP/20-43
7	4617	24	MP/20-44
8	4618	25	MP/20-48
9	4620	26	P-30
10	4621	27	P-69
11	7003	28	Assamese local (Local check)
12	SM/20-3	29	BNCA local
13	SML/103	30	Rangpuria
14	SML/104	31	Badami
15	SML/112	32	Lady rosetta
16	HT/12-830	33	Kufri Surya (Improved variety check)
17	HT/19-4		

3. Result and Discussion

3.1 Analysis of Genetic Parameters for Different Yield and Yield-attributing Traits

All clones showed significant differences in the observed traits, indicating the presence of genetic variation among the clones for all the observed morphological traits which could support further selection. The significant variation among genotypes was probably associated with their diverse origins, including genotypes from Peru, local varieties from north-eastern India and clones developed at CPRI, Shimla (Table 2).

3.1.1 Performances of Genotypes

Based on the overall mean performance for yield and its component traits, the genotypes 4621, MP/20-44 and HT/19-4 had the highest tuber yield/plant; 4611, SML/112, 4614 and SM/20-3 had maximum average tuber weight; 4611, 4621 and SM/20-3 exhibited higher plant height, leaf area index, number of branches/plant, number of stems/hill, tuber volume, marketable tuber yield/ha, total yield /ha. These potato clones could therefore be utilised for breeding potato varieties for high yields and other traits. The local potato genotypes, including Assamese local, Rangpuria, BNCA local and Badami, showed high dry matter content, which may explain their good storability under farmers' field conditions.

Table 2. Analysis of variance (ANOVA) of potato genotypes for tuber yield and its component traits

Sl. No.	Traits	Mean of Sum of Square			CV (%)
		Replications (d.f.=2)	Genotypes (d.f.=32)	Error (d.f.=64)	
1.	Plant height	170.32**	121.53**	26.20	12.08
2.	Number of stems/ hill	0.10	5.88**	2.50	29.26
3.	Number of branches/ plant	5.60*	15.00**	1.33	16.24
4.	Stem diameter	0.33**	0.23**	0.01	14.42
5.	Shoot dry weight	22.17**	34.00**	4.45	19.48
6.	Leaf area index	1.38**	4.50**	0.10	9.88
7.	NDVI values	0.00	0.01**	0.001	3.14
8.	Number of tuber/ plant	0.03	18.54**	3.15	22.38
9.	Average tuber weight	706.42**	358.64**	59.34	26.52
10.	Number of eyes/ tuber	23.91**	19.49**	1.60	13.55
11.	Total soluble solid	0.03	2.10**	0.05	5.08
12.	Dry matter content of tuber	1.73	7.22**	0.75	13.84
13.	Tuber volume	318.07**	1158.37**	48.02	16.82
14.	Tuber yield/ plant	18236.60**	16024.80**	1641.50	19.25
15.	Marketable yield/ ha	9197.64**	5813.15**	1070.55	28.47
16.	Non marketable yield/ ha	0.36	179.26**	1.37	6.96
17.	Total yield/ ha	9397.06**	6220.80**	1143.10	27.43

**, ** Significant at 5% and 1% level, respectively*

3.1.2 Genetic Coefficient of Variation

The phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all traits, indicating an environmental influence on trait expression. Among the yield-attributing traits studied, tuber volume had the highest values of PCV (49.63 %) and GCV (46.69 %). High GCV and PCV were recorded in marketable yield/ ha (34.6,44.8), average tuber weight (34.38,43.42), total yield/ha (33.38,43.21) and tuber yield/plant (32.90,38.12). Moderate GCV and PCV were observed in plant height (13.31, 17.98). These findings indicate variability among genotypes for traits with moderate to high GCV and PCV values. Selection for these traits could therefore help identify desirable potato genotypes. These results are consistent with the findings of Tripura *et al.* (2016) for the number of tubers/plant, average tuber weight, tuber yield in potato; Singha and Ullah (2020) for the number of tubers per plant. Annigeri and Hire*ma**th* (2022) reported high GCV and PCV for unmarketable yield /ha, marketable yield/ha, total yield/ ha, number of tubers/plant.

