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DECODING GENETIC VARIABILITY, TRAIT ASSOCIATIONS AND MULTIVARIATE DIVERGENCE TO IDENTIFY ELITE PARENTS IN CABBAGE (*BRASSICA OLERACEA* VAR. *CAPITATA* L.)

Abinash Mishra[1], Anita Mohanty[2], Pradyumna Tripathy[3], Dibya Sundar Kar[4], Ankita Mishra[5], Disha Baishnabi[6], Akash Kumar Parida[7], Aurobinda Behera[8*], Jyoti Ranjan Das[9], Rohitash Kumar[10], Dibyajita Swain[11]

[1]Department of Vegetable Science, College of Agriculture, Odisha University of Agriculture and Technology, Bhubaneswar, Odisha, India
[2]All India Coordinated Research Project on Vegetable Crops, Odisha University of Agriculture and Technology, Bhubaneswar, Odisha, India
[3]Department of Vegetable Science, College of Agriculture, Odisha University of Agriculture and Technology, Bhubaneswar, Odisha, India
[4]Krishi Vigyan Kendra, Dhenkanal, Odisha, India
[5]Department of Plant Breeding and Genetics, College of Agriculture, Odisha University of Agriculture and Technology, Bhubaneswar, Odisha, India
[6]Department of Vegetable Science, College of Agriculture, Odisha University of Agriculture and Technology, Bhubaneswar, Odisha, India
[7]Department of Vegetable Science, College of Agriculture, Odisha University of Agriculture and Technology, Bhubaneswar, Odisha, India
[8]Department of Vegetable Science, College of Agriculture, Odisha University of Agriculture and Technology, Bhubaneswar, Odisha, India
[9]Department of Vegetable Science, College of Agriculture, Odisha University of Agriculture and Technology, Bhubaneswar, Odisha, India
[10]Department of Vegetable Science, College of Agriculture, Odisha University of Agriculture and Technology, Bhubaneswar, Odisha, India
[11]Department of Vegetable Science, College of Agriculture, Odisha University of Agriculture and Technology, Bhubaneswar, Odisha, India
[*]**Corresponding author:** Aurobinda Behera; E-mail: aurobindabehera.rs24@ouat.ac.in

ABSTRACT

Choosing parents that are both high yielding and genetically distant is the starting point of any cabbage hybrid programme. Eighteen cabbage genotypes (thirteen advanced AICRP lines and five cultivars) were evaluated for fifteen quantitative traits in a randomized block design with three replications during the *rabi* season of 2022–23 at Bhubaneswar, India. The genotypes differed significantly ($P \leq 0.01$) for fourteen traits; plant height was the exception. The top yielders were 2022/CABHYB-1 (295.33 q/ha), Pragati (284.58 q/ha) and 2021/CABHYB-5 (278.88 q/ha), which were statistically on par, followed by 2021/CABHYB-1 (252.78 q/ha). Net head weight showed the highest genotypic and phenotypic coefficients of variation (30.48 and 31.55%). Net, marketable and gross head weight and yield had high heritability (91.0–93.3%) together with high genetic advance as per cent of mean (47.1–60.6%), which points to mainly additive gene action. Yield was positively and significantly correlated with frame spread east–west (r = 0.64), gross head weight (0.63), marketable head weight (0.58), equatorial diameter (0.54), polar diameter (0.52), net head weight (0.49) and frame spread north–south (0.48) and negatively with stalk length (–0.49). In the path analysis, frame spread east–west (0.522), polar diameter (0.298) and marketable head weight (0.222) had the largest positive direct effects on yield (residual effect 0.548). Mahalanobis D^2 analysis placed the genotypes in six clusters and clusters I and VI were the farthest apart ($D^2 = 1377.16$). Five principal components with eigenvalues above one explained 88.72% of the variation. The first component (39.73%) was a head weight–yield axis on which 2022/CABHYB-1 and Pragati scored highest. Ward clustering agreed moderately with the Tocher grouping (adjusted Rand index = 0.38). Frame spread and head weight can therefore be used as selection criteria and 2022/CABHYB-1, Pragati, 2021/CABHYB-5 and 2021/CABHYB-1 are suitable parents for crossing with genotypes of the divergent clusters I and III.

KEYWORDS: *Brassica oleracea* var. *capitata*; Heritability; Path coefficient; Mahalanobis D^2; Principal component analysis; Parental selection

INTRODUCTION

Cabbage (*Brassica oleracea* L. var. *capitata* L., 2n = 2x = 18) is one of the main cole crops of the family Brassicaceae and is grown as a garden, market and field crop in more than ninety countries (Chiang *et al*., 1993). The crop is believed to have been domesticated in the eastern Mediterranean and Asia Minor from wild cabbage, *B. oleracea* var. *sylvestris*, also called colewort (Chiang *et al*., 1993). India ranks second in the world in cabbage production, next to China (FAO, 2026). Within the country, cabbage was grown on about 0.40 million ha in 2017–18 and produced about 9.04 million tonnes (MoA&FW, 2018) and production has kept rising since then through expansion of area (Kar *et al*., 2026). West Bengal and Odisha are the leading cabbage states and together supply about one-third (34.45%) of the national output (Kar *et al*., 2026). For Odisha, this makes it worthwhile to identify high-yielding parents that suit its warm and humid growing conditions.

Cabbage heads supply vitamins C and K, dietary fibre and minerals, along with health-promoting phytochemicals such as glucosinolates and phenolic compounds (Chura *et al*., 2021; Zahid *et al*., 2024). Improving head yield and quality is therefore a priority for cabbage breeders in India, who now depend more and more on F_1 hybrids developed from well-characterized parental lines.

How far a crop can be improved depends on how much variability the breeding material holds and on the nature of that variability. Estimates of the genotypic and phenotypic coefficients of variation, heritability and genetic advance separate the heritable part of the variation from the environmental part and show which traits are likely to respond to selection. A

trait with high heritability and high genetic advance is usually under additive gene action and can be improved by direct phenotypic selection (Johnson *et al*., 1955; Singh and Chaudhary, 1985). Yield, however, is a complex polygenic trait. Correlation and path coefficient analyses are therefore used to separate the direct effects of its component traits from the indirect ones and to find dependable indirect selection criteria (Dewey and Lu, 1959).

A breeder planning crosses also needs to know how divergent the available parents are, because crosses between distant parents are more likely to give heterotic hybrids and useful segregants. Mahalanobis' D^2 statistic with Tocher clustering has been the standard tool for this purpose for many years (Mahalanobis, 1936; Rao, 1952). Principal component analysis and hierarchical clustering look at the same multivariate data from a different angle and show which traits are responsible for the grouping (Jolliffe and Cadima, 2016). Only a few studies have used these approaches together on cabbage germplasm suited to the warm-humid conditions of eastern India. The present study was therefore taken up to (i) estimate genetic variability, heritability and genetic advance for fifteen yield-related traits in eighteen cabbage genotypes, (ii) work out the direct and indirect contributions of these traits to yield through correlation and path analysis and (iii) assess genetic divergence using Mahalanobis' D^2, principal component analysis and Ward clustering, so that divergent and high-yielding parents could be identified for cabbage hybridization.

MATERIAL AND METHODS

Experimental site and plant material

The experiment was carried out in the *rabi* season of 2022–23 at the experimental farm of the All India Coordinated Research Project (AICRP) on Vegetable Crops, Odisha University of Agriculture and Technology (OUAT), Bhubaneswar, Odisha, India (20°15′ N, 85°52′ E; 25.5 m above mean sea level). The soil of the site is sandy loam. The material consisted of eighteen genotypes, of which thirteen were advanced AICRP breeding lines and five were cultivars (Table 1).

Table 1. Cabbage genotypes used in the study.

