

Construction and Utilization of *Oryza glaberrima* Introgression Lines in the Background of *O. sativa* L.

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**Construction and Utilization of *Oryza glaberrima*
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General Introduction

Asian rice, *Oryza sativa* L., is a major food crop in the world and the most common cultivated rice. African rice, *Oryza glaberrima* Steud., is an endemic cultivar in West Africa. Taxonomically *O. glaberrima* belongs to *O. sativa* complex (A-genome) in the genus *Oryza* (Vaughan 1994). Phylogenetic analyses based on isozymes, chloroplast DNA and nuclear DNA (Second 1985, Dally and Second 1990, Ishii *et al.* 1988, 1995, Wang *et al.* 1992, Doi *et al.* 1995) revealed that *O. glaberrima* was cultivated from *O. barthii* A. Chev. (formerly *O. breviligulata* A. Chev *et* Roehr.) while *O. sativa* was believed to be differentiated from *O. rufipogon* Griff. Geographical distribution of the A-genome species was shown in Fig. 1. Other A-genome wild species, *O. nivara* Sharma *et* Shastri, *O. longistaminata* Chev. *et* Roehr., *O. glumaepatula* Steud. (sometimes called *O. rufipogon*) and *O. meridionalis* Ng are known to exist in Asia, Africa, Latin America and Australia, respectively.

Morphological key characters of *O. glaberrima* are the lack of secondary and tertiary branching of panicles, short and rounded ligule, generally awnless spikelets and non-shattering (Vaughan 1994). Pubescent leaves and sparse spikelets are also generally found in this species. Physiologically it has strong seed dormancy and annual growth habit quite different from those of *O. sativa*. Although *O. glaberrima* has interesting characters

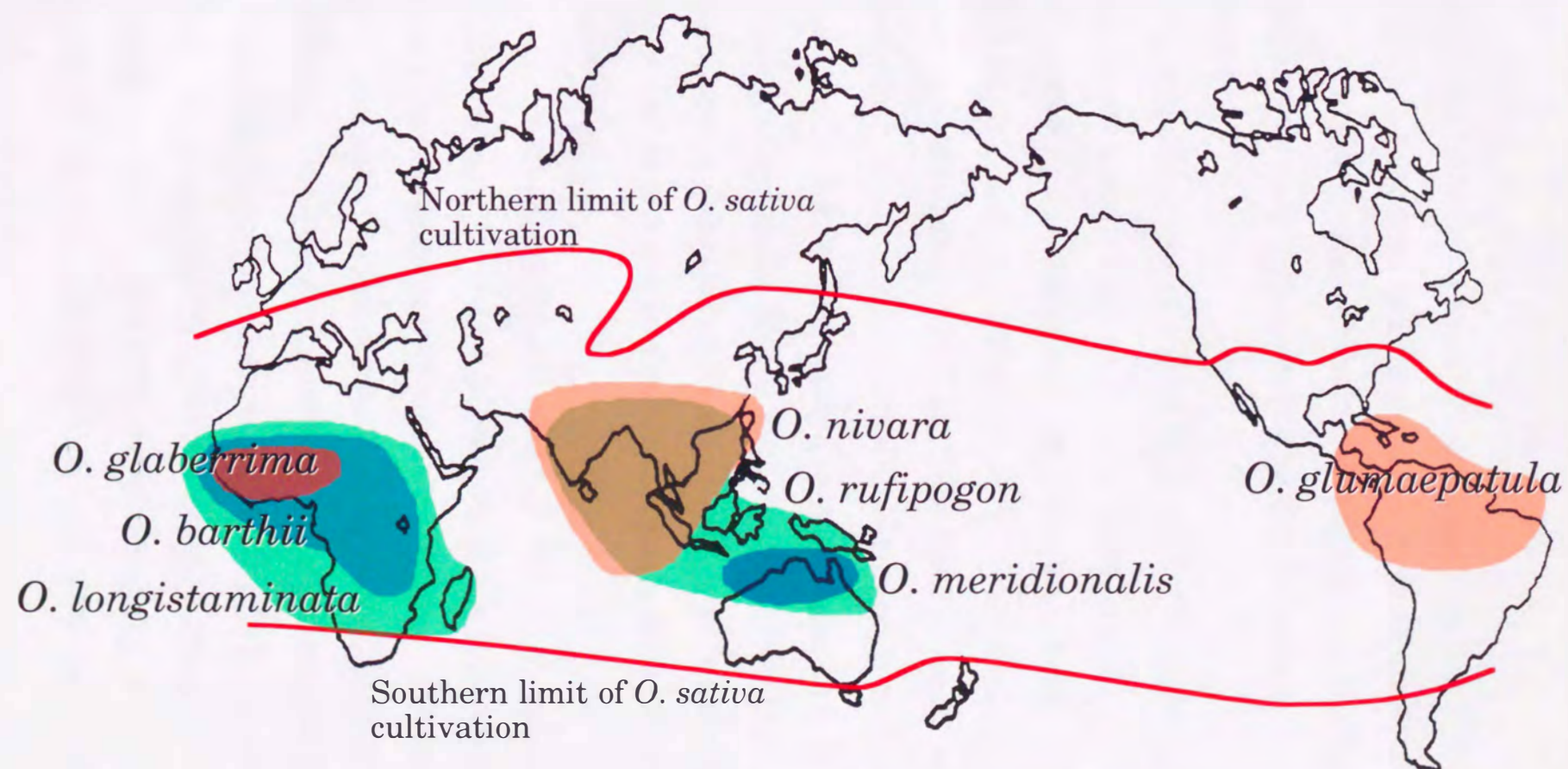


Fig. 1. Geographical distribution of A-genome species in the genus *Oryza*.

such as mentioned above, it has not been extensively used in rice breeding program and molecular-marker-assisted genetic analysis in rice. One of the most possible reasons is that F1 hybrids between *O. sativa* and *O. glaberrima* show complete male sterility.

Using RFLP markers, well-saturated linkage maps of rice were constructed. Traits of agronomic importance, such as disease and insect resistance and even quantitative trait loci (QTLs) were mapped onto them (e. g. Tsunematsu *et al.* 1995, Xiao *et al.* 1995; 1996, Lin *et al.* 1996, Redoña and Mackill 1996). QTLs control many traits of agronomic importance. Development of molecular markers enabled geneticists and breeders to systematically detect QTLs (Lander and Botstein 1989). To manipulate the selection of desired genotypes, molecular markers can be employed instead of expensive evaluations over years and locations.

Currently international effort in molecular-marker-assisted genetic analysis is directed to identify QTLs. Molecular markers are used in mapping populations derived from distantly related crosses and many QTLs are ordinarily detected in the mapping populations. However, simultaneous QTL mapping based on conventional populations such as F2, BC1F1, or recombinant inbred lines makes it difficult to precisely evaluate the phenotypic effect of each QTL. In other words, accuracy of QTL analysis is limited by environmental variance although the

progeny test or replication of recombinant inbreds is effective (Lander and Botstein 1989, Burr and Burr 1991). Hence, it is also difficult to fine-map each of the QTLs in these populations. This difficulty attributes to the great genetic variation in mapping populations.

Some new concepts, such as advanced backcross (AB) QTL analysis (Tanksley and Nelson 1996) and introgression line (IL) analysis (Eshed and Zamir 1994, 1995, Eshed *et al.* 1996), were proposed to overcome these difficulties. These methods utilize backcross progeny (BC2, BC3, BC4) with a more uniform genetic background. AB QTL analysis employs BC2F1 or BC3F1 populations while IL analysis uses fixed lines with a small chromosome segment from the donor. Both new methods, therefore, enable researchers to generate isogenic lines for each QTL in the background of an elite breeding line more rapidly than the conventional methods. Isogenic lines are important to evaluate precisely the phenotype of each plant or line, resulting in fine mapping of QTLs.

In rice, it is generally difficult to obtain many crossed F1 seeds sufficient for repeated or multilocal evaluation as reported in AB QTL analysis in tomato (Bernacchi *et al.* 1998). Introgression lines, therefore, are more rational in rice for such purposes. Systematically bred introgression lines using marker assisted selection (MAS) were developed or are currently developed in some plant species other than tomato, such as

Brassica (Ramsay *et al.* 1996).

To analyze the genetics of traits specific to *O. glaberrima* and to exploit fully the genetic potential of the species, a series of *O. glaberrima* introgression lines (GILs) in the background of *O. sativa* was developed in the present study. Each GIL carrying homozygous chromosome segments from *O. glaberrima* was selected using RFLP markers. MAS was done ahead of the phenotypic selection, while conventional breeding methods gave priority to phenotypic selection.

During breeding of GILs, a large variation of heading date and pollen sterility was observed. Heading date, which is related to many characters of agronomic importance such as grain yield or stress avoidance, is an important character of rice. Sterility is a major key trait for utilizing alien germplasm in rice breeding as well as hybrid rice breeding. Although complete male sterility is observed in hybrids between two cultivated rice species, genetic information about the phenomenon is still very limited (Yabuno 1977, Sano *et al.* 1979, Sano 1983, 1986, 1990).

The present thesis described the following subjects: The first step was the construction of an RFLP linkage map as a framework of MAS for the development of GILs (Chapter I). In the BC₂F₁ generation, QTL analysis for heading and pollen fertility was done (Chapter II). The construction of a series of GILs was described in Chapter III. Some of the detected QTLs were identified using genetically simplified segregating

General Materials and Methods

An *O. glaberrima* accession, IRGC 104038, from Senegal kindly supplied by the International Rice Germplasm Center, the International Rice Research Institute, Los Baños, Philippines was used as a donor parent. A Japonica rice variety, *O. sativa* cv. Taichung 65, was used as a recurrent parent. In the initial cross, Taichung 65 was used as a female parent, while in backcrosses it was used as a male parent with (BC)F1 plants as female parents. Therefore, all the progeny carried cytoplasm from Taichung 65.

The breeding scheme of the plant materials was shown in Fig. 2. Using BC1F1 population (65 plants), a framework RFLP linkage map was constructed. The plants in this population were backcrossed with Taichung 65 and derived BC2F1 plants were used for QTL mapping of heading date and pollen sterility. BC3F1 plants were selected using RFLP markers and its selfed progeny (BC3F2) were selected again for fixed GILs. A BC3F5 population from one of these lines was used to verify a QTL for heading date found in BC2F1. On the other hand, to produce isogenic lines of QTLs for pollen sterility, backcrossing was continued to BC6F1 with phenotypic and marker assisted selection. One of the derived BC6F1 populations was used for mapping a QTL for pollen sterility.

Procedure of DNA extraction and RFLP detection fundamentally followed the procedure described by Ban (1996)

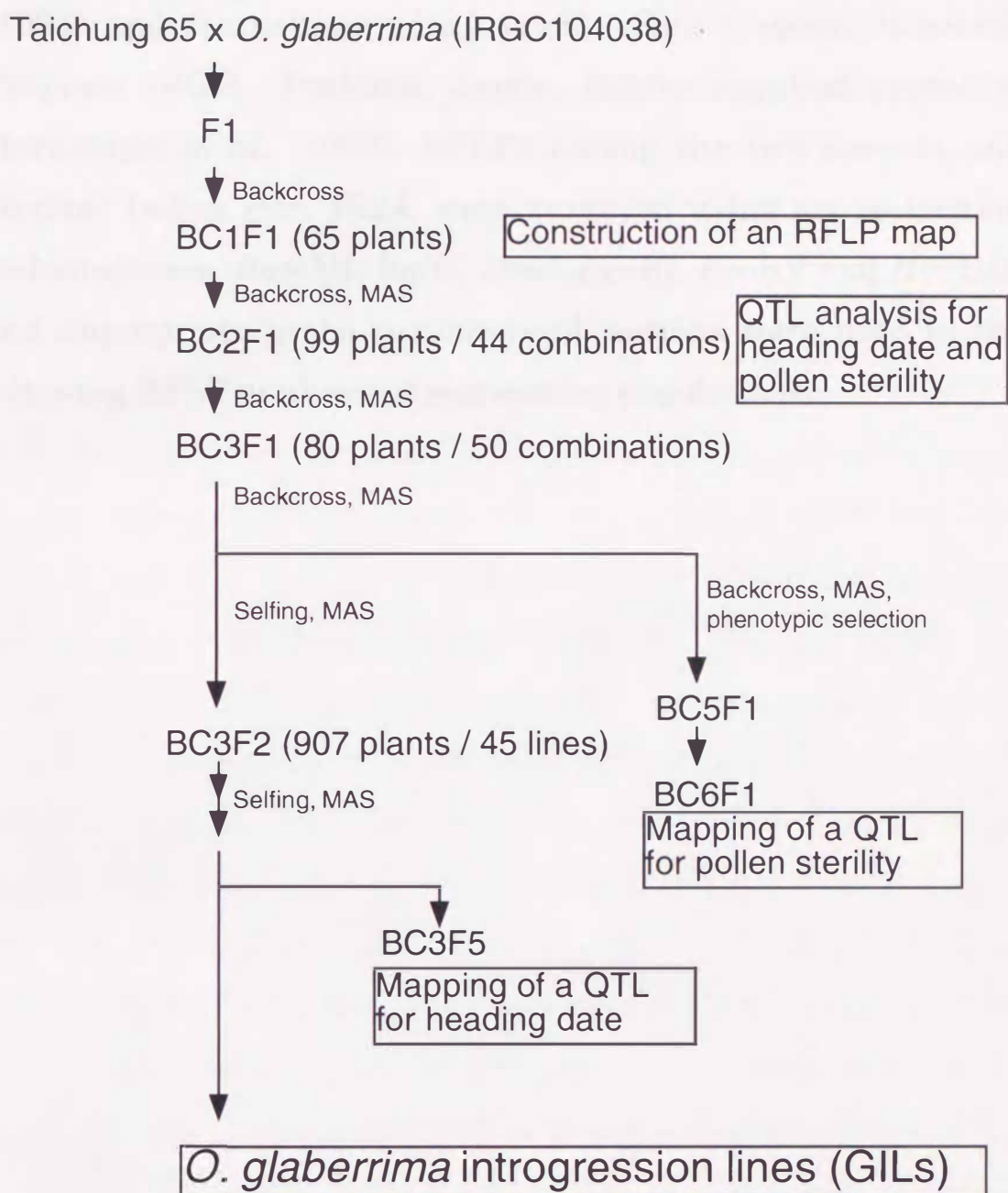


Fig. 2. Scheme to construct *O. glaberrima* introgression lines in the background of *O. sativa* cv. Taichung 65. Production of plant materials used in the present study was also shown. The initial cross were made using Taichung 65 as a female parent and all backcrosses were made using Taichung 65 as a pollen parent so that all the progenies carried cytoplasm of Taichung 65.

and Nagamura (1996). RFLP probes used were of Saito *et al.* (1991) and Harushima *et al.* (1998). Rice Genome Research Program (RGP), Tsukuba, Japan, kindly supplied probes of Harushima *et al.* (1998). RFLPs among the two parents and another Indica rice, IR24, were surveyed using six restriction endonucleases (*Bam*HI, *Bgl*II, *Dra*I, *Eco*RI, *Eco*RV and *Hind*III) and appropriate probe-enzyme combinations were used in the following RFLP analyses of segregating populations.

Materials and Methods

Seeds were sown in a randomized block design in the field. The parent and Tetra Yang 43 as the pollen parent DNA of 201/2

Chapter I

Construction of an RFLP Linkage Map Using a Backcross Population between *Oryza sativa* L. and *O. glaberrima* Steud.

Introduction

As a first step towards construction of GILs, an RFLP linkage map based on a backcross population was constructed. A precise linkage map is essential for conducting MAS. Since GILs will be selected through entire genome, an RFLP linkage map that covers whole rice genome is required. *O. glaberrima* has not been used for molecular-marker-assisted genetic analysis in rice while RFLP maps based on intraspecific crosses (McCouch *et al.* 1988, Saito *et al.* 1991, Tsunematsu *et al.* 1996, Harushima *et al.* 1998), interspecific backcross (Causse *et al.* 1994) and crosses between wild species other than the *O. sativa* complex in the genus *Oryza* (Jena and Kochert 1991, Jena *et al.* 1994) were constructed. The map will also give some additional information about differentiation between *O. sativa* and *O. glaberrima*.

Materials and Methods

Backcrosses were performed using F1 plants as the female parent and Taichung 65 as the pollen parent. DNA of 65 BC1F1

plants was extracted and used for RFLP mapping.

RFLPs were surveyed among three rice varieties, Taichung 65, IR24 (an Indica variety of *O. sativa*), and *O. glaberrima*, using six restriction endonucleases (*Bam*HI, *Bgl*II, *Dra*I, *Eco*RI, *Eco*RV and *Hind*III).

Recombination values were estimated using the maximum likelihood equation (Allard 1956), and the recombination values were converted into the genetic map distances (cM) using Kosambi function (Kosambi 1944).

Results

Crossability of F1 and backcrossed progenies

F1 seeds were easily derived from the cross, Taichung 65 x *O. glaberrima*, and they germinated normally. Crossability of F1 hybrids with Taichung 65 pollens appeared to be lower than in the case of the interspecific cross described by Oka (1988) (approximately 30%). However, 5 to 40 seeds were generated from each of the F1 plants following a standard crossing method.

Detection of RFLPs between O. sativa and O. glaberrima

RFLPs between Taichung 65 and *O. glaberrima* were examined. Out of 415 recordable probe-enzyme combinations (75 probes and 6 enzymes), 245 polymorphic combinations were observed. The frequency of the RFLPs was 59%. In the same

manner, RFLPs were detected in the intraspecific combination between Taichung 65 and IR24 and the frequency was 51%. The frequency of RFLPs detected from the interspecific combination between Taichung 65 and *O. glaberrima* was slightly higher than that from the intraspecific combination. Almost all the probes showed polymorphism between Taichung 65 and *O. glaberrima* and were used for the interspecific mapping.

