Using Association Mapping to Identify Fusarium Head Blight Resistance QTL within Contemporary Barley Breeding Germplasm

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Barriers to MAS in Barley

- Trait phenotype easy to score
- Marker Technology
- Use of “un-adapted” parents for QTL mapping
- Linkage drag
- Marker doesn’t have predicted value

Association mapping within breeding germplasm may be a way to overcome some of the barriers between mapping and breeding

Benefits of Association Mapping

- Not restricted to bi-parental populations

- Test multiple alleles at a time

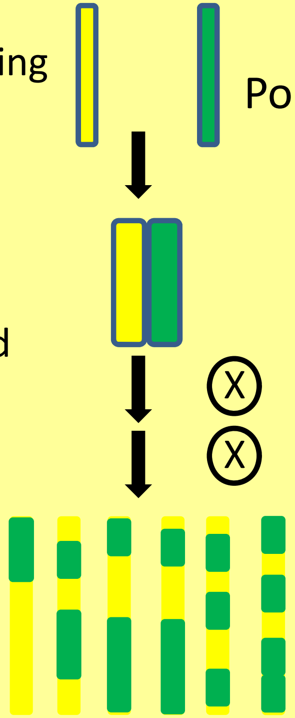
- More appropriate estimate of allelic effects

- Use data routinely generated in breeding
  - Alleles identified are segregating in breeding populations
  - Can quickly utilize the results of mapping for improvement

