

## 「구두발표」

### 1. 유전, 육종, 품절 분야

자포니카 잡초성 벼와 통일형 벼 간 RIL 집단 이용

진화 관련 형질 유전자 분석

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**Mapping of genetic factors controlling domestication-related traits using an RIL population from a Korean *japonica* weedy rice and Tongil-type rice**

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### **Objectives**

In order to identify and characterize genetic factors controlling domestication-related traits in an intersubspecific cross population.

### **Materials and Methods**

Plant materials - BC<sub>1</sub>F<sub>6</sub> (80 lines) from a Milyang23\*\*2/Hapcheonaenmi3 cross

Trait measurement - Morphological and quantitative traits including day to

QTL analysis and map construction - Mapmaker V3.0/QGENE

Genotyping - SSR markers

### **Results and Discussion**

1. A total of 257 SSR markers were used in polymorphic survey between the parents. Of these, 182 (70.8%) were polymorphic between the parents. A genetic linkage map was constructed with 4 morphological and 120 SSR marker for a total length of 1,024 cM with an average interval size 9.3cM. Significant skewing of alleles was observed for 18.0% of the markers used in this study: 16.4% of the markers were skewed towards the Milyang23 allele, while 1.6% were skewed towards the Hapcheonaenmi3 allele.

2. The frequency distribution of phenotypes for each traits in the 80 RILs are shown in Fig 1. All the quantitative traits examined were characterized by continuous variation, and showed approximately normal distribution. Most of the traits showed transgressive variation, giving a large apparent variation in the RILs population.

3. Twenty-two putative QTLs were identified using one-way ANOVA (Table 1). The number of QTLs ranged from 2 to 3 per trait. These 22 QTLs were located in 12 intervals distributed on 8 of the 12 chromosomes. Of the 24 genes/QTLs 16 were found to be clustered only on limited regions of chromosomes 1, 2, 3 and 6.

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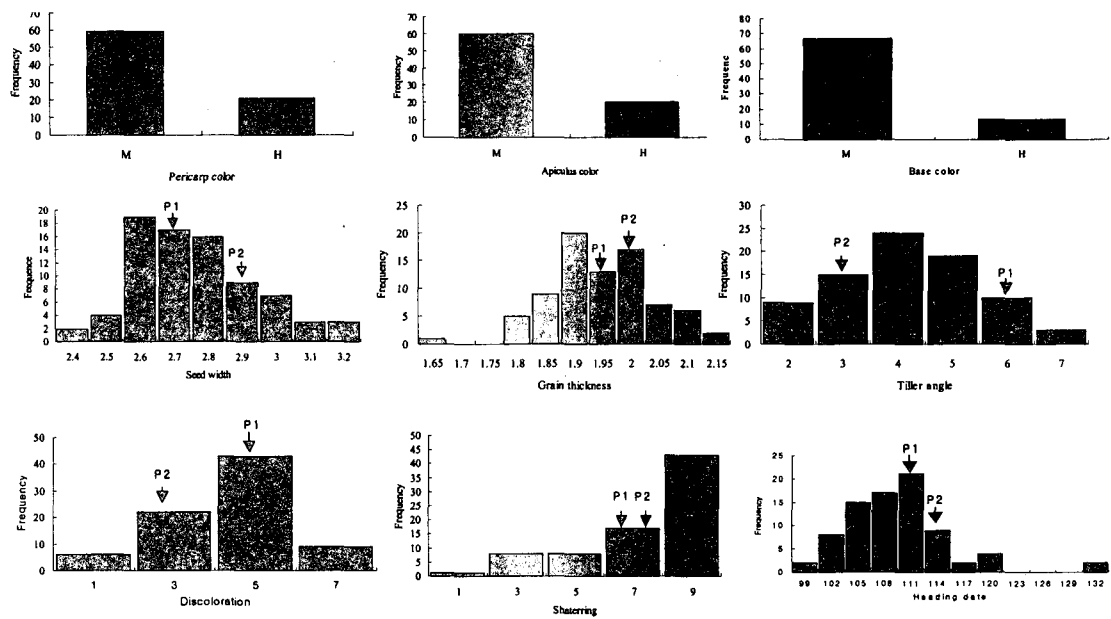


Fig 1. Frequency distribution of phenotypes for each trait (P1: Milyang23, P2: Hapcheonaengmi3)

Table 1. Characteristics of genetic factors underlying domestication-related traits.

Trait	Interval	Chr.	R <sup>2</sup> (%)		Mean		
			Locus	Trait	MM*	HH	Allele effect
Days to heading	RM262-RM526	2	10.7		109.4	115.0	2.80
	RM426-RM168	3	12.8		110.9	106.8	-2.05
	RM539-RM527	6	18.2		109.5	119.8	5.15
	RM214 -RM455	7	16.5	40.9	111.0	106.1	-2.45
Discoloration	RM552-RM6544	11	18.1		4.6	2.5	-1.1
Cold tolerance at seedling stage	RM473-RM431	1	13.5		3.8	0.5	-1.7
	RM253-C	6	8.7	11.6	4.0	2.9	-0.5
Seedling height	RM315-RM414	1	18.1		12.4	14.2	0.90
Shattering	RM166-RM262	2	21.7		7.41	3.86	-1.78
	RM539-RM275	6	24.2	32.6	7.56	5.00	-1.28
Tiller angle	RM232-RM563	3	10.9		4.3	5.3	0.5
Grain length	RM128-PBC121	1	10.8		7.85	7.48	-0.19
	RM166-RM526	2	14.4		7.86	7.33	-0.27
	RM571-RM489	3	14.3		7.89	7.51	-0.19
	RM480-RM421	5	16.3		7.84	7.47	-0.19
	RM539-RM527	6	24.1	35.8	7.80	6.74	-0.53
Grain width	RM570-RM571	3	13.3		2.77	2.92	0.07
	RM527-RM539	6	19.9		2.78	3.09	0.16
	RM271-RM258	10	19.0	23.4	2.78	3.00	0.11
Grain thickness	PBC121-RM128	1	14.6		1.39	1.54	0.15
	RM571-RM570	3	13.8	21.7	1.39	1.54	0.15

\*MM, HH : Milyang23 and Hapcheonaengmi 3 homozygotes, respectively