

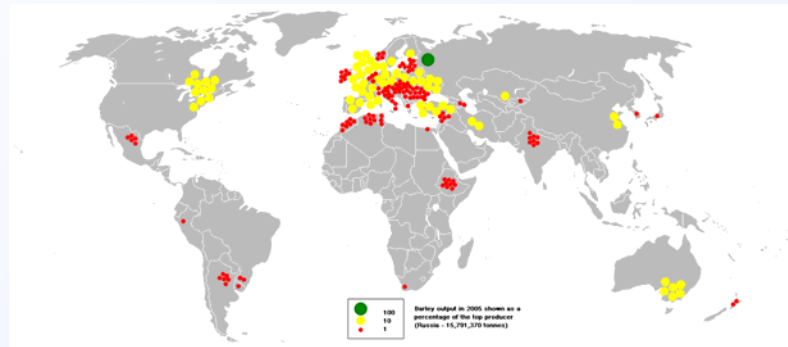
Genomic dissection of tolerance to drought stress in landrace barleys

Robbie Waugh, Michael Baum, Ivan
Matus, David Marshall, Joanne
Russell, Stefania Grando, Salvatore
Ceccarelli, Maria von Korff Schmising,
Timothy Close, Alejandro Del Pozo
and Patrick M. Hayes.

Barley



- 4th main cereal crop, with over 75% grown for animal feed and 138 million metric tonnes grown in 2007
- Grown in over 100 countries and mainly in marginal droughted regions of the world, & where wheat cannot grow
- Genetic dissection of the complex traits that affect the ability of barley to grow in these marginal areas



Exploiting barley diversity



Decreasing diversity from wild to cultivated barley

Domestication, selection and plant breeding



Early domestication
(*H. vulgare ssp spontaneum*)



