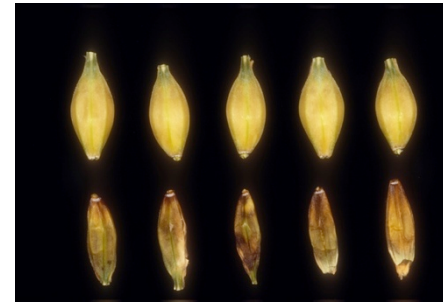


A Meta-analysis of the Genetics of Fusarium Head Blight Resistance in Barley



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St. Paul



Search for Resistance

Sourcing Germplasm

- ◆ USDA-ARS NSGC: USA
- ◆ N.I. Vavilov Institute: Russia
- ◆ NorGen: Sweden
- ◆ ICARDA: Syria
- ◆ ICCI: Israel
- ◆ Plant Gene Resources: Canada



- ◆ In total, over 30,000 accessions evaluated, including wild (*H. vulgare ssp. spontaneum*) and bulbous (*H. bulbosum*) barley

Search for Resistance

US: Screening Nurseries



Search for Resistance

China: Screening Nurseries



Cooperator: Professor Bingxin Zhang
Zhejiang University

Search for Resistance

Standard Controls



Chevron | Stander | CI4196 | ICB111809

Six-rowed | Two-rowed

Search for Resistance

FHB Screening

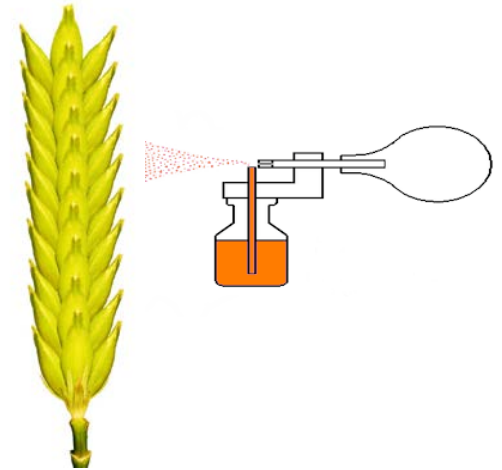
- ◆ From >30,000 *Hordeum* accessions evaluated, <1% had resistance comparable to the 6- and 2-rowed controls



Variation for FHB reaction in China

Type I and Type II Resistance

- ◆ Type I: resistance to initial infection
 - Assayed by spray inoculation of spikes



- ◆ Type II: resistance to spread after initial infection
 - Assayed by single floret inoculation of spikes



Infection Patterns

In the Field



Infection Patterns

- ◆ Barley often shows horizontal spread across a triplet and sometimes vertical



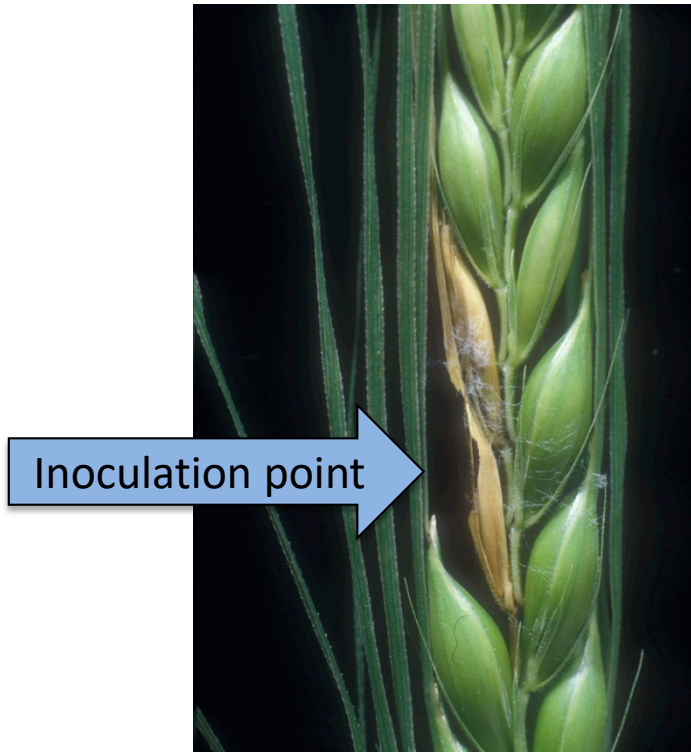
Infection Patterns

- ◆ Barley often shows horizontal spread across a triplet and sometimes vertical



Infection Patterns

- ◆ But this may be due to external mycelial spread or “nesting” and not spread through the rachis



Infection Patterns

- ◆ But this may be due to external mycelial spread or “nesting” and not spread through the rachis



Factors Affecting FHB Severity

Spike traits



2- vs. 6-row



Lax vs. dense



Nodding spikes



Hulled



Hulless

vs.

Factors Affecting FHB Severity

Heading Date and Height

June 26

June 28

July 1

July 8



QTL Mapping Studies for FHB Resistance

Bi/Tri-Parental Mapping Populations

- ◆ Chevron/M69 (C/M69): de la Peña et al. 1999
- ◆ Chevron/Stander (C/S): Ma et al. 2000
- ◆ Clho4196/Foster (Clh/F): Horsley et al. 2006
- ◆ Fredrickson/Stander (F/S): Mesfin et al. 2003
- ◆ Gobernadora/CMB643 (G/CMB): Zhu et al. 1999
- ◆ Chevron/M69 (C/M69): Canci et al. 2004
- ◆ MNS93/Stander (MNS93/S): Canci et al. 2004
- ◆ M92-299/M81 (M92/M81): Canci et al. 2004
- ◆ Zhedar 2/ND9712/Foster (Z/ND/F): Dahleen et al. 2003
- ◆ HOR211/Lacey (H/L): Sallam and Smith, 2005
- ◆ Atahualpa/M81 (AT/M81): Beaubien et al., 2005
- ◆ Quest/W-365 (Quest/W-365): Haas and Steffenson, 2017
- ◆ Harbin RILs: Sato et al., 2008

Meta-analyses of FHB Resistance Loci

- ◆ It is difficult to effectively utilize the many data collected from FHB resistance mapping populations without integration
- ◆ Meta-analysis: integration of previously identified QTLs from multiple linkage maps
- ◆ Integration of multiple QTLs on the same *consensus* map provides a comprehensive picture about the genetic control of FHB resistance and DON accumulation

