The BRIDGE project: From 1 – 20,000 barley genomes

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Barley – a globally grown crop species

Barley Total Harvested Area (ha)

Barley diversity – modern cultivars vs. genetic resources

- Modern cultivars are adapted to and bred for the average conditions in specific geographical regions (climate, latitude, altitude etc.)
- Genetic diversity decreased as a consequence
- Lacking plasticity for further adaptation as climatic conditions become more variable
Global barley diversity

- Phenotypic diversity = Genomic diversity in barley is high
- Allelic Diversity important tool in functional genomics or breeding
- Natural diversity: domesticated / wild genepool
BRIDGE: Biodiversity infoRmatics to close the gap from genome Information to educated utilization of Diversity hosted in GEnebanks

- Interactive haplotype browser
- Comparison to existing marker data to guide pre-breeding

Interfaces to other systems
- EURISCO
- EDBD
- transPLANT
- de.NBI
- SeedSeq
- Digital Seed Bank
- GENESYS

Primary data analysis

Field based phenotyping
BRIDGE project: GBS of >20,000 barley accessions.

- WGS / exome capture of selected accessions
- Historic evaluation data (morphologic and agronomic)
- Passport and geo-reference information
- Ear- and seed phenotyping at harvest
GBS of >20,000 barley accs.

- GBS (PstI/MspI) library preparation (Wendler et al. 2014; >180-plex barcoded)
- Bioinformatics pipeline (Mascher et al. 2013):
  - Minimal read depth per genotype: 2x
  - Maximal fraction of missing calls: 10%
  - Both alleles at least once in homozygous state
Diversity in barley - whole collection

22,621 samples
171,263 SNP

PC1 (1.3 %)
PC2 (1.1 %)

domesticated
wild
unknown
Representativeness of IPK collection
Diversity in domesticated barley
Diversity in domesticated barley
GWAS for row-type

**Genotypes:** SNPs with a MAF ≥1% (19,507 SNPs).

**Software:** GAPIT R package (Lipka et al. 2012), using a mixed linear model, kinship, PC1/2 as covariants
GWAS for awn roughness
GWAS vs BSA for awn roughness

position in reference genome

allele freq.

-\log_{10} (p)

raw1
TILLING to confirm raw1 function

Non-Synonymous  Synonymous  Splice site mutation

8993-1_8 → WT/WT
8993-1_7 → MT/MT
8993-1_2_10 WT/WT
8993-1_2_8 WT/MT
8993-1_2_5 MT/MT
Genebank genomics

- GWAS for simple traits
- GWAS for more complex and agronomically relevant traits
how about historical (legacy) data in genebanks?

unbalanced legacy data from regeneration cycles

→ manual quality assessment

• checking sowing date and off-season sowing date
• checking extreme data points

Outlier detection based on re-scaled median absolute deviation and Bonferroni-Holm test

→ describing the phenotypic diversity of the collection / Estimating heritability and BLUEs

→ examine the data suitability for selection of accessions

re-sampling study
two-fold cross validation

Barley multiplications at IPK Genebank
Value of genebank legacy data for GWAS?
GWAS for resistance to soil-borne viruses

1894 accessions tested

collaboration with JKI QLB, Ordon+Habekuss
The BRIDGE portal

https://bridge.ipk-gatersleben.de
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Summary

BRIDGE – a complete barley ex situ collection characterized by GBS

- Diversity landscape of the collection – what is the context of global diversity
- GWAS
- Collection management
- Better informed selection of genetic resources in pre-breeding
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Genebank genomics highlights the diversity of a global barley collection

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