

# *Adapting durum wheat to drought and crown rot*

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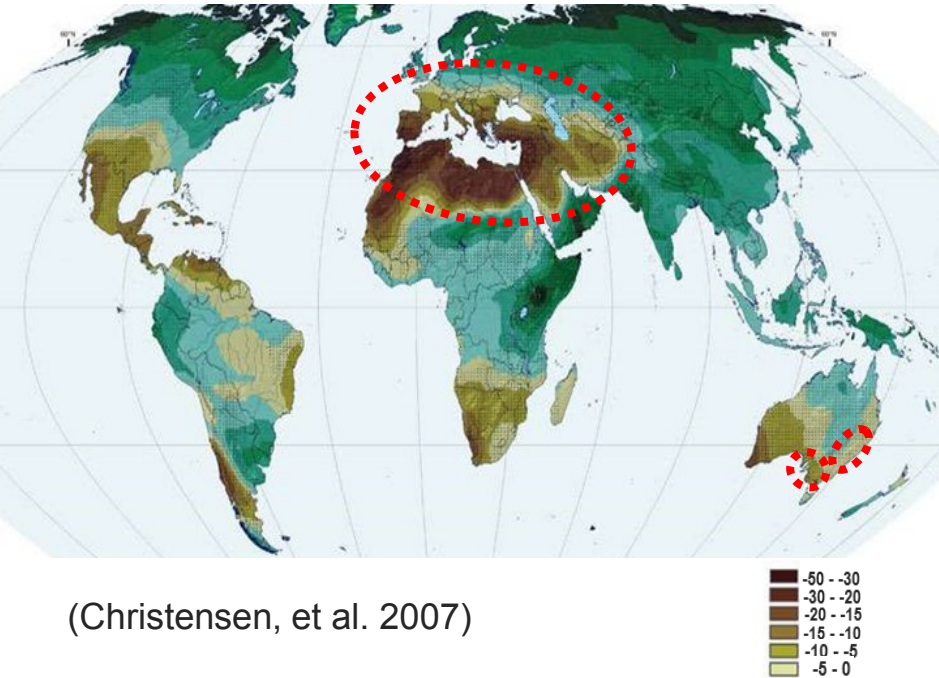
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# Current and future challenges for durum wheat production

↑ Drought

Future drought hotspots coincide with durum regions



↑ Crown rot



Stubble retention



Crown rot caused by *Fusarium* species



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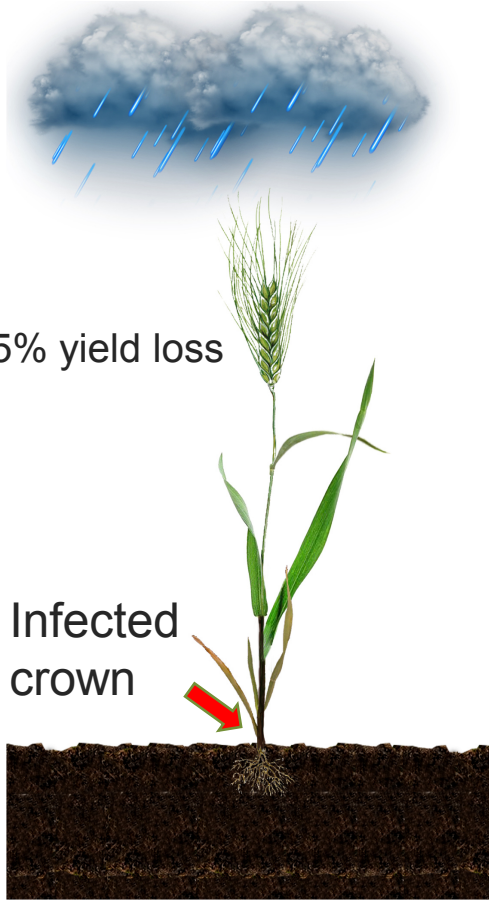
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# How does crown rot cause yield loss?



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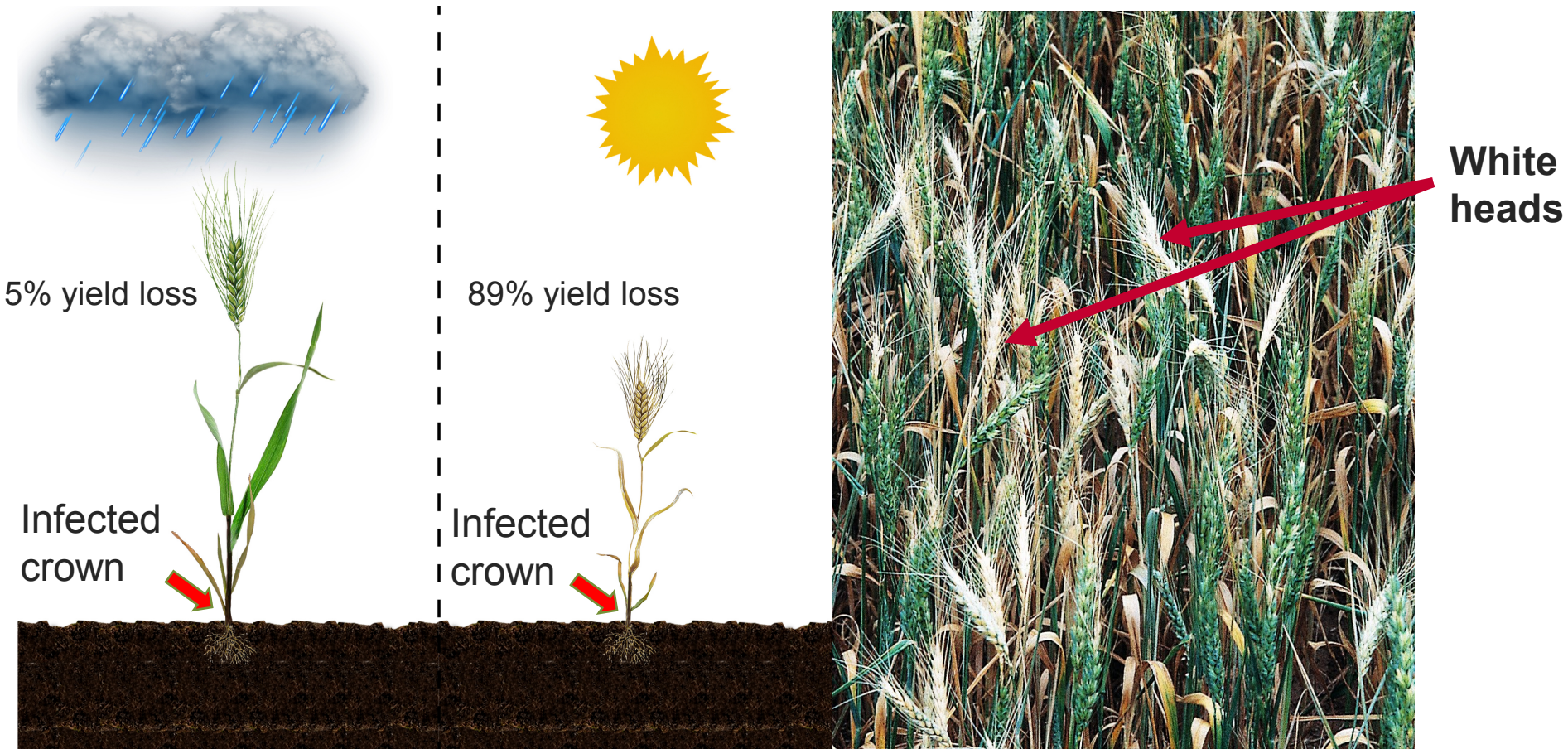
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# How does crown rot cause yield loss?