Sl. No.	Code	Genotype
1	V1	2021/CABHYB-1
2	V2	2021/CABHYB-2
3	V3	2021/CABHYB-3
4	V4	2021/CABHYB-4
5	V5	2021/CABHYB-5
6	V6	2021/CABHYB-6
7	V7	2021/CABHYB-7
8	V8	Green Valley
9	V9	Pulkit
10	V10	2022/CABHYB-1
11	V11	2022/CABHYB-2
12	V12	2022/CABHYB-3
13	V13	2022/CABHYB-4
14	V14	2022/CABHYB-5
15	V15	2022/CABHYB-6
16	V16	Pragati
17	V17	Additi
18	V18	Deepak

Experimental design and observations

The genotypes were grown in a randomized block design (RBD) with three replications. Seedlings were transplanted on 19 November 2022 in plots of 3.0 × 3.0 m at a spacing of 60 × 60 cm and the recommended package of practices was followed uniformly in all plots. In each replication, five plants per genotype were selected at random and observations were recorded on fifteen traits: plant height at harvest (cm); frame spread east–west (E–W) and north–south (N–S) (cm); days to 50% head emergence; polar and equatorial head diameter (cm); stalk length (cm); gross, marketable and net head weight (g); core length (cm); harvest index (%); head shape index (ratio of polar to equatorial diameter); head compactness; and total yield (q/ha). Head compactness was worked out as per Pearson (1931) using $C = N/W^3 \times 100$, where N is the net head weight (g) and W is the mean head diameter (cm), i.e. the average of the polar and equatorial diameters. Harvest index is the ratio of net head weight to gross plant weight, expressed in per cent. Yield per plot was recorded at harvest and converted to quintals per hectare.

Statistical analysis

Plot means were subjected to analysis of variance for RBD (Panse and Sukhatme, 1961). The standard error of the mean (SEm), critical difference (CD) at P = 0.05 and coefficient of variation were calculated for every trait. Genotypic variance was estimated as $\sigma^2_g = (MS_g - MS_e)/r$ and phenotypic variance as $\sigma^2_p = \sigma^2_g + \sigma^2_e$, where MS_g and MS_e are the genotype and error mean squares, $\sigma^2_e = MS_e$ and r is the number of replications. The genotypic and phenotypic coefficients of variation (GCV and PCV) were computed by the method of Burton and DeVane (1953) and grouped as low (<10%), moderate (10–20%) or high (>20%) (Sivasubramanian and Madhavamenon, 1973). Broad-sense heritability ($h^2 = \sigma^2_g/\sigma^2_p$

× 100; Lush, 1949) was grouped as low (<30%), moderate (30–60%) or high (>60%) (Robinson *et al*., 1949). Genetic advance was calculated as $GA = k \cdot h^2 \cdot \sigma_p$, taking k = 2.06 for 5% selection intensity. It was also expressed as a percentage of the mean (GAM) and grouped as low (<10%), moderate (10–20%) or high (>20%) (Johnson *et al*., 1955).

Genotypic and phenotypic correlation coefficients were estimated from the variance and covariance components (Al-Jibouri *et al*., 1958; Weber and Moorthy, 1952). The phenotypic correlations were tested against the t-distribution with n – 2 = 16 degrees of freedom, for which the critical |r| is 0.468 at P = 0.05 and 0.590 at P = 0.01. Path coefficient analysis was done on the phenotypic correlation matrix, keeping yield as the dependent variable (Wright, 1921; Dewey and Lu, 1959). Direct effects were obtained by solving the normal equations. Each indirect effect was calculated as the product of the correlation between two traits and the direct effect of the intermediate trait and the residual effect as $\sqrt{(1 - \Sigma\, p_{iy} r_{iy})}$.

Genetic divergence was measured by Mahalanobis' D^2 statistic (Mahalanobis, 1936) with the pooled error variance–covariance matrix and the genotypes were grouped by Tocher's method (Rao, 1952). Average intra- and inter-cluster D^2 values and cluster means were then worked out as described by Singh and Chaudhary (1985).

Two further multivariate analyses were run to supplement the D^2 analysis. Principal component analysis (PCA) was carried out on the correlation matrix of the genotype means, that is, on standardized data (Jolliffe and Cadima, 2016). Components with eigenvalues above 1 were retained (Kaiser, 1960) and the loadings are reported as correlations between traits and components. The standardized data were also subjected to agglomerative hierarchical clustering by Ward's minimum-variance method with Euclidean distance (Ward, 1963). Agreement between the six-group Ward partition and the Tocher clusters was measured with the adjusted Rand index (Hubert and Arabie, 1985). Boxplots were drawn to show how the genotype means were distributed and values lying beyond 1.5 times the interquartile range were treated as outliers. The multivariate analyses and graphs were prepared in Python 3 using the scikit-learn (Pedregosa *et al*., 2011), SciPy (Virtanen *et al*., 2020) and matplotlib (Hunter, 2007) libraries.

RESULTS

Analysis of variance

Mean squares due to genotypes were highly significant ($P \leq 0.01$) for fourteen of the fifteen traits (Table 2), which shows that the genotypes differed genetically for most traits. Plant height was the only trait in which the genotypes did not differ significantly (F = 1.28). F values were largest for net head weight (42.76), marketable head weight (38.76), gross head weight (34.07), head compactness (32.31) and yield (31.45). The replication effect was significant only for days to 50% head emergence.

Table 2. Analysis of variance (mean squares) for fifteen quantitative characters in eighteen cabbage genotypes.

Character	Replication (df = 2)	Genotype (df = 17)	Error (df = 34)	F (genotype)
Plant height (cm)	12.18	8.83	6.92	1.28 NS
Frame spread E–W (cm)	24.83	41.85**	8.94	4.68**
Frame spread N–S (cm)	23.82	32.43**	9.04	3.59**
Days to 50% head emergence	42.06**	66.03**	3.88	17.02**
Polar diameter (cm)	2.24	5.13**	0.81	6.33**
Equatorial diameter (cm)	0.52	6.81**	0.69	9.87**
Stalk length (cm)	0.07	3.63**	0.17	21.37**
Gross head weight (g)	24660.40	391136.91**	11481.78	34.07**
Marketable head weight (g)	1842.31	296959.00**	7661.04	38.76**
Net head weight (g)	8684.63	272878.75**	6381.05	42.76**
Core length (cm)	0.03	1.10**	0.06	18.28**
Harvest index (%)	12.43	197.17**	15.40	12.80**
Head shape index	0.0100	0.0194**	0.0037	5.24**
Head compactness	0.33	88.87**	2.75	32.31**
Total yield (q/ha)	119.23	8576.05**	272.67	31.45**

*, ** Significant at $P \leq 0.05$ and $P \leq 0.01$, respectively; NS = not significant ($F_{0.05}(17, 34) = 1.93$; $F_{0.01}(17, 34) = 2.54$). Genotype mean squares equal r × variance of the genotype means in Table 3. Mean squares for head shape index are given to four decimal places.

Mean performance and range of variation

Most traits varied over a wide range (Table 3; Figure 1). Yield varied from 135.42 q/ha in 2021/CABHYB-7 to 295.33 q/ha in 2022/CABHYB-1 and the grand mean was 200.95 q/ha. 2022/CABHYB-1, Pragati (284.58 q/ha) and 2021/CABHYB-5 (278.88 q/ha) were statistically on par (CD = 27.40 q/ha). The first two yielded significantly more than all the remaining genotypes, while 2021/CABHYB-5 was on par with 2021/CABHYB-1 (252.78 q/ha), which was in turn on par with 2022/CABHYB-5 (247.74 q/ha). 2022/CABHYB-1 also recorded the highest gross (2434.79 g), marketable (1854.87 g) and net head weight (1720.49 g) and the largest equatorial diameter (17.43 cm). Pragati had the widest frame spread (64.43 cm E–W and 60.47 cm N–S). Days to 50% head emergence ranged from 31.33 in 2022/CABHYB-5 to 45.00 in 2021/CABHYB-2. The most compact heads were found in Deepak (42.97) and 2022/CABHYB-5 (42.96), both

significantly more compact than all other genotypes and the least compact in 2021/CABHYB-1 (20.66). Stalks were shortest in 2021/CABHYB-5 (6.01 cm) and 2022/CABHYB-1 (6.10 cm).

