### Salinity tolerance in P. hallii

By Sonali Singh

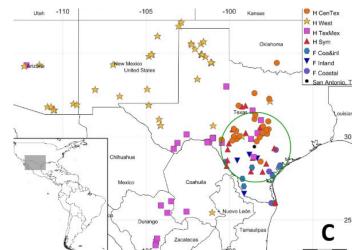
## Introduction

# Why salinity tolerance?

- Salt stress occurs when excessive salts in soil solution cause inhibition of plant growth or plant death
  - Poor irrigation/ drainage systems
  - Previous exposure to seawater
  - High evaporation rates
- High salt levels in soil affect approximately 20% of irrigated lands across the world
- In the future, more land will need to be used to support increased food and biofuel production



- Genetic model for the biofuel producing species, P. virgatum
  - o Diploid vs. tetraploid/octoploid
- P. hallii var. hallii (HAL) is typically found in drier/inland climates
  - o Central Texas, Coastal, Sympatry
- P. hallii var. filipes (FIL) is typically found in more coastal climates



## In the past

- Tobacco plants
  - Upregulation of a specific gene or set of genes, allowing them to combat abiotic stresses
  - Positive responses to genetic manipulation aiming to increase salt tolerance
- ABA-deficient Arabidopsis mutants
  - ABA improved the ability for plants to tolerate abiotic stresses
  - Downregulation of genes that limited ABA

## research questions

1. Are there differences in responses to increased salinity within HAL?

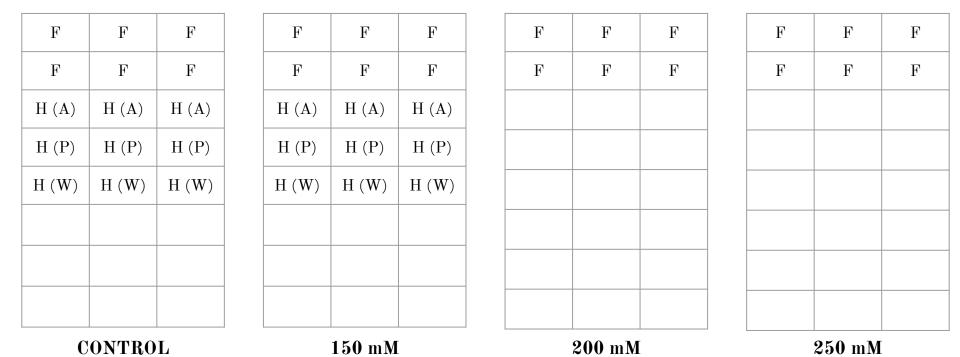
2. Are there differences in responses to increased salinity between HAL and FIL?

3. Is there a difference when QTL mapping HAL and FIL to two reference genomes?

## Methods

#### Experimental Setup

- 1. Germinated 40 seeds from 24 distinct varieties of HAL for 2 weeks in greenhouse
- 2. Transplanted ~20 seeds from 6 varieties of HAL and watered every other day for 3 weeks, after which 6 plants from 3 distinct HAL varieties remained
- 3. Transplanted 24 additional FIL plants to expand experiment
- 4. All plants were grown for 1 more week, being watered every other day
- 5. Began 7 day experimental period of control, 150mM, 200mM, and 250mM salt treatments using 42 total plants (24 FIL and 18 HAL)
- 6. Plants were watered every other day, with the first day consisting of half the treatment concentration to allow for acclimation



- Set number of FIL and HAL in each, randomly assigned to a tray
- Randomized within trays every other day
- Tray position randomized every other day

#### Traits Measured

#### **Above Ground Biomass**

a. Cut plants above root and measured in grams

#### Chlorophyll (A, B and Total)

- a. Measured fresh leaf weight in 5mL test tube
- b. Added 3 mL of 80% acetone and stored in dark for 24 hours
- c. Ran in spectrophotometer

#### **Leaf Water Potential**

a. Measured second-youngest fully grown leaf in pressure bomb

#### **Relative Water Content**

- a. Measured fresh weight of one cut leaf in 5mL test tube
- b. Added 1 mL of water to tube and soaked for 24 hours before measuring turgid weight
- c. Dried leaves for 72 hours and measured dry weight

#### **Osmotic Potential**

- a. Froze one cut leaf for 72 hours
- b. Centrifuged to extract sap
- c. Measured sap in osmometer

