ABSTRACT

The experiment was conducted, at the Research Farm of Tirhut College of Agriculture, Dholi, Muzaffarpur, Bihar, During Rabi 2006-07, evaluating fifty genotypes of toria in R.B.D. design with three replications. Fourteen characters were included in the investigation, to estimate genetic variability, character association, direct and indirect effect on seed yield and genetic divergence for earliness and other yield attributes in toria (Brassica rapa L. var. Toria).

Analysis of variance revealed considerable variability among 50 toria genotypes for all the fourteen characters under study. For all the characters, PCV was higher than GCV. Secondary branches per plant and leaf area index reflected high estimates of GCV and PCV. High estimates of broad sense heritability coupled with high genetic advance as per cent of mean were observed for secondary branches per plant, leaf area index, and specific leaf weight, reflecting greater contribution of genetic component.

Seed yield per plant exhibited positive significant association with total siliqua per plant, harvest index, primary branches per plant, leaf area index, secondary branches per plant and thousand seed weight, while reflected negative significant association with specific leaf weight. Days to 1st flower open (DFFO), days to cessation of flower (DCF) and days to maturity (DM) were positively correlated with each other. Harvest index, thousand seed weight, total siliqua per
plant, and secondary branches per plant exhibited high positive direct effect on seed yield.

$D^2$ statistic using Tocher’s method formed clusters which were reduced to eight by Euclidian cluster analysis and accommodated single genotype clusters in only two Euclidean clusters namely, cluster G (RAUDT-78, RAUDT-17, RAUDT-72 and RAUDT-71) and cluster H (RAUDT-52, RAUDT-67 and RAUDT-15).

Three principal components (PF1, PF2 and PF3) in canonical (vector) analysis explained 58.1% variability with highest element value of secondary branches per plant in $Z_1$, harvest index in $Z_2$ and specific weight in $Z_3$. These three characters also contributed maximum in Tocher’s method cumulatively contributing 68.73% towards total divergence.

Maximum inter cluster distance based on Tocher’s method and Euclidean cluster analysis was found between cluster II & XII, cluster A & H followed by cluster II and XI, cluster D & H, cluster V & XII, Cluster B & H and C & H, respectively.

On the basis of $D^2$ statistic following Tocher’s method and Non-hierarchical Euclidean cluster (Wards minimum Variance Dendrogram) analysis, RAUDT-15, RAUDT-67, RAUDT-55, RAUDT-7, RAUDT-62, DC 9401 and RAUDT-51 were useful parents for yield, earliness and component traits, amongst which the first two genotypes RAUDT-15 and RAUDT-67 with significant superiority in yield, earliness and component traits and RAUDT-78 with high yield and bold seeds may be evaluated in preliminary yield evaluation trial. RAUDT-19 and RAUDT-55 for earliness in DFFO and DM and RAUDT-62 for earliness in maturity have been identified as useful parents for earliness. Eight crosses, involving diverse parents namely, RAUDT-62 x RAUDT-15; RAUDT 62 x RAUDT-67; RAUDT-7 x RAUDT15; RAUDT-7 x RAUDT-67; RAUDT-55 x RAUDT-67; RAUDT-55 x RAUDT-15; DC 9401 x RAUDT-15; and RAUDT-51 x RAUDT-15 could be utilized for exploitation of heterosis and selection of segregants from transgressive breeding programme to develop early, high yielding toria genotypes.

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