

## RFLP(制限酵素DNA断片長多型)を利用したイネの連鎖 地図作成に関する研究

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## 摘要

イネの連鎖地図を一層充実させるために、九州大学農学部育種学教室で作成されてきた従来の連鎖地図(Iwata *et al.* 1984, 1989a, 1989b)とSaito *et al.* (1991)のRFLP連鎖地図との統合を試み、以下の実験を行なった。

(1) イネの12の染色体とRFLP連鎖群との対応関係を明らかにするために、日本型品種日本晴のトリソミックシリーズにインド型品種IR24を交配して得られた日印交雑トリソミックF<sub>1</sub>のシリーズを用いた分析を行なった。日印交雑トリソミックF<sub>1</sub>のDNAをRFLPクローンをプローブとしたサザンハイブリダイゼーションに供し、トリソミックスの過剰染色体に起因する遺伝子量効果を検出してRFLPクローンの座乗染色体を決定した。その結果、染色体1, 5, 7, 8, 9および10に対応するRFLP連鎖群が新たに判明し、染色体2, 3, 4, 6, 11および12に対応するRFLP連鎖群の再確認をすることができた。

(2) 過剰染色体の構造が不明のトリソミックスについて、RFLP連鎖地図に位置づけられているDNAクローンをプローブとしてサザン分析を行ない、遺伝子量効果を検出してその過剰染色体の構造を推定した。その結果、染色体8に関する二次トリソミックス様植物、ならびに、染色体11に関する二次トリソミックス様植物と2種類のアクトトリソミックス様あるいはテロトリソミックス様植物とを見出した。ただし、染色体11に関する2種類のアクトトリソミックス様あるいはテロトリソミックス様植物の過剰染色体の構造の差違は検出できなかった。

(3) インド型品種IR24と日本型標識遺伝子系統との交雑F<sub>2</sub>あるいはF<sub>3</sub>集団を用い、以下の標識遺伝子についてRFLPマーカーとの配列関係を明らかにした。

染色体1：*fs-2*(かすり縞-2)，*d-18*(小丈玉錦型矮性)，*d-2*(夷型矮性)，*rl-2*(捲葉-2)，*spl-6*(病斑葉-6)，*eg*(過剰穎)

染色体2：*tri*(三角粉)，*bl-1*(褐斑葉-1)，*spl-2*(病斑葉-2)

染色体3：*chl-1*(黄緑葉-1)，*fc-1*(細稈-1)，*st(t)*(CM120)(縦縞)，*dl*(垂れ葉)，*spl-3*(病斑葉-3)

染色体4：*d-11*(信金愛国型矮性)，*Ph*(フェノール反応)，*lg*(無葉舌)

染色体5：*d-1*(大黒型矮性)，*st(t)*(CM37)(縦縞)，*spl-7*(病斑葉-7)，*nl-1*(穂首苞葉-1)

染色体6：*dp-1*(内穎發育不全-1)，*spl-4*(病斑葉-4)，*Cl*(小穂叢生)

染色体7：*d-6*(短稈白笹型矮性)，*g-1*(長護穎-1)，*spl-5*(病斑葉-5)，*v-11*(緑変白苗-11)

染色体8：*sug*(甘味胚乳)，*v-8*(緑変白苗-8)

染色体9：*I-Bf*(穎縦筋褐色抑制)，*dp-2*(内穎發育不全-2)，*drp-2*(濡れ葉-2)，*Dn-1*(密穂-1)

染色体10：*spl-10*(病斑葉-10)，*pgl*(淡緑葉)

染色体11：*z-2*(ゼブラ斑葉-2)，*v-9*(緑変白苗-9)

染色体12：*spl-1*(病斑葉-1)，*rl-1*(捲葉-1)

これにより、イネの12の染色体すべてにわたって、従来の連鎖地図とRFLP連鎖地図との対応関係が明らかになった。

(4) 従来、染色体4の連鎖群に属するとされてきた*d-2*は、RFLPマーカーとの連鎖関係により、染色体1に座位が明らかとなった。また、染色体9の*I-Bf*と*dp-2-drp-2-Dn-1*群との配列関係も、RFLPマーカーを介して、*I-Bf-dp-2-drp-2-Dn-1*であることが明らかとなった。

(5) 染色体2の *tri* および *spl-2*, 染色体3の *chl-1*, 染色体4の *lg*, 染色体6の *dp-1* および *spl-4*, 染色体7の *d-6*, *g-1*, *spl-5* および *v-11*, 染色体8の *sug* および *v-8* はいずれも RFLP連鎖地図の末端よりも外側に座位があり, RFLP連鎖地図は飽和していないと考えられた.

(6) 染色体1の *fs-2-XNpb216-XNpb96-d-18-XNpb269-XNpb359-d-2* の領域, 染色体2の *bl-1-XNpb57-XNpb42* の領域, 染色体3の *XNpb164-XNpb249-fc-1-st(t)(CM120)-XNpb51-XNpb15-XNpb182* の領域, 染色体6の *XNpb165-1*, 染色体11の *XNpb389-XNpb78-z-2-gmZ410* の領域および染色体12の *rl-1-XNpb148-XNpb198* の領域では日本型の遺伝子型の分離比が有意に減少していた. 染色体2で見出された分離の歪みはこれまでに報告のない新たなものである.

(7) 本研究により, 従来の連鎖地図と RFLP連鎖地図との対応関係は明らかになったが, 今後, 連鎖地図ならびにこれに位置づけられている遺伝マーカーを基礎的・応用的に利用するには RFLP連鎖地図の一層の拡充が必要である. そのためには, これまで多型が得られず, 連鎖地図作成に用いられてこなかった DNA クローンを用いるための交雑組合せの多様化や新たな DNA マーカーの利用についても検討すべきであると考えた.

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Studies on the construction of a linkage map using RFLP  
(Restriction Fragment Length Polymorphism) in rice

O. Ideta

(Summary)

In order to construct a more detailed linkage map of rice, the study for integration of the classical linkage map and the RFLP linkage map was carried out. The results are as follows.

(1) The relationship between RFLP linkage groups and their respective chromosomes was established via RFLP gene dosage analysis of hybrid primary trisomics. These hybrid trisomics were developed by crossing between Nipponbare primary trisomics (a Japonica cultivar) and IR24 (an Indica cultivar). In this study, six RFLP linkage groups corresponding to the chromosomes 1, 5, 7, 8, 9 and 10 were found out. The previous assignment of six RFLP linkage groups to chromosomes 2, 3, 4, 6, 11 and 12 by chromosome specific marker genes were confirmed.

(2) A secondary-trisomic like plants for chromosome 8, and another secondary-trisomic like plants and two types of acrotrisomic like plants for chromosome 11 were identified through detection of duplication or deficiency of extra chromosomes via RFLP gene dosage analysis.

