

QTL mapping approaches in a eight parent MAGIC population in barley

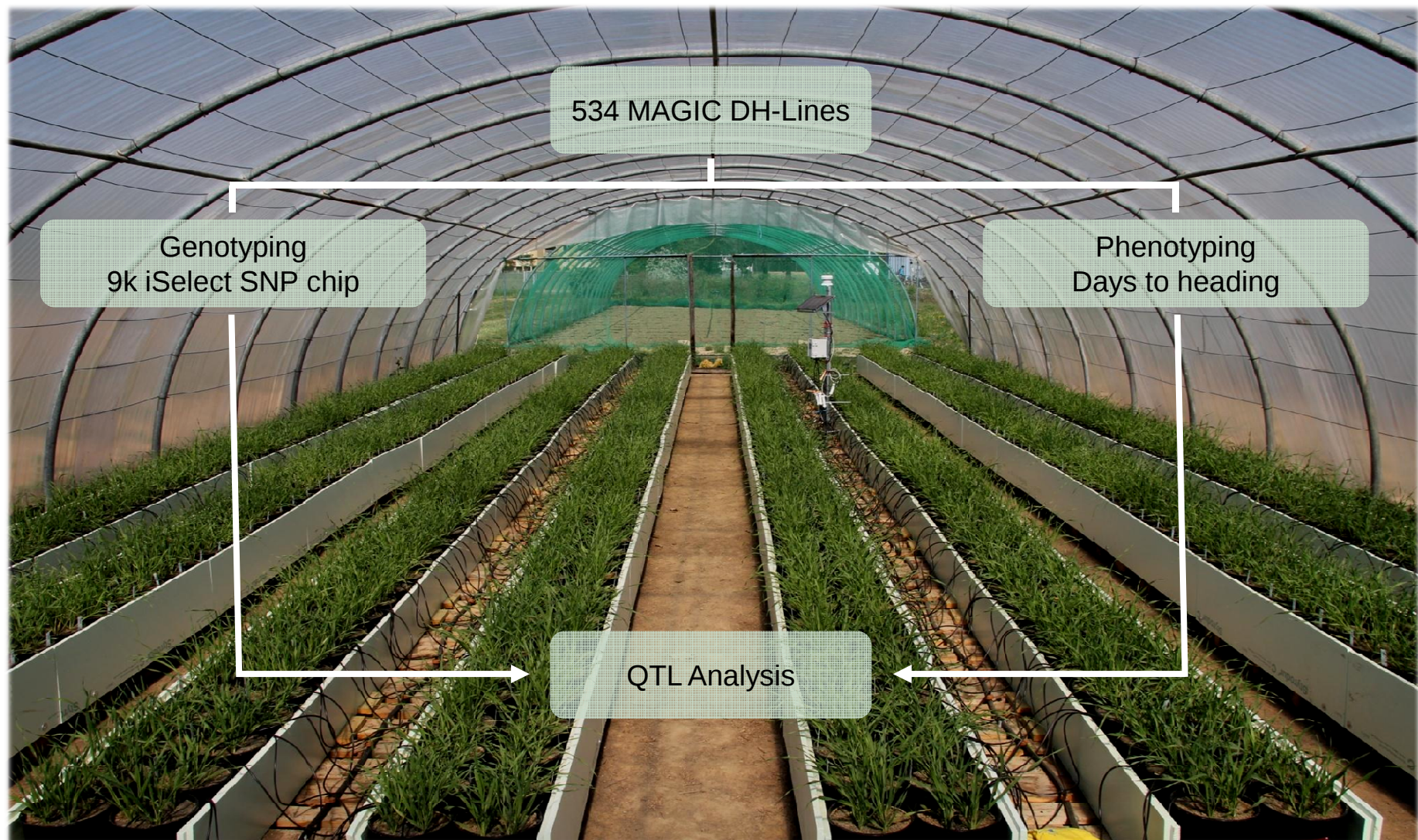
Wiebke Sannemann, Jens Léon

MAGIC workshop

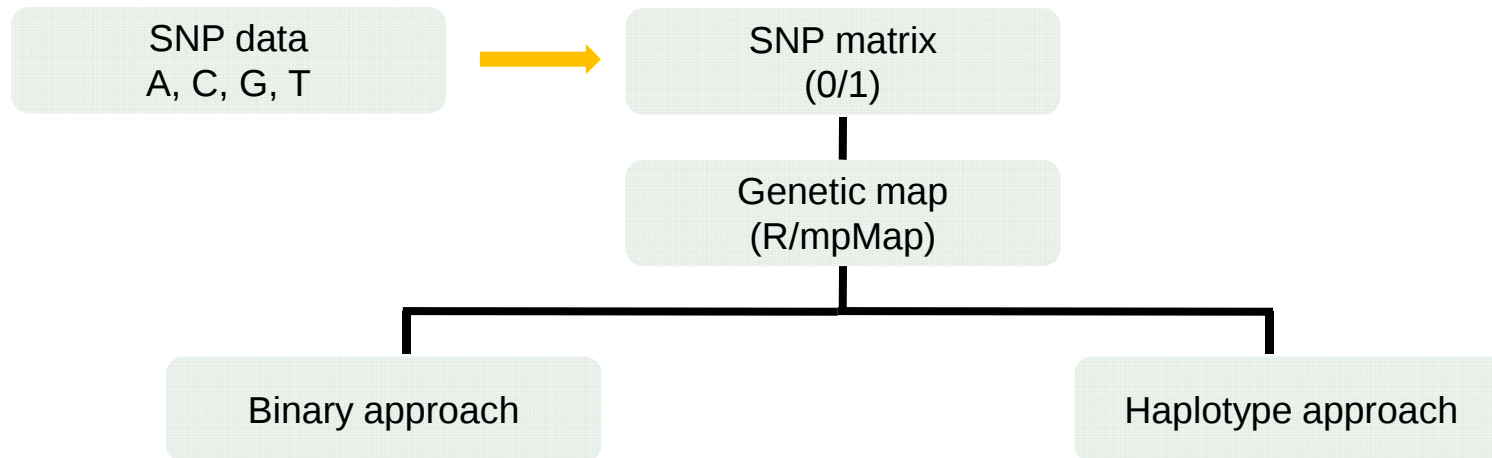
Cambridge, 13.06.2013



Experimentel set up

