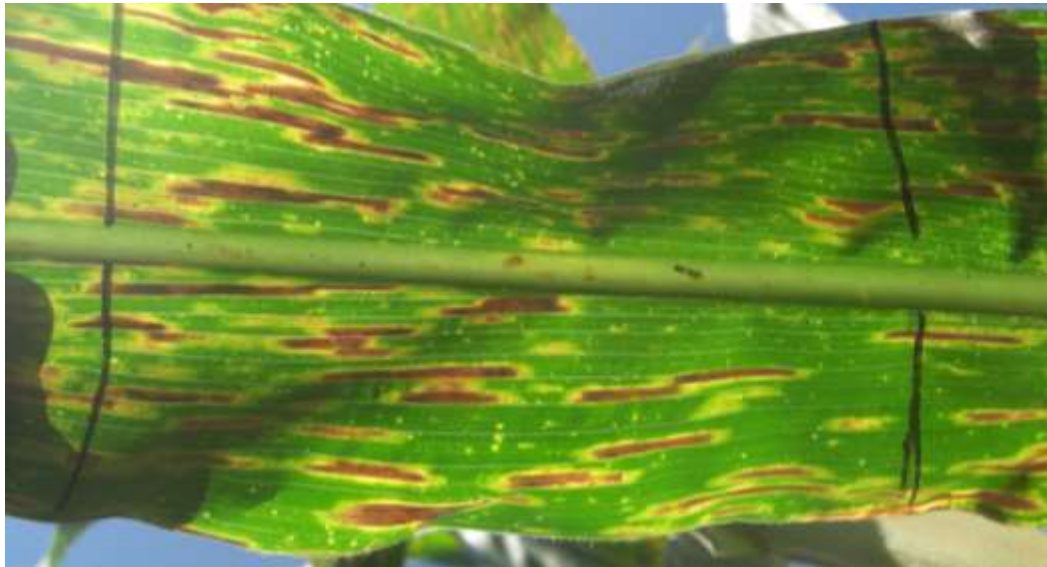


Transcriptional network analysis reveals candidate resistance mechanisms to grey leaf spot in maize



Prof. Dave Berger

Molecular Plant-Pathogen Interactions (MPPI) research group

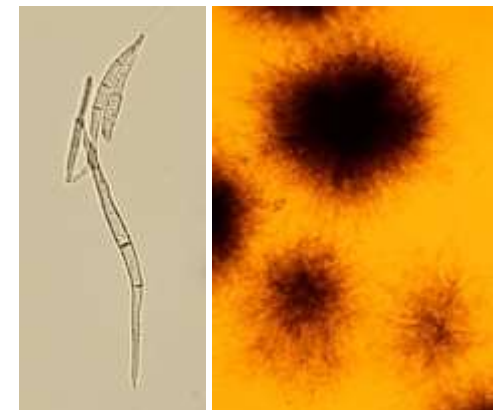


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Grey leaf spot disease of maize

- *Fungal pathogen - **Cercospora zeina***
- *Globally important*
 - *South Africa / East Africa*
 - *USA, Brazil, China*
- *No Till*
- *Yield losses 65%*



