

GENETICS OF GLUCOSINOLATE IN OILSEED RAPE (*BRASSICA NAPUS*)

S. K. GUPTA,* K. S. LABANA AND K. L. AHUJA

Department of Plant Breeding
Punjab Agricultural University
Ludhiana 141004

(Received: June 10, 1988; accepted: January 9, 1989)

ABSTRACT

A diallel set of 8×8 crosses among low, intermediate and high glucosinolate parents was made. The results of this study suggested that, both general and specific combining abilities (gca, sca) are important in the expression of this trait. Both gca and sca components of variance are significant. However, the magnitude of nonadditive component was higher than that of the additive component for glucosinolate content. Heterosis or population improvement programme can be undertaken to evolve low glucosinolate cultivars.

Key words: *Brassica napus*, glucosinolates, combining ability.

Plant breeding in rapeseed mustard is today strongly directed towards improved oil and meal quality. Although the rapeseed meal contains about 40% protein (dry matter basis) with a balance amino acid composition [1], yet its meal cannot be used to its full value because of glucosinolate. It yields some toxic products which create a pungent taste, thereby reducing the palatability of feed [2, 3].

Several techniques have been proposed from time to time for removing glucosinolate. However, in general, most of the methods so far tried are expensive and cause loss of proteins and deterioration of protein quality, or both. This situation has prompted plant breeders in India to study the possibility of reducing glucosinolate content of Indian varieties to an innocuous level by plant breeding methods. Therefore, in the present study, an attempt has been made to know the gene action and combining ability for glucosinolate content in *Brassica napus*. Information derived from this study will be utilized for the development of low glucosinolate varieties.

MATERIALS AND METHODS

Material for the present study comprised eight genetically diverse parents, crossed in an 8×8 diallel set excluding reciprocals. The parents and hybrids were grown in randomized complete block design with three replications. Glucosinolate content was estimated in the seed by the method of Brezezinski and Mendelewski [4]. Combining ability analysis was done following Method 2, Model 1 of Griffing [5].

*Present address: Department of Plant Breeding, H. P. Krishi Vishvavidyalaya, Palampur 176062.

RESULTS AND DISCUSSION

Analysis of variance for combining ability indicated both *gca* and *sca* to be highly significant (Table 1). Thus, both additive and nonadditive gene effects are important in governing the inheritance of this trait. The magnitude of nonadditive genetic component was much greater than the additive component of variance. Thus, to breed for low glucosinolate, which is desirable, heterosis or population breeding can be followed. Further, to exploit the nonadditive gene effects some kind of heterozygosity has to be maintained. The parents Ashai, Christa and Topa are the desirable general combiners for low glucosinolate content (Table 2).

Table 1. Analysis of variance for combining ability

Source	d.f.	M.S.
<i>gca</i>	7	254.46**
<i>sca</i>	28	81.74**
Error	35	5.46
$1/7 \sum_i g_i^2$		24.90
$1/28 \sum_{ij} s_{ij}^2$		76.28

**Significant at 1% level.

The crosses showing desirable *sca* effects are Ashai × Christa, Ashai × Topa, Christa × Bronowski, Christa × Lores, Christa × Topa, Christa × POL-6, GSL-1 × ISN-129, GSL-1 × Topa, GSL-1 × POL-6, Bronowski × Topa, Bronowski × POL-6, Lores × ISN-129, Lores × Topa, Lores × POL-6, and ISN-129 × Topa. These specific crosses can be utilized in building up the gene pools/populations with low glucosinolates. Further, these gene pools will be used for the development of low glucosinolate varieties.

Table 2. Estimates of *gca* (diagonal in bold) and *sca* effects

Varieties	Ashai	Christa	GSL-1	Bronowski	Lores	ISN-129	Topa	POL-6
Ashai	-1.69	-6.13	4.75	13.31	25.65	-0.13	-6.89	4.81
Christa		-3.85	17.92	-10.12	-9.30	1.59	-13.26	-6.33
GSL-1			4.61	18.74	8.18	-12.11	-20.69	-5.03
Bronowski				3.13	20.63	3.97	-17.14	-4.11
Lores					4.08	-6.13	-5.47	-12.73
ISN-129						0.48	0.86	22.47
Topa							-6.98	39.55
POL-6								0.21

SE (S_i) = 1.843; SE ($S_{ij} - S_{ik}$) = 3.13; and SE ($S_{ij} - S_{kl}$) = 2.92.

ACKNOWLEDGEMENTS

The first author is thankful to the ICAR for the financial assistance. Thanks are also due to Dr. S. S. Banga for providing research material and to Dr. D. R. Satija for help in statistical analysis.

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