Comparing genetic diversity within a crop and its wild progenitor: a case study for barley

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SEVERAL OPINIONS ON BARLEY DOMESTICATION HISTORY

„Core Area“ of plant domestication in the Fertile Crescent

Possible areas of barley domestication in the Fertile Crescent
BARLEY

Hordeum spontaneum

Hordeum vulgare
BARLEY DOMESTICATION

Pourkheirandish and Komatsuda 2007
CONSENSUS MAP OF BARLEY DOMESTICATION-RELATED GENES

Pourkheirandish and Komatsuda 2007
DEVELOPMENT AND USE OF THE BARLEY CORE REFERENCE SET **BR816**

**Diverse core collections considered:**
- MPIZ922, B1K, BCC

Max. genetic and phenotypic diversity

**Core Reference Set **BR816** (from 65 countries):**
- **579** wild *H. spontaneum* (whole natural distribution range)
- **109** *H. vulgare*, landraces
- **128** *H. vulgare*, cultivars

**Phenotypic Data available**
Several traits over several years

**Genotypic Data available**
- 300 retrotransposon-based polymorphic SSAP markers
- 400 AFLP marker
- 400 SSR markers
- 1536 BOPA1 marker
- 20 candidate genes have been re-sequenced; more in progress
GENETIC DIVERSITY AMONG EINKORN AND EMMER WHEAT

haplotypes (SNPs) at 17 loci (267/452 lines)

Kilian et al. 2007

Özkan et al. 2010
BR816 AS RESOURCE FOR ALLELE MINING

GENETIC DIVERSITY AT MAJOR FLOWERING PATHWAY GENES IN BARLEY

adapted from Cockram et al. 2007
PpdH1 POLYMORPHIC POSITIONS AMONG 57 HAPLOYPES IN BR816
PpdH1-haplotypes in BR816:
LOSS OF GENETIC DIVERSITY IN CULTIVATED BARLEY

BR816 collection:
898 bp resequenced
57 haplotypes in wild barley
12 haplotypes in domesticated barley
PHENOTYPING OF BR816 (2009)
ASSESSING GENETIC DIVERSITY FOR CROP IMPROVEMENT:

Ongoing work and future research tactics for crop plants and their wild progenitors:

- High-throughput genotyping
- High-throughput phenotyping
- Whole-genome association studies*
- generating new resources*
- Re-sequencing of candidate genes in large collections*
- next-generation sequencing*
- * in situ conservation and collection trips
- Interdisciplinary cooperation
WHOLE-GENOME ASSOCIATION STUDIES IN DIFFERENT BARLEY COLLECTIONS

Linkage Disequilibrium level

HSC  <  LRC  <  HVCC

H. spontaneum  H. vulgare landraces  H. vulgare cultivars

adapted from Tanksley and McCouch 1997
EXAMPLE: EXBARDIV – EUROPEAN CONSORTIUM FOR ASSOCIATION MAPPING IN BARLEY

Hordeum vulgare **Cultivar** Collection
451 lines
128* Winter lines
323* Spring lines

Hordeum vulgare **Landrace** Collection
480 lines
obtained from Stefania Grando, ICARDA

*H. spontaneum* Collection
218 lines
obtained from Eyal Fridman, Jerusalem
DEVELOPMENT OF RESOURCES:
LANDRACE COLLECTION FOR HIGH-RESOLUTION LD-MAPPING

22,093 *Hordeum* accessions at the IPK Genbank (2008)

Spring barley landraces available at IPK
(*6,779 accessions*; including 923 from IPK collection trips)

- Selection based on origin, nomenclature, morphology

Selection of *1600* landraces (2-rowed and 6-rowed)

- Genotyping using 45 SSR markers
- Population structure
- 2x SSD

~ *1000* spring barley landraces (Europe; Africa, Asia)

Primary evaluation at the IPK (2010)

- Illumina
- Phenotyping

Association studies for important agronomic traits
MORE PROGRESS: NEXT-GENERATION SEQUENCING

Wicker et al. in prep
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