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Assessment of genetic variability, heritability and genetic advance for tuber yield and its component traits in potato (*Solanum tuberosum* L.)

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Abstract
Forty-one genotypes of potato wereexamine in Randomized Block Design with three replications during Rabi season 2025-26 at Potato Research Station, Sardarkrushinagar Dantiwada Agricultural University, Deesa. Six characters were included in the present investigation to study the variability, heritability and genetic advance in potato. The analysis of variance was recorded highly significant difference between the genotypes for all traits under studies. The estimates the coefficient of variation relieved that magnitude of phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the characters. High PCV and GCV values were observed for marketable tuber yield followed by total tuber yield, indicating the existence of considerable genetic variability for yield traits. High heritability coupled with high genetic advance as percentage of mean was observed for marketable tuber yield, total tuber yield and tuber dry matter. This combination indicates the predominance of additive gene action and suggests that direct phenotypic selection would be highly effective for improving these traits.

Keywords: Potato, genetic variability, heritability, genetic advance

Introduction
Potato belongs to the family *Solanaceae* and genus *Solanum*, which comprises about 2000 species and the sub-section potato contains 19 series and 235 species, out of which 200 species are tuber bearing (Patel *et al.*, 2018) [12]. However, only two tuber bearing species *viz.*, *Solanum tuberosum* and *Solanum andigenum* have been commercially cultivated throughout the world. The basic haploid chromosome number of *Solanum tuberosum* is believed to be 12. The somatic chromosome number of cultivated potato species is 48 (Tetraploid), which is grown throughout the world. About 74 per cent of tuber bearing species are diploid (2n = 24) and the rest are polyploid *viz.*, tetraploid (2n = 48), pentaploid (2n = 60) and hexaploid (2n = 72).

Potato (*Solanum tuberosum* L.) is one of the most important food crops worldwide. It ranks third after rice and wheat in terms of human consumption (Zeleke *et al.*, 2021) [21]. It having diversified use as vegetable, processed food, livestock feed and raw material for many industrial productIt is one of the most popular vegetables, which is available throughout the year in vegetable market due to its longterm storability. Now-a-day many dehydrated products like diced franules, baries, papad, biscuits, flour, chips, French fries etc. are prepared from the potato. Potato is widely used as raw materials in starch extraction industries.

Potato tuber contains about 75 to 80 percent water, 16 to 20 percent carbohydrates, 2.5 to 3.2 percent crude protein, 1.2 to 2.2 percent true protein, 0.8 to 1.2 percent mineral, 0.1 to 0.2 percent crude fat, 0.6 per cent crude fiber and vitamins B and C (Swaminathan and Pushkarnath, 1962) [12].

Genetic variability studies help in identify novel traits and genetic combinations that can enhance crop productivity, nutritional quality and resilience to stresses. By selecting genotypes with desirabletraits we can develop improved crop varieties that can contribute to food security (Spanoghe *et al.*, 2022) [17]. Tuber yield is a polygenic trait, breeding for genotypes solely based on tuber yield is not very effective. To enhance breeding efficiency, potato breeders must identify the traits contributing to the final yield (Dehari *et al.*, 2024) [5]. Genetic variability forms the fundamental prerequisite for any plant-breeding program to develop superior cultivars. The existence of genetic variation is a crucial factor for genetic improvement in plant breeding and plays a pivotal role in the utilization of germplasm in breeding programs (Kumar *et al.*, 2023) [8]. Genetic parameters such as genotypic and phenotypic coefficients of variation, heritability and genetic advance are key tools for dissecting total variability into heritable and non-heritable components. Genotypic and phenotypic coefficients of variation offer crucial insights into the level of variability present among genotypes. Heritability refers to the degree to which a trait is inherited from one generation to the next. It measures how much of the observed variation in a trait is due to genetic factors. On the other hand, genetic advance represents the progress achieved through selective breeding. High values of both heritability and genetic advance across different yield components suggest promising prospects for selecting highly productive genotypes (Sahu *et al.*, 2023) [14].