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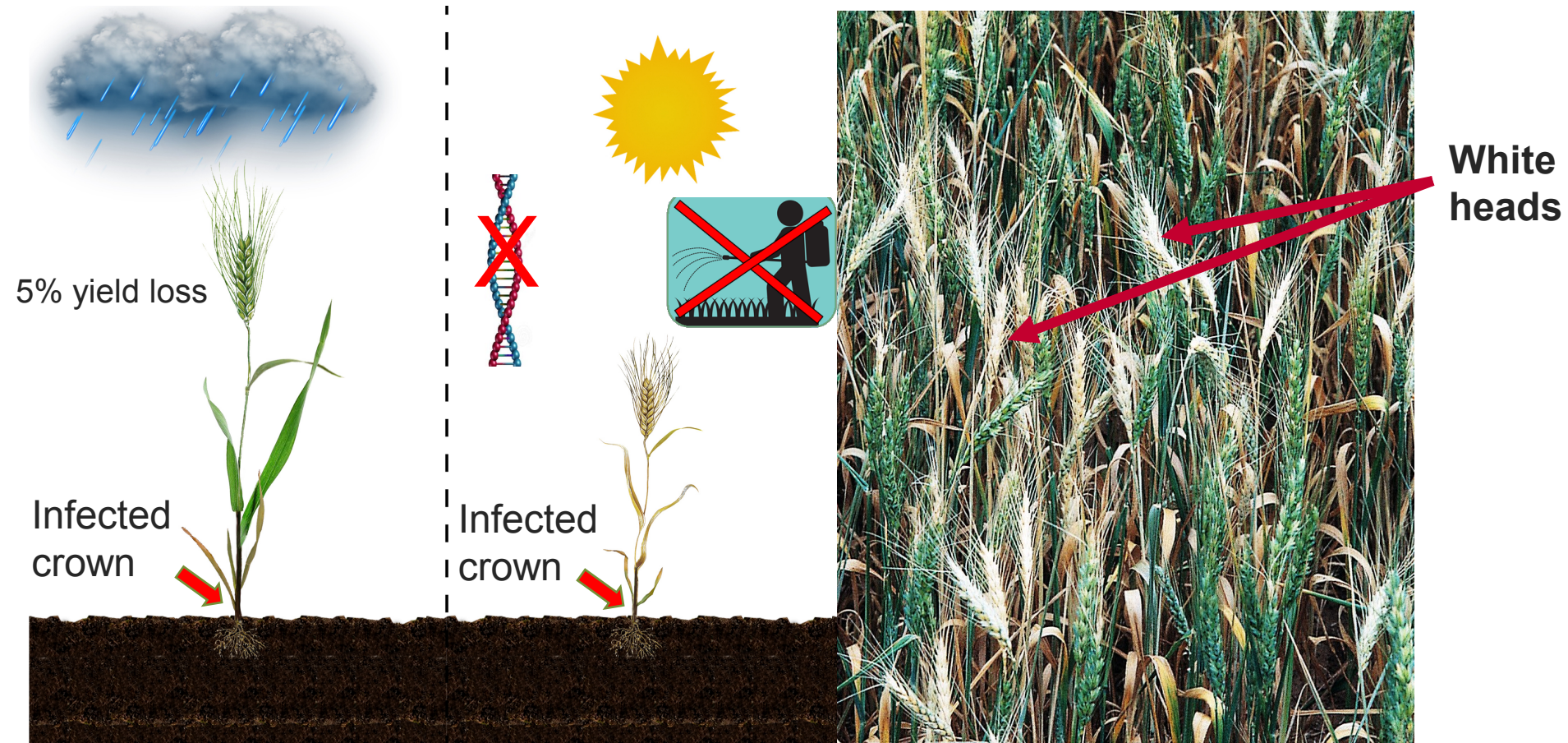
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# How does crown rot cause yield loss?



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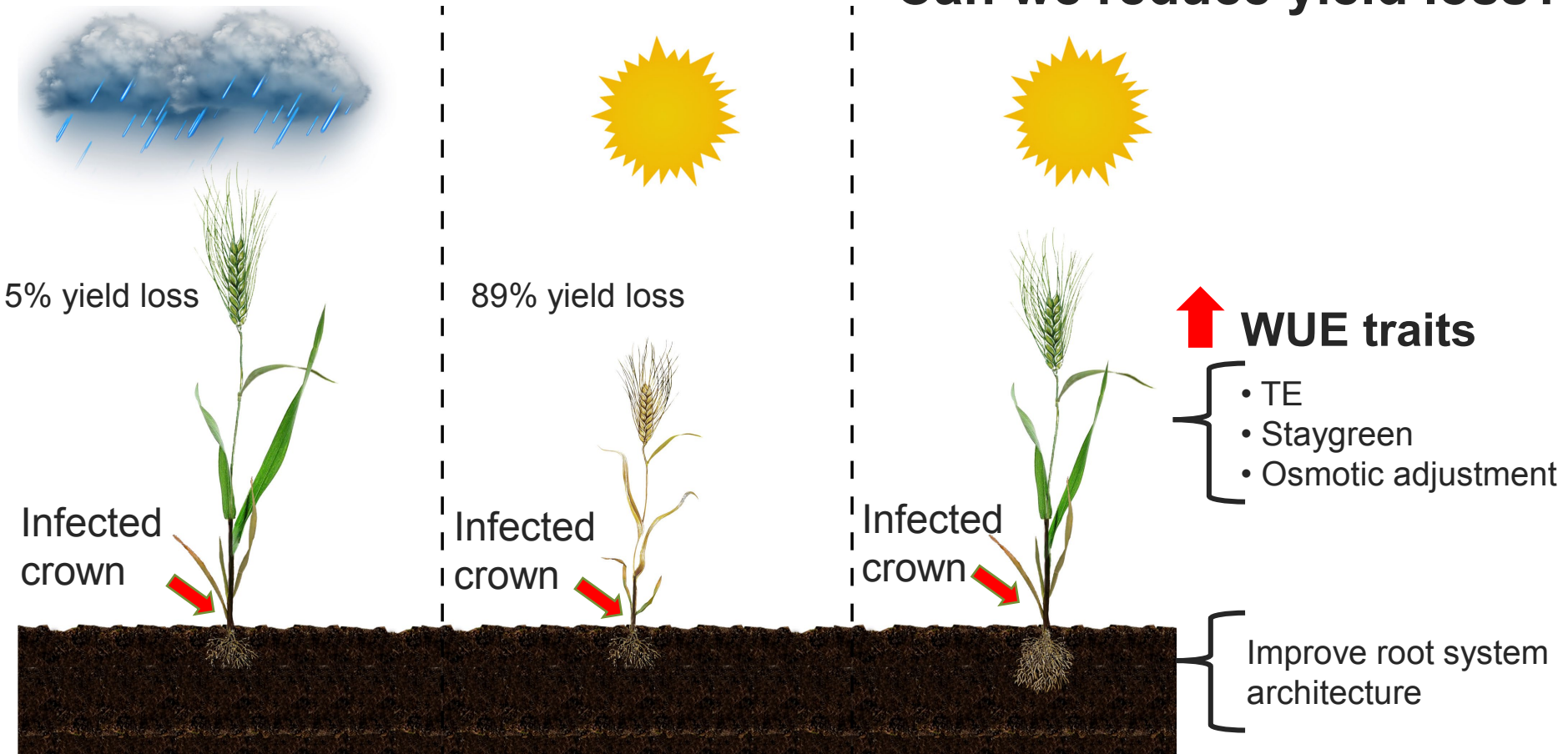


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# How does crown rot cause yield loss?

## Can we reduce yield loss?



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**Can we create populations to  
investigate WUE traits?**



# Establishing populations to fuse ICARDA and Australian germplasm

## ICARDA founder lines

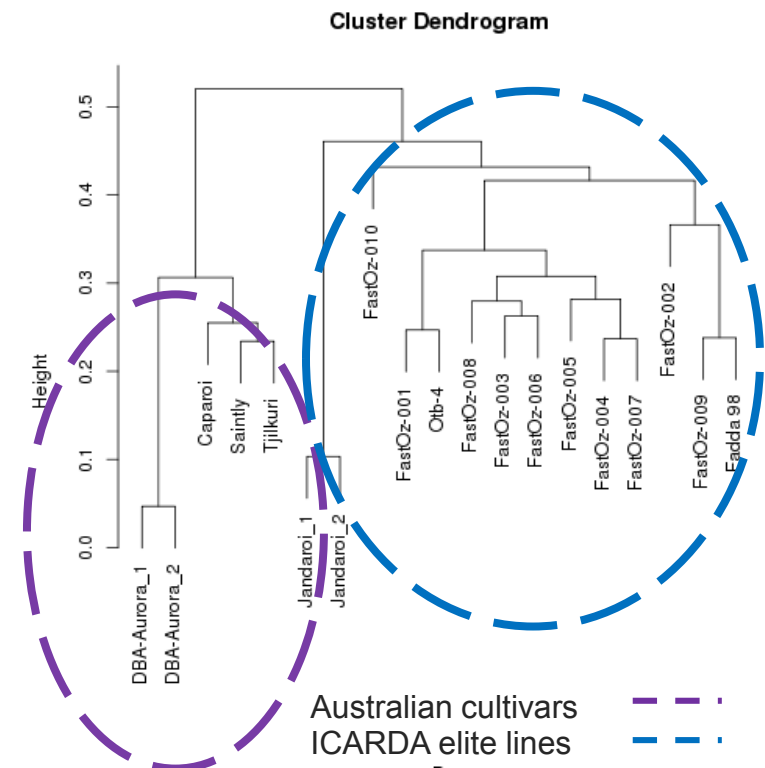
- Adapted to drought and heat
- Tolerance for soil-borne diseases
- Low quality

