Decoding the polyploid wheat genome using gene networks

UNIVERSITY OF BIRMINGHAM

Philippa Borrill

@PhilippaBorrill

Outline

1) Why is polyploidy relevant?
2) Why now?
3) Can we use gene networks to escape polyploidy?

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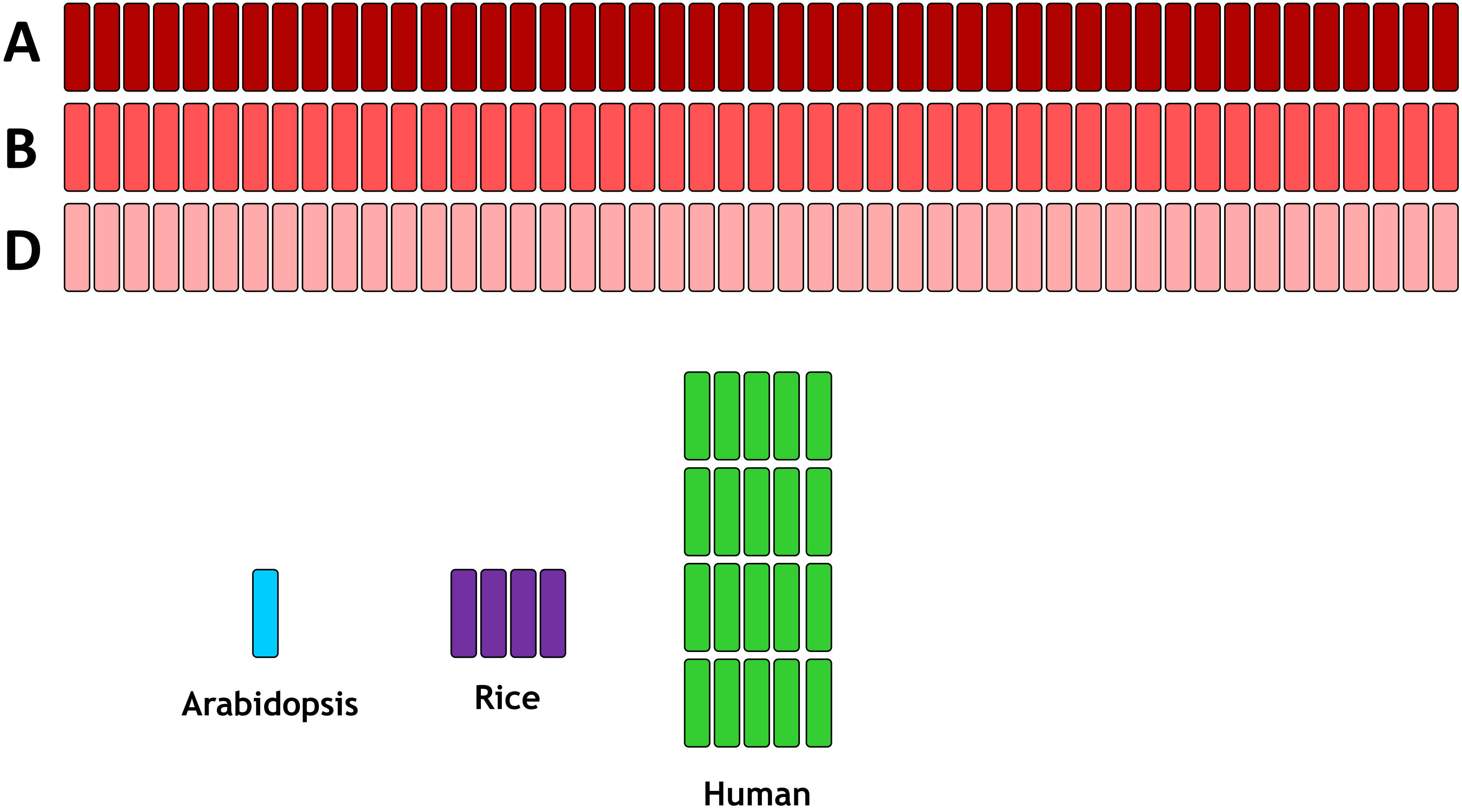
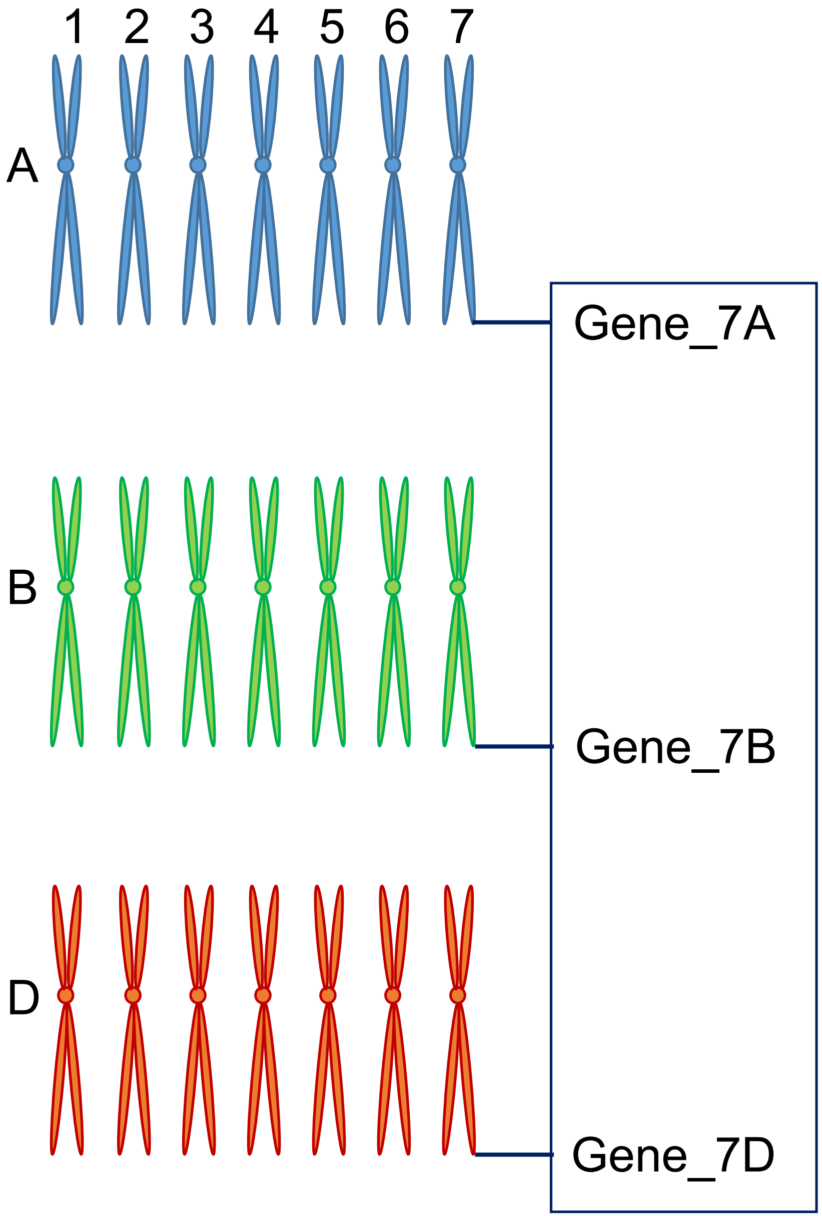
Polyploid plants are abundant

- >70 % of flowering plants have a polyploid evolutionary history
- Many major crops are polyploid

The Challenge of Wheat

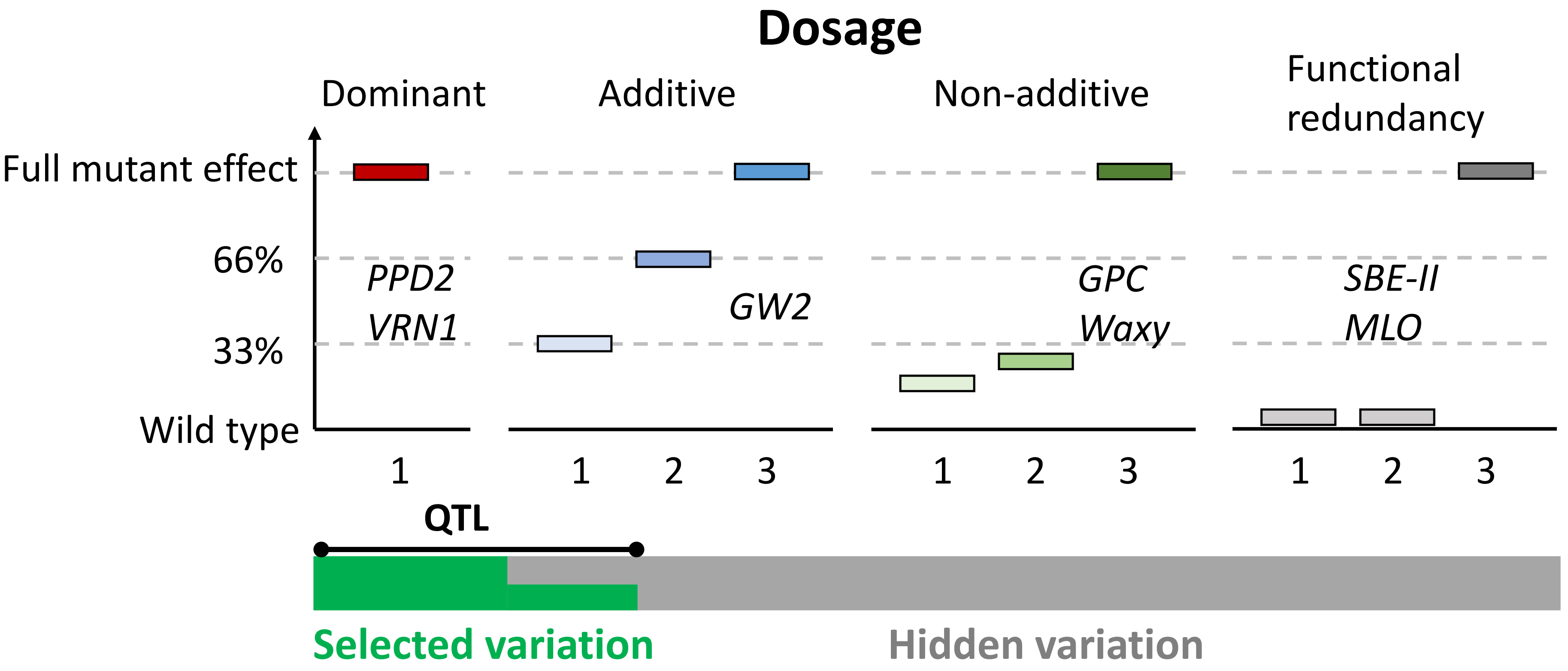


Wheat chromosomes



Homoeologues
>95 % CDS similarity

Functional redundancy hides variation

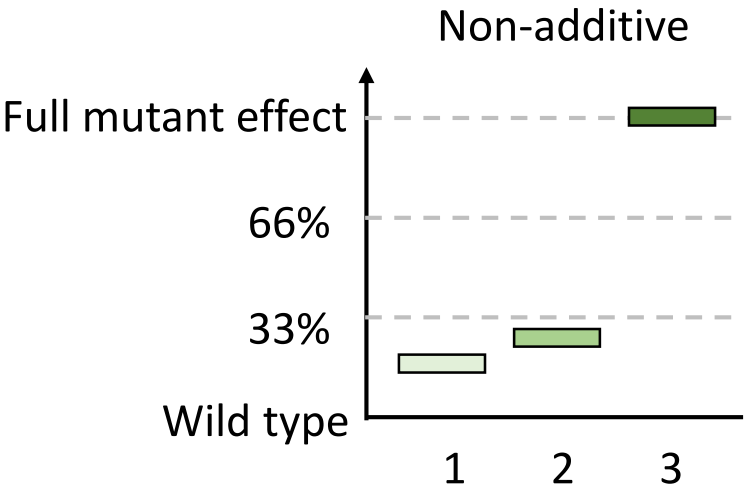


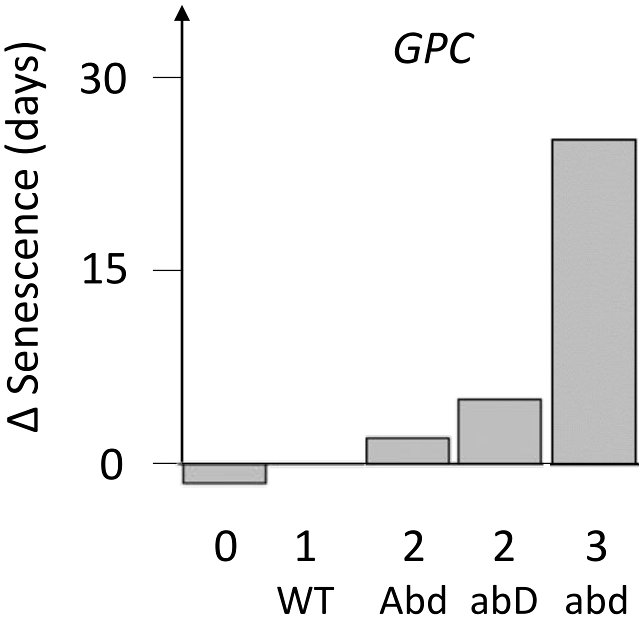
Song *et al.*, 2007, *Nature Genetics*

Wang *et al.*, 2018, *TAG*

Borrill *et al.*, 2019, *Plant J*

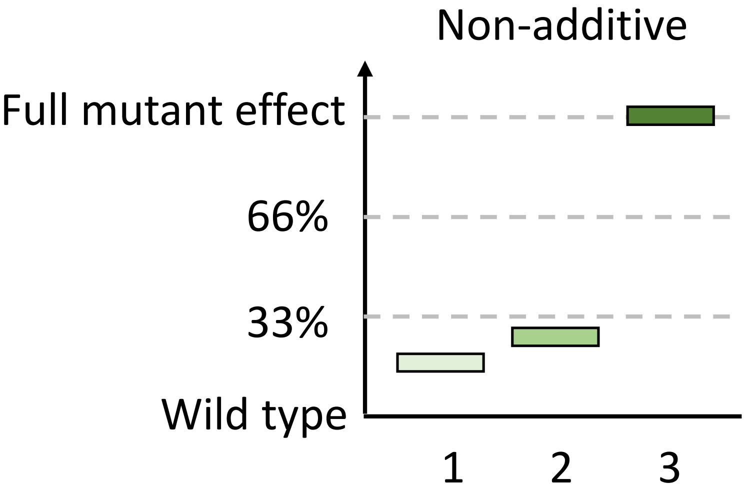
In young polyploids recessive alleles are missed by breeders



