

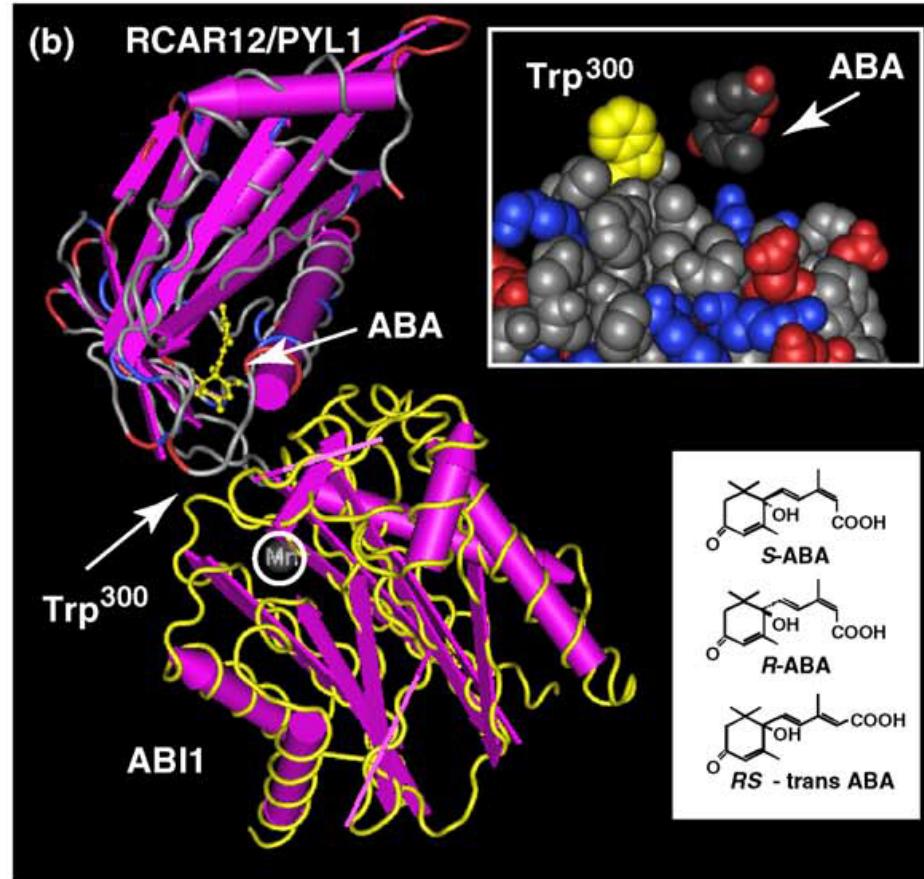


Natural Variation of Gene Regulatory Networks in *Arabidopsis thaliana*

Arthur Korte

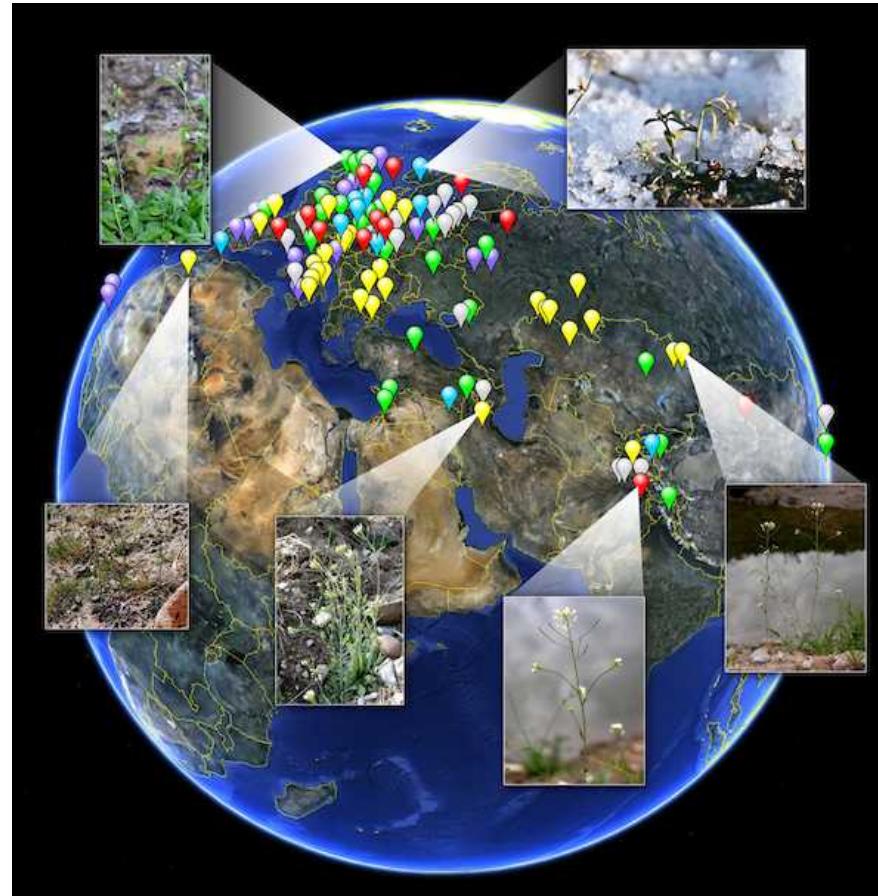
Hannover Mai 14th 2019

PhD in Molecular Biology



How do plants react to stress ?

Postdoc in Population Genetics



Credit:
Photographs/images
were contributed by
Patrick Gooden,
Kathleen Donohue and
Google Earth. Graphic
design: Jamie Simon,
Salk Institute.

How do populations adapt to the environment ?

