

## Genetic Architecture of Yield Components in Toria

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**Abstract:** Diallel analysis, carried out with six inbred lines of toria (*Brassica campestris* L. var. *Toria*), indicated the presence of both additive and non-additive genetic components with the latter being more important for length of main raceme and 1000-seed weight. The ratio  $(H_1/D)^{0.05}$  showed the presence of over-dominance for all the traits. Parents Sangam, TS-61, TH-68 and TC-113 possessed significant gca effects for two or more than two traits at a time and were considered as superior. Likewise, crosses, white flower x TH-68 and Sangam x Tobin attained significant sca effects for most of the component traits and adjudged superior.

**Key words:** Combining ability, toria, yield components.

Seed yield in toria (*Brassica campestris* L. var. *Toria*) is contributed by component traits like siliqua length, length of main raceme, siliquae on main raceme, seeds per siliqua and 1000-seed weight. The studies on genetic components controlling these attributes would help to know the genetic architecture of above traits, and also to identify good combining genotypes, which could finally be utilized in the development of synthetics in toria.

### Materials and Methods

Six inbred lines (White flower, Sangam, TS-61, Tobin, TH-68 and TC-113) were crossed in half diallelic fashion (excluding reciprocals). Fifteen  $F_1$ s, along with six parents, were grown in a randomized block design with three replications, each. Each of the  $F_1$  and parents were represented by a single row of 4.5 m length with row to row distance of 30 cm. The plant to plant distance of 14 cm was maintained for each genotype in all the replications.

The data were recorded on 5 randomly selected plants from  $F_1$ s and parents on yield attributing traits such as siliquae length, length of main raceme, siliquae on main raceme, seeds per siliqua and 1000-seed weight. The above data were subjected to diallel analysis as per methods proposed by Griffing (1956) method 2 and model 1 and Hayman (1954).

### Results and Discussion

The analysis of variance indicated that the genotypes were significantly different for the traits under study: The test of homogeneity of arrays gave significant values for all the traits. The regression coefficient test of covariance for these traits was significant against unity.

The mean squares were significant for general and specific combining ability with respect to all the traits except general combining ability for 1000-seed wt. These results indicated the importance of both additive

Table 1. Genetic components of yield traits in toria

Components/ ratios	Length of main raceme (cm)	Siliquae on main raceme	Siliqua length (cm)	Seeds per siliqua	1000-seed weight (g)
D	54.11* ±13.17	47.39* ±11.89	0.32* ±0.14	3.24* ±0.85	0.07 ±0.03
H <sub>1</sub>	185.87* ±33.34	1.21* ±30.05	1.21* ±0.37	11.10* ±2.17	0.25* ±0.07
H <sub>2</sub>	149.83* 29.87	156.76 ±28.85	1.04 ±0.33	9.28 ±1.94	0.19 ±0.07
h <sub>2</sub>	51.82 ±20.10	36.55 ±18.07	0.24 ±0.22	0.09 ±1.30	0.02 ±0.12
F	72.09 ±32.18	10.59 ±28.92	0.35 ±0.35	1.25 ±2.08	0.12 ±0.04
E	0.47 ±0.067	0.32 ±0.45	0.07 ±0.05	0.29 ±0.42	0.02 ±0.01
(H <sub>1</sub> /D) <sup>0.05</sup>	1.85	1.94	1.94	1.85	1.89
H <sub>2</sub> /4H <sub>1</sub>	0.20	0.22	0.22	0.21	0.19
(4DH <sub>1</sub> ) <sup>0.05</sup> +F	2.12	1.12	1.79	1.05	2.56
(4DH <sub>1</sub> ) <sup>0.05</sup> -F					
h <sup>2</sup> /H <sub>2</sub>	0.35	0.23	0.23	0.01	0.03
Heritability	0.19	0.43	0.14	0.42	2.68

\* Denotes significance at 5% level.

and non-additive genetic variance with the latter being more important for length of main raceme and 1000-seed wt. The additive gene effects were in preponderance for siliquae length, siliqua on main raceme and seeds per siliqua. Many workers have reported the importance of both additive and non-additive gene effects in the inheritance of component traits (Pal and Singh, 1980; Singh and Yadav, 1980).