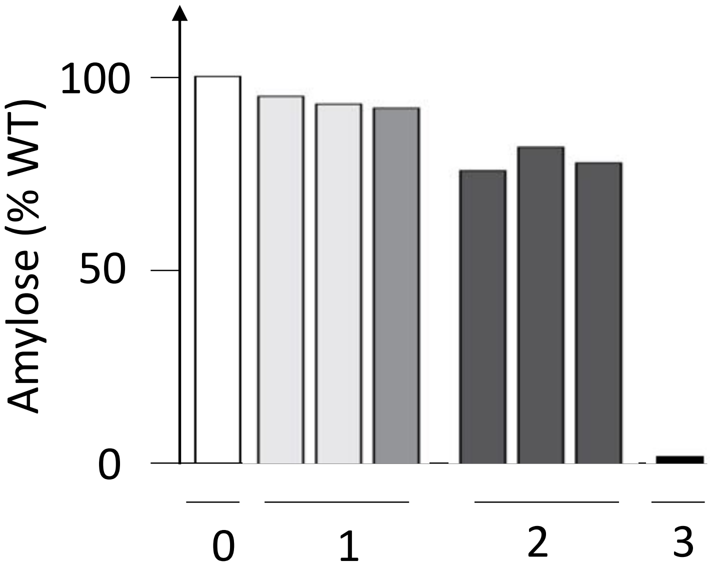


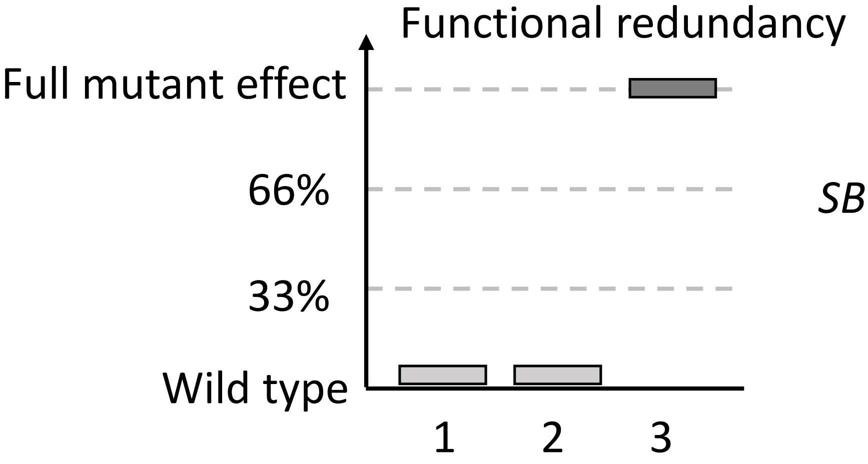
Uauy et al 2006 *Science*; Avni et al 2014 *Planta*;
Borrill et al 2015 *Plos One*.
Borrill, Adamski & Uauy 2015 *New Phytologist*

Incredible potential hiding in the wheat genome

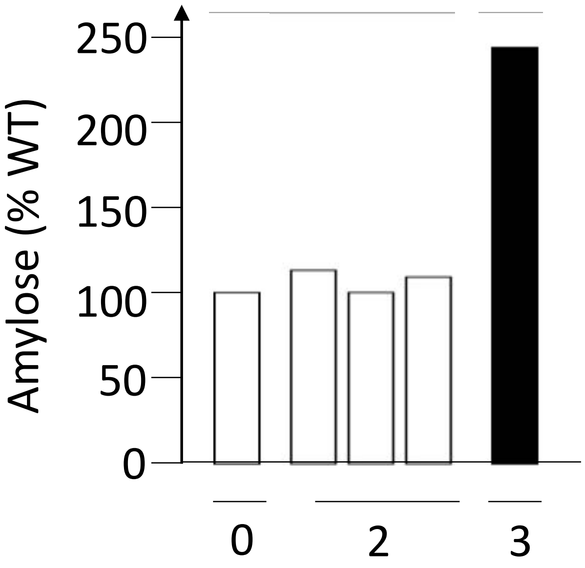


Waxy





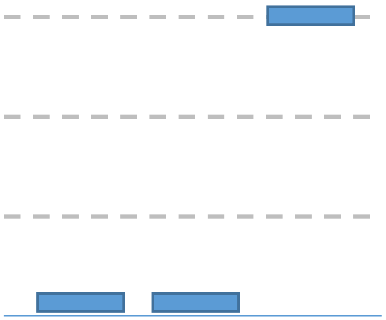
SBE-IIa



Borrill, Adamski & Uauy 2015 *New Phytologist*

1) Why is polyploidy relevant?

- Polyploidy is common in major crop species
- Hides variation



Functional redundancy

Outline

1) Why is polyploidy relevant?
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Fully sequenced wheat genome

Science

ROAD MAP FOR

WHEAT

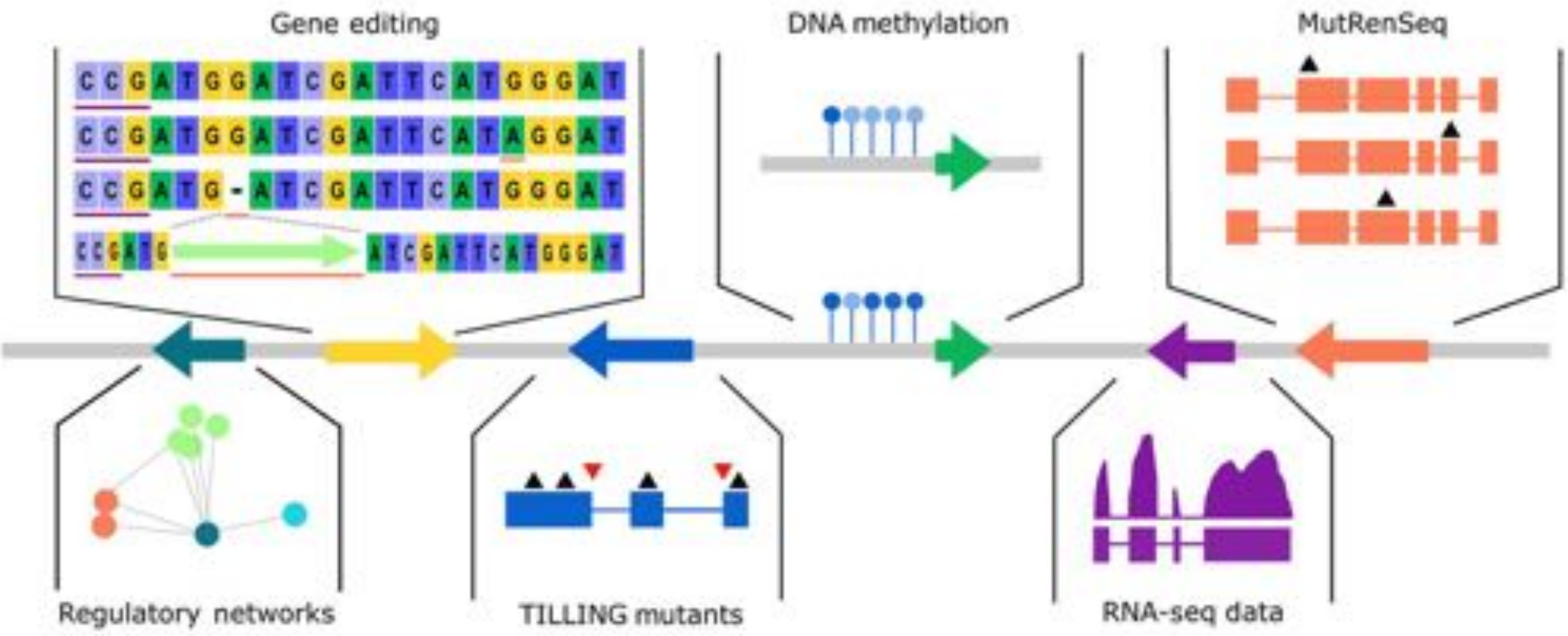
14.5 Gb assembled (genome size ~15.5 Gb -> 94%)

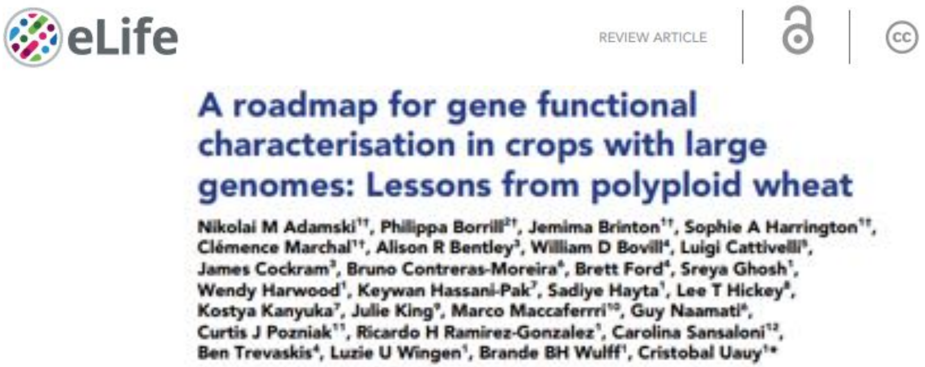
14.1 Gb in 21 pseudomolecules (97%)
1601 superscaffolds (avg 76 per chr.)