www.1001genomes.org



Genomic variation in the *A.thaliana* population (1135 accessions)

10,709,466 SNPs segregate in the population

1,854,599 SNPs are located in coding regions

28,148 SNPs lead to a premature STOP codon

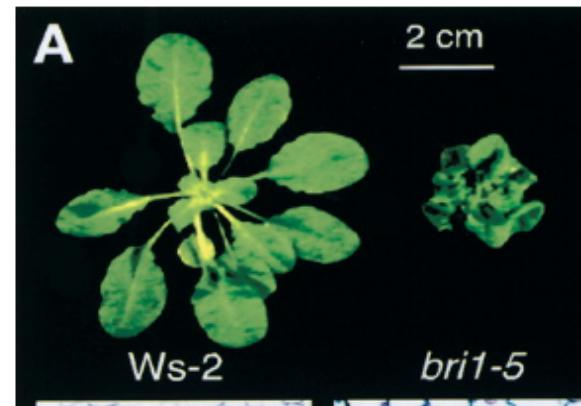


Nearly 10,000 genes are knock-out
in at least 1 accession

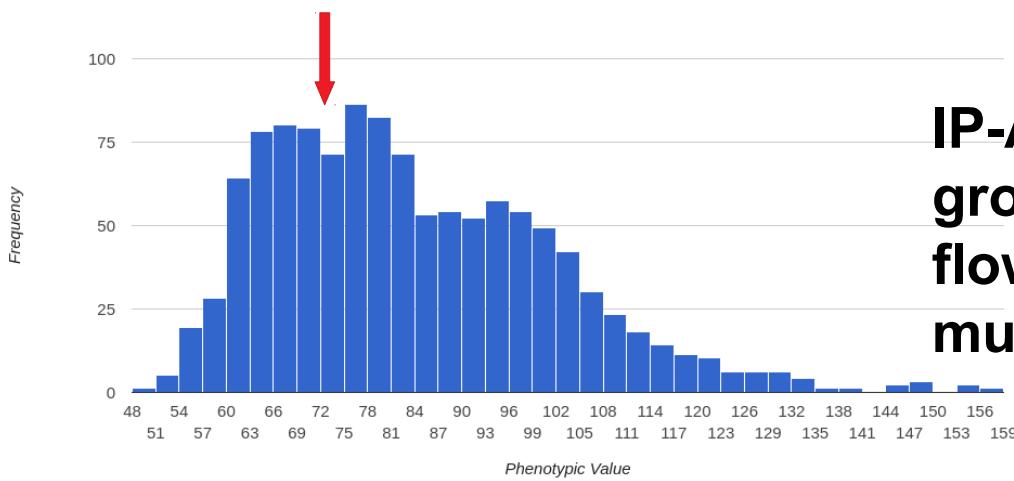
Natural BRI1 knock out in an accession from Portugal (IP-Alo-0)



Natural BRI1 knock out in an accession from Portugal (IP-Alo-0)