Landraces
marginal environments



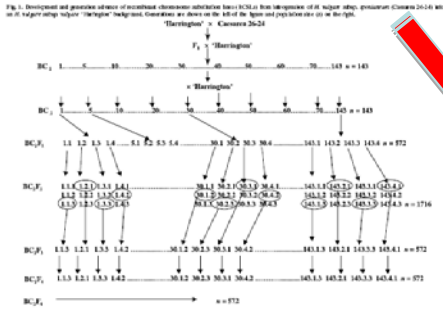
Cultivars

Considerable genetic variation exists;
over 350,000 accessions
conserved

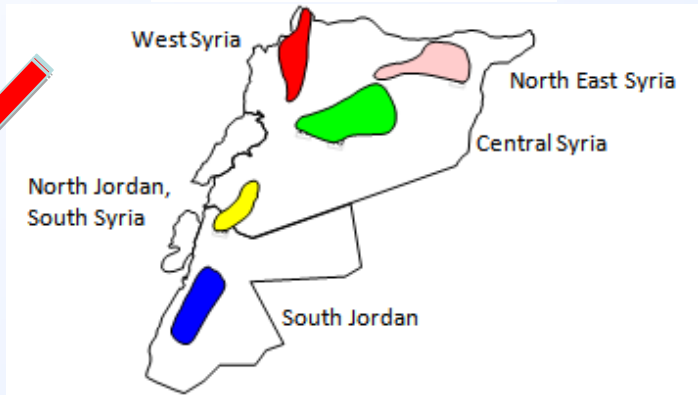
Approach



Genotype 1536 SNPs



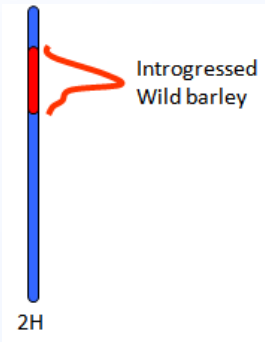
Genotype 1536 SNPs



Phenotype



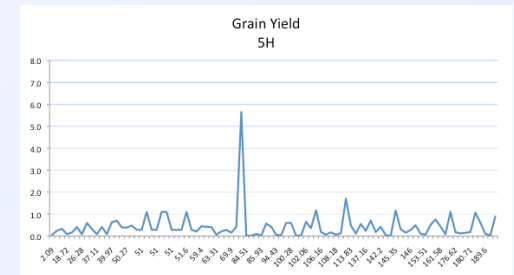
Advanced Backcross QTL analysis



Identify introgressed segments influencing drought

Identify gene/allele conferring drought phenotype

Association mapping analysis



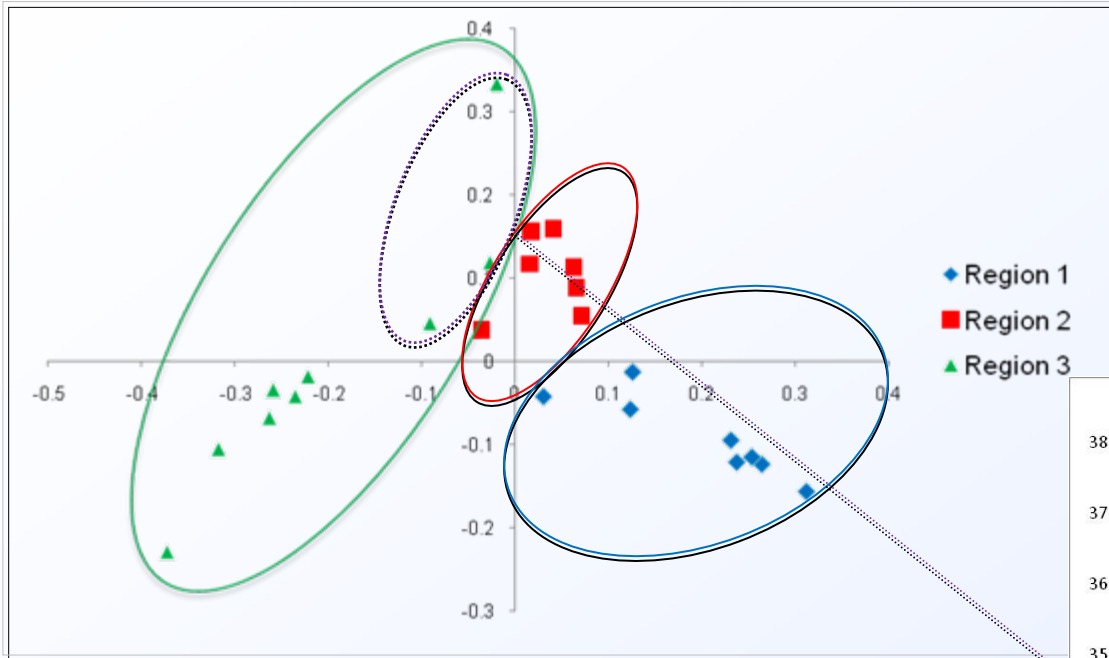
Identify candidate gene regions influencing drought

Association mapping using Syrian Jordanian landrace collection



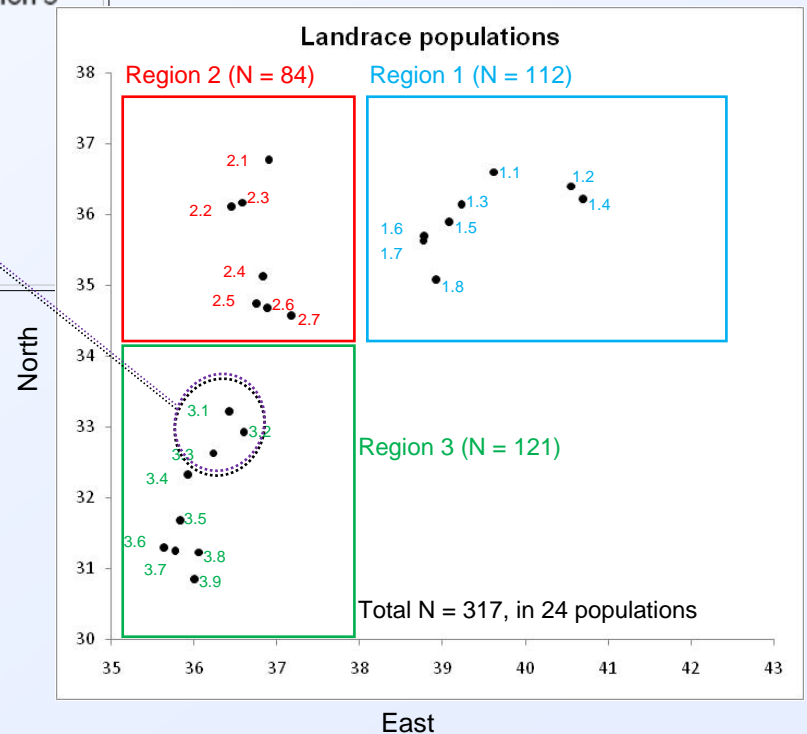
- Advantages
 - Possible to identify associations in pre-existing populations
 - Exploit historical phenotypic information
 - Exploit historical recombination
 - Map many and important traits in the set of relevant germplasm
 - Identification of gene regions, and development of markers for plant breeding
- Disadvantages
 - Account for population structure- a particular problem for barley
- Historical phenotyping
 - Two contrasting field sites
 - Days to heading, grain yield, plant height and thousand kernel weight
- Relevant germplasm
 - 317 SJLCs across 24 populations
 - Genotyped with 1536 SNP markers
- Correct for population structure
 - Kinship matrix, STRUCTURE, PCA others