110,790 genes

IWGSC *et al.*, 2018, *Science*

Integrating genomic resources





eLife

REVIEW ARTICLE

A roadmap for gene functional characterisation in crops with large genomes: Lessons from polyploid wheat

Nikolai M Adamski[1†], Philippa Borrill[2†], Jemima Brinton[1†], Sophie A Harrington[1†], Clémence Marchal[1†], Alison R Bentley[3], William D Bovill[4], Luigi Cattivelli[5], James Cockram[3], Bruno Contreras-Moreira[6], Brett Ford[4], Sreya Ghosh[1], Wendy Harwood[1], Keywan Hassani-Pak[7], Sadiye Hayta[1], Lee T Hickey[8], Kostya Kanyuka[7], Julie King[9], Marco Maccaferrri[10], Guy Naamati[6], Curtis J Pozniak[11], Ricardo H Ramirez-Gonzalez[1], Carolina Sansaloni[12], Ben Trevaskis[4], Luzie U Wingen[1], Brande BH Wulff[1], Cristobal Uauy[1*]

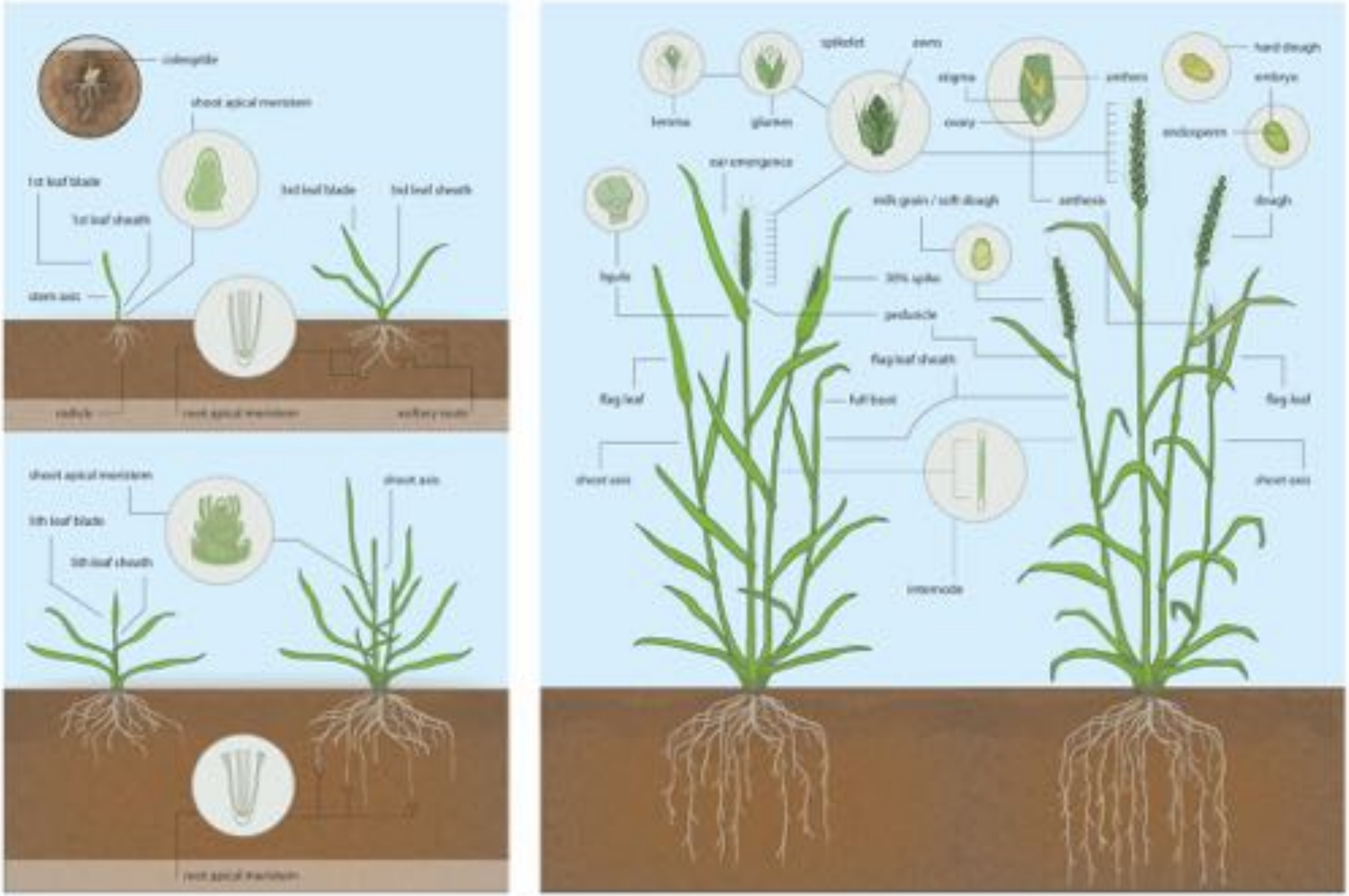
A roadmap for gene functional characterisation in wheat

Cristobal Uauy (cristobal.uauy@jic.ac.uk)

@CristobalUauy

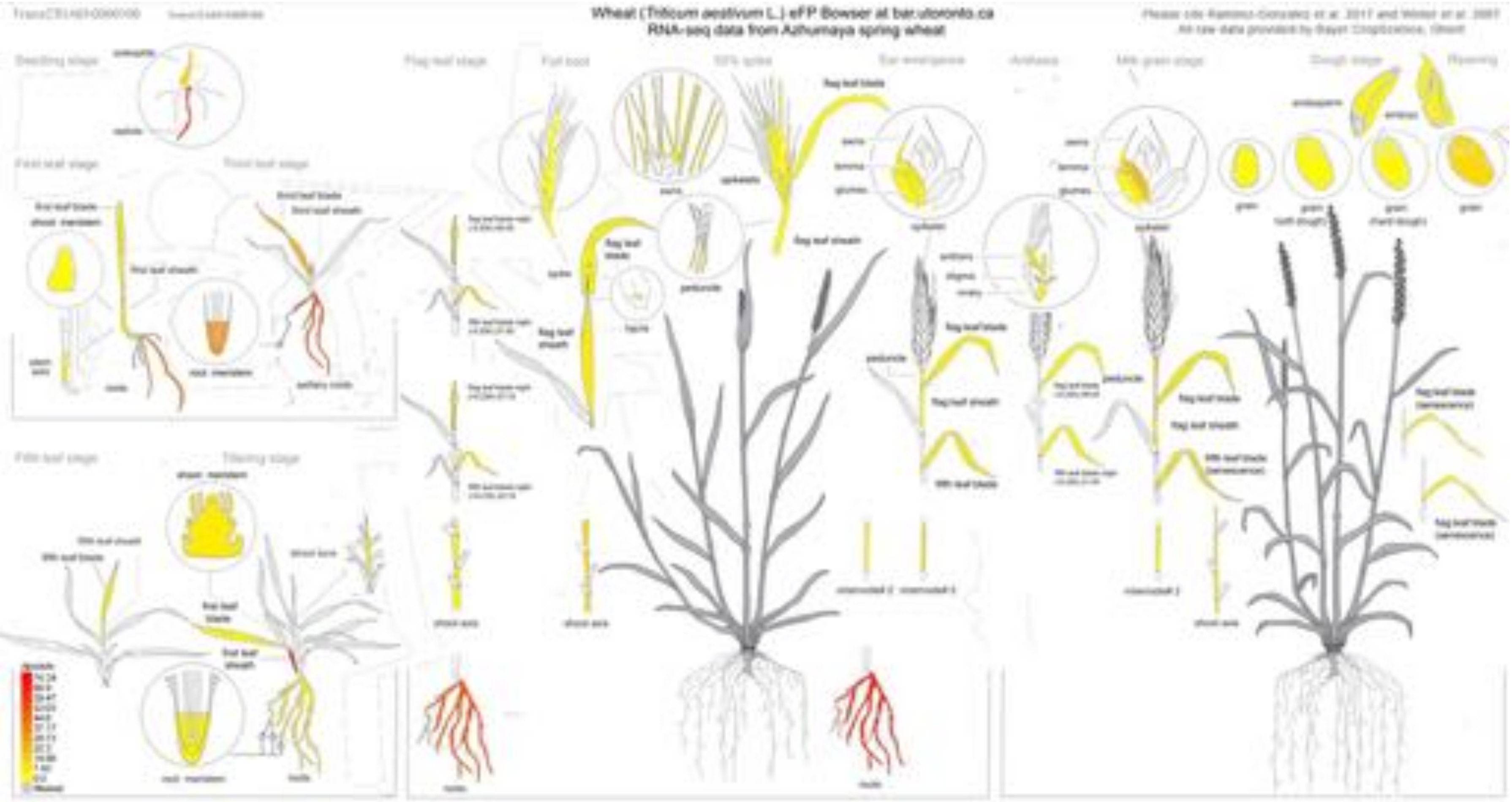
Borrill *et al.*, 2019, *Plant J*
Adamski *et al.*, 2020, *eLIFE*

Over 850 samples; developmental time course, etc



Wheat eFP

http://bar.utoronto.ca/


Wheat (Triticum aestivum L.) eFP Bowser at bar.utoronto.ca
RNA-seq data from Azhurnaya spring wheat

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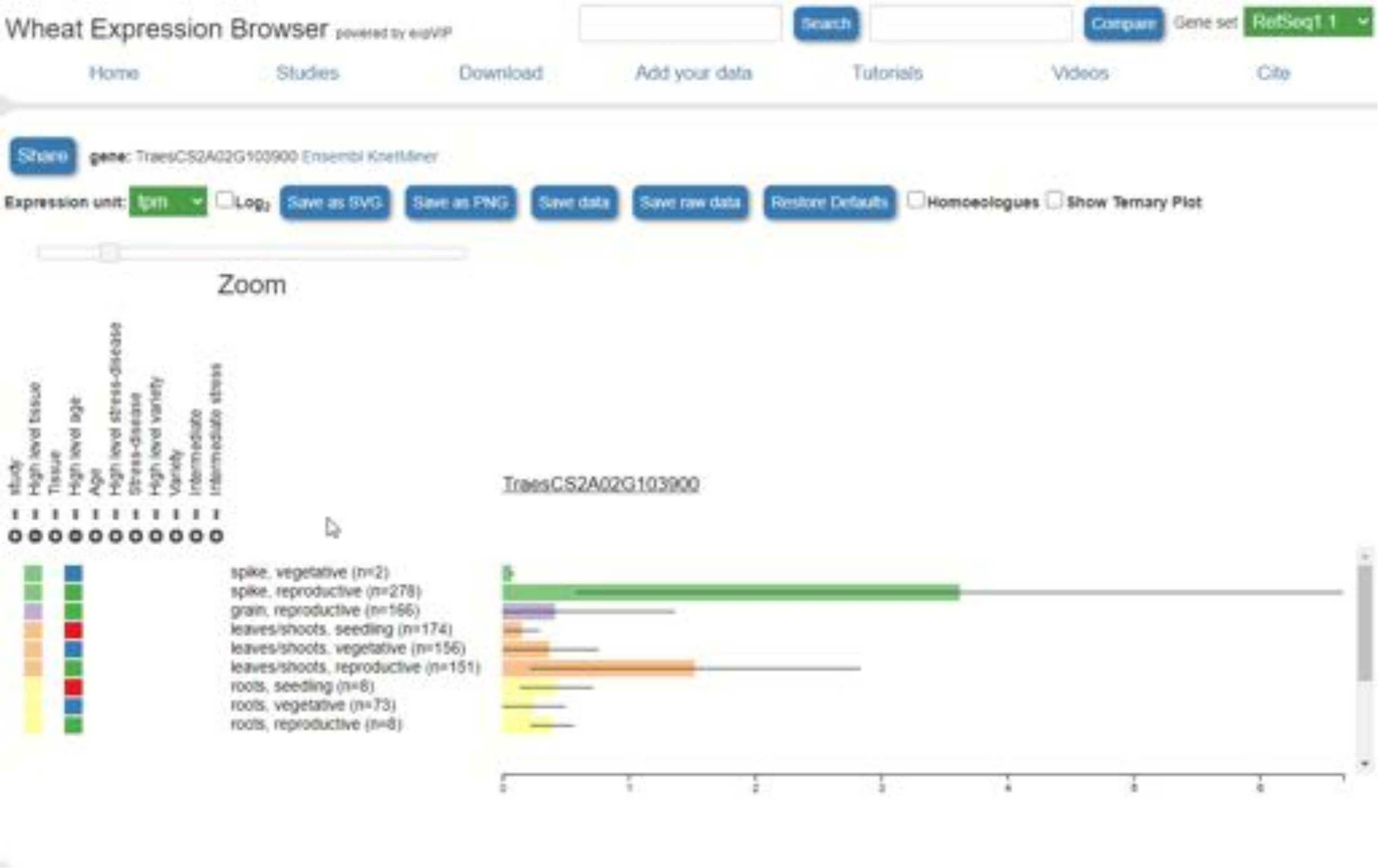
Agriculture and Agri-Food Canada

Crop Science

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

www.wheat-expression.com

>1,000 wheat RNA-Seq samples



gene: TraesCS2A02G103900

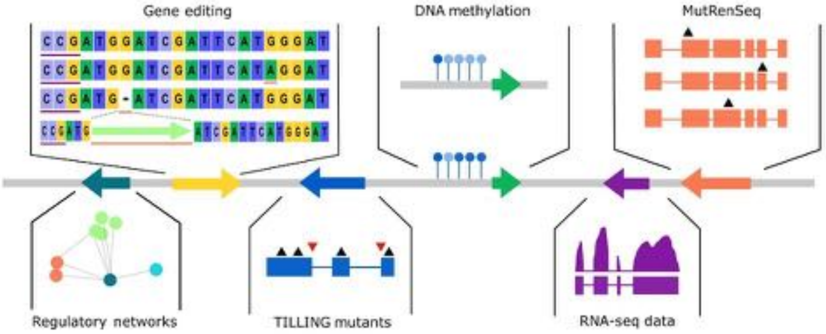
Expression unit: tpm

Gene set: RefSeq1.1

Borrill, Ramirez-Gonzalez *et al.*, 2016, *Plant Physiol*

2) Why now?