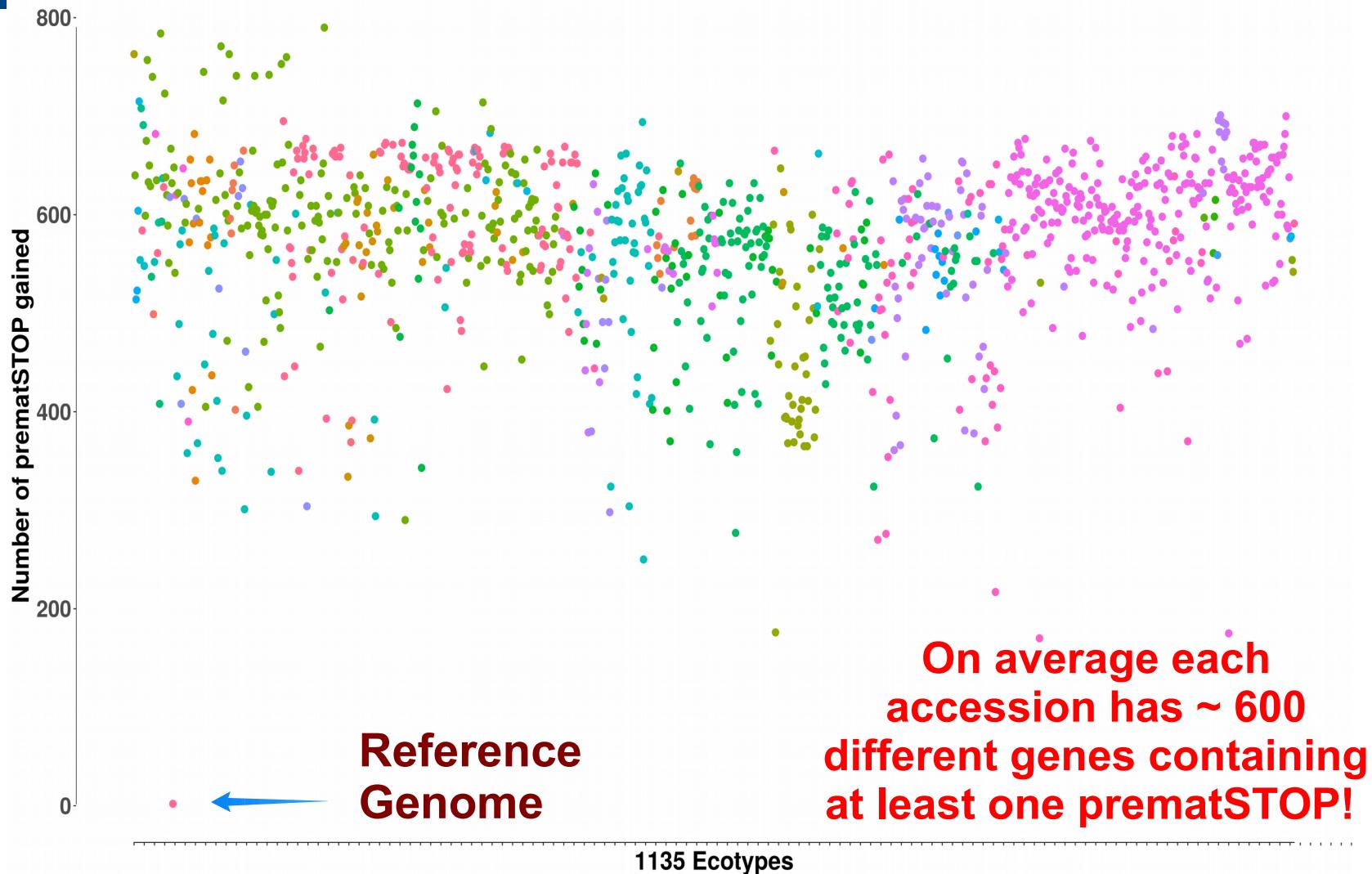


Santiago Mora-García et al. 2004, Genes Dev.



IP-Alo-0 does neither show the growth defect nor the delay in flowering time observed in *bri1* mutants

Frequency of prematSTOP codons by accessions



Co-occurrence of premature Stop codons

Filter for functional prematSTOP by using available RNAseq data (Kawakatsu *et al.* 2016)



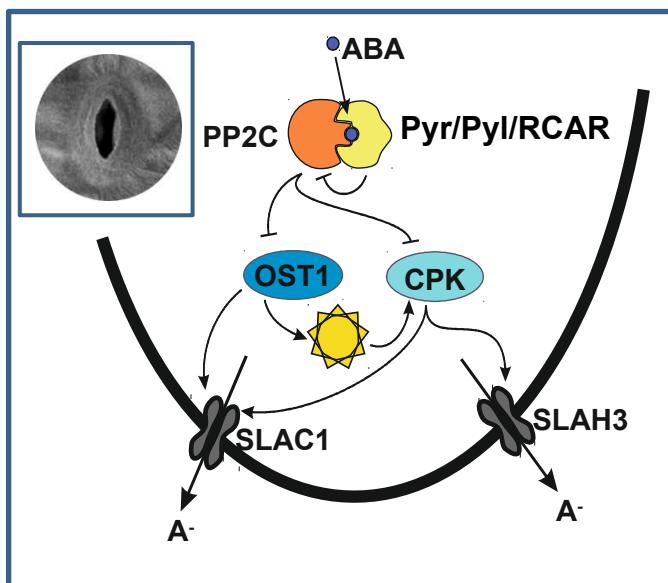
~ 6.000 genes / 16.000 prematSTOP

Gene 1	Gene 2	gene1_count	gene2_count	co-occurrence	P-value over	P-value under
AT2G25850	AT3G45910	27	72	2	0.52	0.75
AT3G55780	AT5G51000	450	435	237	<10 ⁻²⁰	1