3.1.3 Broad Sense Heritability and Genetic Advance

The highest broad-sense heritability was observed for non-marketable yield/ha at 97.7% and the lowest heritability was observed for number of stems/hill (31.1%). High heritability was observed for tuber volume (88.5%), stem diameter (80.7%), tuber yield/plant (74.5%), tuber dry matter content (74%), marketable yield / ha (68.9%), shoot dry weight / plant (68.8%), average tuber weight (62.7%), number of tubers/plant (61.9%) and total yield / ha (60.95%). Traits exhibiting high heritability were considered to have relatively simple inheritance patterns, irrespective of the number of genes governing them. Expected genetic advance as a percentage of the mean was highest for non-marketable yield/ha (92.98%) and the lowest for NDVI values (19.26%). Genetic advance as a percentage of the mean was high for tuber volume (90.49 %), tuber yield/plant (58.50%), average tuber weight (56.09%), marketable yield /ha (55.03%), stem diameter (54.58%), total yield/ha (53.13%), shoot dry weight/plant (49.51%) and tuber dry matter content (41.37%). Similarly, Tripura *et al.* (2016), Hajam *et al.* (2018) and Annigeri and Hire*ma**th* (2022) reported high heritability and genetic advance for various component traits in potato. High heritability coupled with high genetic advance as a percentage of the mean was observed for several traits, including leaf area index, number of branches /plant, stem diameter, number of tubers/plant, average tuber weight, tuber yield/plant, marketable yield/ha, non-marketable yield/ha, tuber volume, number of eyes/tuber, total soluble solid, shoot dry weight(g/plant), tuber dry matter content and total yield/ha indicating a predominance of additive gene action and providing opportunities for effective selection. The observed high heritability coupled with high genetic advance as a percentage of the mean is consistent with earlier work by Ummyiah *et al.* (2010), Tripura *et al.* (2016) for traits such as average tuber weight, total tuber yield, marketable tuber yield, tuber yield/plant. Patel *et al.* (2018) and Ebrahim *et al.* (2020) reported that leaf area index, shoot dry mass, total tuber yield, number of tuber/plant, total soluble solids had high heritability (>60%) and genetic advance as *a* percent*age* of *the* mean (>30%).

Table 3. Genetic variability parameters for seventeen traits

Traits	Range	Mean ± SE	GCV (%)	PCV (%)	h^2bs (%)	GAM (5%)
Plant height (cm)	24.40 - 55.03	42.34 ± 2.96	13.31	17.98	54.80	20.30
Number of stems/ hill	3.78 - 9.22	5.40 ± 0.91	19.65	35.25	31.10	22.57
Number of branches/ plant	0.00 - 10.00	7.16 ± 0.67	29.81	33.94	77.10	53.92
Stem diameter (cm)	0.36 - 1.40	0.91 ± 0.08	29.49	32.83	80.70	54.58
Shoot dry weight (g/plant)	6.00 - 20.67	10.83 ± 1.22	28.96	34.91	68.80	49.51
Leaf area index	1.56 - 6.71	3.35 ± 0.19	36.12	37.45	93.00	71.77
NDVI values	0.39 - 0.86	0.80 ± 0.01	9.82	10.31	90.70	19.26
Number of tuber/ plant	4.83 - 16.15	7.94 ± 1.03	28.53	36.26	61.90	46.24
Average tuber weight (g)	3.99 - 46.02	29.05 ± 4.45	34.38	43.42	62.70	56.09
Number of eyes/ tuber	5.00 - 15.67	9.35 ± 0.73	26.10	29.41	78.80	47.73
Total soluble solid (°Brix)	3.33 - 6.00	4.66 ± 0.14	17.71	18.42	92.40	35.06
Dry matter content of tuber (%)	4.09 - 9.62	6.29 ± 0.50	23.34	27.14	74.00	41.37
Tuber volume (cm^3)	10.33 - 100.67	41.20 ± 4.00	46.69	49.63	88.50	90.49
Tuber yield/ plant (g)	33.50 - 317.07	210.44 ± 23.39	32.90	38.12	74.50	58.50
Marketable yield/ ha (q)	18.10 - 192.76	114.91 ± 18.89	34.60	44.80	68.90	55.03
Non marketable yield/ ha (q)	2.85 - 29.59	16.86 ± 0.68	45.66	46.18	97.70	92.98
Total yield/ ha (q)	**21.14 - 202.44**	**123.22 ± 19.52**	**33.38**	**43.21**	**60.95**	**53.13**