- Wheat genome sequence
- Functional genomic resources



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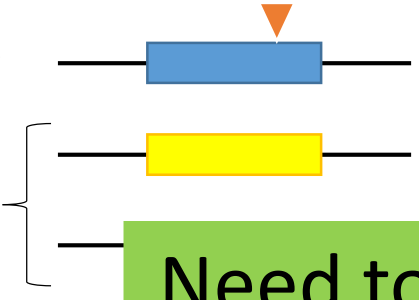


Gene editing

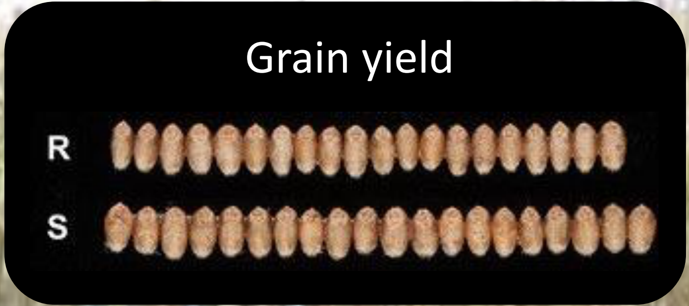
Natural/
induced
variation

Need to predict gene function

Genomics

- Pangenomics
- >7,000 RNA-Seq samples
- Epigenetics

Grain yield

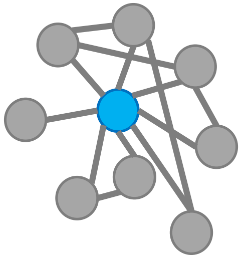


Grain quality

Disease resistance

RNA-seq

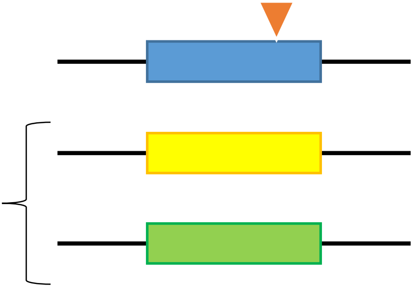
Gene network



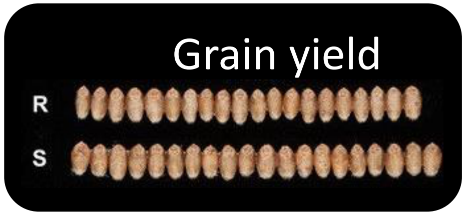
Predict biology

Gene editing

Natural/
induced
variation

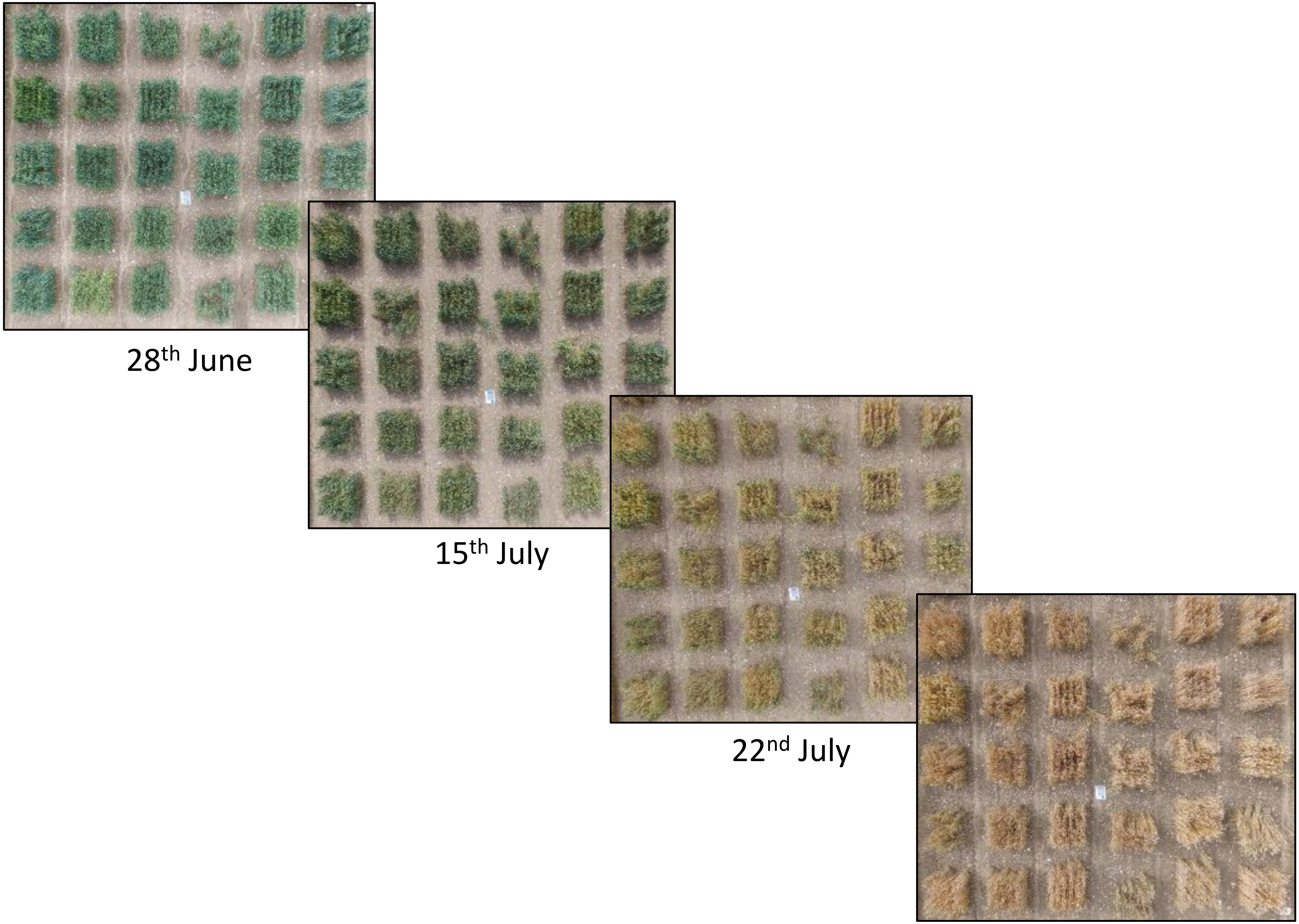


Improvement


Grain yield


Grain quality


Disease resistance



28th June

15th July

22nd July

29th July

Senescence

Yield

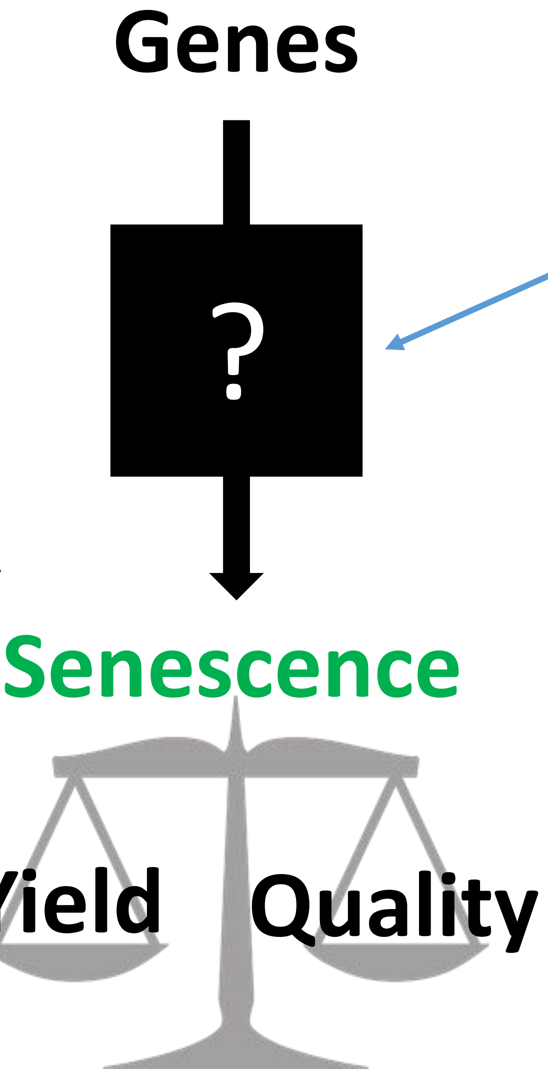
Quality

28th June

15th July

22nd July

29th July



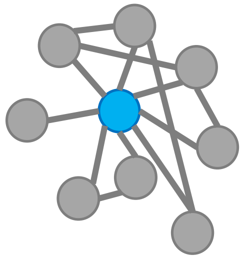
Genes

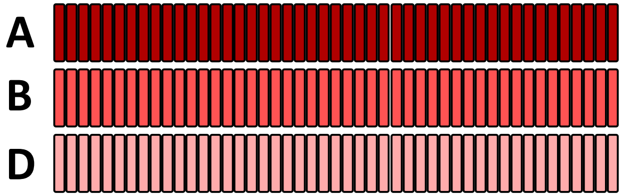
?

