

# Association Mapping of Root Hair Traits in Rice (*Oryza sativa*)

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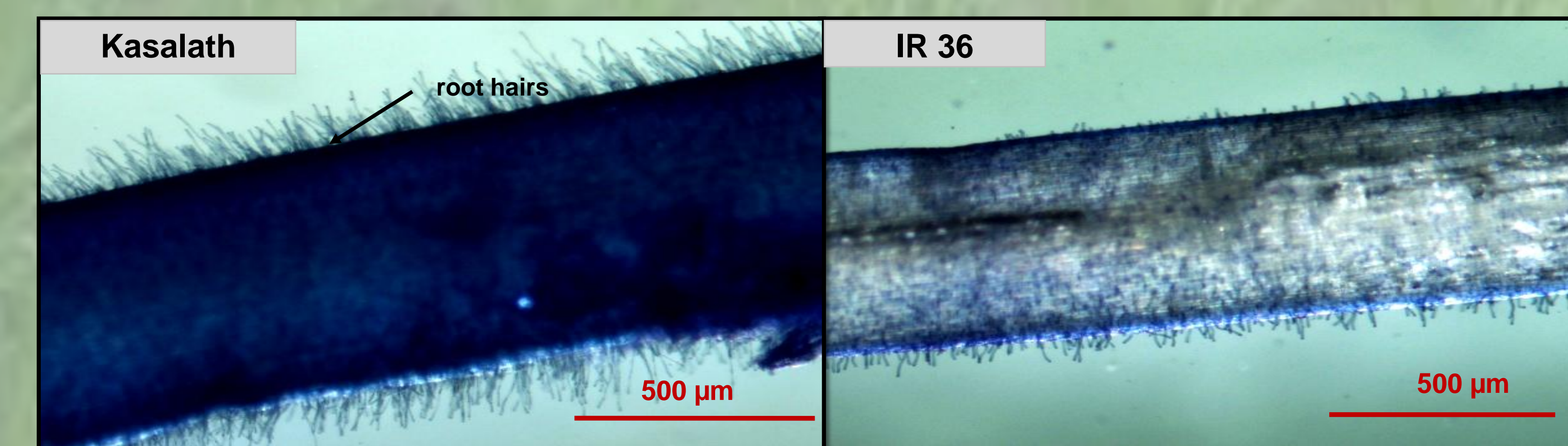
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## INTRODUCTION

Rice is the world's most important crop and a major food source for half of the world's population. Phosphorus deficiency is considered a primary limiting factor for rice production, especially in upland production systems [1]. Upland rice, primarily grown as a subsistence crop, is the dominant rice production system in Latin America and West Africa, where most of the soils are characterized by low phosphorus availability.

Most existing rice cultivars produce low yields in low phosphorus soils. Greater root hair length and density are predicted to confer better performance in low phosphorus soils by increasing the soil volume explored [2]. The overall goal of this study was to characterize the genetic control of root hair traits in rice (*Oryza sativa*).



**Fig 1.** Representative images of root hairs of rice cultivars Kasalath and IR36 showing genotypic difference in root hair length. Plants were grown under high phosphorus. Roots were sampled, stained with Toluidine Blue and root hairs were observed on nodal roots at 5 cm from the root apex.

## METHODOLOGY



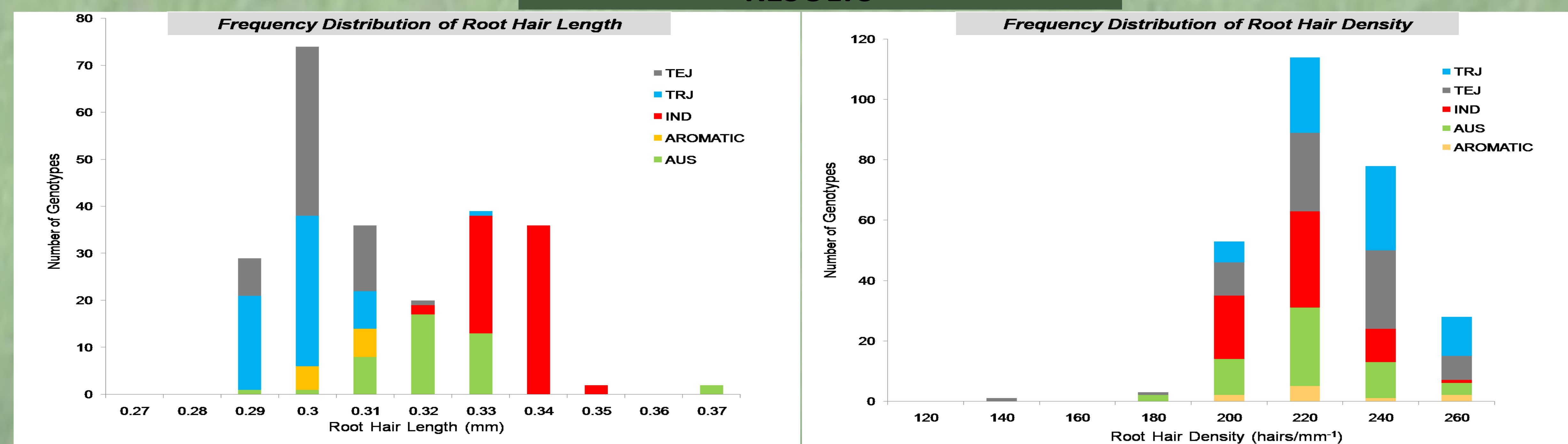
Greenhouse harvest, at 8<sup>th</sup> leaf stage.



