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## An approach to population improvement in self-incompatible turnip-rape

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### ABSTRACT

A total of 233 single plant selections were made from diverse sources of self-incompatible brown-seeded turnip-rape [*Brassica rapa* (Linn.) Thell. emend. Metzger var. *napus* Linn. sensu stricto]. The progenies were tested for important attributes during 1978-79. Ten initial gene pools were constituted with the genotypes selected based on critical norm fixed for corresponding component character. An additional population was constituted with genotypes following beyond the critical mean for 5 out of 10 yield attributes. Intra-genepool selective mating in each resulted in high-yielding populations, particularly in populations where the number of primary branches, plant biomass and single-plant yield were considered for improvement. The study stressed the importance of method of (A) selection of genotypes and (B) selective mating within population in bringing about an overall improvement of seed yield in brown-seeded turnip-rape.

Self-incompatibility poses a problem in the improvement of brown-seeded turnip-rape [*Brassica rapa* (Linn.) Thell. emend. Metzger var. *napus* Linn. sensu stricto]. Pure varieties are difficult to maintain because of inbreeding depression. In the absence of male-sterile lines, commercial exploitation of heterosis is not practicable. Alternatively composites or synthetics are expected to provide a viable approach for genetic upgradation of yield and other important attributes. In this direction, the early attempts were limited. The present study is based on an approach to population improvement in respect of method of selection of base material and selective mating within each population for different component characters.

### MATERIALS AND METHODS

The base material consisted of 233 single-plant progenies selected from diverse sources representing single-crosses, 3-way crosses, varieties and open-pollinated cultivars, based on their phenotypic perfor-

mance in 1977-78. These progenies were evaluated in 1978-79 in a randomized-block design with 2 replications, using plots of 2 rows, each of 3.0 m long, with a distance of 10 cm between plants and 60 cm between rows.

Observations were recorded on random samples of 5 plants in respect of plant height (PHT), number of primary branches (NPR), number of secondary branches (NSR), number of siliquae on primary branch (SPR), number of siliquae on secondary branch (SSR), number of seeds per siliqua (SPS), single-plant biomass in grams (TPY), Single-plant yield (EYD) and row yield (RYD). Harvest index (PHI) was computed for each plant as  $100 \times \text{EYD}/\text{TPY}$ .

As a critical norm of selection ( $M^*$ ), the mean of 233 plants ( $M$ ) grown in 1977-78 was worked out for each character. Individual plant values exceeding  $M$ , say  $n$ , were separated. The mean value of  $n$  provided the critical mean.

$$M^* = (\sum_{i=1}^n x_i)/n \text{ where } x_i = \text{the value}$$

of the character for plant  $i$ , which has a value greater than  $M$ .

The values of progeny means obtained in 1978-79 were scanned and those which

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exceeded  $M^*$  were marked. The corresponding parental seeds (which were reserved in 1977-78) were mixed in equal quantities to obtain an initial gene pool. Thus 10 gene pools were constituted, corresponding to the 10 characters. Each progeny was then scanned for each character mean exceeding the corresponding critical mean. The parental seeds of those progenies which exceeded the critical mean at least for 5 out of 10 characters (50% superiority) were mixed in equal quantities to constitute the 11th gene pool.

The 11 gene pools were raised in big plots (30 rows, each 3 m long) in 1979-80 and subjected to intrapopulation mating by selecting vigorous plants. The resulting composite populations were evaluated in the first phase in 1980-81 and in the second phase in 1981-82, in randomized-block design with 2 replications. A best selection, ('BIDI') and a national check ('Pusa Kalyani') were used as controls. Each plot consisted of 10 rows, each 3 m long, spaced 60 cm apart, with plants spaced at 10 cm within rows. The crop was irrigated.

## RESULTS

The means of 233 single-plant selections and the values of critical norm (Table 1) show clearly the genetic variation that existed in the base material. The variation was subdued for row yield and harvest index, as indicated also by the proportion of plants selected to form the initial gene pool. SPS, PHT and NPR contributed a large proportion of plants in constituting the initial gene pool, followed by SPR and SSR.

The populations generated by selection for NPR, SPR, SPS, TPY and EYD showed substantial improvement in seed yield, over the controls. Selection based on PHT, NSR, SSR, RYD and PHI did not record significant improvement (Table 2).