Genotyping SJLC- 317 accession and 24 populations

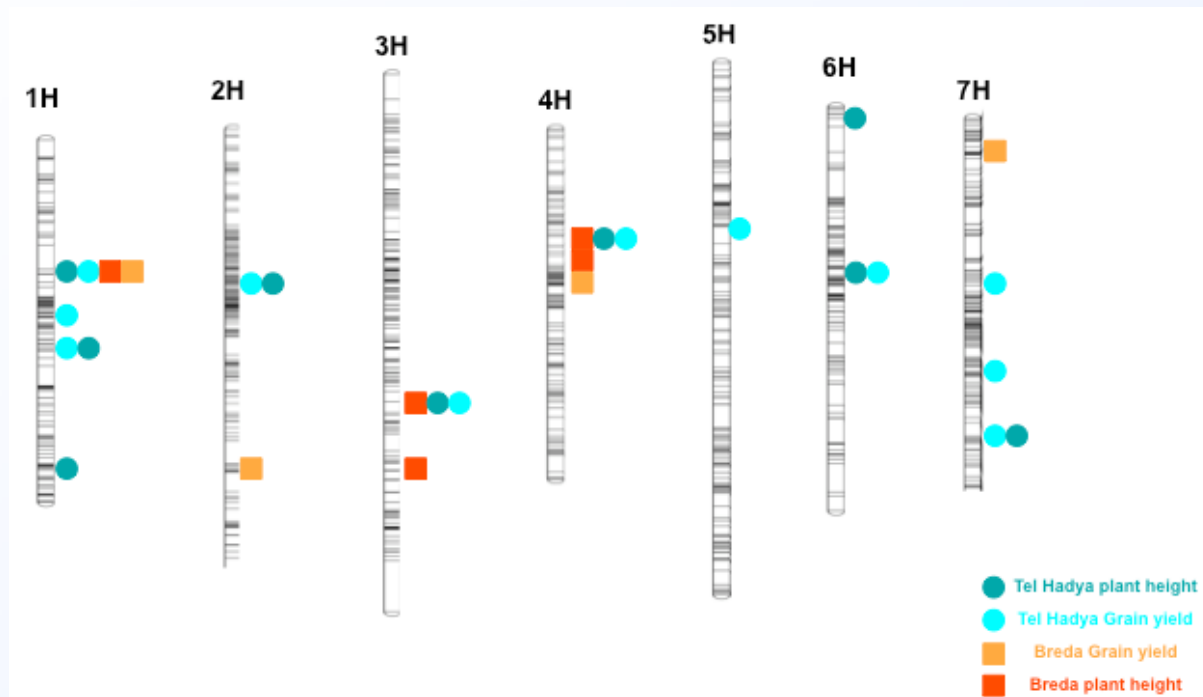


Genetic distances

Geographic distances

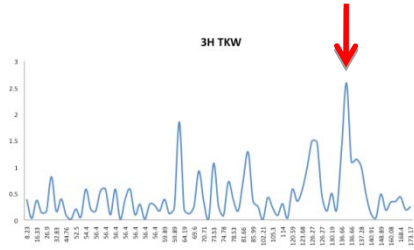


Association analysis and identification of genomic regions

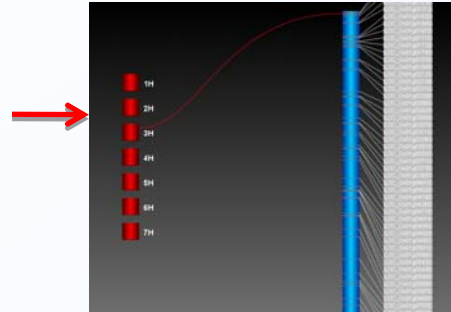


Association using REML and kinship to account for structure

Identifying candidate regions and markers

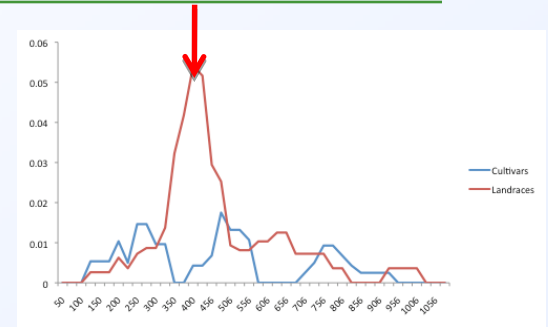


1. Significant association between SNP and TKW



<http://bioinf.scri.ac.uk/strudel/>

2. Alignment with rice, identifying potential candidates

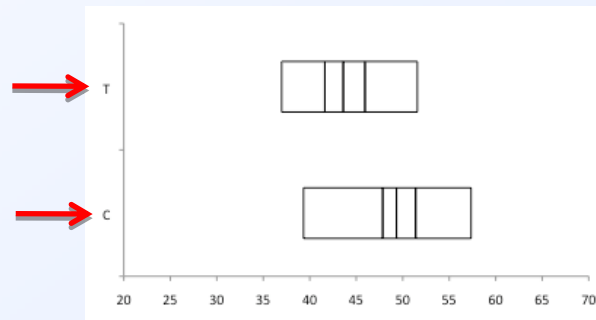


3. Amplification of the candidate gene region, identification of polymorphisms

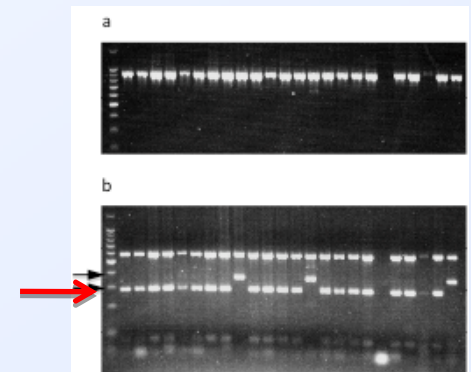
If T then 12% chance that genotype is high yielding