Control of grey leaf spot (GLS) disease

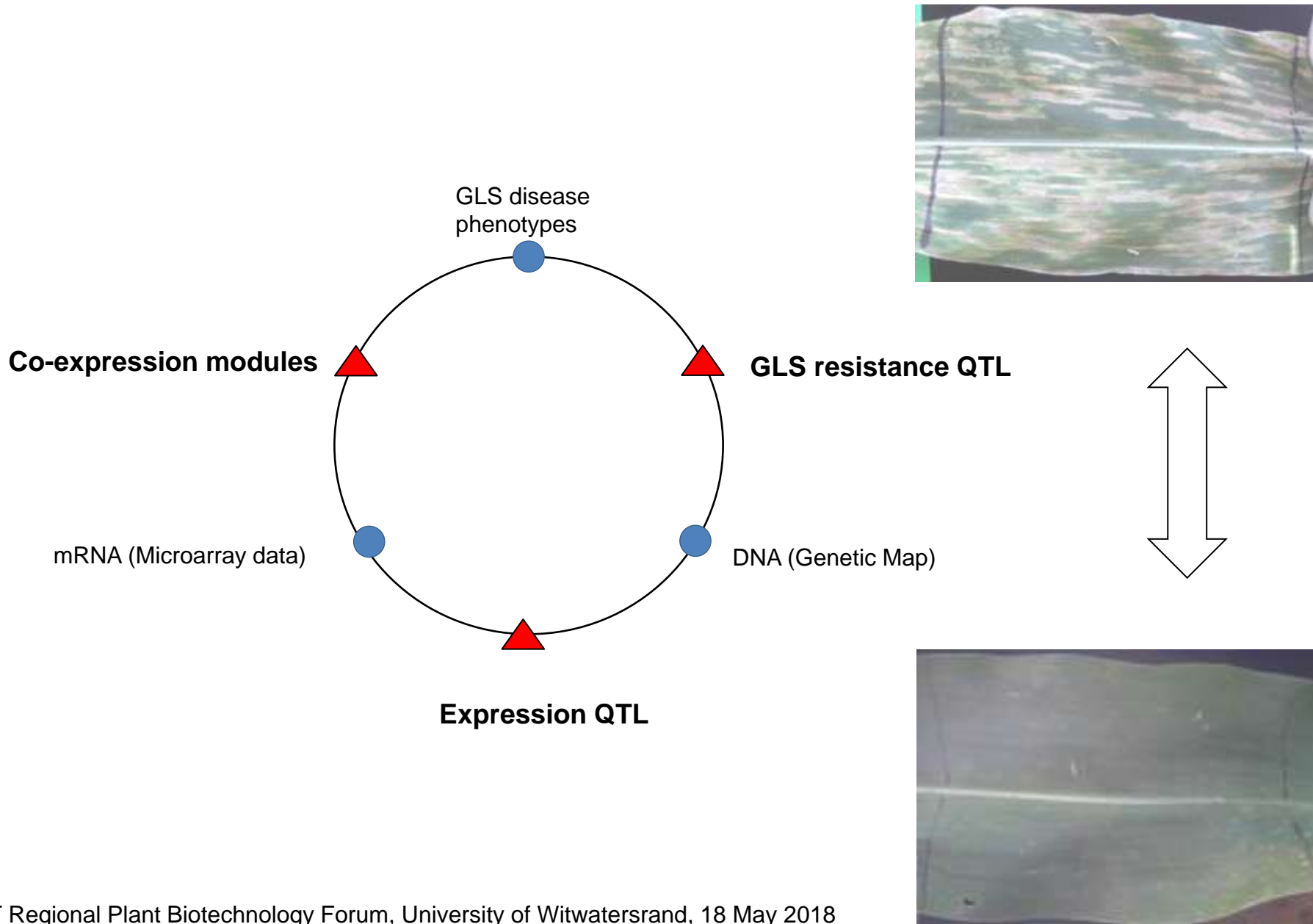
- *Agronomy*
- *Fungicides*
- ***Breeding***



