Plant Archives **Vol. 26, Supplement 1, 2026 pp. 2016-2021** **e-ISSN:2581-6063 (online), ISSN:0972-5210**

Plant Archives

Journal homepage: http://www.plantarchives.org
DOI Url : https://doi.org/10.51470/PLANTARCHIVES.2026.v26.supplement-1.271

EVALUATION OF GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE AMONG THE DIFFERENT YIELD AND QUALITY CHARACTERS OF CHILLI (*CAPSICUM ANNUUM* L.)

Vishal Yadav[1]*, Rajiv[1], Rajat Singh[1], Krishan Kumar[1], Rohit Rawat[1], Rahul Kumar[1], Siddharth Kumar[1] and Anuj Mishra[2]
[1]Department of Vegetable Science, Chandra Shekhar Azad University of Agriculture and Technology,
Kanpur (U.P.), India
[2]Department of Genetics and Plant Breeding, Chandra Shekhar Azad University of Agriculture & Technology,
Kanpur (U.P.), India
*Corresponding author E-mail: yadavvishu65@gmail.com
(Date of Receiving : 07-08-2025; Date of Acceptance : 17-10-2025)

ABSTRACT

The present study was conducted to assess the extent of genetic variability, heritability and genetic advance in chilli (*Capsicum annuum* L.) for yield and quality-related traits. The experimental material consisted of 10 diverse parental genotypes, their 45 half-diallel F_1 crosses and corresponding F_2 progenies, evaluated during rabi 2024-25. Analysis of variance revealed highly significant differences among parents, F_{1s} and F_{2s}, indicating the presence of ample genetic variability. Estimates of genotypic and phenotypic coefficients of variation suggested that yield per plant, fruit length, fruit rot incidence and leaf curl virus incidence exhibited high variability, whereas traits like fruit width, ascorbic acid content and number of branches showed moderate variation. In general, phenotypic coefficients were slightly higher than genotypic. Broad-sense heritability was high for traits such as fruit weight, plant height, number of seeds per fruit, oleoresin content and fruit yield per plant, suggesting reliable transmission of these characters. Genetic advance as percentage of mean was also high for fruit yield, fruit length, fruit rot incidence and leaf curl virus incidence, implying that these traits are largely governed by additive gene action and can respond effectively to selection. Overall, the findings indicate that selection based on yield per plant, fruit length, fruit weight, and resistance-related traits such as fruit rot and leaf curl virus incidence could be highly effective in improving chilli. The study provides useful genetic information to guide breeders in developing high-yielding and quality-rich chilli cultivars suitable for diverse growing environments.

***Keywords* :** Chilli, genetic variability, heritability and genetic advance

Introduction

Chilli (*Capsicum annuum* L.) is one of the most widely cultivated spice crops in the world, valued not only for its pungency and flavour but also for its nutritional and industrial uses. In India, chilli holds a special place as both a dietary staple and a commercial crop, contributing significantly to farmers' income and the spice export industry. Apart from being a source of capsaicin, which imparts pungency, chilli fruits are rich in vitamin C, capsanthin and oleoresin that enhance its quality and market demand. With increasing consumer preference for high-yielding varieties that also meet quality standards, there is a continuous need to develop improved genotypes.

The success of any crop improvement program depends largely on the availability of genetic variation and the breeder's ability to exploit it effectively. Parameters such as genetic variability, heritability and genetic advance provide valuable insights into the inheritance of characters and the scope for selection. While genetic variability indicates the extent of differences present among genotypes, heritability explains how much of this variation is genetically controlled rather than influenced by the environment. Genetic advance, on the other hand, predicts the possible progress expected from selection. Together, these parameters guide breeders in identifying the most promising traits for genetic improvement.

In chilli, traits such as plant height, number of fruits per plant, fruit weight, ascorbic acid content and capsanthin content are complex in nature, often governed by multiple genes and strongly affected by environmental factors. Previous studies in different genetic backgrounds have reported contrasting levels of variability and heritability for these traits, which emphasizes the importance of evaluating new populations under specific agro-climatic conditions. Assessing these genetic parameters in segregating generations can provide deeper insights into the nature of gene action and the expected response to selection.

