

The 9th Workshop on QTL Mapping and Breeding Simulation
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Tactical Applications of Breeding Simulation

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Outline of the presentation

- Parental selection using known genes
- Efficient selection of multiple genes via marker-assisted selection
- Efficient selection of multiple genes and QTL via marker-assisted selection

Parental selection using known gene information

Wang, J.,* H.A. Eagles, R. Trethowan, and M. van Ginkel. 2005. Using computer simulation of the selection process and known gene information to assist in parental selection in wheat quality breeding. **Aust. J. Agric. Res.** 56: 465-473.

Glutenin genes and wheat quality

➤ Six glutenin genes

- *Glu-A1* (1AL), *Glu-B1* (1BL), *Glu-D1* (1DL) for HMW
- *Glu-A3* (1AS), *Glu-B3* (1BS), *Glu-D3* (1DS) for LMW

➤ Two end-use quality traits commonly used by wheat breeders

- Rmax (BU), for maximum dough resistance
- Extensibility (cm), for dough extensibility

➤ Multiple alleles on each gene locus

- *Glu-A1*: 1, 2*, and Null
- *Glu-B1*: 7, 7+8, 7+9, 6+8, 20, 13+16, 14+15, 17+18, and 23+24
- *Glu-D1*: 2+12, 4+12, 5+10, and 2+T2

Selected parents

Parent	Rmax	Extensibility
Silverstar 1	309.80	20.78
Silverstar 2	270.20	20.31
...
Silverstar 7	368.90	20.15
Silverstar 8	329.30	19.68
Westonia	283.70	19.70
Krichauff	312.26	19.39
Machete	312.03	19.95
Diamondbird	368.88	20.16

Four selection schemes

Parent 1 × Parent 2

F1

F2: 1000 individuals

F8: 1000 lines through SSD

R0.04

	Trait to be selected	Lines selected
Step 1	Rmax	40
Step 2	n.a.	