## Australian cultivars

- High quality
- Very susceptible to crown rot

## Ideal populations

- Combine adaptive traits with quality
- Suitable for genetic studies

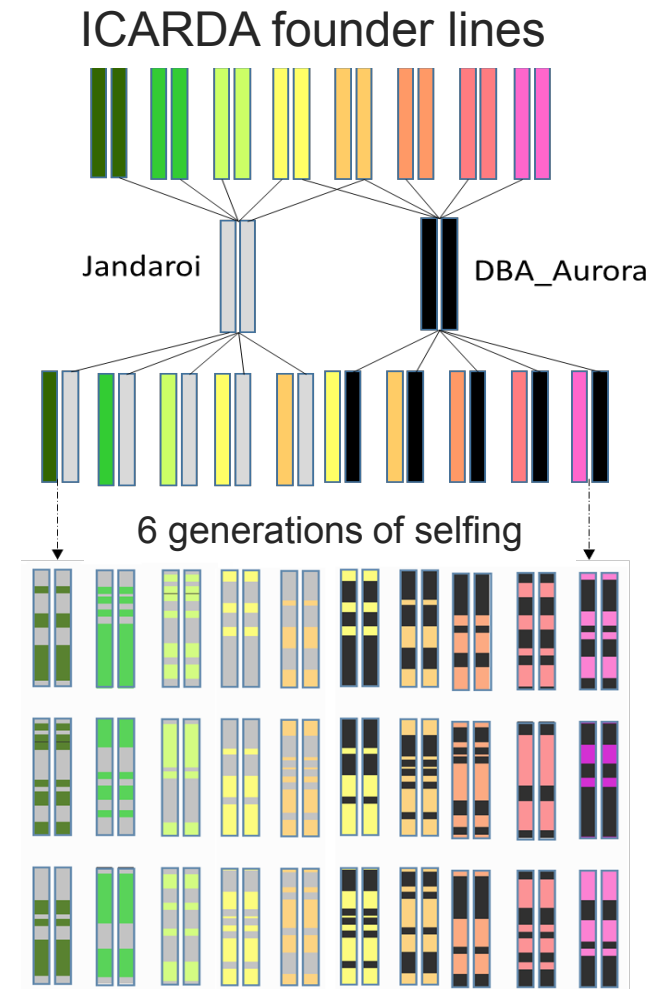


# Durum multi-parent NAM

- Oz reference varieties crossed with ICARDA founders
- 6 selfing generations
- Speed breeding to accelerate population development
- F6 lines genotyped with DArTseq platform



Speed breeding facility, University of Queensland



F6 leaves sampled for genotyping



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# NAM population structure

## Reference parents

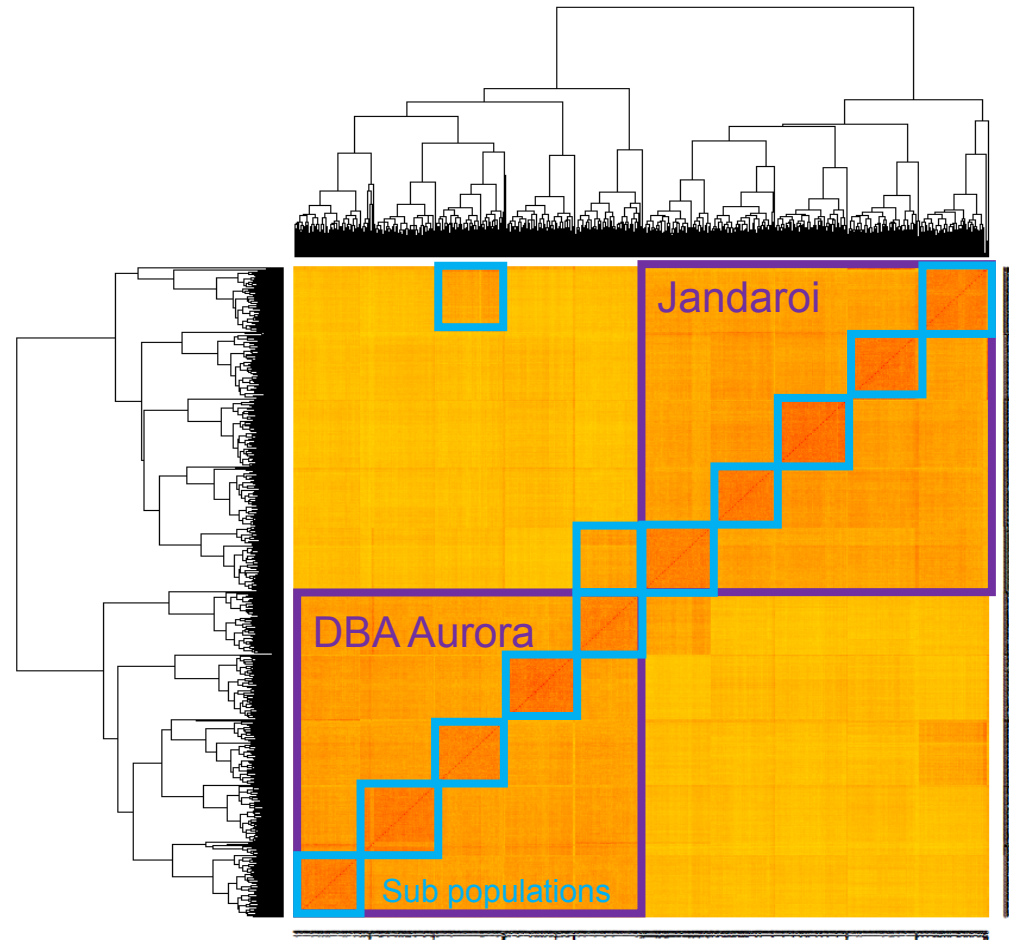
DBA Aurora and Jandaroi

## Founder parents

Fastoz2, Fastoz6, Fastoz10, Kunmiki, Outrob4, Fastoz3, IC-078, Fadda98

## Common founders

Kunmiki and Outrob4



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**Can we phenotype root  
architecture?**

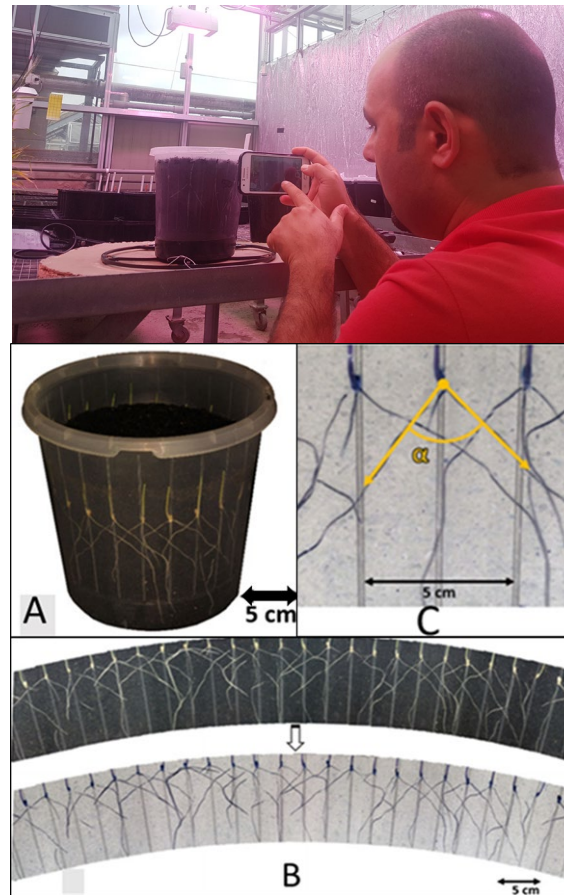


# Phenotyping root angle

## Root angle variation

- Glasshouse: 48.3 - 112 (°)
- Field: 51.7 - 85.8 (°)