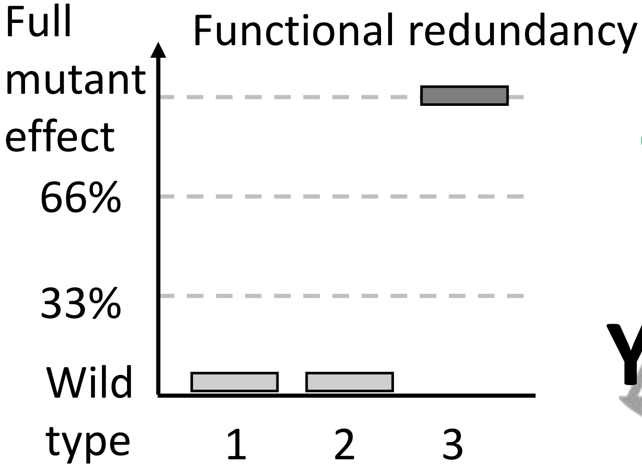
Senescence

Yield **Quality**

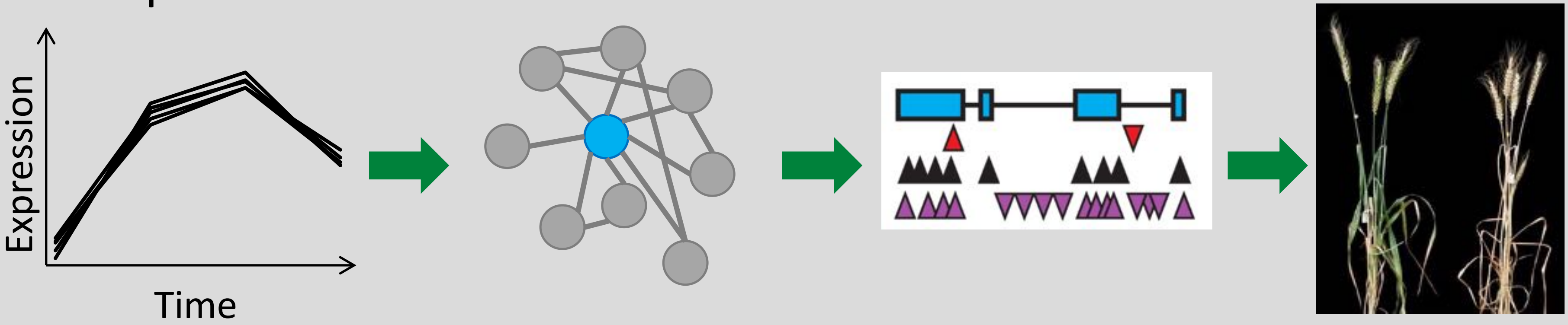
Gene regulatory network modelling

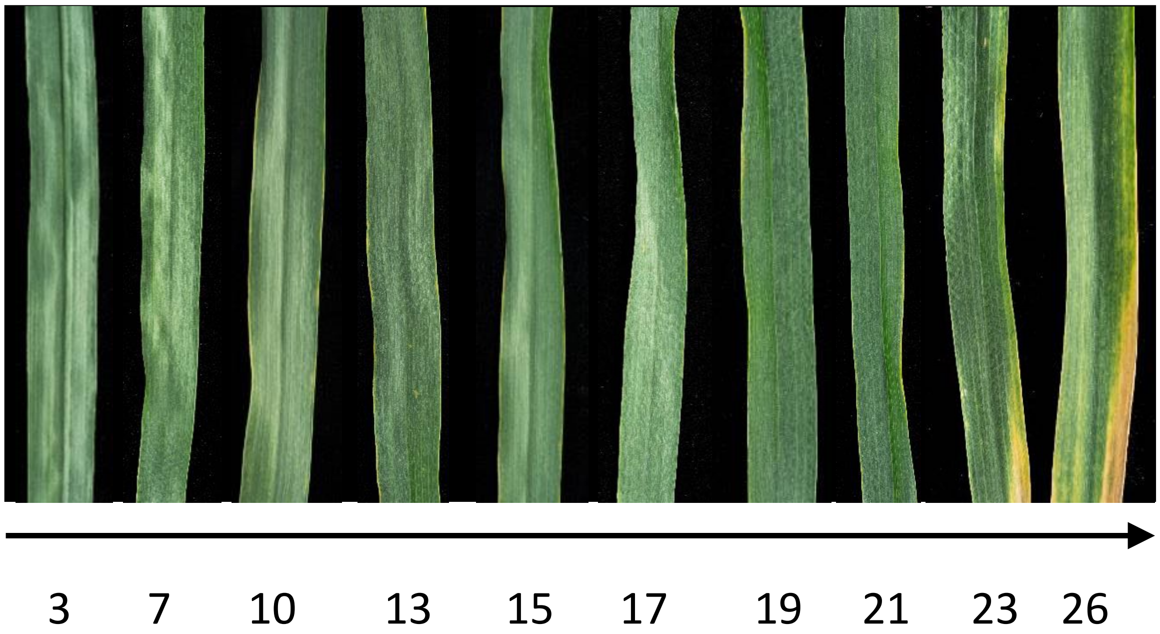






Transcriptional networks

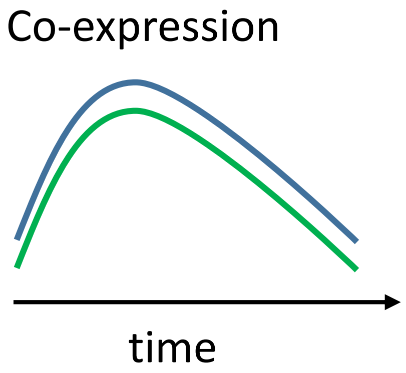


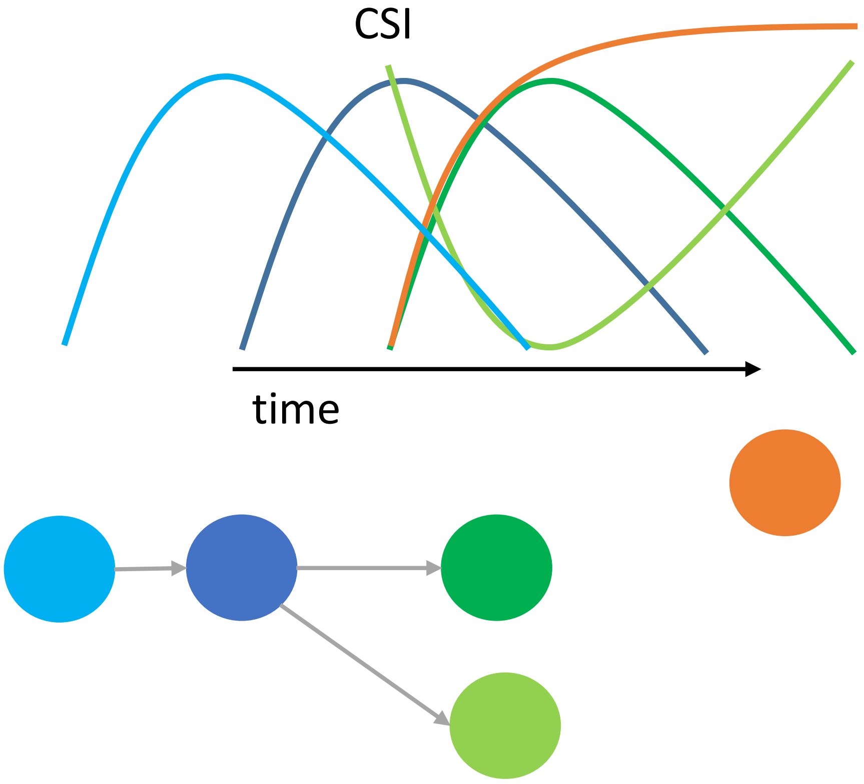


Days after anthesis

Predictive network modelling with CSI

- Co-expression = “guilt-by-association”
- CSI = predictive relationships





Computationally expensive therefore need to prioritise genes to include in CSI

110,790 genes

↓ Expressed

52,905

↓ Differentially expressed

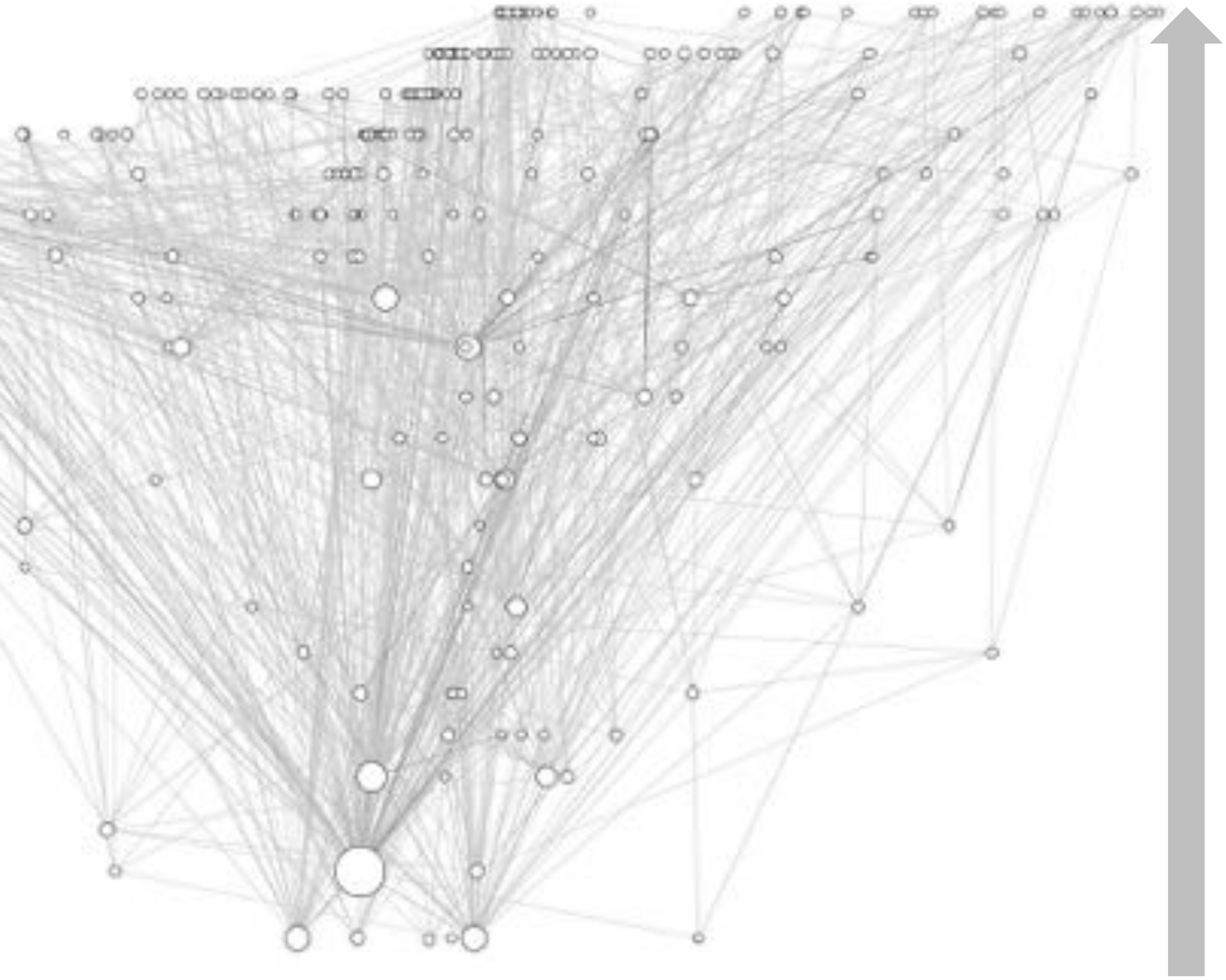
9,533

↓ TFs