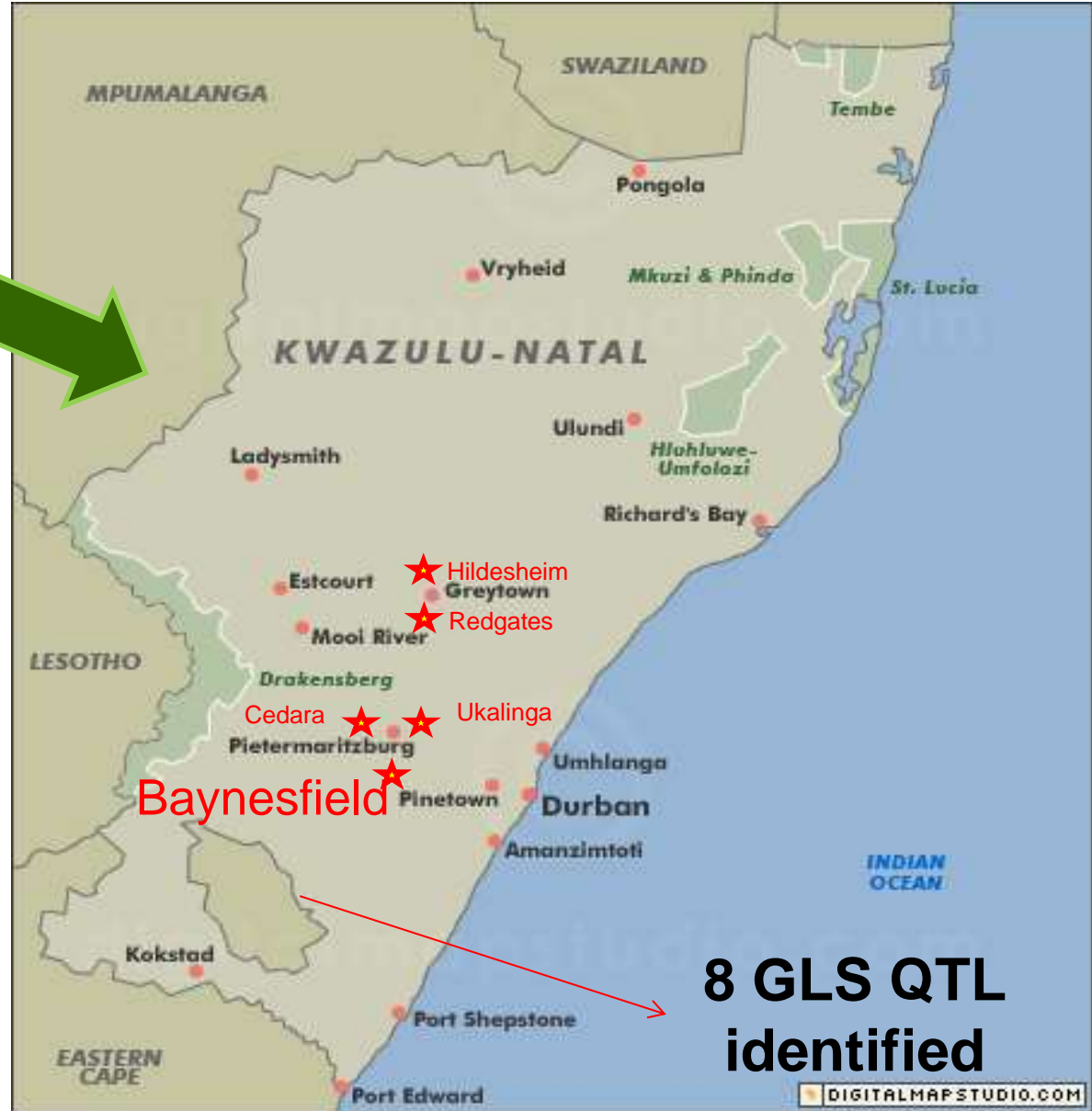
Quantitative resistance



Systems genetics: quantitative resistance to GLS



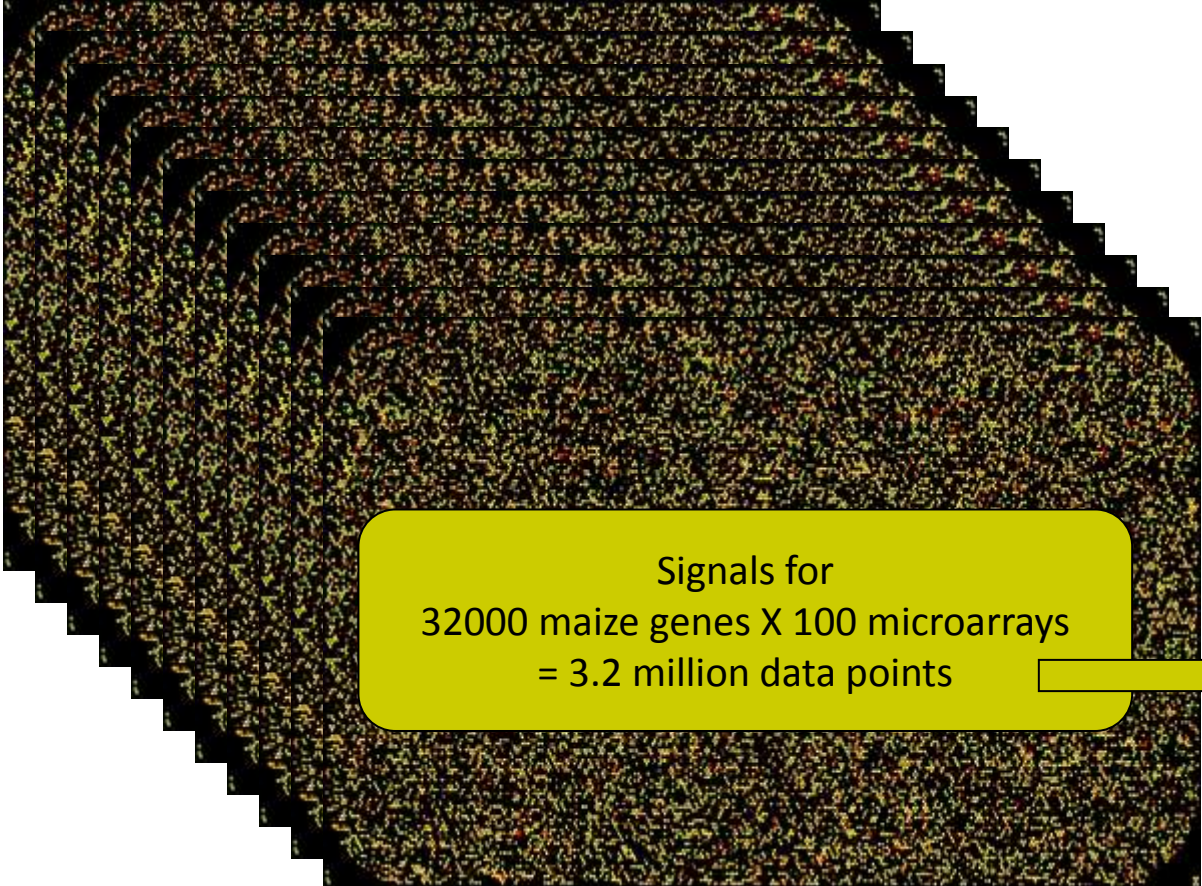
Step 1 - Field trial



Step 2: Global gene expression analysis – 100 RILs