Bi-parental vs Association Mapping Populations

Population Structure

Bi-parental Mapping

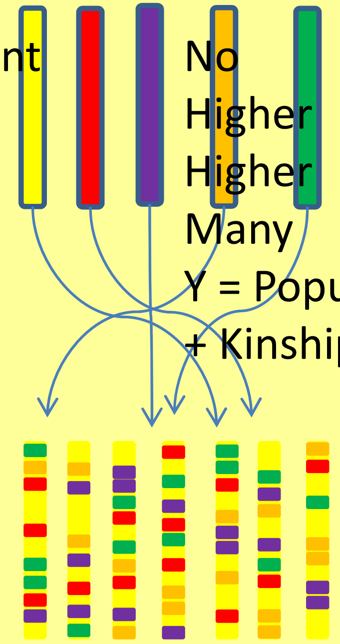


Parents with contrasting phenotypes crossed

Populations are selfed and advanced for multiple generations

Mapping population

Association Mapping



Founders of Breeding Program

Many generations of inter-mating and selection

Current breeding populations

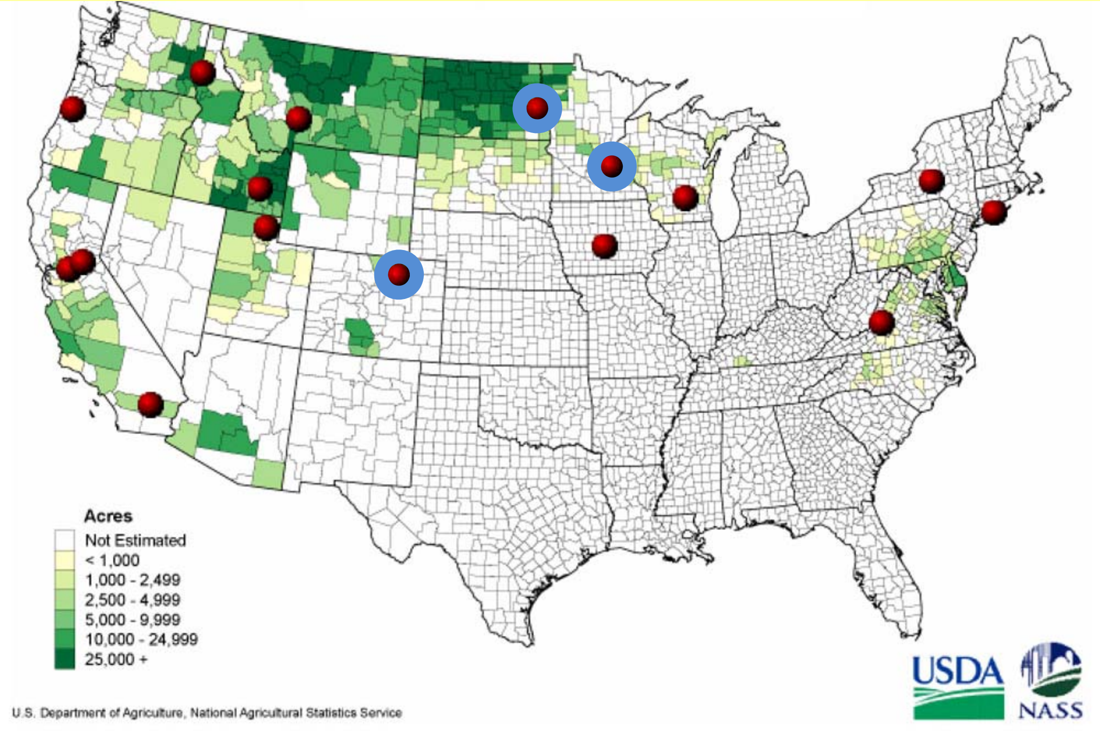
Characteristics

Bi-parental Mapping	Characteristics	Association Mapping
Yes	Population Development	No
Lower	Marker Density	Higher
Lower	Resolution	Higher
Two	Alleles Evaluated	Many
Y = SNP	Genetic Model	Y = Population structure + Kinship +SNP

Mapping Population

(4 programs) x (96 lines/ year) x (2 years) = 768 lines total

Breeders	Program	Row type
Kevin Smith	Minnesota (MN)	6
Blake Cooper	Busch Ag (BA)	2 & 6
Rich Horsley	N. Dakota (N2)	2
Rich Horsley	N. Dakota (N6)	6