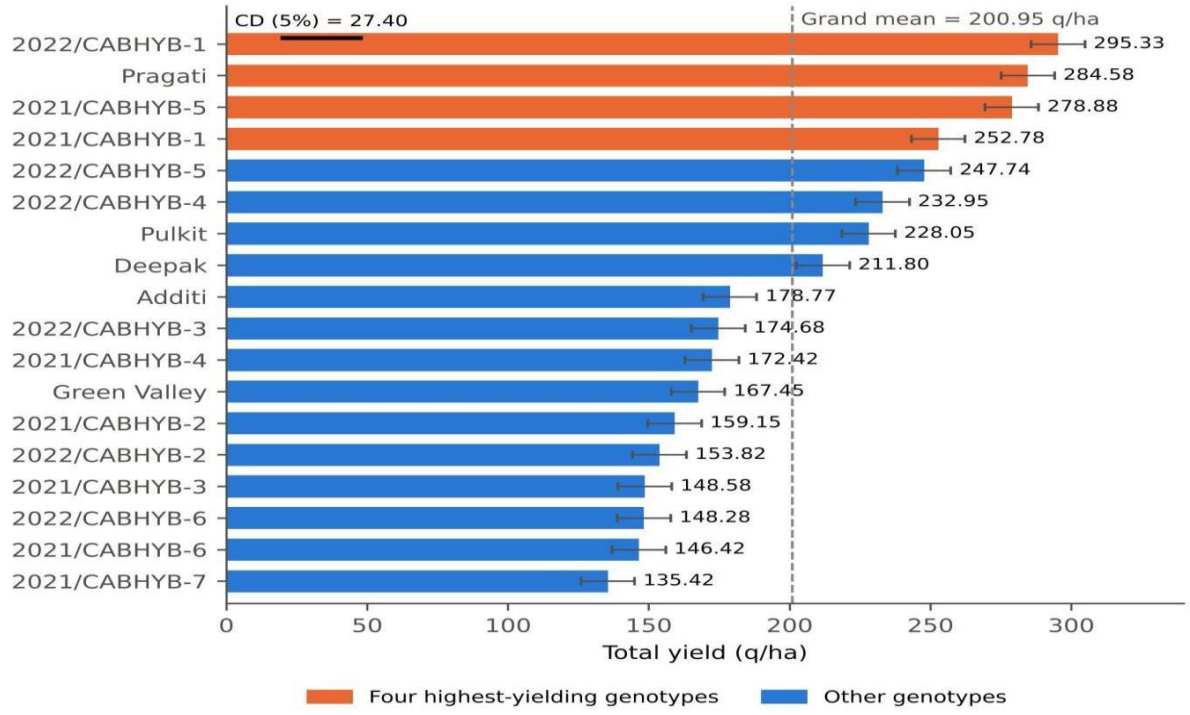


Figure 1. Total yield (q/ha) of eighteen cabbage genotypes. Bars show genotype means ± SEm; the dashed line is the grand mean and the black bar the critical difference at P = 0.05. Orange bars mark the four highest-yielding genotypes.

The boxplots (Figure 2) show that the head weight traits were the most skewed. 2022/CABHYB-1 was a high outlier for gross, marketable and net head weight, Pragati for gross head weight and frame spread N–S and 2021/CABHYB-1 for polar diameter. On the lower side, 2021/CABHYB-4 was an outlier for gross, marketable and net head weight and 2021/CABHYB-2 for net head weight. Yield had no outliers, but its distribution was skewed to the right, with the median (176.73 q/ha) lying below the mean.

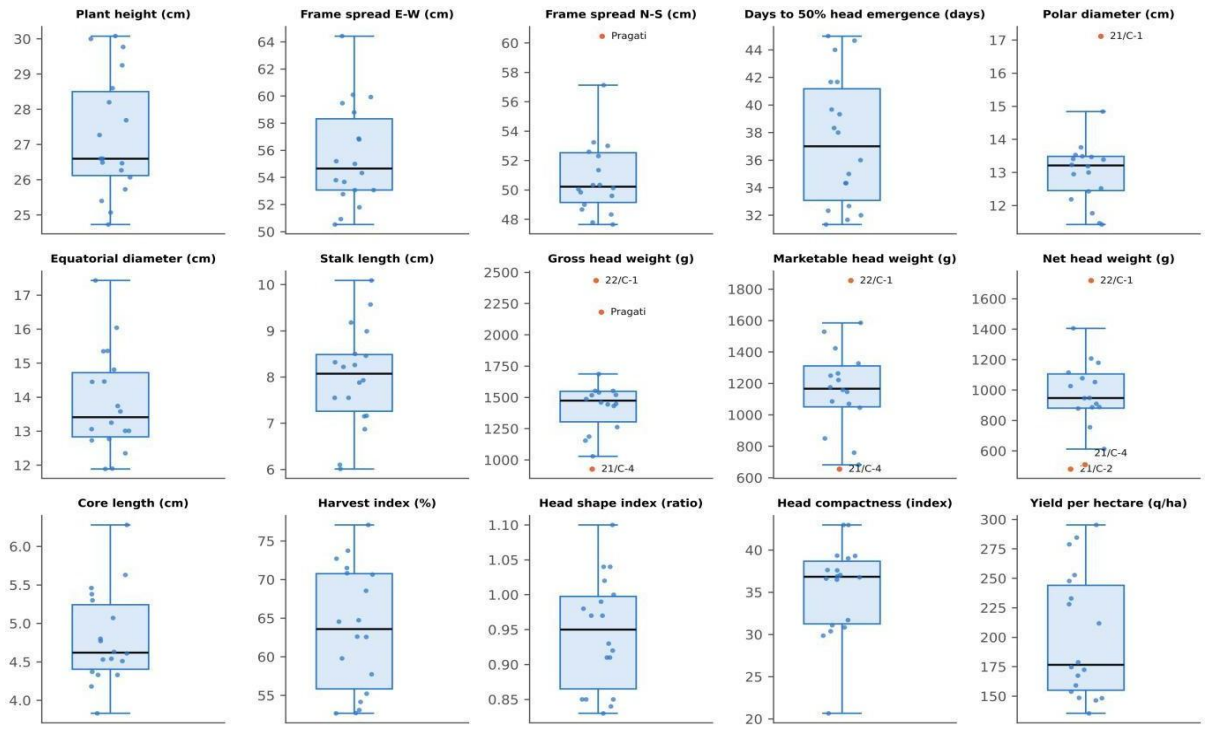


Figure 2. Distribution of genotype means for fifteen quantitative traits in cabbage. Boxes show the median and interquartile range, whiskers extend to 1.5 × interquartile range and orange points are outlying genotypes (21/C-1, 21/C-2, 21/C-4 = 2021/CABHYB-1, -2, -4; 22/C-1 = 2022/CABHYB-1).

Table 3. Mean performance of eighteen cabbage genotypes for fifteen quantitative characters.