Agilent maize 44K microarray



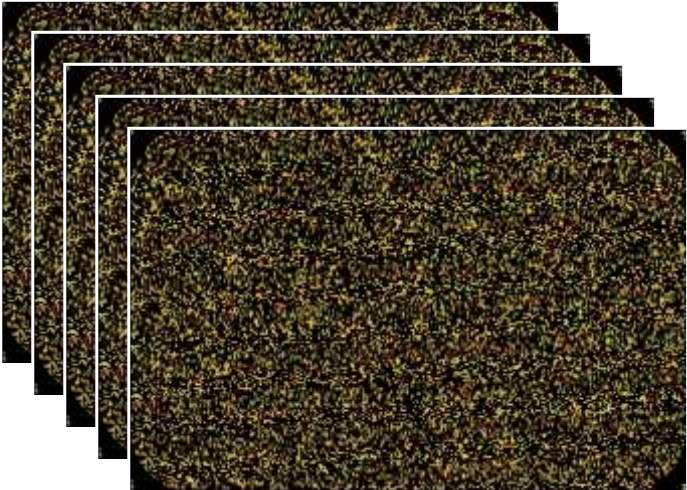
Signals for
32000 maize genes X 100 microarrays
= 3.2 million data points



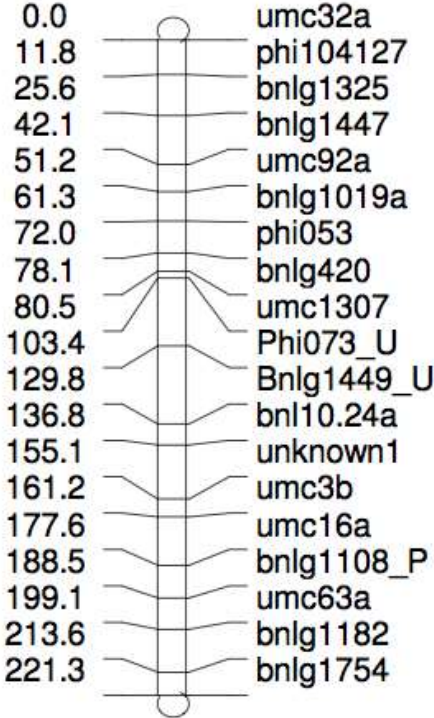
3 co-expression
modules
(statistical correlation with
GLS disease scores)

