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Mapping of quantitative traits LOCIS (QTLs) for plant height in rice

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Abstract

A double haploid mapping population consisting of 75 lines of a cross between the irrigated *indica* variety IR64 and the upland *japonica* variety Azucena was used in the present experiment. The complete set of double haploid lines along with parents was evaluated under two sets of conditions, 1. Transplanted with water stress and 2. Transplanted with no stress over two years. Water stress was imposed at flowering and observations were recorded for plant height traits. A total of five putative QTLs for plant height were detected, which were found to be explaining a minimum of 10.4 per cent to maximum of 17.8 per cent of phenotypic variation, individually. These QTLs were mapped on the rice genome and linked DNA markers have been validated for use in the marker assisted breeding program.

Keywords: Rice, drought, QTL mapping

Introduction

Drought is a major abiotic stress, which limits plant growth and productivity, and is a major cause of yield instability. 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. Considering this aspect in view, a study of identification and molecular mapping of QTLs for plant height in rice was undertaken.

Material and Methods

A population of 75 Double Haploid (DH) lines derived from a cross between the irrigated *indica* variety IR64 and the upland *japonica* variety Azucena^[5] developed at IRRI, was used in the present investigation. IR64 is high yielding improved semidwarf *indica* rice variety suitable for irrigated habitats, were as Azucena is a more drought tolerant *japonica* rice variety. A population of 75 Double Haploid (DH) lines were grown in randomized complete block design with two replications under two different environmental conditions *viz.*, 1. Transplanted with water stress (TD) and 2. Transplanted with irrigated conditions (TI). In both conditions, the seeds were sown in a bed and seedlings were transplanted to a paddy field 31 days later, with single plant⁻¹ hill spaced at 15 X 20 cm. Each plot included three lines with ten plants per line. All normal packages of practices were followed to raise a good crop. The drought condition was imposed by stopping irrigation at 50 per cent flowering stage. Observations were recorded on ten plants in each replication. Observations were recorded for plant height. The mean values over ten plants were considered for analysis. The mean data for two replications under transplanted with water stress, transplanted with irrigated condition were analyzed for QTLs identification. MAPMAKER / QTL 1.1 was used for interval mapping (Locating the QTLs between flanking molecular marker by maximum – likelihood estimation)^[3], and to estimate the percentage of the total phenotypic variance explained by each QTL. A threshold of LOD > 1.5 was used⁻¹ test to claim the presence of a QTL.

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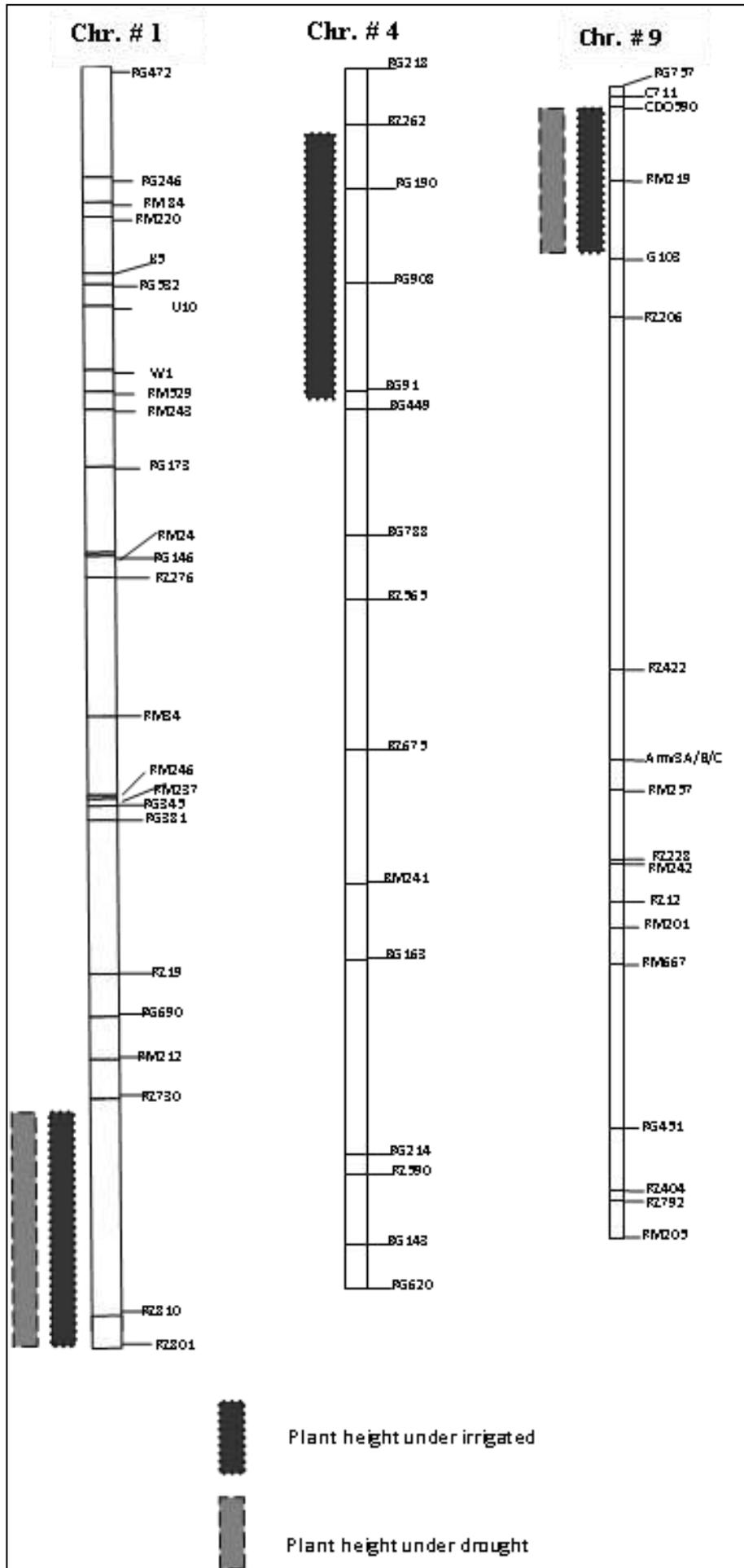


