



Thesis Abstract

Characterization of the *Sub1* Locus Conferring Submergence Tolerance in the Rice (*Oryza sativa* L.) Variety 'Goda Heenati'

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Molecular markers for submergence tolerance would accelerate breeding progress by increasing selection efficiency. Resistance to submergence stress is an important breeding objective in areas where rice cultivars are subjected to complete inundation for a week or more. The characterization of *Sub1* genes would lead to a better understanding of the mechanism of rice submergence tolerance, and facilitate introduction of *Sub1* into susceptible rice cultivars through transformation. Goda Heenati, one of the few rice cultivars showing submergence tolerance, has been reported to possess a major gene different from *Sub1*, the locus controlling tolerance in FR13A and other tolerant cultivars. To understand if the *Sub1* locus plays a role in controlling tolerance in Goda Heenati, an F₂ mapping population was derived from a cross of M-202 (a submergence susceptible *japonica*) and Goda Heenati (a submergence tolerant *indica* variety, was constructed through PCR based SSR markers. A total of 164 F₃ families were screened for submergence tolerance. The map was constructed using 85 microsatellite markers. Only 46 markers were available to construct a linkage map for the 12 chromosomes. This map had a total length of 753.6 cM with an average interval size of 16.4 cM. With the constructed SSR map, four markers were associated with quantitative trait loci for submergence tolerance at seedling stage in chromosome 9 with high LOD peaks 18.42, 14.89, 19.41 and 23.22 at marker loci Rm316, RM464, SSR1 and RM219, respectively. These loci could explain 62.8%, 40.6%, 83.7% and 84.3% of the phenotypic variation. The location of the QTLs was the same as that of AFLP211 and AFLP303, two AFLP (amplified fragment length polymorphism) markers cosegregating with *Sub1* in a high resolution linkage map established previously. Based on these results, it can be concluded that the major QTL identified for Goda Heenati was one of the alleles at the *Sub1* locus, and that *Sub1* is the major determinant of submergence tolerance in all rice cultivars with submergence tolerance identified so far. The sequence of candidate genes in Goda Heenati would probably give an idea of which gene sequences were associated with submergence tolerance. This would be useful information in determining the mechanism of action of the *Sub1* gene.