

Category	: International Rice Research Conference
Select Theme	: Systems physiology
Keyword 1	: Root biology
Endorsement email	:
Keyword 2	: Nutrients (such as mineral uptake, translocation, and regulation)
Keyword 3	:
Title of Entry	: Use of a genome-wide association study to discover novel genes controlling root hair development in rice
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Select only one type of presentation	: 15 minute oral presentation
Abstract	: GWAS (Genome-wide Association Studies) are being used to find markers for important agricultural traits in number of species. We completed GWAS for many root traits in rice ( <i>Oryza sativa</i> ), using 335 lines from the Rice Diversity Panel 1 (RDP1) and 700,000 SNPs. These allowed us to identify potential loci involved in root architecture, anatomy, and morphology. Root hairs are subcellular outgrowths of root epidermal cells. Root hair length and density are important phenes for nutrient acquisition under limiting conditions, as well as being widely studied developmental processes in <i>Arabidopsis</i> . Here, we used GWAS to identify loci involved in the formation and elongation of root hairs across multiple rice subpopulations. In addition to identifying a priori candidates, we also identified many loci that have never been reported to have a relation to root hair growth or formation. One significant SNP was located in a 200kb region in the indica subpopulation that is introgressed from the aus subpopulation. This region, containing 21 genes, confers denser root hairs in genotypes with an aus-like haplotype in an indica background. Very few genes have been identified as playing a role in root hair development in grasses, which have different patterns of epidermal cell differentiation than <i>Arabidopsis</i> . Our results represent the first association study for root hair traits in rice, a trait that could prove to be valuable for breeding for nutrient acquisition, and provide new insight into the developmental patterning and growth of root hairs in rice; information which can be used by breeders for marker-assisted selection and by the research community to understand a basic developmental process.

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