Evaluation of the RFLP map

The RFLP map based on the BC1F1 population is shown in Fig. 3. It includes 101 well-dispersed RFLP markers. Since markers located in telomeric regions (Tsunematsu *et al.* 1996, Harushima *et al.* 1998) were used in this study, the present map covered whole genome. The total map length was 1403.4 cM. Linkage arrangement of the RFLP markers was in good agreement with that of the previously constructed maps (Saito *et al.* 1991, Tsunematsu *et al.* 1996, Harushima *et al.* 1998).

Segregation distortion

Significant segregation distortions were observed in chromosomes 4, 5, 6 and 11 (Table 1). In chromosome 6, a strong distortion towards *O. glaberrima* was detected. In chromosomes 4, 5 and 11, alleles from Taichung 65 were preferentially transmitted to the progenies.

Fig. 3. An RFLP map based on the backcross population (Taichung 65 / *O. glaberrima* (Acc. IRGC 104038) // Taichung 65). Markers with the prefix "XNpb" were supplied by Saito *et al.* (1991). Other markers (Harushima *et al.* 1998) were kindly provided by RGP. Marker intervals are indicated in cM. The total map length is 1403.4 cM.

Table 1. RFLP loci showing segregation distortion.

RFLP locus (chromosome)	Genotype ¹⁾		Total	χ^2 ²⁾
	AA	Aa		
<i>XNpb331</i> (4)	41	24	65	4.446 *
<i>R3166</i> (5)	39	21	60	5.400 *
<i>G260</i> (5)	40	24	64	4.000 *
<i>XNpb297</i> (5)	41	24	65	4.446 *
<i>XNpb209</i> (6)	8	57	65	36.938 ***
<i>XNpb27</i> (6)	5	60	65	46.538 ***
<i>XNpb172</i> (6)	17	48	65	14.785 ***
<i>XNpb179</i> (11)	43	22	65	6.785 **
<i>C477</i> (11)	45	20	65	9.615 **
<i>R3202</i> (11)	42	23	65	5.554 *

1) AA: Number of plants with Taichung 65 / Taichung 65 genotype; Aa: Number of plants with Taichung 65 / *O. glaberrima* genotype.

2) *, **, ***: Significant at 5%, 1% and 0.1% levels, respectively.

Discussion

The linkage orders of the RFLP map constructed in the present experiment were in good agreement with those of the previous maps (Saito *et al.* 1991, Tsunematsu *et al.* 1996, Harushima *et al.* 1998), suggesting that the two species share almost the same chromosome constitution. The total map distance and the intervals between markers obtained from this interspecific cross were not so different from those from the previous intraspecific maps (Saito *et al.* 1991, Tsunematsu *et al.* 1996, Harushima *et al.* 1998), although Oka (1968) reported that preferential pairing of chromosomes could take place to a certain extent in a tetraploid hybrid between *O. sativa* and *O. glaberrima*. This mechanism of free recombination at the same level as intraspecific cross is advantageous to transfer genes from *O. glaberrima* to *O. sativa*.

Strong segregation distortion was observed in chromosome 6. At the *XNpb27* locus, less than 10% of BC1F1 plants were homozygotes for Taichung 65 alleles. In GIL production, the segregation distortion may cause a serious problem as it will be difficult to eliminate *O. glaberrima* alleles from this region.

In *O. sativa* x *O. glaberrima* crosses, a gamete eliminator, *S1*, was reported to be located in the *wx* region (between *XNpb209* and *XNpb27*) on chromosome 6 (Sano *et al.* 1979, Sano 1990). Sano (1990) reported that *S1* behaved a gene complex in

the hybrid. Detailed observation using molecular markers will be able to dissect this complicated loci. The loci showing segregation distortions found in chromosomes 4, 5 and 11 were less serious compared with those in chromosome 6 and therefore not critical for GIL production.

Previous RFLP maps of rice were constructed based on intraspecific crosses, interspecific backcross, and crosses using wild species other than the *O. sativa* section in the genus *Oryza*. The map presented here was based on a new mapping population derived from the cross between *O. sativa* and *O. glaberrima*. Covering the rice genome adequately, it could be used as a framework map for the construction of GILs.

Chapter II

QTL Analysis of Heading Date and Pollen Sterility Using Backcross Progenies between *Oryza sativa* L. and *O.* *glaberrima* Steud.

Introduction

Technique of QTL analysis is appropriate when used as a first survey for genetic analysis in those traits showing continuous variation. Another reason is that QTL analysis can accept phenotypic data that fundamentally contain environmental errors.

Heading date in rice was extensively studied. Major genes were found and summarized in Kinoshita *et al.* (1995). However, it was hardly possible to conduct detailed genetic analysis of the trait without molecular markers because many loci were involved in the trait.

On the other hand, when distantly related species were hybridized, various pre- and post-mating disorders are observed. Oka (1988) summarized post-mating barriers. Among them, F1 sterility is the most important hurdle to overcome in utilization of alien germplasm and hybrid rice breeding. Many loci causing hybrid sterility have been reported (for summary, Kinoshita 1995). Although F1 sterility is commonly found in *O. sativa* x *O. glaberrima* crosses (Yabuno 1977, Sano *et al.* 1979, Sano 1983,

1986, 1990), genetic information about the phenomenon was limited.

BC1F1 plants, used for construction of an RFLP linkage map described in Chapter I, were backcrossed with Taichung 65. In the derived BC2F1 population, large variation for male sterility and heading date was observed. The results of QTL analysis for these two traits are presented in this chapter.

Materials and Methods

Taichung 65 was used as a female parent in the initial cross so that all the progeny carried its cytoplasm. Succeeding backcrosses were performed using F1 or BC1F1 plants as the female parent and Taichung 65 as the pollen parent (Fig. 2). During the 1995 spring-summer season, ninety-nine BC2F1 plants (derived from 44 BC1F1 plants) were grown in pots and subjected to short-day treatment (9 h daylight and 15 h darkness) for 3 weeks (August 4 to August 25) at Kyushu University, Fukuoka, Japan. This treatment could synchronize the heading date of two parents.

These BC2F1 plants were genotyped for RFLP loci, and evaluated for heading date and pollen sterility. All the plants were also backcrossed with Taichung 65 for generating the GILs.

Heading date was recorded as the day when the first spikelet of the plant flowered. Pollen fertility, on the other hand,

was evaluated by observing anthers microscopically. Anthers were collected from spikelets on 1 to 2 days before anthesis and stored in 70% ethanol. Pollen fertility was estimated as the percentage of pollen grains that could be stained by acetic carmine. Pollen grains well stained and filled with the contents were determined as fertile.

QTLs were detected using the QGENE (Nelson 1997), a software for DNA-marker-based genetic analysis on Macintosh.

Results

Heading date and pollen fertility were determined in the BC2F1 population. Frequency distribution of these traits is shown in Figs. 4 and 5. Heading date of two parents were almost the same, and pollen fertility of them were normal. These data were combined with the RFLP genotype of each BC2F1 plant and loaded to the QGENE. The loci affecting these traits were estimated (Figs. 6 and 7) using the "Single-point" and "Interval" commands of the QGENE. Figures 6 and 7 were derived from "Multiplot" command.

On chromosomes 1, 6 and 10, significant ($< 1\%$) QTLs for heading were detected (Fig. 6). In the heterozygous condition, *O. glaberrima* alleles around the RFLP markers *C1211* (chromosome 1) and *XNpb27* (chromosome 6) delayed the heading by 5.5 and 7.8 days, respectively, while another *O.*

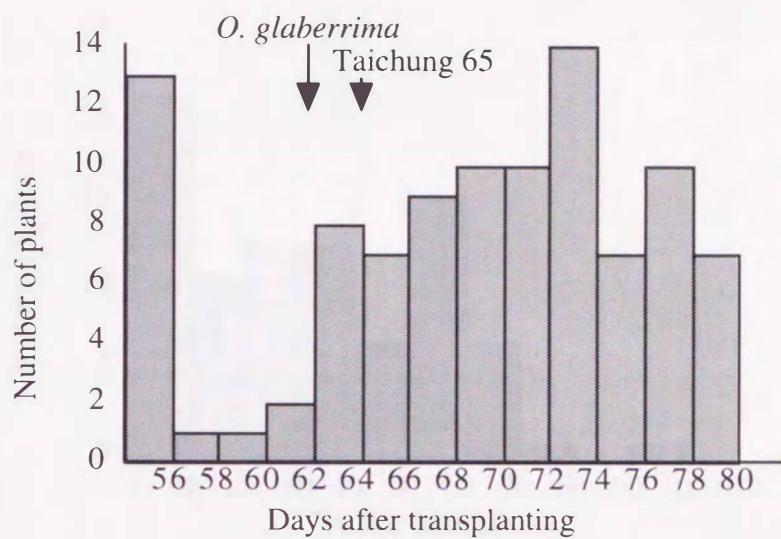


Fig. 4. Frequency distribution for heading in BC2F1 population of Taichung 65 / *O. glaberrima* (Acc. IRGC 104038) // Taichung 65 cross.

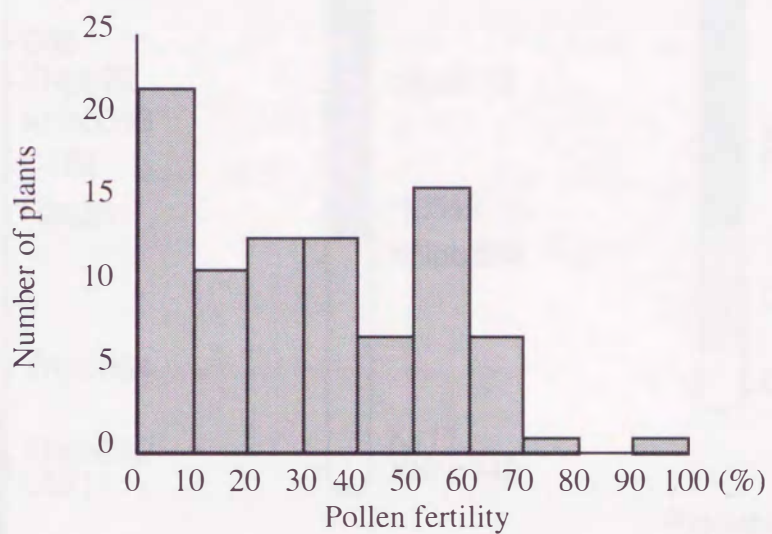


Fig. 5. Frequency distribution for pollen fertility in BC₂F₁ population of Taichung 65 / *O. glaberrima* (Acc. IRGC 104038) // Taichung 65 cross.

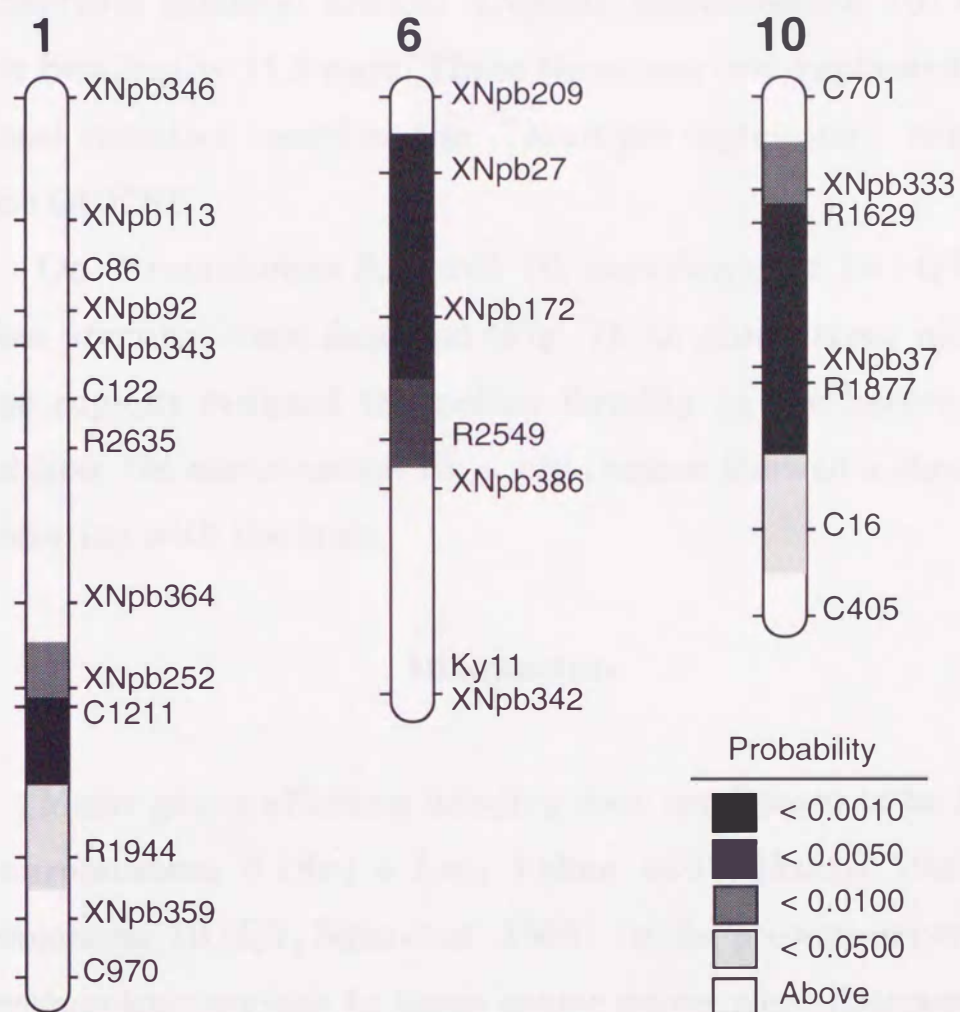


Fig. 6. Putative QTLs for heading detected in the BC2F1 population. Significant (< 1%) regions were detected on chromosomes 1, 6 and 10.

glaberrima allele(s) around *XNpb37* (chromosome 10) caused early heading by 11.2 days. These three markers explained 50.9% of total variation based on the "Multiple regression" command of the QGENE.

On chromosomes 3, 7 and 10, significant ($< 1\%$) QTLs for pollen sterility were detected (Fig. 7). *O. glaberrima* alleles in these regions reduced the pollen fertility in the heterozygous condition. On chromosome 10, a wide region showed a significant association with the trait.

Discussion

Major genes affecting heading date are known to be located on chromosome 6 (*Se1 = Lm*, Yokoo and Kikuchi 1982) and chromosome 10 (*Ef1*, Sato *et al.* 1988). In the present experiment, corresponding regions to these major genes were detected. This indicated that *O. glaberrima* carried loci for heading date similar to those observed within *O. sativa*. Presumably, only in the present interspecific cross combination a QTL for heading could be detected on chromosome 1. This implied that genetic variation of rice could be able to be extended using *O. glaberrima* as a genetic source.

Putative QTLs on chromosome 10 most significantly ($P < 0.001$) reduced pollen fertility. Yabuno (1977) reported the presence of some kinds of cytoplasmic-genic male sterile system

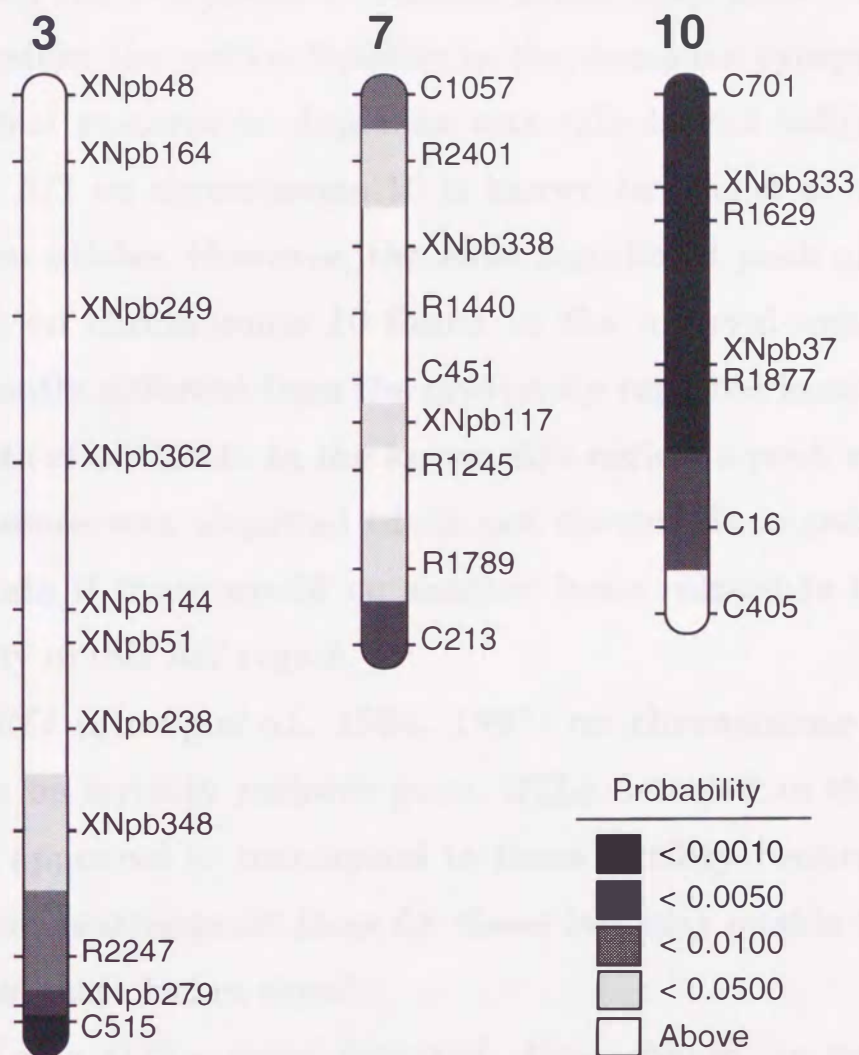


Fig. 7. Putative QTLs for pollen fertility detected in the BC₂F₁ population. Significant (< 1%) regions were detected on chromosomes 3, 7 and 10.

between the two species. Nuclear genes of *O. glaberrima* could not restore the pollen fertility in the Japonica cytoplasm. The strongest restorer in Japonica was called *Rfak* (= *Rfj*, Yabuno 1977). *Rf1* on chromosome 10 is known to consist of a series of restorer alleles. However, the most significant peak of the QTL region on chromosome 10 found in the interval analysis was apparently different from the previously reported location of *Rf1* (Fukuta *et al.* 1992). In the known *Rf1* region, a peak with lower LOD score was observed (data not shown). It is necessary to elucidate if there would be another locus related to the pollen sterility in this *Rf1* region.

