

Genetic variation and association studies in segregating population of rice (*Oryza sativa* L.)

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Genetic variability in a crop is the basic requirement for its further genetic improvement. Release of variability in segregating generations and its assessment is an important aspect in any crop improvement programme. The knowledge of association among the yield and yield contributing characters are very essential for improving the efficacy of selection. In most of the cases quantum of variability and correlations are studied by evaluating the homozygous cultivars but inferences derived become more meaningful only when study is based on individual plant observations in segregating generations (Birader *et al.*, 1991), Therefore, the present study was undertaken with the objectives to obtain estimates of different genetic parameters and correlations in F_2 of rice crosses.

The F_2 population along with its two diverse parents viz., PKV HMT and Shyamla were grown at Zonal Agricultural Research Station, Sindewahi, Distt. Chandrapur (Dr.Panjabrao Deshmukh Krishi Vidyapeeth, Akola, (M.S.)) in randomized block design with three replications during *Kharif*, 2007. Data for grain yield plant⁻¹, panicle length, no. of branches panicle⁻¹, no. of grains panicle⁻¹, biological yield plant⁻¹(g), panicle weight, no. of effective tillers⁻¹, plant⁻¹ plant height (cm) and harvest index were recorded on one hundred and fifty plants selected randomly from each population.

The phenotypic and genotypic coefficients of variations were worked out as per procedure given by Burton (1952) Heritability in broad sense and genetic advance as percentages of mean was calculated by the method adopted by Johnson *et al.* (1955). The correlation coefficients at genotypic levels were calculated according to the procedure given by Miller *et al.* (1958).

Significant differences were found in parents as well as in F_2 populations for grain yield and for different

attributing traits, indicating the presence of genotypic variation. The data presented in Table 1 revealed that grains/panicle⁻¹ had maximum variance followed by panicle weight and biological yield indicated the higher influences of environments on expression of these characters. The results are in agreement with the findings of Maurya (1976). In F_2 population high heritability coupled with high genetic advances were observed for grain yield panicle⁻¹ and biological yield indicated the major contribution of additive genetic variations in the character expression. However, tillers plant⁻¹, panicle length, plant height and harvest index exhibited medium to low estimates of heritability coupled with medium to low genetic advance. This has indicated the contribution of non additive genetic variations in the expression of these characters.

The estimates of genotypic correlation coefficients in all possible combinations among grain yield and its components for the parental as well as in F_2 populations are given in Table 1 in parental population of PKV HMT the grain yield was positively correlated with biological yield, plant height, harvest index and tillers plant⁻¹. Panicle length showed positive relationship with grains panicle⁻¹, panicle weight, biological yield and plant height. Branches panicle⁻¹ had positive association with panicle weight. Biological yield showed positive correlation with plant height while panicle weight was positively correlated with harvest index. In parental population of Shyamala grain yield was positively associated with biological yield, tillers plant⁻¹ and harvest index. Panicle length had positive correlation with branches panicle⁻¹ and grains panicle⁻¹. Branches panicle⁻¹ was positively associated with grains panicle⁻¹ and panicle weight. Biological yield had positive correlation with tillers plant⁻¹ whereas tillers plant⁻¹ had negative correlation with panicle weight.

Correlation estimates in the F_2 population revealed that grain yield was positively associated with the biological yield plant⁻¹ and panicle weight. Panicle length exhibited positive association with branches panicle⁻¹ and plant height. Branches panicle⁻¹ had positive correlation with grains panicle⁻¹. Biological yield plant⁻¹ and grains panicle⁻¹ were positively associated with the panicle

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