R0.2E0.2

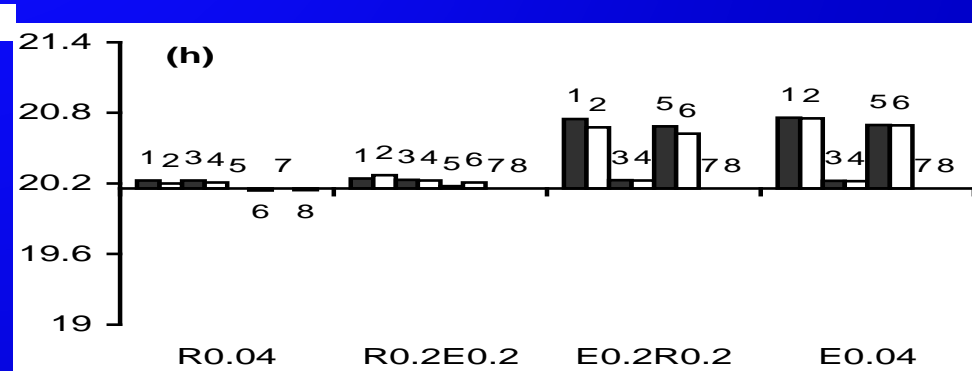
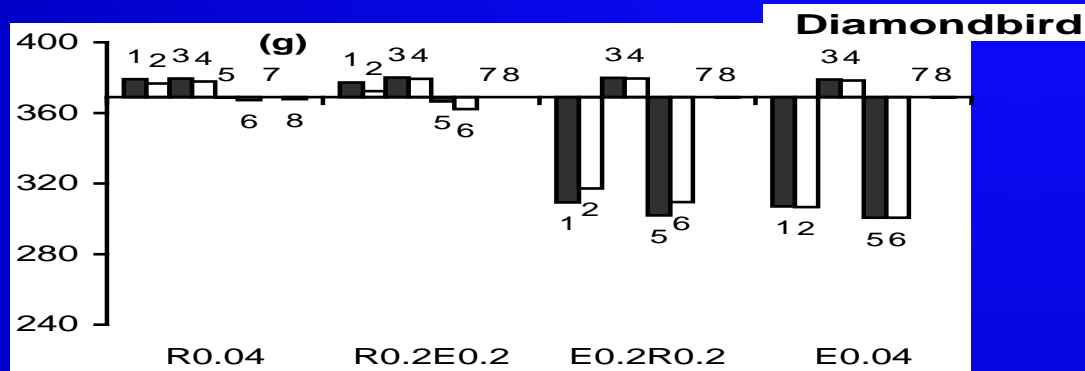
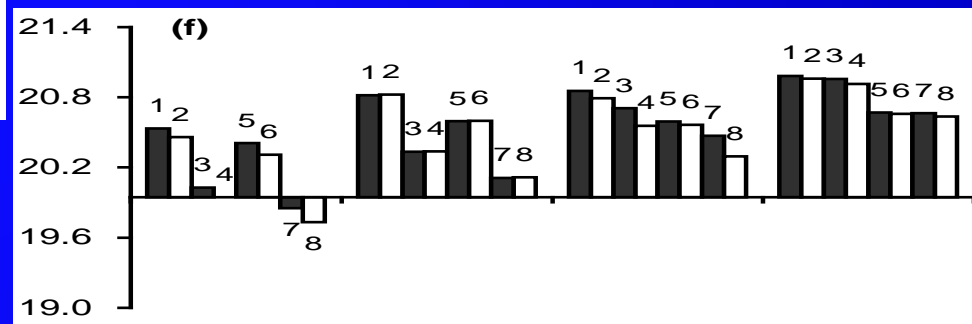
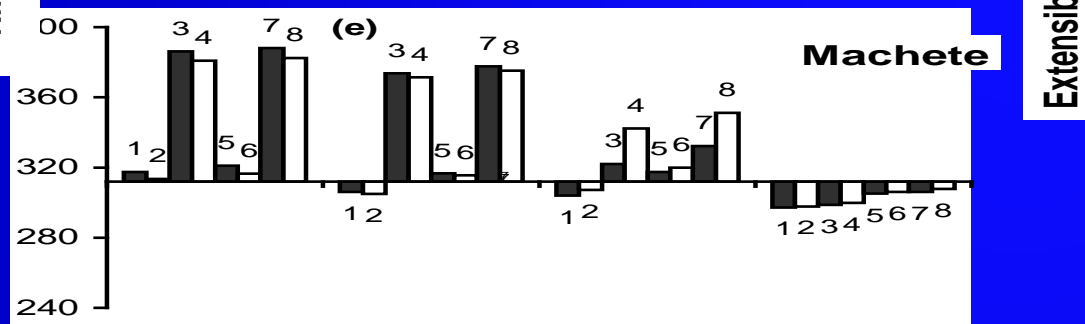
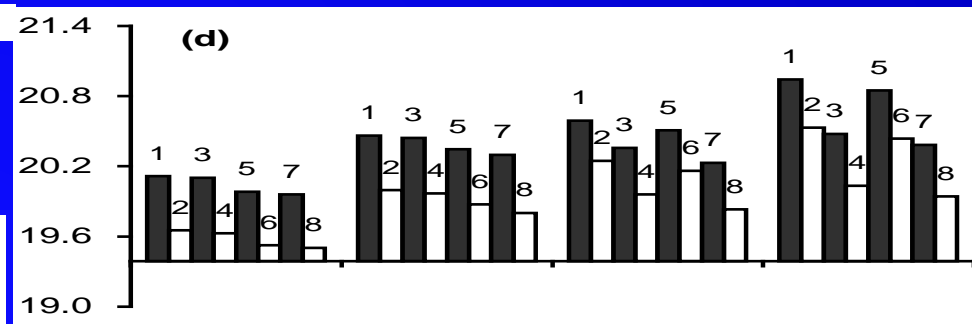
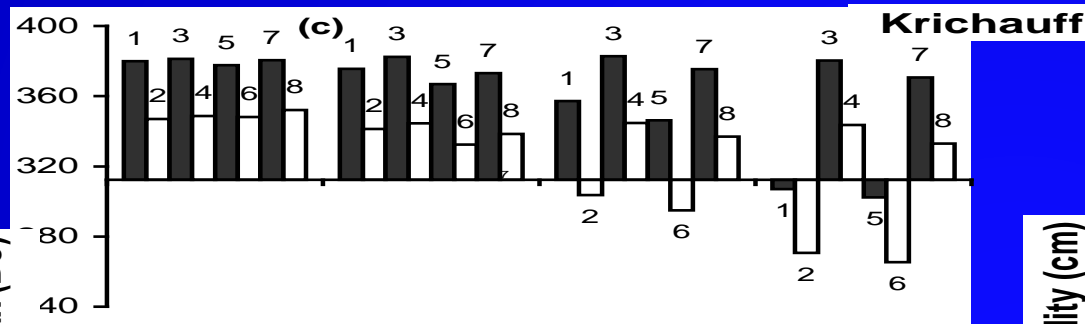
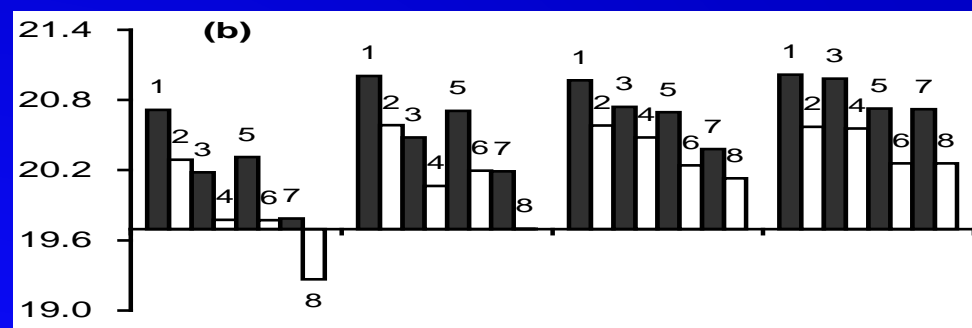
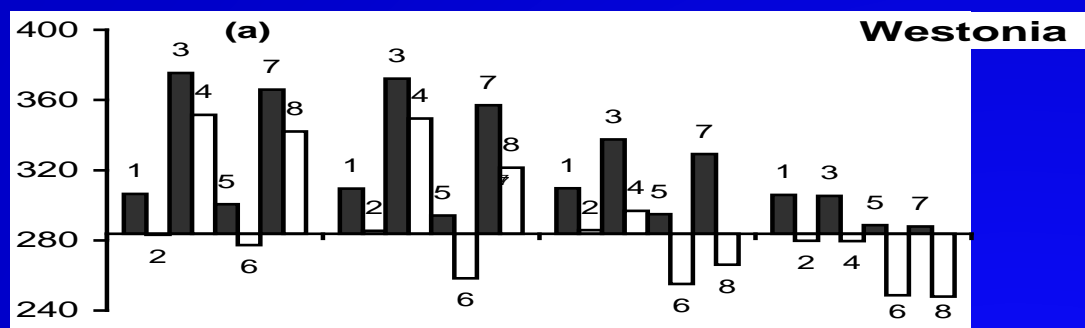
	Trait to be selected	Lines selected
Step 1	Rmax	200
Step 2	Extensibility	40

