Mapping of genes controlling aluminum tolerance in rice: Comparison of different genetic backgrounds

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Abstract: Aluminum toxicity is the main factor limiting the productivity of crop plants in acid soils, particularly in the tropics and subtropics. In this study, a doubled-haploid population derived from the rice (Oryza sativa L.) breeding lines CT9993 and IR62266 was used to map genes controlling Al tolerance. A genetic linkage map consisting of 280 DNA markers (RFLP, AFLP and SSR) was constructed to determine the position and nature of quantitative trait loci (QTLs) affecting Al tolerance. Three characters - control root length (CRL), Al-stressed root length (SRL) and root length ratio (RR) - were evaluated for the DH lines and the parents at the seedling stage in nutrient solution. A total of 20 QTLs controlling root growth under Al stress and control conditions were detected and distributed over 10 of the 12 rice chromosomes, reflecting multigenic control of these traits. The two QTLs of largest effect, qALRR-1-1 and qALRR-8 for root length ratio (a measurement of Al tolerance) were localized on chromosomes 1 and 8, respectively. Three other QTLs in addition to qALRR-8 were apparently unique in the CT9993 x IR62266 mapping population, which may explain the high level of Al tolerance in CT9993. Comparative mapping identified a conserved genomic region on chromosome 1 associated with Al tolerance across three rice genetic backgrounds. This region provides an important starting point for isolating genes responsible for different mechanisms of aluminum tolerance and understanding the genetic nature of this trait in rice and other cereals.

Author Keywords: Abiotic stress; Aluminum toxicity; Oryza sativa L.; QTL mapping; Rice genetics

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