(3) Forty classical markers and 83 RFLP markers were mapped together of all the 12 chromosomes in rice through observing 17 F<sub>2</sub> populations and one F<sub>3</sub> population derived from the crosses between an Indica variety IR24 and Japonica lines with different classical markers. The marker genes mapped in this study were as follows.

chromosome 1

*fs-2* (fine stripe-2), *d-18* (Kotaketamanishiki dwarf), *d-2* (Ebisu dwarf), *rl-2* (rolled leaf-2), *spl-6* (spotted leaf-6) and *eg* (extra glume).

chromosome 2

*tri* (triangular hull), *bl-1* (brown leaf spot-1) and *spl-2* (spotted leaf-2).

chromosome 3

*chl-1* (chlorina-1), *fc-1* (fine culm-1), *st(t)* (CM120) (stripe), *dl* (drooping leaf) and *spl-3* (spotted leaf-3)

chromosome 4

*d-11* (Shinkane-aikoku dwarf), *Ph* (Phenol staining) and *lg* (liguleless).

chromosome 5

*d-1* (Daikoku dwarf), *st(t)* (CM37) (stripe), *spl-7* (spotted leaf-

7) and *nl-1* (neck leaf-1).

chromosome 6

*dp-1* (depressed palea-1), *spl-4* (spotted leaf-4) and *Cl* (Clustered spikelets).

chromosome 7

*g-1* (long sterile lemmas-1), *d-6* (Tankanshirasasa dwarf), *spl-5* (spotted leaf-5) and *v-11* (virescent-11).

chromosome 8

*v-8* (virescent-8) and *sug* (sugary endosperm).

chromosome 9

*I-Bf* (Inhibitor for brown furrows of hull), *dp-2* (depressed palea-2), *drp-2* (dripping-wet leaf-2) and *Dn-1* (Dense panicle-1).

chromosome 10

*spl-10* (spotted leaf-10) and *pgl* (pale green leaf).

chromosome 11

*z-2* (zebra-2) and *v-9* (virescent-9).

chromosome 12

*spl-1* (spotted leaf-10) and *rl-1* (rolled leaf-1).

(4) The gene *d-2*, which had been belonged to linkage group 4, was found to be located on chromosome 1 through the detection of linkages between *d-2* and several RFLP markers mapped on chromosome 1. The locus of unlocated gene *I-Bf* was determined and the liner order of classical marker genes *I-Bf-dp-2-drp-2-Dn-1* on chromosome 9 was established.

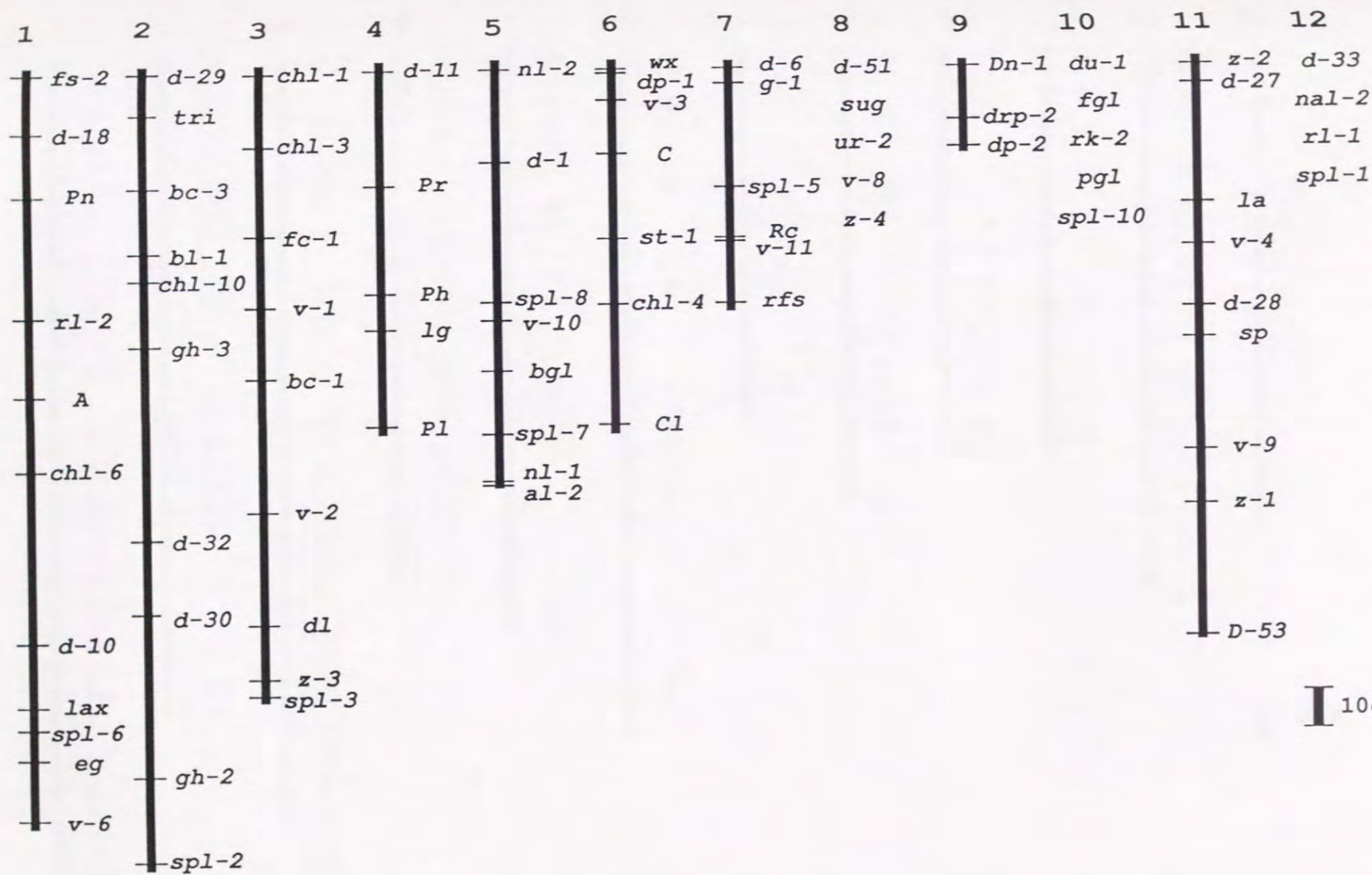
(5) Genes *tri*, *spl-2* (chromosome 2), *chl-1* (chromosome 3), *lg* (chromosome 4), *dp-1*, *spl-4* (chromosome 6), *d-6*, *g-1*, *spl-5* (chromosome 7), *sug* and *v-8* (chromosome 8) were estimated to be located beyond the terminal ends of the RFLP linkage map. The RFLP linkage map was revealed not to be saturated.

