Targeting the aluminum tolerance gene *Alt3* region in rye, using rice/rye micro-colinearity

Miftahudin[1, 2], T. Chikmawati[1, 2], K. Ross[3], G. J. Scoles[4] and J. P. Gustafson[1, 3]

(1) Department of Agronomy, University of Missouri–Columbia, Columbia, MO, 65211

(2) Department of Biology, Bogor Agricultural University, Bogor, 16144, Indonesia

(3) USDA–ARS, Plant Genetic Research Unit, University of Missouri–Columbia, Columbia, MO, 65211

(4) Department of Plant Sciences, University of Saskatchewan, 51 Campus Dr., Saskatoon, SK, S7N 5A8, Canada

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Abstract

Characterization and manipulation of aluminum (Al) tolerance genes offers a solution to Al toxicity problems in crop cultivation on acid soil, which composes approximately 40% of all arable land. By exploiting the rice (*Oryza sativa* L.)/rye (*Secale cereale* L.) syntenic relationship, the potential for map-based cloning of genes controlling Al tolerance in rye (the most Al-tolerant cereal) was explored. An attempt to clone an Al tolerance gene (*Alt3*) from rye was initiated by using DNA markers flanking the rye *Alt3* gene, from many cereals. Two rice-derived, PCR-based markers flanking the *Alt3* gene, B1 and B4, were used to screen 1,123 plants of a rye F_2 population segregating for *Alt3*. Fifteen recombinant plants were identified. Four additional RFLP markers developed from rice genes/putative genes, spanning 10 kb of a 160-kb rice BAC, were mapped to the *Alt3* region. Two rice markers flanked the *Alt3* locus at a distance of 0.05 cM, while two others co-segregated with it. The rice/rye micro-colinearity worked very well to delineate and map the *Alt3* gene region in rye. A rye fragment suspected to be part of the *Alt3* candidate gene was identified, but at this level, the rye/rice microsynteny relationship broke down. Because of sequence differences between rice and rye and the complexity of the rye sequence, we have been unable to clone a full-length candidate gene in rye. Further attempts to clone a full-length rye *Alt3* candidate gene will necessitate the creation of a rye large-insert library.