Material and Methods
The research material for present study comprises Fortyone potato genotypes (Table-1). The field trial was conducted at Potato Research Station, Sardarkrushinagar Dantiwada Agricultural University, Deesa. The experiment was carried out in Randomized Block Design (RBD) with three replications during rabi 2025-26. Each genotype was represented by six row of 3.0 m length. The inter and intra row distances were 50 and 20 cm, respectively. All the

recommended package of practices was followed for successful harvesting of the crop. The data were recorded from five randomly selected plants from each entry in each replication for Days to emergence (%), Foliage senescence (%), Plant vigor (1-5), Marketable tuber yield (t/ha), Total tuber yield(t/ha) and Tuber dry matter (%). The mean of the data recorded were used for statistical analysis. Standard statistical procedures were employed to conduct the analysis of variance (Panse and Sukhatme, 1967) [11], genotypic and phenotypic coefficients of variation (Burton and Devane, 1953) [4], heritability (Allard, 1960) [2] and genetic advance (Lush, 1949; Johnson *et al.*, 1995) [9,7].

Table 1: List of potato genotypes under study.

Sr. No	Genotype	Source
1	AICRP-C-5	CPRI, Shimla
2	AICRP-C-6	CPRI, Shimla
3	AICRP-C-8	CPRI, Shimla
4	AICRP-C-11	CPRI, Shimla
5	AICRP-C-14	CPRI, Shimla
6	AICRP-C-17	CPRI, Shimla
7	AICRP-C-20	CPRI, Shimla
8	AICRP-FF-04	CPRI, Shimla
9	AICRP-P-1	CPRI, Shimla
10	AICRP-P-4	CPRI, Shimla
11	AICRP-P-7	CPRI, Shimla
12	AICRP-P-9	CPRI, Shimla
13	AICRP-P-14	CPRI, Shimla
14	AICRP-P-24	CPRI, Shimla
15	AICRP-P-42	CPRI, Shimla
16	AICRP-P-45	CPRI, Shimla
17	AICRP-P-46	CPRI, Shimla
18	AICRP-P-48	CPRI, Shimla
19	AICRP-P-57	CPRI, Shimla
20	AICRP-P-76	CPRI, Shimla
21	AICRP-P-77	CPRI, Shimla
22	AICRP-P-82	CPRI, Shimla
23	AICRP-P-85	CPRI, Shimla
24	AICRP-P-94	CPRI, Shimla
25	AICRP-P-96	CPRI, Shimla
26	AICRP-P-101	CPRI, Shimla
27	AICRP-P-102	CPRI, Shimla
28	AICRP-P-106	CPRI, Shimla
29	AICRP-P-115	CPRI, Shimla
30	AICRP-P-116	CPRI, Shimla
31	AICRP-P-117	CPRI, Shimla
32	AICRP-P-118	CPRI, Shimla
33	AICRP-P-119	CPRI, Shimla
34	AICRP-P-120	CPRI, Shimla
35	AICRP-P-121	CPRI, Shimla
36	AICRP-P-125	CPRI, Shimla
37	AICRP-P-126	CPRI, Shimla
38	AICRP-P-128	CPRI, Shimla
39	AICRP-P-132	CPRI, Shimla
40	AICRP-P-135	CPRI, Shimla
41	AICRP-P-136	CPRI, Shimla

Results and Discussion

The analysis of variance revealed highly significant differences among the forty-one potato genotypes for all the six characters studied *viz.*, emergence percentage, foliage senescence, plant vigor, marketable tuber yield, total tuber yield and tuber dry matter content (Table 2). The mean sum of squares due to treatments was significant for all traits, indicating the existence of substantial genetic variability among the experimental material the presence of highly significant differences among genotypes has also been reported by several earlier workers including Luthra (2001), Patel *et al*. (2018) and Aishwarya, *et al*. (2024) [10,12,1] in potato.