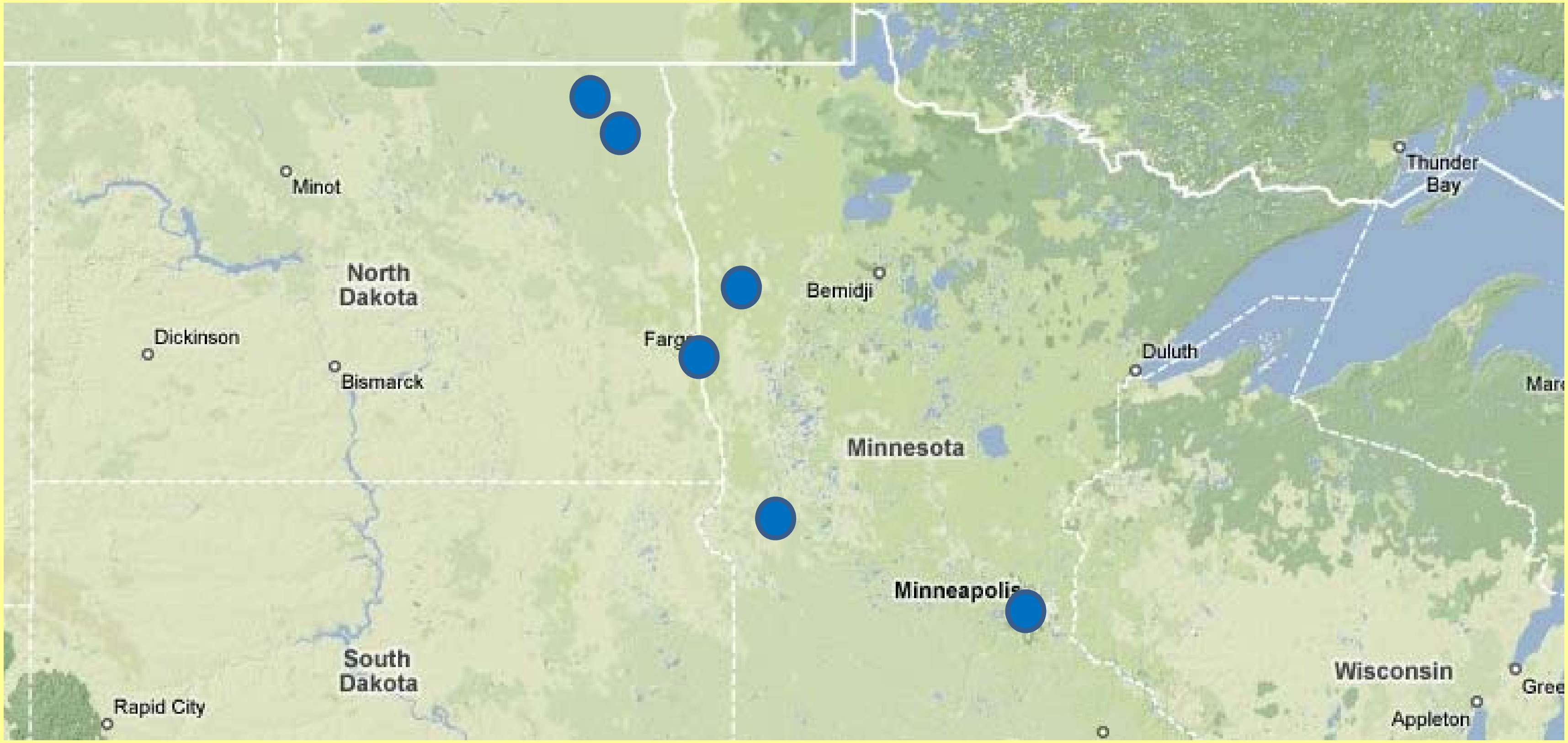


Mapping Sets

Mapping Set	# of lines	Program
CAP I (2006)	384	MN, BA, N2, N6
CAP I six-row	224	MN, BA, N6
CAP I two-row	160	BA, N2
CAP II (2007)	384	MN, BA, N2, N6
CAP II six-row	243	MN, BA, N6
CAP II two-row	141	BA, N2