3.2 Correlation Analysis among Yield and Yield-Attributing Traits

Tuber yield/ha exhibited significant positive correlations at both the genotypic and phenotypic levels with marketable yield/ha, tuber yield/plant, average tuber weight, tuber volume, plant height, leaf area index, stem diameter, non-marketable yield/ha and shoot dry weight, whereas tuber yield/plant showed significant positive correlations with plant height, average tuber weight, marketable yield/ha, tuber volume, non-marketable yield/ha, stem diameter and shoot dry weight at both the genotypic and phenotypic levels, indicating that these traits could be selected for enhancement of tuber yield. Tuber yield per plant was found to be negatively and significantly correlated with tuber dry matter content. This indicated that tuber yield and tuber dry matter content might not be improved simultaneously through selection. Independent selection for these traits would be effective. Associations among component traits revealed positive and highly significant correlations of average tuber weight with marketable yield/ ha, tuber yield/ plant, plant height, tuber volume, stem diameter, shoot dry weight at the phenotypic and genotypic levels. The number of tubers/plant exhibited positive and highly significant correlations at both phenotypic and genotypic levels with tuber dry matter content, number of stems/ hill, total soluble solids content. Similar trends in correlation coefficients for potato were also reported by Rangare and Rangare (2017), Luthra *et al.* (2018) and Hajam *et al*. (2018).

Table 4. Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients between components traits of total yield/ha

Traits	Plant height	Number of stems/ hill	Leaf area index	Number of branches/plant	Stem diameter	Number of tuber/ plant	Average tuber weight	Tuber yield/plant	Marketable yield/ ha	Non-marketable yield /ha	Tuber volume	NDVI values	Number of eyes/ tuber	Total soluble solid	Shoot dry weight	Tuber dry matter content	Total yield /ha
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
1		-0.817**	0.168	-0.1385	0.287 **	-0.458 **	0.787 **	0.669 **	0.757 **	0.351 **	0.569 **	0.177	0.465 **	-0.216 *	0.411**	-0.352 **	0.750 **
2	-0.243 *		0.245 *	0.532 **	-0.539 **	0.417**	-0.722 **	-0.648 **	-0.616 **	-0.455 **	-0.148	-0.105	-0.424 **	0.457 *	-0.472**	0.724 **	-0.607 **
3	0.129	0.090		0.475 **	0.326 **	-0.235 *	0.355 **	0.170	0.367 **	0.087	0.481 **	0.119	-0.014	-0.061	0.454**	0.1992	0.367 **
4	-0.095	0.212 *	0.412 **		0.073	0.048	-0.010	-0.114	-0.016	0.191	0.130	0.247 *	-0.078	-0.144	0.277 **	0.094	-0.017
5	0.265 **	-0.290 **	0.294 **	0.153		-0.531 **	0.564 **	0.387 **	0.390 **	0.404 **	0.298 **	0.283 **	0.287 **	-0.240 *	0.324 **	-0.272 **	0.395 **
6	-0.266 **	0.450 **	-0.214 *	-0.004	-0.401 **		-0.753 **	-0.330 **	-0.353 **	-0.394 **	-0.412 **	0.039	-0.119	0.264 **	-0.504**	0.418 **	-0.359 **
7	0.635 **	-0.306 **	0.317 **	0.025	0.470 **	-0.658 **		0.812 **	0.815 **	0.462 **	0.704 **	0.244 *	0.500 **	-0.313 **	0.561 **	-0.485 **	0.827 **
8	0.596 **	-0.258 **	0.173	-0.078	0.350 **	-0.247 *	0.784 **		0.847 **	0.532 **	0.643 **	0.089	0.723 **	-0.382 **	0.381 **	-0.540 **	0.864 **
9	0.684 **	-0.223 *	0.321 **	0.001	0.351 **	-0.228 *	0.755 **	0.865 **		0.356 **	0.779 **	0.391 **	0.578 **	-0.377 **	0.390 **	-0.473 **	0.998 **
10	0.255 *	-0.230 *	0.080	0.158	0.356 **	-0.279 **	0.343 **	0.437 **	0.259 **		0.296**	-0.110	0.329 **	-0.623 **	0.277 **	-0.481 **	0.357 **
11	0.499 **	-0.064	0.464 **	0.112	0.273 **	-0.338 **	0.609 **	0.595 **	0.657 **	0.269 **		0.280 **	0.238 *	-0.241 *	0.347 **	-0.354 **	0.788 **
12	0.158	-0.010	0.111	0.211 *	0.254 *	0.077	0.183	0.091	0.318 **	-0.108	0.246 *		-0.048	-0.094	0.026	-0.128	0.405 **
13	0.293 **	-0.246 *	-0.008	-0.016	0.285 **	-0.057	0.314 **	0.512 **	0.374 **	0.301 **	0.176	-0.046		-0.263 *	0.095	-0.238 *	0.576 **
14	-0.145	0.264 **	-0.042	-0.108	-0.203 *	0.182	-0.237 *	-0.331 **	-0.296 **	-0.591 **	-0.210 *	-0.097	-0.220 *		-0.085	0.568 **	-0.338 **
15	0.364 **	-0.191	0.385 **	0.224 *	0.308 **	-0.369 **	0.439 **	0.314 **	0.306 **	0.225 *	0.354 **	0.013	0.110	-0.052		-0.145	0.413 **
16	-0.262 **	0.314 **	0.175	0.020	-0.261 *	0.261 *	-0.354 **	-0.428 **	-0.361 **	-0.416 **	-0.277 **	-0.106	-0.180	0.455 **	-0.103		-0.467 **
17	0.673 **	-0.203 *	0.316 **	-0.002	0.346 **	-0.239 *	0.790 **	0.880 **	0.989 **	0.263 *	0.660 **	0.322 **	0.364 **	-0.268 **	0.310**	-0.362 **	