Objectives

- ◆ Construct a consensus map based on previous mapping studies for FHB resistance
- ◆ Conduct a meta-analysis of QTL for FHB resistance and DON accumulation along with important agro-morphological traits
- ◆ Provide recommendations for the way forward in breeding for FHB resistance

Consensus Map Construction

Difficulties

- ◆ In some previous mapping populations:
 - Different markers used (i.e. SSR), limited allelic diversity, poor marker coverage, and small population sizes
- ◆ Need to integrate all markers types into one consensus map

Creating Consensus Maps

LPMerge Method

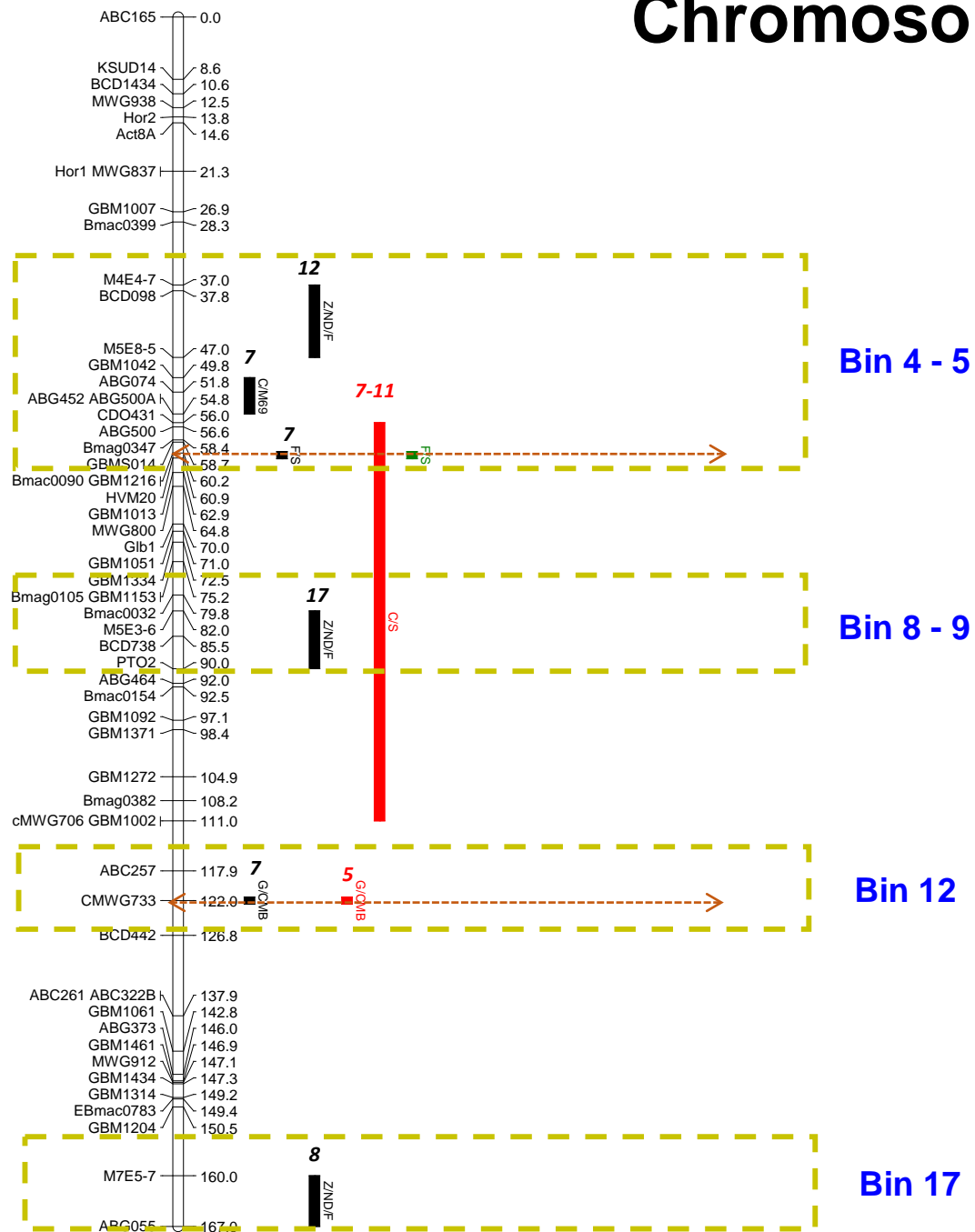
- ◆ Constructed using linear programming implemented in LPmerge package in R (Endelman and Plomion, 2014)
- ◆ Reduces mean error between linkage maps and the consensus map to ensure that marker order is preserved
- ◆ Advantages: removes marker constraints to resolve any conflicts in marker order
- ◆ Produces a graphical representation of marker order
- ◆ Eight maps were used to generate the consensus map

Summary Statistics for Consensus Map

	Chromosome							
Population	1H	2H	3H	4H	5H	6H	7H	Total
Muñoz et al. consensus map	141.9	171.3	178.5	145.2	188.2	188.2	160.9	
Varshney et al. consensus map	139.8	156.4	157.5	133.3	183.7	139.9	157.1	
Zhedar2/ND9712/Foster (Z/ND/F)	182.0	242.0	178.0	158.0	220.0	147.0	153.0	
Chevron/M69 (C/M69)	97.4	154.1	122.3	85.9	157.2	95.2	162.1	
Chevron/Stander (C/S)	103.4	144.3	171	97.1	176.7	95.5	142.0	
Gobernadora/CMB643 (G/CMB)	169.0	230.0	203.0	148.0	201.0	159.0	198.0	
Fredrickson/Stander (F/S)	100.5	212.6	177.8	164.4	195.3	190.5	212.3	
Clho4196/Foster (4196/F)	135.0	119.0	136.0	92.0	135.0	84.0	78.0	
Average (cM)	133.6	178.7	165.5	128.0	182.1	137.4	157.9	1,083.3
Consensus map distance	182.0	179.3	178.5	152.8	231.4	206.7	168.4	1,299.0
Number of Markers	572	790	727	584	802	582	731	4,788

