

## Molecular dissection of drought related QTLs in rice using microsatellite markers

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A double haploid mapping population consisting of 75 lines of a cross between the irrigated *indica* variety IR64 and the upland *japonica* variety Azucena (Guiderdoni *et al.*, 1992) was used in the present experiment. The complete set of double haploid lines along with parents was evaluated for molecular mapping. A set of 264 microsatellite markers was used for parental polymorphism screening of which 60 markers were found polymorphic. Thirty-one of these markers were associated with QTLs of different traits and are distributed on eight different rice chromosomes. These markers can be successfully used to transfer some of the QTLs into different genetic backgrounds.

Key words : QTLs, Rice, Drought.

### INTRODUCTION

Drought is a major abiotic stress, which limits plant growth and productivity, and is a major cause of yield instability. In the rainfed lowland ecosystem of eastern India, drought stress has been identified as the foremost constraint to higher yield. Future increase in production area will come mostly from rainfed lowlands. These areas may experience frequent (intermittent) and severe (prolonged) water deficits at any time during the rice growing cycle. Hard pans in the soil can block root growth and impede water extraction in rainfed low land areas and even in irrigated fields.

However, most measures of agricultural productivity, such as size, shape, yield and quality are influenced by many genes (polygenes), so that traits in a population do not fall into discrete classes, but show a continuous range of phenotypes. Quantitative variation in phenotype can be explained by the combined action of many discrete genetic factors, each having a rather small effect on the overall phenotype, and the influence of environments. As a result, breeding for quantitative traits tends to be a less efficient and time-consuming process. These genes cannot be studied individually using the methods of classical Mendelian genetics because their effects are lost in the statistical fog of all other background variation. Recently QTL mapping studies in rice revealed two important results on the genetic basis of quantitatively inherited traits. First, identification of few QTLs each having relatively large phenotypic effect and second, the complex

phenotype tend to show greater QTL X E interaction, which makes marker-aided selection (MAS) for QTL to genetic improvement of complex trait difficult. By knowing above fact, the study was under taken to identify polymorphic microsatellite markers for indirect selection.

### MATERIALS AND METHODS

The present study was conducted at the Department of Biotechnology, Indira Gandhi Agricultural University, Raipur (C.G.) during 2003-2004, with the main objective of Molecular dissection of drought related QTLs in rice using microsatellite markers

A population of 75 Double Haploid (DH) lines derived from a cross between the irrigated *indica* variety IR64 and the upland *japonica* variety Azucena (Guiderdoni *et al.* 1992) developed at IRRI, was used in the present investigation. IR64 is high yielding improved semidwarf *indica* rice variety suitable for irrigated habitats, Azucena is a more drought tolerant *japonica* rice variety.

*Development of molecular marker system for indirect selection :*

*Genomic DNA extraction :*

In order to extract the total genomic DNA, the seedlings were grown in glass house for six weeks. Leaves of 6-weeks-old plants were collected. DNA was extracted by the method as described by Dellaporta *et al.* (1983) with slight modifications.

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