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Towards Cloning of *Pup1* — A Major Locus for Tolerance to P Deficiency

MATTHIAS WISSUWA

International Rice Research Institute (IRRI), Crop, Soil, and Water Sciences Division, The Philippines

Abstract

Phosphorus deficiency is a major abiotic stress limiting growth and productivity of rice in rainfed rice production areas throughout the world. It is associated with highly weathered, P fixing soils and low fertilizer use by resource-poor farmers. There is considerable genetic variation in rice with respect to its tolerance to P deficiency and ability to take up P from low-P soils. Developing cultivars with improved P-deficiency tolerance that would contribute to increased yield stability should therefore be feasible and molecular techniques may offer a more efficient way of obtaining this goal compared to traditional plant breeding methods. Previous studies have identified a major QTL for P uptake from a P deficient soil, *Pup1*. At present *Pup1* is thought to cosegregate with marker S10043 in a 0.8 cM interval defined by S13126 and S13752. The corresponding interval on the rice physical map spans 9 BACs, of which three have been fully sequenced at the time of writing. The availability of genome sequence data could facilitate efforts to clone the *Pup1* locus if potential target genes can be identified based on hypothesis on gene function. Physiological studies suggest that the *Pup1* gene is expressed in root tissue where it either leads to higher root growth per unit P (higher internal efficiency) or improves P uptake per unit root size (external efficiency). Available sequence data was screened for potential genes that would be related to internal or external efficiency. Several target genes were identified. The probability that any of those genes would be synonymous with *Pup1* is discussed based on additional evidence from physiological studies.

Keywords: Target genes, phosphorus deficient soil, rainfed rice production