

Enhanced Resolution of Plasticity to Environmental Stimuli in Meristems and Individual Root Cell Types of Rice



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Abstract

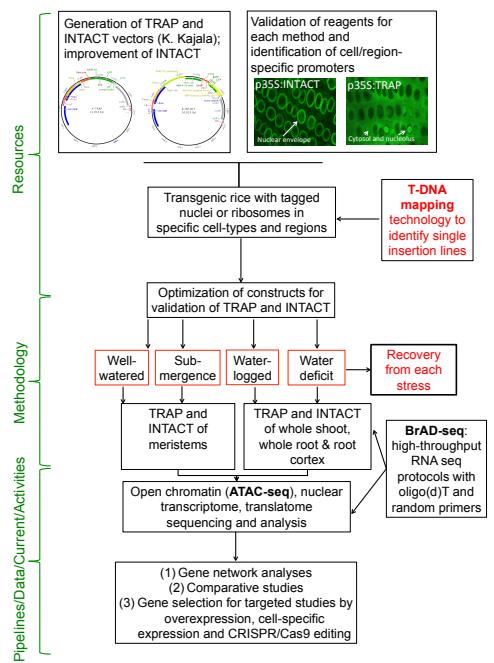
Too little and too much water due to climatic events is a significant cause of global food insecurity. Crops are less productive under water-limited conditions and all major crops, with the exception of rice (*Oryza sativa*), die within a few days of flooding. To complement our analyses of the key submergence-tolerance gene *SUB1A*, an ERF-VII transcription factor, we retooled INTACT (Isolation of Nuclei Tagged in specific Cell Types) and TRAP (Translating Ribosome Affinity Purification) for rice. ATAC-seq (Assay for Transposase Accessible Chromatin) was coupled with INTACT to monitor chromatin. We used these technologies to monitor responses to submergence, waterlogging and water deficit, and the return to homeostasis. The data uncover multiple layers of reversible chromatin and mRNA regulation including nuclear retention, turnover, alternative splicing, translation and *trans*-regulation by non-coding RNAs.

We are asking: How does gene activity in stem cells (meristems) of roots and shoots differ? How do flooding and water-deficit stress influence plasticity of specialized cell types in the root?

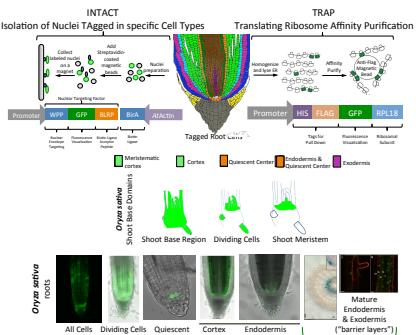
Our challenges and successes have been:

- To optimize TRAP and INTACT in rice
- To identify cell-specific promoter for certain root cell types
- To integrate INTACT with "tagmentation" (ATAC-seq)
- To limit rRNA and organelle contamination in nuclear RNA and ribosome footprint libraries.
- To establish pipelines for multi-scale data analysis

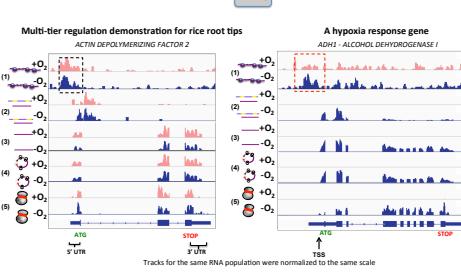
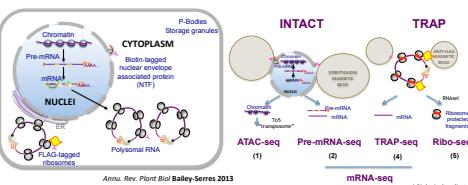
1. Project Workflow



2. Establishment of INTACT and TRAP lines in rice



3. Open chromatin, nuclear RNA and polysomal mRNA analyses in root meristematic regions under submergence



Tracks for the same RNA population were normalized to the same scale

Chromatin accessible regions by DNase I and ATAC-seq overlap

Most regions are located near transcript starts

70% ATAC peaks 17% DNase I peaks

5'-UTR 3'-UTR

Density

ATAC-seq

DNase I

ATAC-seq