341 genes

Borrill *et al.*, 2019, *Plant Physiol.*

295 genes



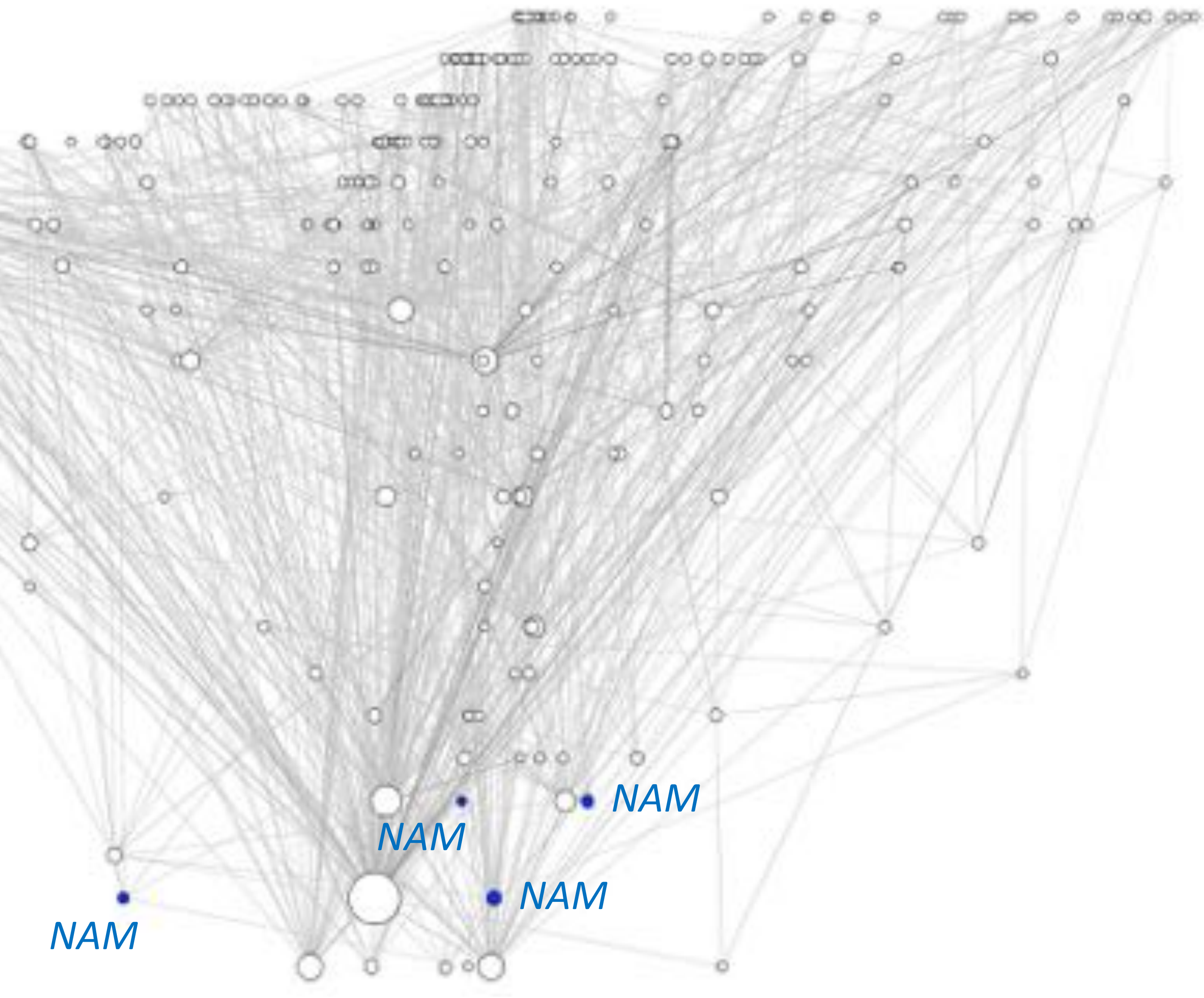
NAM

Uauy *et al*., 2006, *Science*

Borrill *et al*., 2019, *Plant Physiol.*

NAM

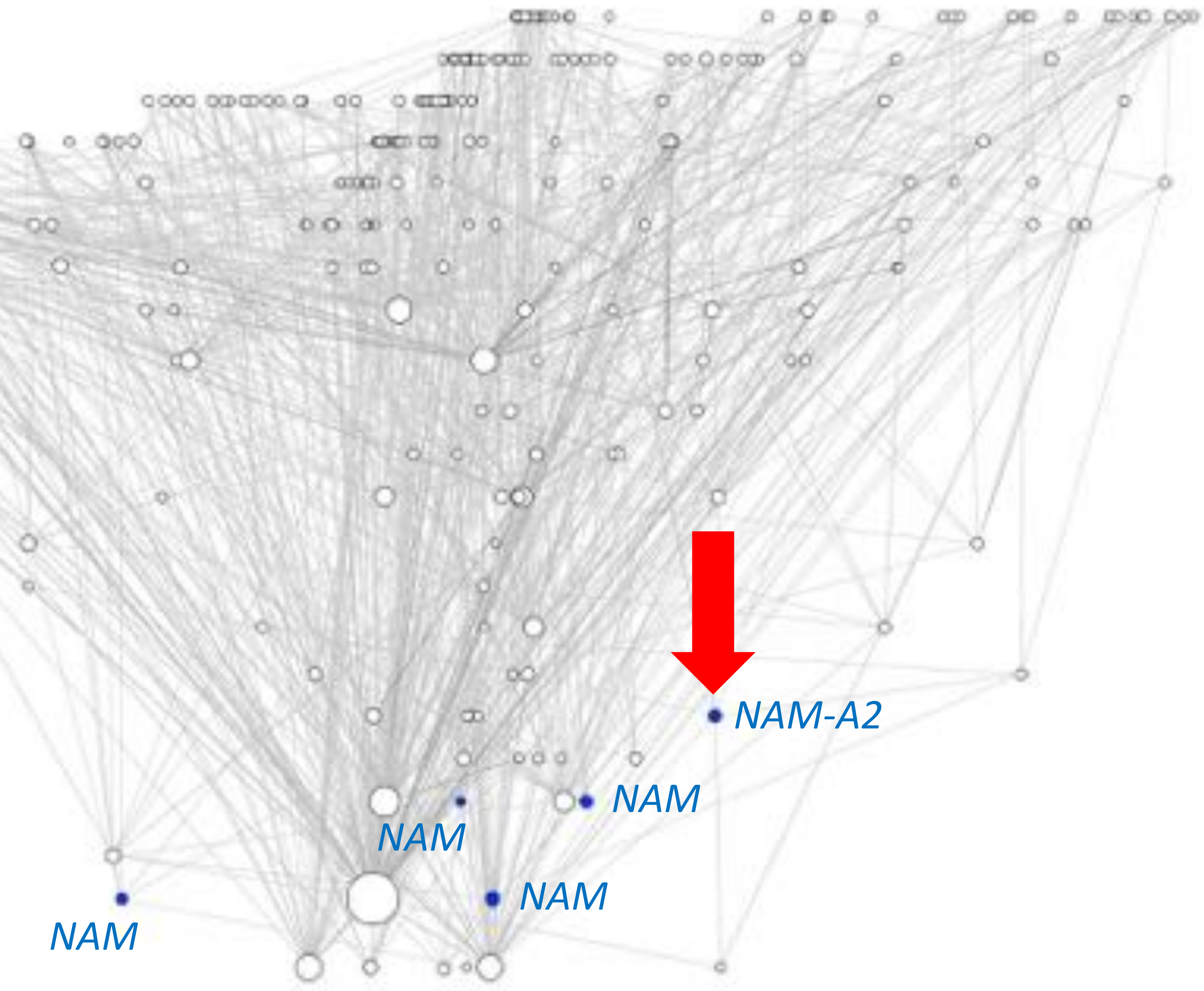
Uauy *et al*., 2006, *Science*



Borrill *et al*., 2019, *Plant Physiol.*

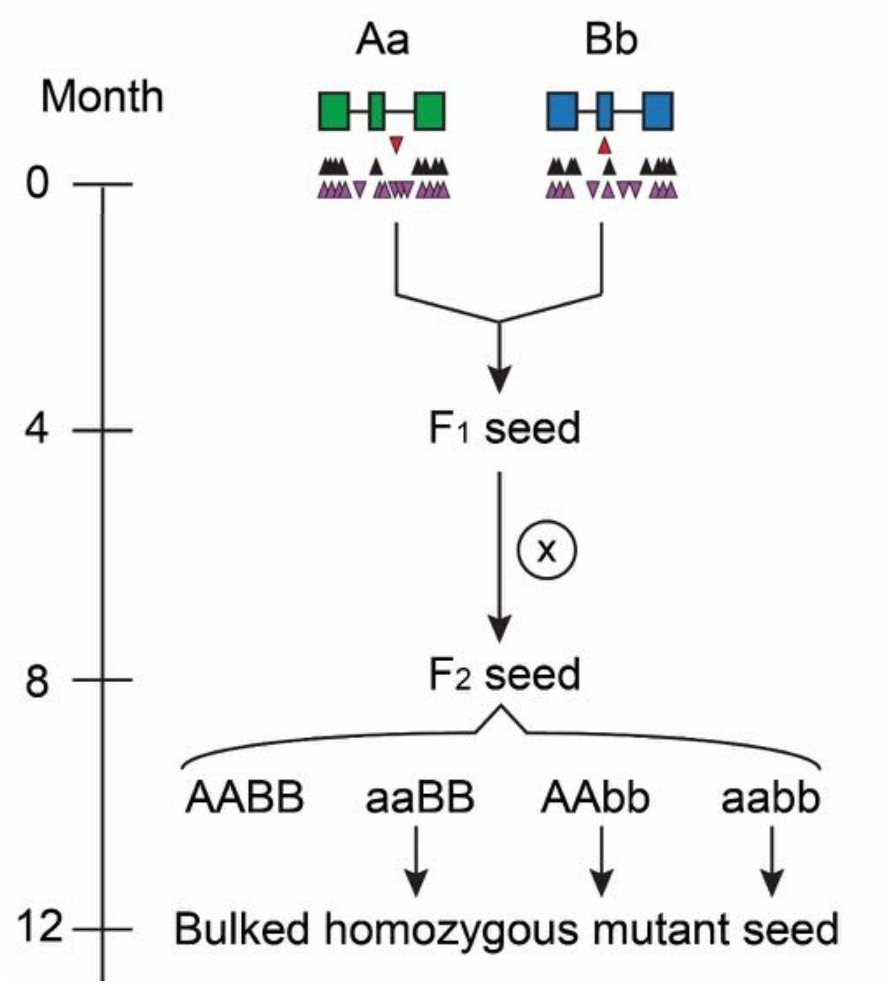
NAM

Uauy *et al.*, 2006, *Science*



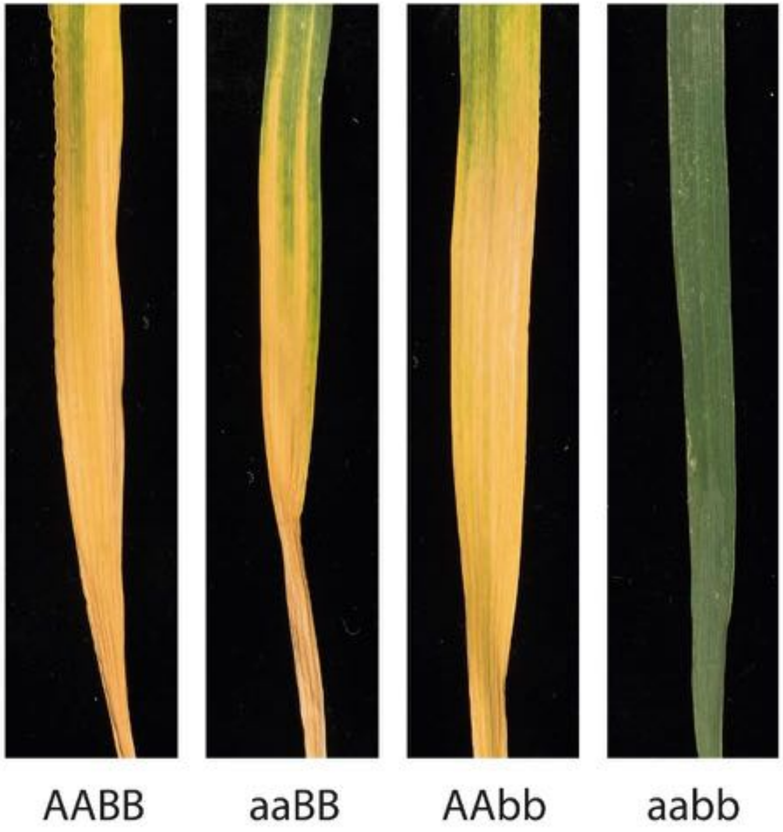
Borrill *et al.*, 2019, *Plant Physiol.*

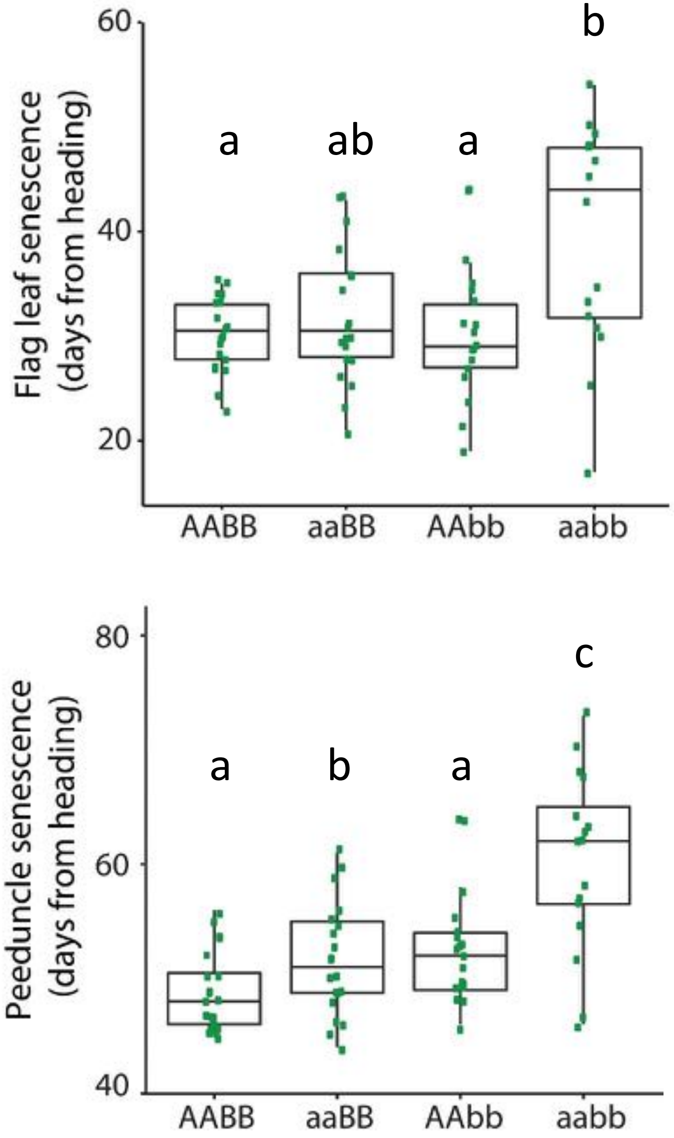
Develop double mutants for candidate genes



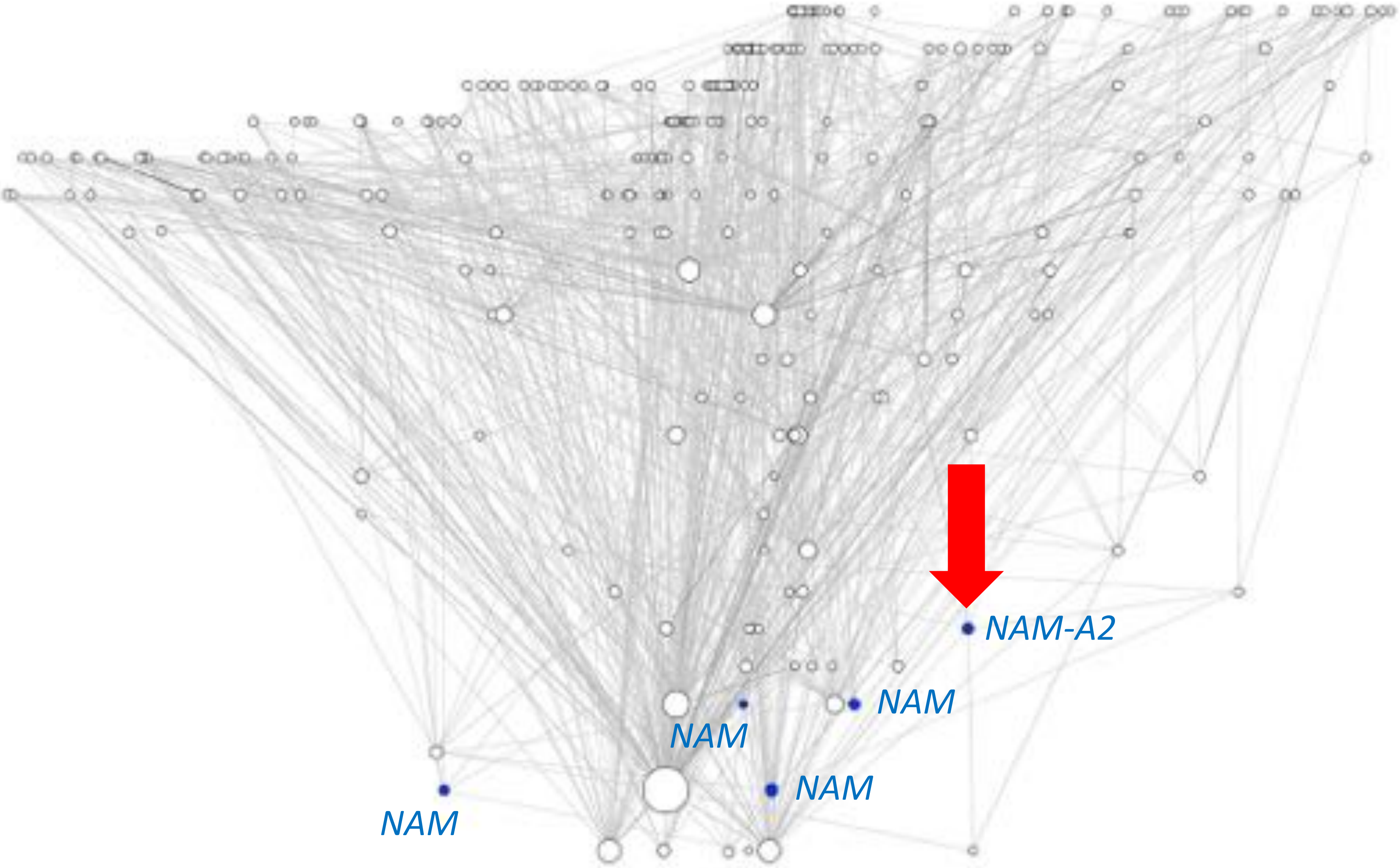
Borrill *et al.*, 2015 *New Phytologist*

