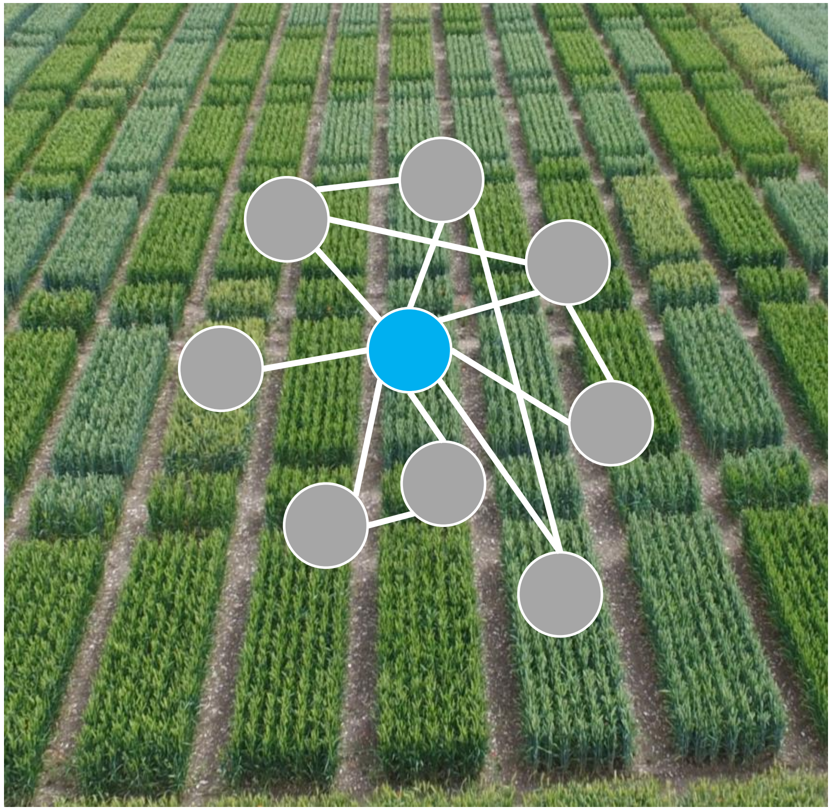
Gene Networks to Predict Gene Function

Philippa Borrill



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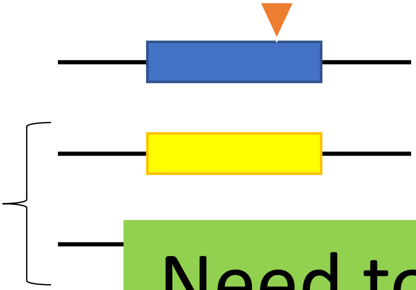


Gene editing

Natural/
induced
variation

Need to predict gene function

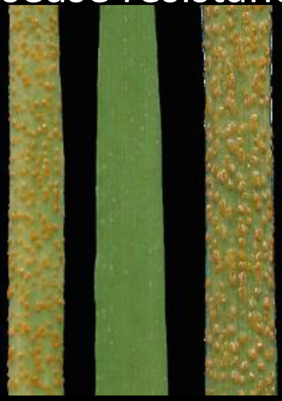
Genomics

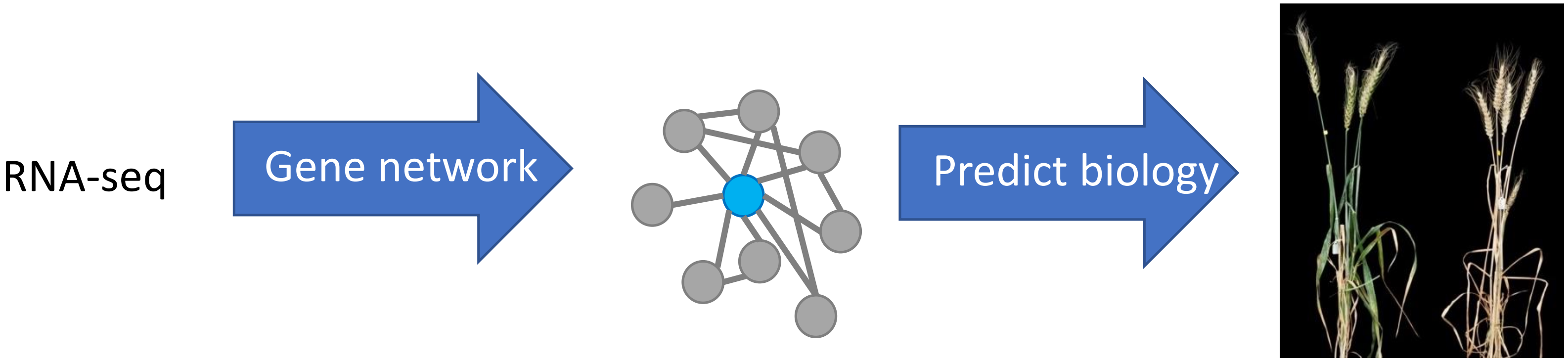
- >1,500 RNA-Seq samples

Grain yield

Grain quality

Disease resistance

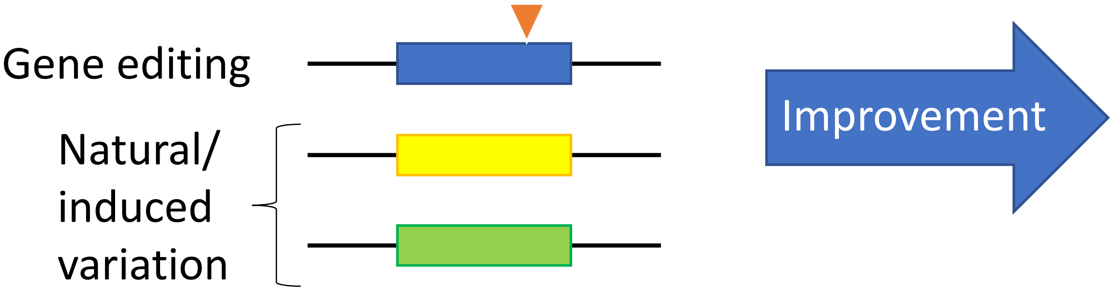




RNA-seq

Gene network

Predict biology



Gene editing

Natural/
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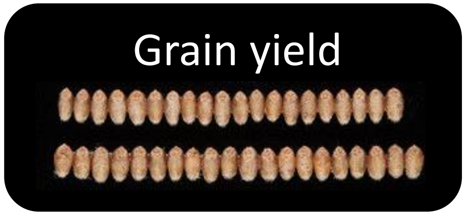
variation