Chromosome 1H

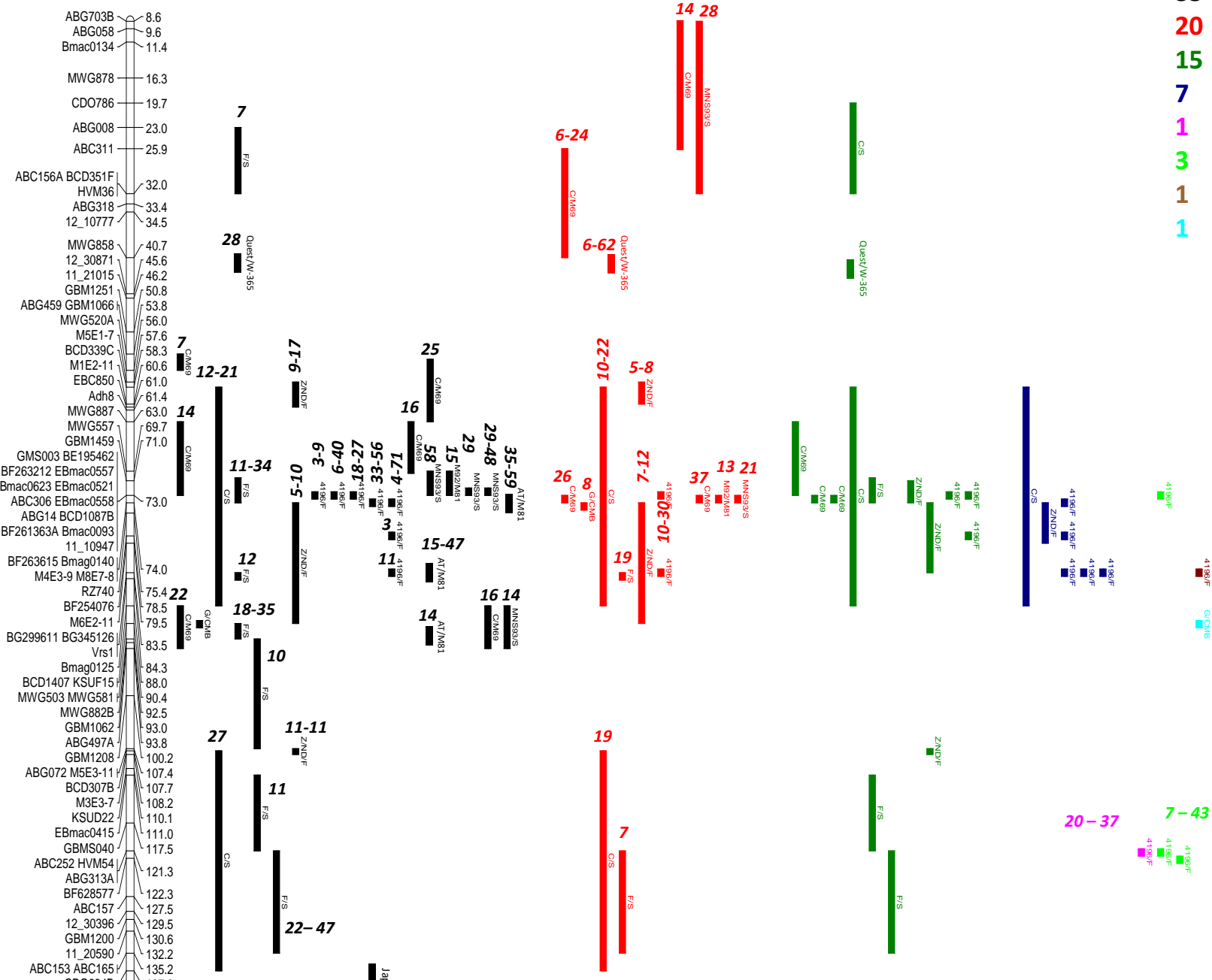
# QTL	Trait
6	FHB
2	DON
1	HD



Chromosome 2H

QTL Trait

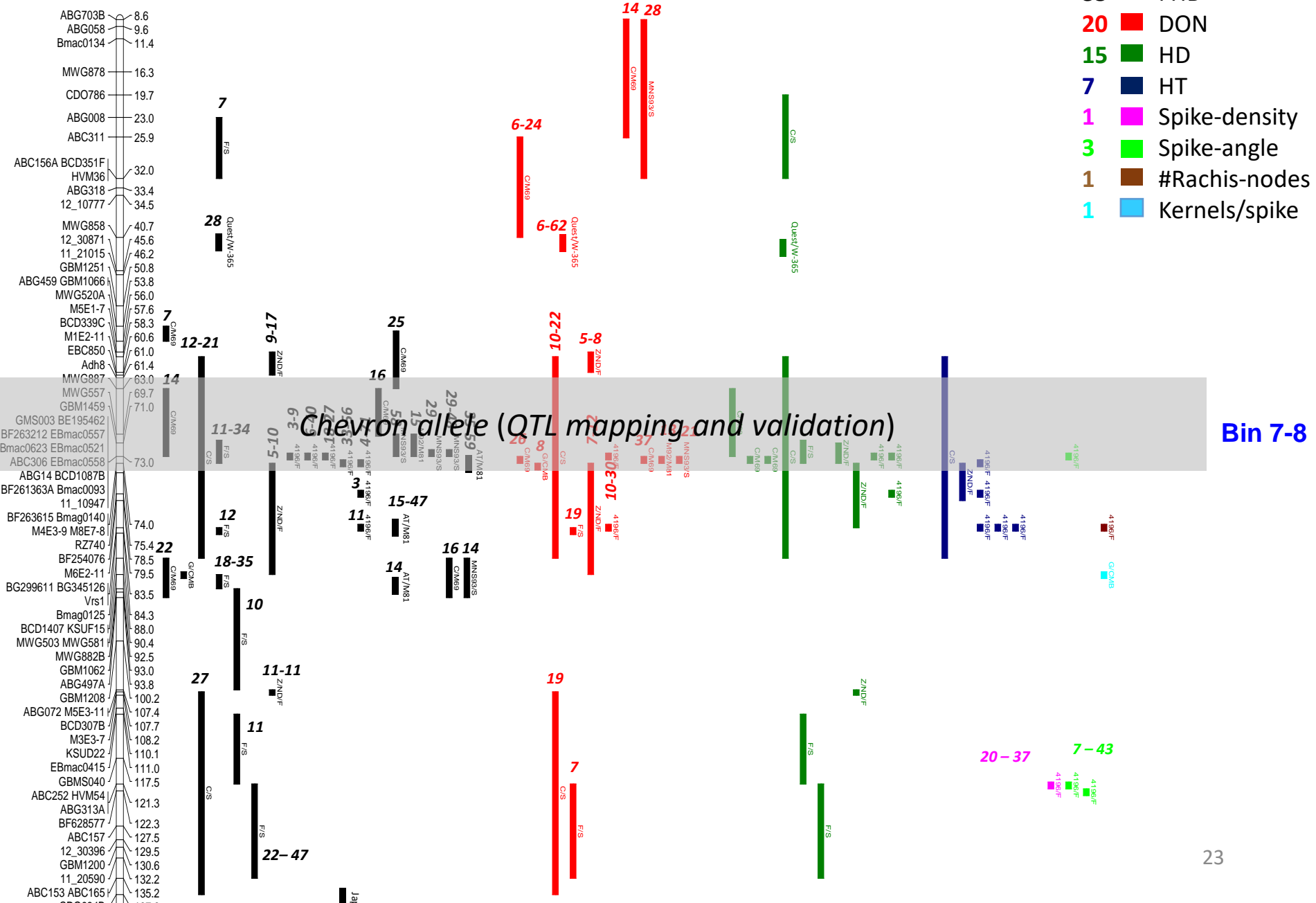
- 35 ■ FHB
- 20 ■ DON
- 15 ■ HD
- 7 ■ HT
- 1 ■ Spike-density
- 3 ■ Spike-angle
- 1 ■ #Rachis-nodes
- 1 ■ Kernels/spike