### Clear pot



### 'Shovelomics'



Richard et al. (2015) Plant Methods



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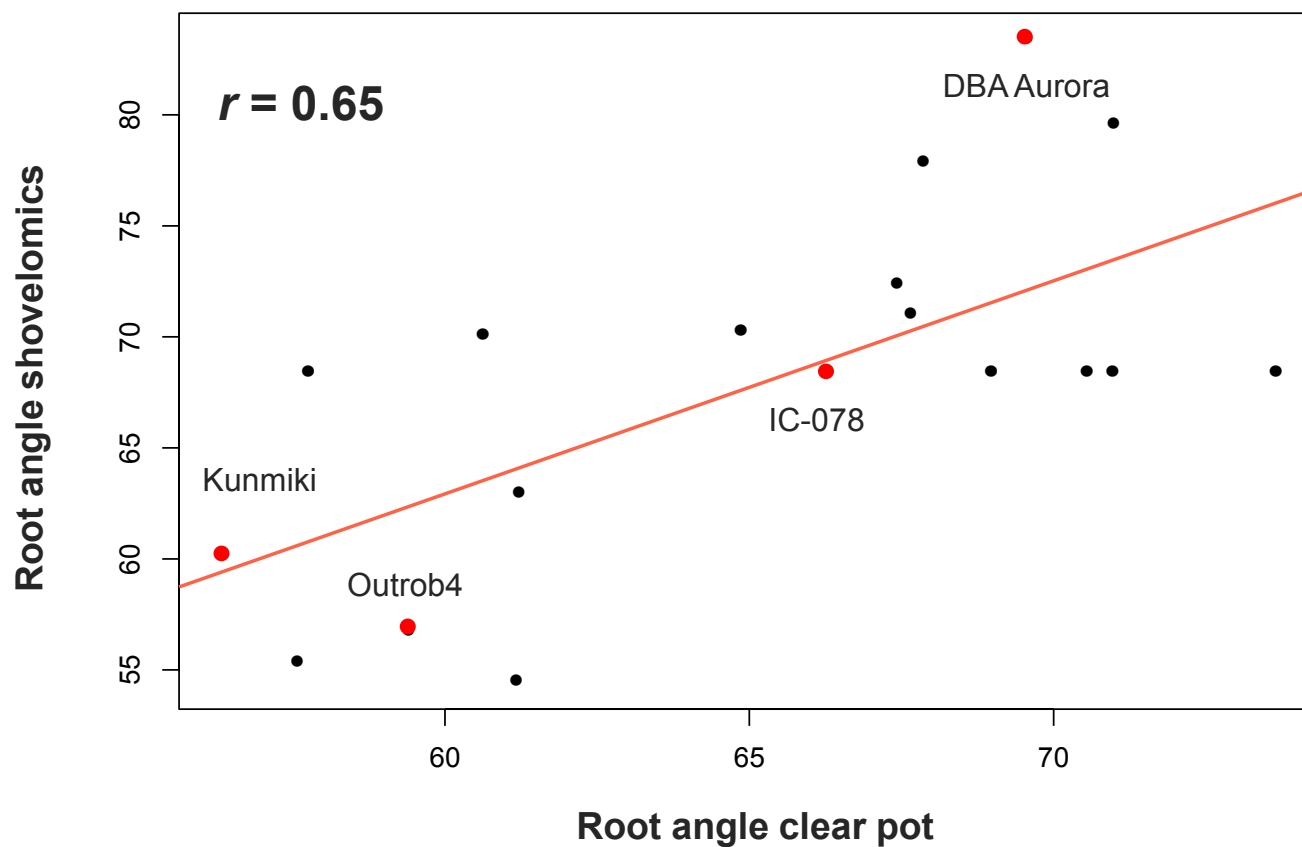
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# Clear pot vs shovelomics

Good correlation between glasshouse and field



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**What are the genomic regions  
controlling root architecture?**

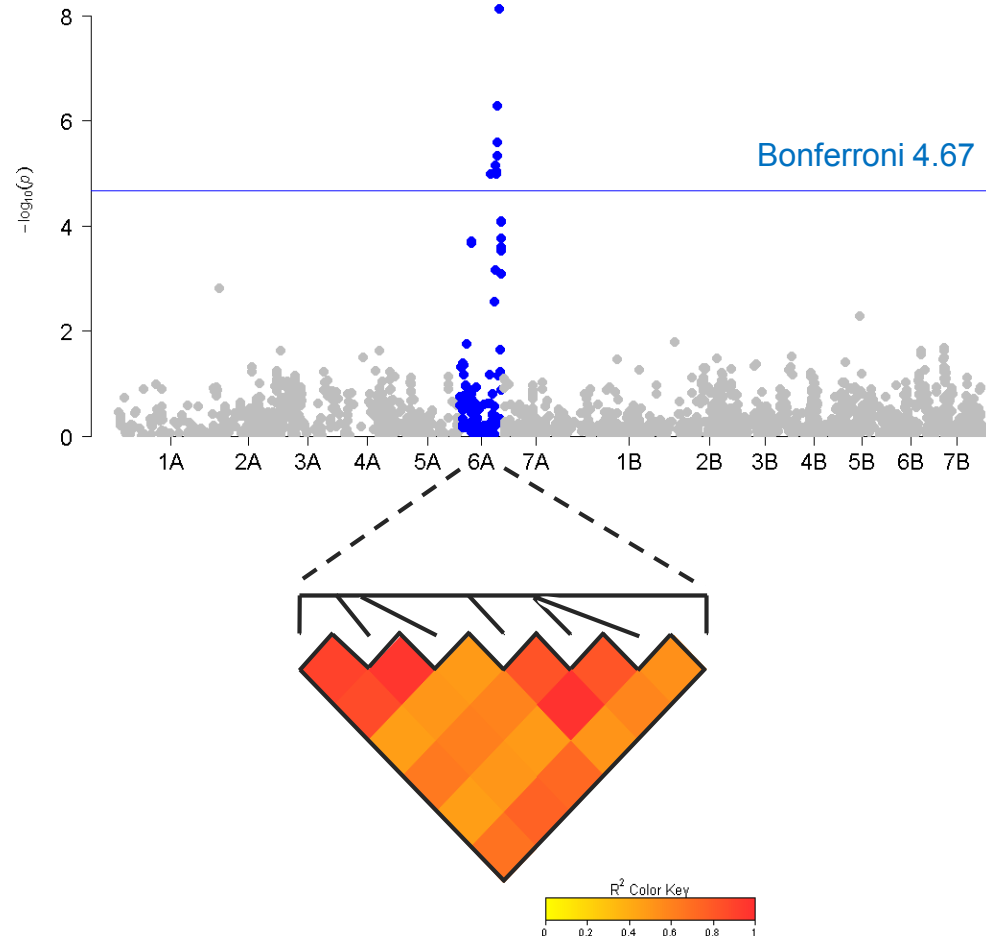
# GWAS for root angle

## Methods

- Subset of 393 NAM lines
- 2,541 high quality DArTseq SNPs
- GenABEL R package

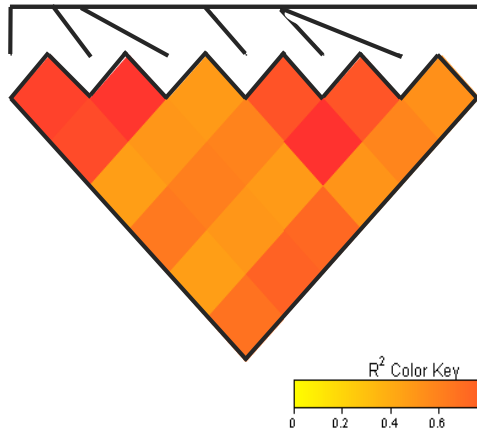
## Results

- Major root angle QTL on 6A
- Associated markers in high LD ( $r^2 = 0.46 - 0.99$ )

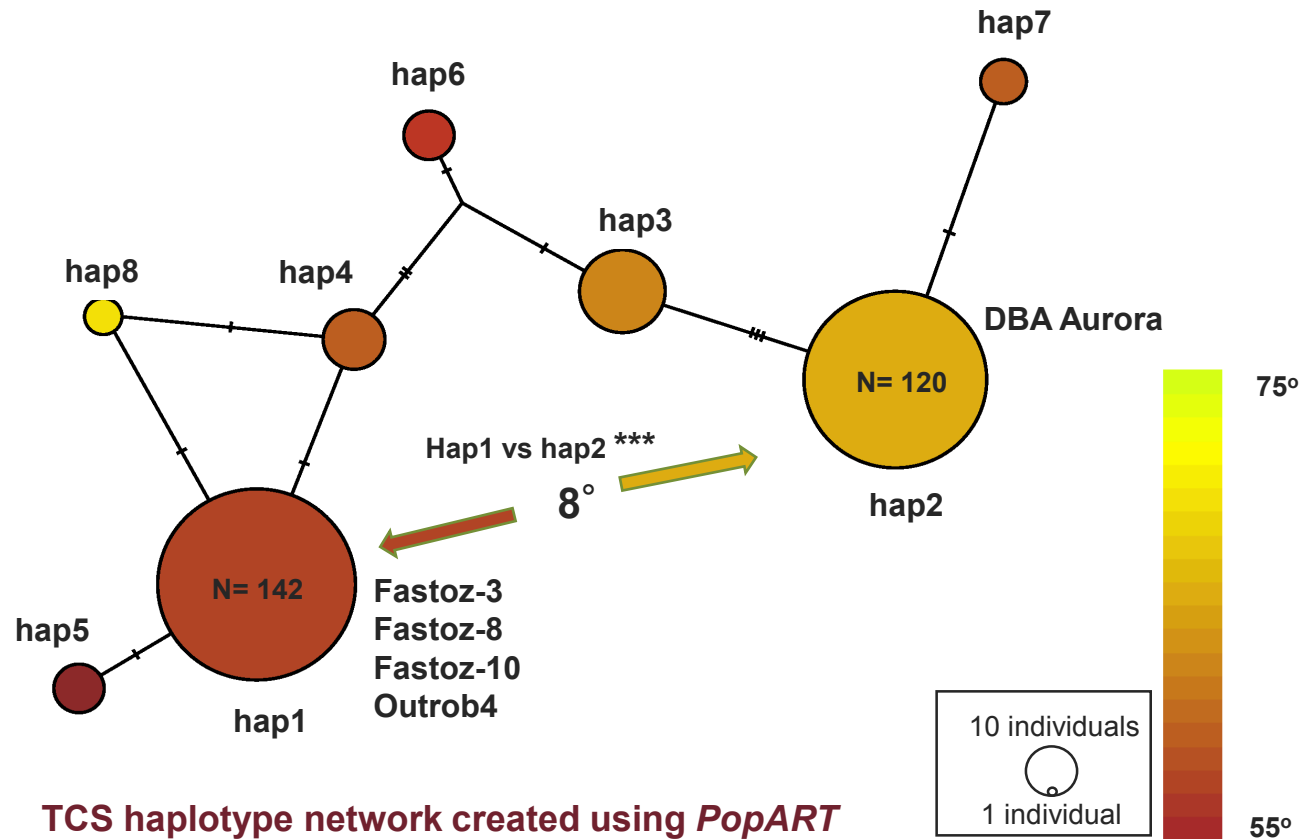
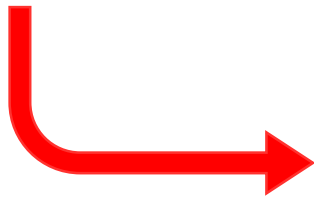