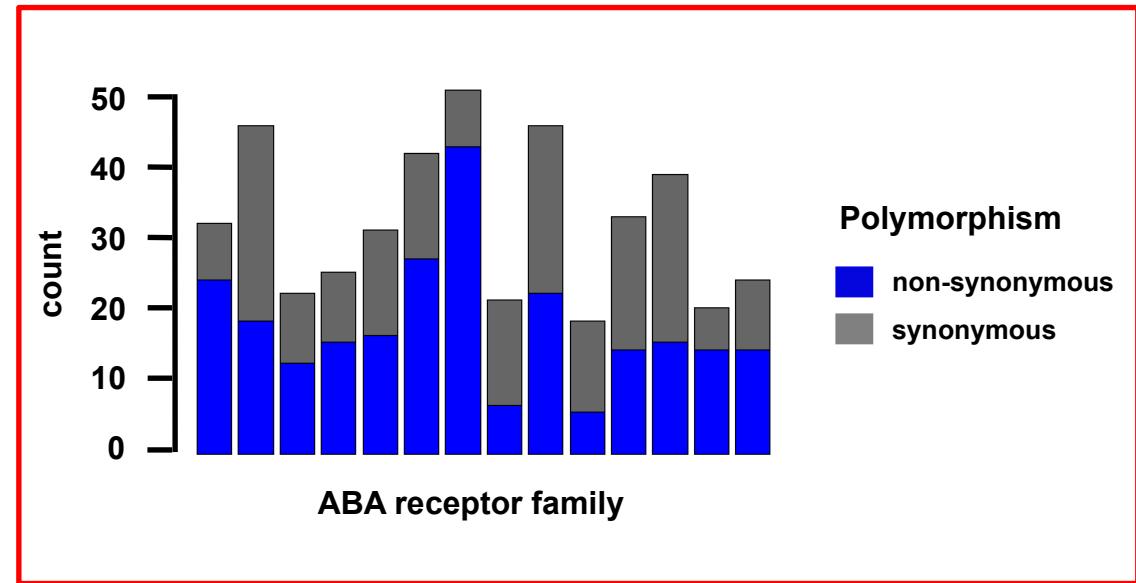
Many genes are knocked-out together more (or less) often than expected