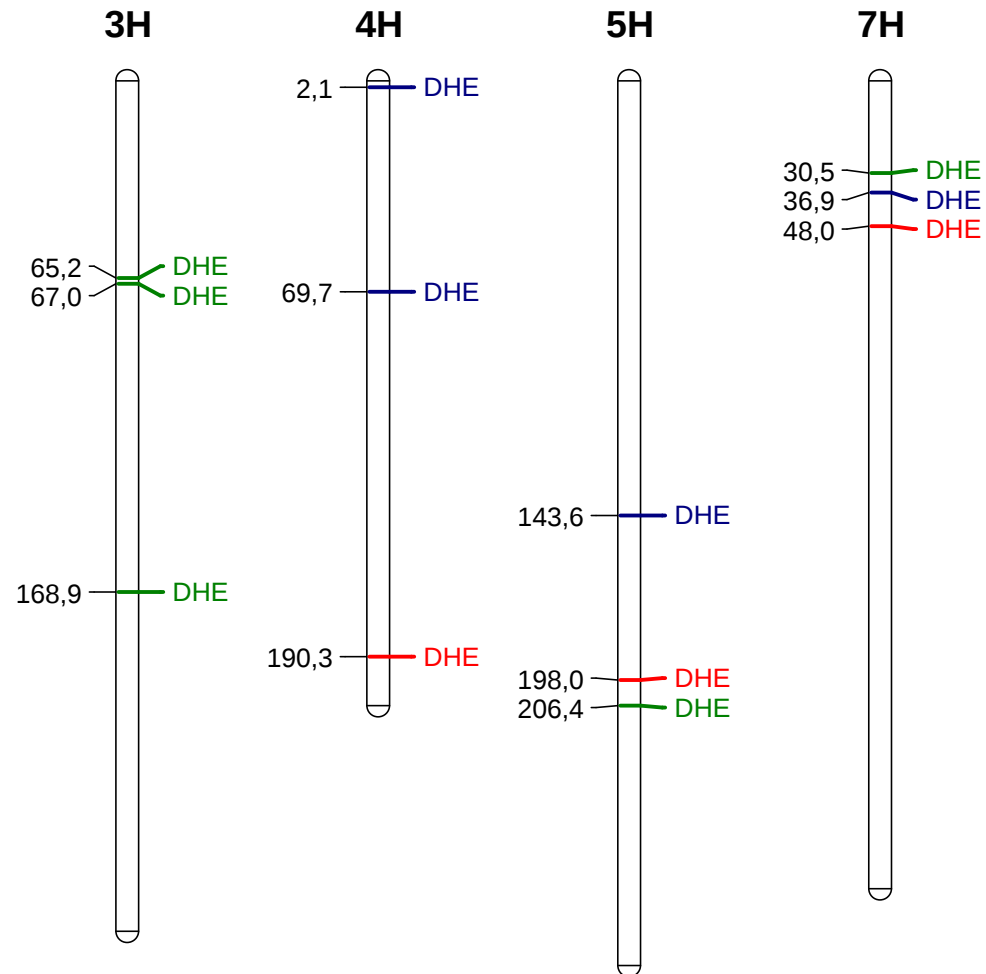


Two mapping approaches

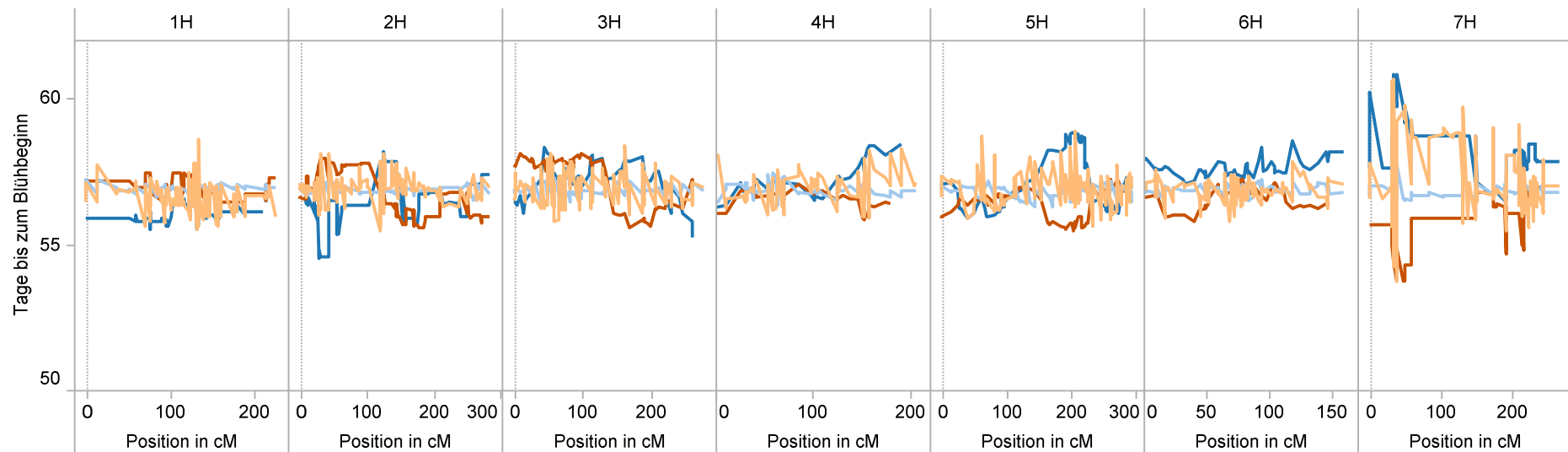


Chromosom	Marker	G106	G108	G111	G112	G114	G115	G118	G125	G127	G128
7H	SNP1236	1	2	2	4	2	0	2	2	7	7
7H	SNP1247	1	2	2	4	2	0	2	2	7	7
7H	SNP1240	1	2	2	4	2	0	2	2	0	0
7H	SNP1371	1	3	3	1	2	0	2	2	1	1
7H	SNP1237	1	3	3	1	2	0	2	2	1	1
7H	SNP1373	1	1	6	1	5	0	2	8	1	1
7H	SNP1383	1	1	6	1	5	0	2	8	1	1
7H	SNP1377	1	1	6	1	5	0	2	8	1	1
7H	SNP1375	1	1	6	1	5	0	2	8	1	1
7H	SNP1410	1	1	6	1	5	0	2	8	1	1
7H	SNP1376	1	1	6	1	5	0	2	8	1	1