Fusarium Evaluation

Each line was evaluated at four locations in a RCB with two reps

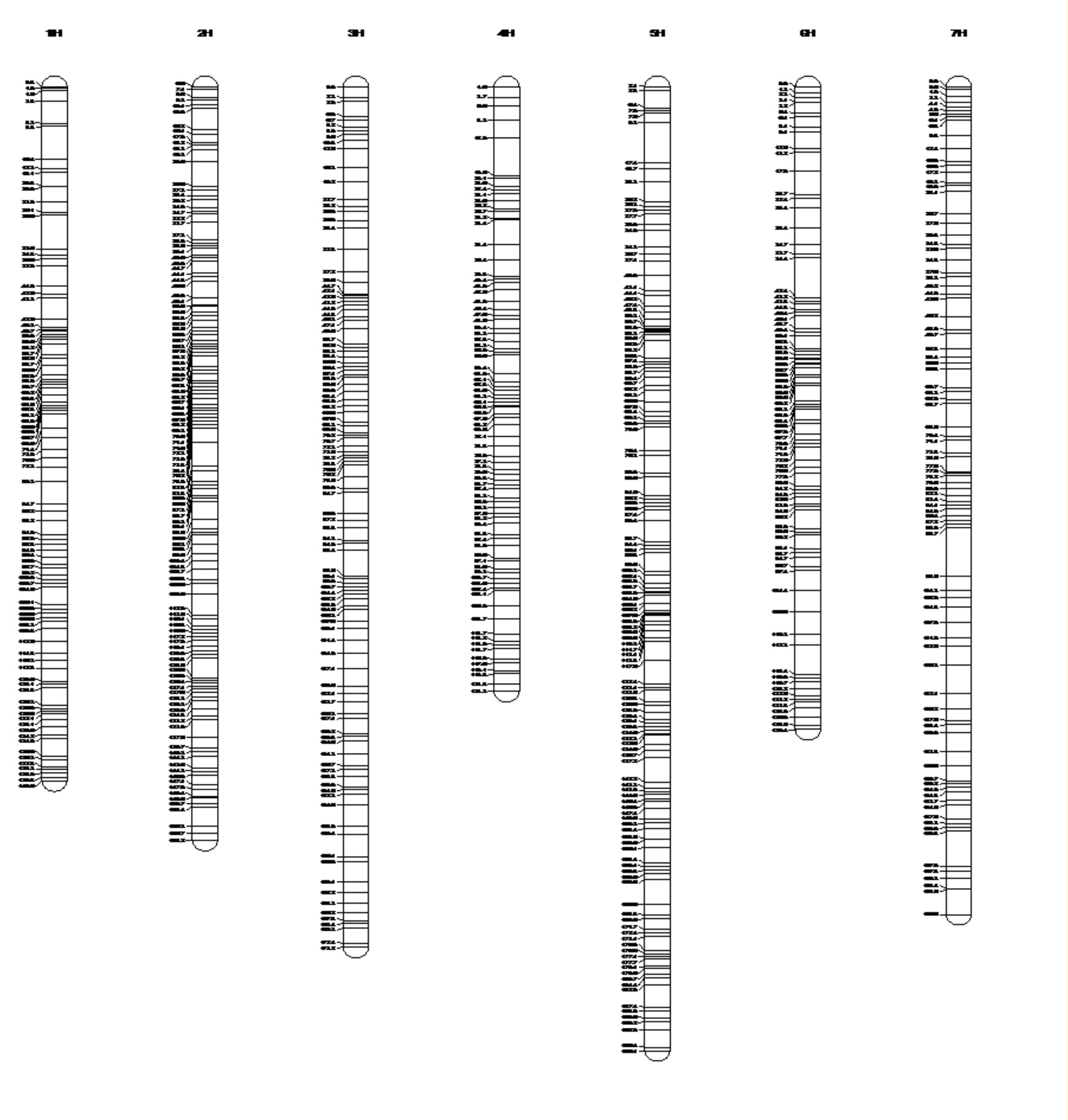


Distribution of SNP Markers

