

# Plasticity of rice to water extremes: Farmers' genes to mechanisms

Julia Bailey-Serres<sup>1,2\*</sup>

<sup>1)</sup> Center for Plant Cell Biology, Department of Botany and Plant Sciences, University of California, Riverside, CA, 92521, USA

<sup>2)</sup> Plant Ecophysiology, Institute of Environmental Biology, Utrecht University, 3584CH, Utrecht, The Netherlands

## 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 complete submergence. To complement our studies on genes such as *SUBIA*, (an ERF-VII transcription factor that provides robust submergence tolerance) and *AG1* (a TREHALOSE 6-P PHOSPHATASE that promotes establishment of young seedlings underwater), we have retooled INTACT (Isolation of Nuclei TAgged in specific Cell Types) and TRAP (Translating Ribosome Affinity Purification) for rice. These technologies enable us to follow dynamics in chromatin, nuclear pre-mRNAs and ribosome-bound mRNAs in meristems and diverse cell types. With these technologies we can better interpret responses to stresses and reestablishment of homeostasis. These include stress acclimation strategies involving changes in metabolism and development, such as dynamics in suberin deposition in sub-epidermal layers of roots that limit water loss under drought and oxygen escape during waterlogging. Our new data uncover dynamic and reversible regulation at multiple levels of gene regulation and provide new insights into processes of stress resilience. Supported by US NSF-PGRP Plasticity (IOS-1238243), Secretome (IOS-1546879) and REU (DBI-146129) grants.

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Corresponding Author\*

Julia Bailey-Serres

Batchelor Hall UC Riverside Riverside, CA, 92521, USA

+1-951-827-3738

+1-951-827-4438

E-mail: julia.bailey@ucr.edu