Code	PH	FS-EW	FS-NS	D50 %	PD	ED	SL	GW	MW	NHW	CL	HI	HSI	HC	YPH
V1	30.08	56.80	50.33	44.00	17.12	14.45	7.55	1487.19	1221.90	888.37	4.61	57.73	1.10	20.66	252.78
V2	27.69	53.07	50.05	45.00	11.77	12.35	8.50	1029.36	682.96	481.43	4.51	52.71	0.91	29.86	159.15
V3	26.27	52.77	48.33	44.67	12.19	12.77	6.87	1154.54	850.23	755.88	5.63	55.22	0.98	31.70	148.58
V4	27.27	50.93	49.00	41.67	11.47	11.90	9.57	928.15	656.15	509.28	4.54	54.15	0.93	30.38	172.42
V5	26.49	56.87	52.60	32.00	13.39	15.35	6.01	1520.61	1158.80	948.41	6.28	64.73	0.85	30.84	278.88
V6	25.73	55.20	50.13	34.33	11.43	13.58	10.09	1459.81	1045.80	886.58	5.30	59.79	0.85	36.77	146.42
V7	30.00	53.80	51.35	34.33	13.00	13.06	7.55	1517.56	1085.75	878.57	5.38	62.61	0.99	37.59	135.42
V8	29.77	55.00	49.60	31.67	13.23	11.89	7.15	1186.72	759.52	612.91	5.46	52.67	1.04	31.09	167.45
V9	29.25	60.10	57.13	32.67	12.95	12.73	7.16	1448.24	1070.23	946.74	4.77	62.57	0.97	37.04	228.05
V10	28.20	59.93	53.00	32.33	14.84	17.43	6.10	2434.79	1854.87	1720.49	4.80	70.65	0.85	39.01	295.33
V11	26.60	51.80	48.67	39.33	13.19	13.01	9.18	1262.55	1146.63	1207.53	4.33	77.08	1.02	36.61	153.82
V12	25.40	53.07	50.34	39.67	13.41	16.04	8.99	1687.41	1585.49	1406.22	5.07	72.71	0.83	36.89	174.68
V13	26.60	58.80	52.31	38.00	12.52	15.36	8.32	1539.52	1423.79	1115.16	4.37	73.74	0.84	37.63	232.95
V14	24.73	53.67	47.65	31.33	13.47	13.25	7.88	1431.82	1263.70	1077.69	4.63	70.82	1.04	42.96	247.74
V15	25.07	50.53	47.79	36.00	12.43	13.01	8.46	1444.29	1175.71	909.90	3.83	64.55	0.97	39.30	148.28
V16	28.60	64.43	60.47	41.67	13.76	14.46	8.26	2183.26	1529.05	1179.59	4.33	53.10	0.91	39.33	284.58
V17	26.07	54.33	49.84	35.00	13.49	14.81	7.93	1552.85	1249.81	1052.72	4.18	68.55	0.92	36.49	178.77
V18	26.47	59.48	53.24	38.33	13.53	13.74	8.22	1552.35	1327.43	1026.13	4.53	71.50	1.00	42.97	211.80
Mean	27.24	55.59	51.21	37.33	13.18	13.84	7.99	1490.06	1171.55	977.98	4.81	63.60	0.94	35.40	200.95
CV (%)	9.66	5.38	5.87	5.28	6.83	6.00	5.16	7.19	7.47	8.17	5.09	6.17	6.44	4.69	8.22
SEm ±	1.52	1.73	1.74	1.14	0.52	0.48	0.24	61.86	50.53	46.12	0.14	2.27	0.035	0.96	9.53
CD (5%)	NS	4.96	4.99	3.27	1.49	1.38	0.68	177.80	145.24	132.55	0.41	6.51	0.101	2.75	27.40

Genotype codes as in Table 1. PH = plant height (cm); FS-EW/FS-NS = frame spread east–west/north–south (cm); D50% = days to 50% head emergence; PD/ED = polar/equatorial diameter (cm); SL = stalk length (cm); GW/MW/NHW = gross/marketable/net head weight (g); CL = core length (cm); HI = harvest index (%); HSI = head shape index; HC = head compactness; YPH = total yield (q/ha); NS= not significant.

Variability, heritability and genetic advance

PCV was higher than GCV for every trait (Table 4; Figure 3). For most traits the two values were close, but for plant height they were far apart (GCV 2.93%, PCV 10.09%), which means that the variation in plant height was mostly environmental. Both GCV and PCV were high (>20%) for net head weight (30.48 and 31.55%), marketable head weight (26.51 and 27.54%), yield (26.18 and 27.44%) and gross head weight (23.87 and 24.93%). GCV was moderate (10.32–15.14%) for head compactness, stalk length, harvest index, core length, days to 50% head emergence and equatorial diameter and low (<10%) for plant height, frame spread, polar diameter and head shape index.

Eleven traits had high heritability (>60%), from 63.99% for polar diameter to 93.30% for net head weight. Heritability was moderate for frame spread E–W (55.10%), head shape index (58.56%) and frame spread N–S (46.31%) and low for plant height (8.44%). High heritability was accompanied by high GAM (>20%) in net head weight (60.64%), marketable head weight (52.56%), yield (51.46%), gross head weight (47.09%), head compactness (29.79%), stalk length (25.86%), core length (23.25%), days to 50% head emergence (23.05%) and harvest index (22.51%). Polar and equatorial diameter had high heritability but moderate GAM (15.00 and 18.37%) and frame spread E–W and N–S had moderate heritability with low GAM (9.11 and 7.64%).

Table 4. Estimates of genetic parameters for fifteen quantitative characters in cabbage.

Character	Mean	Range	σ^2_g	σ^2_p	GCV (%)	PCV (%)	h^2 (%)	GA	GAM (%)
Plant height (cm)	27.24	24.73–30.08	0.64	7.56	2.93	10.09	8.44	0.48	1.75
Frame spread E–W (cm)	55.59	50.53–64.43	10.97	19.91	5.96	8.03	55.10	5.07	9.11
Frame spread N–S (cm)	51.21	47.65–60.47	7.80	16.84	5.45	8.01	46.31	3.91	7.64
Days to 50% head emergence	37.33	31.33–45.00	20.72	24.60	12.19	13.28	84.22	8.60	23.05
Polar diameter (cm)	13.18	11.43–17.12	1.44	2.25	9.10	11.38	63.99	1.98	15.00
Equatorial diameter (cm)	13.84	11.89–17.43	2.04	2.73	10.32	11.94	74.73	2.54	18.37
Stalk length (cm)	7.99	6.01–10.09	1.15	1.32	13.45	14.40	87.16	2.07	25.86
Gross head weight (g)	1490.06	928.15–2434.79	126551.71	138033.49	23.87	24.93	91.68	701.69	47.09
Marketable head weight (g)	1171.55	656.15–1854.87	96432.65	104093.69	26.51	27.54	92.64	615.71	52.56
Net head weight (g)	977.98	481.43–1720.49	88832.57	95213.62	30.48	31.55	93.30	593.05	60.64
Core length (cm)	4.81	3.83–6.28	0.35	0.41	12.23	13.25	85.21	1.12	23.25

Harvest index (%)	63.60	52.67–77.08	60.59	75.99	12.24	13.71	79.73	14.32	22.51
Head shape index	0.944	0.83–1.10	0.0052	0.0089	7.66	10.00	58.56	0.114	12.07
Head compactness	35.40	20.66–42.97	28.71	31.46	15.14	15.85	91.26	10.54	29.79
Total yield (q/ha)	200.95	135.42–295.33	2767.79	3040.46	26.18	27.44	91.03	103.40	51.46

σ^2_g, σ^2_p = genotypic and phenotypic variance; GCV, PCV = genotypic and phenotypic coefficient of variation; h^2 = broad-sense heritability; GA = genetic advance at 5% selection intensity; GAM = genetic advance as per cent of mean. Estimates for plant height should be interpreted with caution because its genotype mean square was not significant.

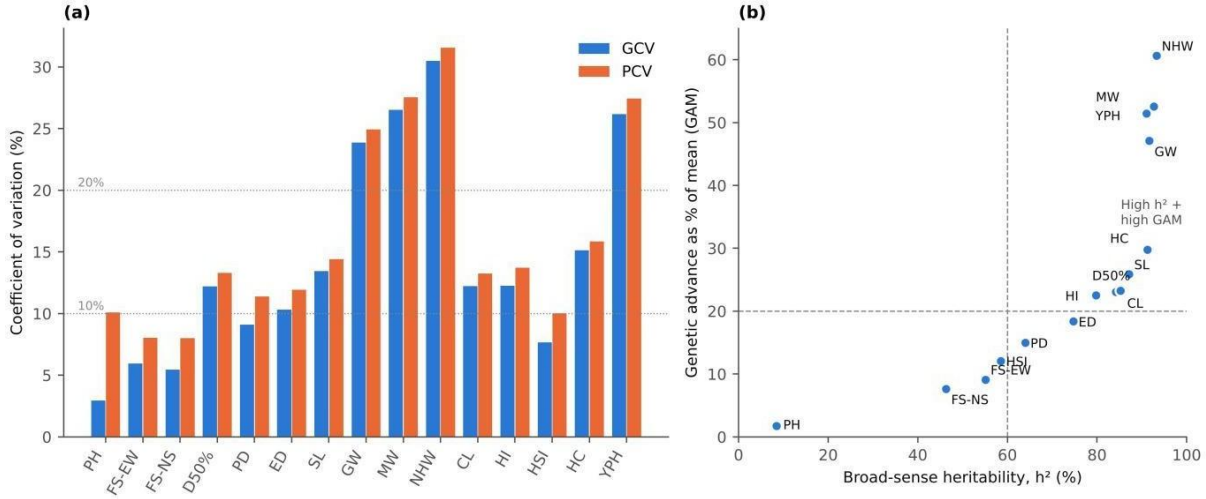


Figure 3. a. Genotypic (GCV) and phenotypic (PCV) coefficients of variation; dotted lines mark the 10 and 20% class limits. b. Broad-sense heritability (h^2) plotted against genetic advance as per cent of mean (GAM); dashed lines mark the 60% (h^2) and 20% (GAM) class limits. Trait abbreviations as in Table 3.