(6) The segregation distortions were detected on five regions. In the regions of *fs-2-XNpb216-XNpb96-d-18-XNpb269-XNpb359-d-2* on chromosome 1, *bl-1-XNpb57-XNpb42* on chromosome 2, *XNpb164-XNpb249-fc-1-st(t) (CM120)-XNpb51-XNpb15-XNpb182* on chromosome 3, *XNpb165-1* on chromosome 6, *XNpb389-XNpb78-z-2-gmZ410* on chromosome 11 and *rl-1-XNpb148-XNpb198* on chromosome 12, the Japonica/Japonica allele frequencies of both classical and RFLP markers showed significantly less than the normal frequency of 25%. On the segregation distortion newly found on chromosome 2, more investigation is needed.

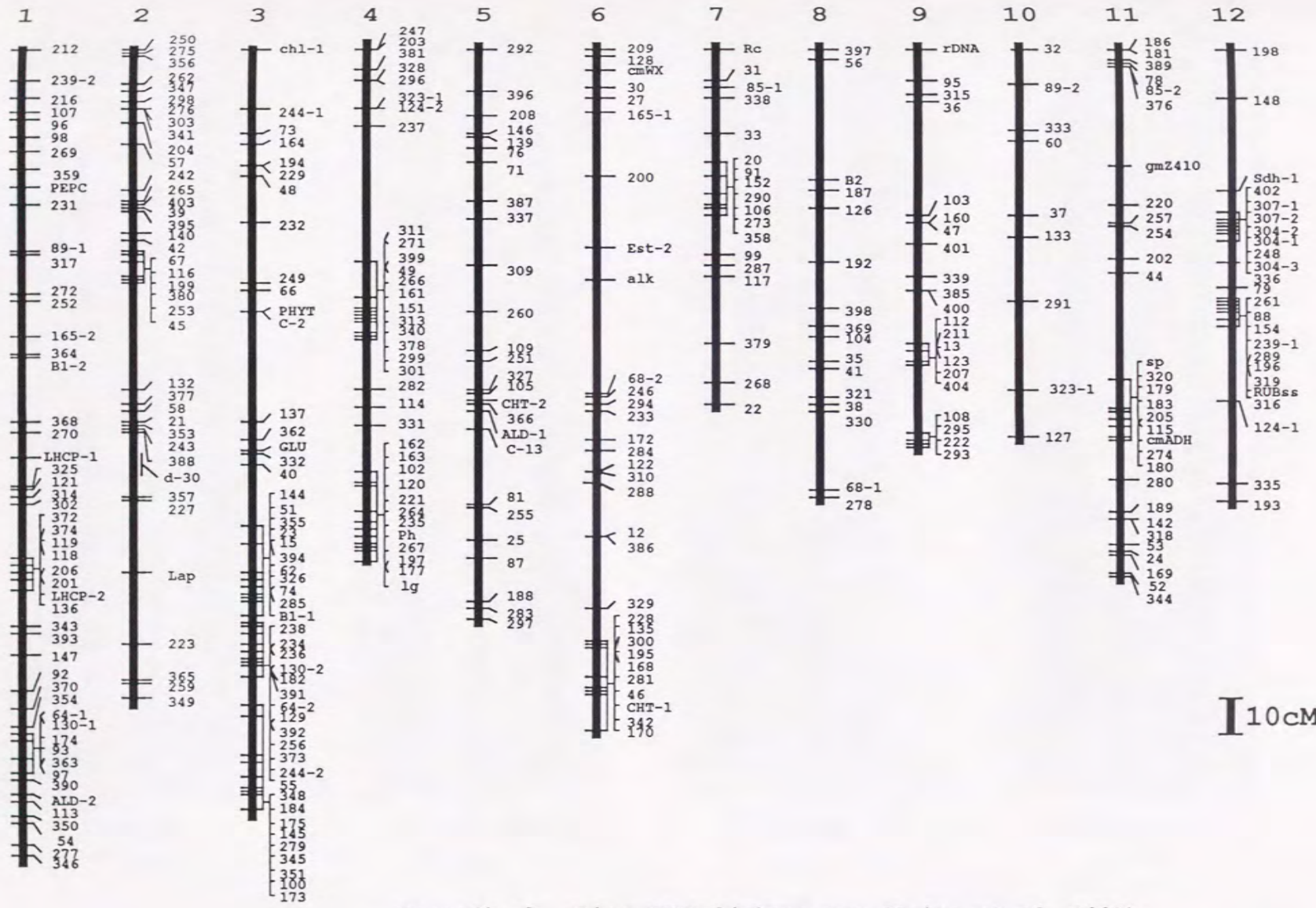
(7) The relationship between the classical linkage map and the RFLP linkage map was established. This information is useful

to estimate linkages between classical marker genes and RFLP markers. But, only a more fully saturated linkage map of rice can offer opportunities for applications in genetics and breeding. More various cross combinations for employing DNA clones which have not been used for previous mapping efforts and new kinds of DNA markers would be useful to construct a more highly detailed linkage map.

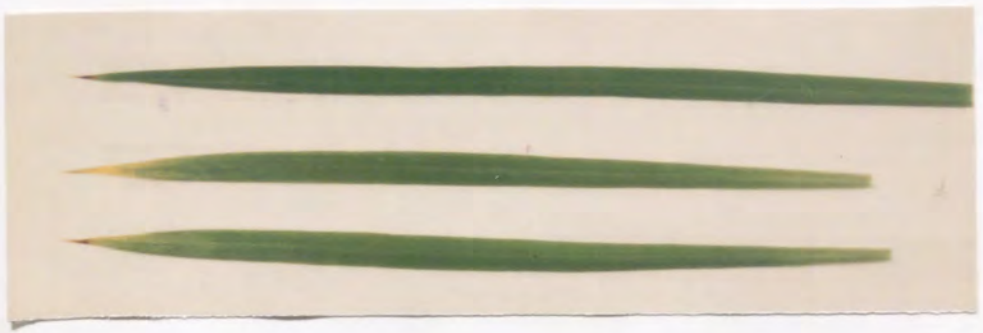




Appendix 1. Rice classical linkage map (Iwata et al. 1984, 1989a, 1989b).