Rf4 (Zhang *et al.* 1994, 1997) on chromosome 7 is also known as fertility restorer gene. QTLs detected in the present study appeared to correspond to these fertility restoration loci. GILs or near-isogenic lines for these loci may enable to further analyze these loci in detail.

Once QTLs were detected, they should be verified by different methods. These methods include those using simple, single-generation segregating populations as well as comparison between a series of overlapping introgression lines. Using genetically simplified segregating populations, two of the QTLs detected in this chapter were confirmed. These experiments were described in chapters IV and V.

Chapter III

Construction of a Series of Introgression Lines of *Oryza glaberrima* Steud. in *O. sativa* L.

Introduction

In the previous chapters, an RFLP linkage map based on the BC1F1 population was constructed and QTL analysis of heading date and pollen sterility was done using the BC2F1 population. The present chapter describes the construction of GILs.

Materials and Methods

Succeeding backcrosses were continued to BC3F1 generation. All backcross progeny were made using BCF1 plant as the female parent and Taichung 65 as the pollen parent (Fig. 2). DNA of 65 BC1F1 plants were extracted and used for RFLP mapping using 104 RFLP markers described in Chapter I. The same BC1F1 plants were backcrossed with Taichung 65. MAS throughout whole genome using 101 RFLP markers was continued in 99 BC2F1 plants and 80 BC3F1 plants. For fixed GILs, 907 plants from 45 BC3F2 lines from the selected BC3F1 plants were genotyped and MAS was conducted to make each line to carry homozygous introgressed chromosome segments

overlapping those of the next lines. Eighty eight candidate BC3F2 plants for GILs from 22 BC3F2 lines were selected. Two BC3F3 plants from a BC3F2 plant were harvested. In 1997, resulting 156 BC3F4 lines were grown. The genotypes of chromosomal regions which were heterozygous in the BC3F2 were determined in the BC3F4.

Results

High sterility observed in BCF1 populations

In the BC1F1 population, all plants were highly sterile, no selfed seeds being obtained. This high sterility was still observed in BC3F1s. One hundred and seventeen BC3F1 plants out of 281 were highly sterile. Spikelet fertility of BC3F2 plants derived from BC3F1 plants ranged from 0% to more than 80%. As a result, GILs were strongly selected for fertility.

Genome coverage of GILs

In the BC3F1 population, the average length of introgressed chromosome segments was 32.7 cM. Fig. 8 represents the introgressed chromosome segments in the GILs (for details, see Appendix). Most of the GILs had two or more introgressed chromosome segments from *O. glaberrima*, with an average of 3.4 segments. The average length of introgressed segments was 32.5 cM. In spite of high sterility in BC3F1, almost

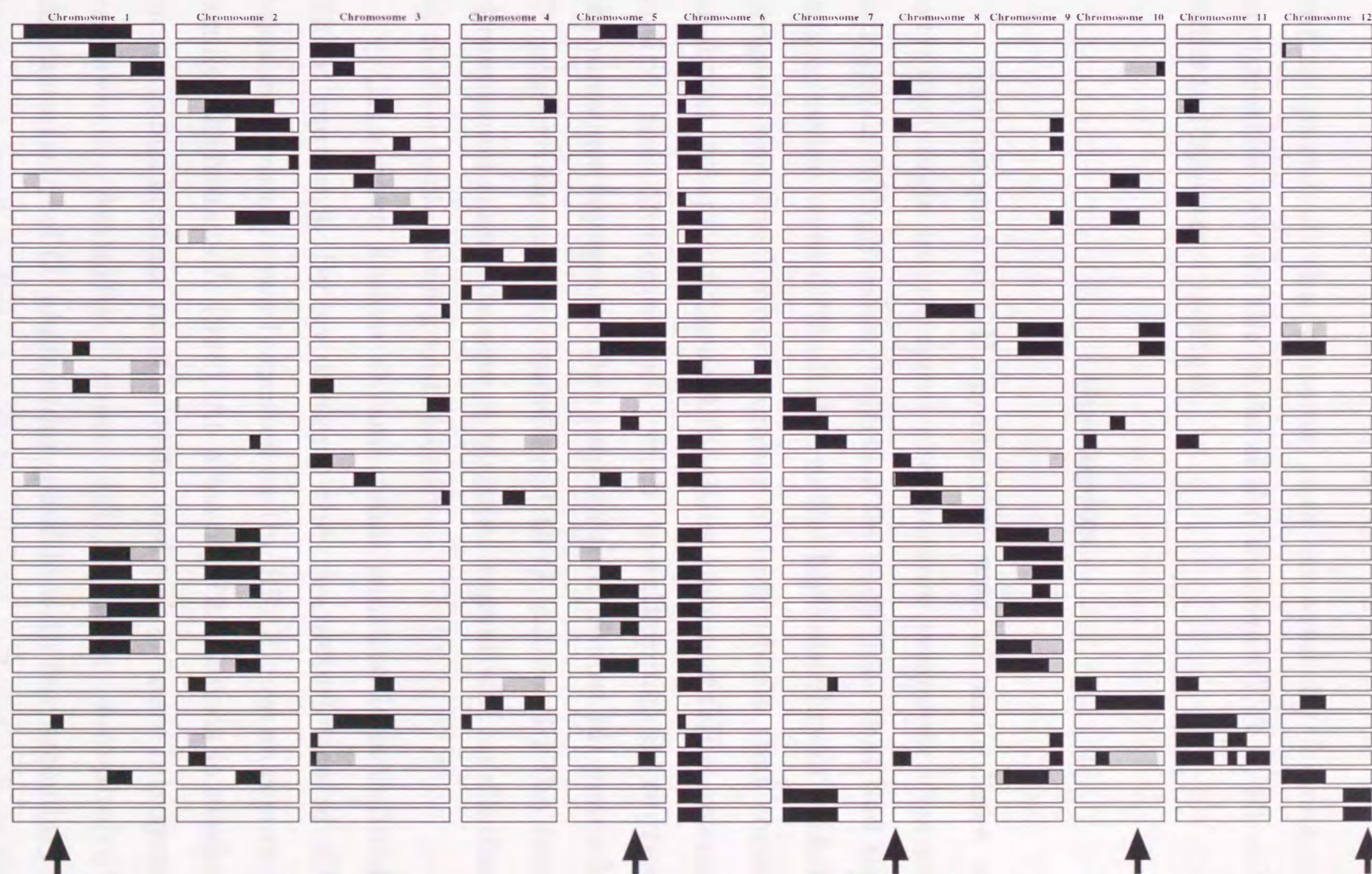


Fig. 8. Genotypes of *O. glaberrima* introgression lines. Only a sub-set (43 out of 156 plants) is presented to show coverage for the genome. The solid black, white and grey regions represent donor, recurrent and heterozygous segments, respectively. Arrows indicate chromosome regions which could not be covered in the present GILs.

entire parts of the genome was covered by homozygous introgression, except the parts of chromosomes 1, 5, 7, 10 and 12 indicated by arrows on Fig 8.

Discussion

Initial goal of GIL production was to make lines each carrying single introgressed chromosome segments that make contiguous introgression. Selection for such lines that had single introgression were difficult due to the high sterility of backcross progeny and the limited number of individuals that could be analyzed. In spite of these difficulties, obtained GILs covers the entire rice genome well with overlapping introgressed chromosome segments. This implies that almost all genes from *O. glaberrima* can be transferred to *O. sativa*. In the future, chromosome segments except targeted region will be eliminated by further backcrossing and selection.

GILs have known chromosomal constitutions defined by RFLP markers. By evaluating the characteristics of GILs, relevant genes are easily located on the RFLP map as reported in tomato (Eshed *et al.* 1996). At present, F2 analysis is needed to locate genes because most of GILs had two or more introgressed segments. Actually, some GILs have morphological characteristics of *O. glaberrima* (panicle with few secondary and tertiary branch, pubescence on leaves and spikelets, short ligule

etc.). Some of the non-*O. sativa*, non-*O. glaberrima* traits were observed only in hybrid progeny (seed shattering, awnness, spreading panicle branch etc.). F2 analysis of such characters are underway. However, expression of these traits were not distinct when compared with *O. glaberrima*, suggesting that the inheritance of these key characters of *O. glaberrima* were oligogenic or polygenic, *i.e.* controlled by QTLs. It was also difficult to find segregants with the typical key characters in early backcross generations as well as in F1s. Therefore, the key characters of *O. glaberrima* were controlled by mostly recessive QTLs.

Theoretically, when near-isogenic lines or ILs were used for QTL detection, increased numbers of replication were needed compared with the conventional way using RI or F2 populations (Kaepler 1997). For the initial detection of QTLs, QTL analysis using conventional mapping populations, especially recombinant inbred lines, are efficient. In spite of this limited statistical power of IL analysis, a series of ILs must be a powerful tool for QTL identification because of its uniform genetic background. However, in distant crosses as those made in the present study, high sterility prevents the utilization of F2 or recombinant inbred lines.

Results of QTL analysis using conventional generations can make researchers to identify putative QTLs, and the QTL analysis as a initial survey for relatively major QTLs make it

easier to find minor QTLs through the backcross-selfing cycles during construction of ILs. When QTLs for the trait of interest could be both dominant and recessive like the key characters of *O. glaberrima* in the present study, QTL analysis using a population backcrossed with the donor parent would be also efficient to identify QTLs, although this goes against the paradigm of IL analysis that integrates QTL analysis with isogenic line breeding. Whether such as "opposite" backcross QTL analysis was possible or not, results of QTL analysis may provide important information for detailed analysis of quantitative traits.

In the present study, MAS was performed in all the backcross generations. This monitoring will help to minimize the occurrence of very small unexpected introgressions that is difficult to detect in later generations. In spite of this advantage, however, following alternative method is proposed as an approach to produce a series of introgression lines:

- 1) Backcross continuously until BC4F1 or BC5F1 generation
- 2) then select the plants with one or two introgressed (donor) chromosome segment(s) from the large BCF1 population as far as possible and
- 3) select the plants carrying homozygous target segments from the selfed progeny of the selected BCF1 plants.

Presumably this method leads to more "isogenic" introgression lines and is totally more efficient. Moreover, if a trait of interest segregates in the progeny of step 3), it can be easily identified

and mapped as a single Mendelian factor. It is expected that even minor QTLs can be detected in the backcrossed progeny as reported by the group of RGP (Yamamoto *et al.* 1996, Shimizu *et al.* 1997).

On chromosome 6, a gamete eliminator locus, *S1*, was reported (Sano *et al.* 1979, Sano 1990). It causes abortion of gametes carrying allele from *O. sativa*, resulting transmission of only gametes carrying allele from *O. glaberrima*. This gene was involved in the present cross combination. In the region between *XNpb209* and *XNpb27*, more than 70 lines out of 156 were fixed with chromosome segments from *O. glaberrima*.

Since the waxy (*wx*) locus was closely linked to *S1* (2.4% to 3.4%, Sano *et al.* 1990), *wx* could have been used as a selective marker for the fixation of an *O. sativa* allele. Because of high frequency of *S1*, it is hardly possible to eliminate the *O. glaberrima* allele from this region without using large F₂ populations. PCR-based markers will enable to select plants with favorable genotypes in the seedling stage. This marker system will be discussed later.

In rice, many loci concerning sterility has been reported (for review, Kinoshita *et al.* 1995). Hybrid sterility between two cultivated rice involves both genic (Sano *et al.* 1979, Sano 1990) and cytoplasmic-genic (Yabuno 1977) sterility. Previous QTL analysis using the BC₂F₁ population described in Chapter II revealed some chromosome regions related to the pollen sterility.

GILs for the region between *XNpb333* and *R1629* (chromosome 10), and between *R1245* and *C213* (chromosome 7) could not be obtained due to sterility. Presumably pollen sterility loci in these regions also caused spikelet sterility and this fact supported the results of the previous QTL analysis. *S1* and QTLs detected in Chapter II as well as other undetected minor sterility loci including duplicate gametic lethals (Oka 1974) would account for the high sterility observed in BCF1 populations. When the *S1* allele from *O. glaberrima* included in many backcrossed progeny was combined with other pollen sterility genes, anthesis was presumably prevented in the plant, resulting in spikelet sterility.

GILs for the regions between *XNpb346* and *XNpb113* (chromosome 1), *R3166* and *G260* (Chromosome 5) and *R3375* and *XNpb402* (Chromosome 12) were not obtained. These regions were certainly segregated in BC3F2 populations, although homozygous plants could not be selected. *O. glaberrima* alleles of these regions were eliminated by selfing followed. Segregation distortion or sterility caused by recessive allele(s) from *O. glaberrima*, including the delay of heading or the hybrid weakness, were presumed to be the cause of these hybrid breakdown. It needs further confirmation to reveal why this region could not be introgressed. By going back to earlier generation before selfing, these phenomena will be verified.

The authors employed the RFLP marker system, which is the most reliable choice currently available in rice, but more

laborious than the PCR-based marker system. A high-throughput system of genetic marker analysis is essential. Ghesqui re *et al.* (1997) emphasized the need for PCR-based markers. One of the most promising marker systems, microsatellite markers (SSR / SSLP), is currently developed in rice (McCouch *et al.* 1997), but it is still insufficient. The International Rice Genome Sequencing Project (<http://www.staff.or.jp/rgp/News/Newsletter.html>) will greatly facilitate the development of genetic markers.

As a genetic resource for rice breeding, *O. glaberrima* had not been used extensively. Recently similar projects as the present study are initiated by researchers of France (Ghesqui re *et al.* 1997) and C te d'Ivoire (Jones *et al.* 1997). *O. glaberrima* has potential for increasing rice yield especially under low-input conditions (Ghesqui re *et al.* 1997). Systematically produced GILs are useful to exploit fully the genetic potential of *O. glaberrima*.

For realization of rice genetics, a series of introgression lines will provide good genetic materials. They will provide materials for "library" for phenotypic selection and multilocal evaluations that enable direct correspondence of the QTL to the trait. Involved genes were conventionally located by comparison between lines carrying overlapping introgressed segments. Recombinants with small introgression (*i.e.* near-isogenic lines) can be obtained by a few additional backcrosses. GILs also provide the ideal materials for studying epistasis

between identified genes or QTLs. As such materials for rice genetics and breeding, developed GILs will be distributed to any interested institution.

Introduction

Following a QTL analysis, fine mapping of QTLs is needed for MAS or map-based cloning of identified QTLs. However, due to limited available power of QTL analysis, an identified QTL is not located on a precise map position, but in a chromosome region. Fine mapping of a QTL and isolation of QTLs in the putative candidate region is a task of considerable difficulty with mapping of quantitative traits.

QTL analysis in the IR29 population revealed three QTLs for heading date on chromosomes 1, 5 and 10. In this study, the QTL on chromosome 10 was targeted as a single Mendelian locus. The QTL on chromosome 10 was mapped as a single Mendelian locus.

Materials and Methods

Yield, panicle length, panicle weight, heading date were identified using the IR29 population. The weather conditions and three times sowing were made and a BILF4 plant QTLF4 was developed for the panicle length of the QTL for heading date on chromosome 10. The QTL for heading date on chromosome 10 was mapped as a single Mendelian locus.

Chapter IV

RFLP Mapping of a QTL for Heading Date Found on Chromosome 10

Introduction

Following a QTL analysis, fine mapping of QTLs is needed for MAS or map-based cloning of identified QTLs. However, due to limited statistical power of QTL analysis, an identified QTL is not located on a precise map position, but in a chromosome region. Precise map position of a QTL and number of QTLs in the putative chromosome region is still uncertain when compared with mapping of qualitative traits.

QTL analysis in the BC2F1 population revealed three QTLs for heading date on chromosomes 1, 6 and 10. In this chapter, the QTL on chromosome 10 were mapped as a single Mendelian factor.

Materials and Methods

Three putative QTL regions for heading date were identified using the BC2F1 population. Then another backcrossing and three times selfing were made and a BC3F4 plant (BC3F4 151) heterozygous for the putative region of the QTL for heading date on chromosome 10 (hereafter referred to as

Ef(t)) was selected using RFLP markers (*XNpb37*, *R1877*, *C16*) (Fig. 2). Its selfed progeny, the BC3F5 population consisting of 147 plants, were used as the mapping population of *Ef(t)*. The seeds of the mapping population were sown on December 11, 1997, and the seedlings were transplanted on January 1, 1998, at the International Rice Research Institute, Los Baños, Philippines.