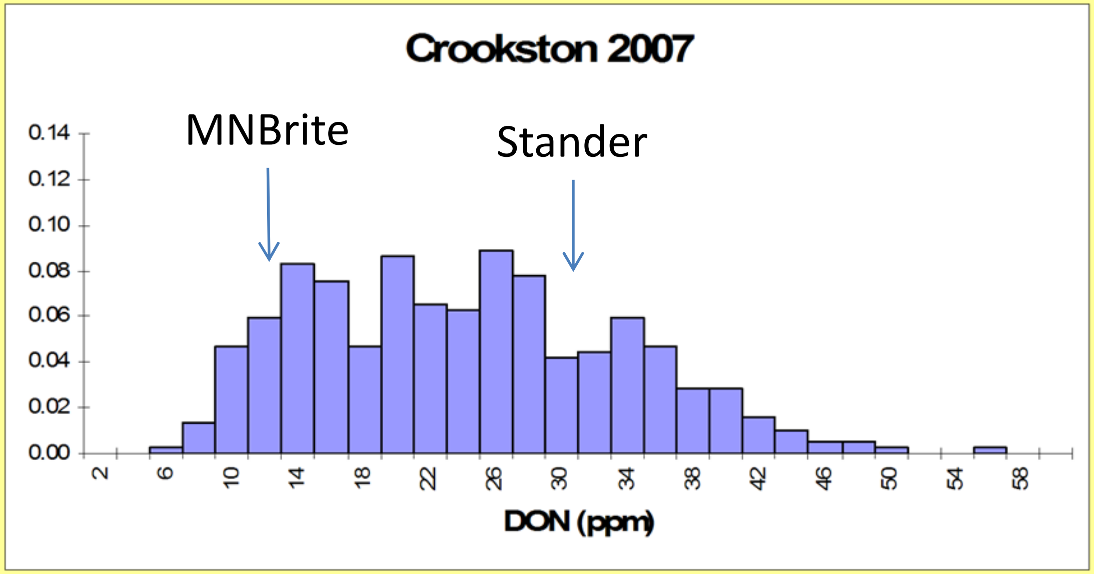
BOPA1

1414 mapped SNP Markers

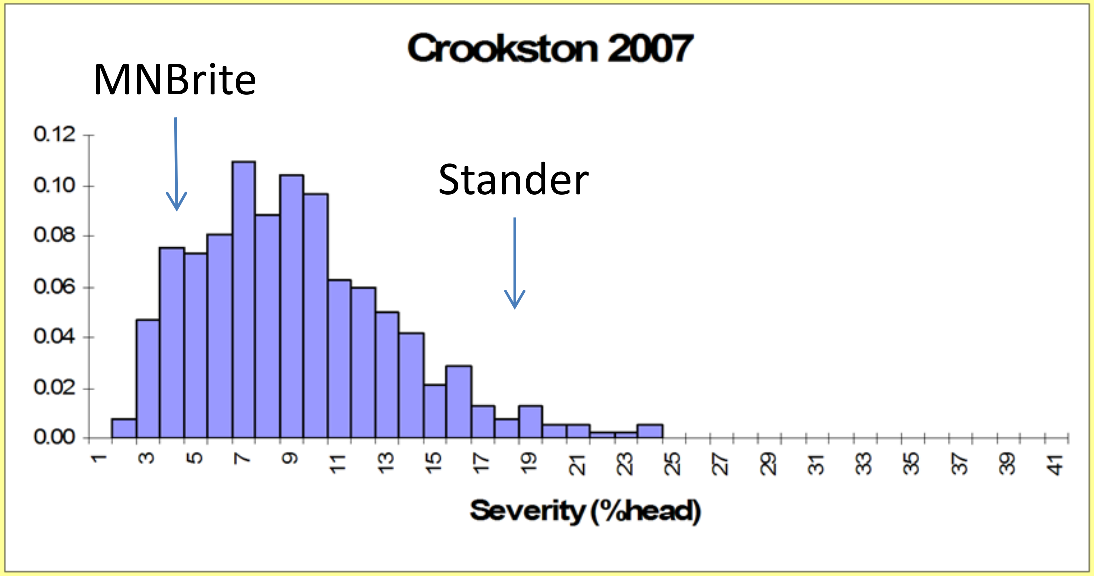
CAP I	1173
CAP I 6	564
CAP I 2	1113
CAP II	1127
CAP II 6	614
CAP II 2	1067