Considering this background, the present study was designed to evaluate genetic variability, heritability and genetic advance for yield and quality-related traits in chilli. The work was carried out using a set of ten diverse parents and their half-diallel crosses, along with F_1 and F_2 generations, under field conditions at Kanpur. The findings are expected to help in identifying characters with higher breeding potential and to provide a scientific basis for designing effective selection and hybridization strategies for improvement of chilli in terms of both yield and quality.

Materials and Methods

The present investigation entitled "Studies on Heterosis, Combining Ability and Gene Action for Yield and Quality Contributing Traits in Chilli (*Capsicum annuum* L.) was conducted in Randomized Block design with three replications during rabi 2024-25 at Main Experimental Station, Department of Vegetable Science, Chandra Sekhar Azad University of Agriculture & Technology, Kalyanpur, Kanpur, (U.P), 208002. The experimental material for the present investigation, generated by crossing 10 lines varieties / genotypes and half diallel fashion to produce 45 F_1. All the 100 treatments (10 parents + 45 F_1 + 45 F_2) were evaluated for the study of genetical analysis of different characters in chilli. The observations were recorded on five randomly selected plants per treatment from each replication for eighteen plants growth, yield and quality traits *viz.*, plant height, number of branches, days to 50% flowering, days to fruiting, days to ripening, fruit length, fruit width, number of fruits plant^{-1}, average fruit weight, number of seed per fruit, fruit yield plant^{-1}, fruit yield hectare^{-1}, ascorbic acid content, capsanthin content, oleoresin content, leaf curl virus incidence, fruit rot incidence. Analysis of variance was done by method suggested by Panse and Sukhatme (1967). The genotypic and phenotypic coefficients of variation were calculated using the formulae of Burton (1952) and Johnson *et al.* (1955). The heritability and genetic advance were calculated according to Allard (1960) and genetic advance as per cent of mean was estimated using the method of Johnson *et al.* (1955).

Result and Discussion

Analysis of variance

The analysis of variance (ANOVA) unveiled significant differences among the genotypes mean sum of squares (MSS) for all the traits under study and has been tabulated following table. Mean sum of squares due to parents and crosses were significant for all eighteen characters studied in parent, F_1 and F_2 viz., plant height (388.455, 98.805 and 74.53), number of branches (0.777, 1.059 and 0.495), days to 50% flowering (48.19, 23.27, 22.15), days to fruiting (79.787, 22.71 and 19.85), days to ripening (74.37, 40.35 and 37.37), fruit length (7.01, 6.90 and 6.91), fruit width (0.079, 0.135 and 0.101), number of fruits plant-1(219.45, 117.88 and 125.49), average fruit weight (1.802, 1.178 and 1.299), number of seed per fruit (154.63, 176.92 and 102.56), fruit yield plant-1 (2170.9, 15617.9 and 16360.8), fruit yield hectare-1 (3473.5, 2498.86 and 2617.72), ascorbic acid content (1001.0, 874.46 and 583.64), capsanthin content (514.91, 332.94 and 206.97), oleoresin content (9.59, 19.56 and 18.05), leaf curl virus incidence (277.41, 282.62 and 213.76), fruit rot incidence (3.69, 5.98 and 4.45) thereby indicating the presence of sufficient genetic variability among the genotypes for these characters