Appendix 2. Rice RFLP linkage map (Saito et al. 1991).



virescent-8  
(v-8)



virescent-4  
(v-4)



stripe (CM37)  
(st)



Normal  
(+)

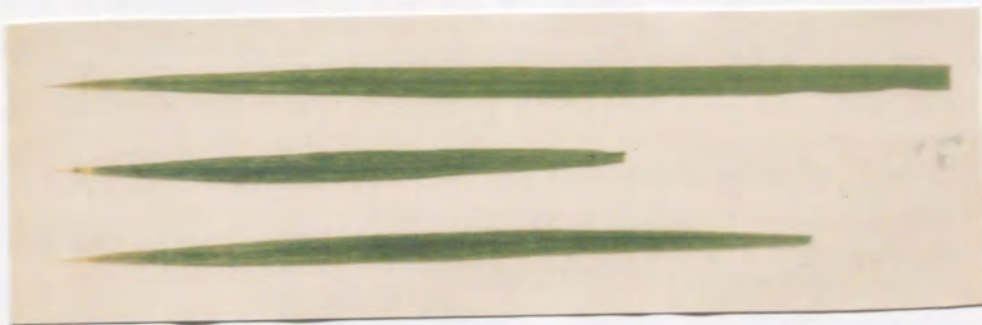
Appendix 3. Marker genes tested in this study.



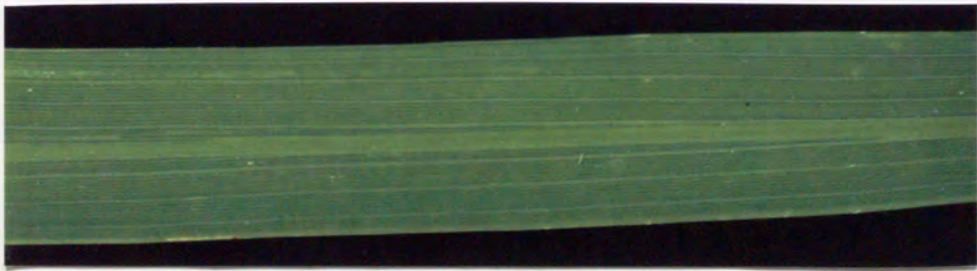
virescent-11  
(v-11)



virescent-10  
(v-10)



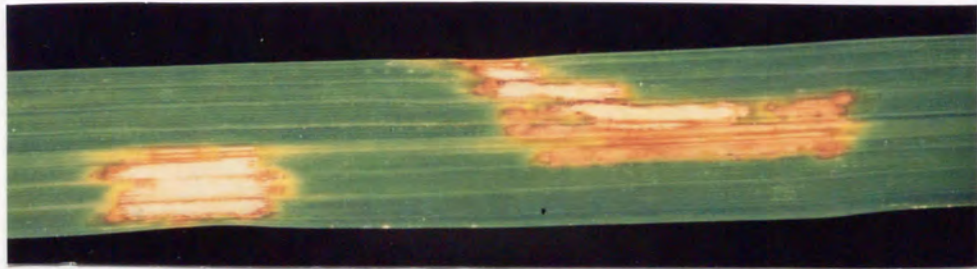
virescent-9  
(v-9)



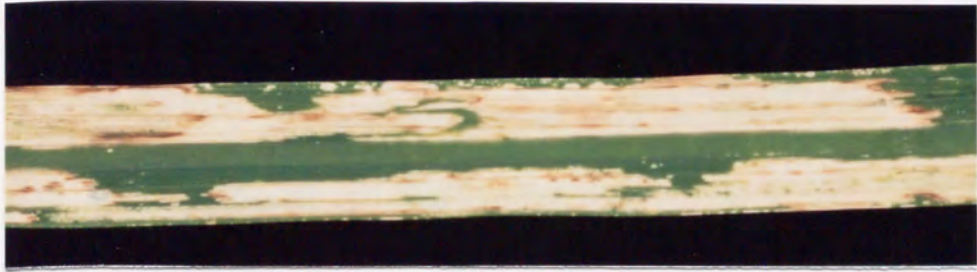
Normal  
(+)



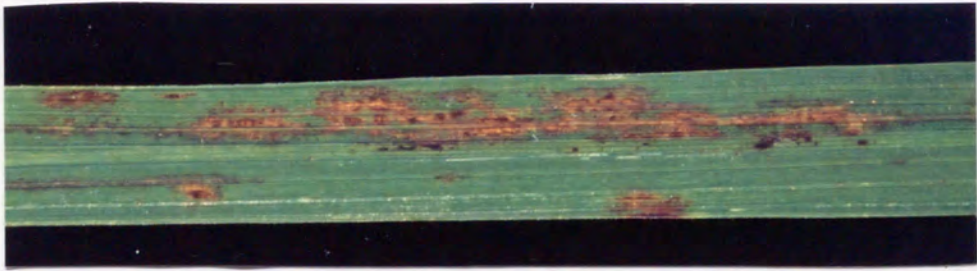
brown leaf spot-1  
(bl-1)



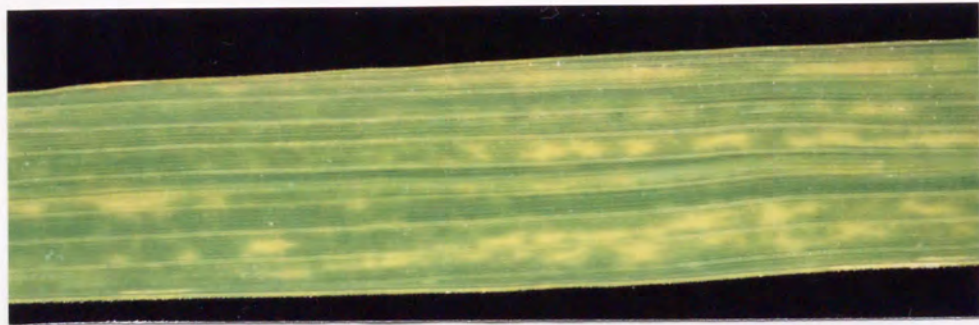
spotted leaf-1  
(spl-1)



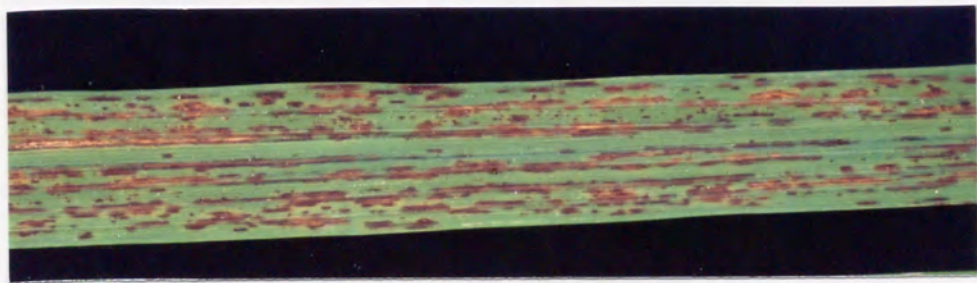
spotted leaf-2  
(spl-2)