Improvement



Grain yield

Grain quality

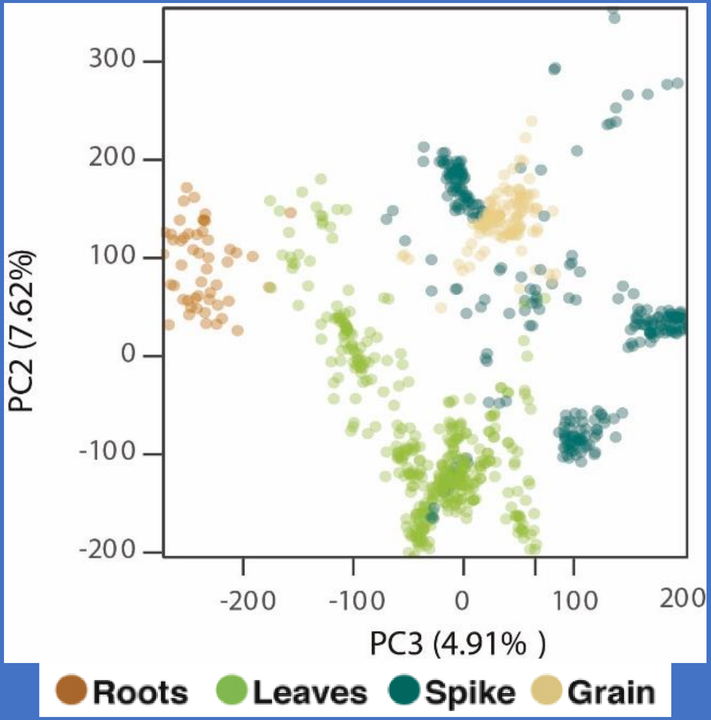
Disease
resistance

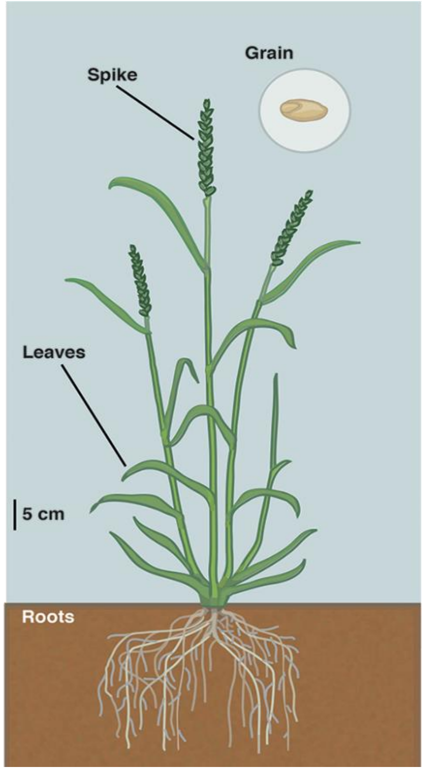
Combining datasets

Origin	# studies	# samples
Public	27	499
New datasets	7	351
Total	34	850

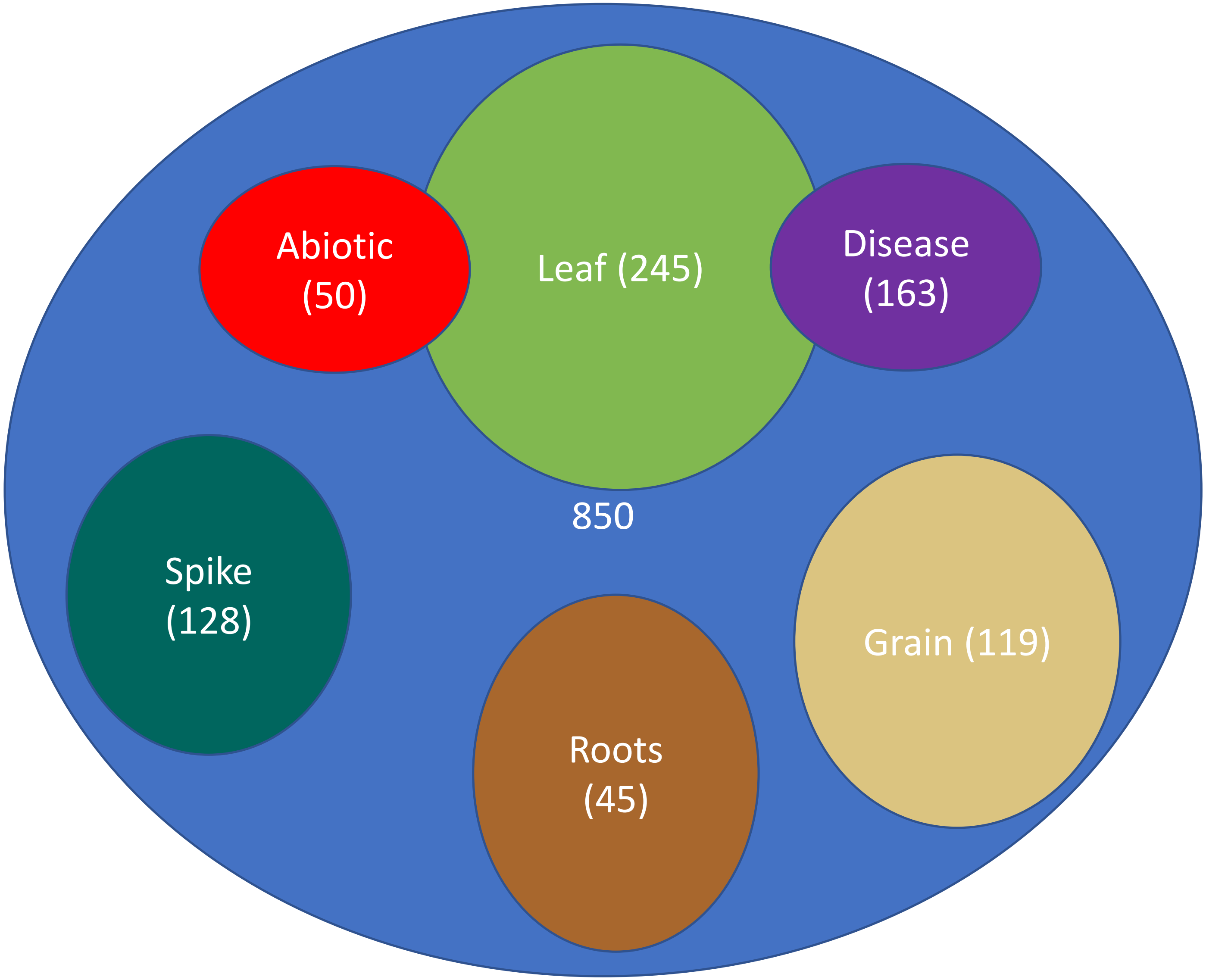
Ramirez-Gonzalez, Borrill *et al.*, *Science* 2018

Datasets used for network analysis





Datasets used for network analysis:



Abiotic (50)

Leaf (245)

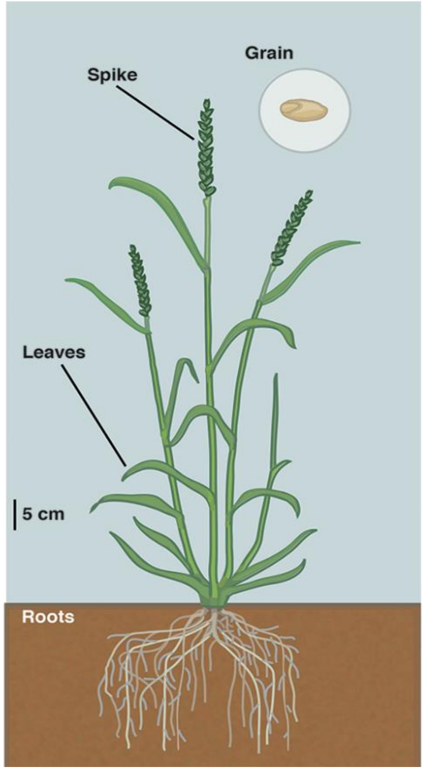
Disease (163)

850

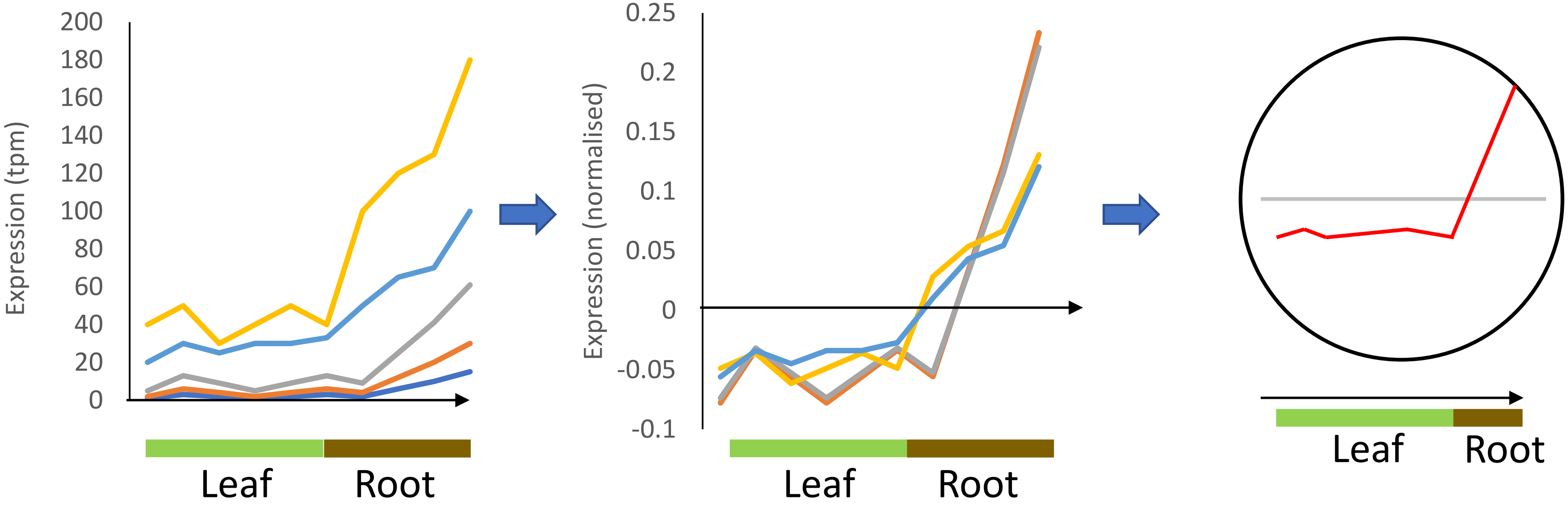
Spike (128)