Correlation analysis

At the phenotypic level (Table 5; Figure 4), yield had significant positive correlations with frame spread E–W (0.64), gross head weight (0.63), marketable head weight (0.58), equatorial diameter (0.54), polar diameter (0.52), net head weight (0.49) and frame spread N–S (0.48) and a significant negative correlation with stalk length (–0.49). Its correlations with days to 50% head emergence (–0.19), head shape index (–0.13), harvest index (0.14), head compactness (0.04) and core length (0.02) were not significant. Among the component traits, the three head weights were closely correlated with each other (0.79–0.90) and with equatorial diameter (0.71–0.79). Harvest index was correlated with marketable (0.57) and net head weight (0.65). Head compactness was correlated with marketable head weight (0.47), net head weight (0.48) and harvest index (0.50), while equatorial diameter was negatively correlated with head shape index (–0.51). The genotypic correlations (Table 6) showed the same pattern and were generally larger in magnitude. With yield, they were 0.85 for frame spread E–W, 0.69 for frame spread N–S, 0.67 for gross head weight, 0.65 for equatorial diameter, 0.64 for polar diameter, 0.62 for marketable head weight, 0.50 for net head weight and –0.53 for stalk length.

Table 5. Phenotypic correlation coefficients among fifteen quantitative characters in eighteen cabbage genotypes.

	PH	FS-EW	FS-NS	D50%	PD	ED	SL	GW	MW	NHW	CL	HI	HSI	HC	YPH
PH	1.00														
FS-EW	0.35	1.00													
FS-NS	0.24	0.82**	1.00												
D50%	0.05	–0.11	–0.03	1.00											
PD	0.21	0.27	0.20	0.01	1.00										
ED	–0.13	0.31	0.19	–0.16	0.38	1.00									
SL	–0.26	–0.31	–0.20	0.30	–0.36	–0.25	1.00								
GW	0.05	0.55*	0.43	–0.23	0.43	0.71**	–0.30	1.00							
MW	–0.09	0.43	0.30	–0.21	0.42	0.79**	–0.20	0.86**	1.00						
NHW	–0.10	0.31	0.21	–0.27	0.38	0.73**	–0.18	0.79**	0.90**	1.00					
CL	0.06	–0.01	0.02	–0.24	–0.07	0.01	–0.38	–0.08	–0.18	–0.11	1.00				
HI	–0.32	–0.05	–0.16	–0.30	0.18	0.45	0.04	0.26	0.57*	0.65**	–0.19	1.00			

HSI	0.16	–0.12	–0.14	0.08	0.42	–0.51*	–0.10	–0.27	–0.29	–0.30	–0.15	–0.13	1.00		
HC	–0.29	0.21	0.19	–0.40	–0.27	0.17	0.12	0.40	0.47*	0.48*	–0.26	0.50*	–0.20	1.00	
YPH	0.12	0.64**	0.48*	–0.19	0.52*	0.54*	–0.49*	0.63**	0.58*	0.49*	0.02	0.14	–0.13	0.04	1.00

*, ** Significant at $P \leq 0.05$ ($|r| \geq 0.468$) and $P \leq 0.01$ ($|r| \geq 0.590$) with 16 df. Abbreviations as in Table 3.

Table 6. Genotypic correlation coefficients among fifteen quantitative characters in eighteen cabbage genotypes.

	PH	**FS-EW**	**FS-NS**	**D50 %**	**PD**	**ED**	**SL**	**GW**	**MW**	**NHW**	**CL**	**HI**	**HSI**	**HC**	**YPH**
PH	1.00														
FS-EW	–	1.00													
FS-NS	–	0.98	1.00												
D50%	–	–0.15	–0.06	1.00											
PD	–	0.50	0.20	–0.01	1.00										
ED	–	0.56	0.38	–0.18	0.57	1.00									
SL	–	–0.38	–0.25	0.36	–0.52	–0.35	1.00								
GW	–	0.81	0.73	–0.30	0.55	0.86	–0.34	1.00							
MW	–	0.63	0.49	–0.24	0.59	0.93	–0.20	0.93	1.00						
NHW	–	0.49	0.37	–0.30	0.49	0.90	–0.20	0.87	0.97	1.00					
CL	–	0.01	–0.05	–0.26	–0.06	0.06	–0.48	–0.09	–0.21	–0.15	1.00				
HI	–	0.03	–0.09	–0.37	0.16	0.56	0.03	0.34	0.65	0.74	–0.25	1.00			
HSI	–	–0.25	–0.38	0.09	0.32	–0.62	–0.09	–0.43	–0.39	–0.39	–0.17	–0.22	1.00		
HC	–	0.23	0.27	–0.46	–0.28	0.19	0.14	0.44	0.49	0.53	–0.29	0.58	–0.28	1.00	
YPH	–	0.85	0.69	–0.20	0.64	0.65	–0.53	0.67	0.62	0.50	0.01	0.14	–0.16	0.04	1.00

Genotypic correlations involving plant height are not reported (–) because the genotypic variance of plant height was not significant ($h^2 = 8.4\%$), which makes the corresponding estimates unstable (absolute values > 1 were obtained). Abbreviations as in Table 3.

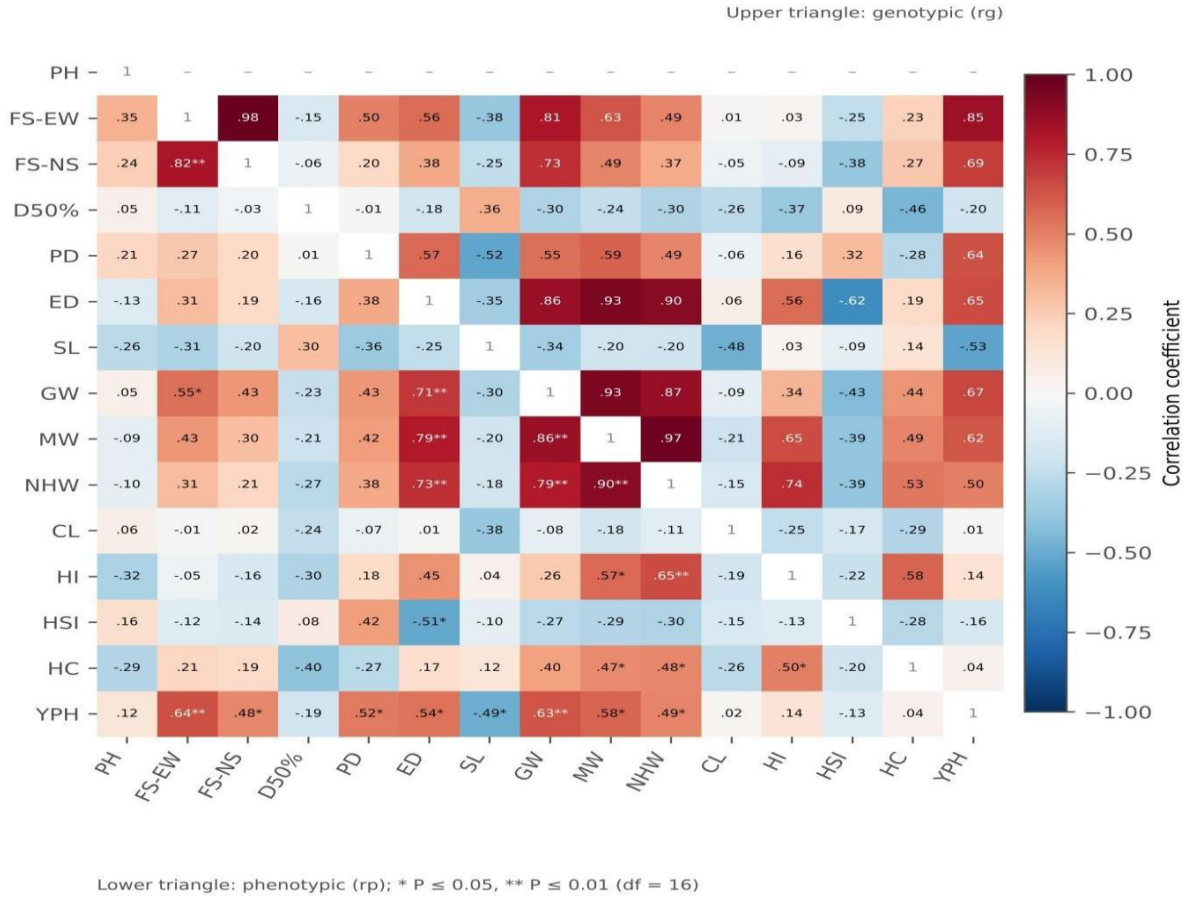


Figure 4. Phenotypic (lower triangle) and genotypic (upper triangle) correlation coefficients among fifteen traits in cabbage. *, ** Phenotypic correlation significant at P ≤ 0.05 and P ≤ 0.01 (16 df). Genotypic correlations involving plant height are omitted (–). Trait abbreviations as in Table 3.

