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Inter-trait association and genetic variability assessment in cabbage under Lucknow conditions

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ABSTRACT

The studies on inter-trait association and genetic variability assessment were carried out in 30 diverse cabbage genotypes for 11 quantitative characters. The study showed high range for marketable yield, days to maturity and leaf length. The highest estimates of PCV and GCV were for stalk length followed by core length and yield and low for leaf width followed by polar length and days to maturity. A high estimate of heritability was noticed for yield followed by leaf length and equatorial length. High heritability in broad sense indicated that large proportion of phenotypic variance was attributable to the genotypic variance and were less influenced by environment. High genetic gain (%) was observed for yield, whereas it was low for days to maturity and polar length. Positive and significant association of yield was observed with all the characters except days to maturity and stalk length at both genotypic and phenotypic level indicating that selection based on these characters either in combination or alone will result in identifying the genotypes having high yield potential. The gross weight, leaf length, stalks length and head weight had maximum direct effect on yield followed by number of non-wrapper leaves and equatorial length.

Key words: Cabbage, variability, correlation, path analysis.

INTRODUCTION

Cabbage (*Brassica oleracea* var. *capitata* L.; $2n = 2x = 18$) is one of the most important cole crops grown under temperate to tropical climatic conditions in more than 90 countries of the world (Singh *et al.*, 13) where the leading countries are China, India, Russia, Korea, Japan and the USA. In India, it is next only to cauliflower with regard to acreage and production. It is a rich source of protein comprising all essential amino acids, especially sulphur containing amino acids, minerals such as calcium, iron, magnesium, sodium, potassium, phosphorus and antioxidants and is reported to have anti-carcinogenic properties (Singh *et al.*, 12). Improvement in any crop depends on the magnitude of genetic variability and the extent of transmission of characters from one generation to the next. The yield and its component characters are polygenic in nature, hence considerably influenced by the environmental factors. The knowledge of inter-relationships among the various components and their direct and indirect effects on yield are the important pre-requisites to bring genetic improvement in cabbage. Thus, the present study was conducted to examine the magnitude and the direction of variability, heritability, genetic advance, and inter-relationship of yield components in 30 diverse cabbage genotypes.

MATERIALS AND METHODS

The experimental materials comprised of 30 cabbage genotypes of tropical and subtropical origin belongings to white, red and savoy types. Each genotype was planted in a plot (3.0 m × 2.7 m) area in randomized block design with three replications. There were 25 plants in each plot planted at row and plant spacing of 60 cm × 45 cm. All the standard package of practices and plant protection measures were timely adopted to raise the crop successfully. Five randomly selected plants from each replication were utilized for recording observations, *viz*., days to maturity, number of non-wrapper leaves, core length, stalk length, equatorial length, leaf length, leaf width, polar length, gross weight, head weight and yield at the Horticultural Research Farm of the Department of Applied Plant Science (Horticulture), BBAU, Lucknow during the winter season for three years. The mean values obtained from two years data were used for estimating the analysis of variance (Panse and Sukhatme, 9). The genotypic and the phenotypic coefficients of variation were calculated by the formula given by Burton (4). Heritability in broad sense and genetic advance as percent of mean were computed by following the methods of Allard (2) and Johnson *et al.* (7), respectively. Correlation and path coefficient analysis were calculated as per formulae suggested by Al-jibouri *et al.* (1), Miller *et al.* (8) and Dewey and Lu (6), respectively.

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RESULTS AND DISCUSSION

The estimates of genetic parameters of variability, *viz.,* phenotypic and genotypic coefficients of variation (PCV and GCV) along with heritability in broad sense (h^2) and genetic advance (GA) as percentage of mean for different traits are given in Table 1. The data revealed that there were significant differences among genotypes for various component traits. High ranges for yield (11.10-56.60), leaf width (19.95-46.02) and days to maturity (71.20-110.53) were observed. The higher phenotypic coefficient variation than those of genotypic coefficient of variation indicated the predominant role of environment in the expression of traits, which is in confirmation with the results obtained by Singh *et al.* (13). The estimate of PCV and GCV were high for stalk length (PCV = 40.42, GCV = 39.21), followed by yield (PCV = 37.07, GCV = 36.87) and core length (PCV = 37.43, GCV = 36.02), whereas leaf width (PCV = 21.51, GCV = 21.12), followed by polar length (PCV = 16.85, GCV = 16.47) and days to maturity (PCV = 12.91, GCV = 11.50) indicating maximum variability in these traits and have ample scope for effective improvement through selection. These results were in broad conformity to those of Yadav (15) in cabbage. Narrow differences between PCV and GCV gave evidence to the genotypes that the variability existing in them was mainly due to their genetic makeup.