If we use synonymous SNPs as a control we don't observe this co-occurrence

Guard Cell signalling



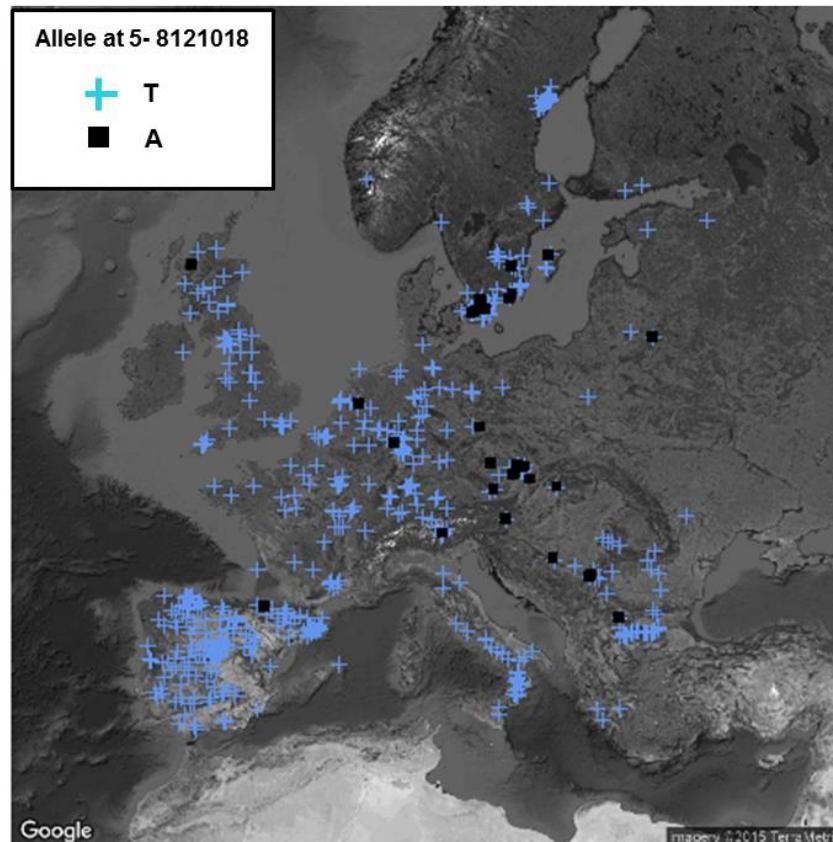
Scherzer et al. Mol Plant 2015



Korte et al. unpubl.

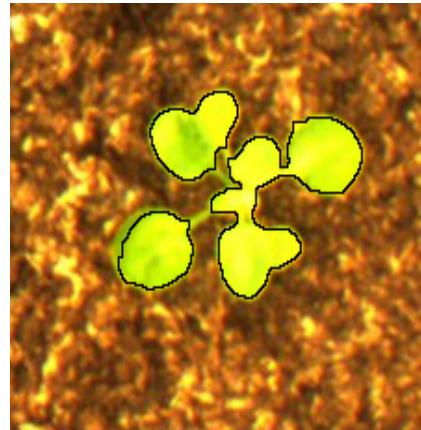
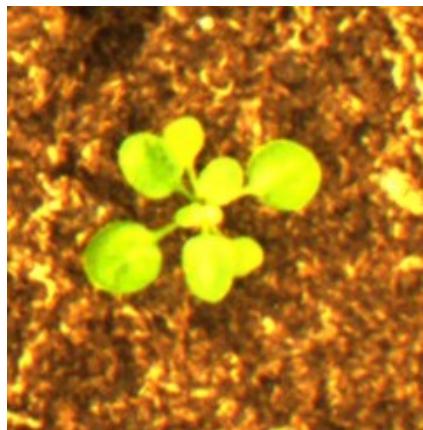
Gene	OST1	SLAC1	SLAH3
Synonymous	23	19	49
Non-synonymous	15	22	42
Splice sites	9	1	8
Alternative Start	4	0	2
Premature Stop	0	0	0

Distinct geographic distribution of different Alleles

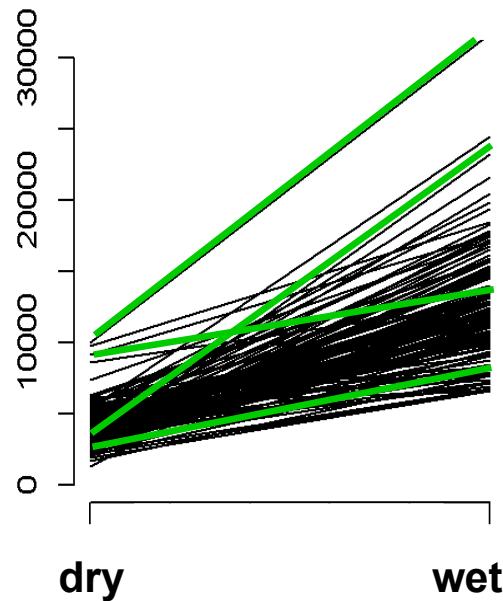


How does natural variation in signalling networks optimize plant performance ?