Grain (119)

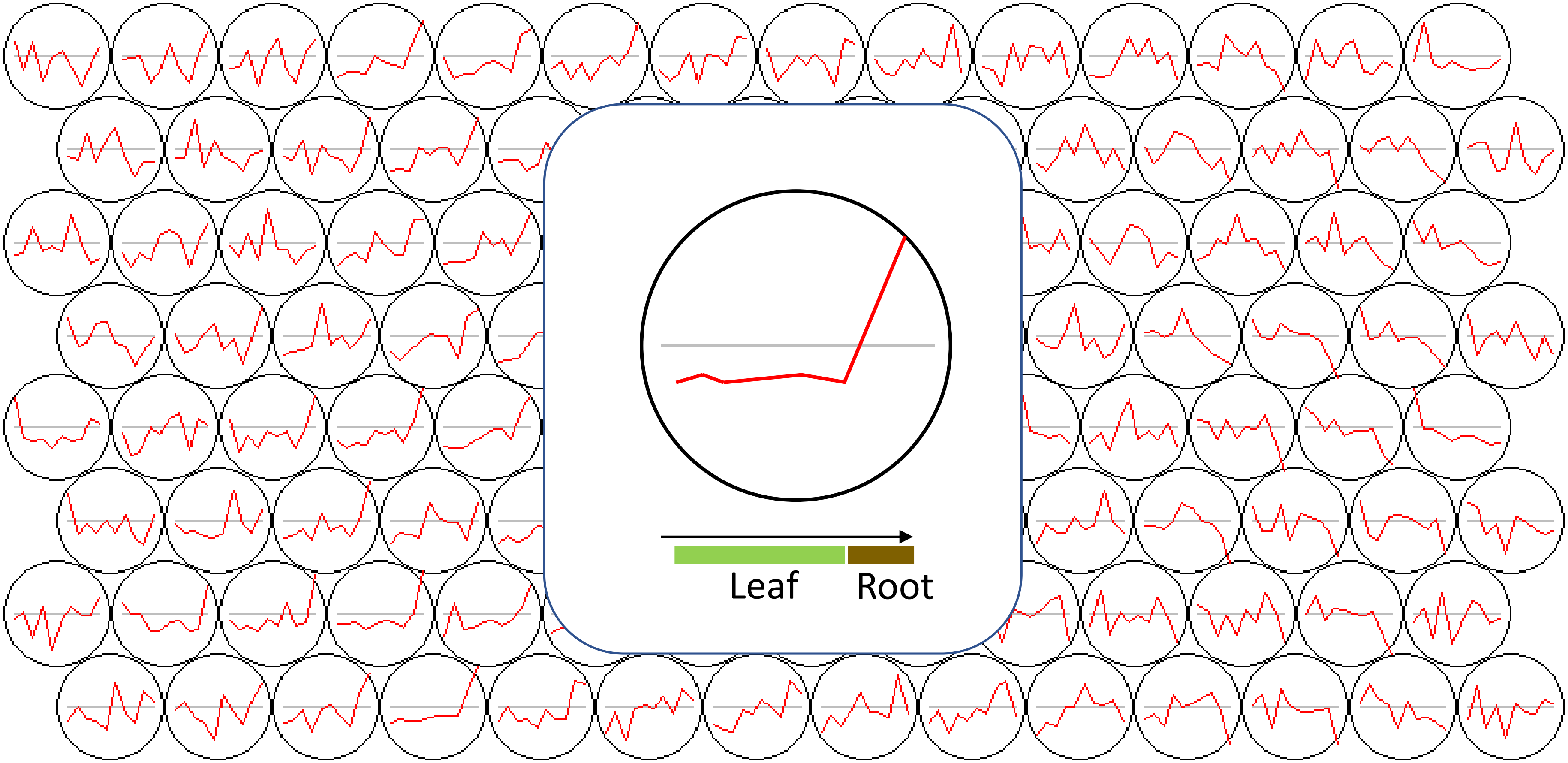
Roots (45)



Co-expression

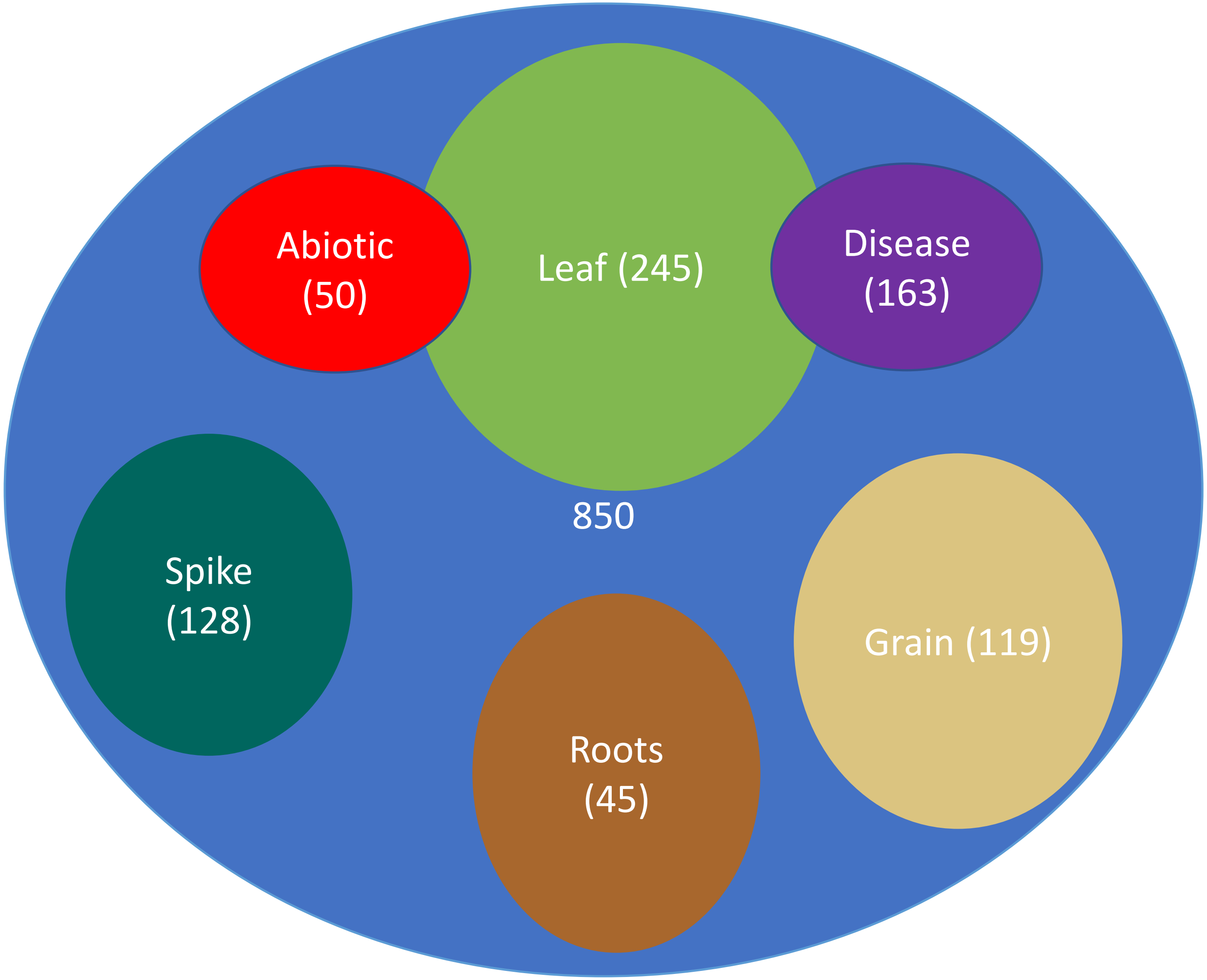


Many patterns of co-expression



Co-expression patterns can gives clues about gene function

Datasets used for network analysis



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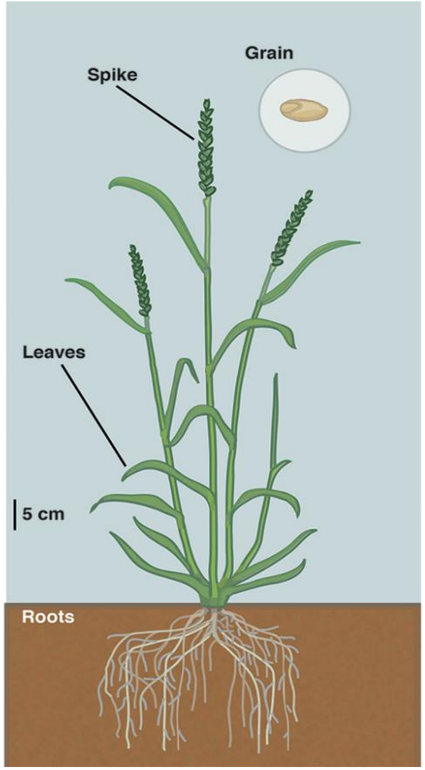