The components of genetic effects along with derived genetic ratios for different traits (Table 1) indicated that estimates of D (additive genetic components) and H<sub>1</sub> (dominance component) were significant for

all the traits. However, the magnitude of H<sub>1</sub> was higher than D for all the traits which was further confirmed when (H<sub>1</sub>/D)<sup>0.05</sup>, which measured the mean degree of dominance, fell in the range of over-dominance. The estimates of quantitative proportions of dominant and recessive genes among the parents measured by (4DH<sub>1</sub>)<sup>0.05</sup> +F/(4DH<sub>1</sub>)<sup>0.05</sup> -F showed that for every one recessive gene there were one to three dominant genes. However, the number of genes differentiating the parents (h<sup>2</sup>/H<sub>2</sub>) were very low perhaps because the genes with positive and negative effects were not uniformly distributed. The ratio H<sub>2</sub>/4H<sub>1</sub>, which measures the symmetrical

Table 2. Estimation of general combining ability effects for yield traits of toria

Parents	Length of main raceme (cm)	Siliquae on main raceme	Siliqua length (cm)	Seeds per siliqua	1000-seed weight (g)
White flower	-0.458	-0.616*	-0.177	-0.719*	-0.120
Sangam	1.829*	3.647*	-0.063	0.884*	-0.053
TS-61	1.829*	4.213*	-0.034	-0.260	0.063
Tobin	-3.327*	-2.681*	0.141	0.510	0.063
TH-68	-1.787*	-3.650*	0.319*	0.899*	0.041
TC-113	1.974	1.088*	0.186	-1.318*	0.006
S.E.(d)	0.527	0.436	0.206	0.416	0.112

\* Denotes significance at 5% level.

distribution of positive and negative alleles and theoretically should be equivalent to 0.25, indicated limited deviation in values for all the traits. The heritability (n.s.) was moderate to high for various traits.

The perusal of data presented in Table 2 indicated that parents Sangam (length of main raceme, siliquae on main raceme, seeds per siliqua), TS-61 (length of main raceme, siliqua on main raceme), TH-68 (siliqua length, seed per siliqua) and TC-113 (length of main raceme, siliqua on main raceme) possessed significant gca effects for at least two traits. Likewise, the crosses White flower x TS-61 (length of main raceme, siliquae on main raceme), White flower x TH-68, Sangam x Tobin (length of main raceme, siliquae on main raceme, seeds per siliqua), TS-61 x Sangam, Tobin x TC-113 and TH-68 x TC-113, (length of main raceme, siliquae on main raceme) attained significant sca effects for two or more than two traits. The high specific combining ability effects of all the above crosses were observed to be resultant of at least one good combining parent.

The results indicated the importance of both additive and non-additive gene effects

for all the traits. The high estimates of mean degree of dominance for all the traits and number of gene differentiating parents indicated strong allelic interactions. This suggested the presence of relatively high non-additive gene effects, coupled with significant additive gene effects, in the present experimental population for most of the traits. It would, therefore, be worthwhile to channelize the available material into two-pronged line of work, viz., the genetic upgrading of this material by a suitable breeding procedure which might exploit the observed kind of gene action and secondly, to utilize the outstanding inbreds, such as Sangam, TS-61, TH-68 and TC-113 for evolving synthetics. Besides, base population with new recombinations can also be developed, if cross combinations indicated above, exhibiting significant sca effects for various traits, are composited and allowed to intermate for few generations to ensure adequate recombinations.

## References

- Griffing, B. 1956. Concept of general and specific combining ability in relation to diallel crossing system. *Australian Journal of Biological Sciences* 9: 463-493.

- Hayman, B.I. 1954. The theory and analysis of diallel crossed. *Genetics* 39: 336-356.
- Pal, R. and Singh, H. 1980. Combining ability in rapeseed. *Indian Journal of Agriculture Sciences* 50: 9-13.
- Singh, H. and Yadav, C.K. 1980. Gene action and combining ability for seed yield, flowering and maturity in rapeseed. *Indian Journal of Agriculture Sciences* 50: 655-658.