Path coefficient analysis

Frame spread E–W had the highest positive direct effect on yield (0.522), followed by polar diameter (0.298) and marketable head weight (0.222) (Table 7). The direct effects of gross head weight (0.077) and net head weight (0.020) were negligible. Their significant correlations with yield came mostly through frame spread E–W (0.287 and 0.162), marketable head weight (0.191 and 0.200) and polar diameter (0.128 and 0.113). Equatorial diameter had a negative direct effect (–0.146), but its correlation with yield was positive because of indirect effects through marketable head weight (0.176), frame spread E–W (0.162) and polar diameter (0.113). Frame spread N–S also had a small negative direct effect (–0.081) and nearly all of its correlation with yield was due to its indirect effect through frame spread E–W (0.428). The negative direct effect of stalk length (–0.260) was strengthened by negative indirect effects through frame spread E–W (–0.162) and polar diameter (–0.107). Direct effects were also negative for head shape index (–0.239), head compactness (–0.233), plant height (–0.196), core length (–0.116) and days to 50% head emergence (–0.111). The residual effect was 0.548, so the fourteen traits accounted for 70% of the variation in yield.

Table 7. Direct (bold, diagonal) and indirect effects of fourteen characters on total yield per hectare, based on phenotypic correlations.

Character	PH	FS-EW	FS-NS	D50%	PD	ED	SL	GW	MW	NHW	CL	HI	HSI	HC	r with YPH
PH	**–0.196**	0.183	–0.019	–0.006	0.063	0.019	0.067	0.004	–0.020	–0.002	–0.007	0.005	–0.038	0.068	0.12
FS-EW	–0.069	**0.522**	–0.067	0.012	0.081	–0.045	0.080	0.042	0.096	0.006	0.001	0.001	0.029	–0.049	0.64**
FS-NS	–0.047	0.428	**–0.081**	0.003	0.060	–0.028	0.052	0.033	0.067	0.004	–0.002	0.003	0.033	–0.044	0.48*
D50%	–0.010	–0.057	0.002	**–0.111**	0.003	0.023	–0.078	–0.018	–0.047	–0.005	0.028	0.005	–0.019	0.093	–0.19
PD	–0.041	0.141	–0.016	–0.001	**0.298**	–0.056	0.093	0.033	0.093	0.008	0.008	–0.003	–0.100	0.063	0.52*
ED	0.026	0.162	–0.015	0.018	0.113	**–0.146**	0.065	0.055	0.176	0.014	–0.001	–0.007	0.122	–0.040	0.54*

SL	0.051	–0.162	0.016	–0.033	–0.107	0.037	**–0.260**	–0.023	–0.044	–0.004	0.044	–0.001	0.024	–0.028	–0.49*
GW	–0.010	0.287	–0.035	0.026	0.128	–0.104	0.078	**0.077**	0.191	0.016	0.009	–0.004	0.065	–0.093	0.63**
MW	0.018	0.224	–0.024	0.023	0.125	–0.116	0.052	0.066	**0.222**	0.018	0.021	–0.009	0.069	–0.110	0.58*
NHW	0.020	0.162	–0.017	0.030	0.113	–0.107	0.047	0.061	0.200	**0.020**	0.013	–0.011	0.072	–0.112	0.49*
CL	–0.012	–0.005	–0.002	0.027	–0.021	–0.001	0.099	–0.006	–0.040	–0.002	**–0.116**	0.003	0.036	0.061	0.02
HI	0.063	–0.026	0.013	0.033	0.054	–0.066	–0.010	0.020	0.127	0.013	0.022	**–0.016**	0.031	–0.117	0.14
HSI	–0.031	–0.063	0.011	–0.009	0.125	0.075	0.026	–0.021	–0.064	–0.006	0.017	0.002	**–0.239**	0.047	–0.13
HC	0.057	0.110	–0.015	0.044	–0.081	–0.025	–0.031	0.031	0.104	0.010	0.030	–0.008	0.048	**–0.233**	0.04

Residual effect = 0.548 (R^2 = 0.700). Each row sums to the phenotypic correlation of that character with yield (last column). Abbreviations as in Table 3.

Genetic divergence by Mahalanobis' D^2 and Tocher clustering

The eighteen genotypes fell into six clusters (Table 8). Cluster II was the largest with six genotypes, clusters I and III had four each and cluster V had two. Clusters IV (Pragati) and VI (2022/CABHYB-1) had a single genotype each. Among the clusters with more than one genotype, the intra-cluster distance was highest in cluster V (223.94) and lowest in cluster III (94.21) (Table 9). The inter-cluster distance was greatest between clusters I and VI (1377.16), followed by III and VI (1137.04), III and V (969.87), I and IV (854.41) and III and IV (797.63). Clusters IV and VI were the closest (226.64), which means that Pragati and 2022/CABHYB-1 are fairly similar to each other.

Cluster VI (2022/CABHYB-1) recorded the highest means for equatorial diameter, gross, marketable and net head weight, harvest index and yield, along with the earliest head emergence and the shortest stalk (Table 10). Cluster IV (Pragati) had the widest frame spread, the latest head emergence (41.67 days) and the most compact heads (39.33). Cluster V had the highest polar diameter (15.26 cm) and, among the clusters with more than one genotype, the highest yield (265.83 q/ha), followed by cluster II (212.33 q/ha). Head weights were lowest in cluster I (gross head weight 1074.69 g) and yield was lowest in cluster III (145.98 q/ha).

Table 8. Distribution of eighteen cabbage genotypes into six clusters by Tocher's method based on Mahalanobis' D^2.

Cluster	No. of genotypes	Genotypes
I	4	2021/CABHYB-2, 2021/CABHYB-4, 2021/CABHYB-3, Green Valley
II	6	2022/CABHYB-4, Deepak, Pulkit, 2022/CABHYB-5, Additi, 2022/CABHYB-3
III	4	2022/CABHYB-2, 2022/CABHYB-6, 2021/CABHYB-6, 2021/CABHYB-7
IV	1	Pragati
V	2	2021/CABHYB-1, 2021/CABHYB-5
VI	1	2022/CABHYB-1

Table 9. Average intra-cluster (diagonal) and inter-cluster D^2 values among six clusters of cabbage genotypes.

Cluster	I	II	III	IV	V	VI
I	**118.20**	374.07	295.49	854.41	617.85	1377.16
II		**117.05**	241.27	307.30	507.20	542.16
III			**94.21**	797.63	969.87	1137.04
IV				**0.00**	400.37	226.64
V					**223.94**	624.36
VI						**0.00**

Diagonal (bold) values are intra-cluster distances; clusters IV and VI are single-genotype clusters.

Table 10. Cluster means for fifteen quantitative characters in cabbage.

