Assessment of genetic variability, correlation and path analysis studies in cabbage (*Brassica oleracea*) under low hill conditions of Himachal Pradesh

PALLAVI SHARMA^{1*}, SHIV PRATAP SINGH¹, B S DOGRA¹, RIYA RANI¹ and ANJALI VERMA¹

College of Horticulture and Forestry (Dr Yaswant Singh Parmar University of Horticulture and Forestry), Neri, Hamirpur, Himachal Pradesh 177 001, India

Received: 24 August 2023; Accepted: 20 September 2023

Keywords: Cabbage, Genotypes, Heritability, Path-analysis, Variability

Cabbage (*Brassica oleracea* var. *capitata* L.) is a member of family cruciferae; basically, a cross pollinated and most important cole crop, with chromosome number 2n=2x=18. It is originated in Mediterranean region from a single wild ancestor i.e. *Brassica oleracea* var. *sylvestris*. It is an excellent source of vitamins, minerals and possess several medicinal properties (Munger 1988). It is an economically beneficial crop mainly due to its high nutritive value, high yield and large scale use in the fast food industry (Thakur and Vidyasagar 2016) but gives less production under low hill conditions. Thus, there is an urgent need to initiate breeding

¹College of Horticulture and Forestry (Dr Yaswant Singh Parmar University of Horticulture and Forestry), Neri, Hamirpur, Himachal Pradesh. *Corresponding author email: pallavishrma23@ gmail.com efforts for genetic improvement of cabbage with respect to various horticultural traits including yield under low hill conditions of Himachal Pradesh. Therefore, the present study was carried out to estimate the extent of variability, heritability, genetic advance, character association and path analysis in cabbage.

The experiment was conducted during 2021 at the College of Horticulture and Forestry (Dr Yaswant Singh Parmar University of Horticulture and Forestry), Neri, Hamirpur, Himachal Pradesh. Twelve genotypes (Supplementary Table 1) were sown in randomized complete block design with three replications and transplanted in field with plot size $2.25~\text{m}\times1.80~\text{m}$ and spacing $60~\text{cm}\times45~\text{cm}$ in the month of October (2021). All the cultural practices were followed as recommended in package of practices. The data was taken for 16 traits by randomly selected five plants from each replication (Table 1).

Table 1 Genetic parameters of variation for horticultural traits in cabbage

Character	Mean	Ra	nge	Coefficient of	f variation (%)	Heritability	Genetic advance as
		Minimum	Maximum	Genotypic	Phenotypic	(%)	per cent of mean
Leaf length (cm)	23.30	18.51	37.88	21.57	24.37	78.30	39.31
Leaf breadth (cm)	23.00	18.42	36.52	21.65	24.33	79.23	39.71
Leaf size (cm ²)	566.44	340.36	1430.18	51.22	57.29	79.93	94.32
Number of non-wrapper leaves	13.03	10.53	16.06	10.83	12.74	72.41	19.00
Days to head formation	91.84	69.16	100.66	8.53	8.59	98.50	17.44
Plant height (cm)	19.77	15.63	39.20	31.82	33.40	90.75	62.44
Plant frame (cm ²)	2394.24	1625.28	4219.30	28.05	33.04	72.07	49.05
Stalk length (cm)	3.26	1.25	5.08	21.46	44.06	23.71	21.52
Core length (cm)	5.46	4.05	6.62	15.63	16.67	87.88	30.18
Polar diameter (cm)	15.23	11.42	18.25	12.73	14.15	80.91	23.58
Equatorial diameter (cm)	14.33	11.99	16.55	9.52	11.21	72.15	16.66
TSS (⁰ B)	4.67	3.88	5.64	9.48	11.15	72.30	16.61
Ascorbic acid (mg/100 g)	42.20	28.06	59.69	18.84	18.94	98.97	38.62
Dry matter (%)	8.02	6.33	10.67	17.76	18.61	91.01	34.90
Gross head weight (g)	1453.93	1038.13	2360.87	22.94	30.92	55.06	35.07
Net head weight (g)	919.00	579.73	1295.26	22.09	30.89	51.13	32.54

Table 2 Genotypic and phenotypic correlation coefficient between net head weight and its component characters in cabbage