Results

Graphical genotype of the BC3F4 plant (BC3F4 151) which was the parent of the mapping population was shown in Fig. 9. Putative region of *Ef(t)* was heterozygous. Although there were another heterozygous region in chromosome 11, and *O. glaberrima* homozygous regions in chromosomes 6, 9 and 11, these regions did not affect the *Ef(t)* mapping.

The frequency distribution of heading date in the BC3F5 mapping population was shown in Fig. 10. A bimodal distribution was observed. Early-heading (60-67 days to heading (DTH)) plants and late heading (69-84 DTH) plants segregated in a ratio of 105 : 42, fitting the expected 3 : 1 ratio ($\chi^2 = 1.000$, $p = 0.32$).

Linkage analysis with RFLP markers revealed that this segregation of heading date was controlled by a major gene that was very tightly linked to *C1369*. Two flanking markers, *C234* and *XNpb37*, were located on the opposite sides of *Ef(t)* with map

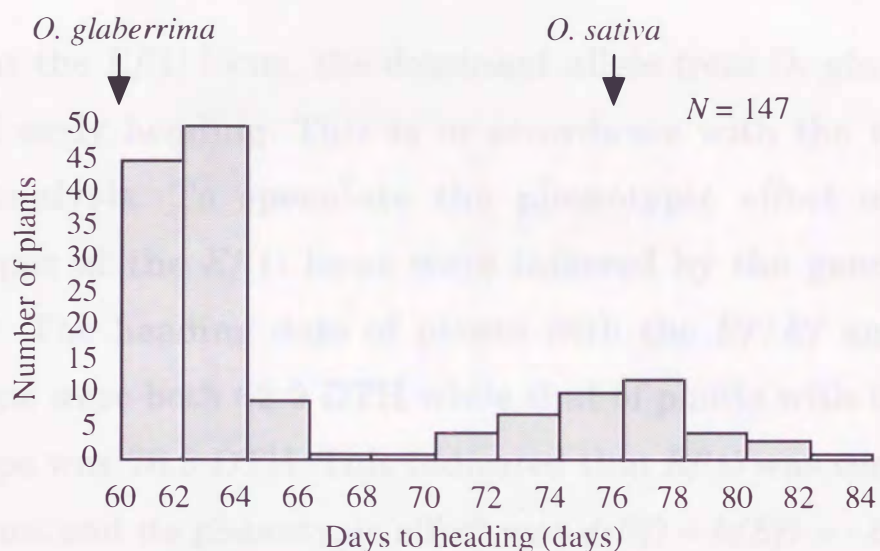


Fig. 10. Frequency distribution of days to heading in the *Ef(t)* segregating population.

distances of 0.3 cM and 0.7 cM, respectively (Fig. 11).

Discussion

At the *Ef(t)* locus, the dominant allele from *O. glaberrima* caused early heading. This is in accordance with the result of QTL analysis. To speculate the phenotypic effect of *Ef(t)*, genotypes at the *Ef(t)* locus were inferred by the genotype at *C1369*. The heading date of plants with the *Ef/Ef* and *Ef/ef* genotype were both 62.9 DTH while that of plants with the *ef/ef* genotype was 76.3 DTH. This indicated that *Ef(t)* was completely dominant and its phenotypic effect was $d(Ef) = h(Ef) = -6.7$ DTH under the conditions of the present experiment.

Characteristics of loci for heading date, especially reaction to day length should be of interest. On the other hand, repeated trials will increase the estimation accuracy of the effects of QTLs. GILs or near-isogenic lines of identified QTLs are helpful in such experiments that need repeated trials or trials in different environments.

Many populations planted during the construction of GILs segregated for heading date. This implied that there were many minor QTLs for heading. The group of Rice Genome Research Program (Yamamoto *et al.* 1996, Shimizu *et al.* 1997) found some additional QTLs for heading after the QTL analysis in the F₂ population. They identified only 5 QTLs in the initial F₂

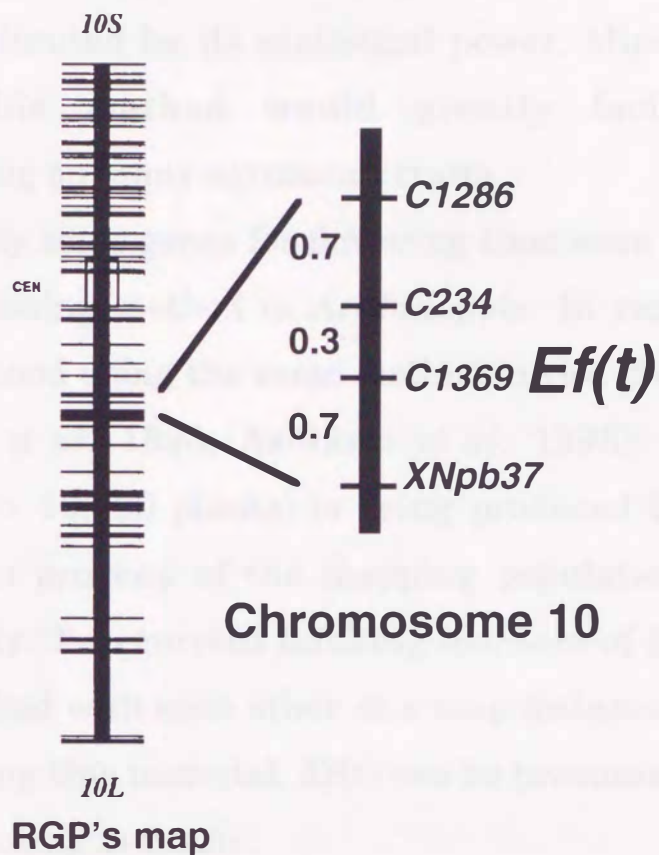


Fig. 11. RFLP linkage map of rice chromosome 10 showing the location of *Ef(t)*. Left vertical bar shows the RGP's RFLP linkage map (Harushima *et al.* 1998).

population (Yano *et al.* 1997). However, 5 additional QTLs were found and mapped as Mendelian factors by repeated backcrossing - selfing cycles. This isogenic-line approach to identify QTLs is supplemental for QTL analysis whose resolution tends to be limited by its statistical power. Minor QTLs found through this method would greatly facilitate better understanding on many agronomic traits.

Recently some genes for flowering time were isolated by the positional cloning method in *Arabidopsis*. In rice, some genes were also cloned using the same method in rice (Song *et al.* 1995, Yoshimura *et al.* 1998, Ashikari *et al.* 1998). Fine-mapping population (> 10,000 plants) is being produced from the *Ef(t)*-heterozygous progeny of the mapping population used in the present study. Two current flanking markers of *Ef(t)*, *C234* and *XNpb37*, linked with each other at a map distance of 1.1 cM (see Fig. 11). Using this material, *Ef(t)* can be presumably isolated by positional cloning in future.

Chapter V

A New Locus Causing High F1 Pollen Sterility Found in Backcross Progeny between *Oryza sativa* L. and *O.* *glaberrima* Steud.

Introduction

Hybrids between *O. sativa* and *O. glaberrima* generally show male-sterility. Oka (1968) reported preferential pairing of homoeologous chromosomes in meiosis of induced tetraploid F1 plants, suggesting that this chromosomal differentiation was related to the sterility. Sano *et al.* (1979; 1983) identified hybrid sterility loci, *S1*, *S2* and *S3* in *O. sativa* x *O. glaberrima* crosses. They caused selective abortion of gametes, *S1* and *S2* affects both male and female gametes while *S3* was a pollen killer. Yabuno (1977) reported that the combination of Japonica (*O. sativa*) cytoplasm and nucleus of *O. glaberrima* produced male sterility. *Rfj* (*Rfak*) was responsible for the full restoration of pollen fertility.

QTL analysis using BC2F1 population detected some loci for pollen sterility as described in Chapter II. The identification of one of the QTLs detected on chromosome 10 (referred to as *S(t)* hereafter) is described in this chapter.

Materials and Methods

Further backcrossing with Taichung 65 was continued after the QTL analysis. BC5F1 plants heterozygous for putative *S(t)* region of chromosome 10 were selected using RFLP markers (*XNpb333*, *R1629*, *R1877* and *XNpb37*) and they were backcrossed with Taichung 65. The resulting BC6F1 population consisting of 57 plants was used as a mapping population (Fig. 2). Flowering spikelets were collected from all plants and stored in 70% ethanol. Pollen fertility was estimated as the percentage of pollen grains that could be stained by the iodostarch reaction.

Results

The mapping population was classified into three groups with discrete pollen fertility; high-sterile (pollen fertility was 0-20%), semi-sterile (40-70%) and fertile (80-100%) (Fig. 12). The numbers of plants in these groups were 28, 23 and 6, respectively (Fig. 13).

When the mapping population was divided into two groups: high-sterile group and semi-sterile plus fertile group, the observed segregation of 28 : 29 fit the expected monogenic ratio of 1 : 1. Linkage analysis using RFLP markers revealed that *S(t)* was located between *G1084* and *R1629* of chromosome 10 (Fig. 14).

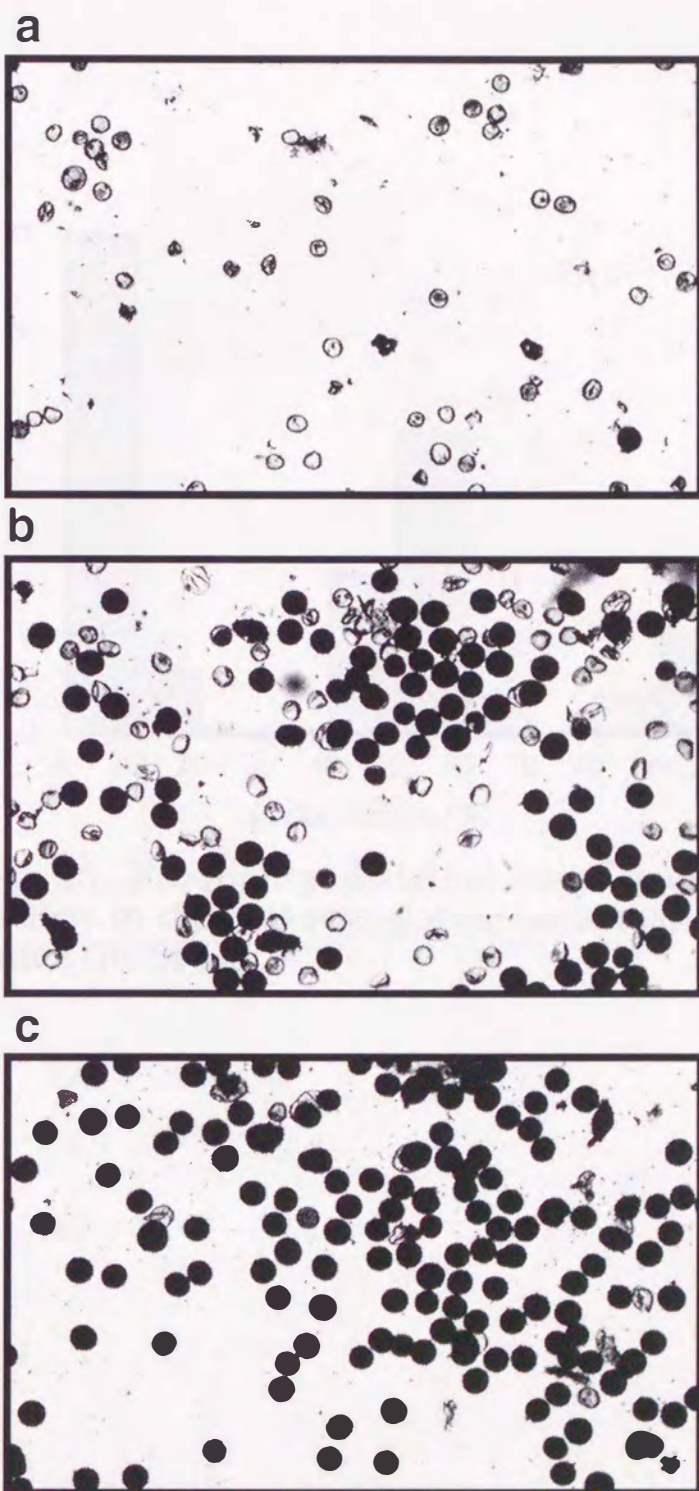


Fig. 12. Pollen grains stained by the iodostarch reaction. The $S(t)$ mapping population segregated into three groups with discrete pollen fertility, high-sterile (a), semi-sterile (b) and fertile (c) groups.

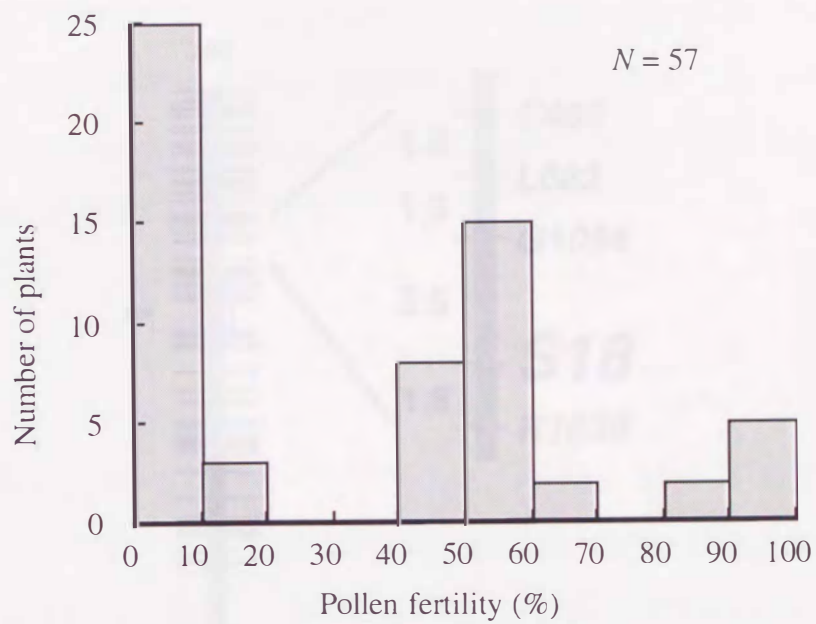


Fig. 13. Frequency distribution of pollen fertility in the $S(t)$ -segregating backcross F1 plants (BC6F1).

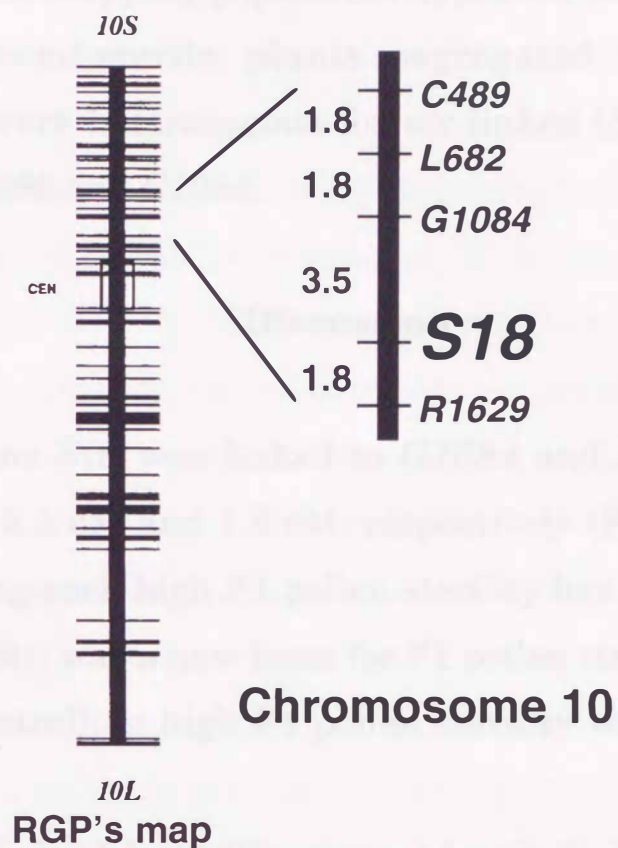


Fig. 14. RFLP linkage map of rice chromosome 10 showing the location of *S18*. Left vertical bar shows the RGP's RFLP linkage map (Harushima *et al.* 1998).

Since a strong segregation distortion towards the *O. glaberrima* allele was observed around the *S1* (Sano 1990) region on chromosome 6 in the BC1F1 and BC2F1 populations, semi-sterility in the mapping population appeared to be due to the *S1* locus. All semi-sterile plants segregated in the present population were heterozygous for *wx*-linked (*S1* region) RFLP markers, *C1496* and *C1084*.

Discussion

The gene *S(t)* was linked to *G1084* and *R1629* with map distances of 3.5 cM and 1.8 cM, respectively (Fig. 14). Since no locus affecting such high F1 pollen sterility has been reported in this region, *S(t)* was a new locus for F1 pollen sterility. Therefore, this gene controlling high F1 pollen sterility was designated as *S18*.

Most of rice F1 sterility caused by single locus were either sporo-gametephytic interaction type (sterile plants show semi-sterility, Oka 1974) or cytoplasmic-male-sterility type (summarized in Virmani and Shinjo 1995). Most of these sterility loci caused semi-sterility. *S18* that causes high F1 pollen sterility in heterozygous condition is unique when considering genetic models of F1 sterility (Oka 1974).