Heritability is used in predicting the expected progress to be achieved through selection (Burton and De Vane, 5; Johnson *et al.*, 7). In the present study, the highest heritability was noticed for yield (98.90%) followed by leaf length (97.30%), equatorial length (97.10%) and leaf width (96.40%). All these traits exhibited more than 90% heritability (Table 1). Number of non-wrapper leaves and head weight showed moderate heritability estimates. Gross weight (78.60) and days to maturity (79.40) showed the low heritability estimates. High heritability in broad sense indicated that the phenotypic variance noted were due to the genotypic variance but have high heritable due to less influence of the environment. High heritability for yield and leaf length has been estimated earlier by Yadav (15) in cabbage. Johnson *et al*. (7) stressed that for estimating the real effects of selection, heritability alone is not sufficient and genetic advance along with heritability is more useful. High genetic advance was observed for yield (18.72), whereas it was low for core length (15.62), stalk length (3.75), polar length (6.50), gross weight (0.96) and head weight (0.72), which are in broad conformity with the finding Rai and Asati (11).

Moderate to high genetic advance for days to maturity (Rai and Asati, 11; Atter *et al.*, 3), leaf width, leaf length, equatorial length, number of non-wrapper leaves and polar length reported by Singh *et al.* (12), which was slightly variance with the present findings. High heritability along with moderate genetic advance was observed for leaf length (11.64), leaf width (11.40) and equatorial length (9.71), these findings were at variance with those of (Rai and Asati, 11) who reported high heritability associated with low genetic advance. High heritability along with moderate genetic advance for these traits may be attributed to the additive gene action linked with non-additive effects and these may be improved through selection followed by hybridization.

However, high heritability associated with high genetic advance was observed for yield, which was

Table 1. Estimates of genetic constants for different morphological and yield traits in some cabbage genotypes.

Trait	Range		Mean	Coefficient of variation		Heritability (%)	Genetic advance	Genetic gain (%)
	Min.	Max.		Phenotypic	Genotypic			
Days to maturity	71.28	110.53	86.96	12.91	11.50	79.40	18.36	21.10
No. of non-wrapper leaves	5.40	23.70	15.16	25.00	24.25	88.90	7.14	47.09
Core length (cm)	2.31	13.85	7.95	37.43	36.02	92.60	5.62	70.69
Stalk length(cm)	2.36	9.46	4.78	40.42	39.21	94.10	3.75	78.45
Leaf width (cm)	14.35	42.75	26.68	21.51	21.12	96.40	11.40	42.73
Leaf length (cm)	15.95	46.02	25.49	22.78	22.47	97.30	11.64	45.66
Equatorial length (cm)	12.10	31.10	20.05	24.19	23.84	97.10	9.71	48.42
Polar length (cm)	12.43	27.40	19.60	16.85	16.47	95.50	6.50	33.16
Gross weight (kg)	1.20	3.55	2.10	28.28	25.03	78.60	0.96	45.71
Head weight (kg)	0.49	2.33	1.24	32.23	30.13	87.40	0.72	58.06
Yield (t/ha)	11.10	56.60	24.78	37.07	36.87	98.90	18.72	75.54

in conformity with the findings of Yadav (15). High heritability coupled with high genetic advances in yield indicates that this trait is likely to respond better to selection. Stalk length along with core length had moderate heritability associated with low genetic advance and these findings were variance with those of Singh *et al.* (14), who reported high heritability associated with moderate genetic advance. Moderate heritability with low genetic advance was observed for head weight (0.72), which is in contrast to the findings of Singh *et al.* (13), who reported low heritability coupled with low genetic advance for this trait. Low heritability in combination with low genetic advance was observed for gross weight (0.96), which differed with the findings of Singh *et al.* (14), who reported high heritability with high genetic advance for this trait. Characters with low heritability coupled with low genetic advance are more under the influence of non-additive gene action and environment and do not respond to selection. High genetic gain (expressed as per cent of mean) was recorded (78.45) followed by yield (75.54), core stalk length (70.69) and head weight (58.06). While, the moderate genetic advance of (48.42), number of non-wrapped leaves (47.09), gross weight (45.71), leaf length (45.66) and leaf width (42.73). These results are in accordance with the findings of Prasad *et al*. (10).

The genotypic correlation coefficients were higher phenotypic correlation coefficients for all the pairs of traits (Table 2). This might be due to the masking effect of environment in the total expression of the genotype resulting in the reduced phenotypic association. The yield displayed positive and significant correlation with all the characters except days to maturity and stalk length. It may be assumed that the selection based on these characters either in combination or alone resulted in identifying the hybrid having high yield potential. The present findings are in accordance with that of Prasad *et al.* (10), and Rai and Asati (11) in cabbage. The yield components mostly exhibited positive and significant inter-relationship among themselves, which indicated the need of their

Table 2. Estimates of genotypic and phenotypic correlation coefficients for morphological traits in cabbage genotypes.