		×	CX	X3 X4 X5	XA	X	9X	7.X	X8	0X	X10	X11	X12	X13	X14	X15	X16
;	(147			1 1		247	137		3	0147	1117	7137	CIA		2137	2117
X	Ü	1.000															
	Ь	1.000															
X2	Ŋ	**686.0	1.000														
	Ь	0.956**	1.000														
X3	Ŋ	**666.0	0.992**	1.000													
	Ь	**\L86.0	**896.0	1.000													
X4	Ŋ	0.065	0.091	0.048	1.000												
	Ь	-0.010	-0.019	-0.027	1.000												
X5	Ŋ	0.324	0.407*	0.374**	0.544**	1.000											
	Ь	0.276	0.358*	0.323	0.441**	1.000											
9X	Ŋ	0.959**	0.924**	**026.0	0.062	0.436**	1.000										
	Ь	0.872**	0.846**	0.901**	0.037	0.423*	1.000										
X7	Ŋ	0.951**	0.962**	0.963**	0.319	0.538**	0.938**	1.000									
	Ь	0.897	0.923**	**668.0	0.195	0.436**	0.811**	1.000									
8X	Ŋ	0.385*	0.428**	0.486**	0.381*	0.799**	0.797**	0.432**	1.000								
	Ь	0.209	0.256	0.197	0.207	0.391*	0.339*	0.355*	1.000								
6X	Ŋ	0.299	0.408*	0.378*	-0.188	0.411*	0.510**	0.338*	0.123**	1.000							
	Ь	0.288	0.367*	0.340*	-0.176	0.386*	0.467**	0.342*	0.576**	1.000							
X10	Ŋ	0.238	0.294	0.246	-0.381*	-0.157	0.280	0.247	0.524**	0.502**	1.000						
	Ь	0.296	0.338*	0.284	-0.280	-0.130	0.284	0.317	0.303	0.450**	1.000						
X11	Ŋ	0.263	0.383*	0.256	-0.113	-0.108	090.0	0.309	0.007	0.200	0.682**	1.000					
	Ь	0.310	0.390*	0.287	-0.005	-0.085	0.105	0.370*	0.064	0.203	0.683**	1.000					
X12	Ŋ	0.524**	0.566**	0.597**	-0.317	0.228	0.695**	0.546**	0.843**	**606.0	0.633**	0.360*	1.000				
	Ь	0.386*	0.439**	0.450**	-0.248	0.178	0.543**	0.407*	0.425**	0.735**	0.371*	0.164	1.000				
X13	Ŋ	0.700**	0.654**	0.717**	-0.029	0.295	0.662**	0.537**	0.176	0.153	-0.209	-0.092	0.345*	1.000			
	Ь	0.604**	0.564**	0.623**	-0.018	0.297	0.632**	0.436**	0.095	0.144	-0.189	-0.079	0.278	1.000			
X14	Ŋ	0.560**	0.476**	0.552**	0.434**	0.408*	0.568**	0.579**	0.231	-0.012	-0.438**	-0.362*	0.062	0.349*	1.000		
	Ь	0.405*	0.353*	0.405*	0.385*	0.385*	0.483**	0.412*	0.146	-0.047	-0.413*	-0.361*	0.082	0.333*	1.000		
X15	Ŋ	0.951**	0.957**	0.947**	-0.022	0.318	0.847**	**826.0	0.310	0.233	0.309	0.365*	0.577**	0.475**	0.544**	1.000	
	Ь	0.825**	0.804**	0.824**	-0.037	0.240	**869.0	0.802**	0.038	0.229	0.381*	0.504**	0.325	0.338*	0.266	1.000	
X16	Ŋ	0.643**	0.637**	0.636**	-0.510**	-0.043	0.521**	0.586**	-0.004	0.227	0.548**	0.507**	0.567**	0.224	0.034	0.813**	1.000
	Ь	0.595**	0.591**	0.596**	-0.324	-0.022	0.446**	0.553**	-0.052	0.196	0.527**	0.595**	0.330*	0.148	-0.081	0.880**	1.000
. 7																	

*Significant at 5% level; **Significant at 1% level.

X1, Leaf length; X2, Leaf breadth; X3, Leaf size; X4, No. of non-wrapper leaves; X5, Days to head formation; X6, Plant height; X7, Plant frame; X8, Stalk length; X9, Core length; X10, Plant diameter; X11, Equatorial diameter; X12, TSS; X13, Ascorbic acid; X14, Dry matter; X15, Gross head weigh; X16, Genotypic correlation with average net head weight.

