How does Association Genetics work in barley?

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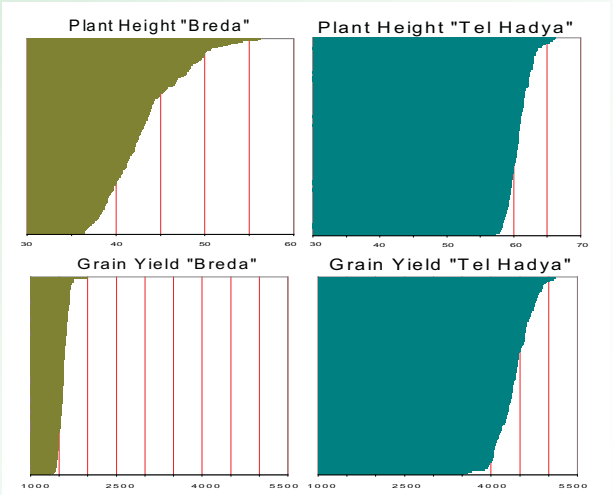
Using biodiversity to reach the gene

Accurate knowledge of the genomic location of genes controlling important agronomic traits is a prerequisite for the successful deployment of molecular marker technology within a breeding programme. Association Genetics benefits from marker saturated genetic maps to effectively use the biodiversity stored in barley natural populations to fine-map traits of economic and agronomic interest.

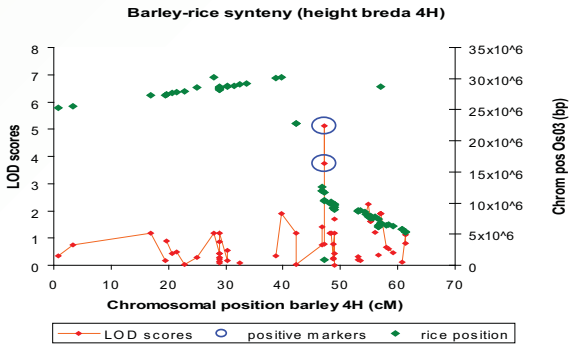


	Days to Heading	Height	Yield	Thousand Kernel Weight
Breda	---	43.25	1580.01	---
TelHadya	102.94	60.88	4419.86	47.86

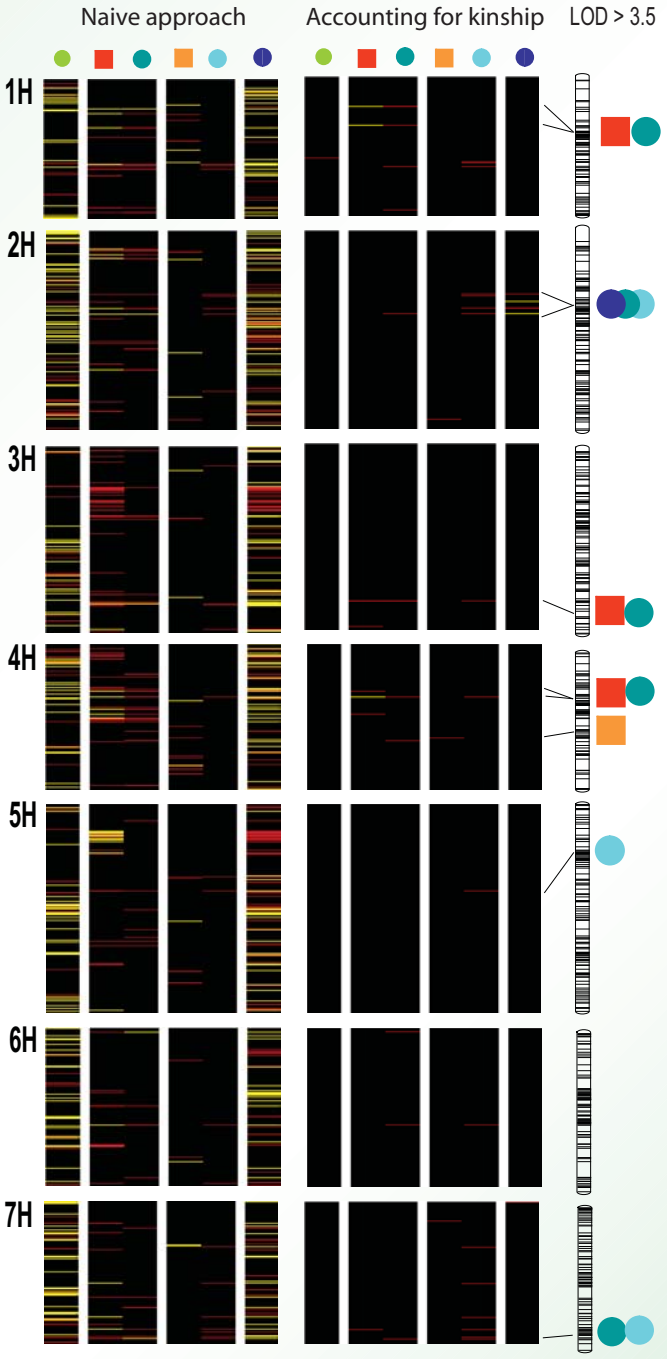
For this example, 1500 SNP-genotypic data was obtained for 200 Syrian and Jordan landraces with phenotypic data available from a dry and a wet location.

Barley-rice synteny

Gene sequence based markers make possible the exploitation of barley synteny with sequenced genomes such as rice and *Brachypodium* to find gene candidates.



Population structure is a major source of false positives



A mixed model framework was used to account for the effects of population structure and kinship. QTLs for yield and height were detected in both dry and wet environments.

LOD > 5 LOD > 4 LOD > 3 LOD < 3

Tel Hadya flowering
Tel Hadya plant height
Tel Hadya Grain yield
Tel Hadya thousand kernel weight
Breda Grain yield
Breda plant height

Association Genetics in barley at SCRI

1) AGOUEB (Association Genetics of UK and European Barley).

UK and European Barley Cultivars + historical data

2) MABDE (Mapping Adaptation of Barley to Drought Environments).

Mediterranean Barley from Landraces to Cultivars + 28 trials around the Mediterranean

3) Genomic dissection of tolerance to drought stress in barley.

Syria and Jordan Landrace Collection (SJLC)

4) ExBARDIV (Genomics-Assisted Analysis and Exploitation of Barley Diversity).

Wild barley, SJLC and European barley cultivars