

Use of Identified QTL to Improve the Efficiency of Breeding for Long Coleoptile Length of Wheat (*Triticum aestivum* L.)

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Introduction

Plant breeders simultaneously select for qualitative traits controlled by one or a small number of major genes, as well as for polygenic traits controlled by multiple genes that may be detected as quantitative trait loci (QTL). However, there are few reported examples of the implementation of QTL markers in line development of self-pollinated crops such as wheat.

Materials and methods

Table 1 Six major genes, their chromosomal locations, and the genotypes of the two wheat parents

Locus symbol ^a	<i>Rht-D1</i>	<i>Rht8</i>	<i>Sr2</i>	<i>VPM</i>	<i>Glu-B1</i>	<i>Glu-A3</i>
Chromosome	4DS	2DL	3BS	7DL	1BL	1AS
Marker type	Codom	Codom	Codom	Dom	Codom	Codom
Distance to the nearest marker (cM)	0.0	0.6	1.1	0.0	0.0	0.0
HM14BS	<i>Rht-D1a</i>	<i>Rht8</i>	<i>sr2</i>	<i>vpm</i>	<i>Glu-B</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>
Target genotype ^b	<i>Rht-D1a</i>	<i>Rht8</i>	<i>Sr2</i>	<i>VPM</i>	<i>Glu-B1i</i>	<i>Glu-A3b</i>

^aAlleles *Rht-D1b* and *Rht8* reduce plant height, allele *Sr2* confers resistance to stem rust, allele *VPM* confers resistance to cereal cyst nematode, and alleles *Glu-B1i* and *Glu-A3b* improve bread wheat dough quality. The six loci are located on different wheat chromosomes, as indicated

^bAlleles in the target genotype were determined by semi-dwarfing with long CL, multiple disease resistances, and excellent grain quality. The two semi-dwarfing alleles can all produce the required plant height. However, *Rht-D1b* also reduces the CL, which is unfavorable for breeding drought-resistant wheat cultivars. *Rht8* reduces plant height without affecting CL, and is therefore the favorable dwarfing allele under drought environments. Other alleles in the target genotype are easily understood as they increase the resistance to some disease, and increase grain quality

Table 2 Additive genetic effects of CL genes used in the simulation study and genotypes of HM14BS, Sunstate and the target genotype with the longest CL

Locus	Chro.	Distance to marker (cM)	Additive effect (mm)	R ² (%)	HM14BS	Sunstate	Genotype with all increased CL alleles
<i>Rht-D1</i>	4DS	0.0	9.5	42.63	<i>Rht-D</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 objectives

To combine Sunstate's favorable disease resistance and grain quality alleles with alleles associated with long CL from HM14BS. We assumed a total of 1000 individuals can be grown, and genotyped by molecular markers in the F₂ generation, and that 200 inbred lines can be generated either through DH or repeated self-pollination. Our first objective was to select inbred lines combining the six desired major genes, i.e. the target genotype in Table 1. These lines will meet requirements for plant height, disease resistance, and grain quality. Our second objective was to select inbred lines combining the six desired major genes together with long CL. In the genetic model defined in Table 2, the greatest CL is 178 mm, when all 17 increased CL genes are combined in one genotype. However, this genotype has an extremely low frequency in a limited-size breeding population, so we set a reasonable target for CL, i.e., CL > 130 mm, which is 30% longer than Sunstate's.

Results and Discussion

Single cross versus backcross

The frequency of the target genotype (i.e. inbred lines combining the six desired major genes and with CL > 130 mm in this study) in breeding populations determines the success of further trait selection. When both major genes and long CL are desired, simulation indicated an F₁-derived population had the largest number of target genotypes.

Increasing target genotype frequency through selection at major gene loci

On average, 6.4 F₂ individuals out of 1000 were retained from Hom3Het3, 19.6 from Hom2Het4, 59.2 from Hom1Het5, and 177.7 from Hom0Het6. The small number of selected F₂ makes further selection difficult, and also increases uncertainty in later generations (Fig. 2B). Therefore, we chose Hom1Het5 for further investigation. In this study, it makes no difference at which loci homozygotes are selected and at which loci allele enrichment is applied, as there is no linkage between the six major genes.

Further increasing target genotype frequency through CL selection

When Hom1Het5 was applied in F₂, an average 19.1 target genotypes could be selected from 200 DH or RIL. When a MAS scheme based on marker score from the known QTL was applied with a selected portion of 0.25 on selected F₂ after Hom1Het5, an average 23.9 target genotypes could be selected (Fig. 2), further increasing the frequency of the target genotype. **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 and would result in net savings in production and time to delivery of long coleoptile wheats containing the six favorable alleles.**

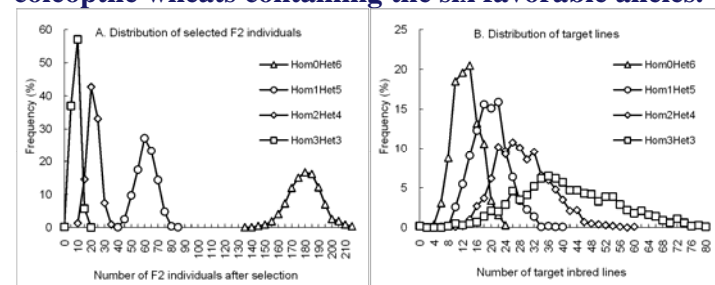


Fig. 1. Comparison of different selection schemes for the six major genes. Frequency was calculated from 1000 simulation runs. A, distribution of the number of selected F₂ individuals; B, distribution of the number of target inbred lines.

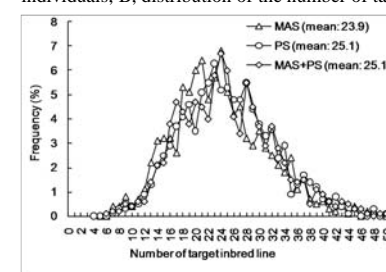


Fig. 2. Frequency distribution of target inbred lines from different selection schemes for coleoptile length. Frequency was calculated from 1000 simulation runs. MAS = marker-assisted selection and PS = phenotypic selection. MAS + PS is a sequential selection scheme where MAS was applied first, followed by PS.