The coefficient of variation was calculated by using methodology developed by Burton and De Vane (1953). Heritability and genetic advance under selection were computed as per Allard (1960) and Johnson *et al.* (1955). Correlation coefficient and path-coefficient analysis were calculated according to AI- Jibouri *et al.* (1958) and Dewey and Lu (1959), respectively as:

Phenotypic coefficient of variation (PCV):

PCV (%) =
$$\frac{\sqrt{\text{Phenotypic variance (Vp)}}}{\text{General mean of population (GM)}} \times 100$$

Genotypic coefficient of variation (GCV):

GCV (%) =
$$\frac{\sqrt{\text{Genotypic variance (Vg)}}}{\text{General mean of population (GM)}} \times 100$$

Heritability:

$$H (\%) = \frac{Vg}{Vp} \times 100$$

where H, Heritability (%); V_g , Genotypic variance $[V_g = (M_g - M_e)/r]$; V_p , Phenotypic variance $(V_g + V_e)$

$$GA = H \times \sigma \rho \times K$$

where H, Heritability (%); σ_p , Phenotypic standard deviation; K, Selection differential at 5% selection index (K = 2.06)

The analysis of variance indicated the significant difference among the genotypes for all the characters under study. The genotypes exhibited large amount of variation for all the 16 characters ranging from 3.26 cm (stalk length) to 2394.24 cm² (plant frame). The wide range of variability observed for leaf size, plant frame, gross head weight and net head weight (Table 1). The range of variability for different characters showed the scope for selection of suitable material for breeding in the improvement of cabbage.

Coefficient of variation: High phenotypic and genotypic coefficient of variation were found for leaf size, stalk length, plant height, plant frame, gross head weight, net head weight, leaf length and lead breadth which indicates the maximum variability present among the genotypes for these trait and have better possibility of exploitation for improvement through selection. Similar results had also been reported by Singh *et al.* (2011), Thakur and Vidyasagar (2016), Kaur *et al.* (2018) and Patwal *et al.* (2019).

Heritability and genetic advance: Heritability gives basic information about traits that help in effective selection. It is ranged from 23.71 to 98.97%. The estimates of heritability in broad sense were categorized as low (<80%), moderate (80–90%) and high (>90%). Highest heritability

was recorded for ascorbic acid, days to head formation, dry matter, plant height, core length and polar diameter (Table 2). Whereas, the moderate level of heritability was observed for the traits, viz. core length and polar diameter. However, the low heritability value was found in the characters, viz. leaf size, leaf breadth, leaf length, number of non-wrapper, TSS, equatorial diameter, plant frame, gross head weight, net head weight and stalk length. Similar levels of heritability were recorded by Singh *et al.* (2011), Soni *et al.* (2013) and Patwal *et al.* (2019).

Genetic advance as percentage of mean varied from 16.61 to 62.44%. It was highest for leaf size, plant height, plant frame, leaf breadth, leaf length, ascorbic acid, gross head weight, dry matter, net head weight and core length; thus suggesting that selection is highly effective for these traits. It shows improvement after one selection cycle in breeding material, which is useful in improvement programme. The present finding was supported by Singh *et al.* (2011), Soni *et al.* (2013), Chura *et al.* (2016) and Kaur *et al.* (2018). Thus selection would be highly effective in those genotypes shows high heritability with high genetic advance for traits, as in additive gene action that means more than one gene governs traits. So, these would be highly effective tools for selection of best genotypes.

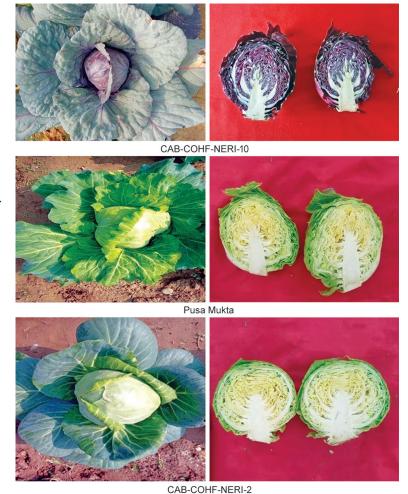


Fig 1 Best genotypes in cabbage variability.

Table 3 Genotypic path coefficient analysis for direct and indirect effects of component characters on net head weight in cabbage

X1, Leaf length; X2, Leaf breadth; X3, Leaf size; X4, No. of non-wrapper leaves; X5, Days to head formation; X6, Plant height; X7, Plant frame; X8, Stalk length; X9, Core length; X10, Polar diameter; X11, Equatorial diameter; X12, TSS; X13, Ascorbic acid; X14, Dry matter; X15, Gross head weight Correlation coefficient were estimated for net head weight which is a very important economic trait and it showed highest positive and significant correlation with gross head weight followed by leaf length, leaf breadth, leaf size, plant height, plant frame, polar diameter, equatorial diameter and TSS (Table 2). It shows their association with traits, as positive or negative relationship with each other, which become beneficial for breeder for effective selection among genotypes. This result is in consonance with findings of Meena *et al.* (2010), Thakur and Vidyasagar (2016), Kaur *et al.* (2018).