❖ We evaluated a subset of 295 *O. sativa* accessions from the Association Mapping Panel, a collection of rice accessions from diverse geographical origins representing the phenotypic diversity of this species.

❖ Plants were grown in the greenhouse to the 8<sup>th</sup> leaf stage, and roots excavated for microscopic evaluation of root hair traits.

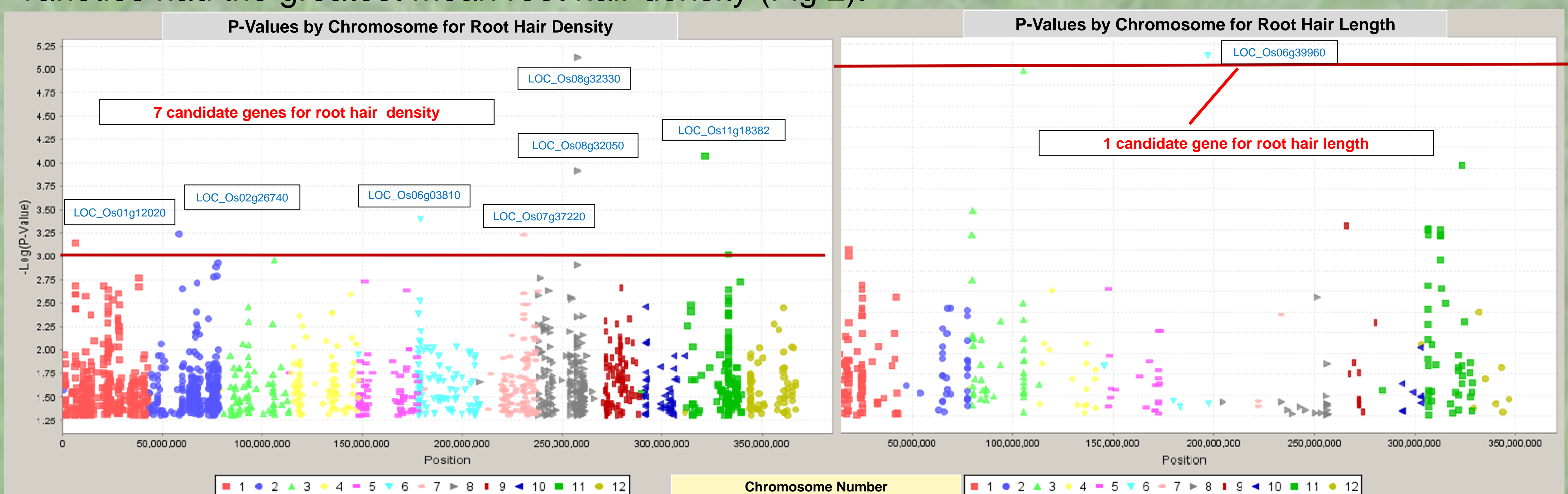
## RESULTS



**Fig 2.** Frequency distribution of root hair length and density across 295 accessions of *O. sativa* diversity panel.

Abbreviations: TEJ = *temperate japonica*; TRJ = *tropical japonica*; IND = *indica*; AROMATIC = *aromatic*; AUS = *aus*.

❖ Genotypic differences were found in root hair characteristics of rice genotypes from the *O. sativa* diversity panel. The *indica* varieties had the longest mean root hair length and the *tropical japonica* varieties had the greatest mean root hair density (Fig 2).



**Fig 3.** Genome-wide association study of root hair traits. *P*-Values are shown from the mixed linear model for root hair density (left) and root hair length (right). The X axis shows the SNPs on each chromosome, y axis is the  $-\log_{10}$  (*P*-Value) for the association. SNPs shown above the red lines are significant markers with *P*-Values < 0.001.

Gene ID	Chromosome	Gene Annotation
LOC_Os06g39960	6	bZIP transcription factor
LOC_Os01g12020	1	Protein precursor, Expressed protein
LOC_Os02g26740	2	Retrotransposon
LOC_Os06g03810	6	Expressed protein
LOC_Os07g37220	7	Inositol-1-monophosphatase, Expressed protein
LOC_Os08g32330	8	Expressed protein
LOC_Os08g32050	8	Retrotransposon
LOC_Os11g18382	11	Expressed protein

**Table 1.** Candidate genes for root hair length and density.

❖ From the preliminary association analysis, seven candidate genes were found on chromosomes 1, 2, 6, 7, 8, 11 for root hair density and one candidate gene was found on chromosome 6 for root hair length (Table 1).

❖ Phenotyping of the entire Association Mapping Panel will permit identification of molecular markers that control root hair traits important for agriculture.

## CONCLUSION

Development of genetic markers for selecting root hair traits in rice should facilitate breeding for improved performance in low-phosphorus soils.

## ACKNOWLEDGMENTS

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## REFERENCES

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