Table 5. Genotypic path coefficient analysis showing direct (bold) and indirect effects of component traits on total yield/ ha

Traits	Plant height	Number of stems/ hill	Leaf area index	Number of branches/ plant	Stem diameter	Number of tuber/ plant	Average tuber weight	Tuber yield /plant	Marketable yield/ ha	Non-marketable yield /ha	Tuber volume	NDVI values	Number of eyes/ tuber	Total soluble solid	Shoot dry weight	Tuber dry matter content	Total yield /ha
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
1	**-0.305**	0.026	-0.002	0.002	-0.023	-0.061	0.329	-0.089	0.772	0.009	-0.024	-0.009	0.000	-0.018	-0.007	0.004	**0.750** **
2	0.250	**-0.031**	-0.003	-0.010	0.042	0.055	-0.302	0.086	-0.628	-0.012	0.006	0.005	0.000	0.038	0.008	-0.008	**-0.607** **
3	-0.052	-0.008	**-0.011**	-0.009	-0.026	-0.031	0.149	-0.023	0.375	0.002	-0.020	-0.006	0.000	-0.005	-0.008	-0.002	**0.367** **
4	0.042	-0.017	-0.005	**-0.018**	-0.006	0.006	-0.005	0.015	-0.017	0.005	-0.005	-0.012	0.000	-0.012	-0.005	-0.001	**-0.018**
5	-0.088	0.017	-0.004	-0.001	**-0.078**	-0.071	0.236	-0.051	0.398	0.010	-0.013	-0.014	0.000	-0.020	-0.006	0.003	**0.395** **
6	0.140	-0.013	0.003	-0.001	0.042	**0.133**	-0.315	0.044	-0.361	-0.010	0.017	-0.002	0.000	0.022	0.009	-0.004	**-0.359** **
7	-0.240	0.023	-0.004	0.000	-0.044	-0.100	**0.418**	-0.107	0.831	0.012	-0.030	-0.012	0.000	-0.026	-0.010	0.005	**0.827** **
8	-0.204	0.020	-0.002	0.002	-0.030	-0.044	0.340	**-0.132**	0.864	0.014	-0.027	-0.004	-0.001	-0.032	-0.007	0.006	**0.864** **
9	-0.231	0.019	-0.004	0.000	-0.031	-0.047	0.341	-0.112	**1.019**	0.009	-0.033	-0.019	-0.001	-0.031	-0.007	0.005	**0.998** **
10	-0.107	0.014	-0.001	-0.003	-0.032	-0.052	0.193	-0.070	0.363	**0.026**	-0.013	0.005	0.000	-0.052	-0.005	0.005	**0.357** **
11	-0.174	0.005	-0.005	-0.002	-0.023	-0.055	0.294	-0.085	0.794	0.008	**-0.042**	-0.014	0.000	-0.020	-0.006	0.004	**0.788** **
12	-0.054	0.003	-0.001	-0.004	-0.022	0.005	0.102	-0.012	0.399	-0.003	-0.012	**-0.049**	0.000	-0.008	0.000	0.001	**0.405** **
13	-0.142	0.013	0.000	0.001	-0.023	-0.016	0.209	-0.096	0.590	0.008	-0.010	0.002	**-0.001**	-0.022	-0.002	0.003	**0.576** **
14	0.066	-0.014	0.001	0.003	0.019	0.035	-0.131	0.051	-0.385	-0.016	0.010	0.005	0.000	**0.083**	0.002	-0.006	**-0.338** **
15	-0.126	0.015	-0.005	-0.005	-0.025	-0.067	0.235	-0.051	0.398	0.007	-0.015	-0.001	0.000	-0.007	**-0.018**	0.002	**0.413** **
16	0.108	-0.023	-0.002	-0.002	0.021	0.056	-0.203	0.072	-0.482	-0.012	0.015	0.006	0.000	0.047	0.003	**-0.011**	**-0.467** **
Residual effect = 0.011																	