Natural variation in growth under water limiting conditions

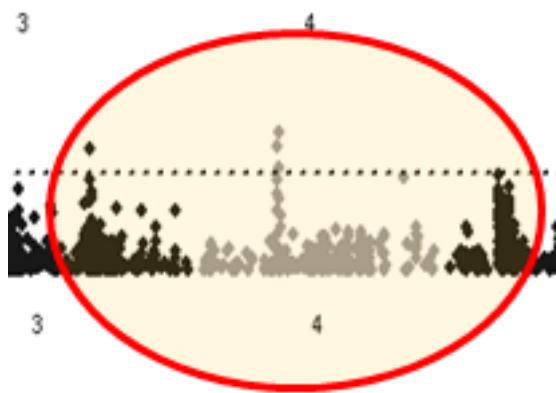


Leaf area after 3 weeks



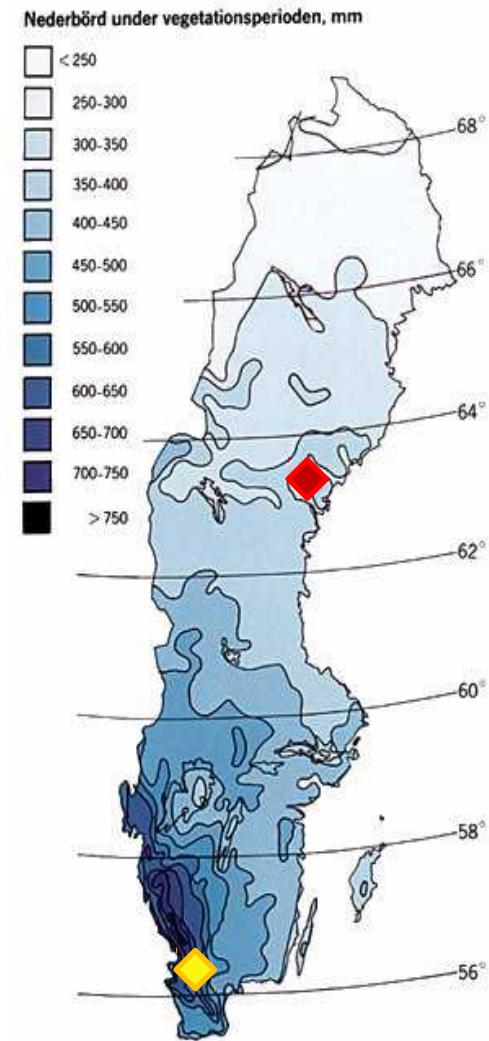
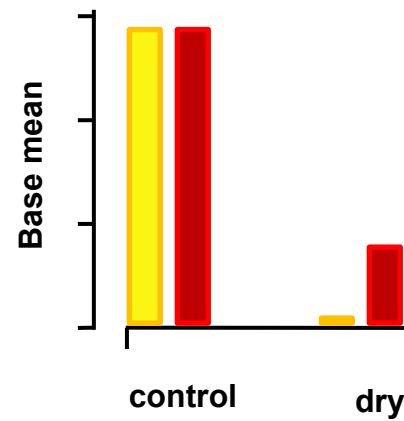
Example : MTMM on Leaf area day 21

MTMM
Trait specific test

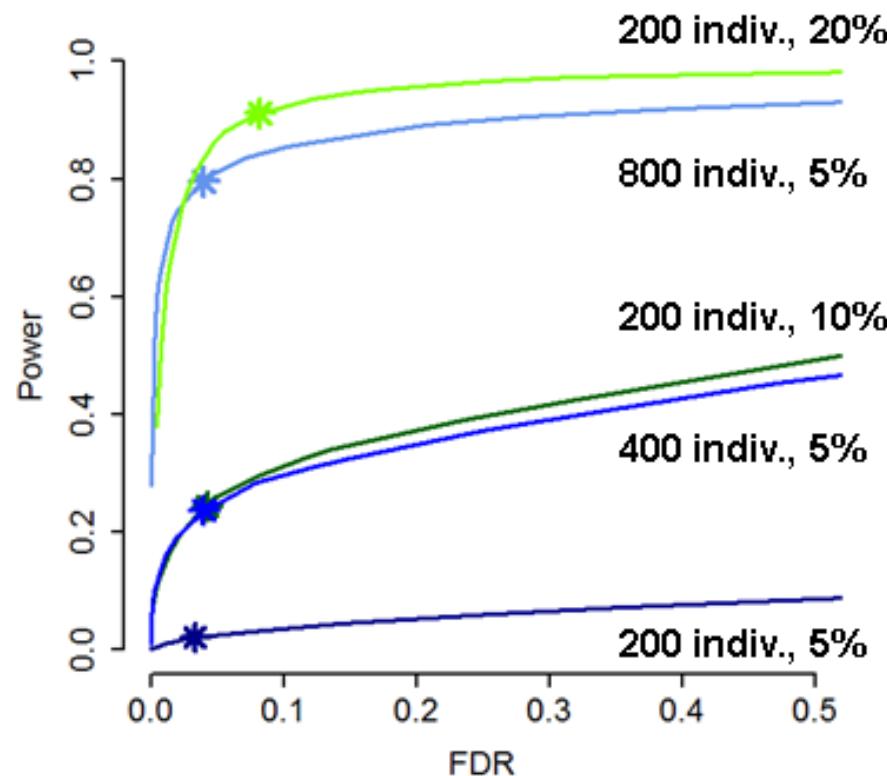


AT4G08950 EXO
(response to
brassinosteroids)