Trait		Days to maturity	Non wrapper leaves	Core length (cm)	Stalk length (cm)	Leaf width (cm)	Leaf length (cm)	Equatorial length (cm)	Polar length (cm)	Gross weight (kg)	Head weight (kg)	Yield (t/ ha)
Days to maturity	P	1.000	-0.015	-0.008	-0.080	-0.040	-0.014	-0.152	0.296*	0.193	-0.035	-0.057
	G	1.000	-0.035	-0.005	-0.073	-0.055	-0.028	-0.173	0.334*	0.261	-0.031	-0.060
Non wrapper leaves	P		1.000	0.198	-0.149	0.159	0.258*	-0.038	0.161	0.008	0.024	0.152
	G		1.000	0.211	-0.166	0.165	0.247	-0.039	0.174	-0.010	0.037	0.163
Core length	P			1.000	-0.165	0.241	0.288*	0.341*	0.237	0.469**	0.557**	0.463**
	G			1.000	-0.174	0.254*	0.300*	0.364**	0.253*	0.531**	0.601**	0.483**
Stalk length	P				1.000	-0.163	-0.085	-0.122	-0.062	-0.197	-0.161	-0.007
	G				1.000	-0.178	-0.096	-0.135	-0.061	-0.205	-0.175	-0.007
Leaf width	P					1.000	0.689**	0.337*	0.215	0.368**	0.375**	0.373**
	G					1.000	0.709**	0.346*	0.222	0.443**	0.405**	0.383**
Leaf length	P						1.000	0.338*	0.299*	0.410**	0.401**	0.520**
	G						1.000	0.345*	0.309*	0.468**	0.438**	0.531**
Equatorial length	P							1.000	0.216	0.473**	0.438**	0.480**
	G							1.000	0.224	0.535**	0.481**	0.490**
Polar length	P								1.000	0.356**	0.154	0.222
	G								1.000	0.414**	0.180	0.230
Gross weight	P									1.000	0.689**	0.613**
	G									1.000	0.825**	0.693**
Head weight	P										1.000	0.643**
	G										1.000	0.691**
Yield	P											1.000
	G											1.000

*, ** Significant at 5 and 1% levels, P = Phenotypic correlation, G = Genotypic correlation.

simultaneous selection for improvement on yield. Similar *inter se* associations of yield contributing traits in cabbage were also reported earlier by Prasad *et al.* (10).

Correlation coefficients indicate only the general association between any two traits without tracing any possible cause of such association. However, the path coefficient analysis at genotypic level is done to partition the correlation co-efficient into direct and indirect effects of different characters on yield (Table 3). The path coefficient analysis revealed that the traits like gross weight (0.519), leaf length (0.251), stalk length (0.160) and head weight (0.160) had the highest positive direct effect on yield followed by number of non-wrapper leaves (0.141) and equatorial length (0.092), which is in agreement with the results of Rai and Asati (11) in cabbage. The days to maturity (-0.135), leaf width (-0.121) and polar length (-0.067) had the direct negative effect but correlation with yield is positive except days to maturity owing to indirect through all the characters. A similar result has also been reported by Rai and Asati (11). Hence, gross plant weight proved to be the most effective selection index while carrying out genetic improvement in cabbage. In yield attributing traits, the residual effect at genotypic level was less compared to the residual effect at phenotypic level. All these characters should be considered simultaneously for effective selection of cabbage genotypes.

From the above findings it may be concluded that besides direct selection for gross weight, stalk length, leaf length and head weight indirect selection for days to maturity to yield improvement can be made possible in cabbage through breeding programme.

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Table 3. Estimate of direct (diagonal) and indirect (off diagonal) effects of various traits towards yield at genotypic level in cabbage genotypes.

Trait	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	Correlation with yield
X_1	**-0.135**	-0.005	0.000	-0.012	0.007	-0.007	-0.016	-0.022	0.136	-0.005	-0.060
X_2	0.005	**0.141**	0.010	-0.027	-0.020	0.069	-0.004	-0.012	-0.005	-0.006	0.163
X_3	0.001	0.030	**0.047**	-0.028	-0.031	0.076	0.034	-0.017	0.276	0.096	0.483^{**}
X_4	0.010	-0.023	-0.008	**0.160**	0.022	-0.024	-0.013	0.004	-0.107	-0.028	-0.007
X_5	0.007	0.023	0.012	-0.028	**-0.121**	0.178	0.032	-0.015	0.230	0.065	0.383^{*}
X_6	0.004	0.038	0.014	-0.015	-0.086	**0.251**	0.032	-0.021	0.243	0.070	0.531^{**}
X_7	0.023	-0.006	0.017	-0.022	-0.042	0.087	**0.092**	-0.015	0.278	0.077	0.490^{**}
X_8	-0.045	0.025	0.012	-0.010	-0.027	0.078	0.021	**-0.067**	0.215	0.029	0.230
X_9	-0.035	-0.001	0.00.0	-0.033	-0.054	0.118	0.049	-0.028	**0.519**	**0.132**	0.693^{**}
X_{10}	0.004	0.005	2825	-0.028	-0.049	0.110	0.044	-0.012	0.428	0.160	0.691^{**}

*, ** Significant at 5 and 1% levels, Residual effect = 0.360, Direct effect = Bold diagonals

X_1 = days to maturity; X_2 = non-wrapper leaves; X_3 = core length (cm); X_4 = stalk length (cm); X_5 = leaf length (cm); X_6 = leaf width (cm); X_7 = equatorial length (cm); X_8 = polar length (cm); X_9 = gross weight (kg), X_{10} = head weight (kg)

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