Mean performance of forty-one potato genotypes for six traits is summarized in Table 3. Emergence percentage ranged from 75.00% (AICRP-P-136) to 96.67% (AICRP-C-17) with an overall mean of 87.72%. Higher emergence was also recorded in AICRP-C-5 (95.56%), AICRP-P-101 (95.56%), AICRP-P-57 (95.00%), AICRP-P-45 (93.34%), AICRP-P-116 (93.89%), AICRP-C-6 (92.78%) and AICRP-P-82 (92.78%). Foliage senescence varied from 46.67% in AICRP-P-136 to 91.67% in AICRP-C-6 and AICRP-P-7, with a population mean of 72.68%. Plant vigor ranged from 4.00 (AICRP-P-132) to 4.92 (AICRP-P-117 and AICRP-P-120) with a mean value of 4.53. Marketable tuber yield exhibited wide variation from 25.75 t ha^{-1} (AICRP-P-4) to 68.47 t ha^{-1} (AICRP-C-17) with a mean value of 42.70 t ha^{-1}. Total tuber yield ranged from 28.52 t ha^{-1} (AICRP-P-121) to 69.35 t ha^{-1} (AICRP-C-17) with an overall mean of 44.83 t ha^{-1}. Genotypes AICRP-C-17, AICRP-P-117, AICRP-C-5, AICRP-P-9 and AICRP-C-14 consistently recorded higher total tuber yield than the population mean. Tuber dry matter varied between 14.27% (AICRP-P-119) and 28.00% (AICRP-P-77) with a mean of 20.74%. Higher tuber dry matter content was recorded in AICRP-P-77 (28.00%), AICRP-P-106 (25.67%), AICRP-P-121 (25.47%), AICRP-P-120 (24.60%), AICRP-P-94 (24.40%) and AICRP-FF-04 (24.40%).

The estimates of genotypic and phenotypic coefficients of variation for six characters of potato genotypes are presented in Table 4 and Fig. 1. The values for the phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were classified as low (<10%), moderate (10- 20%) and high (>20%) according to Sivasubramanian and Menon (1973) [16]. Phenotypic coefficient of variation (PCV) was slightly higher than genotypic coefficient of variation (GCV) for all the characters, indicating that environmental influence on trait expression was relatively low and most of the observed variation was genetically controlled.

High PCV and GCV values were observed for marketable tuber yield (27.61 and 24.79%) followed by total tuber yield (24.88 and 22.03%), indicating the existence of considerable genetic variability for yield traits. Moderate variability was observed for foliage senescence (17.16 and 16.46%) and tuber dry matter (14.54 and 14.15%), whereas emergence (6.58 and 4.71%) and plant vigor (5.58 and 4.29%) exhibited relatively lower variability. Similar findings were reported by Seid *et al*. (2020), Zeleke *et al*. (2021), Anoumaa *et al*. (2022), Gebreselassie (2023), Kumar *et al*. (2023) and Aishwarya, *et al*. (2024) [15,21,3,6,8,1].

Heritability assessment serves as a predictive tool to measure the reliability of phenotypic values. The heritability values, as presented in Table 4 and Fig. 2. were classified by Johnson *et al.*, (1995) [7] as low (<30%), moderate (30-60%) and high (>60%). The broad-sense heritability ranges from 32.51% to 94.72%. In the present study, high estimates of heritability are observed for the traits: tuber dry matter content (94.72%), marketable tuber yield (80.61%) and total tuber yield (78.36%). Moderate heritability is observed for the parameter plant vigor (59.00%), plant emergence (51.35%) and foliage senescence (32.51%). High heritability facilitates effective selection for specific traits. When heritability values are high, it indicates that the expression of traits is primarily influenced by genotype rather than environmental factors. Similar findings were reported by Seid *et al.* (2020), Zeleke *et al.* (2021), Rohit *et al.* (2022), Kumar *et al.* (2023) and Aishwarya *et al.* (2024) [15, 21, 13, 8, 1].

