



Transcriptomics of *Oryza sativa* under Drought Stress

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Introduction

Over 546 million tons of rice are consumed by humans each year. Rice requires flooding for healthy growth, and drought reduces yield by 22 million tons or by 10 kg/person/year.^[1,2,3]

- Plants undergo **stress response** when they sense unfavorable conditions. The molecular mechanisms behind stress response are best understood in the model plant *Arabidopsis thaliana* (*A. thaliana*).
- SIGNAL RESPONSIVE 1 (SR1) is implicated in abiotic and biotic stress response.^[4,5]

SR1: In *A. thaliana*, SR1 is a calcium-dependent, calmodulin-binding transcription factor (TF) involved in the **differential regulation of over 3,000 genes** during abiotic stress response. ^[5,6]

- While the action of SR1 is understood in *A. thaliana*, **its role in rice has not been defined.**

Plan and Impact: Molecular and genetic techniques, coupled with bioinformatics will reveal the action of SR1, a chief regulator of stress response, in the world's second leading staple grain.

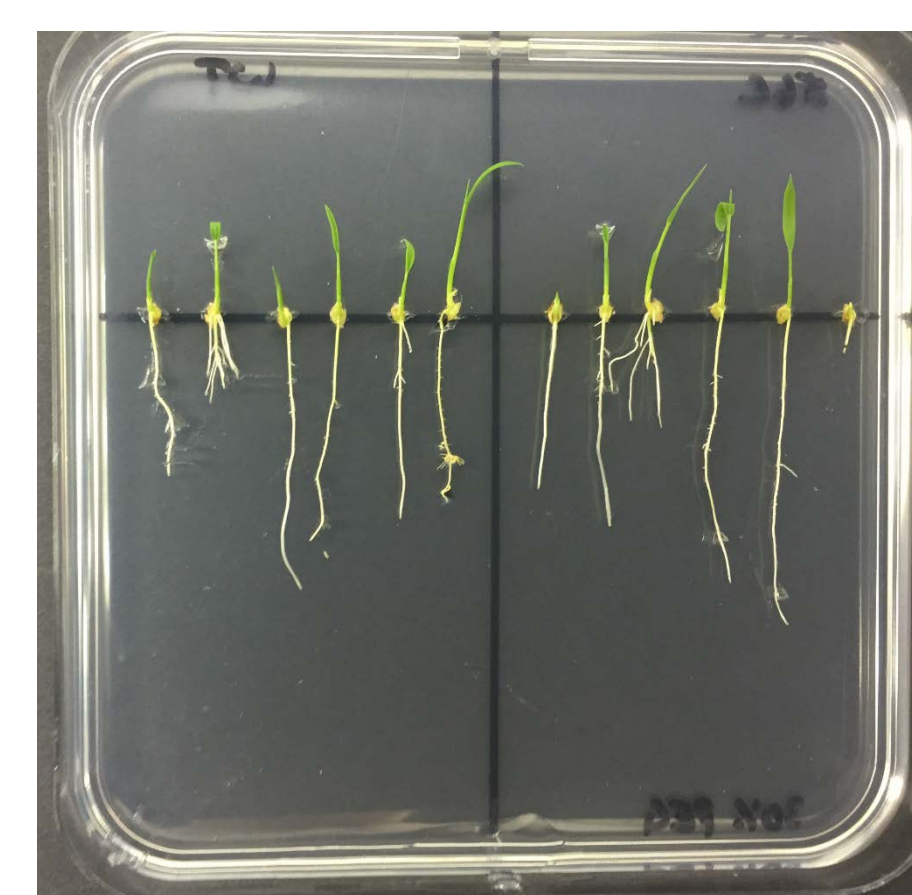


Aims

- Phenotypic analysis of WT and *sr1* under drought and normal conditions.
 - Seedling stage on plates
 - Vegetative stage in soil
- Generate complimented and over-expressed lines.
 - SR1 overexpressed in WT
 - SR1 overexpressed in *sr1*
 - SR1 complimented in *sr1*
- Phenotypic analysis with transgenic lines.
- Transcriptomic analysis.
- Identify direct targets.