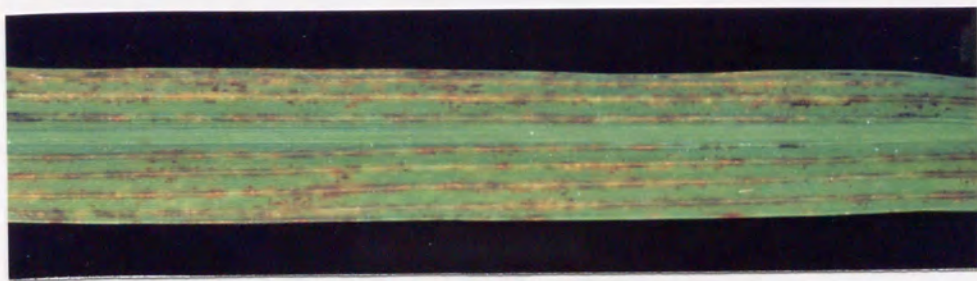
spotted leaf-3  
(spl-3)



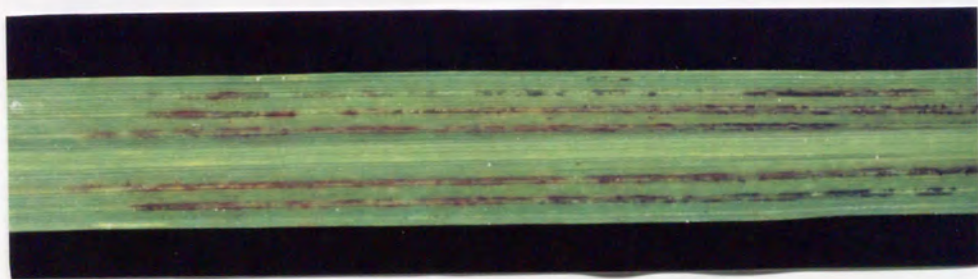
spotted leaf-10  
(*spl-10*)



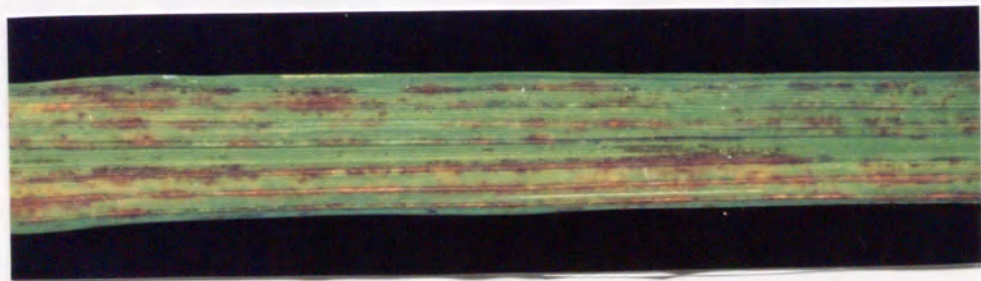
spotted leaf-7  
(*spl-7*)



spotted leaf-6  
(*spl-6*)



spotted leaf-5  
(*spl-5*)

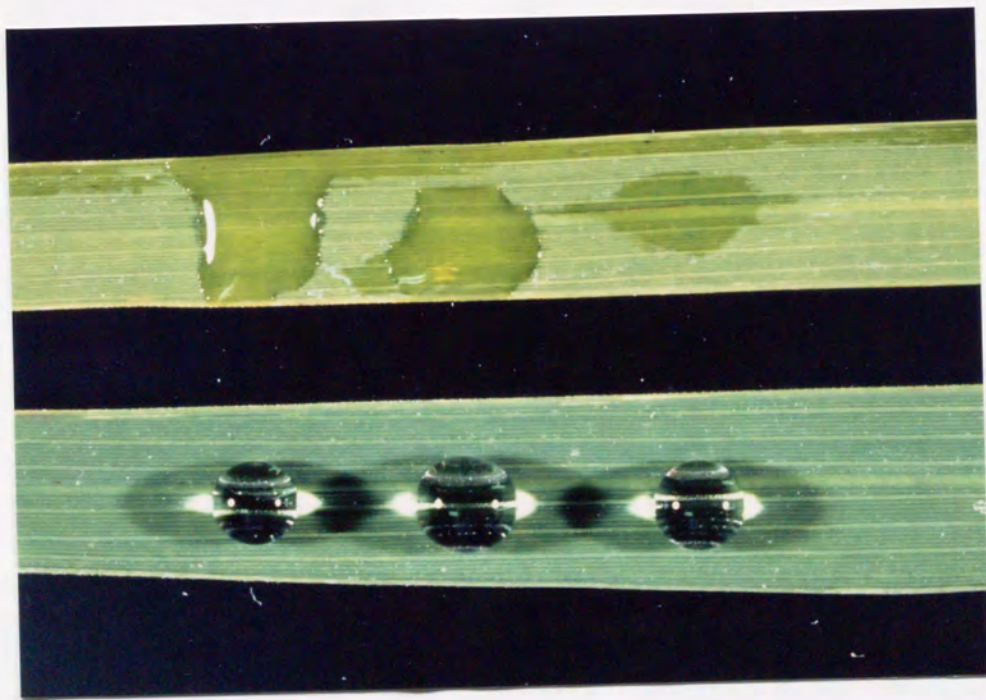


spotted leaf-4  
(*spl-4*)



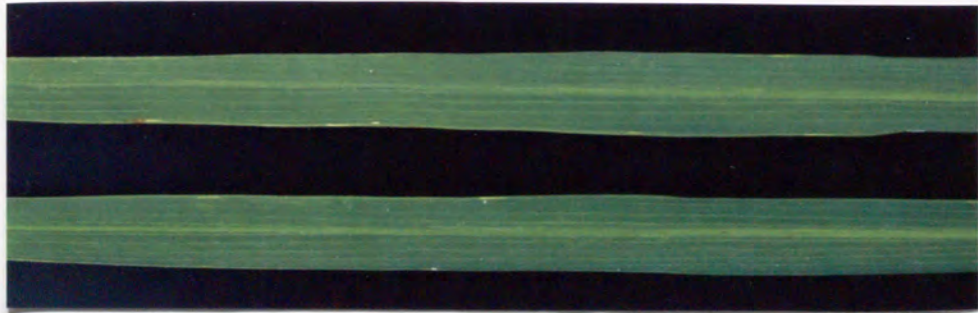
liguleless  
(lg)

Normal  
(+)

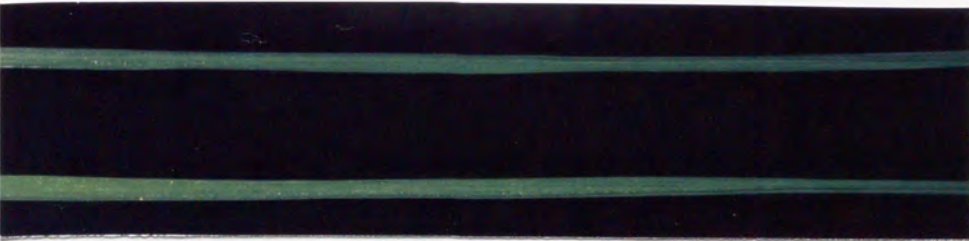


Normal dripping wet leaf-2  
(+)