Variance and Coefficient of variation

The coefficients of variation at genotypic and phenotypic levels were studied among 100 (10 parents + 45 F_1 + 45 F_2) chilli genotypes for plant growth, fruit yield and quality contributing characters rabi seasons. The phenotypic coefficients of variation were higher in magnitude than its genotypic counterpart indicating considerable environmental effect on expression of genes. In parent, high genotypic coefficient of variation was observed for yield per plant, per hectare (24.82) and fruit length (24.04). Medium genotypic coefficient of variation was observed for leaf curl virus incidence (19.45) followed by fruit rot incidence (18.99), plant height (18.31), number of seed per fruit (16.40), fruit weight (16.04), capsanthin content (15.06), fruit width (14.15), ascorbic acid content (13.87), number of fruits per plant (11.62) and number of branches (11.01) and rest character show low genotypic coefficient of variation. While in F_1 high genotypic coefficient of variation was observed for fruit rot incidence (23.34) and leaf curl virus incidence (22.24). Medium genotypic coefficient of variation was observed for fruit length (19.51) followed by yield per plant, per hectare (18.36), fruit width (17.06), number of seed per fruit (16.24), oleoresin content (16.20), capsaicin content (13.19), fruit weight (12.57), number of branches (11.92) and ascorbic acid content (10.26) rest character show low genotypic coefficient of variation. Whereas in F2 high genotypic coefficient of variation was observed for fruit rot incidence (20.70) followed by yield per plant, per hectare (20.68), fruit length (20.22). Medium genotypic coefficient of variation was observed for leaf curl virus incidence (18.69) followed by oleoresin content (16.93), fruit width (14.72), number of seed per fruit (13.62), capsaicin (13.03), fruit weight (12.86) and ascorbic acid (10.31) rest character show low genotypic coefficient of variation.

In parent, high phenotypic coefficient of variation was observed for fruit length (26.28) followed by yield per plant, per plot, per hectare (25.69), capsaicin content (22.24) and leaf curl virus incidence (21.25). Medium phenotypic coefficient of variation was observed for fruit rot incidence (19.32) followed by fruit width (18.72), plant height (18.62), number of seed per fruit (16.85), ascorbic acid content (16.22), fruit weight (16.21), capsanthin content (16.06), number of branches (15.54), number of fruits per plant (13.41) and oleoresin (12.76) and rest character show low phenotypic coefficient of variation. While in F_1 high phenotypic coefficient of variation was observed for fruit rot incidence (24.99) followed by leaf curl virus incidence (22.41), fruit length (20.99), yield per plant, per plot and fruit yield per hectare (20.02). Medium phenotypic coefficient of variation was observed for fruit width (18.65) followed by number of seed per fruit (16.93), oleoresin content (16.39), capsanthin content (16.06), capsaicin content (14.77), number of branches (14.96), ascorbic acid content (14.28) and fruit weight (13.34) and rest character show low phenotypic coefficient of variation. Whereas in F2 high phenotypic coefficient of variation was observed for yield per plant, per plot, per hectare (24.19) followed by fruit rot incidence (22.53), fruit length (22.24) and leaf curl virus incidence (21.13). Medium phenotypic coefficient of variation was observed for oleoresin content (18.92) followed by fruit width (17.49), number of seed per fruit (16.27), capsanthin content (16.06), capsaicin content (15.87), fruit weight (15.84), ascorbic acid content (14.33), number of branches (13.62) and number of fruits per plant (11.47) and rest character show low phenotypic coefficient of variation.

The magnitude of genotypic coefficients of variation (GCV) in parent F_1 and F_2 was moderate to high for most of the growth, yield and quality attributes such as plant height, number of branches, number of seed per fruit, number of fruits per plant, average fruit weight, fruit width, ascorbic acid content, and capsanthin content suggesting sufficient scope for improvement through selection.

Generally, the estimates of PCV were slightly higher than their corresponding GCV values, reflecting the influence of environment on expression of these traits. However, in parent, high phenotypic coefficient of variation was observed for fruit length followed by yield per plant, capsaicin content and leaf curl virus incidence. While in F_1 and F_2 high phenotypic coefficient of variation was observed for fruit rot incidence, leaf curl virus incidence, fruit length, yield per plant and fruit yield per hectare. Similar findings were earlier reported by Patel *et al.* (2015) and Kumar *et al.* (2018) Lata and Sharma (2022), Markram *et al.* (2022), Patel *et al.*, (2022), Saisupriya *et al.* (2022), Shivakumar *et al.* (2025) and Sufiyan (2025) in chilli,