E0.2R0.2

	Trait to be selected	Lines selected
Step 1	Extensibility	200
Step 2	Rmax	40

E0.04

	Trait to be selected	Lines selected
Step 1	Extensibility	40
Step 2	n.a.	



Selection scheme (trait followed by selected proportion)

The best sister lines under each breeding objective and selection scheme

Parent	Objective	R0.04	R0.2E0.2	E0.2R0.2	E0.04
Westonia	High Rmax	3, 7	3, 7	3, 7	1, 3
	High Ext.	1	1, 5	1, 3, 5	1,3,5,7
Krichauff	High Rmax	1,3,5,7	1,3,5,7	3, 7	3, 7
	High Ext.	1,3,5,7	1,3,5,7	1, 5	1, 5
Machete	High Rmax	3,4,7,8	3,4,7,8	4, 8	None
	High Ext.	1,2,5,6	1,2,5,6	1, 2, 3	1,2,3,4
Diamondbird	High Rmax	1,2,3,4	1, 3, 4	3, 4	3, 4
	High Ext.	None	None	1,2,5,6	1,2,5,6

Efficient selection of multiple genes via marker-assisted selection, an example in wheat

Wang, J.,* S.C. Chapman, D.B. Bonnett, G.J. Rebetzke, and J. Crouch. 2007. Application of population genetic theory and simulation models to efficiently pyramid multiple genes via marker-assisted selection. **Crop Science 47: 580-588.**

Nine major genes to be pyramided in wheat

Gene	<i>Rht-B1</i>	<i>Rht-D1</i>	<i>Rht8</i>	<i>Sr2</i>	<i>Cre1</i>	<i>VPM</i>	<i>Glu-B1</i>	<i>Glu-A3</i>	<i>tin</i>
Chr.	4BS	4DS	2DL	3BS	2BL	7DL	1BL	1AS	1AS
Marker	Codom	Codom	Codom	Codom	Dom	Dom	Codom	Codom	Codom
MK-gene distance	0	0	0.6	1.1	0	0	0	0	0.8
HM14BS	<i>Rht-B1a</i>	<i>Rht-D1a</i>	<i>Rht8</i>	<i>sr2</i>	<i>cre1</i>	<i>vpm</i>	<i>Glu-B1a</i>	<i>Glu-A3e</i>	<i>Tin</i>
Sunstate	<i>Rht-B1a</i>	<i>Rht-D1b</i>	<i>rht8</i>	<i>Sr2</i>	<i>cre1</i>	<i>VPM</i>	<i>Glu-B1i</i>	<i>Glu-A3b</i>	<i>Tin</i>
Silverstar+ tin	<i>Rht-B1b</i>	<i>Rht-D1a</i>	<i>rht8</i>	<i>sr2</i>	<i>Cre1</i>	<i>vpm</i>	<i>Glu-B1i</i>	<i>Glu-A3c</i>	<i>tin</i>
Target	<i>Rht-B1a</i>	<i>Rht-D1a</i>	<i>Rht8</i>	<i>Sr2</i>	<i>Cre1</i>	<i>VPM</i>	<i>Glu-B1i</i>	<i>Glu-A3b</i>	<i>tin</i>

One strategy identified by QuLine to combine the nine genes from topcross

- Selection of **Sunstate as the final parent** (having largest number of favorable alleles) in the topcross
- Stage I: Selection for *Rht-B1a* and *Glu-B1i* homozygotes, and enrichment of *rht8*, *Cre1*, and *tin* in TCF1
- Stage II: Selection of homozygotes for one target allele, e.g. *Rht8*, and enrich remaining target alleles in TCF2
- Stage III: Selection of the target genotype in DHs/RILs

Comparison with other strategies

- For this strategy, one target genotype can be selected by screening **< 600 individuals/lines**
- For one-stage selection in advanced generations, one target genotype can be selected by screening **> 3500 lines**
- For one-stage selection in early generations, say TCF2, one target genotype can be selected by screening **millions of individuals**

Efficient selection of multiple genes/QTL via marker-assisted selection, an example in wheat

Wang, J., * S. C. Chapman, D. G. Bonnett, and G. J. Rebetzke. 2009. Simultaneous selection of major and minor genes: use of QTL to increase selection efficiency of coleoptile length of wheat (*Triticum aestivum* L.). **Theor. Appl. Genet.** 119: 65-74.