Table 6. Distribution of potato genotypes in various clusters on the basis of their similar features

Cluster No.	Number of Genotypes in clusters	Names of genotypes
I	22	Assamese Local, BNCA Local, Rangpuria, Badami, Lady Rosetta, 4609, 4610, 4611, 4614, 4615, 4616, 4617, 4618, 4620, 7003, SM/20-3,SML/103, SML/104, SML/112, HT/12-830, MP/19-4, MP/20-6
II	10	MP/20-16 , MP/20-48, HT/19-4, MP/20-42, MP/20-44, P-30, P-69, MP/20-12, MP/20-43, 4621,
III	1	Kufri Surya

Table 7. Mean intra (bold) and inter cluster distance (D^2) among three clusters in potato

Cluster Distances	Cluster 1	Cluster 2	Cluster 3
Cluster 1	257.37	414.59	872.59
Cluster 2		169.69	523.13
Cluster 3			0

Table 8. Mean performance of clusters for seventeen quantitative traits in potato genotypes

Cluster Means	Cluster 1	Cluster 2	Cluster 3	Contribution (%)
Plant height (cm)	42.26	42.56	41.92	0.00
Number of shoots per hill	5.44	5.33	5.11	0.00
Number of branches per plant	6.84	8.06	4.83	0.56
Stem diameter (cm)	0.87	1.00	0.78	2.84
Shoot dry weight (g/plant)	10.89	10.54	12.33	1.51
Leaf area index	3.22	3.60	3.54	13.44
NDVI values	0.80	0.82	0.38	3.40
Number of tuber per plant	7.99	8.06	5.36	0.18
Average tuber weight (g)	27.74	31.82	29.86	0.00
Number of eyes tuber-1	8.98	10.03	10.66	3.40
Total soluble solid (°Brix)	4.99	3.91	4.83	11.74
Tuber dry matter content (%)	6.59	5.61	6.35	0.75
Tuber volume (cm3)	37.31	50.40	34.66	4.92
Tuber yield per plant (g)	190.99	247.79	264.66	0.00
Marketable yield per ha (q)	109.38	130.63	79.32	3.03
Non-marketable yield per ha (q)	12.85	24.42	29.59	54.16
Total yield per ha (q)	117.34	139.81	86.53	0.00

3.3 Path Coefficient Analysis

The highest positive effect on total yield/ha was contributed by marketable yield/ha, followed by average tuber weight and the number of tubers/plant. This suggested that tuber weight and tuber/plant were two important traits contributing directly to yield in potato. Therefore, there is scope to improve tuber yield by selecting plants bearing more tubers with greater average tuber weight. The negative direct effects of stem diameter, number of stems/hill, plant height, tuber dry matter content and shoot dry weight on tuber yield/ha observed in this study indicated that yield improvement through selection of these characters would be ineffective. However, the high negative direct effects of plant height and stem diameter were offset to some extent by high positive indirect effects of average tuber weight. Moderate to high positive indirect effects were exerted on total yield/ha by average tuber weight through marketable yield/ha, tuber yield/plant, plant height, tuber volume, stem diameter, shoot dry weight, number of eyes/tuber, non-marketable yield/ha, leaf area index and NDVI values. Similar findings were also reported by Amadi *et al*. (2008), Singh *et al*. (2015), Rangare and Rangare (2017) and Supriatna *et al*. (2019). In the present investigation, the genotypic residual value was 0.011 which was interpreted as indicating that the seventeen traits studied accounted for 98.9% of the variability, with 1.1% remaining unexplained. The low residual effect (0.011) was interpreted as reflecting the adequacy of the selected traits and their contribution towards tuber yield/ ha.