Heritability

In parent heritability in broad sense was found high for fruit weight (97.92%) followed by plant height (96.75%), Days to fruiting (96.73%), fruit rot incidence (96.57%), number of seed per fruit (94.68%), oleoresin content (94.22%), yield per plant, per hectare (93.38%), capsanthin content (87.98%), days to 50% flowering (86.20%), fruit length (83.69%) and leaf curl virus incidence (83.82%), whereas heritability was medium for days to ripening (78.68%) followed by number of fruits per plant (75.10%), ascorbic acid content (73.17%), fruit width (57.14%) and numbers of branches (50.19%) rest of the traits are low heritable. While in F_1 heritability in broad sense was found high for leaf curl virus incidence (98.49%) followed by oleoresin content (97.65%), number of seed per fruit (92.01%), fruit weight (88.83%), fruit rot incidence (87.20%), fruit length (86.42%), yield per plant, per hectare (84.09%) and fruit width (83.66%) whereas heritability was medium for capsaicin content (77.78%) followed by plant height (71.77%), days to ripening (71.71%) Days to fruiting (70.14%), capsanthin content (66.10%), numbers of branches (63.52%), days to 50% flowering (56.89%), ascorbic acid content (%) and number of fruits per plant (51.30%) and rest of the traits are low heritable. Whereas in F_2 heritability in broad sense was found high for days to ripening (94.19%) followed by fruit rot incidence (84.37%), fruit length (82.71%) and oleoresin content (80.12%), whereas heritability was medium for leaf curl virus incidence (78.24%) followed by yield per plant, per hectare (73.06%), fruit width (70.81%), number of seed per fruit (70.00%), capsaicin content (69.07%), fruit weight (65.96%), days to 50% flowering (60.24%) and ascorbic acid content (51.69%) and rest of the traits are low heritable. similar results are reported by Kumar *et al.* (2020), Deepo *et al.* (2020), Tirupathamma *et al.* (2021), Vyas *et al.* (2021), Lata and Sharma (2022), Markram *et al.* (2022), Patel *et al.*, (2022), Saisupriya *et al.* (2022) and Shivakumar *et al.* (2025).

Genetic advance in percentage of mean (Genetic gain)

In parent, high genetic advance as percentage of mean (genetic gain) was recorded for most of the traits ranging from 49.41% for fruit per plant, per plot and per hectare to 32.69% for fruit weight. Other traits with high genetic advance as percentage of mean were fruit length (45.31%) followed by fruit rot incidence (38.44%), plant height (37.11%), leaf curl virus incidence (36.69%) and number of seed per fruit (32.87%). Medium value of this parameter was recorded for capsanthin content (29.10%) followed by oleoresin content (24.78%), ascorbic acid content (24.45%), fruit width (22.04%), number of fruits per plant (20.75%), days to fruiting (18.24%), number of branches per plant (16.07%) and days to 50% flowering (15.24%). For the rest of traits genetic advance as percentage of mean was found to be low. While in F_1, the highest value of genetic advance as percentage of mean was registered by leaf curl virus incidence (45.47%) followed by fruit rot incidence (44.89%), fruit length (37.37%), fruit yield per plant and per hectare to (34.68%), oleoresin content (32.97%), fruit width (32.13%) and number of seed per fruit (32.09%). Medium value for this parameter was observed for fruit weight (24.41%) followed by capsaicin content (23.66%), number of branches per plant (19.57%) and capsanthin content (15.65%) ascorbic acid content (%). For the rest of traits genetic gain was found to be low. Whereas in F_2, the highest value of genetic advance as percentage of mean was registered by fruit rot incidence (39.16%) followed by fruit length (37.89%), fruit yield per plant and per hectare to (36.41%), leaf curl virus incidence (34.05%) and oleoresin content (31.22%). Medium value for this parameter was observed for fruit width (25.51%) followed by number of seed per fruit (23.47%), fruit weight (21.52%), number of branches per plant (19.57%) and capsanthin content (15.65%) and ascorbic acid content (15.26%). For the rest of traits genetic advance as percentage of mean was found to be low. similar results are reported by Kumar *et al.* (2020), Deepo *et al.* (2020), Tirupathamma *et al.* (2021), Vyas *et al.* (2021), Lata and Sharma (2022), Markram *et al.* (2022), Patel *et al.*, (2022), Saisupriya *et al.* (2022) and Shivakumar *et al.* (2025).