Variation for FHB and DON

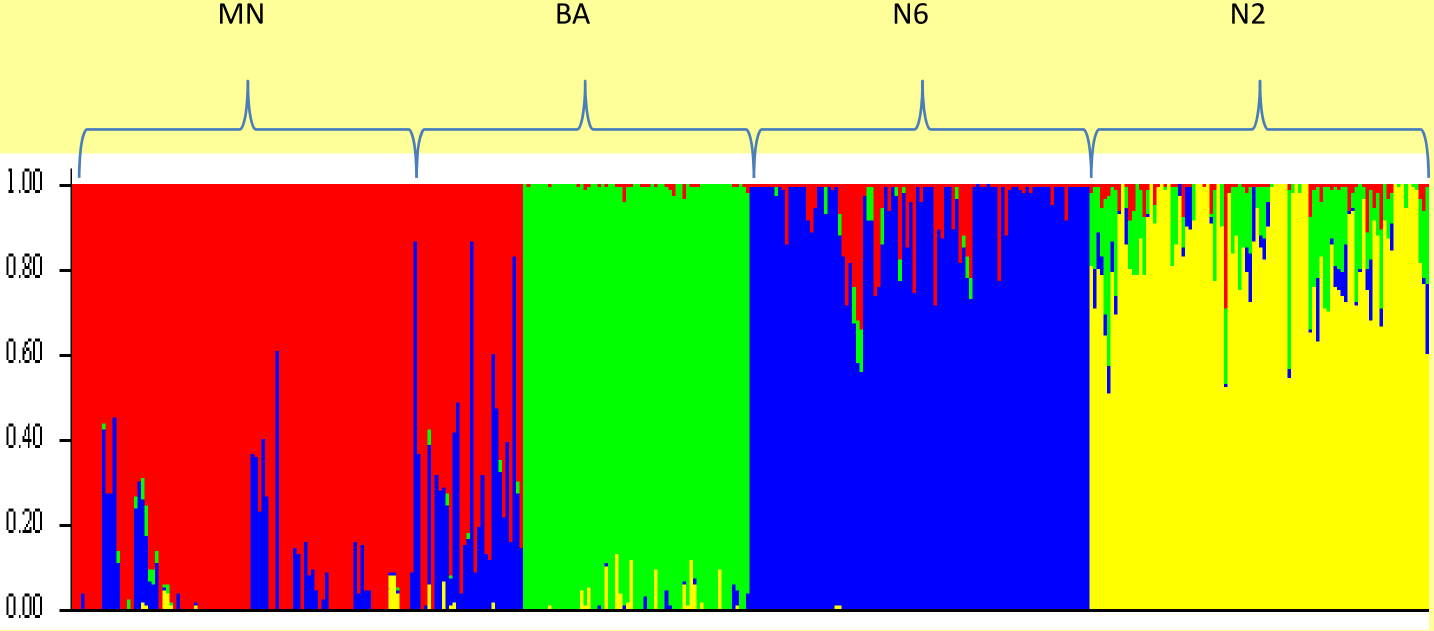


Crookston 2007

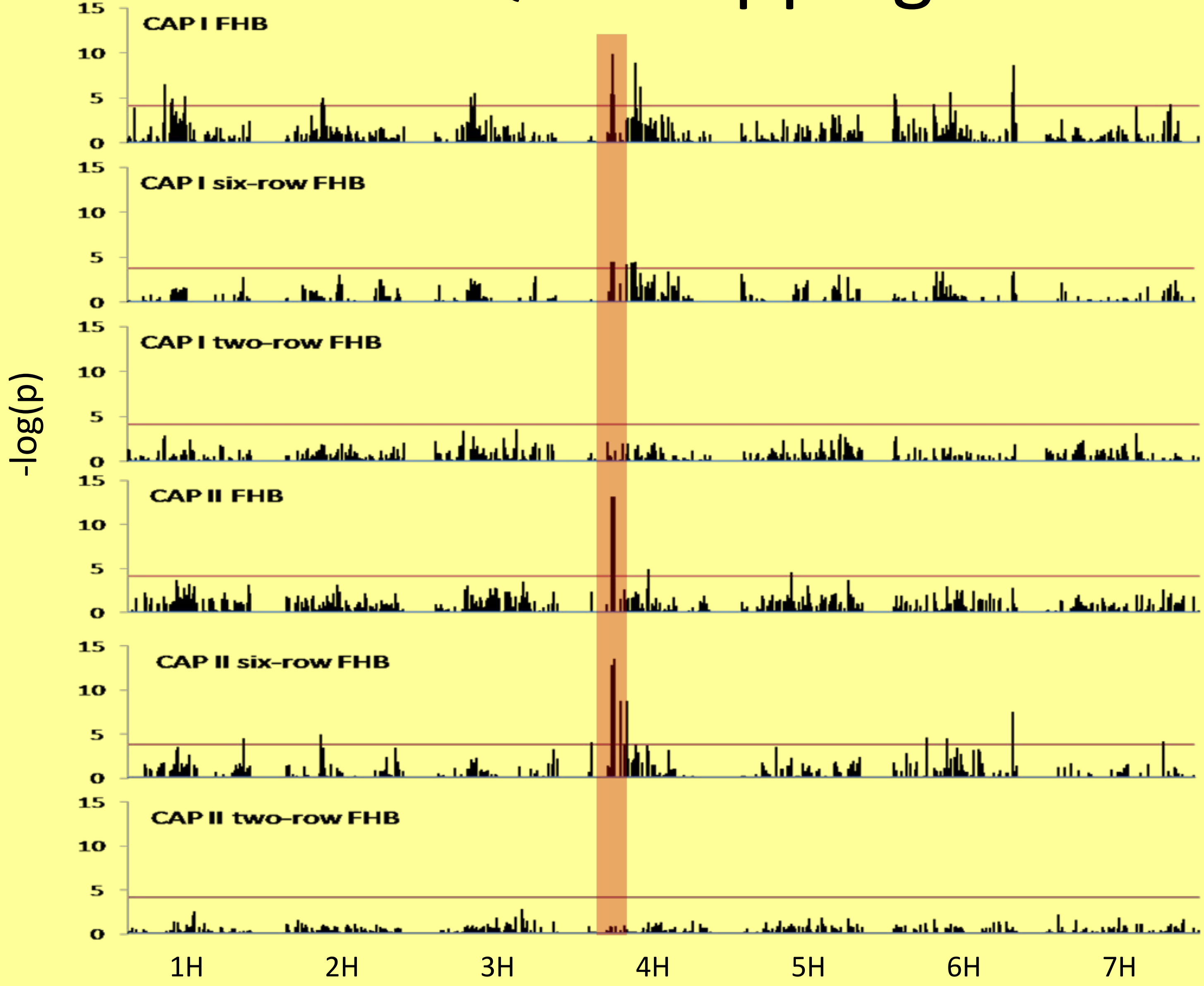


Crookston 2007

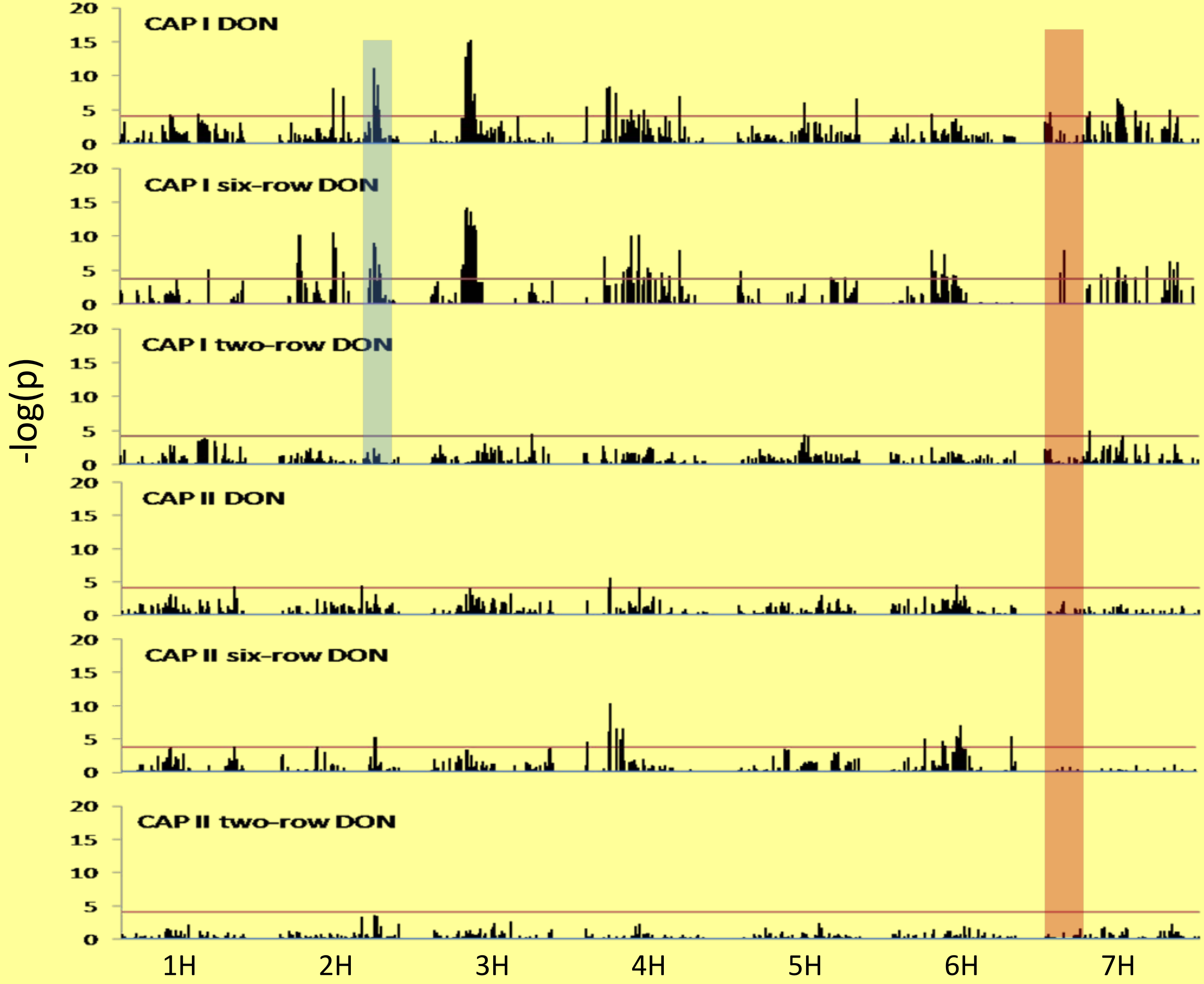
Population Structure CAP I



FHB QTL Mapping



DON QTL Mapping



Summary of FHB and DON QTL Identified with Two Independent Populations

- QTL identified in a mapping set from both CAP I and CAP II

- Resolution is variable and can be more precise than seen in bi-parental mapping populations

- r^2 values are very small which may reflect the underlying genetic architecture of the traits

