MAGIC population in barley

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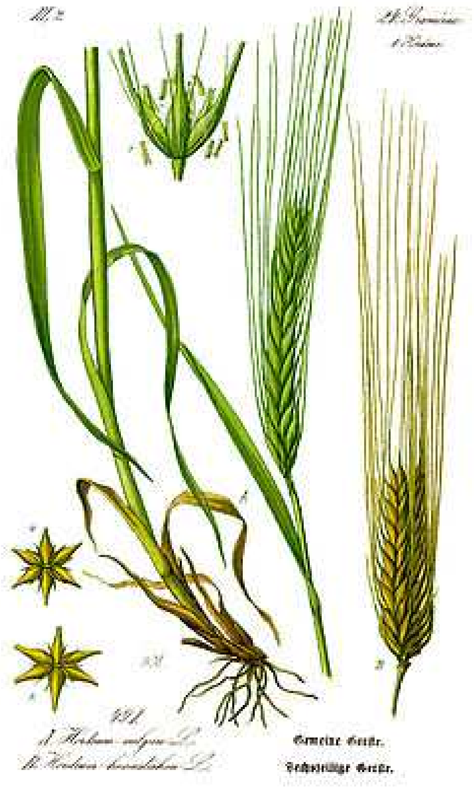
Hordeum vulgare ssp. *vulgare* – cultivated barley

- domesticated 10 000 years ago in the Fertile Crescent
- ranking fifth in terms of acreage
- used for animal feedstock (75%), malting (20%) and human food (5%)

- diploid, self pollinating, highly inbred
- 7 chromosomes (2n=14)
- genome size around 5Gb, ~84% of noncoding DNA
- wild forms are known, available and can be crossed
- used as model crop for other Triticea crops



Prof. Dr. Otto Wilhelm Thomé

Existing barley resources


MPIPZ Cologne

- Gene banks
  - IPK Gatersleben
  - ICARDA
  - International Barley Core Collection
  - etc.
- Populations
  - Composite crosses (CC) with different mating designs all of them are multi parent designs
  - e.g. Oregon Wolfe Barley (OWB)
  - Further mapping populations (often a rather low number of lines)
  - NAM population with wild-forms (public available?)
  - ...

MAGIC Pop in Barley
Selection of parents

Aims:
Parents should represent a highly divers panel
but should be adapted to German growing conditions.

Strategy:
Analysing the pedigrees of German spring barley cultivars.
Selecting the parents or grand parents of the most successful cultivars
Repeat this process until founders (landraces) are selected.

Theses parents should represent the **Founders** of spring barley breeding in Germany.

Additionally a modern cultivar with know sequence, SNP or EST and representing the current type of cultivars should be included as well.

Selected parents

Accession name	**IPK number**	**Year of release**
Ackermanns Bavaria	HOR 100	1903
Ackermanns Danubia	BCC 1427	1912
Barke	Saatzucht Josef Breun GdbR	1996
Criewener 403	HOR 62	1910
Heils Franken	BCC 1433	1895
Heines Hanna	HOR 59	1884
Pflugs Intensiv	BCC 1441	1921
Ragusa	BCC 1359	1929