Genetic advance refers to enhancing the average genotypic value of chosen plants compared to the parental population. The estimates of Genetic advance as a percentage of mean values classified (Johnson *et al.*, 1995) [7] into low (<10%), moderate (10-20%) and high (>20%). In the current investigation, the highest estimates of genetic advance, expressed as a percentage of the mean, were recorded for marketable tuber yield (45.86%), total tuber yield (40.16%) foliage senescence (32.51%) and tuber dry matter content (28.36%) the high value in the genetic advance as a percentage of the mean observed across these traits, indicates the influence of additive genes on their expression. It suggests that selective breeding efforts targeting these traits could yield substantial improvements, thereby enhancing overall trait performance and quality.

On the other hand, the lowest genetic advance as a percentage of the mean was recorded for parameters like emergence percentage (6.96%) and plant vigor (6.78%). It indicates the presence of non-additive gene effects for these traits. Similar findings are also reported by Tessema *et al.* (2022), Kumar *et al.* (2023), Zanzam *et al.* (2023) and Aishwarya *et al.* (2024) [19,8,20,1].

High heritability coupled with high genetic advance as percentage of mean was observed for marketable tuber yield, total tuber yield and tuber dry matter. This combination indicates the predominance of additive gene action and suggests that direct phenotypic selection would be highly effective for improving these traits. Conversely, emergence, foliage senescence and plant vigor recorded moderate to low genetic advance despite moderate heritability, indicating comparatively greater influence of non-additive gene action and environmental factors.

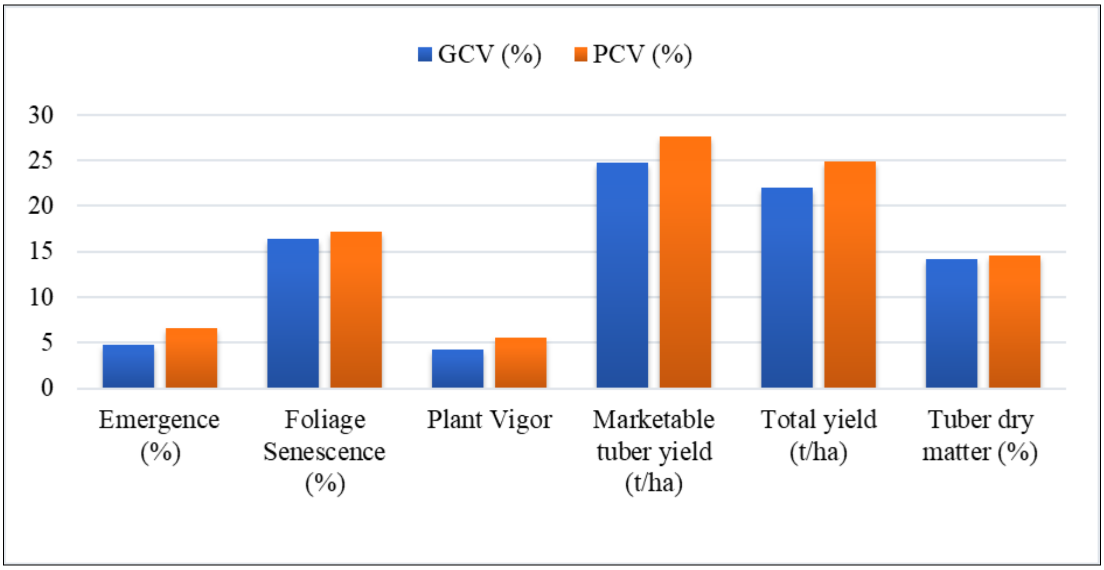

Fig. 1: Genotypic coefficient of variation (%) and phenotypic coefficient of variation (%)