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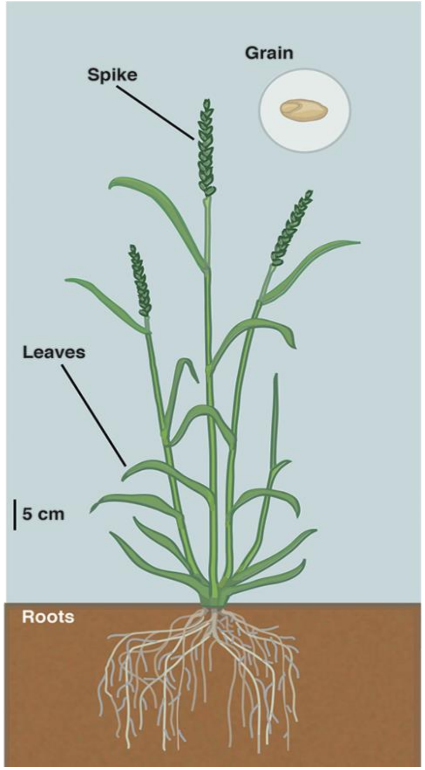


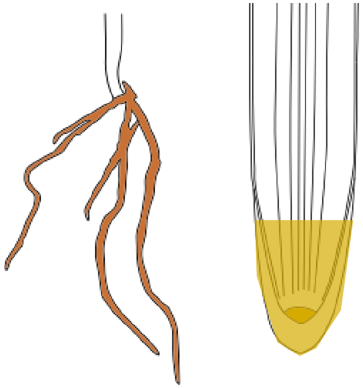
Roots
(45)

