

SHORT COMMUNICATION

Genetic Evaluation of Different Genotypes of Cabbage (*Brassica oleracea* var. *capitata* L.) under Natural Farming Condition in Hill region

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Abstract

The present investigation was carried out to identify the potential genotypes of cabbage for growing under natural farming conditions. About 14 genotypes, including check, were evaluated in a randomized complete block design with three replications during *Rabi*, 2018-19. Analysis of variance for all the traits showed the presence of sufficient variability in the germplasm as revealed by significant differences for all the characters excluding marketable heads per plot. Based upon overall performance, the genotype KGAT-III (123.95 q/ha) gave maximum marketable head yield. However, it was statistically at par with four other genotypes viz., GA-P (118.94 q/ha), M-GA-P (115.52 q/ha), DPCH-112 (108.52 q/ha) and DPCbH-1 (108.08 q/ha) and check variety Pusa Mukta (101.47 q/ha) under natural farming conditions. High PCV estimates were recorded for marketable head yield per plot. High heritability coupled with high genetic advance was observed for net head weight.

Keywords: Cabbage, Genetic advance, Heritability, Natural farming, Variability.

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Introduction

Cabbage (*Brassica oleracea* var. *capitata* L. and chromosome no. $2n=2x=18$), a member of family Brassicaceae, is one of the most important cole-group vegetable crops. It is originated from *B. oleracea* var. *oleracea* L. (syn. *B. oleracea* var. *sylvestris* L.), commonly known as wild cabbage, cliff cabbage or colewort through mutation, human selection and adaptation. Off-late the concept of natural farming is becoming popular for raising vegetable crops without the use of synthetic fertilizers and pesticides. The farming system, as proposed by *Padam Shri* Sh. Subhash Palekar is zero budget natural farming (ZBNF), which was recently also made popular as Subhash Palekar natural farming (SPNF). The farmers have observed improvements in yield, soil conservation, seed diversity, quality of produce, household food autonomy, income and health. They experienced a reduction in farm expenses and on dependence on the borrowed money, which is one of the major problems faced by Indian farmers. Scientific validation of different techniques as suggested by Sh. Subhash Palekar is required at the university level for further adoption and promotion of SPNF. Therefore, in view of producing safe, healthy and quality food present study was carried out to identify the potential genotypes for marketable head yield and other horticultural traits under natural farming conditions (SPNF).

The present investigation was carried out at the experimental farm, Department of Organic Agriculture and Natural Farming,

CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur, Himachal Pradesh., during *Rabi*, 2018-19. The experiment was laid out in randomized complete block design (RCBD) with three replications. Observations were recorded on five randomly selected plants for characters, namely plant spread (cm), number of non-wrapper leaves, gross head weight (g), net weight head (g), polar diameter (cm), equatorial diameter (cm), head shape index, days to harvest, head compactness (g/cm^3), marketable heads per plot, marketable head yield per plot (kg) and TSS ($^{\circ}\text{Brix}$). The data were statistically analyzed as per the methods given by Panse and Sukhatme (1984). The phenotypic and genotypic coefficients of variation were estimated as suggested by Burton and De Vane (1953). Heritability in a broad sense (h^{2bs}) and expected genetic advance were calculated by Burton and De Vane (1953) and Johnson *et al.*, (1955). The statistical analysis for each trait was carried out for each observed character under study using MS Excel and OPSTAT (developed by CCS Haryana Agricultural University, Hisar, India).