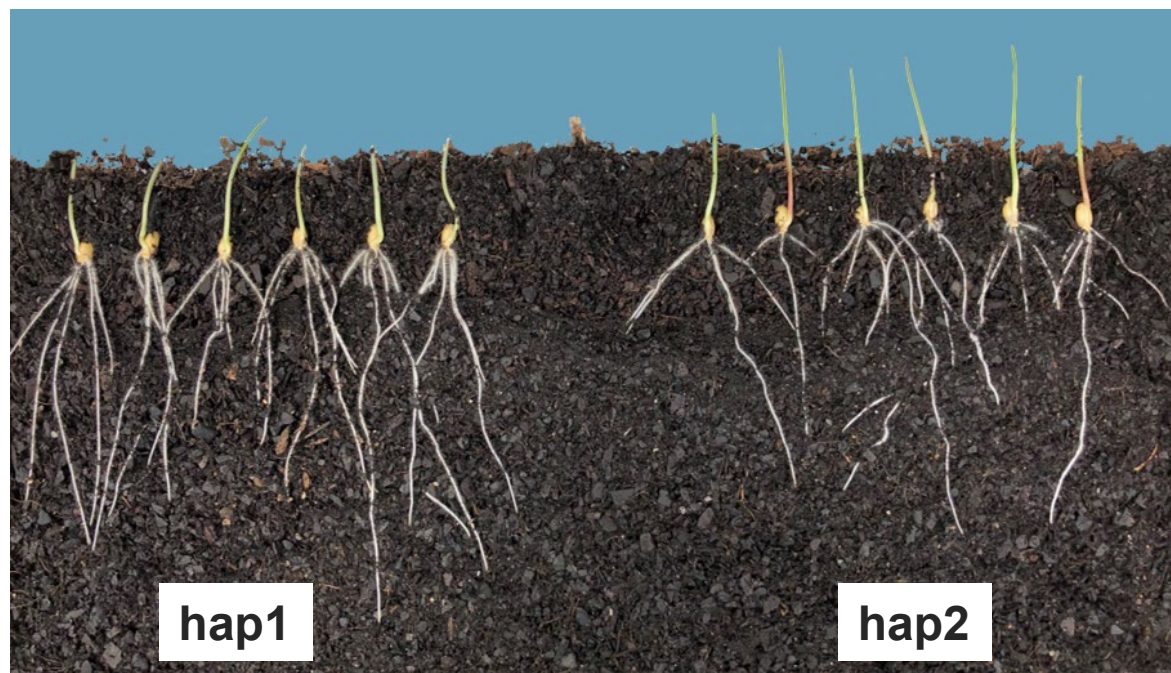
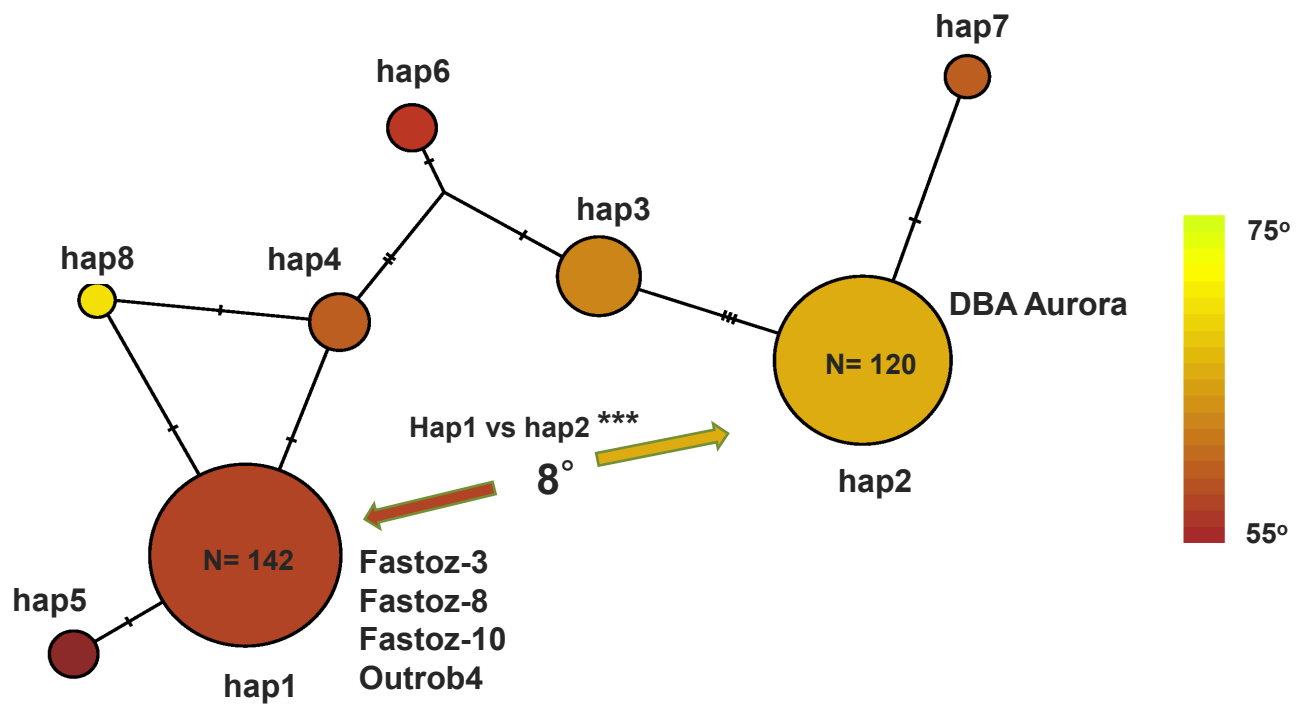


# Haplotype analysis for 6A root angle QTL



Markers used to construct haplotype network







**Does root architecture influence  
field performance?**

# Field evaluation under drought conditions

- Hermitage drought station, Warwick, QLD
- Subset of 168 NAM lines
- Data collection: weekly NDVI measurements, flowering time, plant height, yield



Hermitage research station



Measuring plant height



Counting storms on harvest day!