Chromosome 2H

QTL Trait

- 35 FHB
- 20 DON
- 15 HD
- 7 HT
- 1 Spike-density
- 3 Spike-angle
- 1 #Rachis-nodes
- 1 Kernels/spike

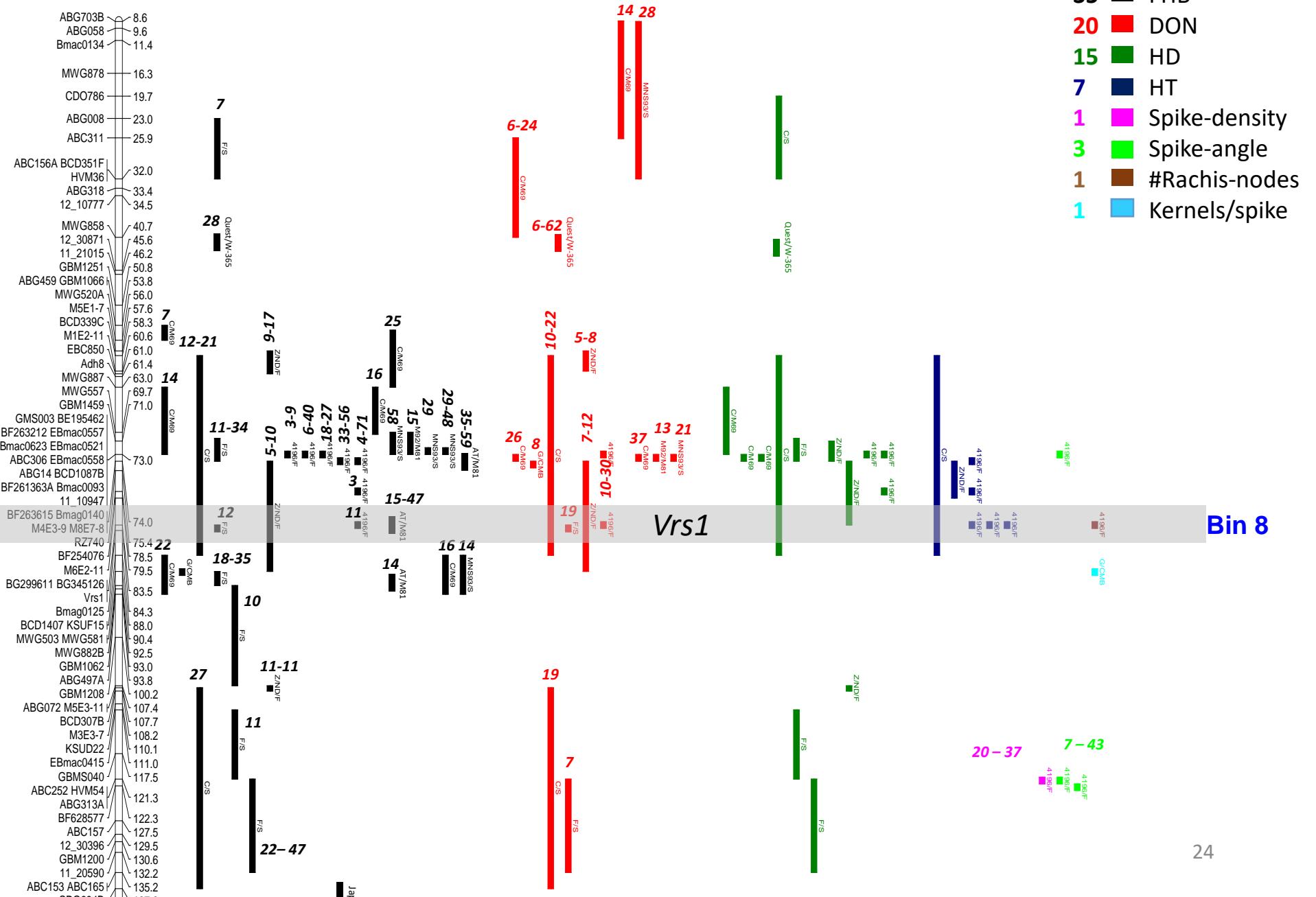


Bin 7-8

Chromosome 2H

QTL Trait

- 35 ■ FHB
- 20 ■ DON
- 15 ■ HD
- 7 ■ HT
- 1 ■ Spike-density
- 3 ■ Spike-angle
- 1 ■ #Rachis-nodes
- 1 ■ Kernels/spike

