

MASTER NEGATIVE NUMBER: 09295.24

Arunachalam, V. and Murty, B.R
Canonical analysis of Sub-specific
Differentiation in Brassica Campestris.
*Journal of Indian Society of Agricultural
Statistics*, 18 (1966): 30-34.

Record no. D-5

Reprinted from "Journal of the Indian Society of Agricultural Statistics"
Vol. XVIII Dec., 1966

CANONICAL ANALYSIS OF SUB-SPECIFIC DIFFERENTIATION IN BRASSICA CAMPESTRIS

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During an analysis of genetic variability among some populations of *Brassica campestris* var. brown sarson, it was found that the self-compatible forms in this crop differed from the self-incompatible forms in a constellation of growth characteristics. It was also observed that genetic associations between yield components in self-compatible types of brown sarson and other self-compatible types in *Brassica campestris* were differing. Therefore, a comparison for factors influencing genetic divergence as assessed by multivariate analyses in both the forms of brown sarson which differ in their breeding structure was attempted.

A group of 40 self-compatible populations representing the spectrum of variability of the material grown in Indo-Gangetic areas and a set of 23 populations of self-incompatible brown sarson grown in separate experiments were analysed separately by multivariate analysis during the years 1961-64. The sample size was 60 plants in 4 replicates in randomised complete block design. The six characters chosen were flowering time, height, number of primary branches, number of secondary branches, number of siliquae on main axis and number of seeds per siliqua.

The Anova of plot means revealed highly significant differences among the varieties for each of the six characters in each group. Although both SC and SI types were grown under comparable conditions in the same field, the amount of genetic variability for individual characters was more in SI types for flowering time and number of fruit bearing branches only while the SC types were equally variable as the SI types for the rest of the characters contrary to the expectations that SC types have limited genetic variability. Tests by Wilks' Λ criterion revealed that the variation among the two groups were parallel when the six characters were considered together.

$$(X^2=481.6, 132 \text{ d.f. (SI type)}) \\ =750.2, 234 \text{ d.f. (SC type)}.$$

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The inter-and intra group analysis using D^2 statistic has revealed considerable divergence between the groups (Table 1).

The number of clusters was eight in *SI* types and nine in *SC* types. Since the sample sizes were the same, and the material grown in the same season and area, the inter-cluster distances could be compared. The average D^2 per comparison was higher in *SI* types (=6.99) than in *SC* types (=5.12). In both the cases, geographical distribution of the varieties could not be related to the genetic divergence as measured by D^2 statistic. However, a comparison of the relative contribution of the individual characters to inter-cluster divergence indicated that height and the number of seeds per siliqua were the largest contributors in the *SC* types (as seen from the table).

Percentage contribution to divergence of

<i>Type</i>	<i>Flowering time</i>	<i>Number of primary branches</i>	<i>Number of secondary branches</i>	<i>Height</i>	<i>Number of Siliquae on main axis</i>	<i>Number of seeds per siliqua</i>
SC	12.6	12.8	7.7	32.8	11.4	22.7
SI	53.4	4.7	11.1	17.4	8.3	5.1

However in *SI* types flowering time and height were important for inter-cluster divergence.

Intra-cluster divergence. The relative importance of the six characters was found to be variable in the *SC* types. However, seeds per capsule, days to flower and height, in general, contributed more than the other characters. In the *SI* types, height and flowering time contributed substantially to the intra-group divergence. It would appear that the forces of evolution within groups were parallel in both the *SC* and *SI* types while the genetic mechanisms in inter-cluster divergence were different in the two groups of incompatibility.

A comparison of the canonical roots has also brought out the diversity of evolutionary mechanisms in *SC* and *SI* types.

In the *SC* types, the first two roots accounted for only 69.7% of the total variation, while in *SI* types, the corresponding value was

82.8%. Actually λ_3 is not significant in *SI* types while it contributed substantially in *SC* types.

Type	Canonical roots				Total
	λ_1	λ_2	λ_3	$\lambda_4 + \lambda_5 + \lambda_6$	
SC Value	137.0	99.5	42.7	60.1	339.3
% contribution to total variation	40.4	29.3	12.6	17.7	100.0
SI Value	264.9	61.0	35.3	32.7	393.9
% contribution to total variation	67.3	15.5	9.0	8.2	100.0

An examination of the first canonical vector (Z_1) supplying the best linear function has indicated the potent role of flowering time and height in *SI* types, while in *SC* types, height, seeds per siliqua, and days to flower were important in that order.

Canonical Vectors	Flowering time	Number of primary Branches	Number of secondary Branches	Height	Number of siliquae on main axis	Number of seeds per siliqua
Z_1 SC	0.4351	0.2491	-0.2310	0.6959	-0.0074	0.4604
SI	0.7593	-0.2984	0.1866	0.5399	-0.0800	0.0422
Z_2 SC	-0.0392	-0.0311	0.1458	0.4895	0.6029	-0.6112
SI	0.1429	0.3615	0.6803	-0.2092	-0.1410	-0.5681

In the case of the second vector, the differences between the *SC* and *SI* types were more pronounced and complex.

The results of this investigation have brought out the diversity of the evolutionary mechanisms operating within a sub species, *Brassica campestris* var. *brown sarson*. It has also revealed that a change in the breeding structure within a population could bring about a substantial change in the character associations and the pattern of distribution of genetic variability without any concomitant geographical diversity, as pointed out by Sewall Wright (1940) that departures from panmixia would change the evolutionary processes in the selective values of genes. Moreover, a closed population due

SUMMARY

Canonical analysis of the evolutionary forces for sub-specific differentiation in *Brassica campestris* var. brown sarson confirmed by D^2 -statistic revealed distinctly different forces. The rapid evolution accompanying a change in breeding system was found to be responsible for the distinctly different genetic architecture in self-compatible and self-incompatible types.

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