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# Phenotyping rate of senescence

- NDVI measurements collected
- Logistic curve
- Staygreen is a consequence of saving water early in the season

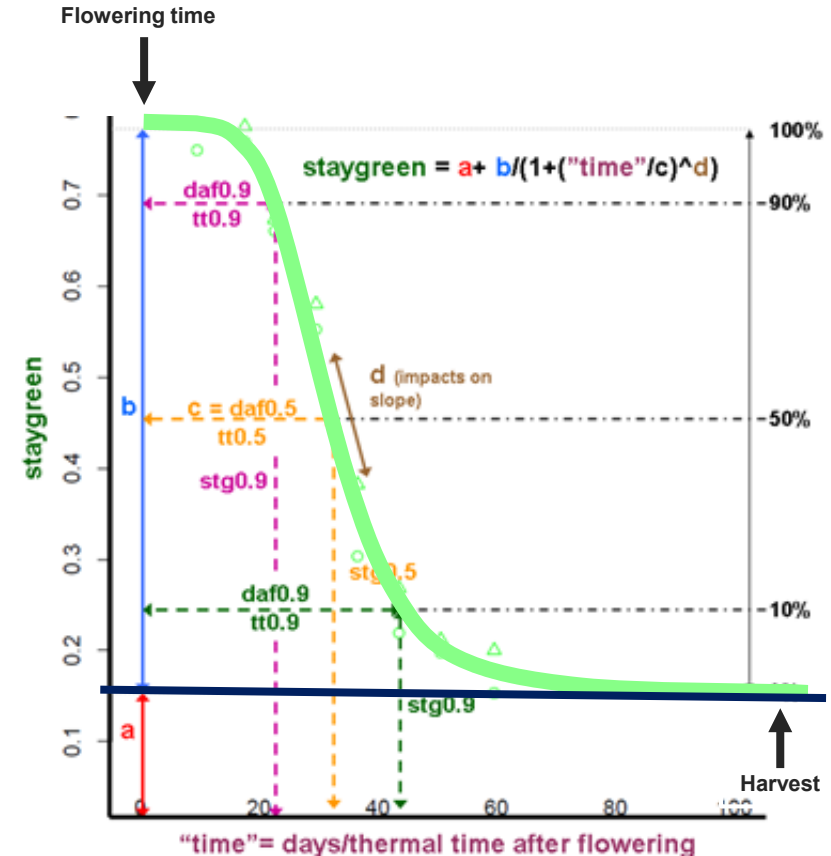


Senescent type

Staygreen type



## Modelling rate of senescence

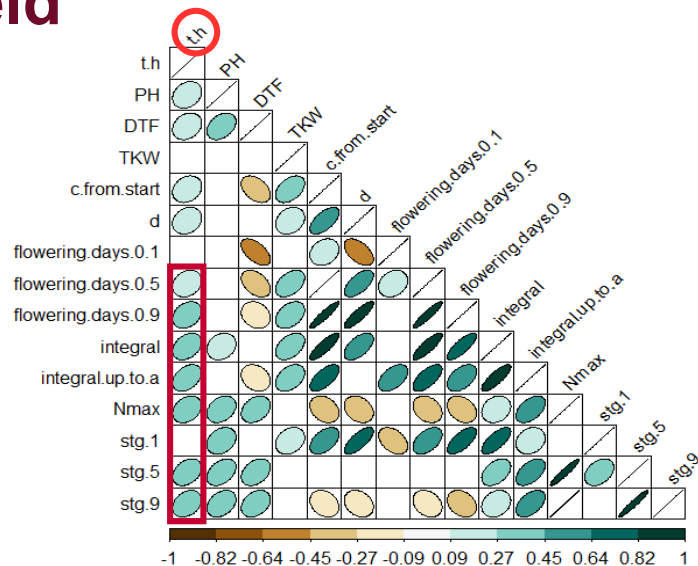


Christopher et al. (2016)



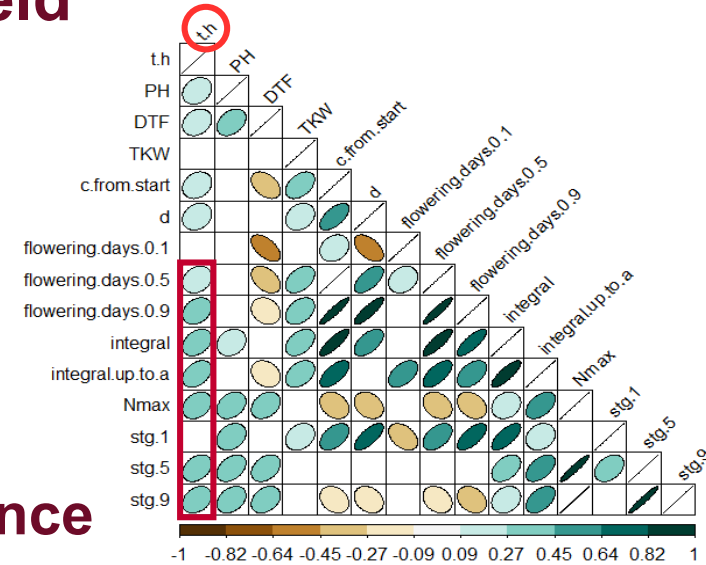
# Correlation between staygreen and yield

- Staygreen traits were significantly correlated with yield

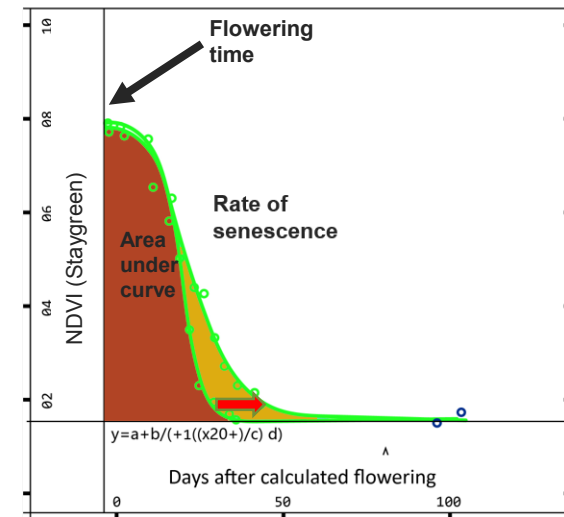
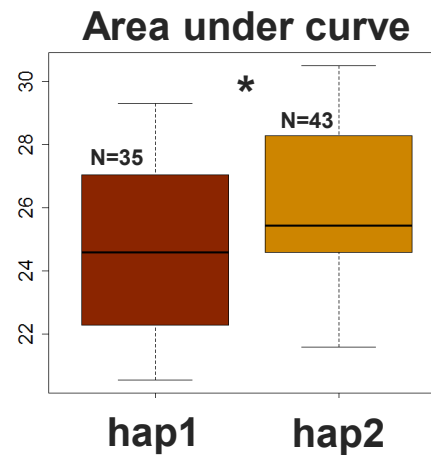
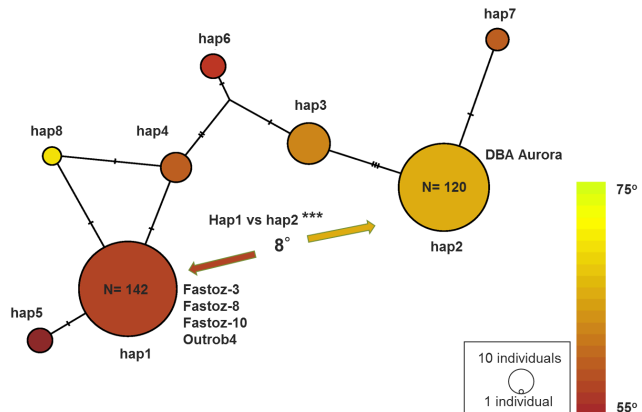


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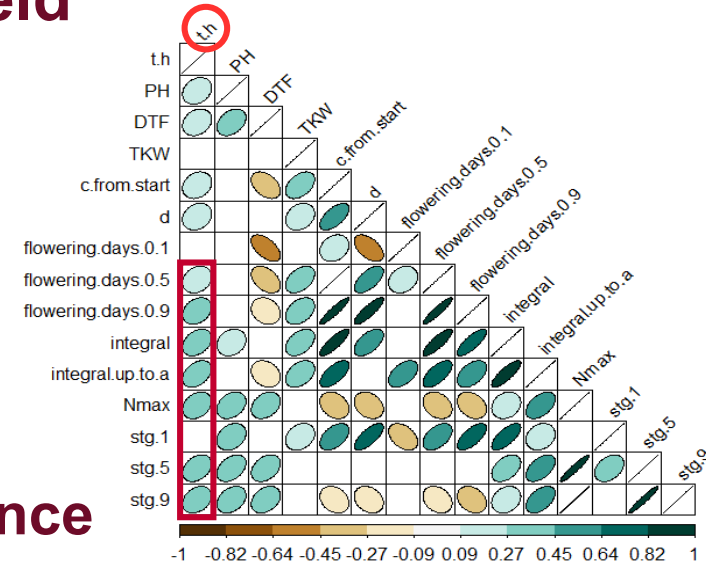