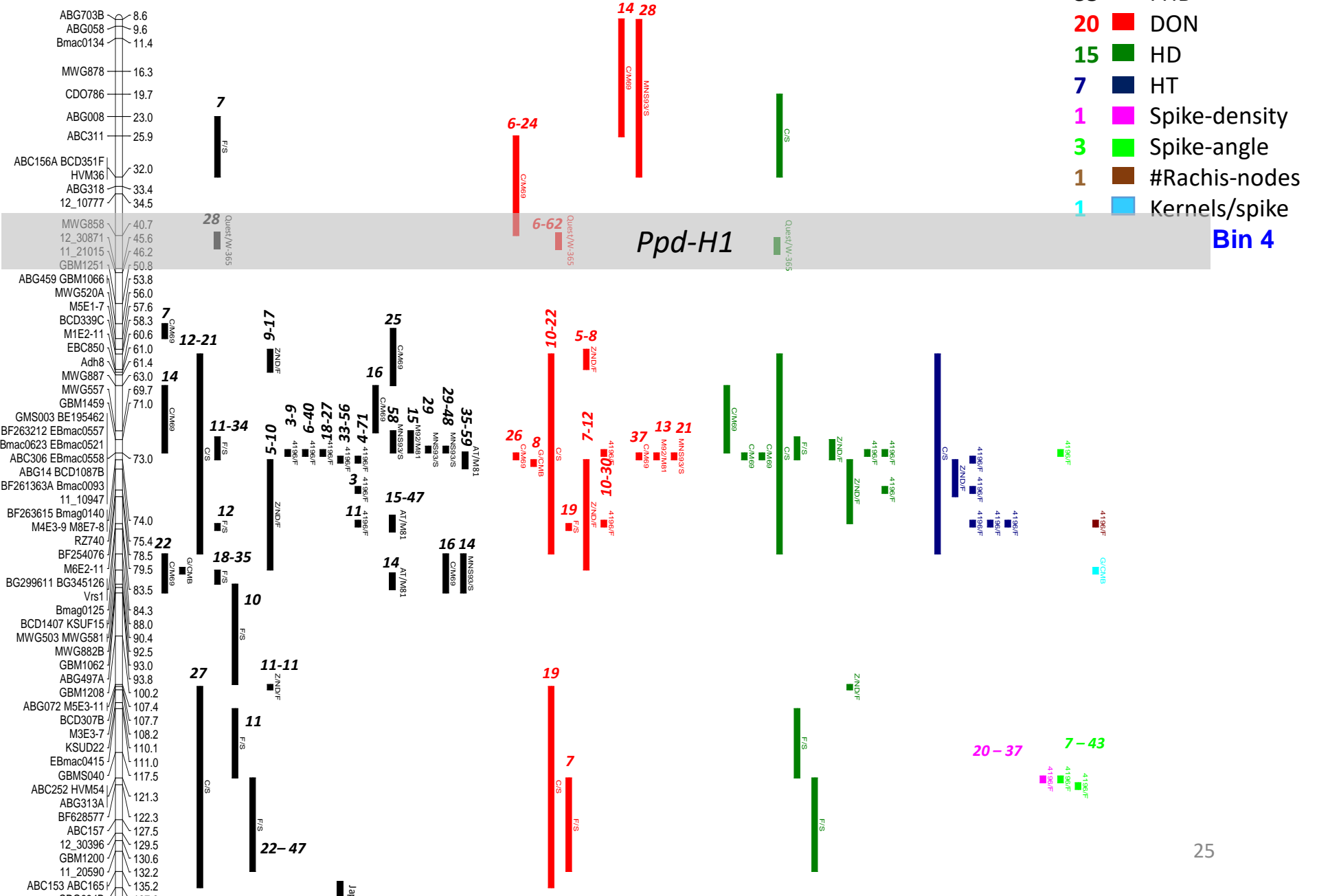


Chromosome 2H

QTL Trait

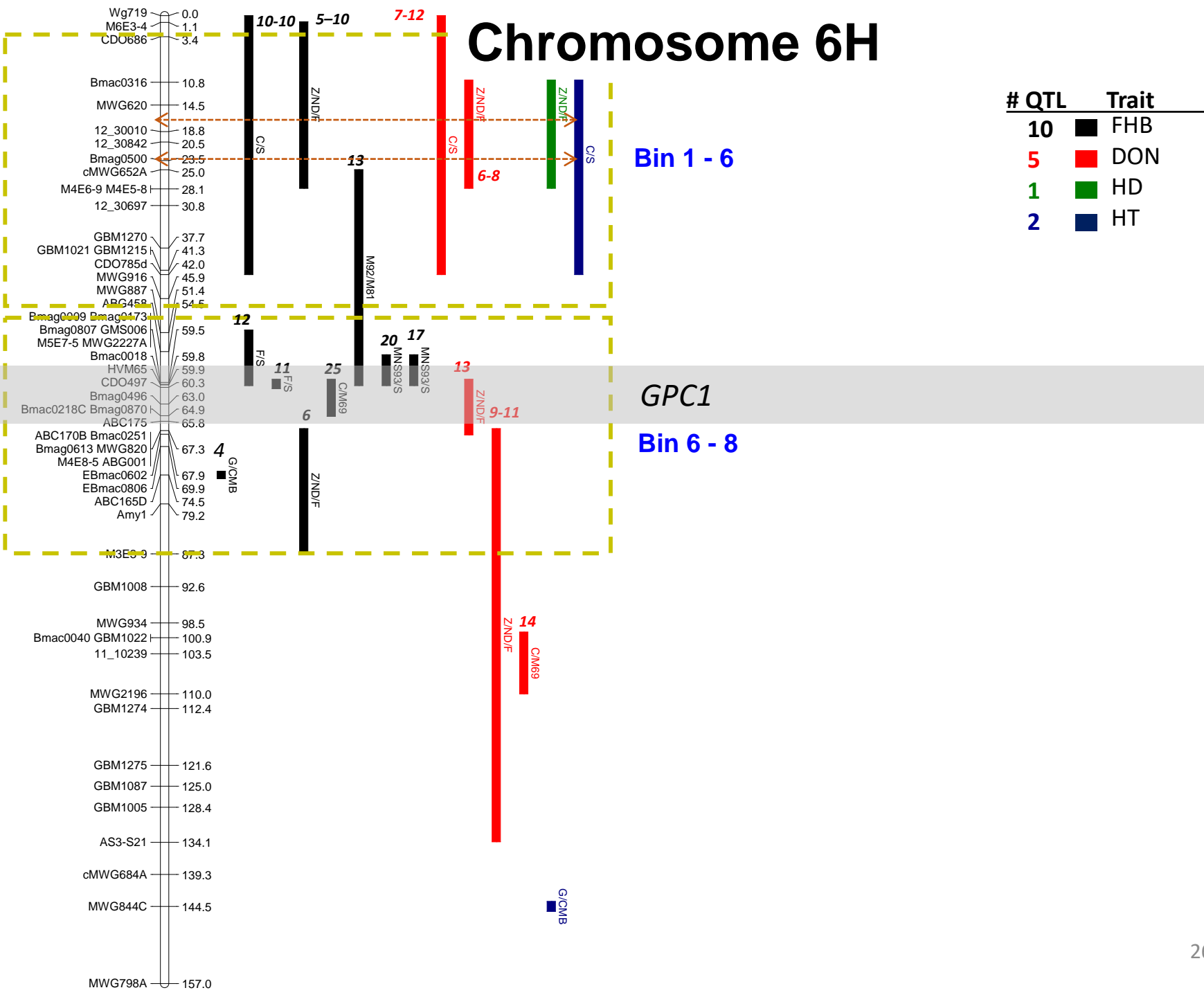
- 35 ■ FHB
- 20 ■ DON
- 15 ■ HD
- 7 ■ HT
- 1 ■ Spike-density
- 3 ■ Spike-angle
- 1 ■ #Rachis-nodes
- 1 ■ Kernels/spike