linkage groups with QTL for DHE



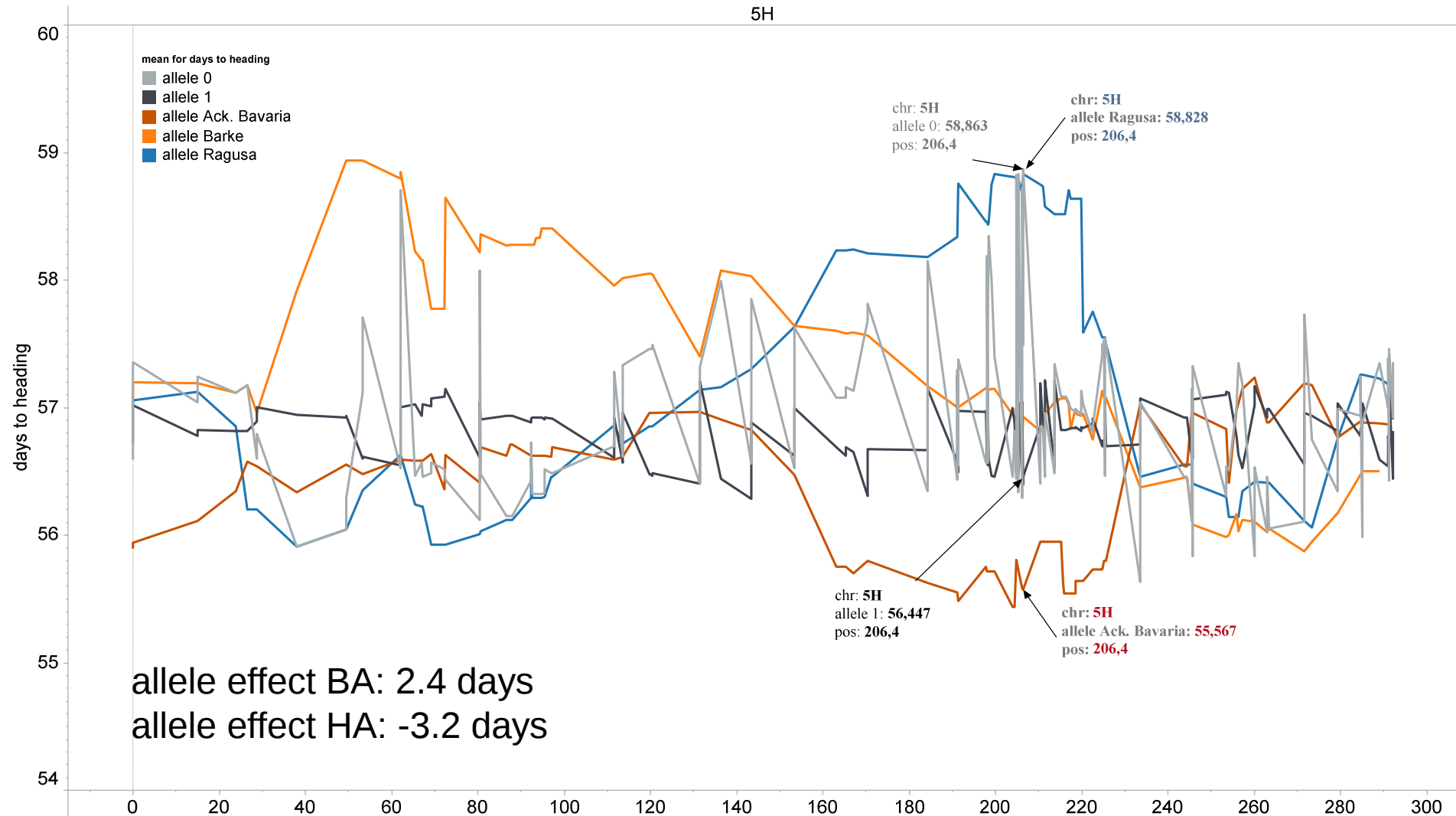
binary approach = blue
haplotype approach = red
both approaches = green



Kennzahlenamen

- Mittelwert bei Allel 0
- Mittelwert bei Allel 1

Comparison of the mapping approaches



Founder ancestry with R/mpMap

	Chromosome							
parents	1H	2H	3H	4H	5H	6H	7H	mean
Ackermanns Bavaria	10.1	11.4	9.9	10.5	9.9	13.2	14.2	11.3
Barke	14.9	9.7	11.7	8.7	14.3	14.7	10.7	12.1
Heils Franken	9.4	12.7	13.6	5.5	8.3	11.1	7.9	9.8
Heines Hanna	12.1	3.7	15.4	20.5	9.3	10.5	7.4	11.3
Pflugs Intensiv	10.0	0.0	2.6	0.0	0.1	0.0	0.0	1.8
Ragusa	9.2	8.6	8.9	10.3	12.1	10.4	9.8	9.9
Ackermanns Danubia	3.9	6.3	9.9	6.2	5.0	2.5	8.2	6.0
Criewener 403	0.2	0.0	0.2	0.0	0.0	0.0	0.0	0.6
unexplained	30.4	47.5	27.9	38.4	41.1	37.6	41.8	37.8

Summary

Binary Approach

- 78 QTL in twelve traits
- small genetic intervals
- lower allele effect
- biased allelic means

Haplotype Approach

- 65 QTL in twelve traits
- greater genetic intervals
- greater allele effect
- contribution of parental allelic mean
- high amount of unexplained founder ancestry
- high computational time



simultaneously use of the approaches

improve founder ancestry

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