Trait	Chrom	cM	bin	r^2
FHB	2H	50-56	6-7	0.010
FHB	4H	24-36	4-7	0.020
FHB	6H	42-61	5-7	0.011
FHB	6H	124-127	?-14	0.017
DON	1H	88	9-12	0.007
DON	2H	125-132	11-13	0.020
DON	3H	52-65	4-7	0.027
DON	4H	3	1	0.009
DON	4H	21-36	2-5	0.015
DON	4H	40-61	5-7	0.008
DON	5H	190-192	13-15	0.012
DON	6H	42-67	5-7	0.007

Location of Resistant Alleles for DON QTL in Breeding Programs

			Frequency Resistant Allele within Program			
Trait	Chrom	cM	MN	BA	N2	N6
DON	1H	88	1.0	0.90	0.74	0.99
DON	2H	125-132	0.54	0.55	0.64	0.12
DON	3H	52-65	0.19	0.57	0.95	0.0
DON	4H	3	0.17	0.49	0.98	0.02
DON	4H	21-36	0.33	0.58	0.99	0.02
DON	4H	40-61	0.29	0.32	0.47	0.51
DON	5H	190-192	0.85	0.81	0.95	0.54
DON	6H	42-67	0.02	0.36	0.73	0.10

Conclusions

- Identified new and previously described QTL regions for FHB and DON

- QTL resolution was variable and in some cases QTL locations were more precise then in a bi-parental mapping study

- Very small effect QTL were identified which may reflect the underlying genetic architecture of complex traits

Acknowledgments

Barley CAP collaborators

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Questions?