

## Deciphering gene regulatory networks controlling root xylem plasticity under drought

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### Abstract

Increased resilience of rice to drought is increasingly needed in rainfed ecosystems and for intermittent wet-dry cultivation. Rice like other cereals responds to drought by promoting deep roots and limiting shallow roots to enhance access to moisture. We are studying the plasticity of xylem development, particularly xylem strand number and diameter, as well as lignification. Plasticity in these traits may be an adaptive strategy for tuning water hydraulics or use efficiency under drought. To address this at the systems level, we profiled ribosome-associated mRNAs (TRAP-seq) and chromatin accessibility (ATAC-seq) within the quiescent center (QC) and meristematic xylem cell population, as defined by the domain of expression of the *QHB/WOX5* promoter (*pQHB*) [1]. This was performed with root systems of plants cultivated under well-water (WW) and moderate water deficit (WD) conditions. In addition to identifying differentially regulated mRNAs, we identified hierarchical gene regulatory networks to predict players of root xylem plasticity under drought [1]. We are validating this network using CRISPR-Cas9 system and defining the downstream targets of these regulators. To gain insight into the root xylem plasticity under drought, we tracked xylem development and lignification in deep and shallow roots using *pQHB:GUS-GFP* lines under WW, WD, and recovery (WDR) conditions. Changes occur in metaxylem strands and lignin deposition in xylem cell walls under WD and WDR. We aim to resolve and manipulate transcription factor-target relationships that orchestrate beneficial xylem plasticity under water extremes. [1] Reynoso et al. (2022) Dev. Cell. 10.1016/j.devcel.2022.04.013. Funded by US NSF IOS-211980.