If C then 78% chance that genotype is high yielding

6. Testing with the theory



5. Re-association of CAPs with TKW

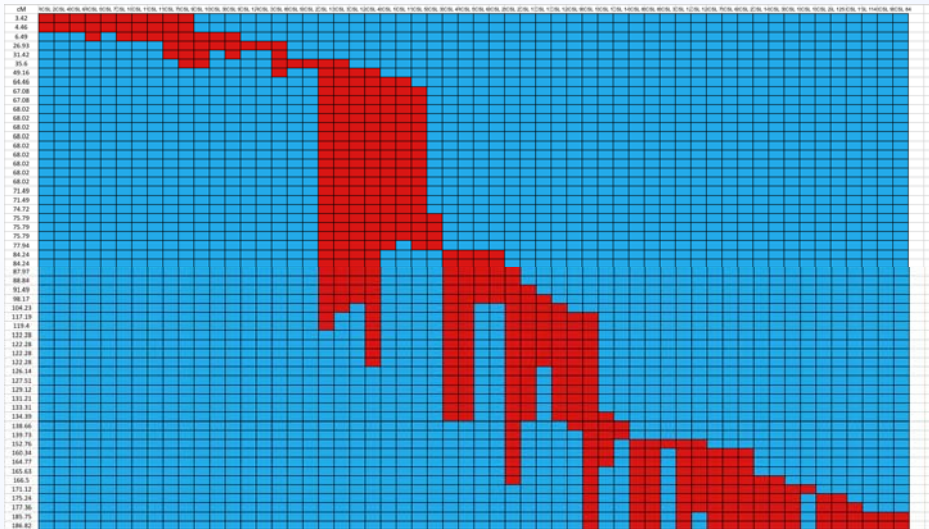


4. Design of CAPs markers, validation in relevant germplasm

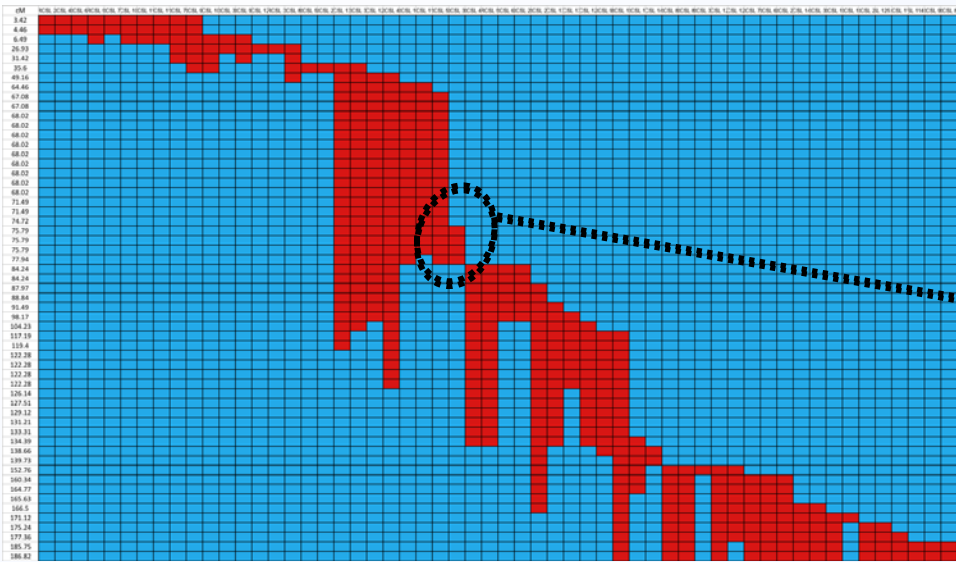
Genotyping and phenotyping RCSLs



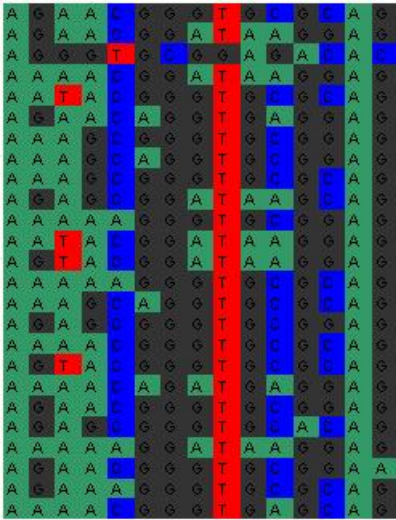
- Ordered series of RCSLs, blue represents 'Harrington' and red the introgressed segments from *H spontaneum*. Each column represents a single RCSL.
- Physiological and agronomic traits measured at contrasting sites in Chile and Syria



Identifying introgressed segments influencing drought



25 haplotypes
(0.706)





- *People*
 - Robbie Waugh
 - Malcolm Macaulay
 - Dave Marshall
 - Linda Milne
 - Paul Shaw
 - Andy Flavell
 - Jordi Comadran
 - Allan Booth
 - Ian Dawson
 - Zhang Zhengzhi
-
- UCLA – Tim Close
 - University of Oregon – Pat Hayes
 - ICARDA – Michael Baum, Stephania Grando
 - INIA – Alejandro del Poza, Ivan Matus