Step 3: eQTL analysis

Gene expression variation (per gene)
 Maize population (100 RILs)

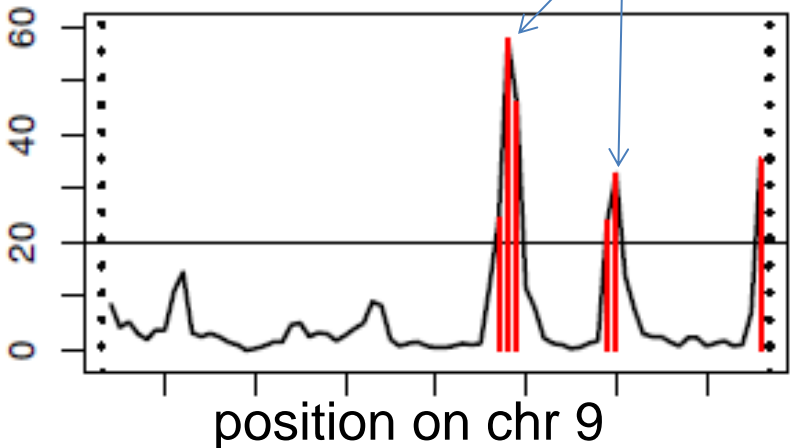


Genetic Map
 (167 markers)



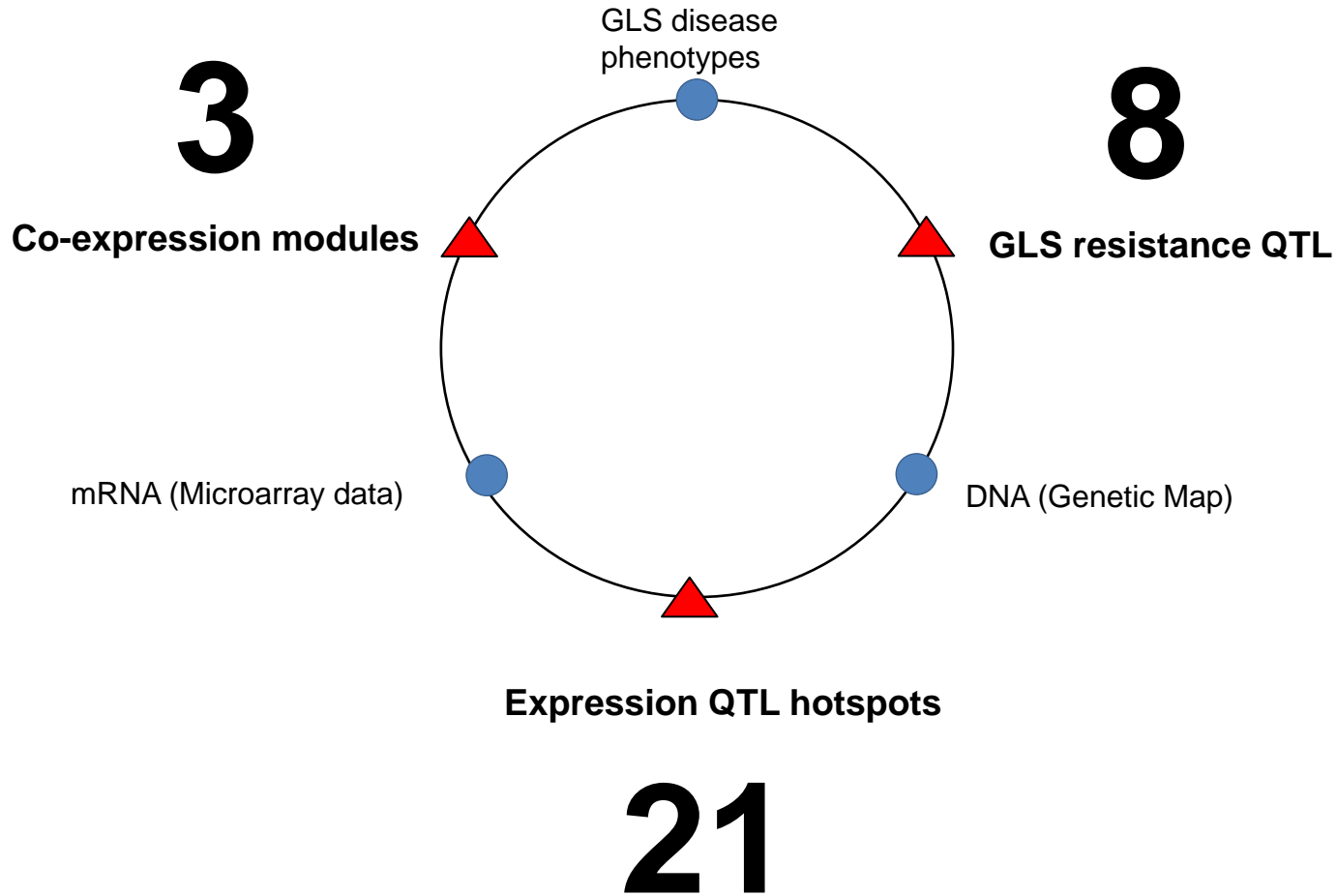
Trans-eQTL “hotspots”