Sano (1979, 1990) reported the F1 sterility locus *S1*. It was found as a locus causing semi-sterility in the progeny from the

cross between *O. sativa* and *O. glaberrima* and tightly linked to the *wx* locus. In the mapping population used in this experiment, *S1* locus still segregated. This made the evaluation of the phenotypic effect of *S18* uncertain. In the high-sterile group, 5 plants out of 28 were homozygous for *S1* region. Pollen fertility of 4 plants out of these 5 plants were 0%, and that of the remaining one plant was 9.7%. High-sterile plants other than these 5 plants showed pollen sterility ranging from 0% to 15.7%. This implies that there was no non-allelic interaction between *S1* and *S18*. However, the level of pollen sterility caused by *S18* should be verified by using a new population without segregation of *S1*.

To identify other pollen sterility loci found in the QTL analysis in the BC₂F₁ population, near-isogenic lines for these sterility loci were already produced by using MAS. Understanding of mechanism of hybrid sterility leads to overcome the reproductive barrier. It is essential for utilizing alien germplasm and breeding high-potential hybrid rice variety.

Summary and Conclusion

To exploit fully the genetic potential of African rice, *Oryza glaberrima* Steud., a series of *O. glaberrima* introgression lines (GILs) in the background of Japonica rice (*O. sativa* L. cv. Taichung 65) was constructed.

As a first step, an RFLP linkage map based on the backcross population (BC1F1) was constructed. It contained 101 well-dispersed RFLP markers. The total map length was 1403.4 cM. This map could be used for the construction of GILs, as it covered the rice genome adequately.

Linkage arrangement of the RFLP markers was in good agreement with that of the previously constructed maps, suggesting that there was no drastic chromosomal differentiation between two cultivated rice species. Since chromosomal rearrangements theoretically cause sterility of various levels, GILs will help to find such small changes although it is very difficult to determine if there are very small linkage rearrangements or not. Recent spreading of large insert genomic libraries may help to prove this question discussed for years.

Significant segregation distortions were observed in chromosomes 4, 5, 6 and 11. In chromosome 6, a strong distortion towards *O. glaberrima* was found. The *S1* locus was thought to be the main cause of this distortion and it was very difficult to eliminate *O. glaberrima* allele(s) from this region in the

construction of GILs. A distorted region on chromosome 5 could not be introgressed to GILs, while regions on chromosomes 4 and 11 were successfully introgressed, proving the effectiveness of MAS.

In the BC2F1 population, QTLs for two quantitative traits, heading date and pollen fertility, were investigated. On chromosomes 1, 6 and 10, significant ($< 1\%$) QTLs for heading were detected. In the heterozygous condition, *O. glaberrima* alleles around the RFLP markers *C1211* (chromosome 1) and *XNpb27* (chromosome 6) delayed heading, while another *O. glaberrima* allele(s) around *XNpb37* (chromosome 10) caused early heading. On chromosomes 3, 7 and 10, significant ($< 1\%$) QTLs for pollen sterility were detected. *O. glaberrima* allele(s) in these regions reduced the pollen fertility in the heterozygous condition. On chromosome 10, a wide region showed a significant association with the trait, suggesting the presence of a strong male-sterility gene.

Succeeding backcrosses were continued to the BC3F1 and GILs were selected from 907 BC3F2 plants. Genotypes of heterozygous regions were determined in the BC3F4 generation. Constructed 156 GILs cover *O. glaberrima* genome well with homozygous overlapping introgressed chromosome segments, in spite of high sterility observed in the BC3F1 plants. Some GILs showed the characteristics of *O. glaberrima* to a certain extent and F2 analysis of these characters will be possible. However, it was impossible to find lines clearly showing typical *O. glaberrima*

phenotype. This implied that two or more QTLs controlled key characters of *O. glaberrima* such as few secondary panicle branch or short rounded ligule. It was also difficult to find segregants with the typical key characters in early backcross generations as well as F1s. It was revealed that recessive minor QTLs were controlling these characters

Due to the *S1* locus causing abortion of gametes carrying *O. sativa* allele, more than 70 GILs were fixed with the *O. glaberrima* allele in the *S1* region on chromosome 6. Because of high frequency of *S1*, it was hardly possible to eliminate the *O. glaberrima* allele from this region without using large F2 populations. PCR-based markers will enable to select plants with favorable genotypes in seedling stage. GILs for regions of chromosomes 7 and 10 were not obtained due to F1 sterility and GILs for the regions in chromosomes 1, 6 and 12 were also not available by unknown reasons.

In contrast to the key characters of *O. glaberrima*, two QTLs for two agronomically important characters were located onto the RFLP map using genetically simplified populations. A QTL for heading date on chromosome 10 was located between RFLP markers *C234* and *XNpb37*, using a BC3F5 segregating population consisting of 147 plants. On the other hand, using 57 BC6F1 plants segregating pollen sterility, a new locus causing high pollen sterility, *S18*, was identified between RFLP markers *G1084* and *R1629* on chromosome 10.

Results of the QTL analysis were very informative when the identification of the loci for heading and pollen fertility was concerned. The capability of the combination of QTL analysis and MAS enabled by molecular markers was confirmed through the present experiments. Using information of the QTL analysis as "navigator", relatively major QTLs were easily identified. On the other hand, loci controlling the key characters of *O. glaberrima* were difficult to identify from the observation of GILs. This implied that the inheritance of these key characters of *O. glaberrima* was oligogenic or polygenic. It was also difficult to find segregants with the typical key characters in early backcross generations as well as F1s. Recessive minor genes controlling these characters are difficult to identify with the breeding scheme of the present study. The reciprocal backcross QTL analysis was proposed to overcome this difficulty.

In addition to breeding strategy of experimental populations, establishment of systems to evaluate quantitatively the characters of interest will be essential in the future genetic analysis of quantitative traits. Once an evaluating system was established, the power of molecular markers will greatly facilitate the genetic analysis of quantitative traits as indicated for the cases of heading date and pollen fertility in the present study.

Although the inheritance of the key characters of *O. glaberrima* was complicated and could not be fully realized, a series of GILs was constructed and some loci for important

characters were identified. A series of GILs is expected to be used as breeding materials fully exploiting *O. glaberrima* as a genetic source, library for phenotypic selection and materials for studying epistasis.

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Appendix 1. RFLP genotypes and phenotypes of the BC2F1 plants used for the QTL analysis described in Chapter II.

BC2F1#	Genotypes ¹⁾										Chromosome 2										Chromosome 3													
	Chromosome 1										Chromosome 2										Chromosome 3													
	X346	X113	C86	X343	C122	R2635	X364	X252	C1211	R1944	X359	C970	C1221	C560	R3393	X45	C499	R1843	X21	X227	G1327	R2510	X48	X164	X249	X362	X144	X238	X348	R2247	X279	C515		
BC2F1 3	1	1	1	1	1	1	1	1	1	1	1	1	3	3	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		
BC2F1 4	1	1	1	1	1	1	1	1	3	3	1	1	3	3	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		
BC2F1 5	1	3	3	1	1	1	1	1	1	1	1	1	1	1	1	1	3	3	0	3	3	0	3	3	3	3	1	1	1	1	3	3	3	
BC2F1 6	1	1	1	1	3	3	1	1	1	1	3	0	3	1	1	1	1	1	1	1	1	1	1	3	3	1	1	1	1	1	3	3	3	
BC2F1 7	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	3	3	1	1	1	1	1	3	3	3	1	1	1	1	1	1	
BC2F1 8	3	3	3	3	1	1	1	1	1	3	3	3	1	1	1	1	1	1	1	1	1	1	1	1	3	3	3	3	1	1	1	1	1	
BC2F1 9	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	3	3	3	1	1	1	1	1	1	1	1	1	1	1	
BC2F1 10	1	1	1	1	1	3	3	3	3	3	3	1	1	1	3	3	3	3	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
BC2F1 11	1	3	1	1	1	1	1	3	3	3	3	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	
BC2F1 12	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	3	3	3	3	3	3	3	3	3	1	1	1	1	1	1	
BC2F1 13	1	1	1	1	1	1	1	1	1	1	1	1	3	3	3	1	1	1	1	1	1	1	1	1	3	3	1	1	1	1	1	1	1	
BC2F1 14	1	1	1	1	0	3	3	3	3	1	1	1	0	3	3	0	3	3	3	3	0	1	1	1	1	1	1	1	1	1	1	1	0	
BC2F1 15	1	1	1	1	1	0	3	3	3	1	1	1	0	3	3	0	3	3	1	1	0	1	1	1	1	1	1	1	1	1	1	1	0	
BC2F1 16	1	1	1	1	1	1	1	1	3	3	3	1	3	3	3	1	1	3	3	3	1	1	1	1	1	1	1	1	1	1	1	1	1	
BC2F1 17	1	1	1	1	0	1	1	1	1	1	1	1	0	1	1	0	1	1	1	3	0	1	1	1	1	0	1	1	1	1	1	1	0	
BC2F1 18	1	3	1	1	1	1	1	1	1	3	3	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	
BC2F1 19	1	1	1	1	1	1	1	1	3	3	3	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	3	3	3	3	
BC2F1 20	1	1	1	1	1	0	1	1	1	1	3	1	0	1	1	0	3	1	1	1	0	1	1	1	1	1	1	1	1	1	1	3	3	
BC2F1 21	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	3	3	3	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	
BC2F1 22	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	3	3	0	3	1	1	1	1	1	1	1	3	1	1	1	1	1	1	
BC2F1 23	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	3	3	3	
BC2F1 24	1	1	1	1	1	1	1	1	1	1	1	1	0	3	3	0	1	1	1	1	0	1	1	3	3	3	1	1	3	1	1	1	0	
BC2F1 25	3	3	3	3	3	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
BC2F1 26	3	3	3	3	3	3	3	3	3	3	3	1	1	1	1	3	3	3	3	3	3	3	3	1	1	1	1	1	1	1	1	1	1	
BC2F1 27	1	1	1	1	1	1	1	1	3	1	3	1	1	1	1	1	1	1	3	1	1	1	1	1	1	3	3	1	1	1	3	3	3	
BC2F1 28	3	3	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	3	3	1	3	3	3	3	3	
BC2F1 29	1	3	1	1	1	3	3	3	3	1	1	1	3	3	3	1	1	1	1	1	1	1	1	1	3	1	1	3	3	3	3	3	3	
BC2F1 30	1	1	1	1	1	1	3	3	3	1	1	1	3	3	3	3	3	3	3	3	1	1	1	1	1	3	3	3	3	3	3	3	3	
BC2F1 31	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
BC2F1 32	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	3	1	1	1	1	1	1	
BC2F1 33	1	1	1	1	1	1	1	1	1	1	0	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	3	1	1	1	1	1	
BC2F1 34	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	3	
BC2F1 35	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	3	3	1	1	1	1	1	1	1	1	
BC2F1 36	1	1	1	1	1	1	1	1	1	3	3	3	1	1	1	1	1	1	3	3	3	3	3	1	1	1	1	1	1	1	1	1	1	
BC2F1 37	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	3	1	1	1	3	3	1	1	1	1	1	3	1	3	
BC2F1 38	1	1	1	1	1	1	1	1	1	3	3	3	1	1	1	0	1	1	1	1	1	1	1	3	3	1	1	1	1	1	1	1	1	
BC2F1 39	1	1	1	1	1	1	1	1	1	3	3	3	1	1	1	0	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	
BC2F1 40	1	1	1	1	0	1	1	1	1	1	1	1	0	1	1	0	0	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	0	
BC2F1 41	1	1	1	1	1	1	1	3	0	3	3	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
BC2F1 42	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	3	1	1	1	1	1	1	1	1	1	1	1	1	3	3	3	3	
BC2F1 43	1	3	3	0	1	1	1	1	1	1	1	3	1	1	1	3	3	1	1	1	1	1	1	1	1	1	1	1	1	3	3	3	3	
BC2F1 44	3	3	0	0	1	1	1	1	1	1	1	3	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
BC2F1 45	1	1	1	1	1	1	1	1	1	1	1	1	3	3	0	3	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	
BC2F1 46	1	1	1	1	1	1	1	1	1	1	1	1	3	3	3	1	1	1	1	1	1	1	1	1	1	1	3	3	3	3	3	3	3	
BC2F1 47	1	1	1	1	1	1	1	1	3	3	3	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
BC2F1 48	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	3	3	3	3	3	3	1	1	1	1	3	3	1	0	1	1	
BC2F1 49	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	3	3	3	1	1	1	1	1	1	1	1	1	3	3	1	1	1	1	
BC2F1 50	1	1	1	1	1	1	1	1	1	0	1	1	1	1	3	3	3	3	1	1	1	1	1	3	3	1	1	1	1	1	1	1	1	
BC2F1 51	1	1	1	1	1	1	1	1	1	0	0	1	1	3	1	1	1	0	3	1	1	1	1	1	1	1	1	1	3	1	1	1	1	
BC2F1 52	1	1	1	1	1	0	3	1	1	0	0	1	1	1	1	1	0	1	3	0	3	1	1	1	1	1	1	3	3	1	1	1	0	
BC2F1 53	1	1	1	1	3	3	3	3	3	0	3	3	1	1	1	1	0	1	1	1	1	1	1	3	3	3	1	1	1	1	1	1	1	
BC2F1 54	1	1	1	1	1	1	1	1	1	1	1	1	3	3	1	1	0	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	
BC2F1 55	1	1	1	1	1	1	1	1	1	3	3	3	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	
BC2F1 56	1	1	1	1</																														

Appendix 1. (Continued)