Root network

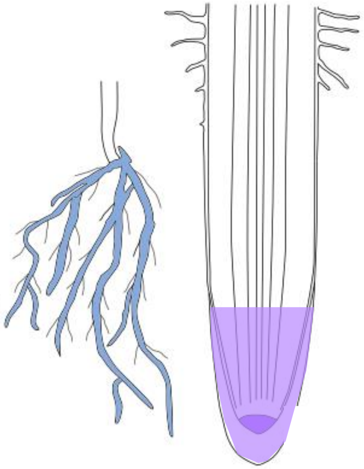
45 root samples

Germination

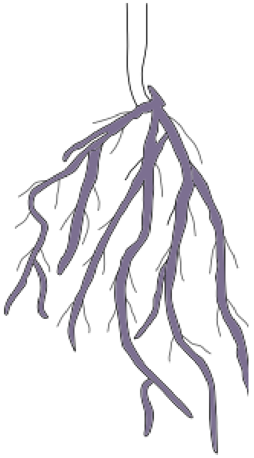
Three leaf stage



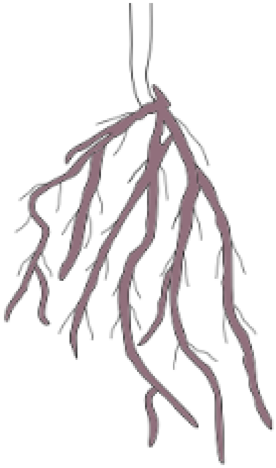
Tillering stage



Flag leaf stage



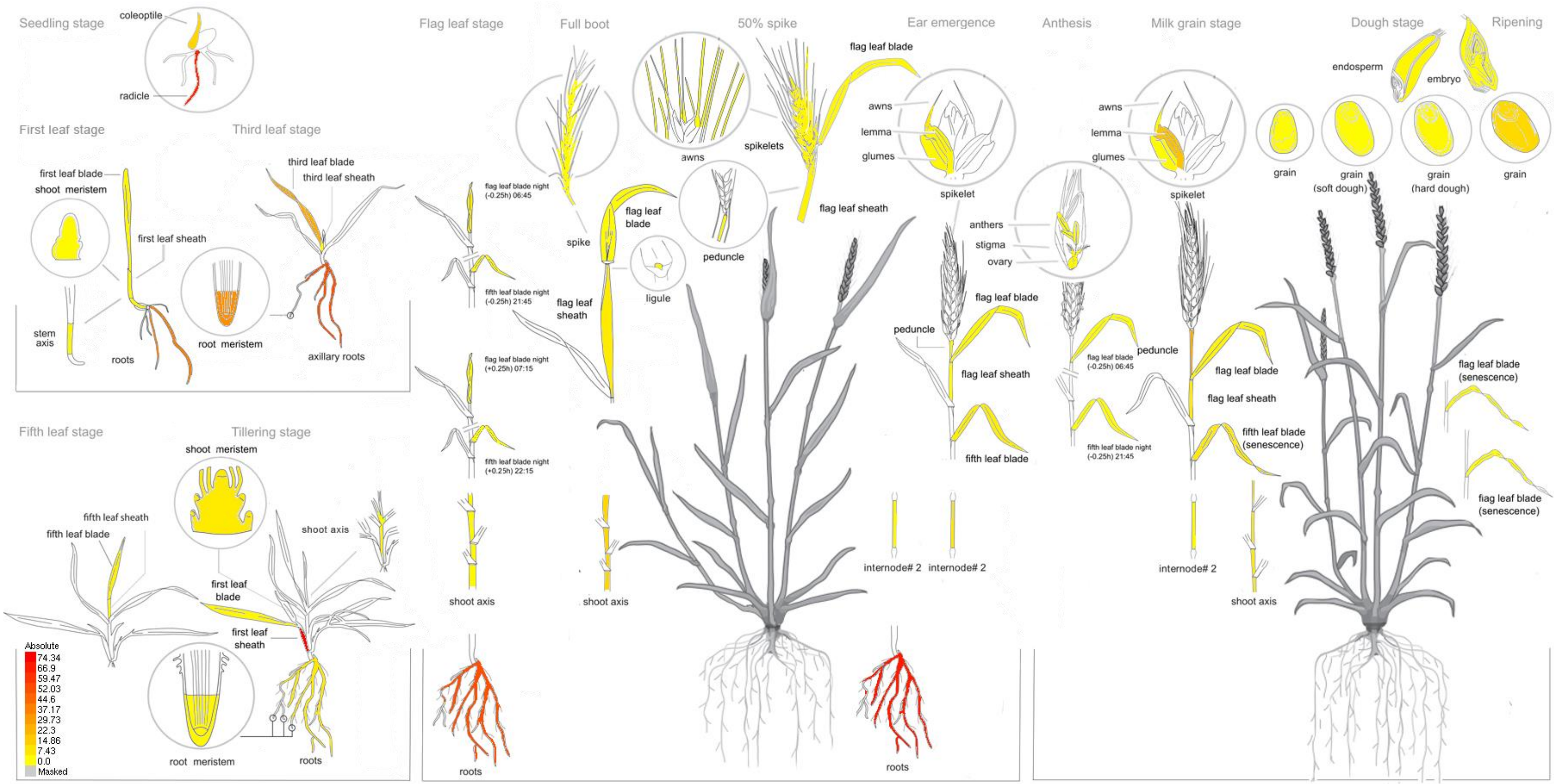
Spike emergence



Bayer CropScience

BASF
We create chemistry

http://bar.utoronto.ca/efp_wheat/cgi-bin/efpWeb.cgi



Ramirez-Gonzalez, Borrill *et al.*, *Science* 2018

John Jacobs
Mark Davey
Fred Van Ex

BASF
We create chemistry

Bayer CropScience

Nicholas Provart

UNIVERSITY OF TORONTO

Andy Sharpe

UNIVERSITY OF SASKATCHEWAN

Yogendra Khedikar

Agriculture and Agri-Food Canada

Root network

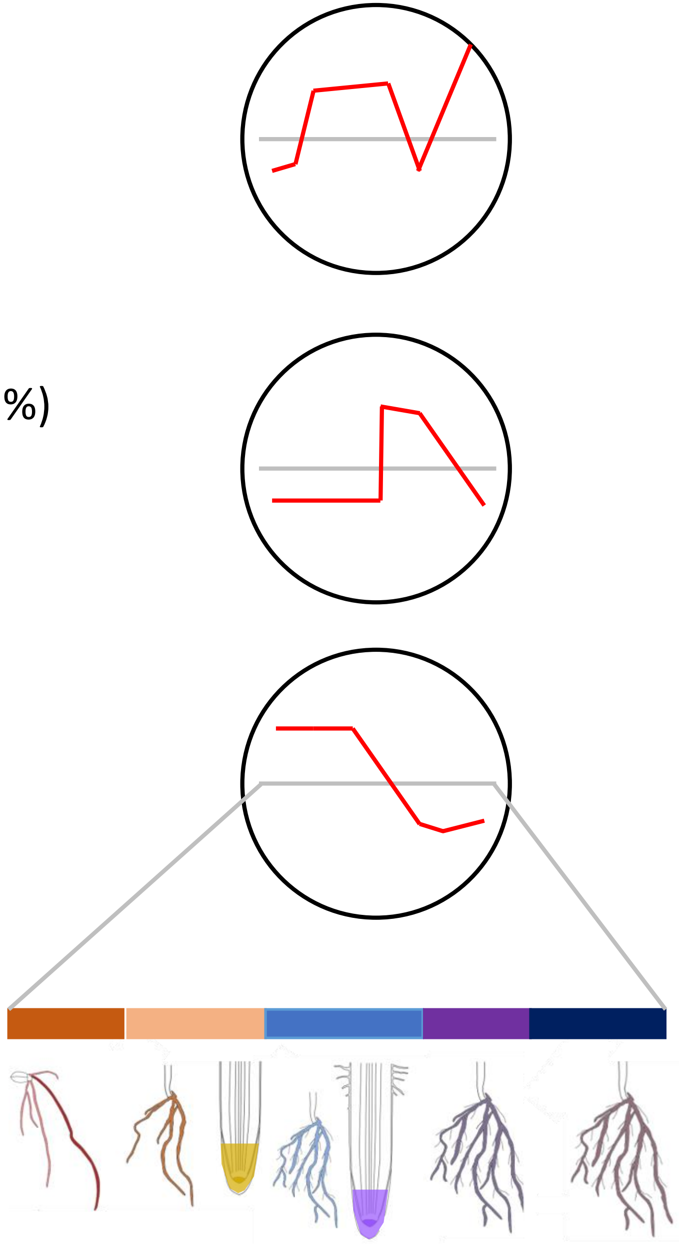
72,370 genes expressed

↓

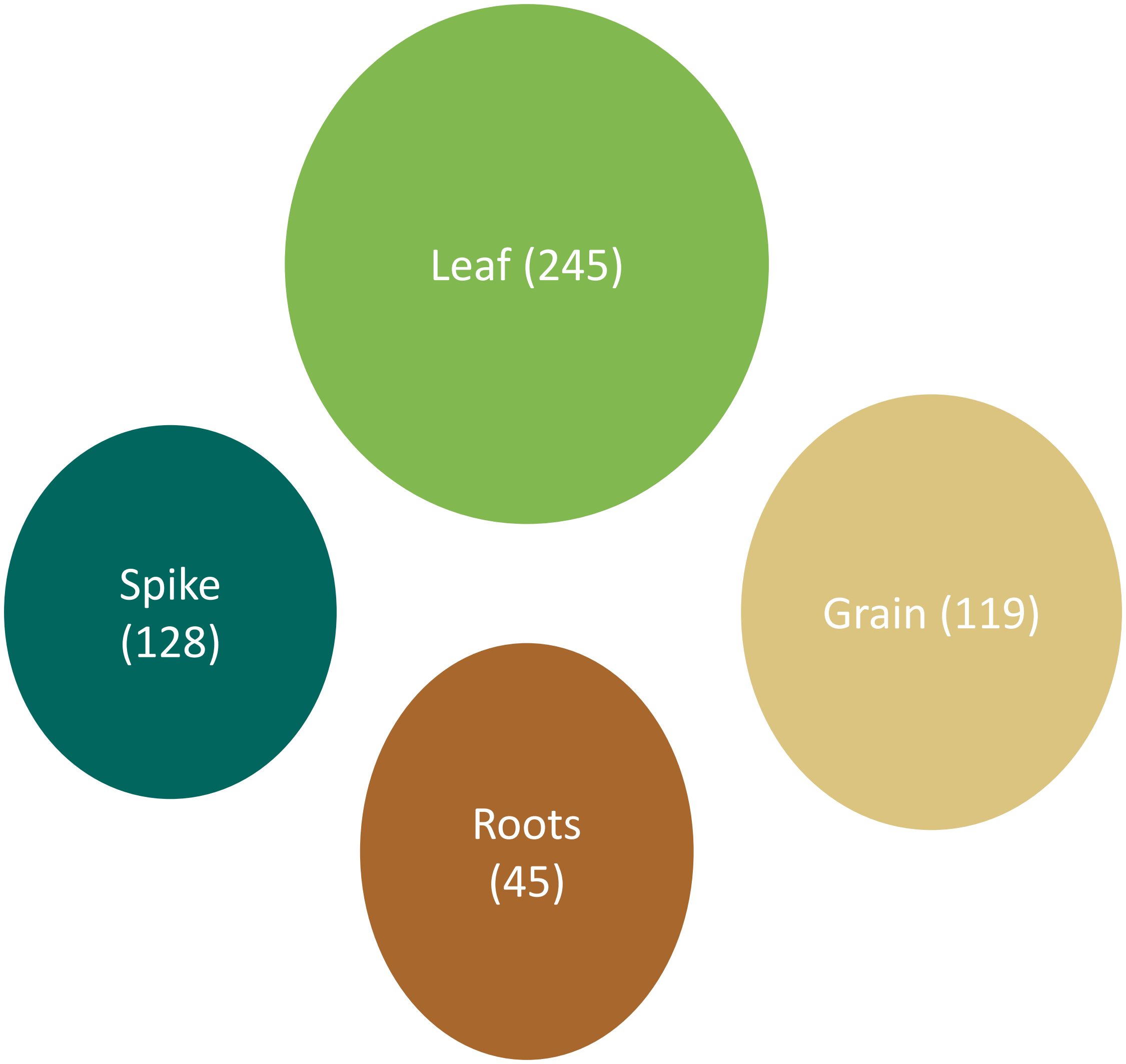
63,686 genes assigned to clusters (88 %)

↓

72 clusters



Network conservation between tissues



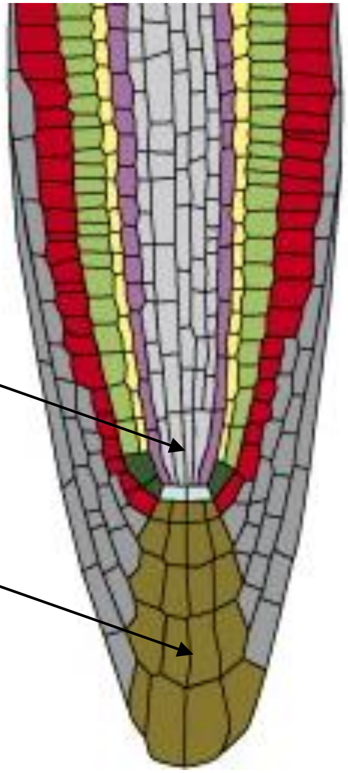
Leaf (245)

Spike (128)

Grain (119)

Roots (45)