Character	I	II	III	IV	V	VI
Plant height (cm)	27.75	26.42	26.85	**28.60**	28.28	28.20
Frame spread E–W (cm)	52.94	56.57	52.83	**64.43**	56.83	59.93

Frame spread N–S (cm)	49.24	51.75	49.48	**60.47**	51.47	53.00
Days to 50% head emergence	40.75	35.83	36.00	41.67	38.00	**32.33**
Polar diameter (cm)	12.16	13.23	12.51	13.76	**15.26**	14.84
Equatorial diameter (cm)	12.23	14.32	13.17	14.46	14.90	**17.43**
Stalk length (cm)	8.02	8.08	8.82	8.26	6.78	**6.10**
Gross head weight (g)	1074.69	1535.36	1421.05	2183.26	1503.90	**2434.79**
Marketable head weight (g)	737.22	1320.08	1113.47	1529.05	1190.35	**1854.87**
Net head weight (g)	589.88	1104.11	970.64	1179.59	918.39	**1720.49**
Core length (cm)	5.04	4.59	4.71	4.33	**5.45**	4.80
Harvest index (%)	53.69	69.98	66.01	53.10	61.23	**70.65**
Head shape index	0.97	0.93	0.96	0.91	**0.98**	0.85
Head compactness	30.76	39.00	37.57	**39.33**	25.75	39.01
Total yield (q/ha)	161.90	212.33	145.98	284.58	265.83	**295.33**

Bold values are the most desirable cluster mean for each character (lowest for days to 50% head emergence and stalk length; highest for all others, including plant height and head shape index for which no direction is implied).

Principal component analysis

Five principal components had eigenvalues above one and together they explained 88.72% of the total variation (Table 11; Figure 5a). PC1 (eigenvalue 5.959; 39.73%) had high positive loadings for marketable (0.944), gross (0.941) and net head weight (0.890), equatorial diameter (0.868), yield (0.774), frame spread E–W (0.732), frame spread N–S (0.594), polar diameter (0.544) and harvest index (0.504). It can therefore be read as a head weight–yield axis. PC2 (20.02%) set plant height (0.851) against harvest index (–0.649), head compactness (–0.632) and stalk length (–0.539). PC3 (10.52%) was related to head shape index (0.634) and polar diameter (0.629) as against core length (–0.559). PC4 (10.41%) was related to core length (0.613) as against stalk length (–0.565), days to 50% head emergence (–0.544) and frame spread N–S (–0.505) and PC5 (8.04%) to days to 50% head emergence (0.552) as against head compactness (–0.545) and head shape index (–0.501).

In the PC1–PC2 biplot (Figure 5b), 2022/CABHYB-1 (PC1 score 6.00) and Pragati (3.44) were placed at the positive end of PC1, near the vectors of head weight, frame spread and yield. They were followed by 2022/CABHYB-4, 2022/CABHYB-3 and 2021/CABHYB-5. The negative end was occupied by three cluster I genotypes, 2021/CABHYB-4 (–4.10), 2021/CABHYB-2 (–3.60) and 2021/CABHYB-3 (–2.76). Along PC2, 2021/CABHYB-1 (3.85) and Green Valley (2.34) stood apart from 2022/CABHYB-3 (–2.38), 2022/CABHYB-6 (–2.28) and 2022/CABHYB-2 (–1.92), which have compact heads and a high harvest index.

Table 11. Eigenvalues, variance explained and trait loadings (correlations with components) of the first five principal components.

Character	**PC1**	**PC2**	**PC3**	**PC4**	**PC5**
Plant height (cm)	0.029	**0.851**	0.047	–0.090	–0.170
Frame spread E–W (cm)	**0.732**	0.440	–0.219	–0.351	–0.165
Frame spread N–S (cm)	**0.594**	0.423	–0.349	**–0.505**	–0.178
Days to 50% head emergence	–0.343	0.161	0.327	**–0.544**	**0.552**
Polar diameter (cm)	**0.544**	0.480	**0.629**	0.198	0.068
Equatorial diameter (cm)	**0.868**	–0.125	0.027	0.139	0.436
Stalk length (cm)	–0.401	**–0.539**	0.105	**–0.565**	0.083
Gross head weight (g)	**0.941**	0.037	–0.025	–0.102	0.008
Marketable head weight (g)	**0.944**	–0.216	0.179	–0.033	0.074
Net head weight (g)	**0.890**	–0.312	0.167	0.082	0.054
Core length (cm)	–0.061	0.324	**–0.559**	**0.613**	0.215
Harvest index (%)	**0.504**	**–0.649**	0.278	0.257	–0.099
Head shape index	–0.369	0.369	**0.634**	0.148	**–0.501**
Head compactness	0.423	**–0.632**	–0.199	–0.140	**–0.545**
Total yield (q/ha)	**0.774**	0.371	0.007	–0.008	0.027
Eigenvalue	**5.959**	**3.004**	**1.578**	**1.561**	**1.207**
Variance explained (%)	**39.73**	**20.02**	**10.52**	**10.41**	**8.04**
Cumulative variance (%)	**39.73**	**59.75**	**70.27**	**80.68**	**88.72**

Loadings with absolute values ≥ 0.50 are shown in bold.

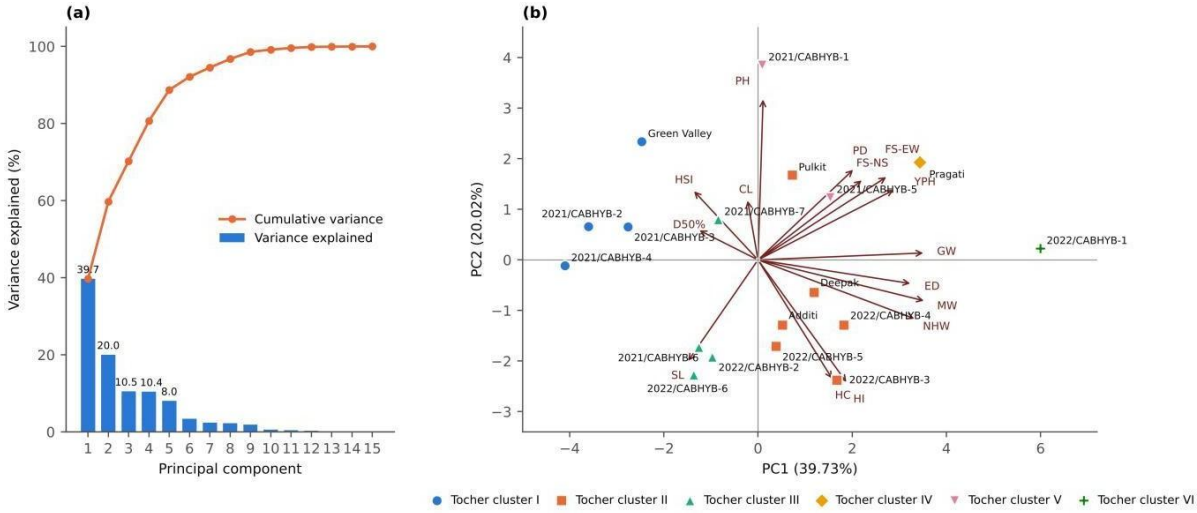


Figure 5. a. Scree plot of the percentage and cumulative variance explained by the principal components. b. Biplot of the first two principal components showing genotype scores (symbols coloured by Tocher cluster) and trait loading vectors. Trait abbreviations as in Table 3.

Hierarchical clustering

Ward clustering split the genotypes into two main groups at the highest linkage distance (10.97) (Figure 6). The first group had 2021/CABHYB-1, -2, -3, -4, -5 and -7, Green Valley and Pulkit. Within it, 2021/CABHYB-2, -3 and -4, all of which belong to Tocher cluster I, formed a tight subgroup. The second group had 2021/CABHYB-6, 2022/CABHYB-2 to -6, Additi and Deepak, along with the high-yielding pair 2022/CABHYB-1 and Pragati. These two merged with each other at a distance of 5.61 and joined the rest of the group at 9.80. The six-group Ward partition agreed moderately with the Tocher clusters (adjusted Rand index = 0.38). Both methods kept 2022/CABHYB-1 and Pragati apart from the rest and put 2021/CABHYB-2, -3 and -4 together. Ward clustering, however, merged most members of Tocher clusters II and III into one group and separated 2021/CABHYB-1 from 2021/CABHYB-5. The standardized heatmap (Figure 6) shows high head weight, frame spread and yield in the 2022/CABHYB-1–Pragati branch and late head emergence with low head weight in the branch of 2021/CABHYB-2, -3 and -4.