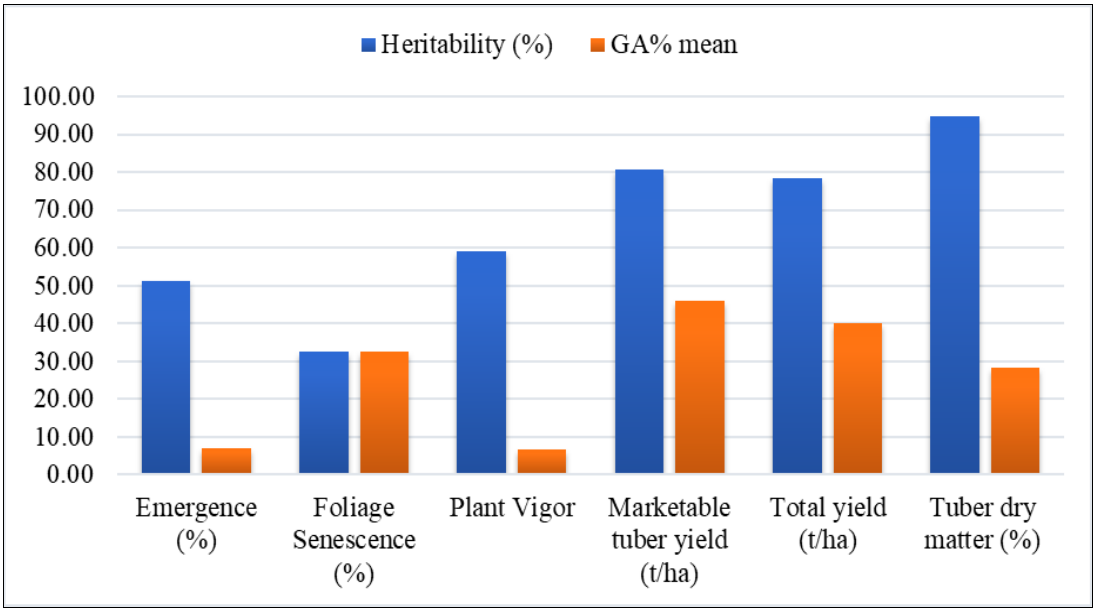

Fig. 2: Heritability (%) and genetic advance as (%) of mean

Table 2: Analysis of variance for tuber yield and its components.

Sr. No	Characters	Mean sum of squares		
		Replication (d.f.=2)	Treatment (d.f.=40)	Error (d.f.=80)
1	Emergence (%)	10.033	67.625**	16.229
2	Foliage Senescence (%)	26.220	441.620**	12.470
3	Plant Vigor	0.014	0.139**	0.026
4	Marketable tuber yield (t/ha)	43.550	363.160**	26.950
5	Total yield (t/ha)	35.430	319.37**	26.930
6	Tuber dry matter (%)	0.997	26.311**	0.480

(**) Significant at 1% level

Table 3: Mean performance of 41 genotypes of potato for six characters.