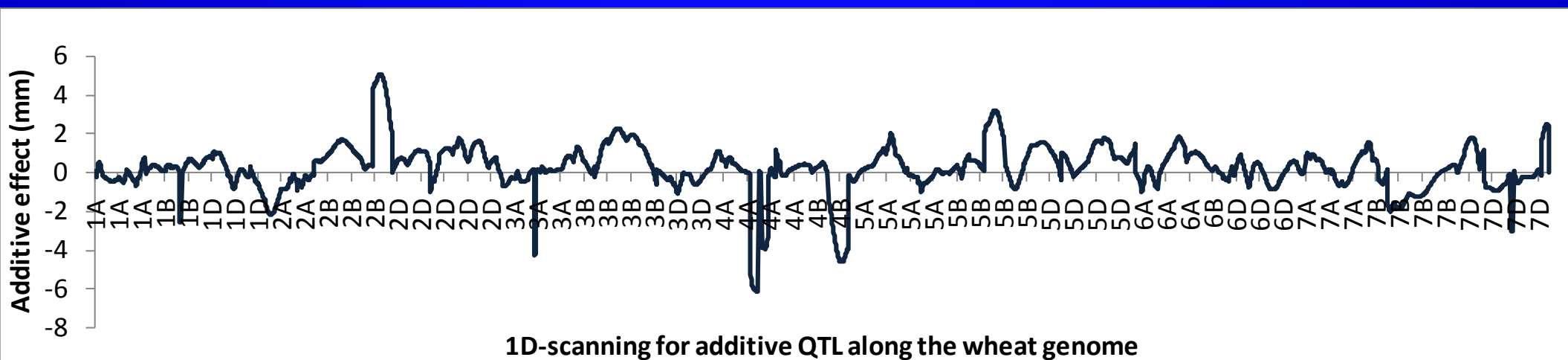
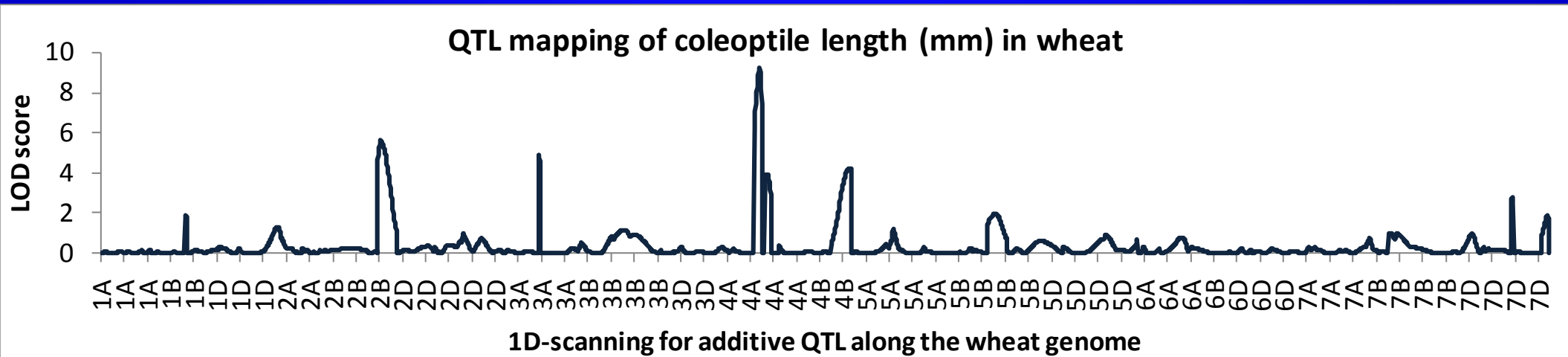
Phenotypic selection for coleoptile length ($h^2_{\text{entry-mean}} = 0.80$)



From Dr. David Bonnett, CIMMYT

CL (coleoptile length) is a typical quantitative trait

- 159 DH lines derived from two Australian wheat cultivars Cranbrook and Halbert (provided by Greg Rebetzke, CSIRO, Canberra, Australia) using Inclusive Composite Interval Mapping (ICIM)



Six major genes in two parental lines

Gene	<i>Rht-D1</i>	<i>Rht8</i>	<i>Sr2</i>	<i>VPM</i>	<i>Glu-B1</i>	<i>Glu-A3</i>
Chr.	4DS	2DL	3BS	7DL	1BL	1AS
Marker	Codom	Codom	Codom	Dom	Codom	Codom
MK-gene distance	0	0.6	1.1	0	0	0
HM14BS	<i>Rht-D1a</i>	<i>Rht8</i>	<i>sr2</i>	<i>vpm</i>	<i>Glu-B1a</i>	<i>Glu-A3e</i>
Sunstate	<i>Rht-D1b</i>	<i>rht8</i>	<i>Sr2</i>	<i>VPM</i>	<i>Glu-B1i</i>	<i>Glu-A3b</i>