NAM-2 phenotyping





Borrill *et al.*, 2019, *Plant Physiol.*



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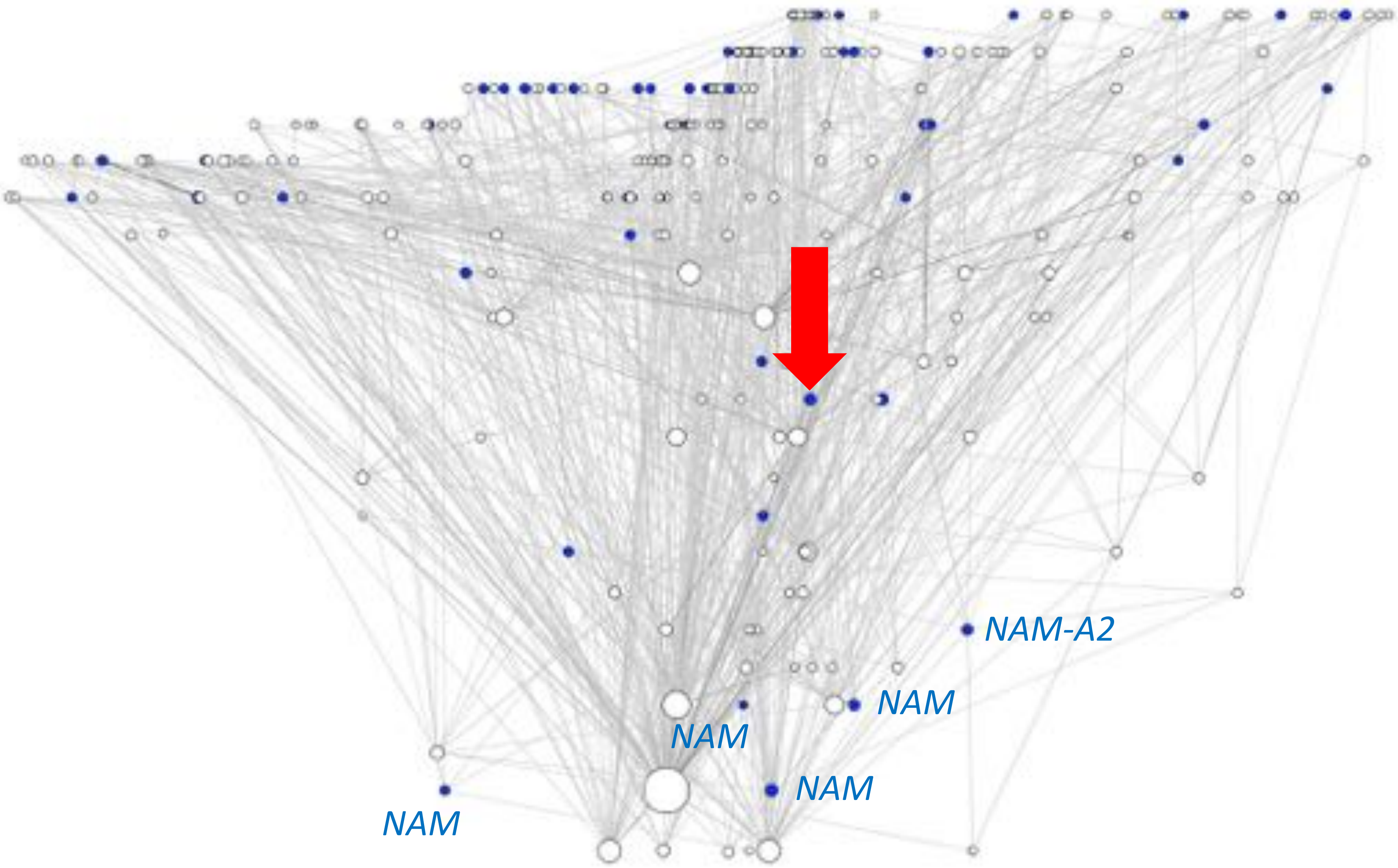

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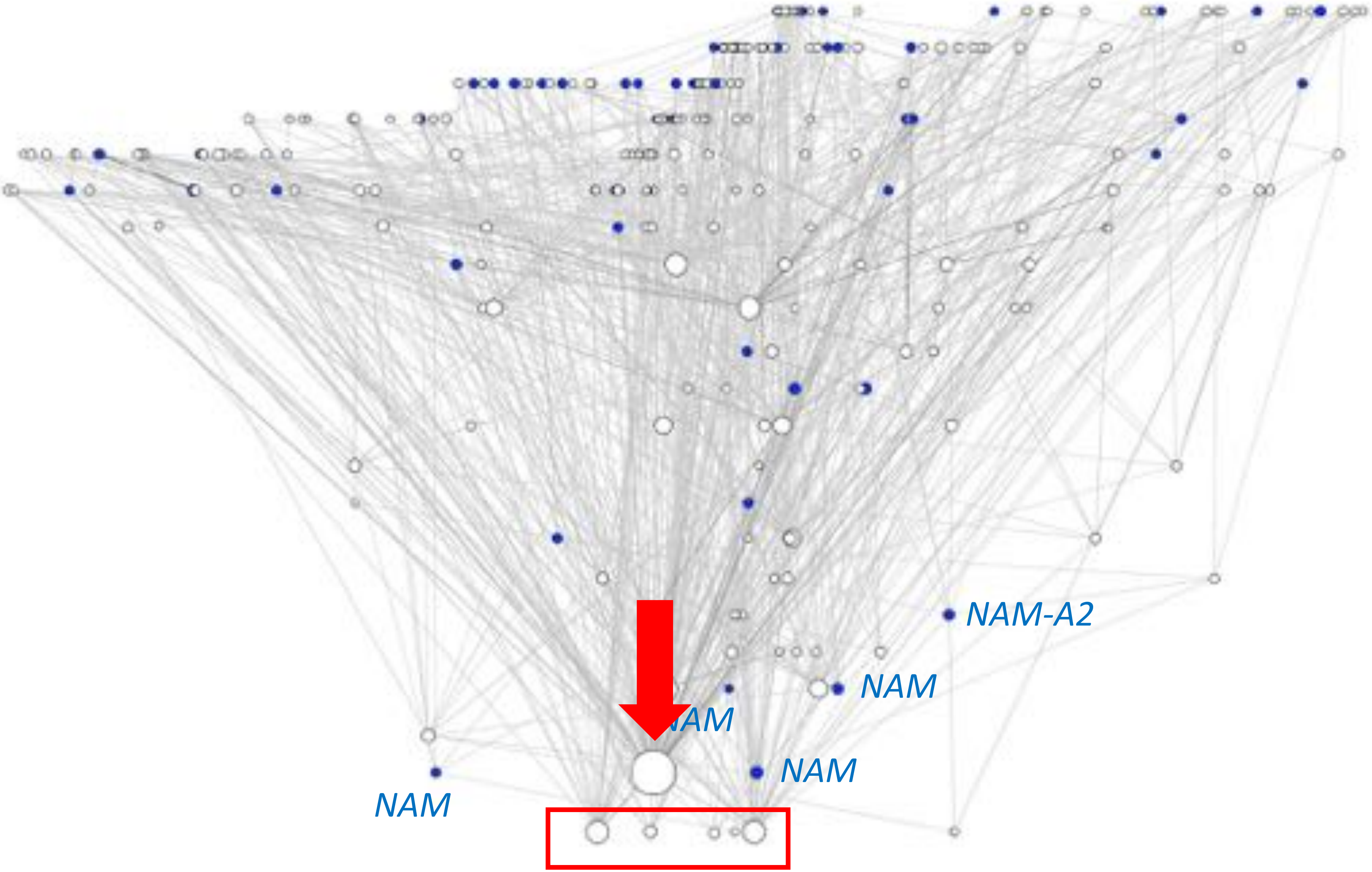


Borrill *et al.*, 2019, *Plant Physiol.*

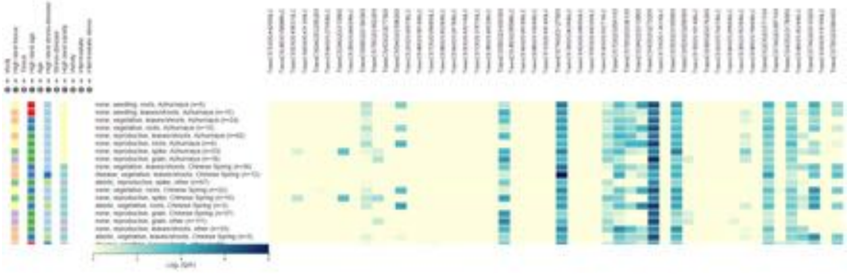
Layering additional information

>200 gene candidates

How to choose which to prioritise?

Other expression data (www.wheat-expression.com)