3.4 Genetic Divergence

Based on Mahalanobis D^2 statistics, in the present investigation, 33 potato genotypes were classified into three clusters. Clustering of genotypes was done based on their morphological differences. Cluster I contained the largest number of genotypes (22) followed by cluster II (10 genotypes). Cluster III was monogenotypic and contained only one genotype. Cluster I was more diverse than the others. The maximum inter-cluster distance was recorded between clusters I and III followed by clusters II and III. Clusters I and II had an inter-cluster distance of 414.59, the lowest recorded value. Genotypes within the same cluster were less divergent than genotypes in different clusters. Genotypes from clusters showing the maximum inter-cluster distance could be used in intervarietal hybridisation to develop divergent recombinants. The maximum intra-cluster distance was observed for the cluster containing the

highest number of genotypes (cluster I). The minimum inter-cluster distance between clusters I and II indicated a close relationship and similarity of traits among their genotypes. In this investigation, inter-cluster distances exceeded intra-cluster distances, indicating genetic diversity among the genotypes. The highest cluster mean values were recorded for important traits, including total yield/ha, marketable yield/ha, tuber volume, average tuber weight, number of tubers/plant and stem diameter in cluster-II. For crosses aimed at obtaining segregating genotypes with improved tuber yield, genotypes such as MP/20-12 and 4621 from cluster II could be considered. Based on inter-cluster distances, clusters I and III were identified as the most divergent and genotypes from these clusters could be selected as parents for future hybridisation programme in potato. The highest relative contribution to total divergence was recorded for non-marketable yield/ha followed by total soluble solids, leaf area index, tuber volume, number of eyes/ tuber, NDVI values, stem diameter, marketable yield/ ha and shoot dry weight. Traits such as average tuber weight contributed less to total divergence. These findings were consistent with those of Barik (2007), Panigrahi *et al.* (2014), Sattar *et al.* (2011) and Prabha *et al.* (2018).

4. Conclusion

The evaluation of 33 potato genotypes revealed significant differences among the 17 measured traits under the experimental conditions at Jorhat. Phenotypic coefficients of variation were consistently higher than genotypic coefficients, while several yield-related traits exhibited comparatively high estimates of variability, heritability and expected genetic advance. Tuber volume showed the largest genotypic and phenotypic coefficients of variation, and non-marketable yield per hectare exhibited the highest broad-sense heritability and genetic advance as a percentage of the mean. The positive correlations of total yield per hectare with average tuber weight, tuber yield per plant and marketable yield indicate that these characters merit consideration during selection. Path analysis likewise identified the strong positive direct contribution of marketable yield per hectare, while correlations and indirect effects emphasised the interconnected nature of yield components. The classification of genotypes into three clusters demonstrated divergence within the experimental material, with the greatest inter-cluster distance occurring between clusters I and III. The results provide a basis for identifying contrasting parental material and prioritising traits in subsequent breeding evaluations. Further confirmation under additional field conditions would be needed before broader conclusions about performance or adaptation are drawn.

5. Limitations

The study assessed 33 genotypes during one rabi season at a single experimental location. Accordingly, the observed variability, correlations and cluster relationships describe the evaluated material under those conditions and should not be interpreted as evidence of stability across environments. The analysis was based on recorded morphological and yield-related traits; it does not independently establish the genetic mechanisms underlying their associations. Additional seasons and locations would be useful to evaluate the consistency of trait expression and the performance of selected genotypes.

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Declaration of AI Use

This manuscript was prepared through the intellectual contributions of the author(s) to the study design, data analysis, interpretation of results, and scholarly content. Grammarly and ChatGPT were used solely to assist with grammatical refinement and reference formatting during manuscript revision. The author(s) accept full responsibility for the accuracy, integrity, and final content of the manuscript.

Competing Interests

Authors have declared that no competing interests exist.