Additive genetic effects of CL genes, genotypes of HM14BS, Sunstate and the genotype with the longest CL

Locus	Chrom	Distance to the nearest marker (cM)	Additive effect (mm)	Additive variance explained (%)	HM14BS	Sunstate	Genotype with all increased CL alleles
<i>Rht-D1</i>	4DS	0.0	9.5	42.63	<i>Rht-D1a</i>	<i>Rht-D1b</i>	<i>Rht-D1a</i>
<i>qCL1</i>	1AS	8.1	2.9	3.97	+	-	+
<i>qCL2</i>	2BS	0.7	2.5	2.95	+	-	+
<i>qCL3</i>	2DS	1.1	4.1	7.94	+	-	+
<i>qCL4</i>	3BS	0.9	2.0	1.89	+	-	+
<i>qCL5</i>	5AL	6.2	4.9	11.34	+	-	+
<i>qCL6</i>	5DS	13.0	3.6	6.12	+	-	+
<i>qCL7</i>	Unidentified		4.0	7.56	-	+	+
<i>qCL8</i>	Unidentified		3.0	4.25	+	-	+
<i>qCL9</i>	Unidentified		3.0	4.25	-	+	+
<i>qCL10</i>	Unidentified		2.0	1.89	+	-	+
<i>qCL11</i>	Unidentified		2.0	1.89	+	-	+
<i>qCL12</i>	Unidentified		2.0	1.89	-	+	+
<i>qCL13</i>	Unidentified		1.0	0.47	+	-	+
<i>qCL14</i>	Unidentified		1.0	0.47	+	-	+
<i>qCL15</i>	Unidentified		1.0	0.47	+	-	+
<i>qCL16</i>	Unidentified		1.0	0.47	+	-	+
<i>qCL17</i>	Unidentified		1.0	0.47	-	+	+
Coleoptile length (mm)					158	97	178

Breeding target ...

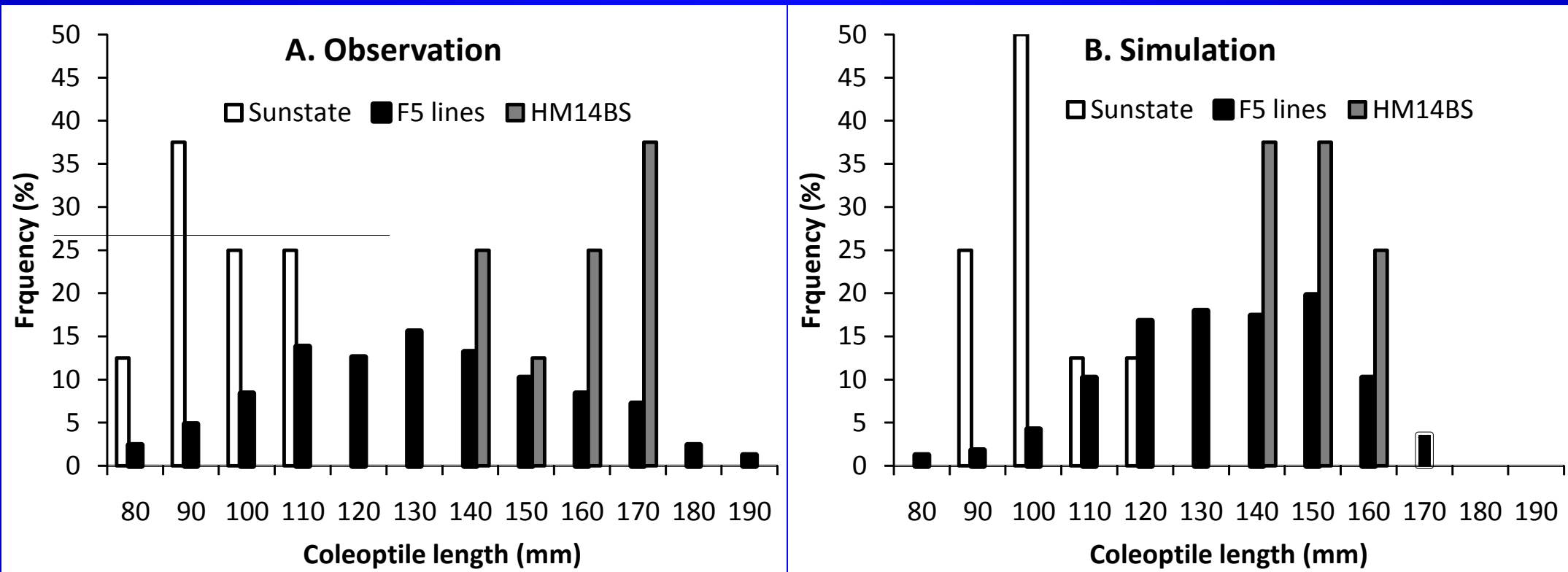
For the six major genes

Gene	<i>Rht-D1</i>	<i>Rht8</i>	<i>Sr2</i>	<i>VPM</i>	<i>Glu-B1</i>	<i>Glu-A3</i>
Target	<i>Rht-D1a</i>	<i>Rht8</i>	<i>Sr2</i>	<i>VPM</i>	<i>Glu-B1i</i>	<i>Glu-A3b</i>