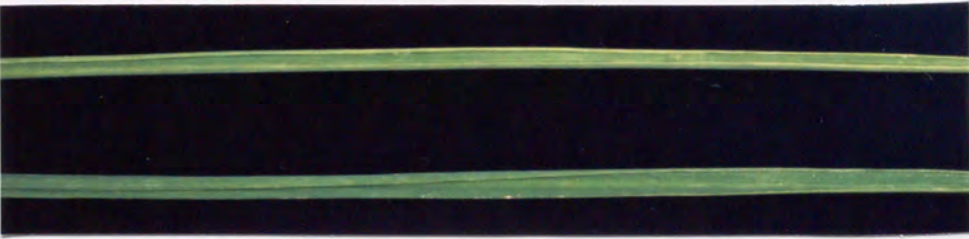
(drp-2)



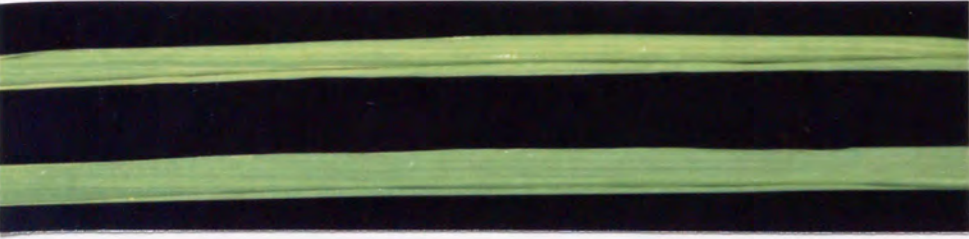
Normal  
(+)



narrow leaf-1  
(nal-1)



rolled leaf-1  
(rl-1)

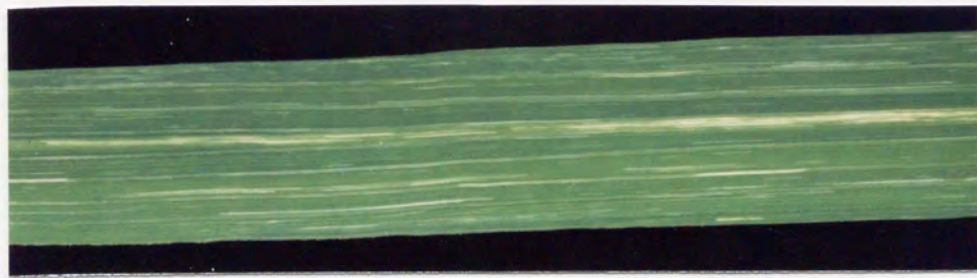


rolled leaf-2  
(rl-2)

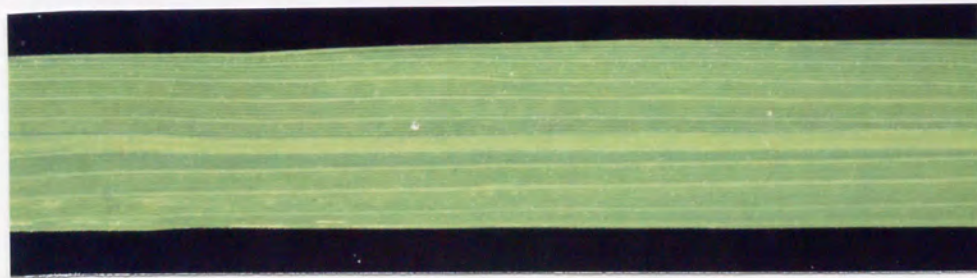




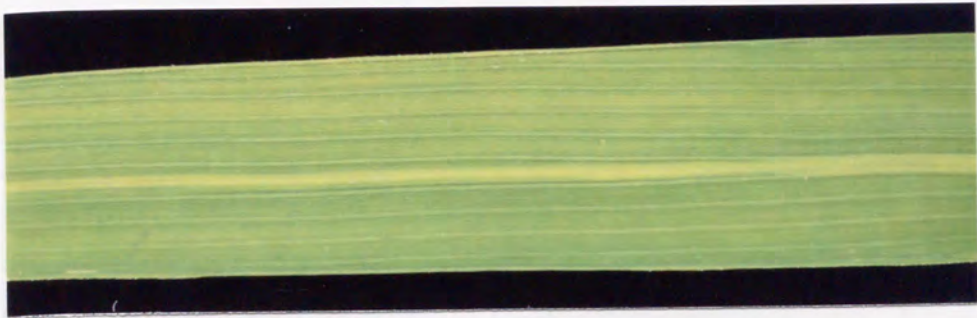
Normal  
(+)



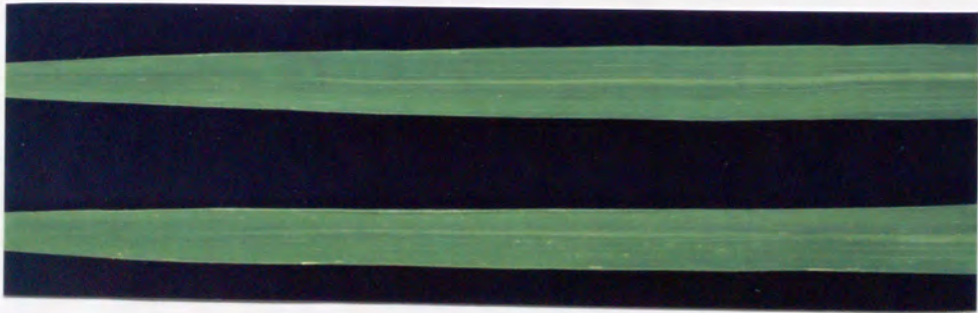
fine stripe-2  
(fs-2)



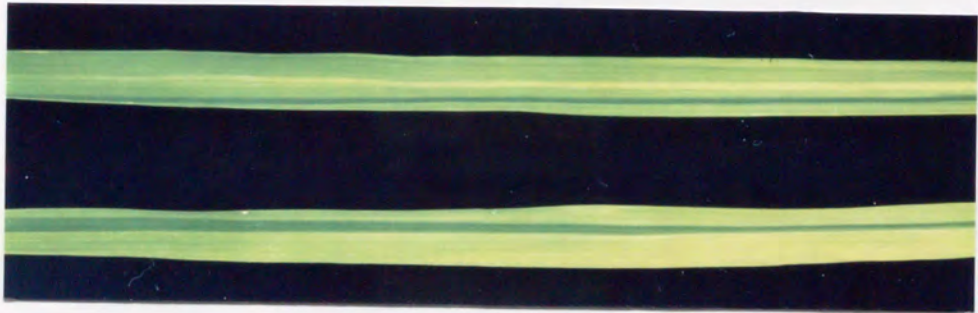
chlorina-1  
(chl-1)