Analysis of variance for the experimental data revealed that mean squares were highly significant for all the studied traits indicating sufficient variability except marketable heads per plot (Table 1). Maximum gross head weight was observed in the genotype Tinnu (740 g) and was statistically significant with the genotype M-GA-P (701.67 g). The genotype GA-(P) (438 g) exhibited the maximum net head weight, followed by the genotype M-GA-(P) (428 g). Meena *et al.*, (2009) and Thakur and Vidyasagar (2016) revealed significant differences for net head weight. The genotype GA-(P) (1.04) had a maximum head shape index and was

statistically significant with eight other genotypes, including check. The genotype KGAT-III ($41.62 \text{ g}/\text{cm}^3$) exhibited maximum head compactness, followed by the genotype M-GA(P) ($39.44 \text{ g}/\text{cm}^3$). These results are closely related to the findings of Thakur and Thakur (2002a) and Atter (2004). The highest marketable yield per plot was observed in KGAT-III (4.47 kg). The range for TSS varied from [$7.57(^{\circ}\text{Brix})$] in GA-(P) to [$8.90(^{\circ}\text{Brix})$] in KTCBHR-35 (Table 2). A high phenotypic coefficient of variation (PCV) was observed only for the marketable head yield per plot (23.24%). Moderate PCV estimates were exhibited for the net weight (18.66%), head compactness (16.96%), gross weight (15.53%), number of non-wrapper leaves (14.93%) and plant spread (13.19%). Moderate GCV estimates were recorded for marketable head yield per plot (18.08%), net weight (16.60%), gross weight (12.69%), head compactness (10.12%) and number of non-wrapper leaves (10.04%). High heritability estimates were exhibited by net head weight (79.15%), gross head weight (66.84%) and marketable head yield per plot (60.49%). A high estimate for the genetic advance was obtained only for net weight (30.43%). However, moderate estimates were obtained for marketable head yield per plot (28.96%), gross weight (21.38%), number of non-wrapper leaves (13.92%) and head compactness (12.44%). High PCV estimates were observed only for the trait marketable head yield per plot (Table 3). Thus, from the present investigation, it may be concluded that the trait viz., net head weight and marketable head yield per plot can be improved by doing effective selection in the early generations for further crop improvement.

Table 1: Analysis of variance for agronomic/horticultural and quality traits in cabbage

S. No.	Sources of variations traits	Replications 2	Genotypes 13	Error 26
1	Plant spread (cm)	15.436	28.450*	13.413
2	No. of non-wrapper leaves	5.672	4.486*	1.290
3	Gross weight (g)	5792.667	20,975.22388*	2951.179
4	Net weight (g)	2,616.500	10,959.342*	884.628
5	Polar diameter (cm)	0.164	1.283*	0.360
6	Equatorial diameter (cm)	0.121	0.580*	0.258
7	Head shape index	0.000	0.005*	0.002
8	Days to harvest	165.452	242.996*	104.299
9	Head compactness (g/cm^3)	64.456	56.7328*	21.342
10	Marketable heads per plot	5.643	1.108	0.745
11	TSS ($^{\circ}\text{Brix}$)	0.032	0.375*	0.076
12	Marketable head yield per plot (kg)	1.479	1.408*	0.252

Significant at 5% level of significance

Table 2: Mean performance of genotypes for agronomic/horticultural and quality traits in cabbage