## Results & Interpretations

#### SIGNIFICANT DIFFERENCES BETWEEN

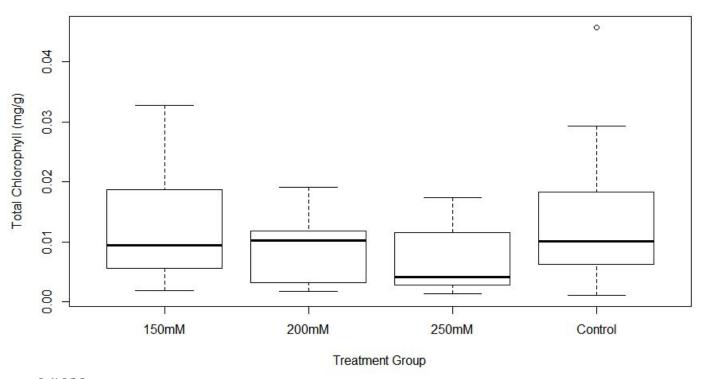
#### Salt Levels

TRAIT	SIGNIFICANT	IN FAVOR OF
Biomass	Yes	Control
Chlorophyll	No	-
Water Potential	Yes	Control
RWC	Yes	Control
Osmotic Potential	Yes	Control

#### SIGNIFICANT DIFFERENCES BETWEEN HAL vs. FIL

TRAIT	SIGNIFICANT	IN FAVOR OF
Biomass	No	-
Chlorophyll	No	-
Water Potential	Yes	HAL
RWC	Yes	FIL
Osmotic Potential	No	-

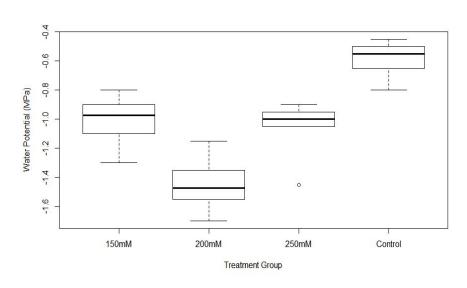
#### Overall Chlorophyll

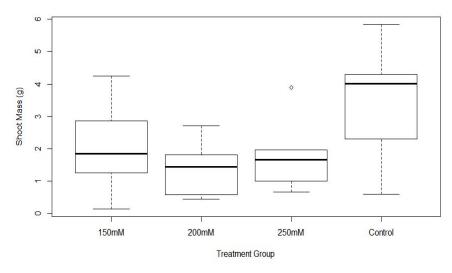


150 p-value = 0.5639 200 p-value = 0.2416250 p-value = 0.08658

#### Overall Water Potential

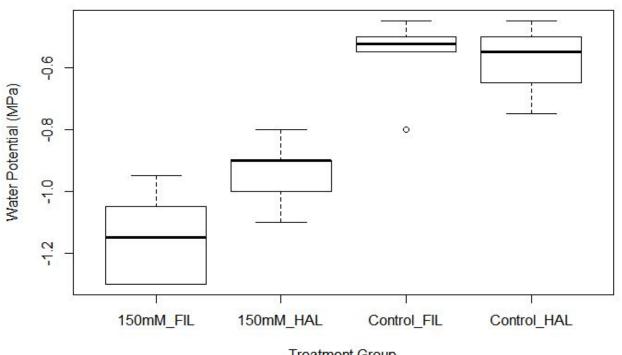
#### Overall Shoot Mass





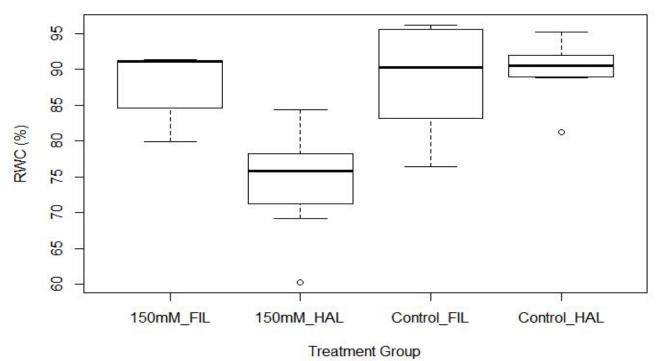
150 p-value: 1.246e-08 200 p-value: 2.525e-5 250 p-value: 0.001196 150 p-value: 0.01046 200 p-value: 0.001465 250 p-value: 0.01976