Root specific cluster – 82 genes



Root procambium

p-value 3.25E-05

Central root cap of primary root

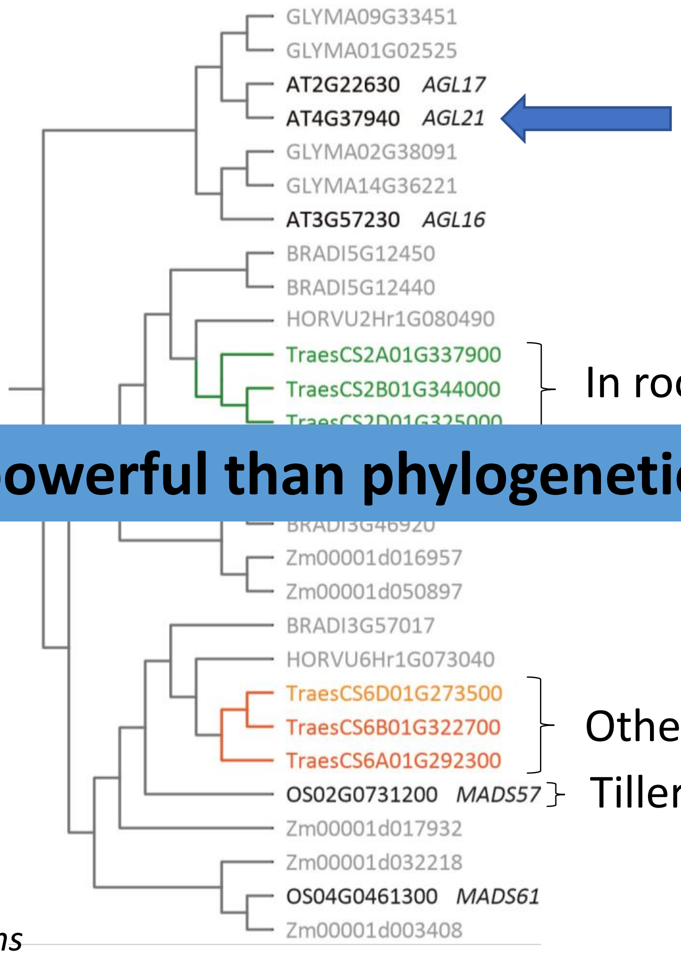
p-value 4.48E-05

Image from: Péret *et al.*, 2009 *Trends in Plant Science*

Root specific cluster

10 TFs: 3 are MADS_II homoeologues

Orthologue *AtAGL21* – role in lateral root development



In root specific cluster

More powerful than phylogenetics alone

nt

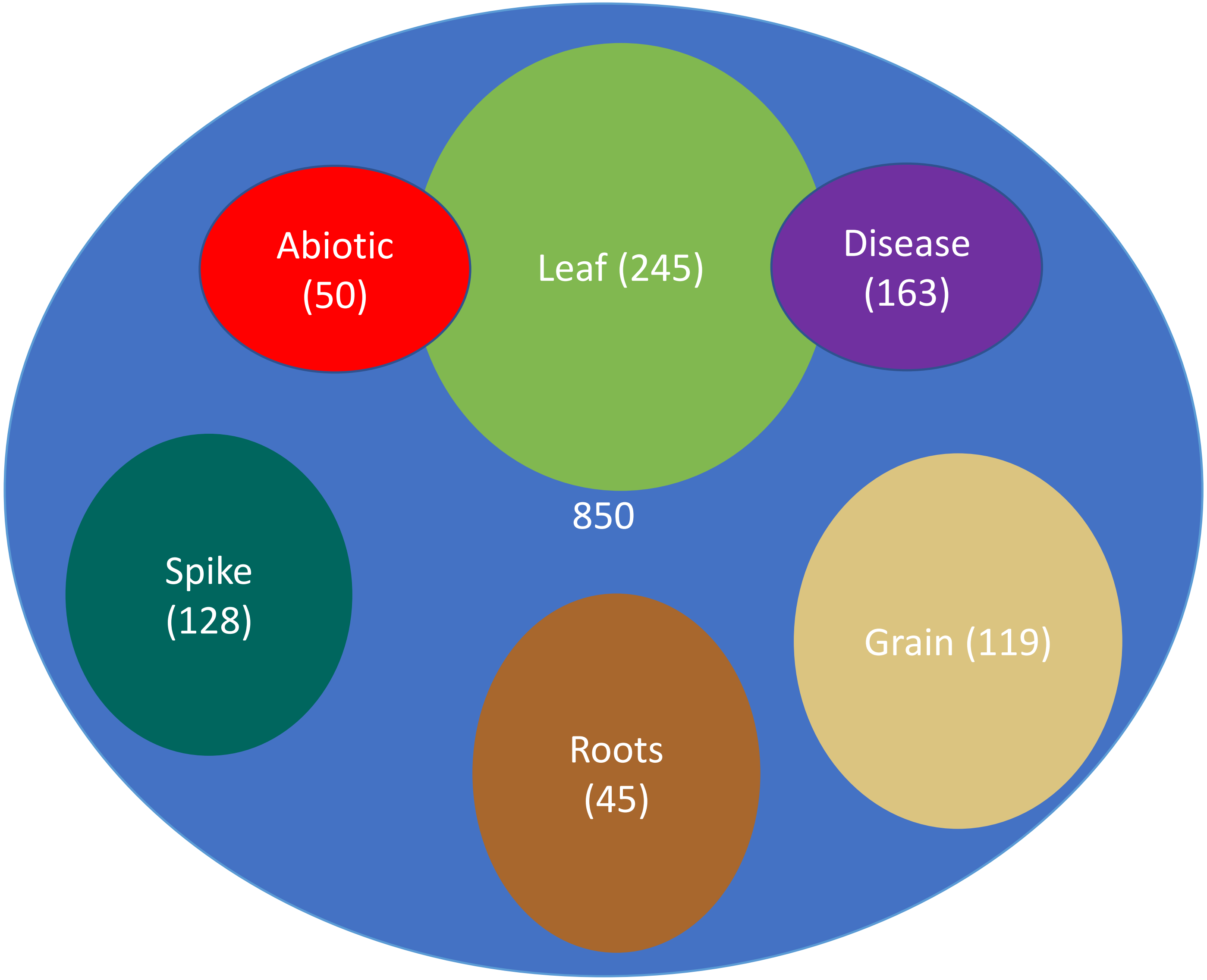
Other clusters

Tillering

Yu *et al.*, 2014 *Molecular Plant*
Guo *et al.*, 2013 *Nature Communications*
CN104140971B

Ramirez-Gonzalez, Borrill *et al.*, *Science* 2018

Datasets used for network analysis



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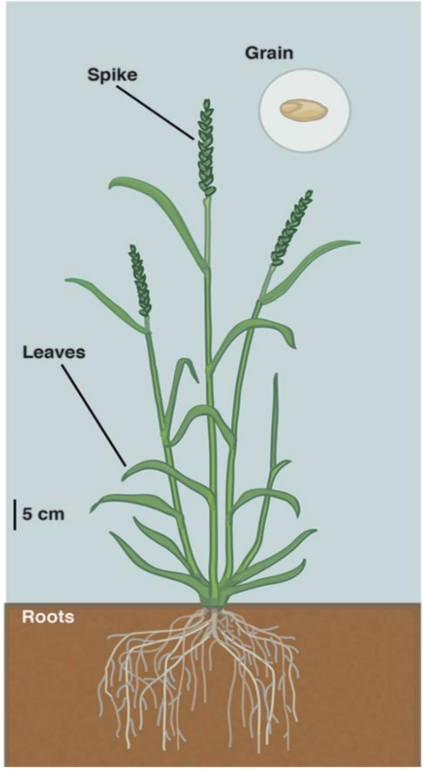


Disease network – 163 samples

All leaf samples from seedling/young vegetative plants

Yellow rust

Powdery mildew

Septoria tritici blotch

Fusarium (crown rot)