Bin 4

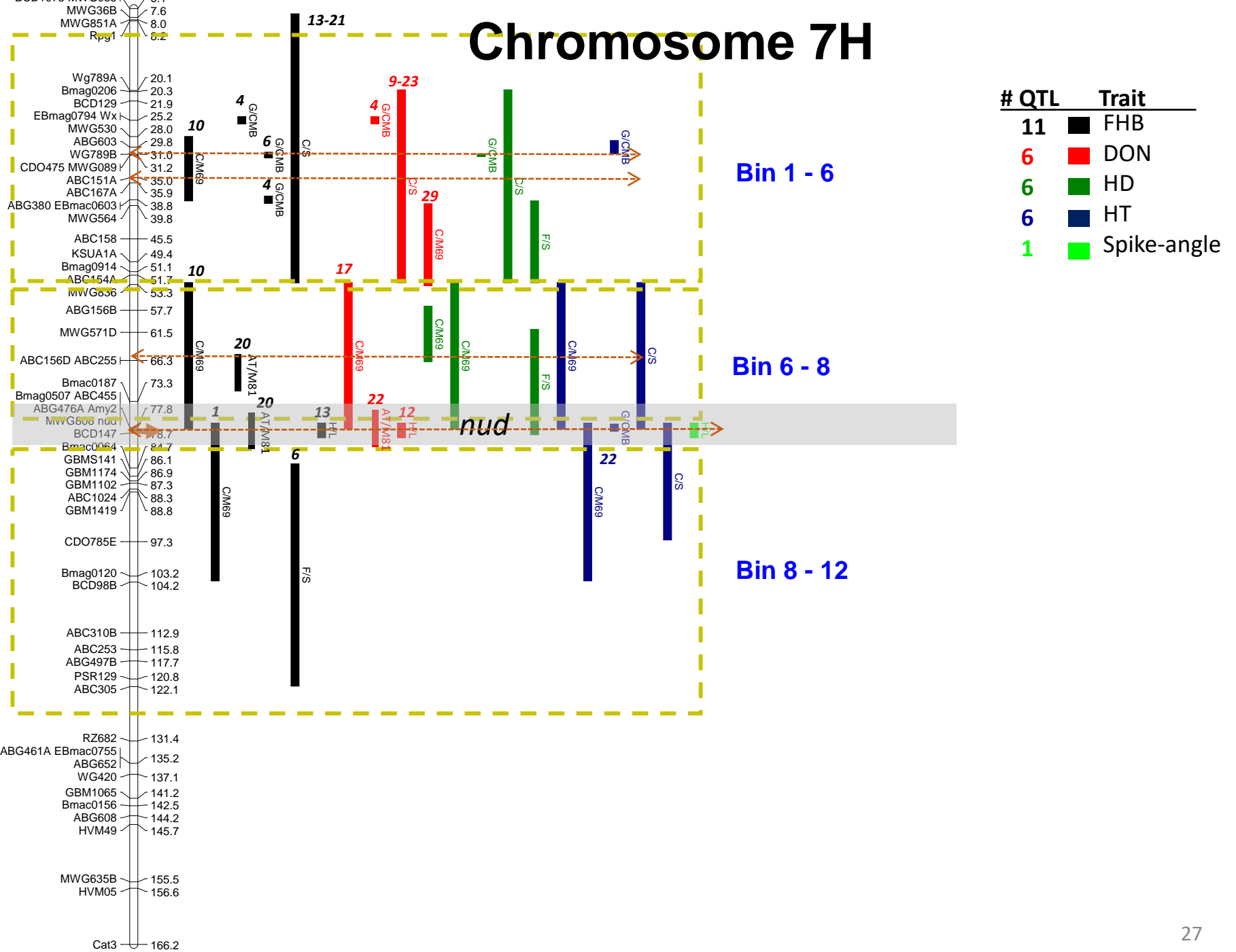


Chromosome 6H

# QTL	Trait
10	FHB
5	DON
1	HD
2	HT



Chromosome 7H



Summary of Identified FHB and DON QTL in Barley

Chrom.	Trait	No. QTL	No. detected in >one site	No. QTL explaining >10%	No. independent of agronomic traits	No. detected >1X, $R^2 > 10\%$, & independent of other traits
1H	FHB	6	0	2	5	0
	DON	2	1	0	2	0
2H	FHB	35	14	26	5	0
	DON	20	6	14	6	1
3H	FHB	9	2	2	2	0
	DON	5	0	1	3	0
4H	FHB	3	2	1	1	0
	DON	2	2	2	1	0
5H	FHB	4	2	3	3	2
	DON	2	0	2	1	0
6H	FHB	10	6	6	3	1
	DON	5	4	4	3	2
7H	FHB	11	1	4	3	1
	DON	6	1	5	2	0
Total	FHB	78				4
	DON	42				3