## Root angle QTL effects on yield performance

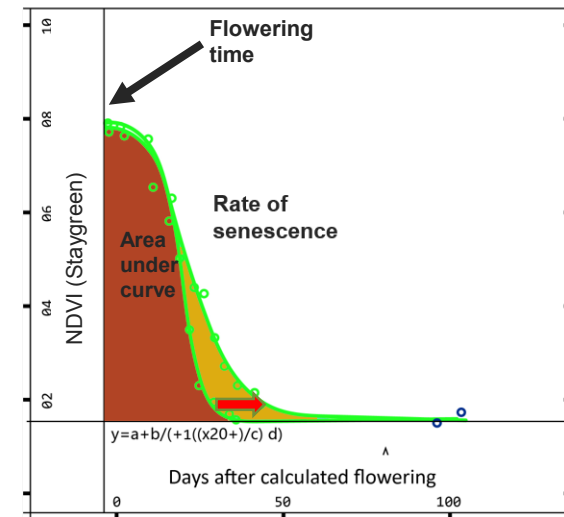
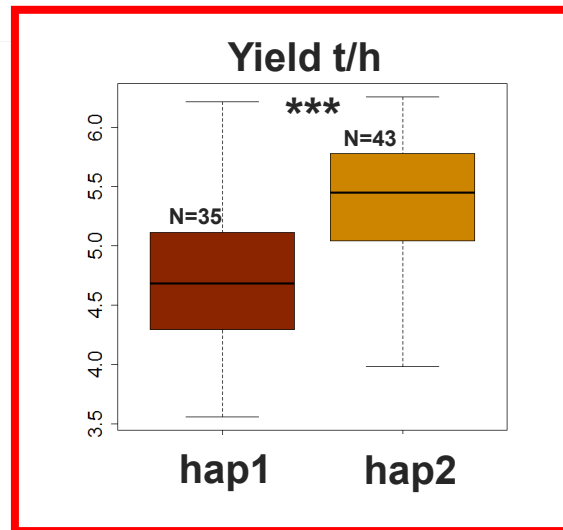
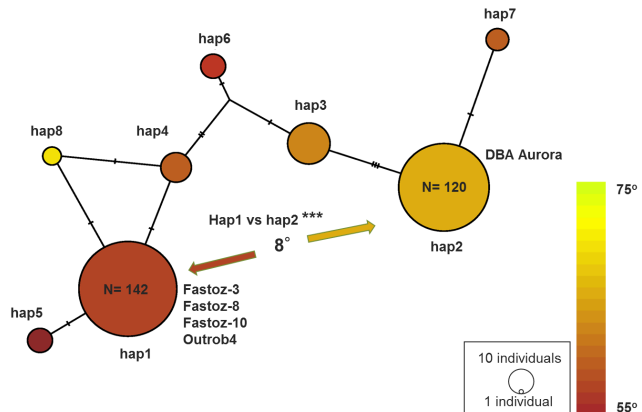


# Correlation between staygreen and yield

- Staygreen traits were significantly correlated with yield



## Root angle QTL effects on yield performance





**Can WUE traits minimise yield loss  
under crown rot?**

# Crown rot experiment

- Similar trial, but **high crown rot pressure**
- Data collection: flowering time, plant height, yield and **crown rot**
- Crown rot assessed as a **severity index**:
  - White heads % 1<sup>st</sup> assessment
  - White heads % 2<sup>nd</sup> assessment
  - Stem browning



Sown on infected stubble



Stem scoring

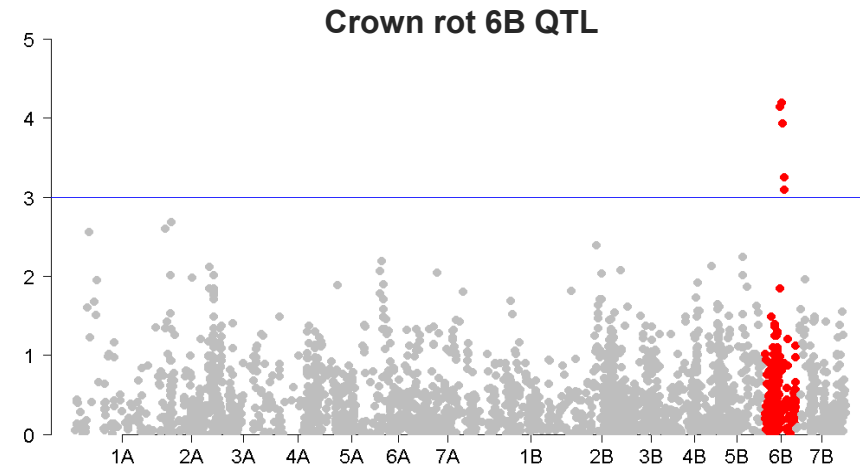


5% white heads

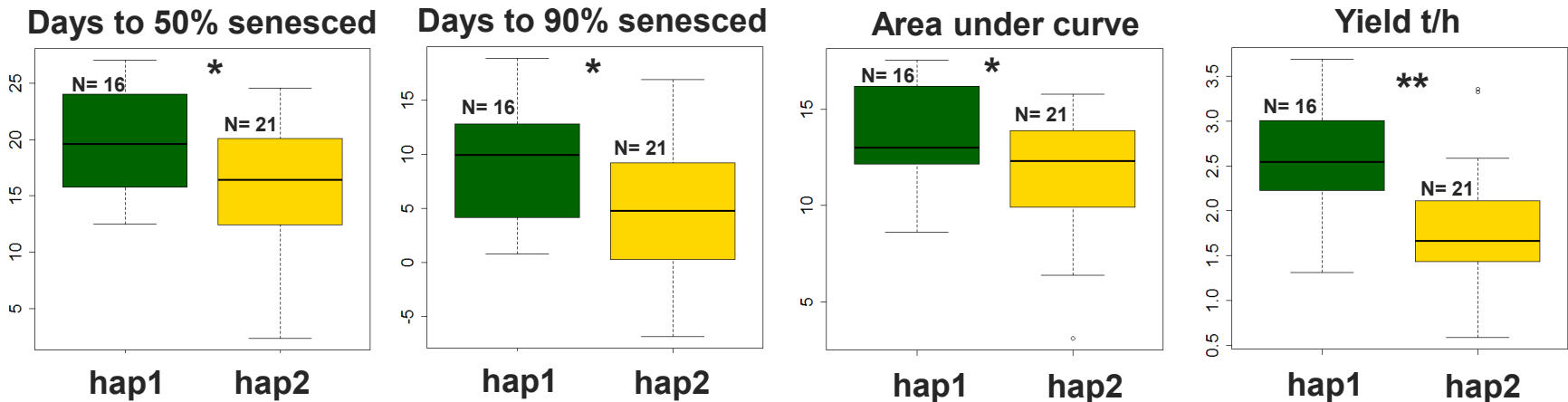
95% white heads

# GWAS for crown rot

- QTL on 6B
- Performed haplotype analysis
- The region is also associated with staygreen traits!