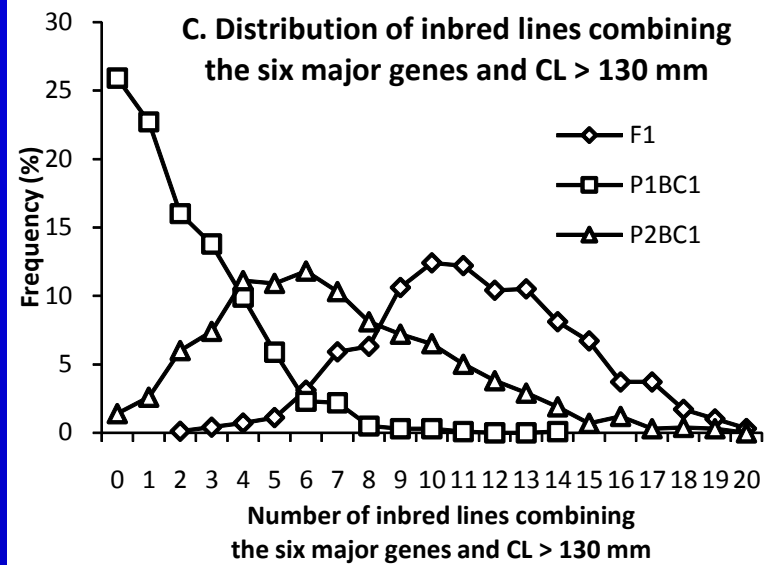
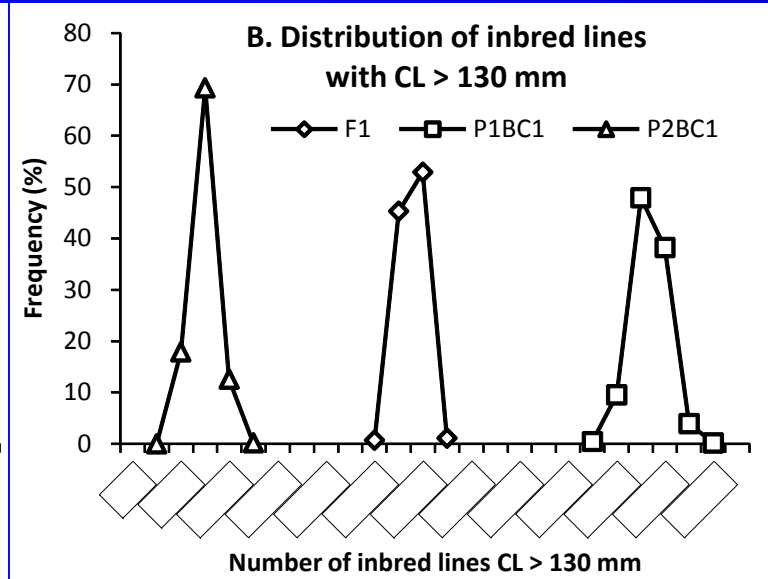
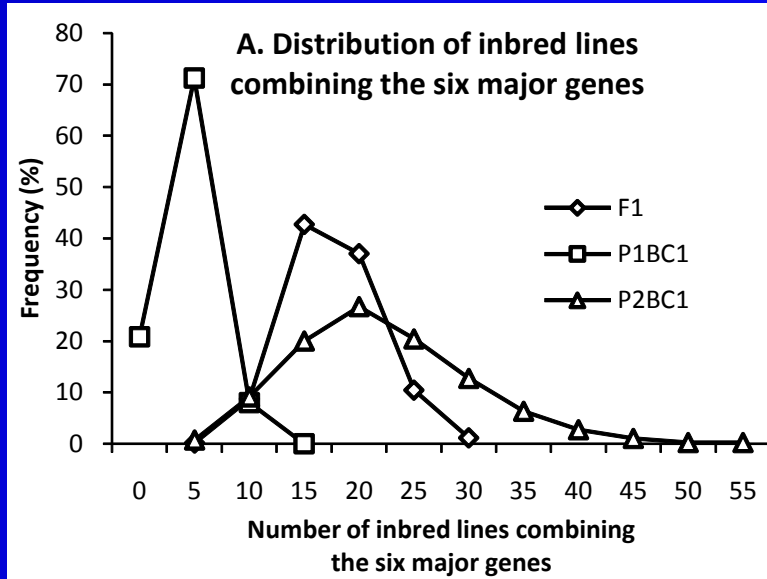
For coleoptile length (CL), $CL > 130$ mm, which is 30% longer than Sunstate's

Target: to select as many as possible inbred lines combining the six desired alleles and having $CL > 130$ mm, so as to have chances to select for other traits, i.e., yield and adaptation.