Meta-analysis of QTL Mapping Studies

Association Mapping Panels

- ◆ Midwest barley breeding lines: Massman et al. 2011
- ◆ Wild barley introgression population (WBIP): Tandukar et al. unpublished

Association Mapping in Midwest Barley Breeding Programs

QTL	Chr.	Pos.	Bin	Associated traits
FHB2H.50-56	2H	50-56	6-7	
FHB4H.24-36	4H	24-36	4-7	HT
FHB6H.42-61	6H	42-61	5-7	
FHB6H.124-127	6H	124-127	14	
DON1H.88	1H	88	9-12	
DON2H.74-78	2H	74-78	8	HD
DON2H.125-132	2H	125-132	11-13	HT
DON3H.52-65	3H	52-65	4-7	HT
DON4H.03	4H	3	1	
DON4H.21-36	4H	21-36	2-5	HT
DON4H.40-61	4H	40-61	5-7	
DON5H.190-192	5H	190-192	13-15	
DON6H.42-67	6H	42-67	5-7	HD - HT

Association Mapping in Wild Barley Introgression Population

QTL	Chrom	Position cM	Bin Position	Associated traits
FHB2H.12_3087 1	2H	45.6	5	HD - HT
FHB2H.11_2101 5	2H	46.2	5	HD - HT
DON2H.12_3087 1	2H	45.6	5	HD - HT
DON2H.11_2101 5	2H	46.2	5	HD - HT
DON2H.11_1094 7	2H	73.0	8	



QTL Mapping

- ◆ Genetics of FHB severity and DON accumulation is complex: many QTL of small effect across genome
- ◆ Many QTL are not robust: detected in one environment only
- ◆ Number of agro-morphological traits co-localizing with QTL for FHB severity & DON accumulation strongly suggests pleiotropy
- ◆ Still, resistance QTL from various sources have been integrated into the breeding programs with some success

Breeding Lines with Reduced DON

Minnesota			North Dakota		
Variety / Line	Yield Bu/A	DON ppm	Variety / Line	Yield Bu/A	DON ppm
Lacey	109	11.6	Lacey	94.8	23.8
Tradition	104	11.4	Tradition	95.4	23.2
Quest	109	7.4	Quest	94.1	15.2
S6M164	107	7.3	ND32889 (6R)	97	16.9
S6M166	110	8.8	ND32898 (6R)	97.1	16.5
			ND32920 (6R)	98.3	12
			Conlon (2R)	85.5	12.2
			Pinnacle (2R)	86.4	20.5
			ND Genesis (2R)	97.9	14.5
			2ND28065 (2R)	101	11.9
			2ND32529 (2R)	103	12.7
			2ND32829 (2R)	97.4	12.2

Genomic Selection

- ◆ Genomic selection aims to predict the genetic value of selection candidates based on the Genomic Estimated Breeding Value (GEBV)
- ◆ Predicted from high-density markers across the genome
- ◆ In contrast to MAS, GEBV is based on **all** markers across the genome, including those with minor effects as well as those major effects
- ◆ Thus, GEBV may capture more genetic variation for the target under selection

Genomic Selection for FHB Resistance

The Way Forward

- ◆ The greater uniformity of materials in breeding nurseries will parse out the contributions of agro-morphological traits on FHB and DON
- ◆ Evaluations done at multiple locations will provide greater confidence and validation of QTL effects
- ◆ Other traits important in breeding can be selected at the same time

Genomic Selection: DON & Yield

Spring Six-row Barley

Year

1

Crossing Block

Parents (greenhouse)

2-3

Inbreeding

F1 (greenhouse)

F2 (field)