Conclusion

The present investigation clearly demonstrated the existence of substantial genetic variability for yield and quality contributing traits in chilli. High GCV and PCV value were recorded for most of the traits Heritability and genetic advance were high for traits like fruit number, ascorbic acid, and fruit yield, indicating potential for effective selection. Moderate estimates for traits like oleoresin suggested both genetic and environmental influences. Thus, based on variability, heritability and genetic advance we can select the best parents to developing more high yielder hybrids varieties.

Table 1 : Analysis of variance for Randomized Block Design

SN	Characters	Source of Variation								
		Parents			F1			F2		
		Replications	Treatments	Error	Replications	Treatments	Error	Replications	Treatments	Error
		[2]	[9]	[18]	[2]	[44]	[88]	[2]	[44]	[88]
1	Plant height	5.450	388.455**	4.30	4.067	98.805**	11.455	54.372	74.53**	37.55
2	Number of branches	0.205	0.777**	0.193	0.042	1.059**	0.170	0.189	0.495**	0.161
3	Days to 50% flowering	0.675	48.192**	2.441	2.500	23.275**	4.693	5.563	22.15**	3.995
4	Days to fruiting	0.355	79.787**	0.889	0.9743	22.710**	2.8218	8.167	19.856**	6.966
5	Days to ripening	4.328	74.373**	6.161	0.272	40.353**	4.690	1.583	37.373**	0.753
6	Fruit length	0.004	7.010**	0.427	0.114	6.901**	0.343	0.119	6.917**	0.450
7	Fruit width	0.008	0.079**	0.015	0.012	0.135**	0.008	0.018	0.101**	0.012
8	Number of fruits plant^{-1}	9.073	219.452**	21.841	35.824	117.88**	28.320	65.201	125.49**	36.234
9	Average fruit weight	0.169	1.802**	0.012	0.014	1.178**	0.047	0.122	1.299**	0.190
10	No. of seed per fruit	1.218	154.637**	2.841	1.495	176.922**	4.979	32.049	102.568**	12.819
11	Fruit yield plant^{-1}	419.20	2170.9**	500.8	775.40	15617.9**	926.5	2364.4	16360.8**	1790.5

12	**Fruit yield hectare^{-1}**	67.10	3473.5**	80.1	124.07	2498.86**	148.23	378.31	2617.72**	286.48
13	**Ascorbic acid content**	173.80	1001.00**	109.02	0.830	874.46**	1.310	36.51	583.64**	138.65
14	**Capsaicin content**	0.021	0.025	0.019	0.0001	0.025**	0.002	0.002	0.023**	0.003
15	**Capsanthin content**	16.33	514.91**	22.44	112.97	332.94**	48.60	23.829	206.970**	74.633
16	**Oleoresin content**	0.105	9.591**	0.192	0.302	19.565	0.155	0.343	18.058**	1.379
17	**Leaf curl virus incidence**	20.585	277.418**	16.776	0.285	282.62**	1.442	6.380	213.762**	18.138
18	**Fruit rot incidence**	0.072	3.693**	0.043	0.644	5.981**	0.279	0.714	4.456**	0.259

Table 2: Genetic variability, Heritability and Genetic advance of parent, F1 and F2