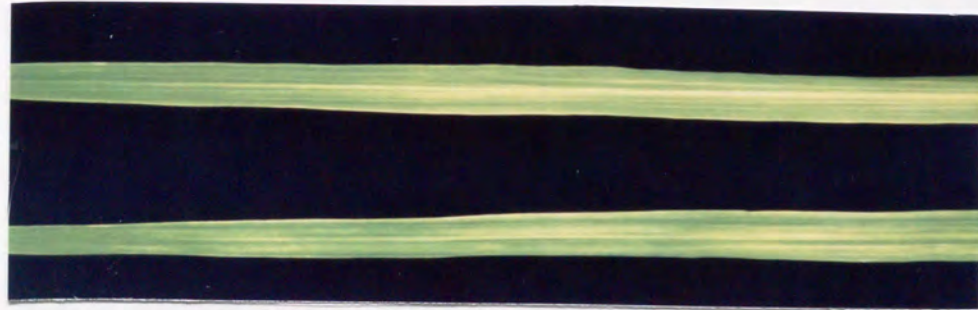
pale green leaf  
(pgl)



Normal  
(+)



stripe (CM120)  
(st)



zebra-2  
(z-2)



Normal (Taichung 65)  
(+)



Daikoku dwarf  
(d-1)



Ebisu dwarf  
(d-2)



Kotaketamanishiki dwarf  
(d-18)

Kikeibanshinriki dwarf  
(d-10)

Tankanshirasasa dwarf  
(d-6)



lazy growth habit  
(1a)



fine culm-1  
(fc-1)



drooping leaf  
(dl)



Shinkane-aikoku dwarf  
(d-11)



Daikoku dwarf  
(d-1)



Clustered spikelets  
(Cl)



Normal  
(+)



short panicle  
(sp)



neck leaf-1  
(nl-1)



lax panicle  
(lax)

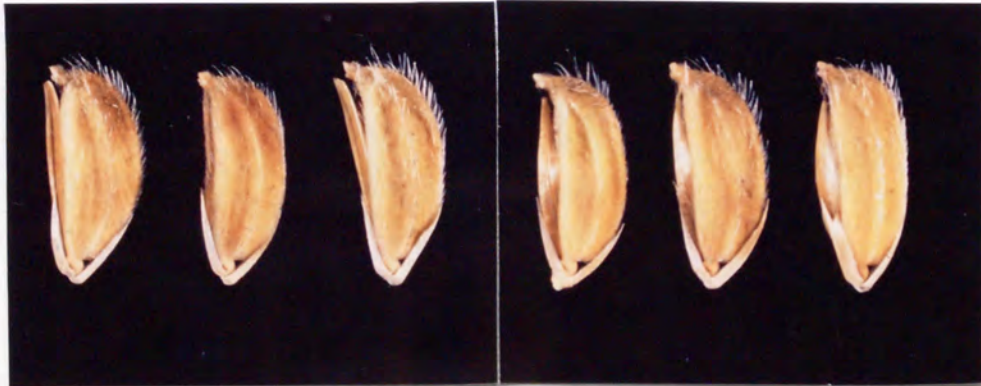


Dense panicle-1  
(Dn-1)



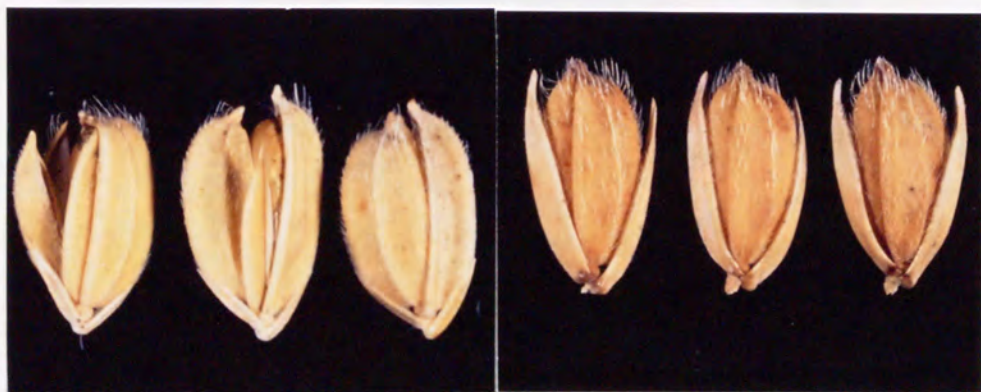
Normal  
(+)

brown leaf spot-1  
(bl-1)



depressed palea-1  
(dp-1)

depressed palea-2  
(dp-2)



extra glume  
(eg)

long sterile lemmas-1  
(g-1)





Inhibitor for brown furrows of hull  
(*I-Bf*)

triangular hull  
(*tri*)



(+)

(*Ph*)

control

stained

Phenol staining (*Ph*)



Normal  
(+)

sugary endosperm  
(*sug*)

