

Assessment of genetic variability in recombinant inbred lines of rice (*Oryza sativa* L.) using phenotypic traits and molecular markers

Soumya Mohanty, J. Kumar, N. Mohanty, G. Gouda, S.K. Pradhan, S.K. Dash and L. Behera

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ABSTRACT: Evaluation of genetic variability of recombinant inbred lines (RILs) was done at phenotypic and molecular levels. The RILs have been developed by single seed descent method from a cross between high yielding *indica* and low yielding NERICA rice cultivars. The coefficient of phenotypic of variations for all the 14 yield and yield component traits were found significant. The highest estimate of PCV and GCV were observed for grain yield per plant. High heritability along with high genetic advance as per cent of mean was recorded for plant height, grain number and secondary branching indicated that the less influence of environmental effect on the inheritance of these traits. Principal component analysis was further used to establish the patterns and interrelationships existing between the RILs. The first four principal components explained 71.28% of the total variability in all the 14 traits. The 24 SSR markers were used to assess genetic diversity at molecular level between RILs. All the 190 RILs could be differentiated and grouped into three major clusters, indicating that these RILs are suitable for mapping of QTLs for yield traits.

Key Words : Rice (*Oryza sativa*), genetic variability, recombinant inbred lines (RILs), QTLs, phenotypic traits, molecular marker technology, simple sequence repeats.