genes

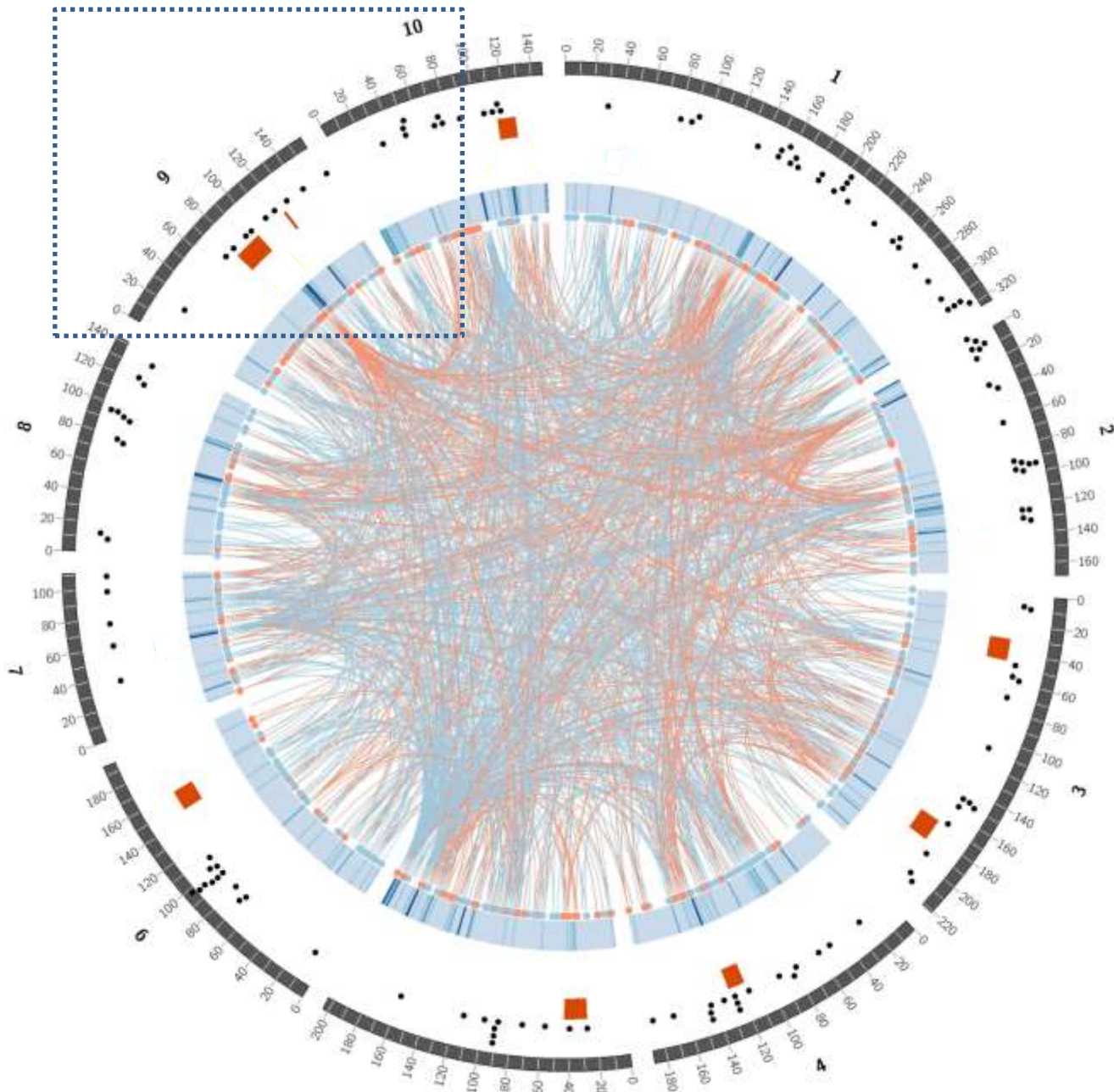


21
 trans-eQTL “hotspots”
 across maize genome