MAGIC **Diallel**

MAGIC – crossing scheme

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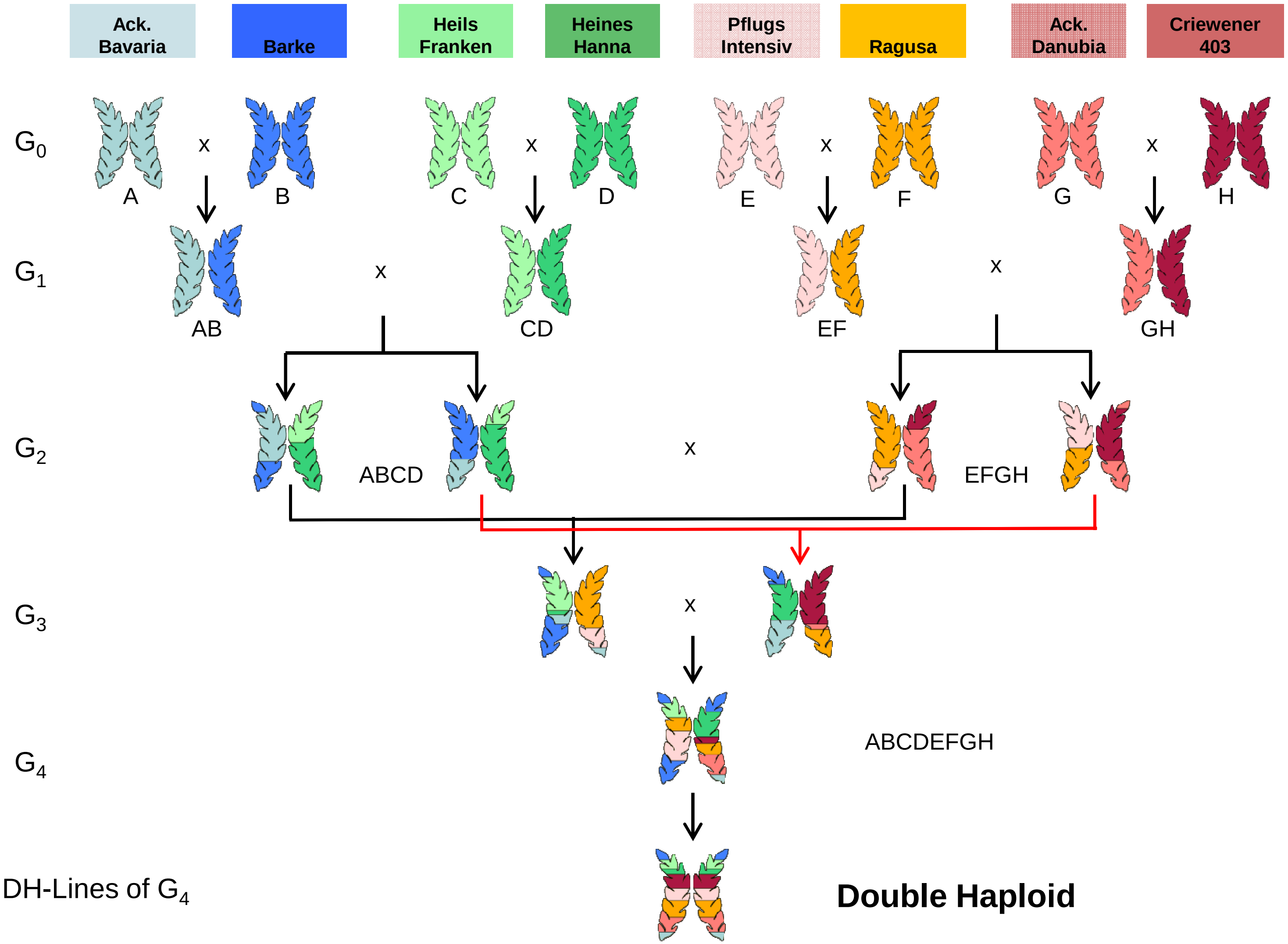

Number of parents

single plants

4 parents/cross

8 parents/cross

16 parents/cross

Equal number per subpopulation

MAGIC barley population

- ~ 5 000 DH-lines
- ~ 1 400 DH-lines with enough seeds for plot experiments
- ~ 534 DH-lines genotyped with SNP marker

Genotyping

- Illumina 9k iSelect chip
  - ca. 5 000 polymorphic SNP marker in MAGIC population

- Genotyping by Sequencing (60 000 SNPs) in cooperation with Cornell University
  - however in another project we received only 1 300 SNP polymorphic markers without too much missing data

- Barley Sequence or “Gene space” has been published in Nov2012

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Decay of LD for DH-lines of Barley MAGIC population

