ABSTRACT

Mapping Of Paranodulation Response QTL in Rice

Paranodules are the nodule like structures induced on roots of non-legumes. These can be induced by several methods, viz., treatment with auxins; hydrolytic enzymes etc. The paranodules thus induced can be colonized by nitrogen fixing bacteria by which non-legumes can also derive benefits of biological nitrogen fixation, like legumes.

Paranodulation response in rice was found to exhibit high degree of genetic variation behaving as a heritable trait. Since, the phenotyping for the paranodulation response is tedious and time consuming; there is a need for developing molecular markers for the trait useful in Marker Aided Selection (MAS) for better paranodulation response. Keeping this in mind, an attempt was made to map the QTL responsible for paranodulation trait.

Perpetuating mapping population of doubled haploid (DH) lines derived from anther culture of IR64 X Azucena was used as experimental material in the present investigation. A total of 121 DH lines were screened for paranodule induction response, by culturing the seedling roots in-vitro in Yoshida’s rice culture medium with 2, 4-D treatment. The phenotypic landscape was super-imposed on the already established SSR marker based genomic grid (269 SSR marker data, Susan Mc Couch, per. Comm.). Analysis with ‘MAPMAKER/QTL’ showed two major QTL responsible for paranodulation trait, both mapped to chromosome 9. \( pnodQ\)-1 being between the markers RM 219 and RM342b, with LOD score of 3.47 and responsible for 22.4% of variation. The other, \( pnodQ\)-2 located between RM342b and RM105, with LOD score of 4.72, responsible for 36.5 % of variation. Further analysis revealed that paranodulation trait is having recessive mode of inheritance. It was
confirmed with high LOD score when recessive model was forced. When both the QTL were considered in one model to know the type of interaction between them, the log likelihood of the two QTL map was less than the sum of log likelihoods of individual QTL maps indicating the epistatic interaction between the two QTL.

This was supported by the earlier studies. In them, it was found that paranodulation is governed by two interacting loci. At individual locus, the dominant allele results in low paranodulation, dominating over the high paranodulating phenotype that has recessive alleles. But, between the loci, there is digenic complementary interaction (duplicate recessive epistasis with 9 low: 7 high segregation ratio).

In the present study, three SSR markers were identified which are flanking the two QTL and in addition, another eight SSR markers which are mapped in this region of chromosome were also selected for validation experiment. Since the marker density was too less, additional 10 SSR primers were designed. Six primers from EST clones (which are related to root characteristics) and another three markers mapped in this region of genome, from RGP site were also chosen, so that final marker density comes to approximately 1 marker/cM.

All these 30 markers were surveyed on twelve upland rice genotypes, which were already characterized for paranodule induction response. Two groups, viz., high paranodulating and low paranodulating were made based on their induction response. Results revealed that, out of 30 primers surveyed, ten primers, viz., RM219, RM342b, RM105, RM316, RM444, RM464, AP005554, AP005811, AP006235 and AP006727 showed polymorphism between IR64 and Azucena, the parents of DH population. However, they could not differentiate the high paranodulating group from the low nodulating group, i.e., the association between banding patterns and high or low paranodulating phenotypes was not always consistent. Nevertheless, phenotype to marker agreement of 50 % and above was observed with only the markers RM105,
AP005811, AP006235, RM464 and AP005554. On chromosome 9 of rice these markers span a region about 29 cM, indicating the need of further high density fine mapping with additional markers in the region.