F3 (greenhouse) Gen Sel*

Winter Nursery

4-5

Line Evaluation

Prelim. Yield Trials

Adv. Yield Trials

6-7

Industry Testing

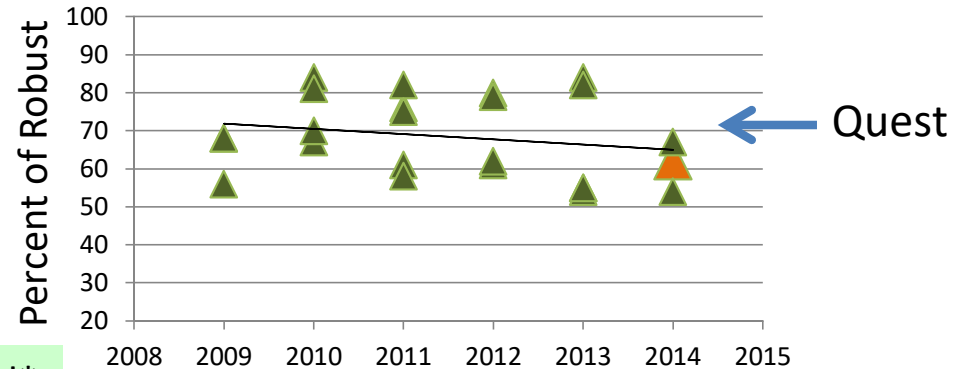
Pilot Malting

Plant-scale Brewing

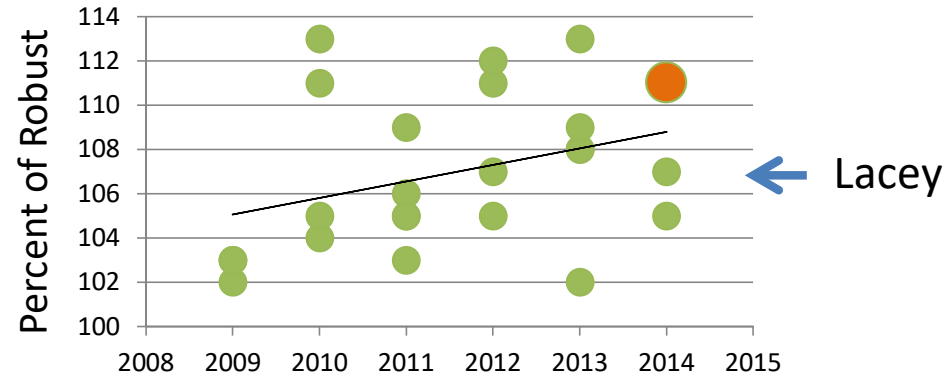
8

Release

DON



Yield



M160

Lacey

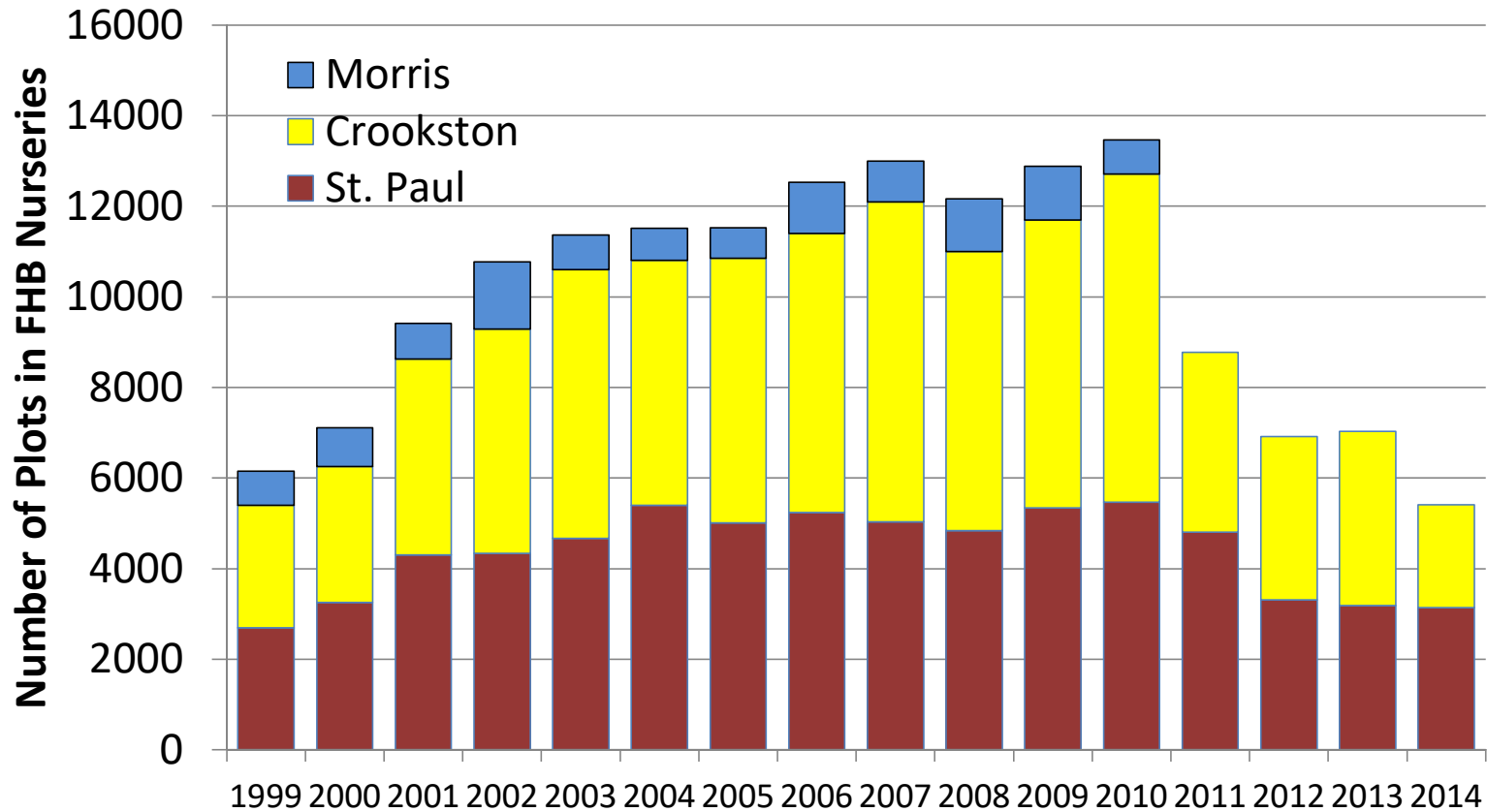


On Using Genomic Selection

- ◆ Genomic selection works--but not all the time
- ◆ Accuracy is greater when the training population is more closely related to the prediction population
- ◆ Technical/logistical issues are not trivial
- ◆ Greatest impacts:
 - Cost of genotyping < less than phenotyping
 - GS can shorten breeding cycle
 - Morale!



Genomic Selection has Reduced Field Resources for FHB Screening



Summary

- ◆ Biparental and association mapping revealed many QTL for low FHB severity and DON across the genome
- ◆ Although many QTL co-locate with agro-morphological traits, some have contributed to cultivars with low FHB and DON, e.g. Quest et al.
- ◆ Genomic selection is a promising method to increase the the accuracy and shorten the breeding cycle for selection of FHB resistance, thereby hastening the release of new, improved varieties

Positive Changes on the Horizon?

- ◆ Two-rowed barley is now the preferred type for malting in the Upper Midwest
- ◆ Autumn-sown facultative barleys are now being bred for the Upper Midwest
- ◆ Two-rowed barleys generally suffer less FHB and DON than six-rowed types
- ◆ Autumn-sown barleys may often escape the most conducive conditions for FHB in the summer

Acknowledgements

Personnel

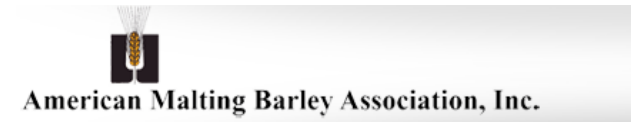
- ◆ B. Steffenson Project
 - ◆ Stephanie Dahl
 - ◆ Tamas Szinyei
 - ◆ Matthew Martin
 - ◆ Matthew Haas
 - ◆ Bullo Mamo
 - ◆ Ahmad Sallam
- ◆ R. Dill-Macky Project
- ◆ K. Smith Project
- ◆ G. Muehlbauer Project
- ◆ Yanhong Dong



- ◆ US Wheat Barley Scab Initiative



- ◆ American Malting Barley Association



- ◆ University of Minnesota



- ◆ Lieberman-Okinow Endowment