Data integration



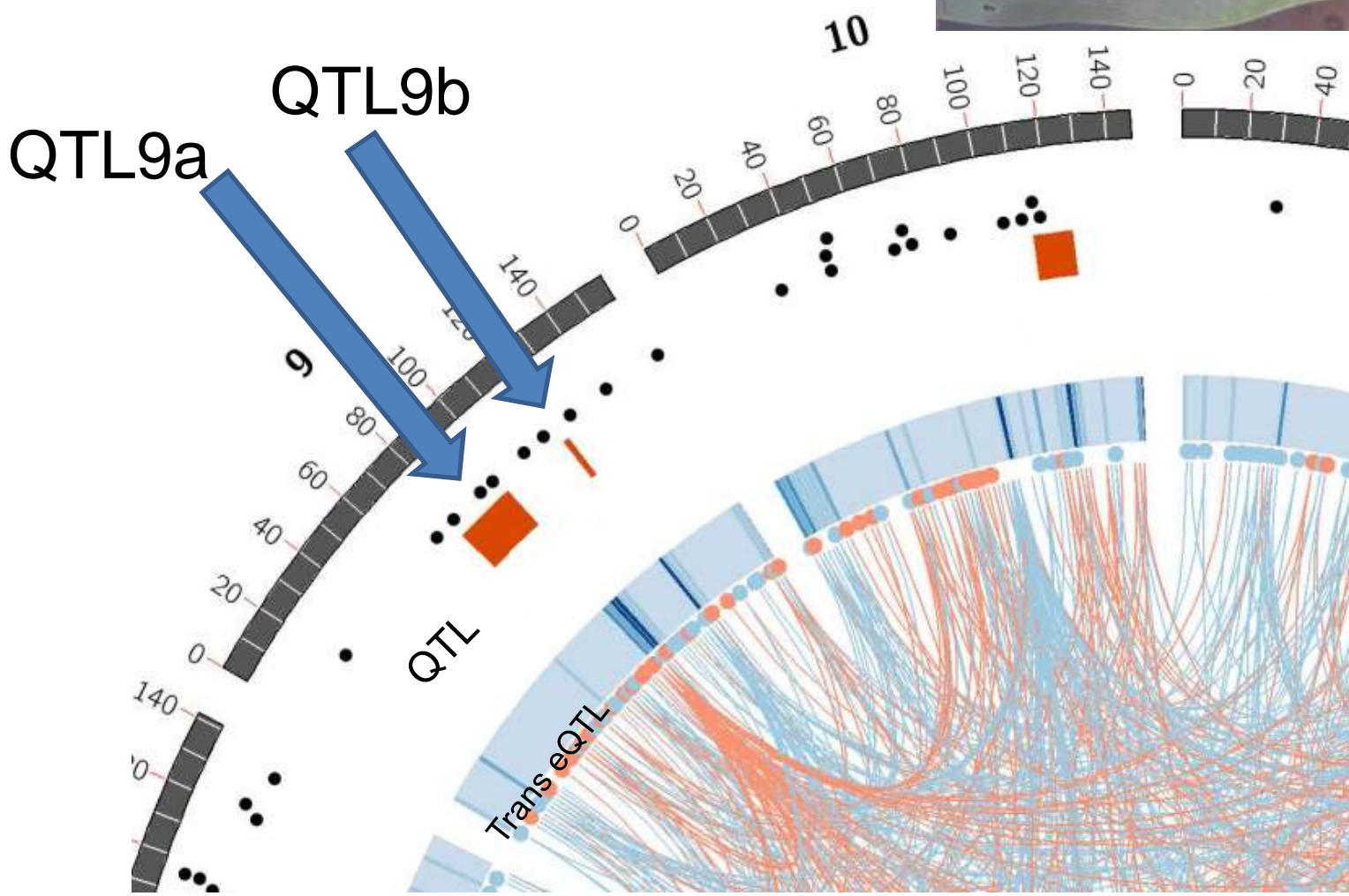
Gene network: R1 co-expression module (1498 genes)