Sr. No.	CharactersGenotypes	Emergence (%)	Foliage Senescence (%)	Plant Vigor	Marketable tuber yield (t/ha)	Total yield (t/ha)	Tuber dry matter (%)
1	AICRP-C-5	95.56	80.00	4.67	58.73	59.33	19.87
2	AICRP-C-6	92.78	91.67	4.50	36.04	38.54	18.87
3	AICRP-C-8	83.33	78.33	4.50	31.70	37.23	23.87
4	AICRP-C-11	85.00	75.00	4.42	26.29	30.61	22.40
5	AICRP-C-14	87.22	78.33	4.75	56.62	57.89	18.67
6	AICRP-C-17	96.67	88.33	4.67	68.47	69.35	19.40
7	AICRP-C-20	85.56	81.67	4.58	45.24	45.72	18.93
8	AICRP-FF-04	82.22	86.67	4.42	27.25	32.97	24.40
9	AICRP-P-1	86.67	86.67	4.58	54.10	54.84	17.83
10	AICRP-P-4	82.78	68.33	4.50	25.75	29.62	23.47
11	AICRP-P-7	85.00	91.67	4.08	32.73	33.46	20.33
12	AICRP-P-9	84.44	86.67	4.58	57.31	58.63	19.67
13	AICRP-P-14	89.44	86.67	4.50	44.20	47.80	22.00
14	AICRP-P-24	84.45	73.33	4.50	35.72	38.86	21.00
15	AICRP-P-42	88.33	73.33	4.50	52.76	53.59	17.93
16	AICRP-P-45	93.34	76.67	4.67	49.37	50.67	19.00
17	AICRP-P-46	94.44	86.67	4.58	45.71	47.34	22.73
18	AICRP-P-48	85.55	56.67	4.67	52.69	53.14	15.93
19	AICRP-P-57	95.00	76.67	4.67	40.22	44.57	21.80
20	AICRP-P-76	86.11	76.67	4.67	53.24	54.78	19.80
21	AICRP-P-77	88.33	63.33	4.75	43.76	47.50	28.00
22	AICRP-P-82	92.78	73.33	4.67	47.56	48.82	20.87
23	AICRP-P-85	85.00	60.00	4.58	55.94	57.42	16.40
24	AICRP-P-94	86.67	63.33	4.83	33.83	44.65	24.40
25	AICRP-P-96	91.67	55.00	4.33	37.73	38.74	17.53
26	AICRP-P-101	95.56	81.67	4.42	49.06	51.07	19.60
27	AICRP-P-102	89.44	76.67	4.67	52.10	53.74	20.53
28	AICRP-P-106	92.78	71.67	4.58	33.13	37.39	25.67
29	AICRP-P-115	91.11	75.00	4.42	43.66	44.80	23.13
30	AICRP-P-116	93.89	73.33	4.83	52.24	52.97	22.20
31	AICRP-P-117	90.56	66.67	4.92	60.26	61.47	22.67
32	AICRP-P-118	84.44	53.33	4.17	34.21	35.84	20.13
33	AICRP-P-119	87.78	50.00	4.25	42.83	43.39	14.27
34	AICRP-P-120	84.44	53.33	4.92	41.67	44.70	24.60
35	AICRP-P-121	83.89	75.00	4.33	26.84	28.52	25.47
36	AICRP-P-125	86.11	86.67	4.33	35.52	36.23	19.13
37	AICRP-P-126	83.89	63.33	4.67	43.48	44.23	19.20
38	AICRP-P-128	82.78	63.33	4.25	28.95	30.43	22.53
39	AICRP-P-132	84.44	73.33	4.00	29.09	29.88	21.73
40	AICRP-P-135	82.22	55.00	4.17	30.31	31.13	18.87
41	AICRP-P-136	75.00	46.67	4.67	34.58	36.06	15.47
	General Mean	87.72	72.68	4.53	42.70	44.83	20.74
	S. Em ±	2.33	2.04	0.09	3.00	3.00	0.40
	CD at 5%	6.55	5.74	0.26	8.44	8.43	1.13

Table 4: Estimates of genetic parameters for tuber yield and its attributing traits in potato

Sr. No.	Characters	Range		Coefficient of variation (%)			h^2 (Broad sense %)	Genetic advance	Genetic advance as % of mean
		Mini.	Max.	Phenotypic	genotypic	Environmental			
1	Emergence (%)	63.33	100.00	6.58	4.71	4.59	51.35	6.11	6.96
2	Foliage Senescence (%)	45.00	95.00	17.16	16.46	4.86	32.51	23.63	32.51
3	Plant Vigor	3.75	5.00	5.58	4.29	3.57	59.00	0.31	6.78
4	Marketable tuber yield	20.31	70.28	27.61	24.79	12.16	80.61	19.58	45.86

	(t/ha)								
5	Total yield (t/ha)	22.47	71.13	24.88	22.03	11.58	78.36	18.00	40.16
6	Tuber dry matter (%)	13.20	28.40	14.54	14.15	3.34	94.72	5.88	28.36

Conclusion

The present investigation demonstrated the existence of ample genetic variability among the evaluated potato genotypes for yield and processing-related traits. Significant differences observed through analysis of variance confirmed the presence of substantial genetic diversity. The relatively small differences between PCV and GCV indicated limited environmental influence on trait expression. High heritability coupled with high genetic advance for marketable tuber yield, total tuber yield and tuber dry matter suggested that these traits are mainly governed by additive gene effects and can be effectively improved through direct phenotypic selection. Among the evaluated entries, AICRP-C-17 emerged as the most promising genotype owing to its superior marketable and total tuber yield, while AICRP-P-77 was identified as a valuable processing genotype because of its exceptionally high tuber dry matter content.

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