

Assessing Relationship between Heterosis and QTL Linked Molecular Divergence and Identification of Heterotic Trait Loci for Yield and Component Traits in Rice (*Oryza Sativa* L.)

Sheel Yadav¹, Ashutosh Singh² and K.K. Vinod²

¹Division of Genomic Resources, National Bureau of Plant Genetic Resources, New Delhi 110012, India.

²Division of Genetics, Indian Agricultural Research Institute, New Delhi 110 012, India.

E-mail: ¹sheel.y85@gmail.com

Abstract—Identification of heterotic pools in rice germplasm would help in selection of parental materials for future hybrid breeding programs. Unlike in the case of maize, conventional techniques to identify heterotic pools have not been promising in rice. Identification of genetic diversity based on random molecular markers, has also not yielded significant breakthrough. We have used 49 microsatellite (SSR) markers linked to QTLs for yield and component traits, reported in earlier studies, to estimate the genetic diversity and relate the genetic distance to heterotic performance of the hybrids between 22 parental lines including two CMS lines i.e. Pusa 6A and IR58025A and 20 restorer lines. All the restorer parents were confirmed to carry the fertility restorer (Rf) gene, using a linked marker, RM6100. As far as we know, attempts to use trait linked SSRs to assess their refining ability to identify heterotic pools in rice is very limited. Three estimates of hybrid performance i.e., relative heterosis, heterobeltiosis and standard heterosis were computed. The mean phenotypic and genotypic diversity of 2.87 and 0.37 respectively, showed sufficient variation among parents. However, both the distance measures (phenotypic and genetic) failed to strike a relation with heterotic performance. The use of these markers led to the identification of quite a few number of markers linked to target traits by single point analysis (RM253, RM273, RM303 & RM 252 for plant height; RM159, RM30, RM472 & RM289 for number of tillers; RM2634, RM5 & RM263 for panicle length; RM202 for filled grains/panicle; RM5 for 1000 seed weight and RM 253 for grain yield/plant). The study reveals that heterosis is a complex function of genomic loci that are interdependent to trait expressing genes, but are independent of the genes themselves.