CTGACTCGTATATATACAGACG
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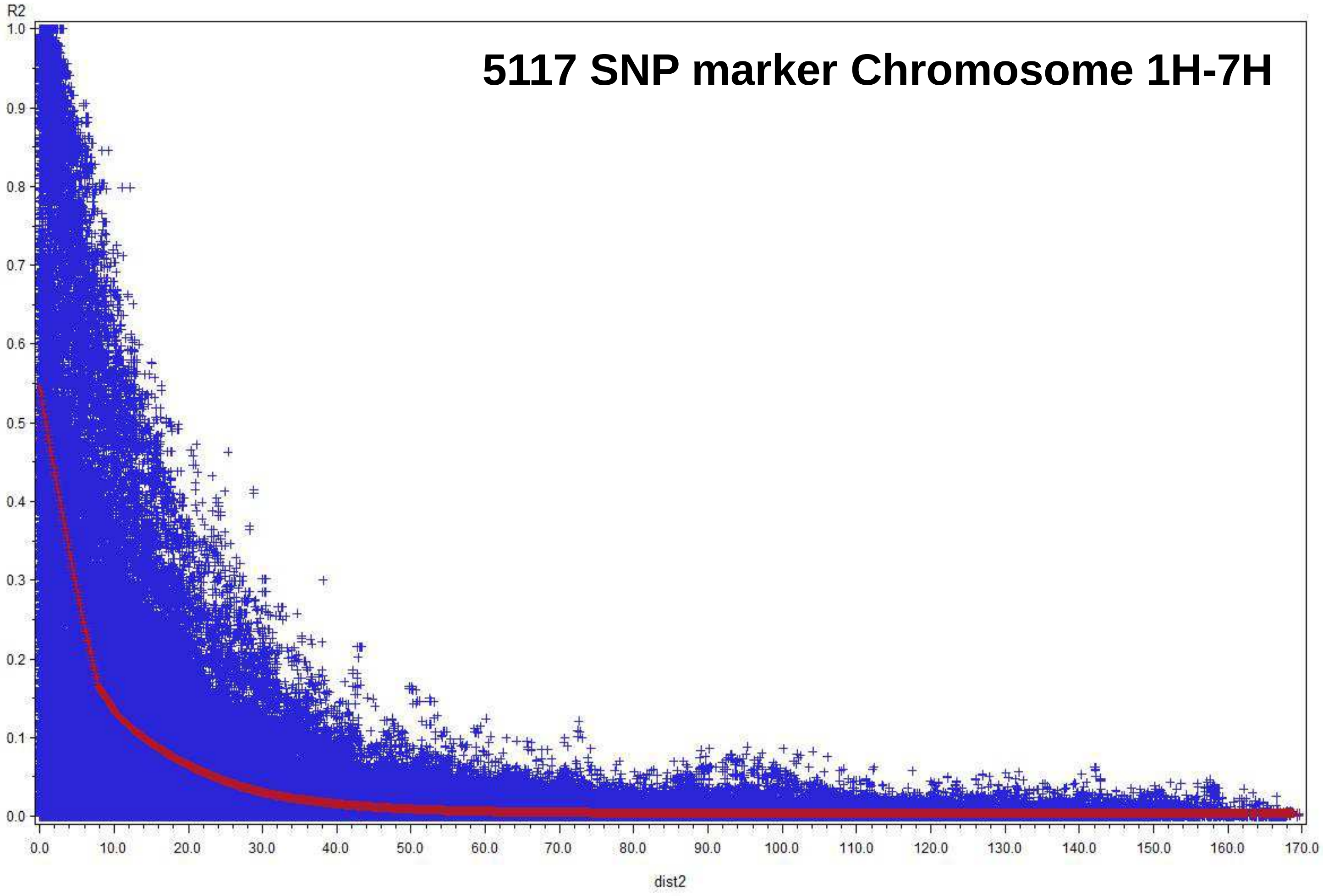

Position in cM from Comadran et al. 2012

MAGIC phenotypic data

Augmented design 2011/2012

- 554 genotypes of spring barley
  - 534 DH-lines
  - 8 parents (2 reps) and check variety (20 reps)
- two water treatments with five weeks reduced water supply

Phenotypic traits

- flowering time
- yield and yield components

Development of a SAS Macro for Mixed Model QTL mapping

Mixed Model Analysis

- Marker (QTL effect or haplotype effect)
- optional: genotype within marker as a random factor
- Random factors (QTL by environment)
- Fixed factors (QTL by treatment)

Advantages

- Multi-locus analysis (forward/backward selection)
- Cross Validation
- Permutation
- Epistatic effects (including by environment or by treatment)
- Multi-trait QTL analysis (however time consuming)

Challenges

Haplotypes *vs*. SNP analysis

We would like to include all markers into a haplotyping process

Talk of Wiebke Sannemann

MAGIC Population in Barley

First PhD thesis finished
First publication on the way

Seeds of the parent are available for cooperation
Seeds of the genotyped MAGIC lines are also available

Further lines will be genotyped

For all relevant QTL regions
Bi-parental crosses from the Diallel are available
as F_1 or DH-lines

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