		Maximum	**Minimum**	**Grand Mean**	**Sem**	**GCV**	**PCV**	**h2(bs)**	**GA**	**GAM**
Plant height	**Parent**	80.96	41.91	61.79	1.20	18.31	18.62	96.75	22.93	37.11
	F1	86.41	64.25	74.93	1.95	7.20	8.50	71.77	9.42	12.57
	F2	80.46	61.04	70.76	3.54	4.96	9.98	24.71	3.60	5.08
Number of branches	**Parent**	5.15	3.48	4.01	0.25	11.01	15.54	50.19	0.64	16.07
	F1	5.83	3.49	4.57	0.24	11.92	14.96	63.52	0.89	19.57
	F2	5.53	3.29	3.83	0.23	8.70	13.62	40.84	0.44	11.46
Days to 50% flowering	**Parent**	56.18	44.03	49.00	0.90	7.97	8.58	86.20	7.47	15.24
	F1	53.63	38.87	46.62	1.25	5.34	7.08	56.89	3.87	8.29
	F2	56.24	42.18	49.27	1.15	4.99	6.43	60.24	3.93	7.98
Days to fruiting	**Parent**	66.58	50.07	56.98	0.54	9.00	9.15	96.73	10.39	18.24
	F1	59.74	45.29	53.71	0.97	4.79	5.72	70.14	4.44	8.27
	F2	62.61	50.31	56.45	1.52	3.67	5.95	38.15	2.64	4.67
Days to ripening	**Parent**	104.34	90.16	95.67	1.43	4.98	5.62	78.68	8.71	9.11
	F1	101.88	82.23	91.09	1.25	3.79	4.47	71.71	6.01	6.60
	F2	104.36	85.78	94.94	0.50	3.68	3.79	94.19	6.98	7.36
Fruit length	**Parent**	8.46	4.16	6.16	0.38	24.04	26.28	83.69	2.79	45.31
	F1	12.09	5.19	7.58	0.34	19.51	20.99	86.42	2.83	37.37
	F2	11.62	5.11	7.26	0.39	20.22	22.24	82.71	2.75	37.89
Fruit width	**Parent**	1.37	0.84	1.03	0.07	14.15	18.72	57.14	0.23	22.04
	F1	1.65	0.83	1.21	0.05	17.06	18.65	83.66	0.39	32.13
	F2	1.50	0.84	1.17	0.06	14.72	17.49	70.81	0.30	25.51
Number of fruits plant^{-1}	**Parent**	80.12	51.92	69.82	2.70	11.62	13.41	75.10	14.49	20.75
	F1	100.59	69.49	77.75	3.07	7.03	9.81	51.30	8.06	10.37
	F2	92.89	60.20	70.83	3.48	7.70	11.47	45.09	7.55	10.65
Average fruit weight	**Parent**	6.35	3.79	4.82	0.07	16.04	16.21	97.92	1.57	32.69
	F1	6.28	3.79	4.88	0.13	12.57	13.34	88.83	1.19	24.41
	F2	6.35	3.76	4.73	0.25	12.86	15.84	65.96	1.02	21.52
No. of seed per fruit	**Parent**	54.25	34.72	43.38	0.97	16.40	16.85	94.68	14.26	32.87
	F1	61.49	32.14	46.62	1.29	16.24	16.93	92.01	14.96	32.09
	F2	57.77	30.44	40.17	2.07	13.62	16.27	70.00	9.43	23.47
Fruit yield plant^{-1}	**Parent**	502.10	258.64	338.72	12.92	24.82	25.69	93.38	167.38	49.41
	F1	631.95	286.57	381.24	17.57	18.36	20.02	84.09	132.19	34.68
	F2	588.44	240.83	337.03	24.43	20.68	24.19	73.06	122.71	36.41
Fruit yield hectare^{-1}	**Parent**	200.84	103.46	135.49	5.17	24.82	25.69	93.38	66.95	49.41
	F1	252.78	114.63	152.49	7.03	18.36	20.02	84.09	52.88	34.68
	F2	235.38	96.33	134.81	9.77	20.68	24.19	73.06	49.09	36.41
Ascorbic acid content	**Parent**	154.51	95.85	124.29	6.03	13.87	16.22	73.17	30.38	24.45
	F1	162.55	100.36	126.57	6.75	10.26	14.28	50.21	14.47	13.34
	F2	144.37	93.97	118.19	6.80	10.31	14.33	51.69	18.04	15.26
Capsaicin content	**Parent**	0.82	0.54	0.66	0.08	7.15	22.24	10.33	0.03	4.74
	F1	0.88	0.52	0.67	0.03	13.03	14.77	77.78	0.16	23.66
	F2	0.81	0.47	0.62	0.03	13.19	15.87	69.07	0.14	22.58
Capsanthin content	**Parent**	104.31	67.63	85.07	2.73	15.06	16.06	87.98	24.76	29.10
	F1	126.94	80.17	104.20	4.03	9.34	11.49	66.10	16.31	15.65
	F2	112.68	77.75	93.90	4.99	7.07	11.60	37.15	8.34	8.88
Oleoresin content	**Parent**	16.96	10.80	14.29	0.25	12.39	12.76	94.22	3.54	24.78
	F1	21.52	11.08	15.71	0.23	16.20	16.39	97.65	5.18	32.97

