



## ***ABSTRACT***

*"Genome-wide association study at the cellular level reveals novel regulators of root development"*

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Development is ultimately regulated at the cellular level. The coordinated growth and development of cells underlie both form and function of tissues and eventually the whole organism. Assuming that assessing natural variation at the cell type level might facilitate the identification of novel developmental regulators using quantitative genetics, we set out to quantify the cellular architecture of the root in more than 200 natural accessions of *Arabidopsis thaliana* utilizing automated confocal microscopy. We found widespread natural variation of morphology at the cell-type level and used this variation to conduct genome wide association mapping. Using expression data to identify candidate genes in proximity of significantly associated genome regions, and subsequent characterization of T-DNA insertion lines for those genes, we identified two novel regulators of root development. While the F-Box family gene KUK is involved in coordinating meristem length and terminal cell size, another novel gene, which we designated AUT, encodes a small protein that regulates the width of the root vasculature. Our work not only uncovered two novel players in root development but also demonstrated the feasibility of GWA at the cellular level to identify causal genes for basic biological processes such as development.