Chitin

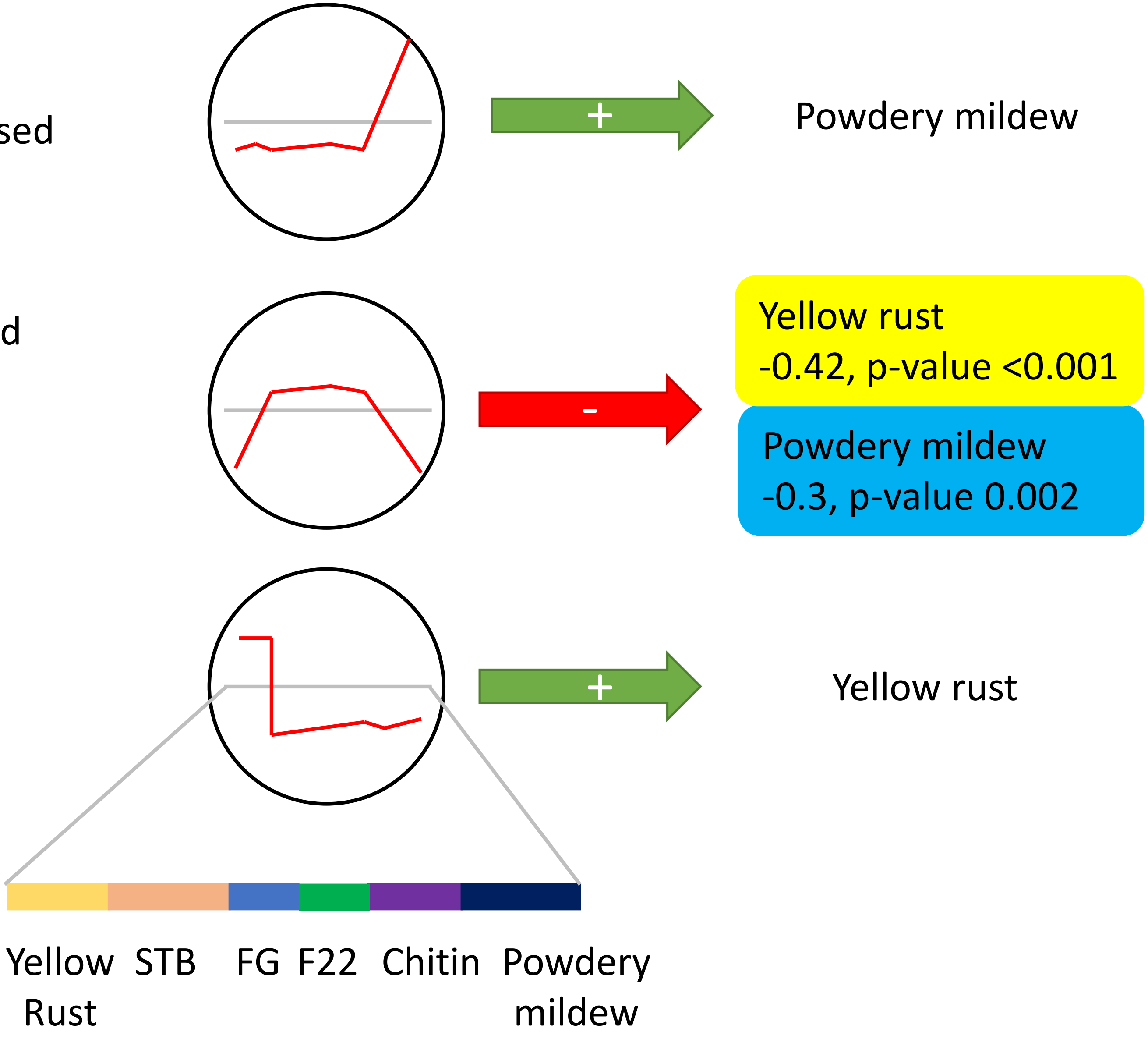
Flg22

Disease network

74,592 genes expressed

55,647 genes assigned to clusters (74.6 %)

69 clusters



+

Powdery mildew

-

Yellow rust
-0.42, p-value <0.001

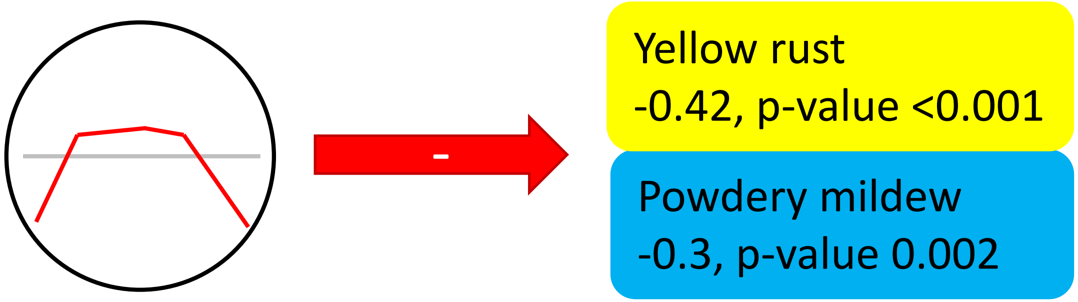
Powdery mildew
-0.3, p-value 0.002

+

Yellow rust

Yellow Rust STB FG F22 Chitin Powdery mildew

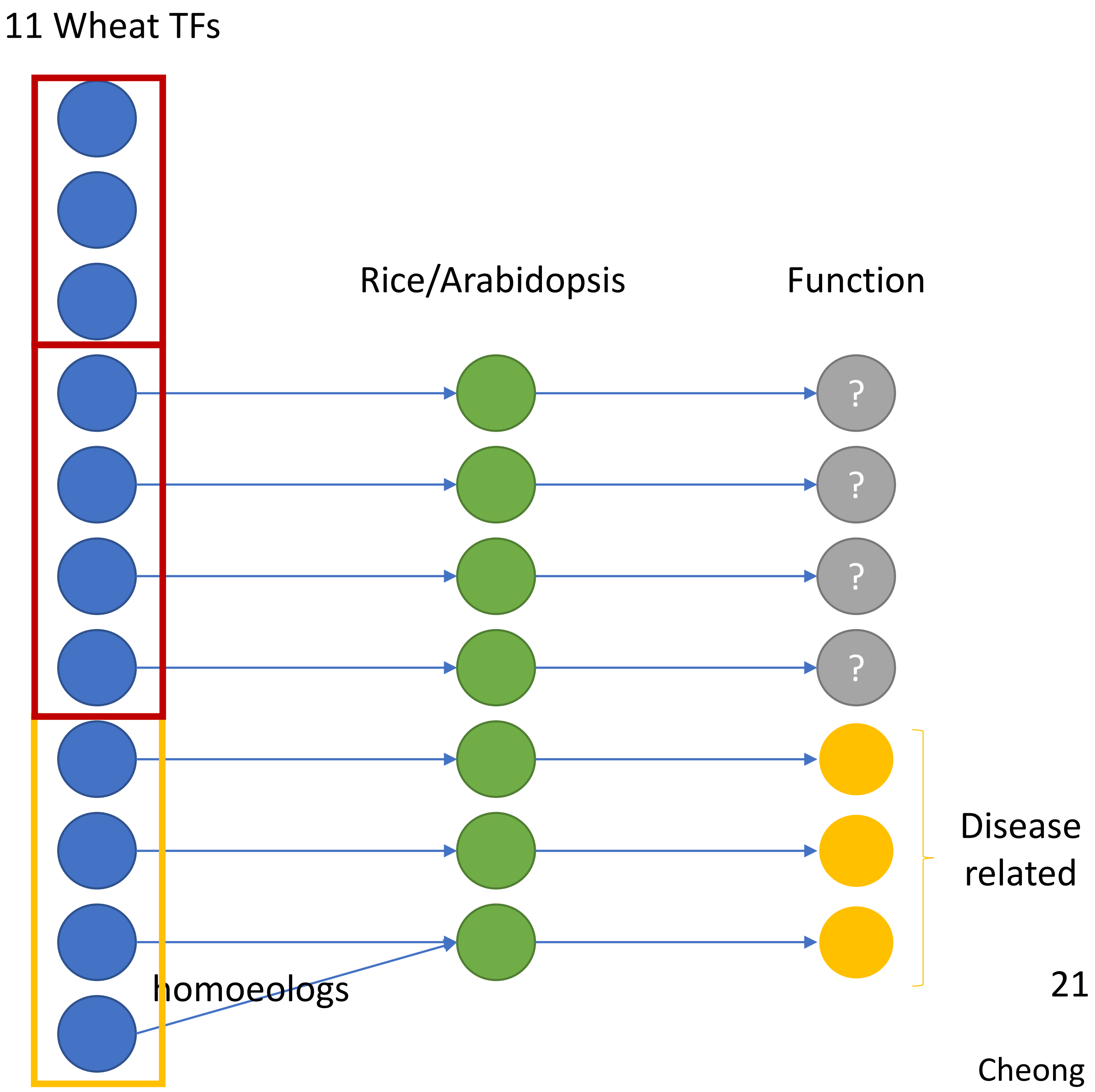
Yellow rust and powdery mildew cluster



Yellow rust
-0.42, p-value <0.001

Powdery mildew
-0.3, p-value 0.002

- 542 genes
- GO enrichment:
    - generation of precursor metabolites and energy
- 11 TFs



11 Wheat TFs

Rice/Arabidopsis

Function

?