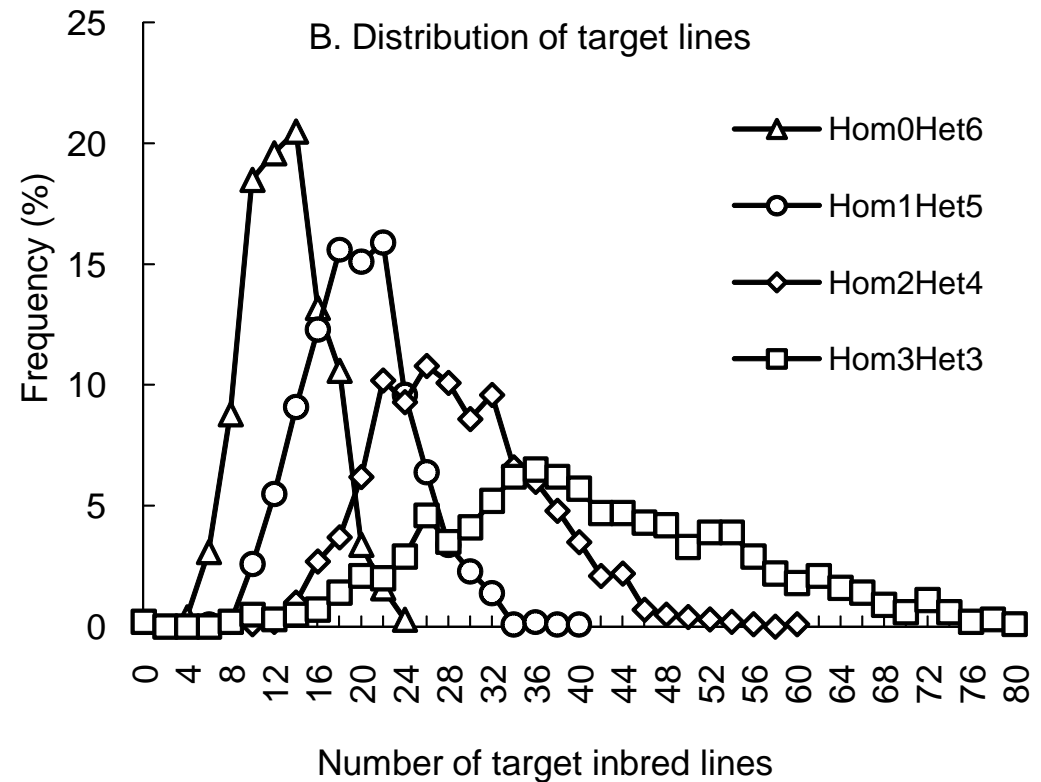
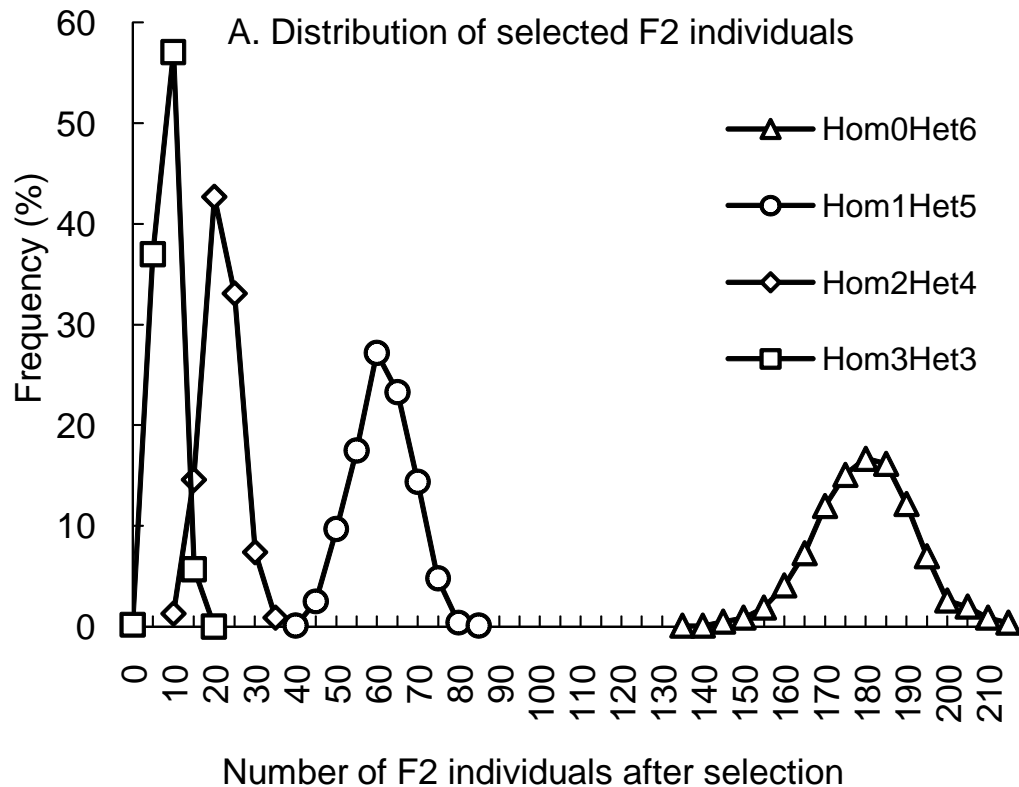
Validating the genetic model