Path coefficient analysis (Table 3) based on net head weight as a dependent variable revealed that leaf breadth had the highest positive direct effect on net head weight followed by gross head weight, plant frame, polar diameter, leaf size, TSS, ascorbic acid, dry matter and days to head formation; hence selection through these positive direct effects could be helpful in improving the dependent trait and negative direct effect should not be effective, as in this case we go for indirect selection. Rai et al. (2003), Meena et al. (2010), Thakur and Vidyasagar (2016) and Kaur et al. (2018) also reported the similar results earlier.

CAB-COHF-NERI-10, Pusa Mukta and CAB-COHF-NERI-2 (Fig 1) were observed as best genotypes for net head weight and other important traits like leaf length, leaf breadth, leaf size, plant height, plant frame, gross head weight, ascorbic acid. These genotypes were superior in their performance in genetic parameters, viz. high variability, heritability and improvement over one selection cycle and also shows high positive correlation and path coefficient analysis. These superior genotypes can be recommended for cultivation or for use in further breeding programmes.

SUMMARY

Cabbage is economically important crop among many sectors. Twelve genotypes were evaluated during September to February (2021-22) at the College of Horticulture and Forestry (Dr Yaswant Singh Parmar University of Horticulture and Forestry), Neri, Hamirpur, Himachal Pradesh to study variability in yield and its contributing characters. In variability parameters, high GCV and PCV value indicating the considerable amount of variation was present in germplasm. High heritability with high genetic advance observed for traits, viz. days to head formation, plant height, ascorbic acid and dry matter content showed the influence of additive gene action and are highly able to transfer from one generation to other generation. Thus, selection would be effective for improvement in these genotypes. Correlation coefficient and path coefficient analysis showed that leaf breadth, gross head weight, plant frame, polar diameter, leaf size; these traits can help in evolving genotypes with higher net head weight through selection. Hence, CAB-COHF-NERI-10 and Pusa Mukta were high in yield and can be used for further breeding programme.

REFERENCES

- Al-Jibouri H W, Millar P A and Robinson H F. 1958. Genotypic and environmental variance and covariance in an upland cotton cross of interspecific origin. *Agronomy Journal* **50**: 633–37.
- Allard R W. 1960. *Principles of Plant Breeding*, pp. 485. John Wiley and Sons, New York.
- Burton G W and De Vane R W. 1953. Estimating heritability in tall fescue (*Festucaa rundinaceia*) from replicated clonal material. *Agronomy Journal* **45**: 478–81.
- Chura A, Negi P S and Pandey V. 2016. Assessment for yield and yield attributing traits in cabbage. *International Journal of Agriculture Innovations and Research* 5: 2319–73.
- Johnson H W, Robinson J F and Cornstock R E. 1955. Estimation of genetic and environmental variability in Soya bean. *Agronomy Journal* 7: 314–18.
- Kaur M, Chandha S, Kumar N, Sehgal N and Kanwar S. 2018. Characters association and path analysis among CMS and SI based cabbage hybrids under mid hill conditions of Himachal Pradesh, India. *International Journal of Current Microbiology* and Applied Sciences 7: 424–30.
- Meena M L, Ram R B, Late R and Sharma S R. 2010. Determining yield components in cabbage (*Brassica oleracea* var. *capitata* L.) through correlation and path analysis. *International Journal*

- of Science and Nature 1: 27-30.
- Munger H M. 1988. Adopation and breeding of vegetable crops for improved human nutrition. *Horticulture and Human Health*, pp. 177. Quebedeaux B and Pedrick A B (Eds).
- Patwal A, Singh A K, Pant S C and Verma S K. 2019. Assessment of genetic components in horticultural traits of cabbage (*Brassica oleracea* var. *capitata* L.) germplasm in mid hills of Uttarakhand. *International Journal of Chemical Studies* 7: 2077–82.
- Rai N, Kumar A and Yadav R K. 2003. Correlation and path coefficient analysis for the yield and its traits in cabbage. *Indian Journal of Hill Farming* **16**: 61–65.
- Singh B K, Sharma S R, Kalia P and Singh B. 2011. Genetic variability for antioxidants and horticultural traits in cabbage. *Indian Journal of Horticulture* **68**: 51–55.
- Soni S, Kumar S, Maji S and Kumar A. 2013. Heritability and genetic advance in cabbage (*Brassica oleracea* var. *capitata* L.) under Lucknow condition. *Hort Flora Research Spectrum* 2: 274–76.
- Thakur H and Vidyasagar. 2016. Character association and path analysis of yield and other horticultural traits in cabbage (*Brassica oleracea* var. *capitata* L.). *An International Quarterly Journal of Life Science* 11: 3129–32.