Fig 1: Putative QTLs for Plant Height

Results and Discussion

A summary of number of QTLs detected under different environmental condition and different season is presented in Table- 1. The identified QTL can be classified in two types, first type represent major gene that affect quantitative traits, which are detected with large LOD score (>10). The second types include most of QTL identified in rice, which have relative small effect. In this study, 5 QTLs were identified and had small phenotypic effect and LOD score of <10 this is expected as a different characters are under different genetic control and depend on its complexity along with variable level of QTL X E interaction. This is in agreement with the [1] who reported that more than 80 per cent of loci identified in rice are of this type.

Under transplanted with irrigated condition, three QTLs were detected. One QTL was detected on chromosome number 1 with LOD score of 2.4 between marker RZ730 - RZ801 having positive additive effect and explained 17.8% of phenotypic variation. Another, QTL was identified on chromosome number 4 with LOD score of 2.7 between marker RZ262 - RG449 having negative additive effect, which explained 17.3% of phenotypic variation. Third QTL was identified on chromosome number 9 with LOD score of

1.9 between CDO590 - G103 markers having positive additive effect, and explained 13.8 % of phenotypic variation. Two QTLs were detected for this trait under transplanted with water stress on chromosome number 1 and 9 with LOD score 2.4 and 1.7. First QTL was detected on chromosome number 1 with LOD score of 2.4 between RZ730 - RZ801 markers having positive additive effect, explained 13.6 % of phenotypic variation. Second QTL was identified on chromosome number 9 with LOD score of 1.7 between CDO590 - G103 marker having positive additive effect, explained 10.4% of phenotypic variation. Number of QTLs identified in this study has been reported by other workers to be present on the same chromosome. e.g. [2] reported the QTLs on chromosome # 1 and 4 for plant height (Figure-1), this genomic segment is closely linked to the map position of *sd-1*, a major gene controlling semi-dwarfism [4]. The identification of QTLs at same position by different workers in different populations has significant implication and can be inferred as real. These QTLs, which are common, stable and if their relative contribution is also high can be the real candidate for MAS and even the map based cloning (Figure- 1).

Table 1: Putative QTLs detected using interval mopping for Plant Height

Character	Regions between DNA markers	Chr. #	Additive effect	per cent Variation explained	LOD
Irrigated	RZ730 - RZ801	1	0.9	17.8	2.4
	RZ262 - RG449	4	-6.4	17.3	2.7
	CDO590 - G103	9	7.8	13.8	1.9
Drought	RZ730 - RZ801	1	4.7	13.6	2.4
	CDO590 - G103	9	3.9	10.4	1.7

Conclusions

Apart from these QTLs numbers of other QTLs were also detected in the present study, which are not reported by the previous workers. The difference in location of QTLs for various traits may be because of different cross combination used in this analysis, as the detection of QTL is based on allelic differences between parental lines, different population size, statistical threshold for detecting putative loci, the number of markers used in the analysis [3].

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