Genotypes ¹⁾		Chromosome 4					Chromosome 5					Chromosome 6					Chromosome 7					Chromosome 8													
BC2F1#	C445	Q4	X331	X311	X237	X247	X292	R3166	G260	X105	X255	X297	X209	X27	X172	R2549	X386	Q11	C1057	R2401	R1440	C451	X117	R1245	R1789	C213	X397	X56	G1073	R1394A	C1107	X41	X278		
BC2F1 3	3	1	1	1	1	1	1	1	1	1	1	1	3	3	3	3	3	1	1	1	3	3	3	3	1	1	3	3	1	1	1	1	1		
BC2F1 4	3	1	1	1	1	1	3	1	1	1	1	1	3	3	3	3	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	3		
BC2F1 5	1	1	1	1	1	1	1	1	1	1	1	1	3	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		
BC2F1 6	1	1	1	1	1	1	1	1	1	1	1	1	3	3	3	3	3	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		
BC2F1 7	3	3	1	1	1	1	1	1	1	1	1	1	3	3	1	1	1	1	1	1	3	3	3	3	3	3	1	1	1	1	1	1	1		
BC2F1 8	3	3	1	1	3	3	3	3	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	3	
BC2F1 9	1	3	3	1	1	3	1	1	1	1	1	1	3	3	3	3	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
BC2F1 10	1	1	1	1	1	1	1	3	3	3	1	1	3	3	1	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	0	1	1	
BC2F1 11	1	1	1	1	1	1	1	1	1	1	1	1	3	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
BC2F1 12	1	1	1	1	3	3	1	1	1	1	1	1	3	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
BC2F1 13	1	1	1	1	3	1	1	1	1	1	1	1	3	3	1	1	3	1	1	3	3	3	3	1	1	1	1	1	1	1	1	1	1	1	
BC2F1 14	1	1	1	1	1	0	3	3	3	0	3	3	3	3	1	1	1	1	1	1	0	0	1	1	1	1	0	3	3	1	1	3	3	3	
BC2F1 15	1	1	1	1	1	0	1	1	1	0	1	1	3	3	3	1	1	1	1	1	0	0	1	1	1	1	1	3	3	1	1	1	1	1	
BC2F1 16	1	1	1	1	1	1	3	1	1	1	1	3	3	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
BC2F1 17	1	1	1	1	1	0	3	3	1	0	3	3	3	3	0	1	0	1	1	0	0	1	1	1	1	1	1	1	1	1	1	3	3	3	
BC2F1 18	1	3	1	1	1	3	1	1	1	1	1	1	3	3	1	3	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
BC2F1 19	1	1	1	3	3	1	3	3	1	1	1	1	3	0	1	1	0	1	1	3	3	3	3	3	3	3	1	1	1	3	3	1	1	1	
BC2F1 20	1	1	1	3	1	1	3	3	3	0	1	1	1	0	3	1	0	1	3	1	1	1	1	1	1	1	0	1	1	1	3	3	3	3	
BC2F1 21	1	1	1	3	3	1	1	1	1	3	1	1	3	3	3	3	0	1	1	1	1	3	3	3	1	1	1	1	1	1	3	3	3	3	
BC2F1 22	3	3	3	3	3	3	1	1	1	1	1	1	3	3	1	1	0	1	1	3	3	1	3	3	1	1	1	1	1	1	1	1	1	1	
BC2F1 23	1	1	1	1	1	1	1	1	3	3	3	1	3	3	1	1	0	1	1	1	1	1	1	1	1	1	1	3	3	3	1	1	1	1	
BC2F1 24	1	1	1	1	3	0	3	3	1	0	1	1	3	3	1	1	0	1	1	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	
BC2F1 25	1	1	1	3	3	3	1	1	1	1	1	1	3	3	1	1	0	3	3	3	3	3	3	3	1	1	1	1	1	1	1	1	1	1	
BC2F1 26	1	1	1	1	1	1	1	1	1	1	1	1	3	3	3	1	0	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	
BC2F1 27	1	1	1	1	1	1	1	3	3	1	1	1	3	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	3	3	3	1	1	
BC2F1 28	3	1	1	3	3	1	1	3	3	3	1	1	0	1	3	3	3	1	1	3	1	1	1	1	1	1	1	3	3	1	1	0	3	1	
BC2F1 29	1	1	1	3	3	1	3	3	1	1	1	1	3	3	1	1	1	1	1	3	3	3	3	3	3	3	3	1	1	1	1	3	3	1	
BC2F1 30	1	1	1	3	3	1	3	3	1	1	1	1	3	3	1	1	3	3	1	3	3	3	3	3	3	3	3	3	3	1	1	1	1	1	
BC2F1 31	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	3	3	1	1	1	3	3	3	3	3	3	1	1	1	1	1	1	1	
BC2F1 32	3	1	1	1	1	1	1	1	3	3	1	1	3	3	1	1	3	3	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	
BC2F1 33	3	1	1	1	1	1	1	1	3	3	3	1	0	1	1	1	3	3	1	1	1	1	1	1	1	3	3	1	1	1	1	1	1	1	
BC2F1 34	1	1	1	1	1	1	1	1	3	3	3	1	3	1	1	1	0	1	1	1	3	3	3	3	3	3	3	1	1	1	1	3	1	1	
BC2F1 35	1	1	1	1	1	1	1	1	1	1	1	1	3	3	3	1	0	1	3	3	3	3	3	3	3	3	1	3	3	3	3	3	3	3	
BC2F1 36	1	1	1	1	1	1	1	1	1	1	1	3	3	3	1	1	0	1	3	3	3	3	3	3	3	3	3	3	3	1	1	0	1	1	
BC2F1 37	1	1	1	1	1	1	1	1	1	1	1	1	3	3	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	
BC2F1 38	3	3	3	3	3	1	1	1	1	1	1	1	3	3	1	1	0	1	3	3	1	1	1	1	1	3	3	1	1	1	1	0	1	1	
BC2F1 39	1	1	1	1	1	1	3	1	1	1	1	1	3	3	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	
BC2F1 40	3	3	3	3	3	0	3	1	1	0	1	1	3	3	1	1	0	1	3	3	0	1	1	1	3	3	1	1	1	1	1	0	1	1	
BC2F1 41	3	3	3	3	3	3	3	1	1	1	1	1	3	3	1	1	0	1	3	3	1	1	1	1	1	1	1	1	1	1	1	0	1	1	
BC2F1 42	1	1	1	1	1	1	1	1	1	3	1	1	3	3	1	1	0	3	1	1	1	1	1	1	1	1	1	3	3	3	3	3	3	1	
BC2F1 43	1	1	1	1	1	1	3	1	1	1	1	1	3	3	1	1	0	3	3	3	1	3	3	3	3	3	3	1	1	3	3	3	3	3	
BC2F1 44	1	1	1	1	1	1	1	1	1	1	1	1	0	3	1	1	0	1	3	3	1	1	3	0	0	3	1	0	1	1	0	1	1	1	
BC2F1 45	3	3	3	1	1	1	1	1	1	1	1	1	0	3	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	3	3	3	3	
BC2F1 46	3	3	3	3	1	1	1	1	1	1	1	1	3	3	1	1	0	1	1	1	1	1	1	1	1	1	1	3	3	3	3	3	3	3	
BC2F1 47	3	3	3	1	1	1	1	1	1	1	1	1	3	3	3	3	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	
BC2F1 48	1	1	1	1	1	3	1	1	1	1	1	1	3	3	1	1	0	1	3	1	1	1	3	3	3	3	3	3	3	1	1	1	1	1	
BC2F1 49	1	1	1	1	1	3	1	1	1	1	1	1	3	3	3	1	0	1	3	3	3	1	1	1	1	1	1	1	1	1	1	1	1	1	
BC2F1 50	1	1	1	1	1	1	1	1	1	1	1	1	3	3	3	1	0	1	1	3	3	1	1	1	1	1	1	1	1	1	1	1	1	1	
BC2F1 51	1	1	1	1	1	1	1	1	1	1	3	1	3	3	3	1	0	1	1	3	3	3	3	3	1	1	1	1	1	1	1	1	1	1	
BC2F1 52	1	1	1	1	1	0	3	3	1	0	3	3	3	3	1	1	0	3	3	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
BC2F1 53	1	1	1	1	3	3	1	1	1	1	1	1	3	1	3	3	3	3	3	3	3	1	1	1	1	1	1	1	1	1	1	1	1	1	
BC2F1 54	1	1	1	1	1	3	3	3	1	1	1	1	0	1	1	1	0	1	1	1	1	1	1	1	1	1	1	3	3	3	3	3	3	3	
BC2F1 55	3	1	1	1	1	1	1	1	1	1	1	1	1	3	3	1	0	1	1	1	1	1	1	1	1	1	1	3	3	1	1	1	1	1	
BC2F1 56	3	1	1	1	1																														

Appendix 1. (Continued)

	Genotypes ¹⁾																				Pollen fertility	2)	Heading date (m/d)							
	Chromosome 9					Chromosome 10					Chromosome 11					Chromosome 12														
	X36	X103	R1751	R2638	X293	C701	X333	R1629	X37	R1877	C16	C405	X181	G1465	C1003	X257	X179	C477	R3202	X344-1	X52	C901	C1069	C449	X402	R3375	C1336	X344-2		
BC2F1#																														
BC2F1 3	1	1	1	1	1	3	3	1	1	1	1	1	1	1	1	1	1	1	1	1	3	3	1	0	3	3	3	3	8.3%	9/17
BC2F1 4	1	1	3	3	1	3	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	-	9/17
BC2F1 5	1	1	1	1	1	3	0	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	0	2.2%	9/15
BC2F1 6	1	1	3	3	3	3	3	3	1	1	1	1	3	3	3	3	1	1	1	1	1	1	1	0	1	1	1	0	0.0%	9/15
BC2F1 7	3	1	1	1	3	1	1	1	1	1	1	1	3	3	3	3	1	1	1	1	1	1	1	0	1	1	0	1	34.0%	9/16
BC2F1 8	3	1	1	1	1	1	1	1	1	1	1	1	3	3	3	3	3	3	1	1	1	1	1	0	1	1	1	1	30.0%	9/7
BC2F1 9	1	1	1	1	1	3	3	3	1	1	1	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	1	1	0.0%	9/16
BC2F1 10	3	3	3	3	3	1	1	1	1	1	1	1	1	1	1	3	3	3	3	3	3	3	3	3	3	3	1	1	51.4%	9/11
BC2F1 11	1	1	1	1	1	1	1	1	1	1	1	1	3	3	1	1	1	1	1	3	3	3	1	3	3	3	1	1	59.1%	9/11
BC2F1 12	1	1	1	1	1	1	1	1	1	1	1	3	3	3	1	1	1	1	1	1	1	1	1	0	1	1	1	1	51.5%	9/2
BC2F1 13	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	3	3	3	3	42.3%	9/17
BC2F1 14	1	3	0	3	3	1	1	1	1	1	3	3	1	1	3	3	3	3	3	3	3	3	3	3	3	3	1	1	46.4%	9/13
BC2F1 15	3	3	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	3	3	3	3	3	3	3	1	1	35.9%	9/8
BC2F1 16	1	1	3	3	3	1	1	1	1	1	3	3	1	1	3	3	3	3	3	3	3	3	1	3	3	3	1	1	55.0%	9/7
BC2F1 17	0	3	1	1	1	0	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	56.1%	9/10
BC2F1 18	1	1	1	1	1	3	3	3	1	1	1	1	3	3	3	1	1	1	1	1	1	1	3	3	3	3	1	1	14.6%	9/4
BC2F1 19																														

(To be continued)

Appendix 1. (Continued)

	Genotypes ¹⁾																																
	Chromosome 1													Chromosome 2										Chromosome3									
BC2F1#	X346	X113	C86	X343	C122	R2635	X364	X252	C1211	R1944	X359	C970	C1221	C560	R3393	X45	C499	R1843	X21	X227	G1327	R2510	X48	X164	X249	X362	X144	X238	X348	R2247	X279	C5	
BC2F1 81	1	1	1	1	1	1	3	3	3	1	1	1	1	1	1	1	1	1	1	1	3	3	3	1	3	1	1	1	1	1	1	1	1
BC2F1 82	1	1	3	3	3	3	3	1	1	1	1	1	1	1	1	1	1	1	1	1	3	3	1	3	3	1	1	1	1	1	1	1	1
BC2F1 83	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	3	3	3	1	1	1	1	1	1	1	1	1	1
BC2F1 84	1	1	0	0	1	1	3	1	1	1	1	1	1	1	1	1	1	3	3	3	3	3	1	3	3	1	1	1	1	1	0	1	1
BC2F1 85	1	1	0	1	1	1	1	1	1	1	3	3	3	1	3	3	1	1	1	1	1	1	1	1	1	1	3	3	1	1	1	1	1
BC2F1 86	1	1	0	1	3	3	3	3	3	3	3	3	3	3	3	3	1	1	1	1	1	1	1	3	3	3	3	1	3	1	1	1	1
BC2F1 87	1	1	0	1	3	3	3	3	3	3	3	3	3	1	1	0	1	1	1	1	1	1	1	3	3	3	3	1	1	1	1	1	1
BC2F1 88	1	1	0	1	1	1	3	1	1	1	1	1	1	3	3	3	3	3	1	1	1	1	3	3	3	1	1	1	1	3	3	3	3
BC2F1 89	1	1	0	1	3	3	3	1	1	1	1	1	1	3	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	3	3	3
BC2F1 90	1	1	0	1	3	3	3	1	1	1	1	1	1	1	3	3	3	3	1	1	1	1	3	3	3	1	1	1	1	3	3	3	3
BC2F1 91	1	1	0	1	1	1	1	1	1	1	1	1	1	3	3	3	3	0	1	1	1	1	1	1	1	3	3	3	1	1	1	3	3
BC2F1 92	1	3	3	3	3	1	1	1	1	1	1	1	1	3	3	3	3	3	3	3	3	3	1	1	1	3	3	3	1	1	1	3	3
BC2F1 93	1	3	3	3	3	1	1	1	1	1	3	3	3	1	1	3	3	3	3	3	3	1	1	1	1	3	3	3	1	1	1	1	3
BC2F1 94	1	1	0	1	1	1	1	1	1	1	1	1	1	3	3	3	1	1	1	1	1	1	1	1	1	1	3	3	1	1	1	1	1
BC2F1 95	1	1	0	1	1	1	3	3	3	1	1	1	1	3	3	3	3	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
BC2F1 96	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	3	3	3	1	1	1	1	1	3	3	3	3	1	1	1	1	1	1
BC2F1 97	1	1	0	1	1	1	3	3	3	1	1	1	1	3	3	1	3	1	1	1	1	1	1	3	3	3	3	1	1	1	1	1	1
BC2F1 98	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	0	1	1	1	1	0
BC2F1 99	1	1	0	1	1	1	1	1	0	1	1	3	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1
BC2F1 100	1	1	0	1	3	3	3	3	3	3	3	3	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
BC2F1 101	1	1	0	1	1	3	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1

(To be continued)

Appendix 1. (Continued)

	Genotypes ¹⁾																																		
	Chromosome 4						Chromosome 5						Chromosome 6						Chromosome 7						Chromosome 8										
BC2F1#	C445	Q4	X331	X311	X237	X247	X292	R3166	G260	X105	X255	X297	X209	X27	X172	R2549	X386	Q11		C1057	R2401	R1440	C451	X117	R1245	R1789	C213	X397	X56	G1073	R1394A	C1107	X41	X28	
BC2F1 81	1	1	1	1	1	1	1	1	3	0	3	1	3	3	1	1	0	3		3	3	3	3	1	1	1	0		1	1	1	1	3	3	3
BC2F1 82	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	0	1		1	1	1	1	1	1	1	0		1	1	1	0	1	1	
BC2F1 83	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	0	1		1	1	1	1	1	1	1	0		1	1	3	3	0	3	1
BC2F1 84	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	0	1		3	3	1	1	1	1	1	0		1	1	0	3	0	3	3
BC2F1 85	1	1	1	3	3	3	1	1	1	1	1	1	3	3	3	1	0	1		1	1	1	1	1	1	1	0		3	3	1	1	0	1	1
BC2F1 86	1	1	1	1	3	3	1	1	1	1	1	1	3	3	3	1	0	1		1	1	1	1	1	1	1	0		1	1	1	1	0	1	1
BC2F1 87	1	1	1	1	1	1	1	1	3	1	1	1	3	3	3	1	0	1		3	3	3	3	1	1	1	0		3	3	1	1	0	1	1
BC2F1 88	1	1	1	1	1	1	1	1	1	1	1	1	3	3	1	3	3	1		3	3	3	3	3	1	1	0		1	1	1	1	0	1	1
BC2F1 89	1	1	1	1	1	1	3	1	1	1	1	1	3	3	1	1	0	3		3	3	3	3	1	1	1	0		1	1	1	1	0	1	1
BC2F1 90	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	3	3	3		3	1	1	1	1	1	1	0		1	1	1	1	0	1	1
BC2F1 91	1	1	3	1	1	1	1	1	1	0	3	1	1	3	3	3	3	1		3	3	3	1	1	1	1	0		1	1	3	3	3	3	3
BC2F1 92	1	1	3	1	1	1	1	1	1	0	3	3	1	1	1	1	0	1		3	3	3	1	1	1	1	0		1	1	1	1	0	1	1
BC2F1 93	1	1	1	1	1	3	1	1	1	0	1	1	3	3	3	3	3	1		3	3	3	1	1	1	1	0		1	1	3	3	3	3	1
BC2F1 94	3	3	1	1	1	3	1	1	1	1	1	1	3	1	1	1	0	1		1	1	3	3	3	3	3	0		3	3	3	3	0	1	1
BC2F1 95	1	3	3	3	3	1	1	1	1	1	3	3	3	3	3	1	0	1		1	3	3	3	3	3	3	0		3	3	3	3	3	1	1
BC2F1 96	1	1	1	1	1	1	1	1	1	1	3	1	3	3	1	1	0	1		1	3	3	3	3	3	3	0		3	3	1	1	0	1	1
BC2F1 97	3	3	3	3	1	1	1	1	1	1	3	3	3	3	3	1	0	1		1	3	1	1	1	1	1	0		1	1	1	1	0	1	1
BC2F1 98	1	1	1	1	3	0	3	1	1	0	1	1	1	3	3	3	0	1		3	3	3	3	1	1	1	0		1	1	1	3	0	3	3
BC2F1 99	3	1	1	1	1	1	1	1	1	1	1	1	3	3	3	1	0	3		3	3	1	1	1	1	1	0		1	1	1	1	0	1	1
BC2F1 100	1	3	1	1	1	1	1	1	1	1	1	1	3	3	3	1	0	1		1	1	1	1	1	1	1	0		1	1	1	1	0	1	1
BC2F1 101	1	1	1	1	1	1	1	1	1	0	1	1	3	1	1	1	0	1		1	1	1	1	1	1	1	0		1	1	1	1	0	1	1

(To be continued)

Appendix 1. (Continued)

BC2F1#	Genotypes ¹⁾																										Pollen fertility	2)	Heading date (m/d)	
	Chromosome 9					Chromosome 10					Chromosome 11					Chromosome 12														
	X36	X103	R1751	R2638	X293	C701	X333	R1629	X37	R1877	C16	C405	X181	G1465	C1003	X257	X179	C477	R3202	X344-1	X52	C901	C1069	C449	X402	R3375	C1336	X344-2		
BC2F1 81	3	3	3	3	1	3	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	27.8%	9/12
BC2F1 82	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	3	3	3	1	1	1	1	1	1	1	1	1	97.4%	9/4
BC2F1 83	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	-	9/2
BC2F1 84	1	1	1	1	1	1	1	3	3	3	3	1	0	1	1	1	1	1	1	1	1	1	3	1	1	3	3	1	7.0%	8/25
BC2F1 85	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	3	3	3	1	3	1	1	1	1	1	1	1	61.1%	9/10
BC2F1 86	1	3	3	3	3	3	3	3	1	1	1	1	1	1	1	1	3	3	1	1	1	1	3	3	1	1	1	1	0.0%	9/15
BC2F1 87	1	1	1	1	1	1	3	3	3	3	3	1	1	1	3	3	3	3	3	3	1	3	3	1	1	1	1	1	0.0%	9/14
BC2F1 88	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	37.0%	9/9
BC2F1 89	1	1	3	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	41.0%	9/11
BC2F1 90	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	-	8/31
BC2F1 91	1	1	1	3	3	1	1	1	3	3	1	1	1	1	3	3	3	1	1	1	1	1	3	3	3	1	1	1	27.6%	9/2
BC2F1 92	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	3	3	3	1	1	1	1	1	1	1	1	3	1	49.1%	9/3
BC2F1 93	3	3	3	3	1	3	3	3	3	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	11.0%	9/17
BC2F1 94	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	41.8%	9/8
BC2F1 95	1	1	1	3	3	1	1	3	3	3	3	3	1	1	1	3	3	3	3	3	3	3	1	1	3	3	1	1	-	9/1
BC2F1 96	1	1	1	1	3	1	1	3	3	3	3	1	3	3	3	3	3	3	3	3	3	3	1	1	3	3	3	3	25.0%	8/25
BC2F1 97	1	1	0	3	1	1	1	3	3	1	1	1	3	3	3	3	3	3	3	3	3	3	1	1	1	1	1	3	51.4%	9/4
BC2F1 98	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	3	3	1	1	1	1	1	1	28.4%	9/19
BC2F1 99	1	1	1	3	3	1	1	1	1	1	1	1	1	1	1	1	3	3	3	3	3	3	1	1	1	1	1	1	25.4%	9/18
BC2F1 100	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	3	3	1	1	1	1	1	1	1	1	1	0	64.3%	9/12
BC2F1 101	1	3	1	0	1	1	1	1	1	0	0	1	1	1	1	1	3	3	3	0	3	1	1	1	1	1	1	0	57.0%	9/11

1): 1, 3 and 0 represents Taichung 65 homozygous, heterozygous and missing data, respectively.