	F2	19.11	10.26	13.93	0.68	16.93	18.92	80.12	4.35	31.22
Leaf curl virus incidence	**Parent**	58.05	32.68	47.92	2.36	19.45	21.25	83.82	17.58	36.69
	F1	64.07	23.66	43.53	0.69	22.24	22.41	98.49	19.79	45.47
	F2	56.69	30.38	43.21	2.46	18.69	21.13	78.24	14.71	34.05
Fruit rot incidence	**Parent**	8.04	4.31	5.81	0.12	18.99	19.32	96.57	2.23	38.44
	F1	10.07	3.66	5.91	0.31	23.34	24.99	87.20	2.65	44.89
	F2	9.35	3.96	5.72	0.29	20.70	22.53	84.37	2.24	39.16

References

Allard, R.W. (1960). Principles of Plant Breeding. John Wiley and Sons, London. p. 83-88.

Burton, G.W., Devane, E.H. (1953). Estimating the heritability in tall fescue (*Festuca arundinancea*) from replicated clonal material. *Agronomy Journal*, **45**, 478-481.

Deepo, Dm., Sarker, A., Akter, S., Islam, Md. M., Hasan, M. and Zeba N. (2020). Diversity and path analysis in Chilli (*Capsicum annuum* L.) based on morphological traits in Northern region of Bangladesh. *Turkish Journal of Agriculture - Food Science and Technology* **8**, 179-185 145.

Farwah S, Hussain K, Rizvi S, Hussain SM, Raishid M, Saleem S. (2020). Genetic variability, heritability and genetic advance studied in chilli (*Capsicum annuum* L.) genotypes. *International Journal of chemical Studied*, **8**(3),1328-1331.

Johnson, H.W., Robinson, H.F., Comstock, R.E. (1955). Genotypic and phenotypic correlation in soybean and their implication in selection. *Agronomy Journal*, **47**, 477-483.

Kempthorne, O. (1957). An Introduction to Genetic Statistics. John Wiley and Sons, New York.

Kumar, Tg., Patel, Hb., Jayashree. and Gowda, Dc. (2020). Genetic variability studies in green Chilli (*Capsicum annuum* L.). *International Journal of Chemical Studies,* **8**, 2460-2463

Lata, H. and Sharma, A. (2022). Evaluation, genetic variability, correlation and path analysis studies in Chilli (*Capsicum annuum* L.) genotypes. *Himachal journal of agricultural research*, **48**(1), 56-64.

Markam, D. and Sharma, D. (2022). Assessment of genetic variability, heritability and genetic advance for yield and yield attributing traits in Chilli (*Capsicum annuum* L.). *The Pharma Innovation Journal,* **11**(10), 471-474.

Panse, Vg. and Sukhatme, Pv. (1954). Statistical methods for agricultural workers. Statistical methods for agricultural workers.

Patel, Dk., Patel, Br., Patel, Jr. and Kuchhadiya, Gv. (2015). Genetic variability and character association studies for green fruit yield and quality component traits in Chilli (*Capsicum annuum* L.), *Electronic Journal of Plant Breeding*, **6**(2), 472-478.

Saisupriya, P., Saidaiah, P. and Pandravada, Sr. (2022). Analysis of genetic variability, heritability and genetic advance for yield and yield related traits in Chilli. *International Journal of Bio-resource and Stress Management* **13**(4), 387-393.

Shivakumar, M., Biradar, K., Naidu, G., and Prabhu, S. (2025). Genetic variability in local collections of byadgi Chilli (*Capsicum annuum* L.) for qualitative and quantitative traits. *Journal of Farm Sciences*, **38**(1), 10-14.

Sufiyan, A. (2025). Genetic variability analysis of hot pepper (*capsicum annuum*. L) Landraces at Haramaya University, Eastern Ethiopia. *Indian Journal of Advanced Botany*, 5(1), 10-17.

Vyas, D., Kar, S. and Thakur, P. (2021). Genetic variability, heritability and correlation association studies for yield and its components in Chilli (*Capsicum annuum* L.) *the pharma innovation journal*, **10**(8),1681-1683.