The differences in yield were significant between the 2 phases (Table 3), though all other sources were found insignificant. The yield of second-phase population was consistently lower because of the loss caused by hailstorm. Definite clues to the trends of improvement can

Table 1. Mean of 233 plant selections (M), critical norm ( $M^*$ ), number of plants constituting gene pool (n) and range of variation in turnip-rape

Character	n	n*	M	$M^*$	Range of variation in the constituted gene pool	
					Minimum	Maximum
PHT @	40	17.2	157.1	146.7	146.8	106.8
NPR	38	16.3	7.4	8.7	8.8	12.2
NSR	31	13.3	6.2	9.3	9.4	25.0
SPR	33	14.2	43.2	50.3	50.5	65.7
SSR	33	14.2	10.4	15.5	15.6	26.8
SPS	45	19.3	16.0	18.2	18.3	23.1
TPY	24	10.3	54.6	67.0	71.0	114.0
EYD	24	10.3	10.7	13.9	14.0	26.3
RYD	15	6.4	577.6	660.2	662.2	964.6
PHI	5	2.1	19.5	20.0	30.0	30.0
All characters	22	9.4	—	—	—	—

n\* = n expressed as a percentage of 233 plants;  
@ = dwarf plants desirable.

Table 2. Comparative yield performance of different constituted populations

Population	Seed yield (kg/ha)			Percentage increase over	
	I phase	II phase	Average	Best selections	'Pusa Kalyani'
PHT	1,516	903	1,209.5	—	—
NPR	1,721	1,278	1,499.5	21.8	13.6
NSR	1,612	1,028	1,320.0	7.2	0.1
SPR	1,734	1,167	1,450.5	17.9	9.9
SSR	1,584	972	1,278.0	3.9	—
SPS	1,666	1,236	1,451.0	17.9	10.0
TPY	1,885	1,180	1,532.5	24.5	16.2
EYD	1,749	1,097	1,432.0	16.4	8.6
RYD	1,653	958	1,305.5	6.0	—
PHI	1,380	833	1,106.5	—	—
All characters	1,680	750	1,215.0	—	—
'Pusa Kalyani' (National Check)	1,680	958	1,319.0	—	—
Best selection	1,544	917	1,230.5	—	—

Table 3. ANOVA of yield (kg/ha) of the populations over the 2 phases

Source	df	Mean squares
Population	12	61488
Composites (CP)	10	63187
Checks (CK)	1	54946
CP vs CK	1	51036
Years	1	4962540*
Population × year	12	11290
Error	24	45688

\*P = 0.05.

be obtained only by checking the yields of these populations in later phases.

#### DISCUSSION

The importance of population breeding in developing high-yielding varieties of different crops has been emphasized by Gardner (1961) and Lonquist (1967). The creation and maintenance of well-buffered and co-adapted genotypes were advocated as the most economic way of genetic upgradation of open-pollinated crops where production of hybrids on a large scale is not a viable practice (Allard, 1960).

Since self-incompatibility enforces cross-pollination, population breeding is a worthy approach in turnip-rape. The

superiority of this approach lays in selection of well-defined base material, its evaluation by progeny tests and constitution of gene pool from the parent material. The method resembles in a way that of recurrent selection schemes. The performance of the gene pool was improved by selective mating within the population that was found to be potent (Arunachalam and Katiyar, 1978; Arunachalam and Bandyopadhyay, 1979; Katiyar and Arunachalam, 1981). The population generated by selection for plant biomass was the best among the 11 populations (see also Campbell and Kondra, 1978; Thurling, 1974). The accumulation of desirable genes as a result of selection (Allard, 1960; Thomas *et al.*, 1972), appreciable amount of heterosis (Allard, 1960), strong correlation of some desirable attributes with yield (Campbell and Kondra, 1978; Thurling, 1974, in rapeseed), desirable gene recombinations and dissociation of linkage blocks (Murty, 1978; in turnip-rape; Miller and Rawlings, 1967; in cotton) and positive additive interactions (Marshall and Allard, 1974; in sorghum) were some reported factors relevant for the recorded improvement in these populations.

Our studies bring out some salient results of direct applied importance : (i)

superior populations can be generated by selecting for number of primary branches, single-plant yield, plant biomass, siliquae on the primary branches and seeds/siliqua; (ii) an approach dependent on a genetically diverse and well-defined base, selection of constituent plants of the gene pool on progeny test, recombination through selective mating within population appears to be a short-term viable strategy for toning up yield levels in the crop.

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