2): -: Missing data.

Appendix 2. Detailed genotypes of GILs and BCF1 plants.

Plant/ line#	Genotypes ¹⁾									Chromosome 2								Chromosome 3																							
				Chromosome 1																																					
	BC3 F1#	BC2 F1#	B1 F1#	C970	X359	R1944	C1211	X252	X364	R2635	C122	X343	X92	C86	X113	X346	R2510	G1327	X227	X21	R1843	C499	X45	R3393	C560	C1221	C515	X279	R2247	X348	X238	X51	X144	X362	X249	X164	X48				
BC2F1 85				1	1	1	3	3	3	3	3	3	3	3	3	3	1	3	3	1	1	1	1	1	1	1	1	3	3	1	1	1	1	1	1	1	1	1	1	1	
BC2F1 75				1	0	1	3	3	3	3	3	3	3	0	0	3	1	1	3	3	1	0	1	1	1	1	1	1	1	1	1	1	1	0	1	3	1	1	1	1	
BC3F1 65				1	1	1	3	3	3	3	3	3	3	0	0	3	1	1	1	1	1	0	1	1	1	1	1	0	1	0	1	1	0	1	3	1	1	1	1	1	
GIL 15	65	75	85	1	1	1	2	2	2	2	2	2	2	0	0	2	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	0	1	0	1	0	1	1	1	
GIL 16	65	75	85	1	1	1	2	2	2	2	2	2	2	0	0	2	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	0	1	0	1	0	1	1	1	
GIL 17	65	75	85	1	1	1	2	2	2	2	2	2	2	0	0	2	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	0	1	0	1	2	1	1	1	
GIL 18	65	75	85	1	1	1	2	2	2	2	2	2	2	0	0	2	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	0	1	0	1	2	1	1	1	
BC1F1 64				3	3	3	3	3	3	3	3	3	3	3	1	1	1	3	3	3	0	1	1	1	1	1	1	1	1	1	1	2	3	3	3	3	3	3	3	3	
BC2F1 53				3	3	0	3	3	3	3	3	3	1	0	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	3	3	3	3	
BC3F1 58				3	3	3	3	3	3	3	3	3	1	0	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	3	3	
GIL 19	58	53	64	2	1	0	0	1	2	2	2	1	0	0	0	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	0	1	1	0	1	1	2	2	2
GIL 20	58	53	64	0	3	3	3	2	2	2	1	1	0	0	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	2	2	2
BC1F1 60				3	3	3	3	3	3	3	3	3	1	1	1	1	1	1	3	3	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	3	3	3	3	
BC2F1 39				3	3	3	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	3	3	3
BC3F1 46				3	3	3	1	1	1	1	1	1	1	0	1																										

(To be continued)

Appendix 2. (Continued)

	Genotypes¹⁾																																							
	Chromosome 4				Chromosome 5				Chromosome 6				Chromosome 7				Chromosome 8																							
Plant/ line#	BC3 F1#	BC2 F1#	B1 F1#	X247	X237	X311	X331	C45	X292	R3166	G660	X105	X255	X297	X209	X27	X172	R2549	X386	Q11	X342	C1057	R2401	X338	R1440	C451	X117	R1245	R1789	C213	X278	X41	C1107	R1394A	G1073	X56	X397			
BC1F1 85				1	1	3	3	1	1	1	3	3	3	3	3	3	3	3	3	3	3	3	1	1	3	3	3	3	3	3	1	1	1	3	3	3	3	3		
BC2F1 75				1	1	1	1	1	1	1	3	3	3	3	3	3	3	3	1	0	1	0	1	1	0	1	1	3	3	3	3	1	1	0	3	0	3	1		
BC3F1 65				1	1	1	1	1	1	1	3	3	3	3	3	3	3	1	1	1	0	1	0	0	1	1	1	1	1	1	1	1	1	1	1	3	3	3	1	
GIL 15	65	75	85	1	1	1	1	1	1	1	2	2	3	1	2	2	1	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
GIL 16	65	75	85	1	1	1	1	1	1	1	2	2	3	1	2	2	1	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
GIL 17	65	75	85	1	1	1	1	1	1	1	2	2	3	3	2	2	1	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
GIL 18	65	75	85	1	1	1	1	1	1	1	2	2	3	3	0	2	1	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
BC1F1 64				3	3	1	1	1	1	3	3	1	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3		
BC2F1 53				3	3	1	1	1	1	1	1	1	1	1	3	3	3	3	3	3	0	3	3	0	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
BC3F1 58				1	1	1	1	1	1	1	1	1	1	1	1	3	3	3	3	0	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
GIL 19	58	53	64	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
GIL 20	58	53	64	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
BC1F1 50				3	3	3	3	3	3	3	1	1	1	1	3	3	1	1	1	1	1	3	3	3	1	1	1	1	1	0	3	3	3	3	3	3	3	3	3	3
BC2F1 39				1	1	1	1	1	1	3	1	1	1	1	3	3	1	1	0	1	0	1	1	0	1	1	1	1	1											

(To be continued)

Appendix 2. (Continued)

			Genotypes ¹⁾																																				
			Chromosome 9					Chromosome 10					Chromosome 11					Chromosome 12																					
Plant/ line#	BC3 F1#	BC2 F1#	B1 F1#	X36	X103	R1751	X13	X293	C701	X333	R1629	X37	R1877	C16	C405	X52	X344-1	R3202	C477	X179	X44	X257	C1003	G1455	X181	X344-2	X24	X193	C1336	R3375	X402	C449	X148	C1069	C901				
BC2F1 35				1	1	1	3	3		1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
BC2F1 75				1	1	1	0	1		1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	0	0	1	1	1	1	1	1	1		
BC3F1 65				1	1	1	0	1		1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		
GIL 15	65	75	85	1	1	1	1	1		1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		
GIL 16	65	75	85	1	1	1	1	1		1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		
GIL 17	65	75	85	1	1	1	1	1		1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		
GIL 18	65	75	85	1	1	1	1	1		1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		
BC1F1 64				3	3	3	3	3		1	3	3	3	3	3	3	1	1	1	1	1	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	
BC2F1 53				3	1	1	1	1		1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	0	0	1	1	1	1	1	1	1	1	
BC3F1 56				3	1	1	1	1		1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	
GIL 19	58	53	64	3	1	1	1	1		1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	
GIL 20	58	53	64	1	1	1	1	1		1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
BC1F1 58				3	3	3	3	3		1	1	1	1	3	3	3	1	1	1	1	1	1	1	1	1	1	1	3	3	3	3	3	3	3	3	3	3	3	
BC2F1 39				1	1	1	3	3		1	1	1	1	3	3	3	1	1	1	1	0	0	1	1	1	1	1	3	0	0	3	0	3	3	3	0	3	3	
BC3F1 46				1	1	1	1	1		1	1	1	1	3	3	3	1	1	1	1	1	1	1	1	1	1	3	3	3	1	1	1	1	1	1	1	1	1	
GIL 23	46	39	56	1	1	1	1	1		1	1	1	1	3	3	2	1	1	1	1	1	1	1	1	0	1	0	0	0	1	1	1	1	1	1	1	1	1	
GIL 24	46	39	56	1	1	1	1	1		1	1	1	1	3	3	2	1	1	1	1	1	1	1	1	0	1	0	0	0	1	1	1	1	1	1	1	1	1	
GIL 25	46	39	56	1	1	1	1	1		1	1	1	1	2	2	2	1	1	1	1	1	1	1	1	0	1	0	0	1	0	1	1	1	1	1	1	1	1	
GIL 26	46	39	56	1	1	1	1	1		1	1	1	1	2	2	2	1	1	1	1	1	1	1	1	0	1	0	1	0	1	1	1	1	1	1	1	1	1	
BC1F1 17				3	3	3	3	3		1	1	1	1	3	3	3	0	0	3	3	3	3	3	3	1	1	1	0	1	1	1	0	3	3	3	0	3	3	
BC2F1 15				3	3	3	0	1		1	1	1	1	1	1	1	3	3	3	1	1	0	1	1	1	1	1	0	0	1	1	1	3	3	3	0	3	3	
BC3F1 24				1	1	1	1	1		1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
GIL 27	24	15	17	1	1	1	1	1		1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	0	1	0	1	1	1	1	1	1	1	1	
GIL 28	24	15	17	1	1	1	1	1		1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	0	1	0	1	0	1	1	1	1	1	1	1	
GIL 29	24	15	17	1	1	1	1	1		1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	0	1	0	1	0	1	1	1	1	1	1	1	
GIL 30	24	15	17	1	1	1	1	1		1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	0	1	0	1	0	1	1	1	1	1	1	1	
BC1F1 29				1	1	3	3	1		3	3	1	1	1	3	3	0	3	3	1	1	1	3	3	3	3	0	1	1	1	1	1	1	1	1	1	1	1	1
BC2F1 22				1	1	3	1	1		3	3	1	1	1	1	1	3	3	3	1	1	0	1	3	3	3	1	0	0	1	1	1	1	1	1	1	1	1	
BC3F1 30				1	1	1	1	1		3	3	1	1	1	1	1	1	1	1	1	1	1	1	3	3	3	1	1	1	1	1	1	1	1	1	1	1	1	
GIL 31	30	22	29	1	1	1	1	1		1	1	1	1	1	1	1	1	1	1	1	1	1	2	0	3	0	1	0	1	0	1	1	1	1	1	1	1	1	
GIL 32	30	22	29	1	1	1	1	1		1	1	1	1	1	1	1	1	1	1	1	1	1	2	0	2	0	1	0	1	0	1	1	1	1	1	1	1	1	
GIL 33	30	22	29	1	1	1	1	1		2	2	1	1	1	1	1	1	1	1	1	1	1	1	0	1	0	1	0	1	0	1	1	1	1	1	1	1	1	
GIL 34	30	22	29	1	1	1	1	1		2	2	1	1	1	1	1	1	1	1	1	1	1	1	0	1	0	1	0	1	0	1	1	1	1	1	1	1	1	
BC1F1 61				1	1	1	1	3		1	1	1	3	3	1	1	1	1	1	1	1	1	1	1	1	3	3	3	3	3	3	3	3	3	3	3	3	3	
BC2F1 46				1	1	1	1	3		1	1	1	3	3	1	1	1	1	1	1	0	1	1	1	1	1	1	0	0	1	1	1	1	1	1	1	1	1	
BC3F1 55				1	1	1	1	3		1	1	1	3	3	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	
GIL 35	55	48	61	1	1	1	1	2		1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	0	1	0	1	0	1	1	1	1	1	1	1	1	
GIL 36	55	48	61	1	1	1	1	2		1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	0	1	0	1	0	1	1	1	1	1	1	1	1	
GIL 37	55	48	61	1	1	1	1	2		1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	0	1	0	1	0	1	1	1	1	1	1	1	1	
GIL 38	55	48	61	1	1	1	1	1		1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	0	1	0	1	0	1	1	1	1	1	1	1	1	
GIL 39	55	48	61	1	1	1	1	3		1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	0	1	0	1	0	1	1	1	1	1	1	1	1	
GIL 40	55	48	61	1	1	1	1	2		1	1	1	3	3	1	1	1	1	1	1	1	1	1	0	1	0	1	0	1	0	1	1	1	1	1	1	1	1	
BC1F1 12				1	1	1	1	1		3	3	5	1	1	1	3	3	3	3	3	3	3	3	3	3	3	1	1	1	1	3	3	3	3	3	3	3	3	
BC2F1 12				1	1	1	1	1		1	1	1	1	1	3	1	3	3	3	1	0	1	1	3	3	3	1	0	0	1	1	1	1	1	1	1	1	1	
BC3F1 18				1	1	1	1	1		1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
GIL 41	18	12	12	1	1	1	1	1		1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	0	1	0	1	0	1	1	1	1	1	1	1	1	
GIL 42	18	12	12	1	1	1	1	1		1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	0	1	0	1	0	1	1	1	1	1	1	1	1	
GIL 43	18	12	12	1	1	1	1	1		1	1	1	1	1	2	1	1	1	1	1	1	1	1	0	1	0	1	0	1	0	1	1	1	1	1	1	1	1	
GIL 44	18	12	12	1	1	1	1	1		1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	0	1	0	1	0	1	1	1	1	1	1	1	1	
BC1F1 43				1	3	3	3	3		1	3	3	3	3	3	1	1	1	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	
BC2F1 26				1																																			

(To be continued)

Appendix 2. (Continued)

Appendix 2. (Continued)

[illegible]

(To be continued)

Appendix 2. (Continued)

Plant/ line#	Genotypes ¹⁾			Chromosome 9										Chromosome 10										Chromosome 11										Chromosome 12											
	BC3 F1#	BC2 F1#	B1 F1#	X36	X103	R1751	X13	X293	C701	X333	R1629	X37	R1877	C16	C405	X52	X344-1	R3202	C477	X179	X44	X257	C1003	G1465	X181	X344-2	X24	X193	C1336	R3375	X402	C449	X148	C1069	C901										
BC1F1 17				3	3	3	3	3	1	1	1	1	1	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3			
BC2F1 14				1	3	0	3	3	1	1	1	1	1	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3			
BC3F1 23				1	1	1	1	1	1	1	1	1	1	3	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		
GIL 73	23	14	17	1	1	1	1	1	1	1	1	1	1	2	2	1	0	1	1	2	2	2	2	1	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
GIL 74	23	14	17	1	1	1	1	1	1	1	1	1	1	3	0	1	0	1	1	2	2	2	2	1	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
GIL 75	23	14	17	1	1	2	2	2	1	1	1	1	1	2	2	1	0	1	1	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
GIL 76	23	14	17	1	1	2	2	2	1	1	1	1	1	2	2	1	0	1	1	1	1	1	1	1	1	0	1	0	1	1	1	2	2	2	2	2	2	2	2	2	2	2	2	2	
GIL 77	23	14	17	1	2	2	2	2	1	1	1	1	1	1	1	1	0	2	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
GIL 78	23	14	17	1	2	2	2	2	1	1	1	1	1	1	1	1	0	2	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
BC1F1 9				1	1	3	3	3	3	3	3	1	1	1	1	1	0	1	1	1	1	3	3	3	3	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
BC2F1 6				1	1	3	3	3	3	3	3	1	1	1	1	1	1	1	1	1	0	3	3	3	3	3	1	0	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
BC3F1 7				1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
GIL 85	7	6	9	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
GIL 86	7	6	9	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
GIL 87	7	6	9	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
GIL 88	7	6	9	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
GIL 89	7	6	9	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
GIL 90	7	6	9	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
GIL 91	7	6	9	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
GIL 92	7	6	9	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
BC1F1 85				3	3	3	3	3	3	3	3	3	3	3	1	1	1	1	3	3	3	3	3	3	3	1	0	1	1	1	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3
BC2F1 91				1	1	1	3	3	1	1	1	3	3	1	1	1	1	1	3	3	0	3	3	3	1	1	1	0	0	1	1	3	3	0	3	3	3	3	3	3	3	3	3	3	3
BC3F1 72				1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
GIL 93	72	91	95	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
GIL 94	72	91	95	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
GIL 95	72	91	95	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
GIL 96	72	91	95	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
BC1F1 29				1	1	3	3	1	3	3	1	1	1	3	3	3	3	3	1	1	1	3	3	3	3	3	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
BC2F1 22				1	1	3	1	1	3	3	1	1	1	1	1	1	3	3	3	1	1	0	1	3	3	3	1	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
BC3F1 30				1	1	1	1	1	3	3	1	1	1	1	1	1	1	1	1	1	1	1	1	3	3	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
GIL 97	30	22	29	1	1	1	1	1	0	2	1	1	1	1	1	1	1	1	1	1	1	1	2	0	2	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
GIL 98	30	22	29	1	1	1	1	1	0	2	1	1	1	1	1	1	1	1	1	1	1	1	2	0	2	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
GIL 99	30	22	29	1	1	1	1	1	0	2	1	1	1	1	1	1	1	1	1	1	1	1	1	0	2	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
GIL 100	30	22	29	1	1	1	1	1	0	2	1	1	1	1	1	1	1	1	1	1	1	1	2	0	2	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
GIL 101	30	22	29	1	1	1	1	1	0	2	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
GIL 102	30	22	29	1	1	1	1	1	0	2	1	1	1	1	1	1	1	1	1	1	1	1	2	0	2	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
GIL 103	30	22	29	1	1	1	1	1	0	2	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
GIL 104	30	22	29	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	2	0	2	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
BC1F1 30				1	1	1	1	3	1	1	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3
BC2F1 36				1	1	1	1	3	1	1	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3
BC3F1 76				1	1	1	1	3	1	1	3	3	3	3	3	3	0	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3
GIL 111	76	96	98																																										

Appendix 2. (Continued)

[illegible]

(To be continued)

Appendix 2. (Continued)