#### HAL vs. FIL Water Potential



Control p-value: 0.6286 150 p-value: 0.03037 Treatment Group

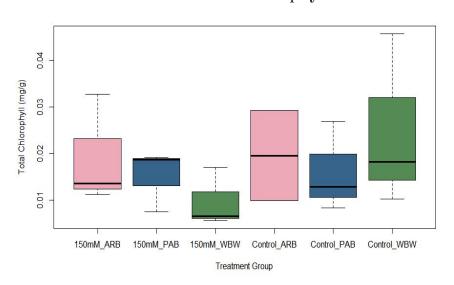
#### HAL vs. FIL RWC



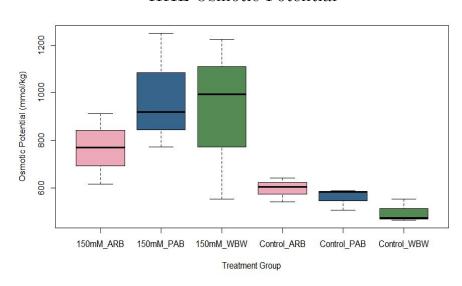
Control p-value: 0.6736 150 p-value: 0.02256

#### Variation Within HAL

HAL Total Chlorophyll



#### HAL Osmotic Potential

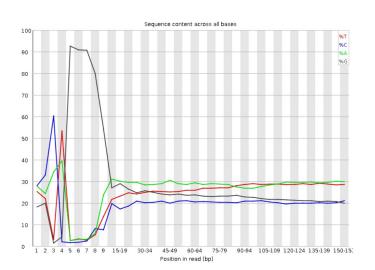


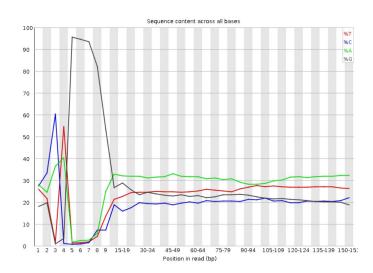
### Bioinformatics

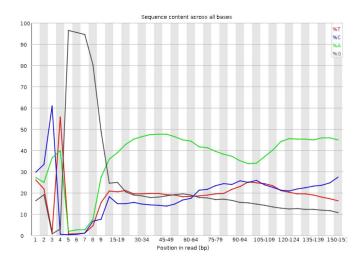
#### Coding Setup

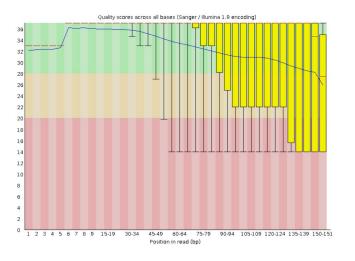
- 1. Bunzip the files
  - a. Converting from binary format (BAM) to a readable format (SAM)
- 2. Quality report
  - a. Quality filter to trim primer sequences
- 3. Mapping
  - a. Unspliced mapping using BWA
- 4. Filter mapping results
  - a. Trim out low quality regions
- 5. Analysis
  - a. Convert SAM back to BAM and get a matching percentage

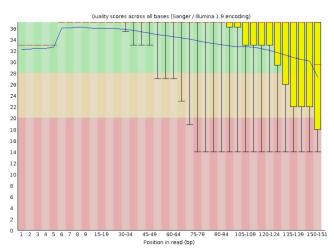
### Quality Trimming AS DONE IN STEP 2





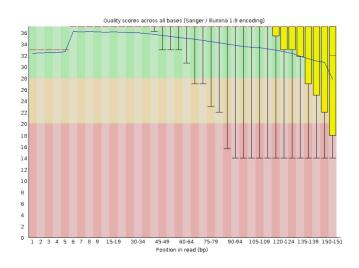






#### Quality Trimming

AS DONE IN STEP 4



## Conclusions & Future Directions

## Looking back

Are there differences in responses to increased salinity within HAL?

Yes, but our treatment size was not large enough to look into these statistically.

Are there differences in responses to increased salinity between HAL and FIL?

Overall, FIL reacts better to salt stress, with the exception of water potential.

Is there a difference when QTL mapping HAL and FIL to two reference genomes?

There is a reference bias when mapping HAL and FIL to the same genome.

#### Future Directions

- Repeat HAL vs. FIL experiment in greenhouse, collect RNA, and do RNAseq on those specific plants to correlate phenotypic and genomic expression
- Add on another variable of environment and grow both HAL and FIL in their natural environment and the other variety's environment
- Extend the length of the treatment to measure long term effects under more subtle conditions

#### References

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- Metternicht, G. I., and Zinck, J.A. (2003). Remote sensing of soil salinity: potentials and constraints. *Science Direct* 85, 1-20.
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