References

Aishwarya, K. R., Singh, D., Pradeep, S. D., Mehta, T., Singh, K., Fandan, R., Nitwal, R., & Singh, J. P. (2024). Correlation and path coefficient analysis among yield and yield associated traits in potato (*Solanum tuberosum* L.) accessions in the 'Terai' region of Uttarakhand. *Journal of Scientific Research and Reports, 30*(6), 975–983. https://doi.org/10.9734/jsrr/2024/v30i62116

Allard, R. W. (1999). *Principles of plant breeding* (2nd ed.). John Wiley & Sons. https://www.wiley.com/en-us/-p-9780471023098

Amadi, C. O., Ene-Obong, E. E., Okocha, P. I., & Dung, E. A. (2008). Path analysis of yield of some potato hybrids and their progenitors in Northern Guinea Savanna of Nigeria. *Production Agriculture and Technology, 4*(2), 28–37.

Annigeri, S. V., & Hiremath, S. M. (2022). Studies on correlation and path analysis in potato (*Solanum tuberosum* L.) genotypes. *The Pharma Innovation Journal, 11*(2), 2855–2860. https://www.thepharmajournal.com/archives/2022/vol11issue2/PartAL/11-2-402-758.pdf

Barik, S. B. (2007). *Genetic diversity in potato (Solanum tuberosum L.)* [Master's thesis, Indira Gandhi Krishi Vishwavidyalaya]. Krishikosh Institutional Repository. https://krishikosh.egranth.ac.in/server/api/core/bitstreams/b567a7b0-7452-485d-bb29-b3ec536944f4/content

Burton, G. W., & DeVane, E. H. (1953). Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agronomy Journal, 45*(10), 478–481. https://doi.org/10.2134/agronj1953.00021962004500100005x

Dewey, D. R., & Lu, K. H. (1959). A correlation and path-coefficient analysis of components of crested wheatgrass seed production. *Agronomy Journal, 51*(9), 515–518. https://doi.org/10.2134/agronj1959.00021962005100090002x

Ebrahim, S., Mohammed, W., & Abebe, T. (2020). Genetic variability, heritability and genetic advance in potato (*Solanum tuberosum* L.) for processing quality, yield and yield related traits. *International Journal of Plant Breeding and Crop Science, 7*(3), 928–936.

Gomez, K. A., & Gomez, A. A. (1984). *Statistical procedures for agricultural research* (2nd ed.). John Wiley & Sons. https://www.wiley.com/en-us/Statistical%2BProcedures%2Bfor%2BAgricultural%2BResearch%2C%2B2nd%2BEdition-p-9780471870920

Hajam, M. A., Khan, S. H., Bhat, T. A., Parray, E. A., Rather, A. M., Hajam, M. A., Reyaz, L., Bhat, I. A., & Wani, M. A. (2018). To estimate the phenotypic, genotypic variability, heritability (bs) and genetic advance for quantative characters of potato. *The Pharma Innovation Journal, 7*(7), 346–350. https://www.thepharmajournal.com/archives/2018/vol7issue7/PartF/7-7-107-483.pdf

Luthra, S. K., Gupta, V. K., Kaundal, B., & Tiwari, J. K. (2018). Genetic analysis of tuber yield, processing and nutritional traits in potato (*Solanum tuberosum*). *The Indian Journal of Agricultural Sciences, 88*(8), 1214–1221. https://doi.org/10.56093/ijas.v88i8.82539

Mahalanobis, P. C. (1936). On the generalized distance in statistics. *Proceedings of the National Institute of Sciences of India, 2*(1), 49–55. https://cir.nii.ac.jp/crid/1570854176374874752?lang=en

Panigrahi, K. K., Sarkar, K. K., Baisakh, B., & Mohanty, A. (2014). Assessment of genetic divergence in potato (*Solanum tuberosum* L.) genotypes for yield and yield attributing traits. *International Journal of Agriculture, Environment and Biotechnology, 7*(2), 247–254. https://doi.org/10.5958/2230-732X.2014.00241.1

Patel, A. B., Patel, R. N., Gami, R. A., Patel, J. A., & Patel, P. C. (2018). Genetic variability among the potato (*Solanum tuberosum* L.) genotypes as affected by harvesting period for processing purpose and tuber yield. *Current Agriculture Research Journal, 6*(3), 372–377. https://doi.org/10.12944/CARJ.6.3.16

Prabha, N., Nanda, H. C., & Sharma, S. K. (2018). Genetic divergence analysis in potato (*Solanum tuberosum* L.). *International Journal of Current Microbiology and Applied Sciences, 7*(2), 3152–3157. https://doi.org/10.20546/ijcmas.2018.702.379