R1 Co-expression module correlated with Resistance (1498 genes)

QTL9a – overlap trans eQTL hotspot (135 genes)

QTL9b – overlap trans eQTL hotspot (88 genes)



Conclusions - resistance

“R1 resistance gene network” in sub-tropical maize

Jasmonate signalling

Callose deposition

Meyer et al. BMC Plant Biology 17, 197, (2017)

Christie et al. Plant Journal, 89, 746-763 (2017)



“WikiProtocol” – Systems genetics experiment

Christie et al. The Plant Journal 89, 746-763, (2017).

What:

Plant population segregating for trait

Identify relevant tissue/time point

Skills – Field, Lab, Bioinformatics

How:

Phenotype (e.g. GLS disease 1-9 scale)

Genotype (e.g. maize SSR map)

Gene expression profile (e.g. microarray)

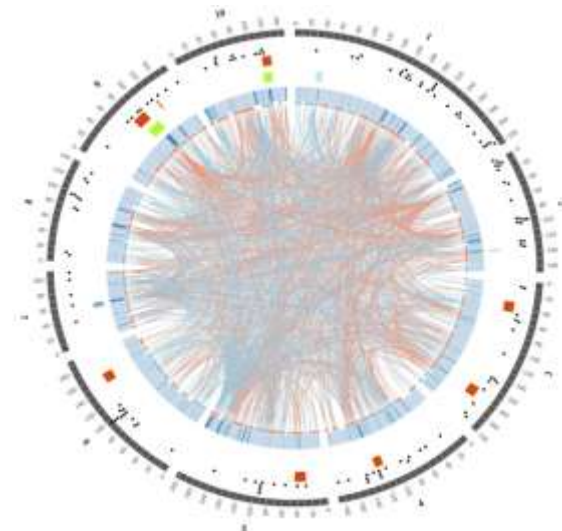
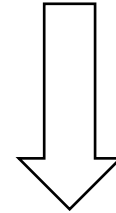
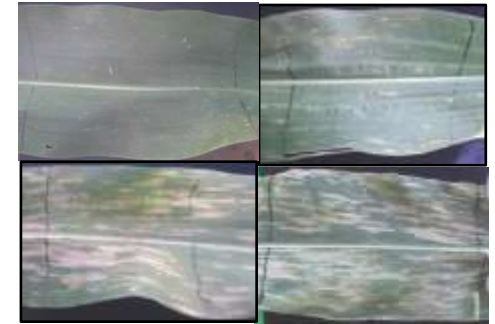
Identify:

- a. QTL
- b. Gene co-expression modules
- c. expression QTL

Integrate co-expression, QTL, eQTL data

Why:

Identify genes, regulators, processes relevant to trait



Acknowledgements



Dr Nanette Christie
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Dr Bridget Crampton



Dr. Shane Murray



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