Genotype	Plant spread (cm)	No. of non-wrapper leaves	Gross weight (g)	Net head weight (g)	Polar diameter (cm)	Equatorial diameter (cm)	Head shape index	Days to harvest	Head compactness	Marketable heads per plot	Marketable head yield per plot (kg)	Marketable head yield (q/ha)	TSS
M-GA(P)	30.54	10.74	701.67	428.00	10.26	10.30	1.00	138.67	39.44	9.67	4.16	115.52	8.17
KTCBH-R35	30.04	7.94	410.00	230.00	8.41	9.44	0.90	127.34	32.45	9.34	2.16	59.81	8.90
DPCH-112	25.54	8.27	646.00	404.00	9.75	10.70	0.92	139.34	38.08	9.67	3.91	108.52	8.47
DPCb-131	33.21	10.87	596.00	322.00	10.17	10.32	0.99	144.67	30.48	9.67	3.13	86.83	8.34
KGAT-II	34.23	10.80	628.00	358.67	10.01	10.06	1.00	139.34	35.58	10.00	3.59	99.72	8.70
KGAT-III	33.22	10.67	620.67	404.34	9.86	10.09	0.98	150.00	41.62	11.00	4.47	123.95	8.27
Glory-7	33.50	11.07	486.34	261.34	9.53	9.46	1.01	151.34	31.43	9.34	2.45	68.04	7.84
I-4-4	34.36	10.00	646.00	342.67	10.40	10.30	1.02	138.00	30.95	9.67	3.29	91.37	8.10
S-Glory-1	33.78	10.14	646.67	371.67	9.78	10.36	0.95	146.67	36.43	9.00	3.35	92.92	8.20
DPCbH-1	30.69	10.34	598.67	363.34	10.08	10.55	0.96	132.34	33.42	10.67	3.90	108.08	7.80
DPCb-1101	32.19	12.54	639.00	333.34	9.45	9.74	0.98	141.34	38.00	9.00	3.00	83.33	8.47
GA(P)	31.35	10.34	600.67	438.00	11.28	10.90	1.04	140.00	32.07	9.67	4.27	118.39	7.57
Pusa Mukta	33.73	8.87	547.00	339.67	10.68	10.52	1.00	120.34	28.80	10.67	3.66	101.47	8.20
TINNU	39.47	11.34	740.00	290.00	10.08	10.54	0.96	152.00	26.56	9.67	2.80	77.57	8.07
Grand mean	32.56	10.28	607.62	349.07	9.97	10.23	0.97	140.1-010	33.95	9.79	3.43		8.22
SE(d)±	2.99	0.92	44.35	24.28	0.49	0.41	0.03	8.33	3.77	0.70	0.40		0.22
CD(5%)	6.14	1.90	91.19	49.92	1.00	0.85	0.06	17.14	7.75	-----	0.84		0.46
CV(%)	11.24	11.05	8.94	8.52	6.01	4.96	4.03	7.28	13.61	8.82	14.61		3.34
Range	25.54-39.47	7.94-12.54	419.00-740.00	230-438	8.41-11.28	9.44-10.9	0.90-1.04	120.34-150	26.56-41.62	9.00-11.00	2.16-4.47	59.81-123.95	7.57-8.90

Table 3: Estimates of PCV, GCV, heritability and genetic advance for marketable yield and other traits in cabbage

S. No.	Traits	PCV (%)	GCV (%)	h^2bs (%)	GA as percentage of mean
1	Plant spread (cm)	13.185(M)	6.877(L)	27.203(L)	7.389(L)
2	No. of non-wrapper leaves	14.934(M)	10.044(M)	45.235(M)	13.916(M)
3	Gross weight (g)	15.525(M)	12.693(M)	66.838(H)	21.376(M)
4	Net weight (g)	18.660(M)	16.601(M)	79.150(H)	30.425(H)
5	Polar diameter (cm)	8.191(L)	5.558(L)	46.052(M)	7.77(L)
6	Equatorial diameter (cm)	5.908(L)	3.206(L)	29.452(L)	3.584(L)
7	Head shape index	5.346(L)	3.347(L)	39.189(M)	4.316(L)
8	Days to harvest	8.758(L)	4.853(L)	30.713(M)	5.541(L)
9	Head compactness (g/cm ³)	16.958(M)	10.118(M)	35.597(M)	12.435(M)
10	Marketable heads per plot	9.511(L)	3.553(L)	13.953(L)	2.734(L)
11	TSS (brix)	5.096(L)	3.841(L)	56.807(M)	5.963(L)
12	Marketable head yield per plot (kg)	23.244(H)	18.078(M)	60.489(H)	28.964(M)

PCV = Phenotypic coefficient of variation {Low (L): <10%, Moderate (M): 10-20%, High (H): >20%}

GCV = Genotypic coefficient of variation {Low (L): <10%, Moderate (M): 10-20%, High (H): >20%}

h^2bs = Heritability (broad sense) {Low (L): <30%, Moderate (M): 30-60%, High (H): >60%}

GA = Genetic advance {Low (L): <10%, Moderate (M): 10-30%, High (H): >30%}

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