Rangare, S. B., & Rangare, N. R. (2017). Classificatory analysis of potato (*Solanum tuberosum* L.) genotypes for yield and yield attributing traits. *The Pharma Innovation Journal, 6*(9), 94–102. https://www.thepharmajournal.com/archives/2017/vol6issue9/PartB/6-8-41-719.pdf

Robinson, H. F., Comstock, R. E., & Harvey, P. H. (1949). Estimates of heritability and the degree of dominance in corn. *Agronomy Journal, 41*(8), 353–359. https://doi.org/10.2134/agronj1949.00021962004100080005x

Sattar, M. A., Uddin, M. Z., Islam, M. R., Bhuiyan, M. K. R., & Rahman, M. S. (2011). Genetic divergence in potato (*Solanum tuberosum* L.). *Bangladesh Journal of Agricultural Research, 36*(1), 165–172. https://doi.org/10.3329/bjar.v36i1.9240

Singh, J., Kumar, D., Sood, S., Bhardwaj, V., Kumar, R., & Kumar, S. (2024). Genetic variability and association studies for yield and its attributes in cultivated potato (*Solanum tuberosum* L.). *Vegetable Science, 51*(1), 148–153. https://doi.org/10.61180/vegsci.2024.v51.i1.20

Singh, P., Sharma, P. K., Banjara, N. C., Sahu, N. P., & Sharma, R. (2015). Variability, heritability genetic advance, correlation and path analysis between yield and yield components in potato (*Solanum tubersum* L.). *Ecology, Environment and Conservation, 21*(2), 1093–1097. https://www.envirobiotechjournals.com/issues/article_abstract.php?aid=6073&iid=192&jid=3

Singh, R. K., & Chaudhary, B. D. (1979). *Biometrical methods in quantitative genetic analysis* (Rev. ed.). Kalyani Publishers. https://ci.nii.ac.jp/ncid/BB10261908

Singh, R. K., & Chaudhary, B. D. (1985). *Biometrical methods in quantitative genetics analysis*. Kalyani Publishers. https://kalyanipublishers.co.in/uploads/subjectPDF/1.pdf

Singha, L., & Ullah, Z. (2020). Genetic variability studies for yield and it's attributing traits in potato (*Solanum tuberosum* L.). *International Journal of Current Microbiology and Applied Sciences, 9*(2), 1974–1983. https://doi.org/10.20546/ijcmas.2020.902.225

Supriatna, J., Nuraeni, A., Fajarfika, R., & Sahat, J. P. (2019). Correlation and path coefficient analysis of heat stress tolerance characters in potato. *Journal of Physics: Conference Series, 1402*(3), Article 033035. https://doi.org/10.1088/1742-6596/1402/3/033035

Thakur, N., Sood, S., Kumari, M., Dipta, B., Mankar, P., Kaur, R. P., Mangal, V., Bhardwaj, V., Kumar, V., & Singh, B. (2026). Multivariate analysis and genetic diversity for tuber yield and quality traits in potato (*Solanum tuberosum* L.). *Scientific Reports*. https://doi.org/10.1038/s41598-026-74243-7

Tripura, A., Das, A., Das, B., Priya, B., & Sarkar, K. K. (2016). Genetic studies of variability, character association and path analysis of yield and its component traits in potato (*Solanum tuberosum* L.). *Journal of Crop and Weed, 12*(1), 56–63. https://www.cropandweed.com/archives/2016/vol12issue1/11.pdf

Ummyiah, H. M., Khan, S. H., Wani, K. P., Hussain, K., & Junaif, N. (2010). Genetic variability in potato (*Solanum tuberosum* L.). *The Asian Journal of Horticulture, 5*(1), 61–63.

Yadav, S. (2026). Methodological approaches to hybridisation and selection in the initial generations of potato (*Solanum tuberosum* L.) clones. *Plant Cell Biotechnology and Molecular Biology, 27*(9–10), 1–9. https://doi.org/10.56557/pcbmb/2026/v27i9-1010932

Yousaf, M. F., Tomar, V., Romé, H., Bagge, M., Timmermann, M., Chu, T. T., & Jensen, J. (2025). Rate of double reduction and genetic variability in yield, quality, and senescence related traits in tetraploid potato (*Solanum tuberosum* L.). *Frontiers in Plant Science, 16*, Article 1560123. https://doi.org/10.3389/fpls.2025.1560123

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