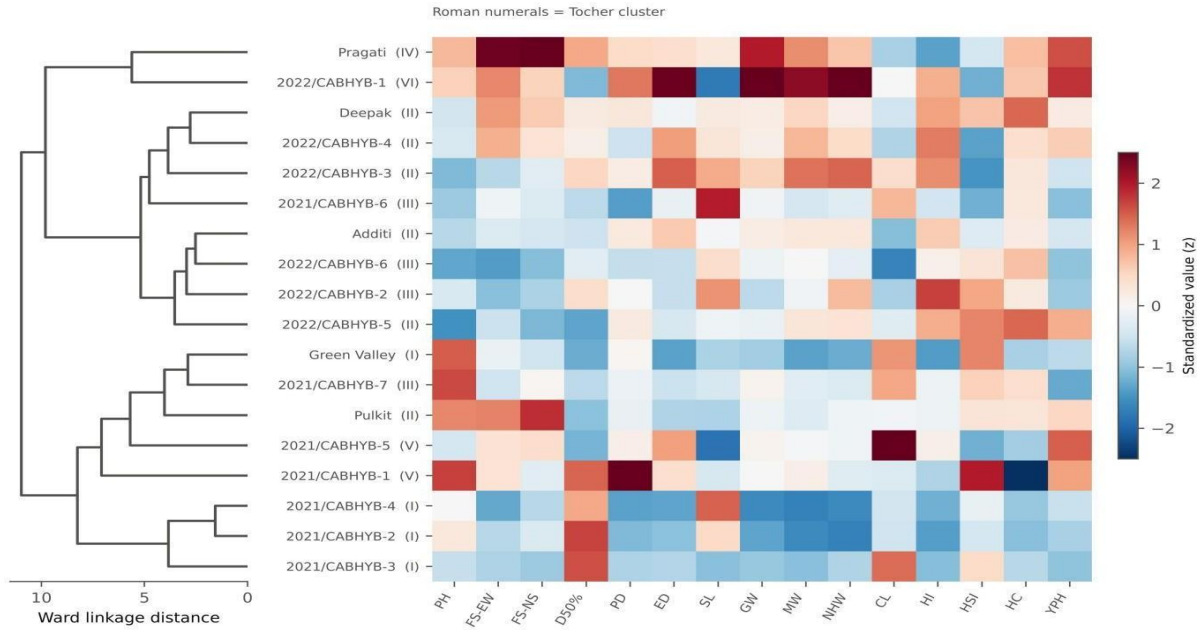


Figure 6. Dendrogram of eighteen cabbage genotypes from Ward's minimum-variance clustering on standardized data, with a heatmap of standardized trait values (z scores). Roman numerals after the genotype names indicate Tocher clusters. Trait abbreviations as in Table 3.

DISCUSSION

Significant differences among the genotypes for fourteen of the fifteen traits show that the material has enough variability for selection. Earlier workers reported similar variability in cabbage (Singh *et al*., 2013a; Sharma *et al*., 2023) and cauliflower (Singh *et al*., 2023). Plant height did not vary significantly and its heritability was very low (8.44%), so this trait is of little use for distinguishing these genotypes under the conditions of the present study. 2022/CABHYB-1, Pragati and 2021/CABHYB-5 yielded 39–47% more than the grand mean and this advantage went with heavier heads and wider frames. Comparable variation for head and yield traits has been reported in Indian and exotic cabbage germplasm (Singh *et al*., 2013a; Zahid *et al*., 2024).

For most traits the gap between PCV and GCV was narrow. The environment thus had only a limited influence on their expression and the phenotypic values can be taken as a fair guide to the genotypic values. Net, marketable and gross head weight and yield showed high GCV, high heritability and high GAM together. Such traits are governed largely by additive gene action and should respond to simple phenotypic selection (Johnson *et al*., 1955; Singh and Chaudhary, 1985). Similar results for head weight and yield were reported in cabbage (Singh *et al*., 2013a; Zyada and Ismail, 2018; Sharma *et al*., 2023) and for head mineral traits as well (Singh *et al*., 2013b; Chura *et al*., 2021). Head compactness, stalk length, core length, harvest index and days to 50% head emergence also had high heritability with high GAM and can be improved by selection. Frame spread, on the other hand, had moderate heritability and low GAM. Non-additive gene action and the environment probably play a larger part in this trait, so selection in later generations or heterosis breeding may work better for it. One caution is needed here. Broad-sense heritability estimated from a single season and location includes the genotype × environment interaction variance and it therefore tends to overestimate the heritable portion.

Yield was positively correlated with frame spread, head diameters and head weights and negatively with stalk length. The same associations were reported earlier in cabbage (Kaur *et al*., 2018; Sharma *et al*., 2023) and cauliflower (Singh *et al*., 2023; Singh *et al*., 2025). Because the three head weights were strongly correlated among themselves, selection for any one of them will improve the other two as well. For most pairs of traits the genotypic correlation was higher than the phenotypic correlation. The associations are therefore largely genetic and are masked to some extent by environmental effects.

The path analysis showed that frame spread E–W, polar diameter and marketable head weight acted on yield directly. Gross head weight, net head weight, equatorial diameter and frame spread N–S were associated with yield mainly through these three traits. Frame spread E–W, polar diameter and marketable head weight have significant positive correlations with yield as well as positive direct effects and so they are the most dependable indirect selection criteria. Path analyses in cabbage point in the same direction (Singh *et al*., 2013a; Kaur *et al*., 2018; Sharma *et al*., 2023). The negative direct effects of stalk length, head shape index and head compactness suggest that plants with short stalks and round, moderately compact heads are desirable for yield. The residual effect of 0.548 means that about 30% of the variation in yield came from factors not included in the model, for example plant stand at harvest and losses from head splitting. Since fourteen highly inter-correlated predictors were fitted to only eighteen genotype means, the individual direct effects, especially those of the head weights, should be interpreted with caution.

The six Tocher clusters and the large inter-cluster distances, particularly between clusters I and VI and between III and VI, show that the material is genetically quite divergent. The genotypes did not cluster strictly by origin. AICRP lines of both the 2021 and 2022 series were spread over several clusters and the cultivars Deepak, Pulkit and Additi grouped with 2022 lines. This agrees with diversity studies in which morphological divergence was unrelated to geographic or institutional origin (Rana *et al*., 2023). The PCA confirmed that head weight, head diameter, frame spread and yield (PC1) were the main sources of multivariate variation. Ward clustering, on its own, separated the high-yielding pair 2022/CABHYB-1 and Pragati as well as the late, low-yielding lines of cluster I. Only moderate agreement between Ward and Tocher clustering (adjusted Rand index = 0.38) is to be expected, because D^2 takes the error covariance among traits into account whereas Ward clustering works on standardized Euclidean distance. The groupings common to both methods are therefore the most reliable.

For breeding, 2022/CABHYB-1, Pragati and 2021/CABHYB-5 are the most promising parents, as they combine the highest yields with membership of divergent clusters (VI, IV and V). Clusters IV and VI are, however, fairly close to each other ($D^2 = 226.64$). Crosses of 2022/CABHYB-1 or Pragati with genotypes of the most distant clusters I and III and of 2021/CABHYB-5 with cluster III, are therefore more likely to give heterotic combinations. Deepak and 2022/CABHYB-5 can be used as donors for head compactness. The genotypes were evaluated for one season at one location only, so they need to be tested over environments to confirm their stability before being used widely in hybridization.

CONCLUSION

The eighteen cabbage genotypes showed significant variability for fourteen of the fifteen traits studied. Net, marketable and gross head weight and yield had high GCV, heritability and GAM, so direct selection for these traits will be effective. Frame spread E–W, polar diameter and marketable head weight turned out to be the most dependable indirect selection criteria for yield. Mahalanobis' D^2, PCA and Ward clustering all identified 2022/CABHYB-1 and Pragati as distinct, high-yielding genotypes. 2022/CABHYB-1, Pragati, 2021/CABHYB-5 and 2021/CABHYB-1 are recommended as parents for crossing with genotypes of the divergent clusters I and III.

Acknowledgments

The authors thank the All India Coordinated Research Project (AICRP) on Vegetable Crops, Odisha University of Agriculture and Technology, Bhubaneswar, for providing the experimental facilities and genetic material.

Funding

This research received no specific grant from any funding agency in the public, commercial or not-for-profit sectors.

Conflicts Of Interest

The authors declare no conflict of interest.

Data Availability

Genotype means for all traits are given in Table 3. Plot-level data are available from the corresponding author on reasonable request.

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