?

?

?

Disease related

homoeologs

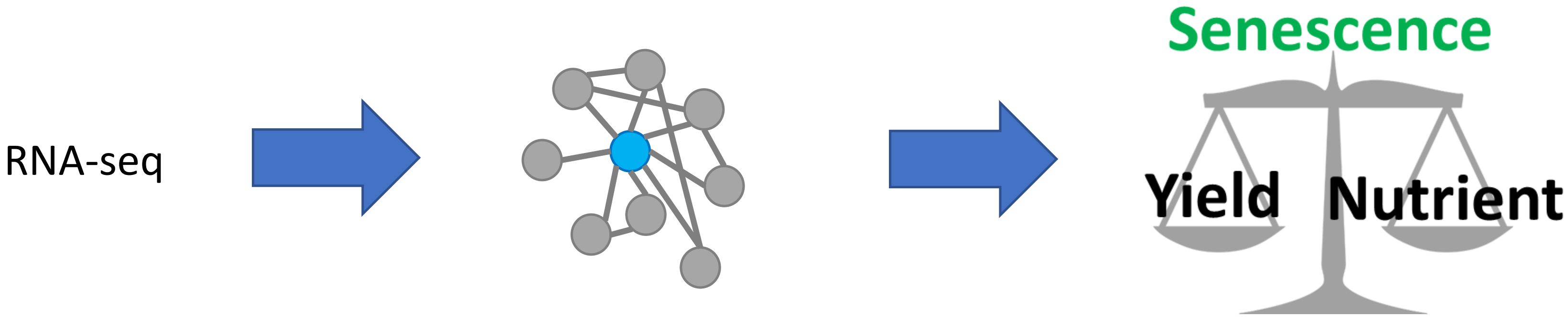
AtJAZ12

OsWRKY80

OsVOZ2

21 DPI *Xanthomonas oryzae*

Cheong *et al.*, 2013, *PLOS ONE*

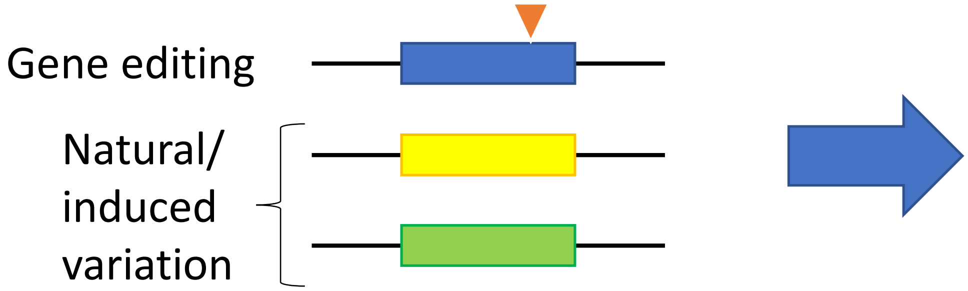


RNA-seq

Senescence

Yield

Nutrient



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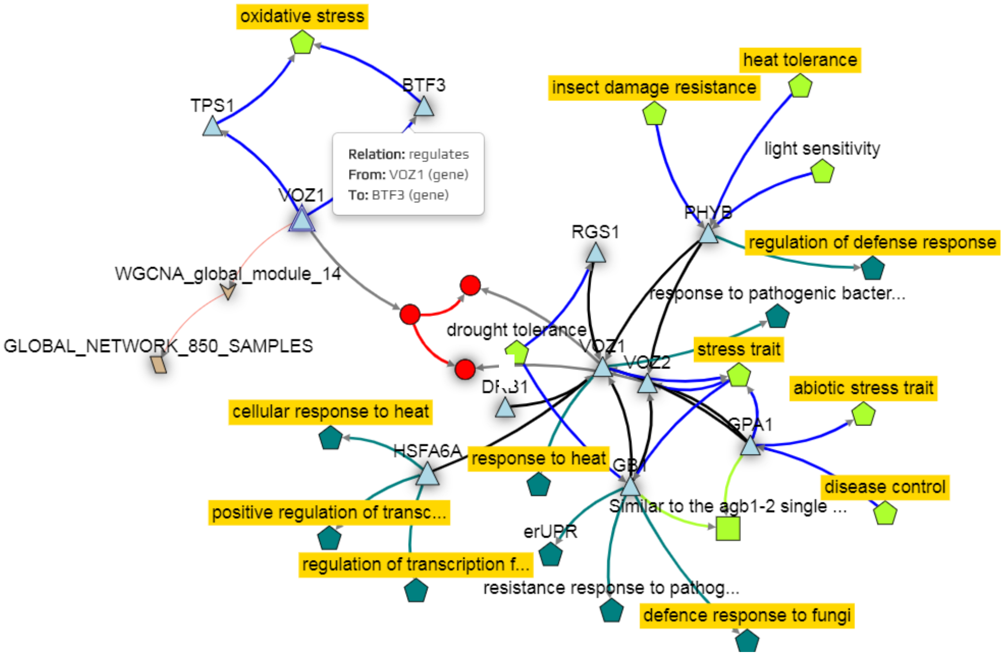
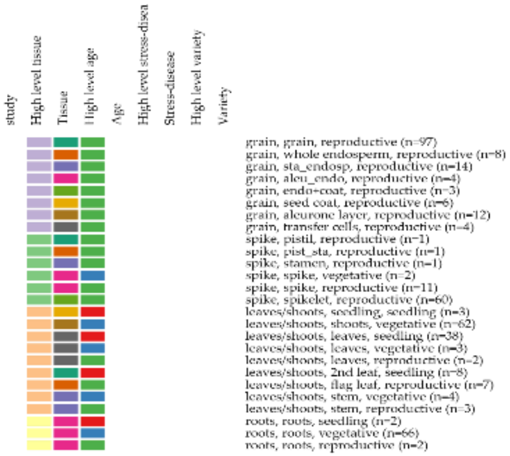
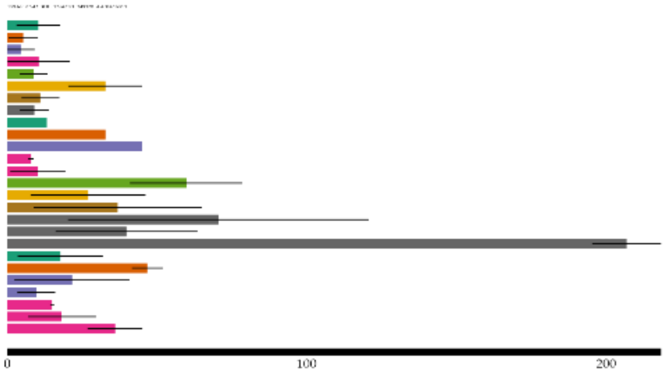
knetminer.rothamsted.ac.uk



www.wheat-expression.com





Acknowledgements

Cristobal Uauy
Ricardo Ramirez-Gonzalez
Tobin Florio
Sophie Harrington
Jemima Brinton

John Innes Centre

Keywan Hassani-Pak

ROTHAMSTED RESEARCH

DFW

IWGSC

Annotations
Manuel Spannagl
Daniel Lang

PGSB

Genie3
Andrea Braeutigam

Universität Bielefeld

eFP
Yogendra Khedikar
Nicholas Provart
Andy Sharpe

Agriculture and Agri-Food Canada
UNIVERSITY OF TORONTO
UNIVERSITY OF SASKATCHEWAN

RNA-seq data

Boulos Chalhoub	INRA SCIENCE & IMPACT
Burkhard Steurnagel	John Innes Centre
Curtis Pozniak	UNIVERSITY OF SASKATCHEWAN
Rudi Appels	LA TROBE UNIVERSITY THE UNIVERSITY OF MELBOURNE Murdoch UNIVERSITY
Vijay Tiwari	UNIVERSITY OF MARYLAND
Raju Datla	Canada NRC·CNRC
Mark Davey	Bayer CropScience
Rob Davey	Earlham Institute

eFP browser: http://bar.utoronto.ca/efp_wheat/cgi-bin/efpWeb.cgi

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