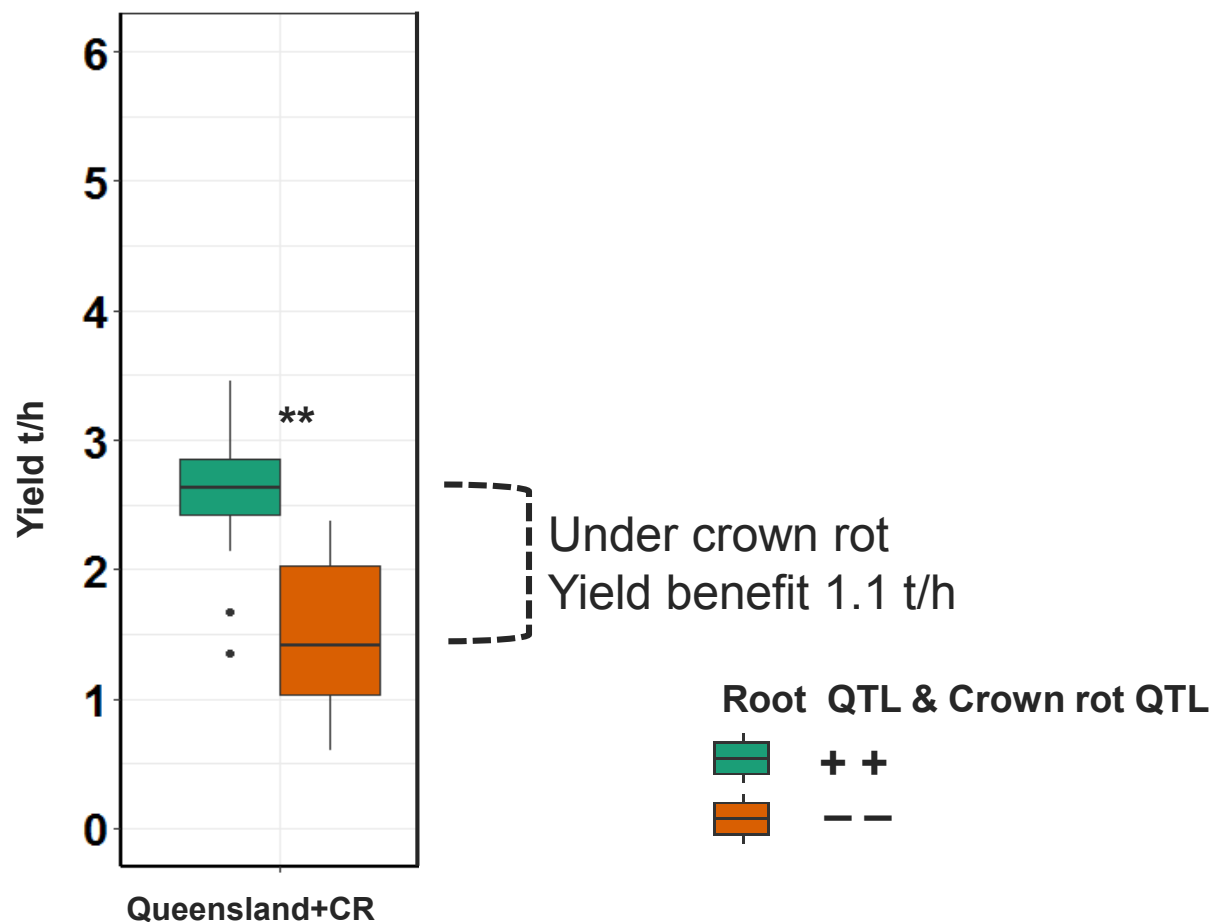


**Tolerance to crown rot achieved by modulating canopy development**





# Can we combine root and crown rot QTL?



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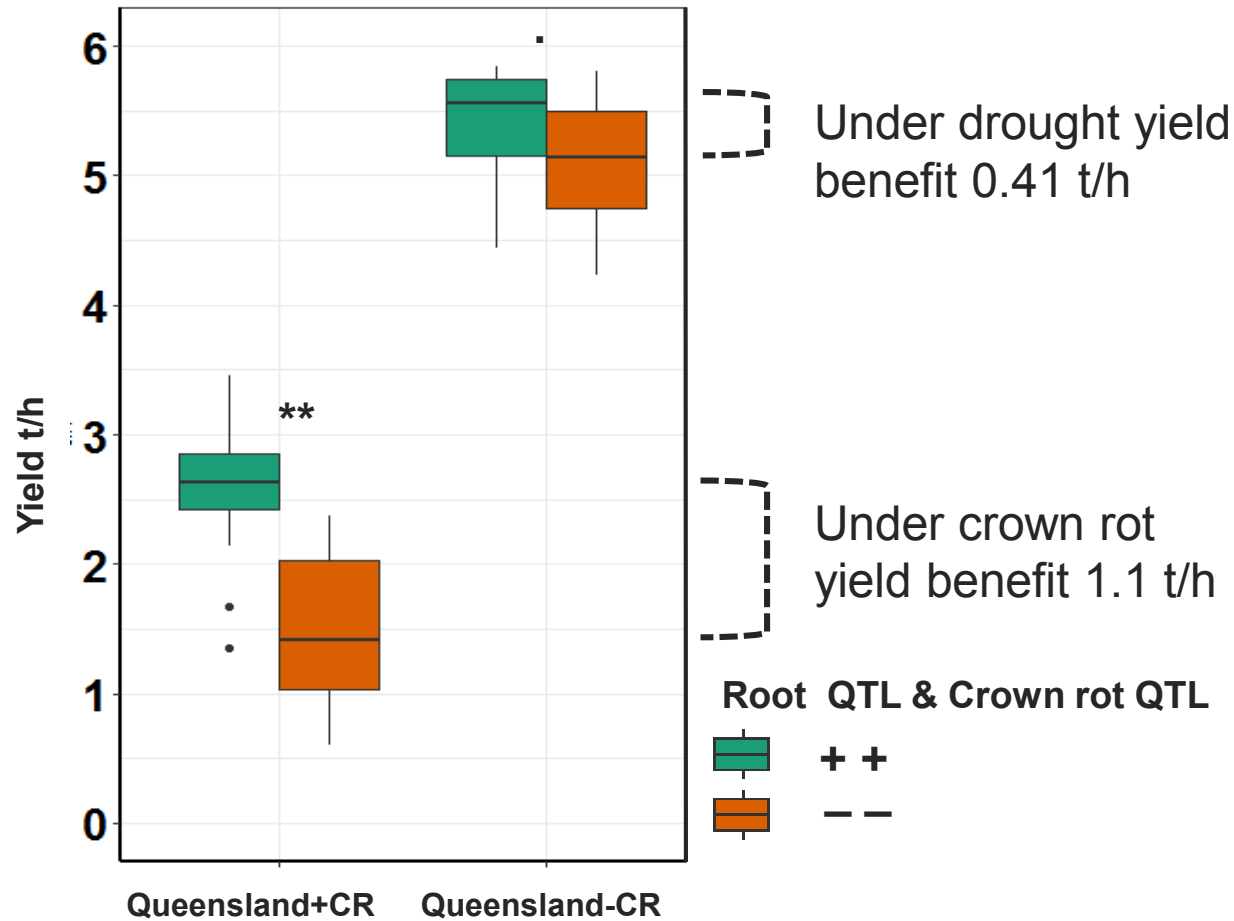


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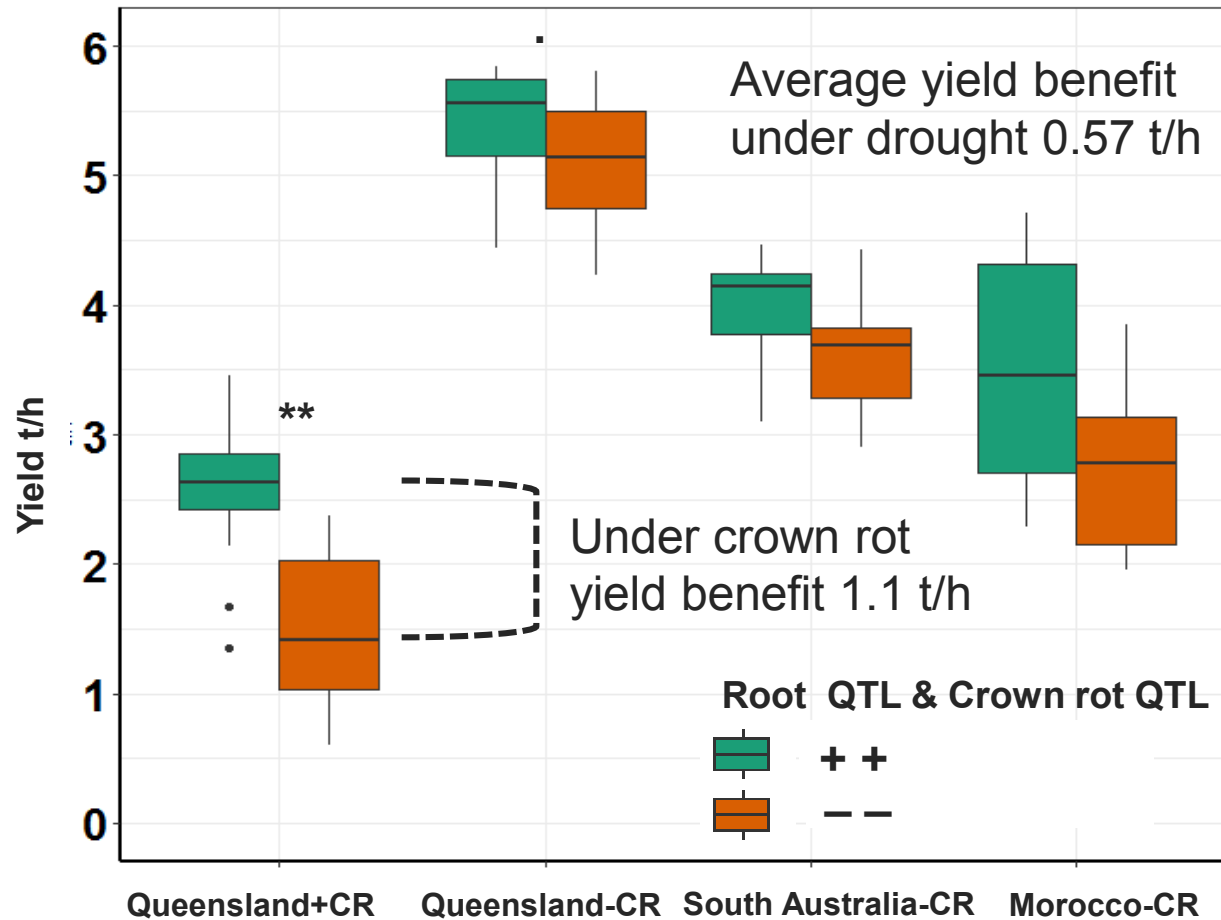


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# Can we combine root and crown rot QTL?



# Can we combine root and crown rot QTL?





# Take home messages

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- Powerful NAM population for studying WUE traits
- Major QTL for root architecture on 6A & crown rot on 6B
  - Opportunity to optimise WUE traits to enhance yield under drought and crown rot

## What's next?

- Validate trait combinations in a more diverse environmental context
- Combine favourable alleles using a genomic selection strategy

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University of Queensland Research Scholarship (UQRS)







# Questions?



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