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Variability studies in hybrid rice (Oryza sativa L.) across locations

P.V. Padmavathi, P.V. Satyanarayana and Lal Ahamed M Acharya N.G. Ranga Agricultural University, Bapatla, India

Rice is a staple food crop in India, providing 43% of calorie requirement for more than 70% of Indian population. Assessment of genetic variability present in any crop species is an essential prerequisite for formulating an effective breeding programme. Effective selection not only depends on estimation of genetic variation among the genotypes but also on the proportion of heritable variation and the expected genetic gain that would be obtained. Four wild abortive source CMS lines were crossed with thirteen restorers in line x tester design to obtain 52 hybrids at Maruteru, Andhra Pradesh during kharif, 2010. These 52 hybrids along with their parents and three checks (viz., MTUHR 2089-hybrid check, MTU 1075 and MTU 1010-varietal checks) were evaluated in a randomized block design with two replications and a spacing of 20 x15 cm at four different agroclimatic zones of Andhra Pradesh viz., Maruteru, Warangal, Jagtial and Ragolu locations to estimate the genetic variability parameters for yield and yield contributing characters. Pooled analysis of variation revealed significant difference for genotypes and locations for all the characters. The estimates of phenotypic coefficient of variation (PCV) were slightly higher than those of genotypic coefficient of variation (GCV). High PCV and GCV were observed for no. of filled grains panicle⁻¹ and grain yield plant⁻¹. High estimates of heritability coupled with high genetic advance as per cent of mean was observed for characters viz., number of filled grains panicle⁻¹, test weight and grain yield plant⁻¹ indicating preponderance of additive gene action which could be exploited through simple selection methods.

Biography

P.V. Padmavathi, completed my M.Sc (Ag) in the Dept. of Genetics and Plant Breeding, Agricultural College, Bapatla of Acharya N.G. Ranga Agricultural University and doing Ph.D in the same Department of the same university.

padmaphd05@gmail.com