

Molecular mapping of genes conferring aluminum tolerance in rice (*Oryza sativa* L.)

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Abstract: Crop productivity on acid soil is restricted by multiple abiotic stress factors. Aluminum (Al) tolerance seems to be a key to productivity on soil with a pH below 5.0, but other factors such as Mn toxicity and the deficiency of P, Ca and Mg also play a role. The development of Al-tolerant genotypes of rice is an urgent necessity for improving crop productivity in developing countries. Inhibition of root growth is a primary and early symptom of Al toxicity. The present study was conducted to identify genetic factors controlling the aluminum tolerance of rice. Several parameters related to Al tolerance, most importantly the relative root growth under Al stress versus non-stress conditions, were scored in 188 F₃ selfed families from a cross between an Al-tolerant Vietnamese local variety, Chiembau, and an Al-susceptible improved variety, Omon269-65. The two varieties are both *Oryza sativa* ssp. *indica*, but showed a relatively high level of DNA polymorphism, permitting the assembly of an RFLP map consisting of 164 loci spanning 1,715.8 cM, and covering most of the rice genome. A total of nine different genomic regions on eight chromosomes have been implicated in the genetic control of root and shoot growth under aluminum stress. By far the greatest effects on aluminum tolerance were associated with the region near WG110 on chromosome 1. This region does not seem to correspond to most of the genes that have been mapped for aluminum tolerance in other species, nor do they correspond closely to one another. Most results, both from physiological studies and from molecular mapping studies, tend to suggest that aluminum tolerance is a complex multi-genic trait. The identification of DNA markers (such as WG110) that are diagnostic for aluminum tolerance in particular gene pools provides an important starting point for transferring and pyramiding genes that may contribute to the sustainable improvement of crop productivity in aluminum-rich soils. The isolation of genes responsible for aluminum tolerance is likely to be necessary to gain a comprehensive understanding of this complex trait.

Author Keywords: Abiotic stress tolerance; Molecular-marker; Quantitative trait locus (QTL); Restriction fragment length polymorphism (RFLP); Rice

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