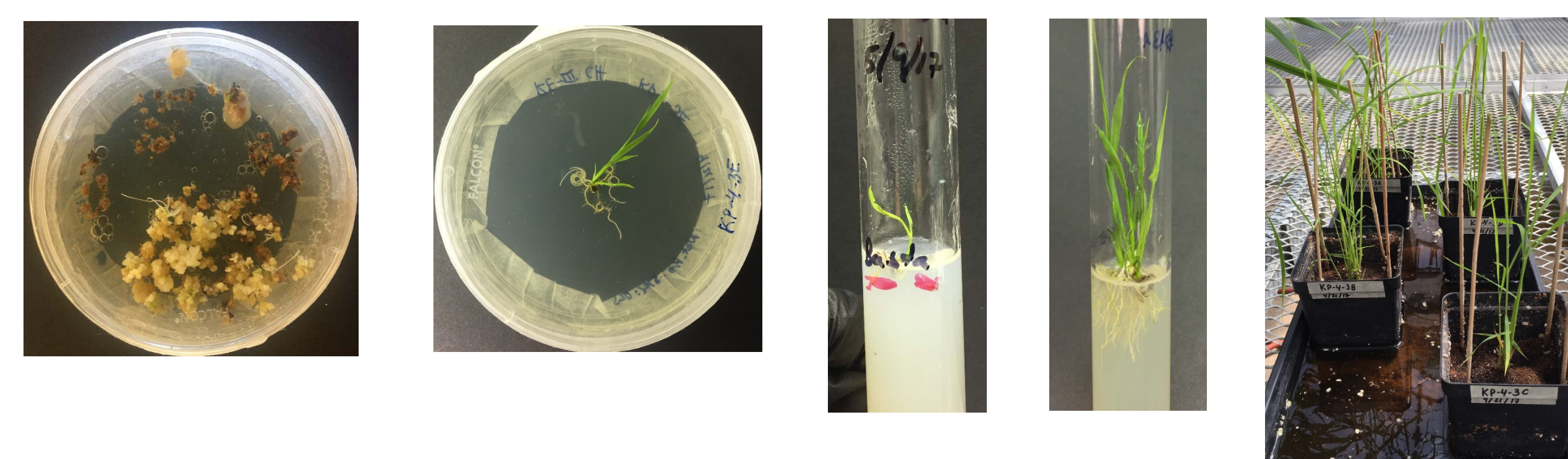
Approaches

1) *In vitro* Drought Tolerance Assay



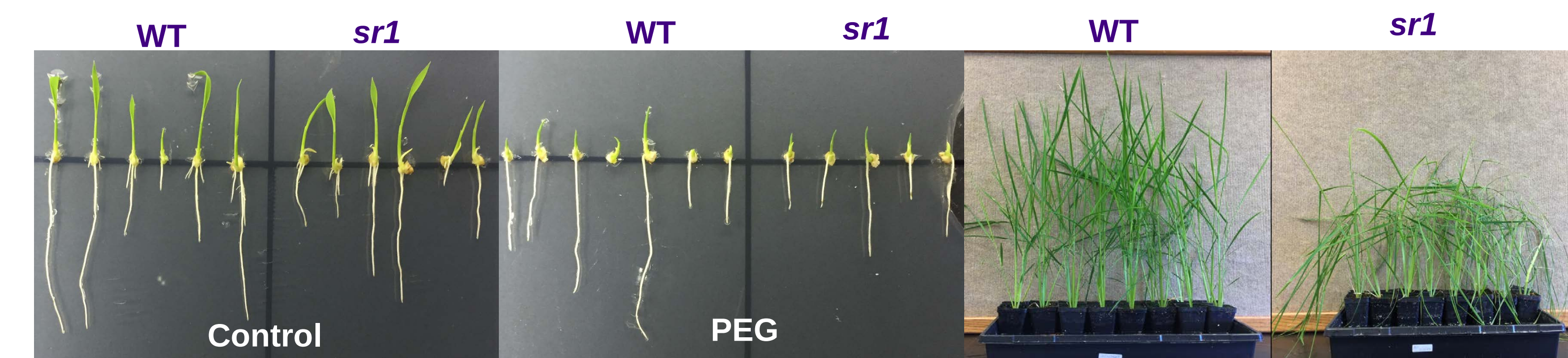
- MS media with and without poly ethylene glycol (PEG).
- WT and *sr1* are plated after de-hulling and sterilization.
- Embryos are excised after sterilization.

2) *Agrobacterium*-mediated transformation



- Calli induction and transfection.^[7]
- Selection
- Transgenics

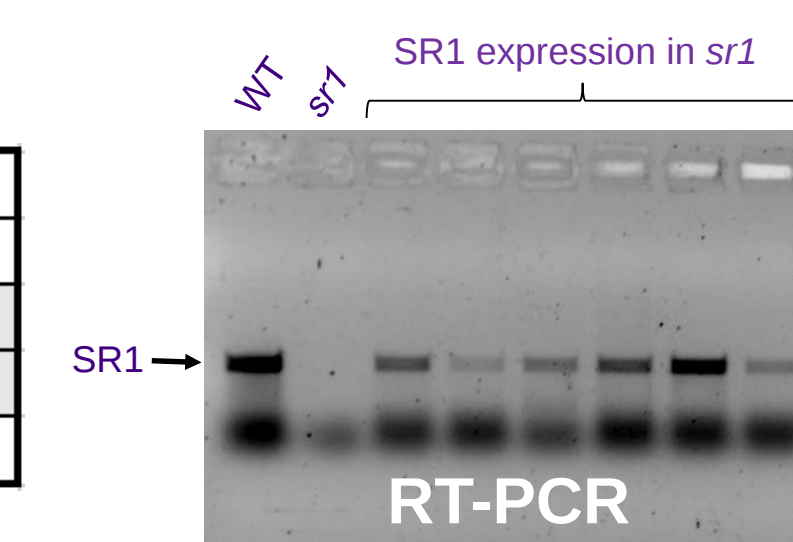
Preliminary Findings



Aim 1. WT and Mutant embryos germinated on PEG. 6 days after plating.

Aim 1. WT and Mutant plants. 8 days of water withholding.

Construct	Independent Lines	Verified by	
		Genomic PCR	RT-PCR
Overexpressed in WT	-		
Overexpressed in <i>sr1</i>	In process		
Complimented in <i>sr1</i>	1 - 6	Yes	Yes



Aim 2. Generation of transgenic lines



Aim 2. Transgenic complimented line at flowering stage

Future Work

- Generation of overexpressed transgenic lines.
- Phenotypic characterization of transgenics.
- RNA-seq analysis.
- ChIP-seq.

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