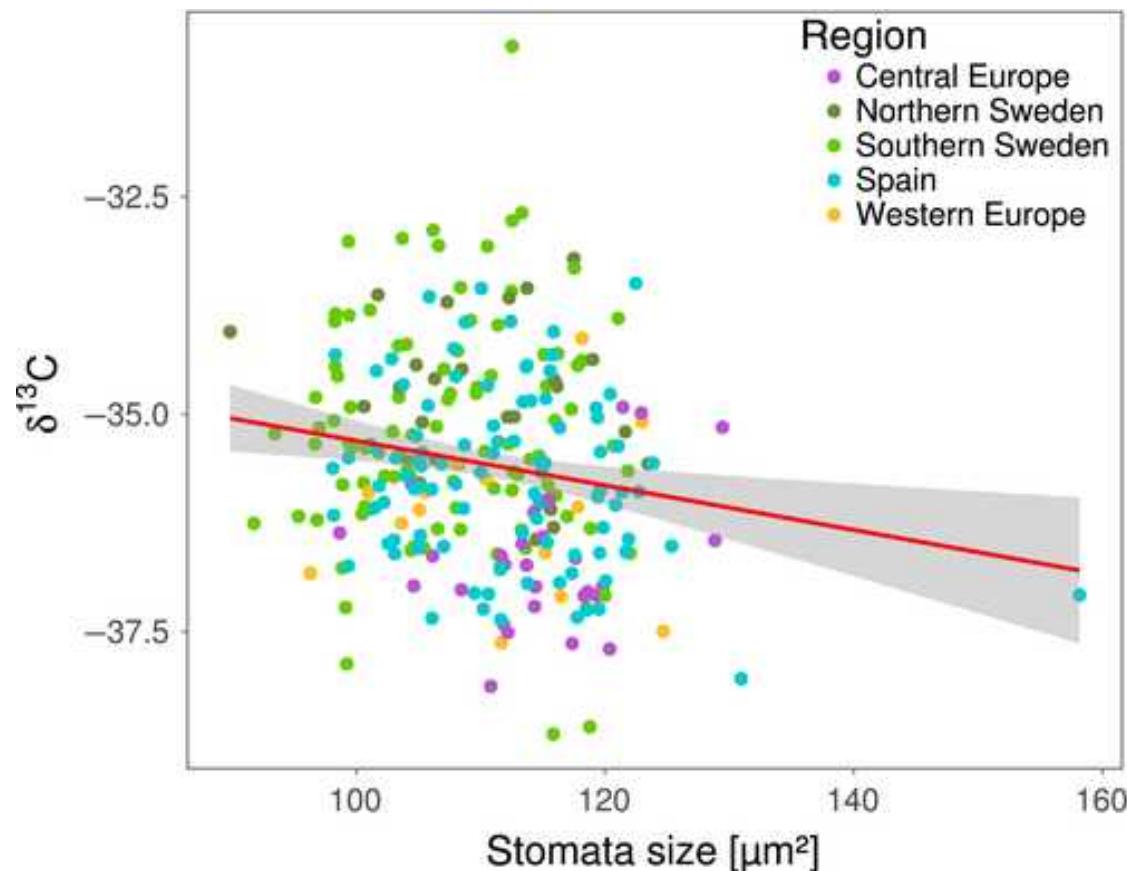
RNA expression
of AT4G08950



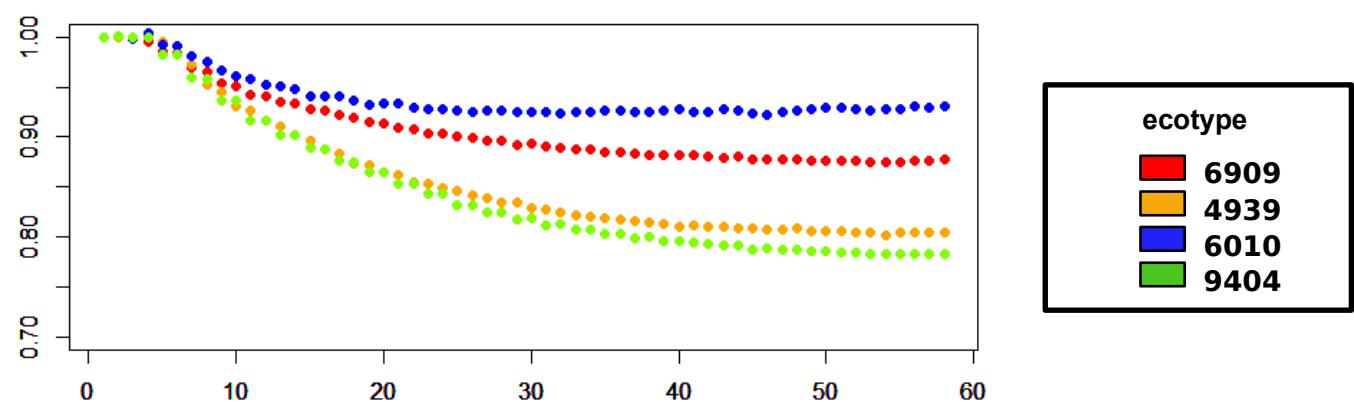
GWAS on cellular traits



Natural variation in water-use efficiency



Natural variation in transpiration rates after increased CO₂ levels

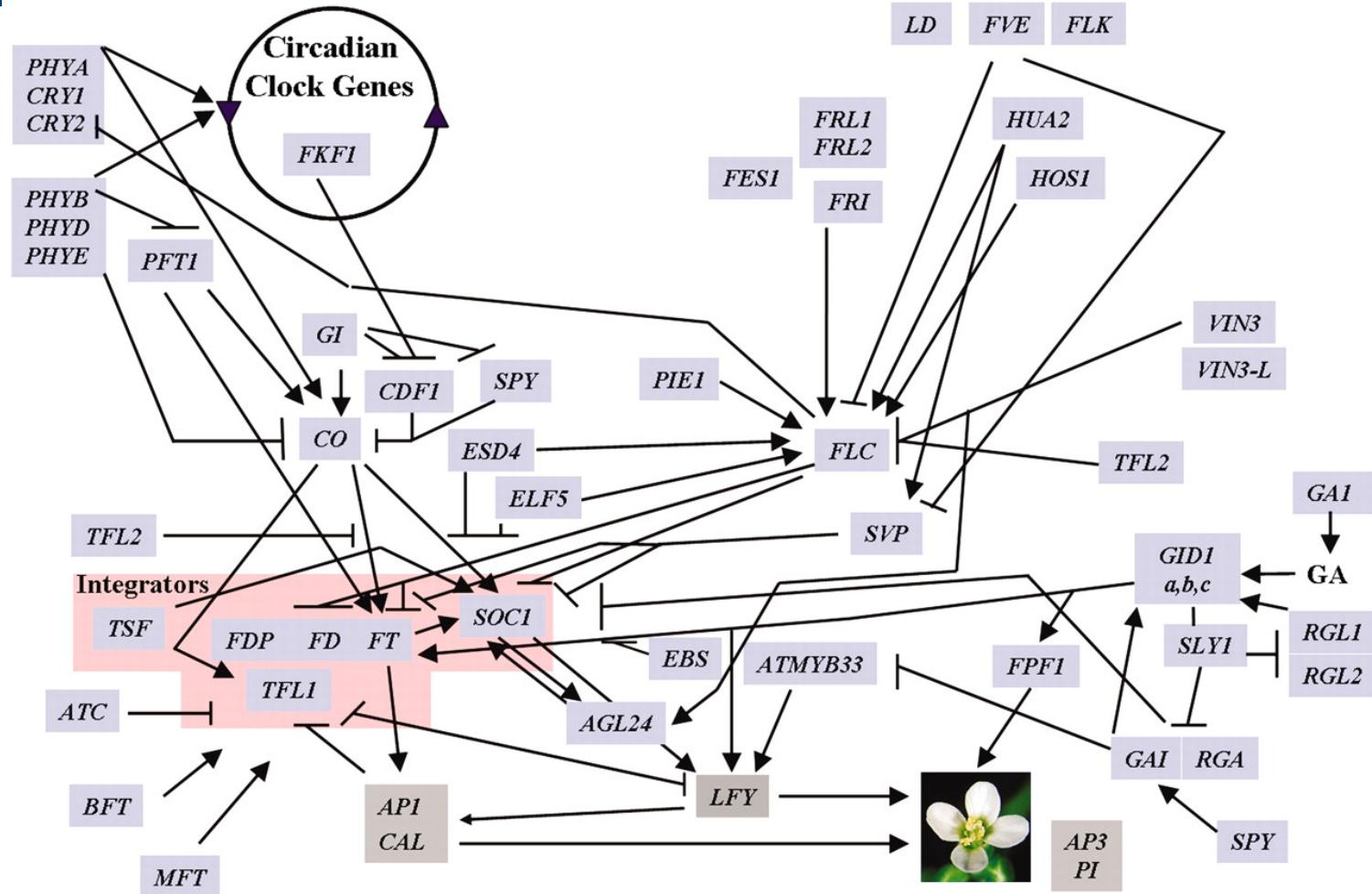


Understand the molecular networks that optimize guard cell performance

**Generation of cell type specific transcriptomes
under different environmental conditions**

**Link phenotypic differences not only with genetic
differences, but integrate transcriptional data as well**

Signalling pathways are complex



Acknowledgments



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