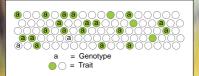
Genomics-assisted Analysis and Exploitation of Barley Diversity (EXBARDIV)

Project Goal

To establish an incremental association mapping approach based on different population types for the discovery of new gene alleles in barley which can be exploited for crop breeding.

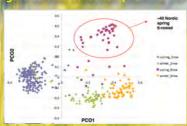
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A strong association between a trait and a marker implies a close physical linkage in the genome (IF the population of individuals is unstructured)



The EXBARDIV Consortium



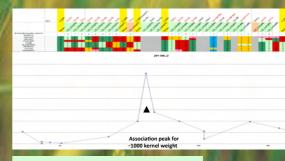
Andy Flavell, University of Dundee at SCRI Klaus Pillen, Max Plack Institute, Koln Alan Schulman, MTT Agrifood Helsinki Andreas Graner, IPK Gatersleben Luigi Cattivelli, CRA Fiorenzuola Søren Rasmussen, Copenhagen University Joanne Russell, Scottish Crop Research Ins

Field Plot Data	Seed yield parameters	Seed Content	Plant Parameters	Biotic Stress	Abiotic Stre
Frost	Grain Number (seeda/ear)	Grain protein	Above ground biomass	Powdery mildew resistance	Frost tolerance (Fv/Fm value a freezing)
Heading	Grain yield (weight/area	Grain total - Pi	Above ground N content at maturity	Leaf rust resistance	
Height	1000 kernel weight	Grain phytate	Leaf N content during shooting & flowering	Net blotch resistance	
Ear length	Grain area (X x Y)	Grain β-glucan	1 200	Leaf stripe resistance	
Maturity	Grain shape (width /length)	Grain N content	Visit Service	Rhynchosporium resistance	
Lodging	Grain hardness	Grain micro nutrients	1		
Leaning	Grain volume (X x Y x Z)	Grain starch content	Ell visit	1000	
Brackling		Arabinoxylan content	20.00	10.00	
Necking		Starch digestibility	10 100		
PlotWt		Plant sterols	STATE OF THE PARTY		
PlotMoi		'Blue value'	1000		
PlotLen					
PlotWid				ALC: UNKNOWN	

Current work & the Future

The most promising association candidate regions for 1000 kernel weight identified from trials conducted last year and this are being tested by a 'focussed' approach to narrow down the candidate region to a few genes using Next Generation sequencing (NGS) of genes across the association interval.

We have collected genes in the vicinity of association peaks, pre-screened them in a panel of 8 cultivars for SNP polymorphism and designing appropriate gene segments and targetting strategies for NGS across the complete cultivar collection. Sequencing is ongoing



Existing Illumina SNPs in barley

No polymorphisms in the 8 cultivars tested