>1,000 RNA-Seq samples

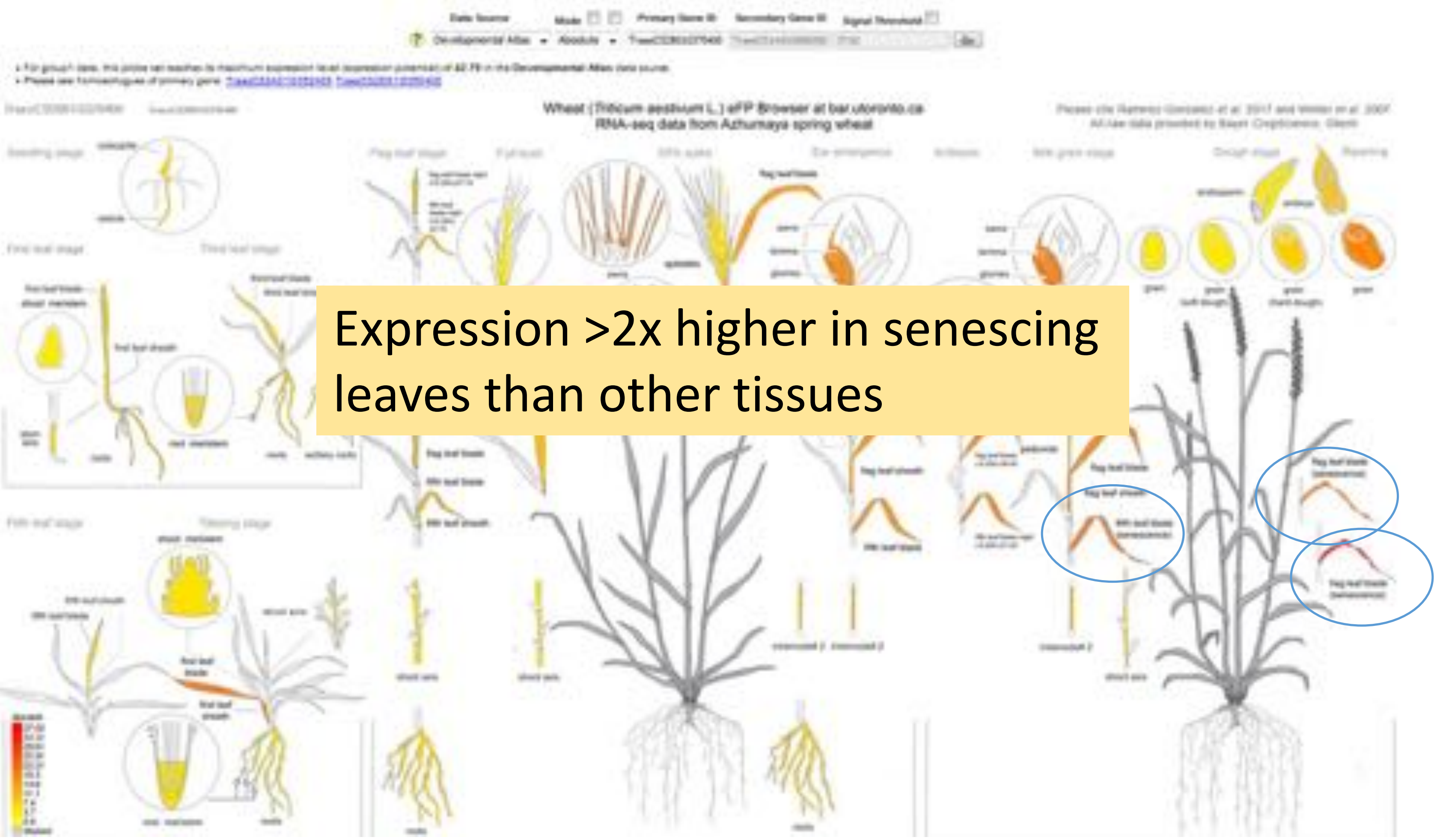


Ortholog information

Gene network information
http://knetminer.rothamsted.ac.uk/

Wheat eFP

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



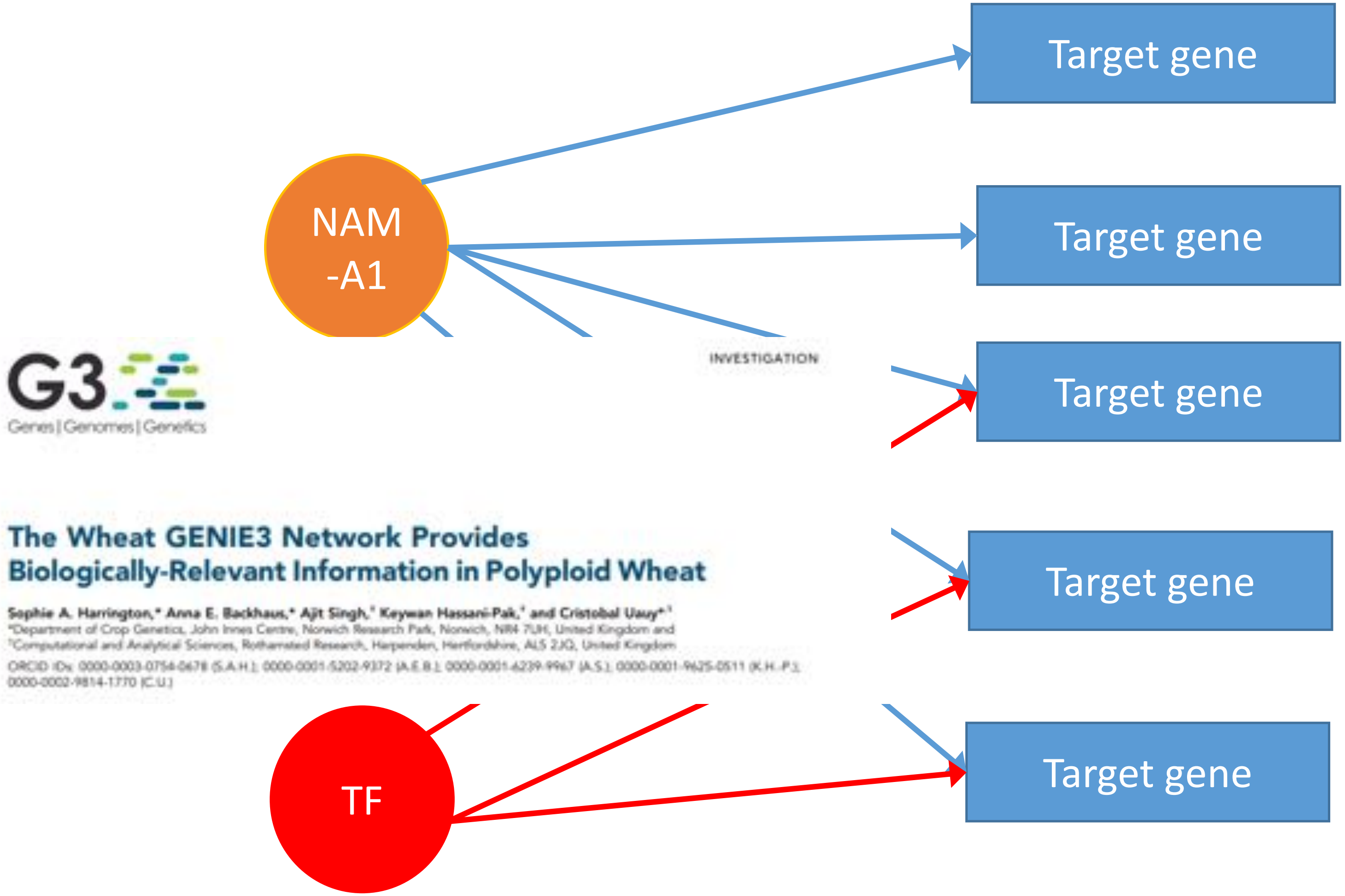
Wheat (Triticum aestivum L.) eFP Browser at bar.utoronto.ca
RNA-seq data from Azhurnaya spring wheat

Expression >2x higher in senescing leaves than other tissues

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

Genie3 network

(Available at http://knetminer.rothamsted.ac.uk/)



G3 Genes | Genomes | Genetics

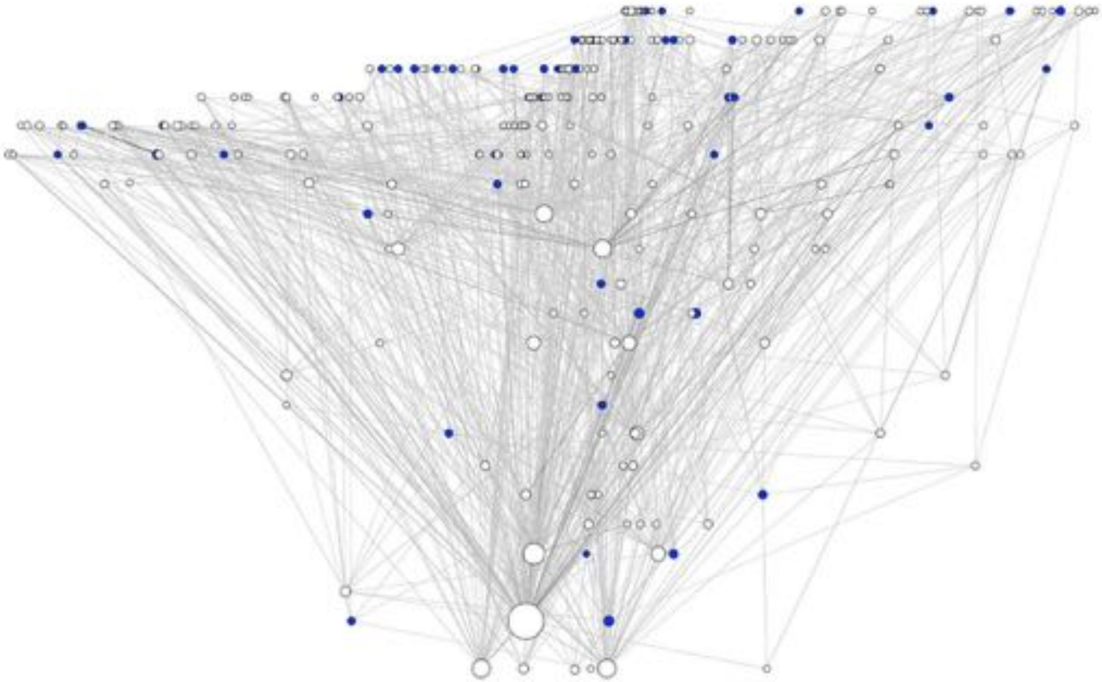
INVESTIGATION

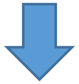
The Wheat GENIE3 Network Provides Biologically-Relevant Information in Polyploid Wheat

Sophie A. Harrington,* Anna E. Backhaus,* Ajit Singh,† Keywan Hassani-Pak,† and Cristobal Uauy*,1
*Department of Crop Genetics, John Innes Centre, Norwich Research Park, Norwich, NR4 7UH, United Kingdom and
†Computational and Analytical Sciences, Rothamsted Research, Harpenden, Hertfordshire, AL5 2JQ, United Kingdom
ORCID IDs: 0000-0003-0754-0678 (S.A.H.); 0000-0001-5202-9372 (A.E.B.); 0000-0001-6239-9967 (A.S.); 0000-0001-9625-0511 (K.H.-P.); 0000-0002-9814-1770 (C.U.)

Ramirez-Gonzalez, Borrill *et al.*, 2018, *Science*
Harrington *et al.*, 2020 *G3*

Future TFs to characterise



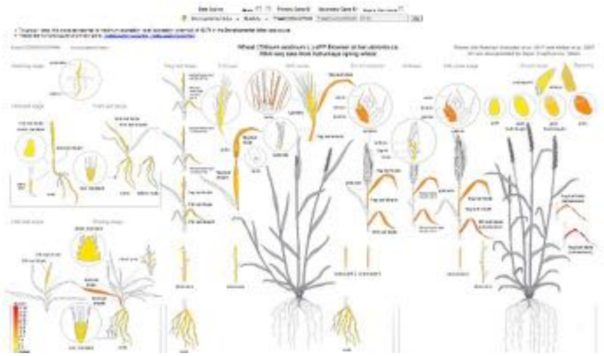


20 TFs with additional evidence

Rice orthologs frequently involved in:

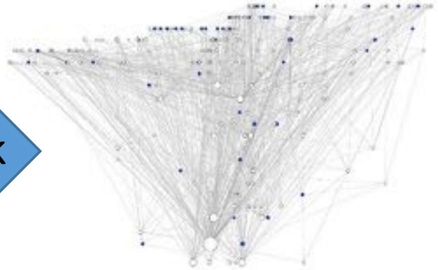
- Nitrate response
- Drought

3) Can we use gene networks to escape polyploidy?

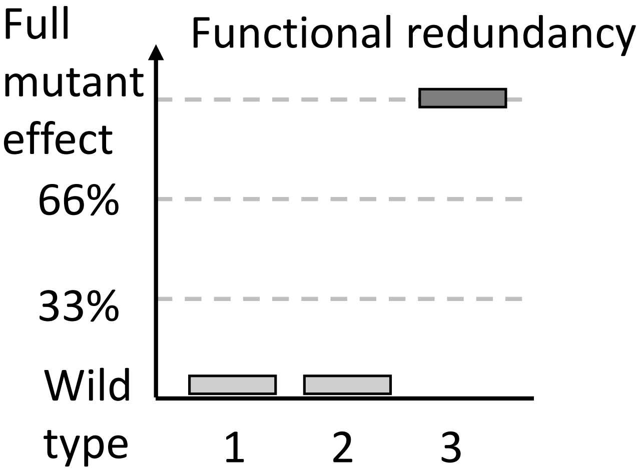


RNA-seq

Gene network



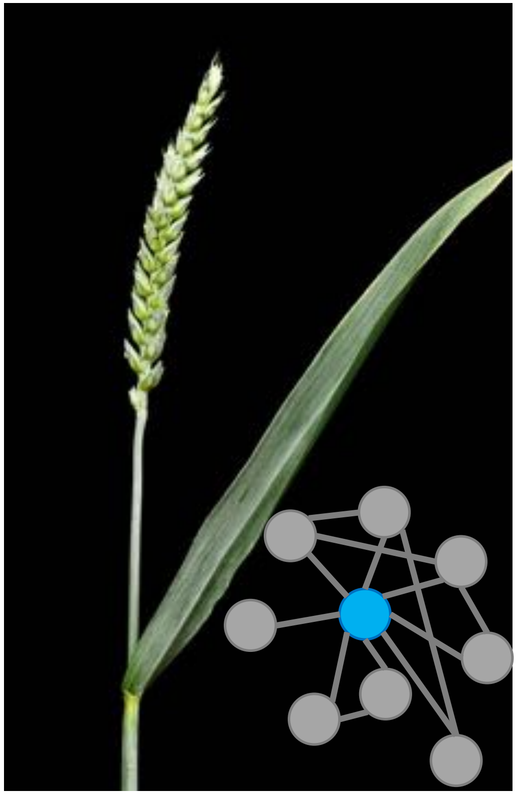
Predict biology



Conclusions

1) Why is polyploidy relevant?
2) Why now?
3) Can we use gene networks to escape polyploidy?

- Polyploidy challenge and opportunity
- New resources for wheat (genome, TILLING, expression)
- Gene networks can unmask polyploidy



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James Simmonds

www.borrilllab.com

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UKRI Biotechnology and Biological Sciences Research Council

THE ROYAL SOCIETY

UNIVERSITY OF BIRMINGHAM

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Conclusions

1) Why is polyploidy relevant?

Challenge and opportunity

2) Why now?

New resources for wheat

3) Can we use gene networks to escape polyploidy?

Gene networks can unmask polyploidy

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