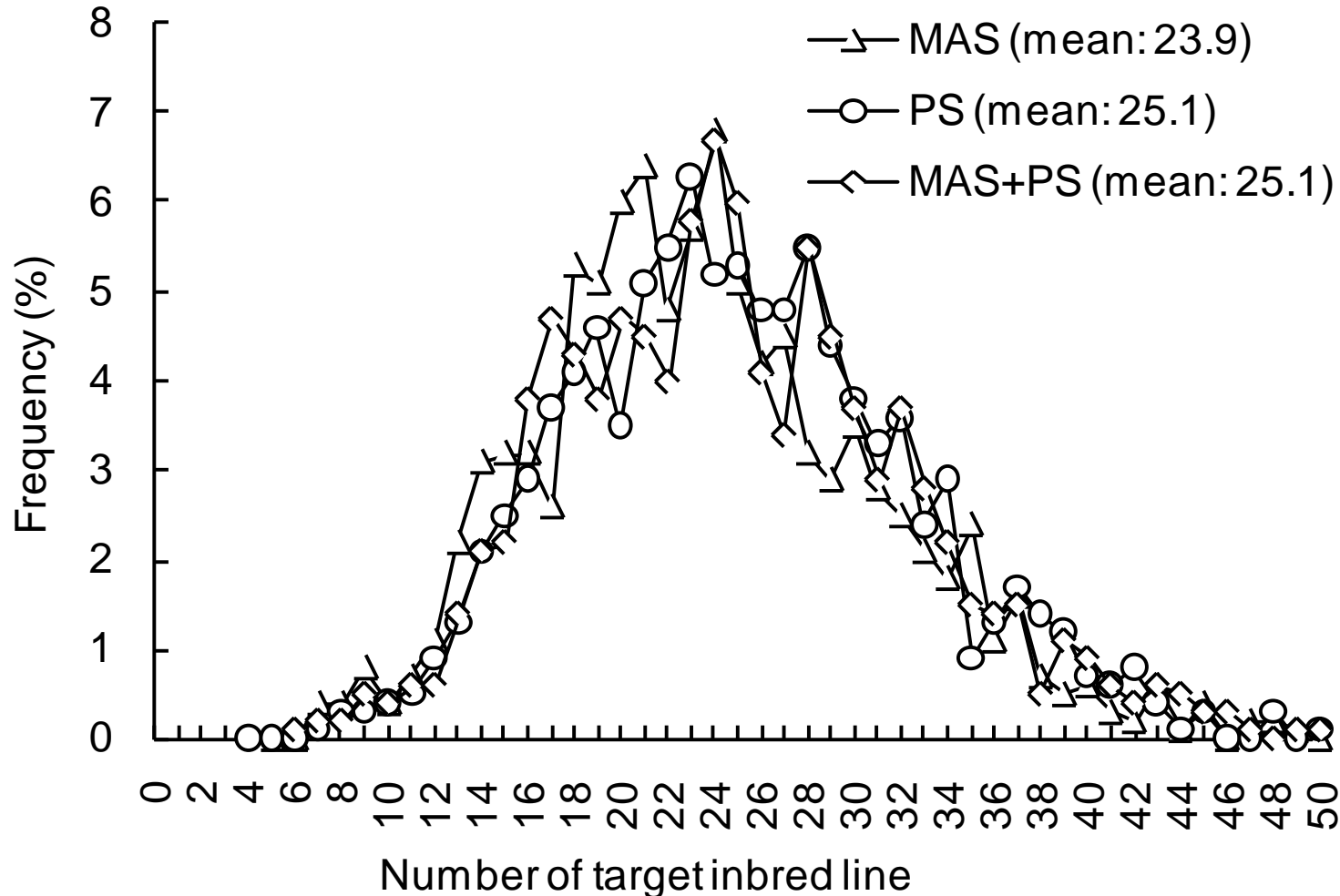
Do we need backcrossing?



Comparison of various MAS strategies in selecting the six major genes (1000 F2 individuals and 200 RILs)



Comparison of MAS and phenotypic selection (PS) for coleoptile length



The chance or number game of plant breeding

Conclusions

- An average of **2.4** individuals with the target genotype were present in unselected F₁-derived doubled haploid (DH) or recombinant inbred line (RIL) populations of size 200.
- A selection scheme for the six major genes in F₂ increased the number of target individuals to **19.1**, and additional marker-assisted selection (MAS) for CL increased the number to **23.9**.
- Phenotypic selection (PS) of CL outperformed MAS in this study due to the high heritability of CL, incompletely linked markers for known QTL, and the existence of unidentified QTL.
- However, a selection scheme combining MAS and PS was equally as efficient as PS (**25.1** target genotypes selected) and would result in net savings in production and time to delivery of long coleoptile wheats containing the six favorable alleles.