Plant/ line#	Genotypes ¹⁾																																						
	Chromosome 4				Chromosome 5				Chromosome 6				Chromosome 7				Chromosome 8																						
	BC3 F1#	BC2 F1#	B1 F1#	X247	X237	X311	X331	C445	X292	R3166	G260	X105	X255	X297	X209	X27	X172	R2549	X386	Q11	X342	C1057	R2401	X338	R1440	C451	X117	R1245	R1789	C213	X278	X41	C1107	R1394A	G1073	X56	X397		
BC1F1 96				3	3	3	3	3	3	0	1	1	3	3	3	3	3	1	1	1	1	1	1	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3
BC2F1 95				1	3	3	3	3	1	1	1	1	3	3	3	3	3	1	0	1	0	1	1	3	0	3	3	3	3	3	3	0	1	1	3	3	3	3	3
BC3F1 78				1	1	1	1	1	0	1	1	1	3	3	3	3	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	3
GIL 149	76	96	98	1	1	1	1	1	1	1	1	1	3	3	2	2	1	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	
GIL 150	76	96	98	1	1	1	1	1	1	1	1	1	2	1	2	2	1	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	
GIL 151	76	96	98	1	1	1	1	1	1	1	1	1	1	1	1	2	1	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
GIL 152	76	96	98	1	1	1	1	1	1	1	1	1	1	1	1	2	1	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
GIL 153	76	96	98	1	1	1	1	1	1	1	1	1	2	1	2	2	1	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	
GIL 154	76	96	98	1	1	1	1	1	1	1	1	1	2	1	2	2	1	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	3	
BC1F1 11				3	3	1	1	3	3	3	3	1	1	1	3	3	3	3	3	1	1	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	
BC2F1 8				3	3	1	1	3	3	3	3	3	1	1	3	3	1	1	1	1	0	1	1	1	0	1	1	1	1	1	1	1	3	3	3	3	3	3	
BC3F1 11				1	1	1	1	3	3	1	1	1	1	1	3	3	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
GIL 155	11	8	11	1	1	1	1	2	1	1	1	1	1	1	2	2	1	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
GIL 156	11	8	11	1	1	1	1	2																															

(To be continued)

Appendix 2. (Continued)

Plant/ line#	Genotypes ¹⁾			Chromosome 9								Chromosome 10								Chromosome 11								Chromosome 12										
	BC3 F1#	BC2 F1#	B1 F1#	Chromosome 9					Chromosome 10					Chromosome 11					Chromosome 12																			
				X36	X103	R1751	X13	X293	C701	X333	R1629	X37	R1877	C16	C405	X52	X344-1	R3202	C477	X179	X44	X257	C1003	G1485	X181	X344-2	X24	X193	C1336	R3375	X402	C449	X148	C1069				
BC1F1 96				1	1	1	1	1	3		1	1	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	1	1	1		
BC2F1 96				1	1	1	3	3			1	1	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	1	1		
BC3F1 78				1	1	1	1	1	3		1	1	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	1	1		
GIL 149	76	96	98	1	1	1	1	2			1	1	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	1	1	
GIL 150	76	96	98	1	1	1	1	2			1	1	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	1	1	
GIL 151	76	96	98	1	1	1	1	2			1	1	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	1	1	
GIL 152	76	96	98	1	1	1	1	2			1	1	1	1	0	1	1	1	0	1	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	1	1
GIL 153	76	96	98	1	1	1	1	2			1	1	2	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	1	1	
GIL 154	76	96	98	1	1	1	1	2			1	1	1	2	1	3	1	1	0	0	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	1	1
BC1F1 11				3	3	3	3	3			1	1	1	1	1	1	1	1	1	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	1	1
BC2F1 8				3	1	1	1	1			1	1	1	1	1	1	1	1	1	1	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	1	1
BC3F1 11				3	1	1	1	1			1	1	1	1	1	1	1	1	1	1	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	1	1
GIL 155	11	8	11	1	1	1	1	1			1	1	1	1	1	1	1	1	1	1	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	1	1
GIL 156	11	8	11	1	1	1	1	1			1	1	1	1	1	1	1	1	1	1	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	1	1
GIL 157	11	8	11	3	1	1	1	1			1	1	1	1	1	1	1	1	1	1	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	1	1
GIL 158	11	8	11	1	1	1	1	1			1	1	1	1	1	1	1	1	1	1	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	1	1
GIL 159	11	8	11	3	1	1	1	1			1	1	1	1	1	1	1	1	1	1	1	0	1	2	2	2	2	2	2	2	2	2	2	2	2	2	1	1
GIL 160	11	8	11	3	1	1	1	1			1	1	1	1	1	1	1	1	1	1	0	3	0	0	2	2	2	2	2	2	2	2	2	2	2	2	1	1
GIL 161	11	8	11	3	1	1	1	1			1	1	1	1	1	1	1	1	1	1	1	0	2	0	0	3	0	3	0	3	0	3	0	3	0	3	1	1
GIL 162	11	8	11	1	1	1	1	1			1	1	1	1	1	1	1	1	1	1	0	3	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	1
BC1F1 12 ²⁾				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
BC2F1 10				3	3	3	3	3			1	1	1	1	1	1	1	1	1	1	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3
BC3F1 14				3	3	3	3	3			1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
GIL 163	14	10	12	1	2	1	1	1			1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
GIL 164	14	10	12	1	2	2	3	1			1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
GIL 165	14	10	12	1	1	3	3	2			1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
GIL 166	14	10	12	1	1	1	1	2			1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
GIL 167	14	10	12	3	2	2	2	3			1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
GIL 168	14	10	12	2	2	2	3	3			1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
GIL 169	14	10	12	1	2	2	2	2			1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
GIL 170	14	10	12	1	2	2	2	2			1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
BC1F1 13				3	1	1	1	1			1	1	1	1	1	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3
BC2F1 13				3	1	1	1	1			1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
BC3F1 20				3	1	1	1	1			1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
GIL 171	20	13	13	2	1	1	1	1			1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
GIL 172	20	13	13	2	1	1	1	1			1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
GIL 173	20	13	13	1	1	1	1	1			1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
GIL 174	20	13	13	1	1	1	1	1			1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
GIL 175	20	13	13	1	1	1	1	1			1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1									

1): 1, 2, 3 and 0 represent Taichung 65 homozygous, *O. glaberrima* homozygous, heterozygous and missing data, respectively.

2): Data not available.

Appendix 3. Detailed genotypes of the *Ef* (t) mapping population used in Chapter IV.

Plant	Days to heading	Determined genotypes at <i>Ef</i> (t)	Genotypes at marker loci ¹⁾			
			C1369	C1286	C234	XNpb37
1	62	<i>Ef</i>	3	3	3	3
2	62	<i>Ef</i>	2	2	2	2
3	78	<i>ef</i>	1	1	1	1
4	62	<i>Ef</i>	3	3	3	3
5	61	<i>Ef</i>	3	3	3	3
6	62	<i>Ef</i>	3	3	3	3
7	60	<i>Ef</i>	3	3	3	3
8	61	<i>Ef</i>	2	2	2	2
9	76	<i>ef</i>	1	1	1	1
10	60	<i>Ef</i>	3	3	3	3
11	62	<i>Ef</i>	3	3	3	3
12	62	<i>Ef</i>	2	2	2	2
13	61	<i>Ef</i>	2	2	2	2
14	73	<i>ef</i>	1	1	1	1
15	62	<i>Ef</i>	3	3	3	3
16	62	<i>Ef</i>	3	3	3	3
17	61	<i>Ef</i>	2	3	2	2
18	61	<i>Ef</i>	3	3	3	3
19	61	<i>Ef</i>	2	2	2	2
20	62	<i>Ef</i>	2	2	2	2
21	62	<i>Ef</i>	2	2	2	2
22	62	<i>Ef</i>	3	3	3	3
23	77	<i>ef</i>	1	1	1	1
24	77	<i>ef</i>	1	1	1	1
25	75	<i>ef</i>	1	1	1	1
26	71	<i>ef</i>	1	1	1	1
27	62	<i>Ef</i>	3	3	3	3
28	75	<i>ef</i>	1	1	1	1
29	63	<i>Ef</i>	3	3	3	3
30	64	<i>Ef</i>	3	3	3	3
31	75	<i>ef</i>	1	1	1	1
32	64	<i>Ef</i>	3	3	3	3
33	73	<i>ef</i>	1	1	1	1
34	62	<i>Ef</i>	2	2	2	2
35	62	<i>Ef</i>	3	3	3	3
36	62	<i>Ef</i>	2	2	2	2
37	77	<i>ef</i>	1	1	1	1
38	67	<i>ef</i>	3	3	3	3
39	62	<i>Ef</i>	3	3	3	3
40	74	<i>ef</i>	1	1	1	1
41	62	<i>Ef</i>	2	2	2	2
42	62	<i>Ef</i>	3	3	3	3
43	61	<i>Ef</i>	3	3	3	3
44	61	<i>Ef</i>	3	3	3	3
45	61	<i>Ef</i>	3	3	3	3
46	62	<i>Ef</i>	3	3	3	3
47	62	<i>Ef</i>	3	3	3	3
48	63	<i>Ef</i>	3	3	3	3
49	62	<i>Ef</i>	2	2	2	2
50	81	<i>ef</i>	1	1	1	1
51	62	<i>Ef</i>	3	3	3	3
52	62	<i>Ef</i>	2	2	2	2
53	60	<i>Ef</i>	3	3	3	3
54	74	<i>ef</i>	1	1	1	1
55	79	<i>ef</i>	1	1	1	1
56	73	<i>ef</i>	1	1	1	1
57	61	<i>Ef</i>	3	3	3	3
58	61	<i>Ef</i>	3	3	3	3
59	73	<i>ef</i>	1	1	1	1
60	61	<i>Ef</i>	3	3	3	3
61	80	<i>ef</i>	1	1	1	1
62	61	<i>Ef</i>	3	3	3	3
63	65	<i>Ef</i>	3	3	3	3
64	73	<i>ef</i>	1	1	1	1
65	76	<i>ef</i>	1	1	1	3
66	61	<i>Ef</i>	3	3	3	3
67	61	<i>Ef</i>	3	3	3	3
68	81	<i>ef</i>	1	1	1	1
69	62	<i>Ef</i>	3	3	3	3
70	62	<i>Ef</i>	3	3	3	3
71	61	<i>Ef</i>	3	3	3	3
72	62	<i>Ef</i>	2	2	2	2
73	63	<i>Ef</i>	3	3	3	3
74	63	<i>Ef</i>	2	2	2	2
75	63	<i>Ef</i>	2	2	2	2
76	63	<i>Ef</i>	2	2	2	2
77	83	<i>ef</i>	1	1	1	1
78	74	<i>ef</i>	1	1	1	1
79	64	<i>Ef</i>	2	2	2	2
80	61	<i>Ef</i>	2	2	2	2

(To be continued)

Appendix 3. (Continued)

Plant	Days to heading	Determined genotypes at <i>Ef</i> (t)	Genotypes at marker loci ¹⁾			
			C1369	C1286	C234	XNpb37
81	61	<i>Ef</i>	3	3	3	3
82	63	<i>Ef</i>	3	3	3	3
83	76	<i>ef</i>	1	1	1	1
84	72	<i>ef</i>	1	1	1	1
85	61	<i>Ef</i>	3	1	1	3
86	77	<i>ef</i>	1	1	1	1
87	62	<i>Ef</i>	3	3	3	3
88	69	<i>ef</i>	1	1	1	1
89	76	<i>ef</i>	1	1	1	1
90	60	<i>Ef</i>	3	3	3	3
91	70	<i>ef</i>	1	1	1	1
92	61	<i>Ef</i>	2	2	2	2
93	60	<i>Ef</i>	3	3	3	3
94	61	<i>Ef</i>	3	3	3	3
95	61	<i>Ef</i>	3	3	3	3
96	72	<i>ef</i>	1	1	1	1
97	61	<i>Ef</i>	3	3	3	3
98	62	<i>Ef</i>	3	3	3	3
99	63	<i>Ef</i>	3	3	3	3
100	63	<i>Ef</i>	3	3	3	3
101	61	<i>Ef</i>	2	2	2	2
102	76	<i>ef</i>	1	1	1	1
103	75	<i>ef</i>	1	1	1	1
104	75	<i>ef</i>	1	1	1	1
105	62	<i>Ef</i>	3	3	3	3
106	74	<i>ef</i>	1	1	1	1
107	71	<i>ef</i>	1	1	1	1
108	61	<i>Ef</i>	2	2	2	2
109	63	<i>Ef</i>	3	3	3	3
110	76	<i>ef</i>	1	1	1	1
111	63	<i>Ef</i>	3	3	3	3
112	63	<i>Ef</i>	2	2	2	2
113	77	<i>ef</i>	1	1	1	1
114	61	<i>Ef</i>	3	3	3	1
115	61	<i>Ef</i>	3	3	3	3
116	61	<i>Ef</i>	2	2	2	2
117	62	<i>Ef</i>	2	2	2	0
118	61	<i>Ef</i>	3	3	3	3
119	65	<i>Ef</i>	3	3	3	3
120	78	<i>ef</i>	1	1	1	1
121	65	<i>Ef</i>	3	3	3	3
122	78	<i>ef</i>	1	1	1	1
123	61	<i>Ef</i>	3	3	3	3
124	74	<i>ef</i>	1	1	1	1
125	77	<i>ef</i>	1	1	1	1
126	62	<i>Ef</i>	3	3	3	3
127	71	<i>ef</i>	1	1	1	1
128	61	<i>Ef</i>	2	2	2	2
129	61	<i>Ef</i>	2	2	2	2
130	65	<i>Ef</i>	3	3	3	3
131	61	<i>Ef</i>	3	3	3	3
132	61	<i>Ef</i>	3	3	3	3
133	62	<i>Ef</i>	3	3	3	3
134	61	<i>Ef</i>	3	3	3	3
135	62	<i>Ef</i>	3	3	3	3
136	62	<i>Ef</i>	3	3	3	3
137	61	<i>Ef</i>	3	3	3	3
138	61	<i>Ef</i>	3	3	3	3
139	61	<i>Ef</i>	2	2	2	2
140	64	<i>Ef</i>	3	3	3	0
141	64	<i>Ef</i>	2	2	2	0
142	63	<i>Ef</i>	3	3	3	3
143	61	<i>Ef</i>	3	3	3	0
144	61	<i>Ef</i>	3	3	3	3
145	63	<i>Ef</i>	3	1	3	3
146	62	<i>Ef</i>	3	3	3	3
147	62	<i>Ef</i>	3	3	3	3

1): 1, 2, 3 and 0 represents Taichung 65 homozygous, *O. glaberrima* homozygous, heterozygous and missing data, respectively.

Appendix 4. Detailed genotypes of the *S18* mapping population used in Chapter V.

Plant	Pollen fertility	Determined genotypes at <i>S18</i> ¹⁾	Genotypes at marker loci (chromosome 2)					
			C489 (10)	L682 (10)	G1084 (10)	R1629 (10)	C1496 (6)	C1084 (6)
1	2.0%	3	3	3	3	3	3	3
2	60.2%	1	1	1	1	1	3	3
4	41.5%	1	1	1	1	1	3	3
5	15.7%	3	3	3	3	3	3	3
6	0.0%	3	1	1	1	3	3	3
7	0.0%	3	3	3	3	3	1	1
9	54.7%	1	1	1	1	1	3	3
11	45.1%	1	1	1	1	1	3	3
12	0.0%	3	3	3	3	3	3	3
14	0.0%	3	3	3	3	3	3	3
15	0.0%	3	3	3	3	3	3	3
16	0.0%	3	3	3	3	3	1	1
17	1.6%	3	3	3	3	3	3	3
18	0.0%	3	3	3	3	3	3	3
19	0.0%	3	3	3	3	3	3	3
20	52.7%	1	1	1	1	1	3	3
21	14.5%	3	3	3	3	3	3	3
23	14.1%	3	3	3	3	3	3	3
25	68.1%	1	1	1	1	1	3	3
26	90.6%	1	1	1	1	1	1	1
27	0.0%	3	3	3	3	3	3	3
29	56.0%	1	1	1	1	1	3	3
32	0.0%	3	3	3	3	3	3	3
33	3.2%	3	1	1	3	3	3	3
34	53.1%	1	1	1	1	1	3	3
36	0.0%	3	3	3	3	3	3	3
37	50.0%	1	1	1	1	1	3	3
38	0.0%	3	3	3	3	3	3	3
40	48.1%	1	1	1	1	1	3	3
41	52.9%	1	1	1	1	1	3	3
42	0.0%	3	3	3	3	3	3	3
44	0.0%	3	1	3	3	3	3	3
45	49.9%	1	1	1	1	1	3	3
48	52.5%	1	1	1	1	1	3	3
49	82.4%	1	1	1	1	1	1	1
50	0.0%	3	3	3	3	3	3	3
51	0.0%	3	3	3	3	3	1	1
52	53.8%	1	1	1	1	1	3	3
54	95.0%	1	1	1	1	1	1	1
55	53.2%	1	1	1	1	1	3	3
56	53.6%	1	3	3	3	1	3	3
57	0.0%	3	3	3	3	3	3	3
58	0.0%	3	3	3	3	3	1	1
59	97.8%	1	1	1	1	1	3	3
60	0.0%	3	3	3	3	3	3	3
61	42.3%	1	1	1	1	1	3	3
62	0.0%	3	3	3	3	3	3	3
63	59.0%	1	1	1	1	1	3	3
64	9.7%	3	3	3	3	3	1	1
65	43.2%	1	1	1	1	1	3	3
66	53.6%	1	1	1	1	1	3	3
67	54.6%	1	1	1	1	1	3	3
68	93.4%	1	1	1	1	1	1	1
69	53.5%	1	1	1	1	1	3	3
70	50.9%	1	1	1	1	1	3	3
71	87.2%	1	1	1	1	1	1	1
72	0.0%	3	3	3	3	1	3	3

1), 2): 1, 3 represents Taichung 65 homozygous and heterozygous, respectively.