Appendix 4. Linkage data

Chromosome 1

Gene pair A(a) — B(b)		Segregation mode									Total	$\chi^2$ (linkage)	Recombination value (%)
		AABB	AABb	AAbb	AaBB	AaBb	Aabb	aaBB	aaBb	aabb			
<i>fs-2</i> — <i>XNpb216</i>		32	80	8	-	-	-	0	2	15	137	38.4 **	8.6 ± 2.5
<i>fs-2</i> — <i>XNpb96</i>		33	77	9	-	-	-	0	3	14	136	32.7 **	10.6 ± 2.8
<i>fs-2</i> — <i>d-18</i>		128	-	8	-	-	-	3	-	14	153	35.5 **	9.3 ± 2.5
<i>fs-2</i> — <i>XNpb269</i>		34	76	9	-	-	-	0	3	14	136	32.7 **	10.6 ± 2.8
<i>fs-2</i> — <i>XNpb359</i>		38	73	9	-	-	-	1	3	13	137	29.0 **	12.8 ± 3.0
<i>fs-2</i> — <i>XNpb252</i>		39	53	27	-	-	-	4	6	7	136	2.2	40.4 ± 5.1
<i>fs-2</i> — <i>XNpb314</i>		32	58	30	-	-	-	1	10	6	137	1.8	41.3 ± 5.1
<i>XNpb216</i> — <i>XNpb96</i>		28	5	0	6	70	5	0	5	18	137	130.3 **	8.1 ± 1.7
<i>XNpb216</i> — <i>d-18</i>		32	-	0	76	-	6	7	-	16	137	36.9 **	10.9 ± 2.8
<i>XNpb216</i> — <i>XNpb269</i>		24	9	0	11	63	7	0	7	16	137	82.2 **	13.5 ± 2.2
<i>XNpb216</i> — <i>XNpb359</i>		23	10	0	16	58	8	1	8	14	138	59.3 **	17.8 ± 2.6
<i>XNpb216</i> — <i>d-2</i>		86	-	16	0	-	0	11	-	5	118	2.4	34.6 ± 5.6
<i>XNpb216</i> — <i>XNpb252</i>		8	15	10	26	38	17	9	7	7	137	2.5	>50
<i>XNpb216</i> — <i>XNpb314</i>		9	14	10	19	44	19	5	11	7	138	1.4	49.0 ± 4.3
<i>XNpb96</i> — <i>d-18</i>		33	-	0	78	-	2	3	-	20	136	62.3 **	4.1 ± 1.7
<i>XNpb96</i> — <i>XNpb269</i>		67	9	1	11	138	9	0	4	32	271	311.5 **	6.7 ± 1.1
<i>XNpb96</i> — <i>XNpb359</i>		61	10	0	15	126	8	1	7	27	255	252.0 **	8.7 ± 1.3
<i>XNpb96</i> — <i>d-2</i>		36	-	4	55	-	12	6	-	5	118	6.2 *	30.0 ± 4.9
<i>XNpb96</i> — <i>XNpb252</i>		27	37	13	44	79	35	12	12	12	271	4.5	43.9 ± 3.0
<i>XNpb96</i> — <i>XNpb314</i>		24	36	17	46	77	35	8	18	10	271	1.6	46.2 ± 3.0
<i>d-18</i> — <i>XNpb269</i>		34	79	1	-	-	-	0	0	22	136	77.7 **	0.8 ± 0.8
<i>d-18</i> — <i>XNpb359</i>		39	74	2	-	-	-	0	2	20	137	64.2 **	3.4 ± 1.6
<i>d-18</i> — <i>XNpb252</i>		37	50	27	-	-	-	6	9	7	136	0.8	44.7 ± 5.2
<i>d-18</i> — <i>XNpb314</i>		30	56	29	-	-	-	3	12	7	137	1.0	44.0 ± 5.2
<i>XNpb269</i> — <i>XNpb359</i>		71	1	0	6	135	1	0	7	34	255	394.0 **	3.0 ± 0.8
<i>XNpb269</i> — <i>d-2</i>		35	-	4	54	-	8	7	-	9	117	12.6 **	25.4 ± 4.6
<i>XNpb269</i> — <i>XNpb252</i>		31	36	11	41	76	34	11	16	15	271	10.3 *	40.4 ± 2.9
<i>XNpb269</i> — <i>XNpb314</i>		27	36	15	42	76	33	9	19	14	271	4.8	43.0 ± 3.0
<i>XNpb359</i> — <i>d-2</i>		32	-	3	56	-	6	1	-	9	107	20.2 **	15.6 ± 3.8
<i>XNpb359</i> — <i>XNpb252</i>		34	36	7	37	71	35	7	15	13	255	20.2 **	36.5 ± 2.8
<i>XNpb359</i> — <i>r1-2</i>		12	33	9	9	27	15	3	12	6	126	4.1	45.9 ± 4.4
<i>XNpb359</i> — <i>XNpb368</i>		16	31	8	11	34	11	4	13	5	133	3.3	43.2 ± 4.2
<i>XNpb359</i> — <i>XNpb314</i>		28	36	13	41	71	33	5	17	13	257	8.4	40.4 ± 3.0
<i>XNpb359</i> — <i>XNpb147</i>		10	32	14	12	30	13	3	13	6	133	1.2	>50
<i>XNpb359</i> — <i>XNpb130</i>		13	20	22	12	28	16	5	11	6	133	7.5	>50
<i>XNpb359</i> — <i>XNpb174</i>		14	20	22	11	29	16	4	11	6	133	8.0	>50
<i>XNpb359</i> — <i>sp1-6</i>		15	20	21	12	30	14	5	11	6	134	7.9	>50
<i>XNpb359</i> — <i>XNpb97</i>		15	0	41	14	0	42	5	0	17	134	0.2	48.1 ± 5.3
<i>XNpb359</i> — <i>eg</i>		14	29	13	14	27	15	5	12	5	134	0.4	49.4 ± 4.3
<i>XNpb359</i> — <i>XNpb346</i>		14	22	18	12	31	12	5	10	5	129	4.5	>50
<i>d-2</i> — <i>XNpb252</i>		32	50	14	-	-	-	5	9	7	117	3.8	36.9 ± 5.3

to be continued

chromosome 1 continued

d-2 - XNpb314	33	48	16	-	-	-	7	7	7	118	2.8	41.2 ± 5.5
XNpb252 - r1-2	17	13	3	7	54	8	0	3	18	123	64.7 **	16.7 ± 2.7
XNpb252 - XNpb368	20	11	3	10	59	5	0	5	16	129	68.8 **	15.9 ± 2.5
XNpb252 - XNpb314	59	47	11	44	135	23	3	24	54	400	139.8 **	23.7 ± 1.8
XNpb252 - XNpb147	9	19	7	13	40	21	3	12	5	129	1.5	46.0 ± 4.4
XNpb252 - XNpb130	11	10	13	13	38	23	6	10	5	129	6.4	>50
XNpb252 - XNpb174	12	10	13	13	38	23	4	12	5	130	7.5	50.0
XNpb252 - spl-6	11	12	12	16	36	22	5	12	4	130	4.0	>50
XNpb252 - XNpb97	12	-	23	13	-	61	8	-	13	130	5.4	49.0 ± 5.4
XNpb252 - eg	10	17	8	14	43	17	9	6	6	130	5.7	>50
XNpb252 - XNpb346	7	15	10	14	41	19	10	5	5	126	7.0	>50
r1-2 - XNpb368	19	5	0	7	63	1	1	7	22	125	110.1 **	9.3 ± 1.9
r1-2 - XNpb314	12	10	1	11	55	6	2	10	18	125	46.5 **	19.7 ± 2.9
r1-2 - XNpb147	9	12	3	11	40	21	2	19	8	125	7.5	37.9 ± 4.1
r1-2 - XNpb130	11	11	1	11	31	30	5	15	10	125	17.1 **	38.6 ± 4.2
r1-2 - XNpb174	12	11	1	11	30	30	3	17	10	125	20.8 **	36.9 ± 4.1
r1-2 - spl-6	11	14	2	15	32	28	4	18	10	134	12.6 *	39.7 ± 4.1
r1-2 - XNpb97	11	-	13	13	-	59	7	-	23	126	6.4	38.6 ± 5.2
r1-2 - eg	11	15	2	14	42	19	7	12	13	135	10.8 *	36.7 ± 3.9
r1-2 - XNpb346	6	13	4	14	35	20	9	9	11	121	5.0	46.1 ± 4.5
XNpb368 - XNpb314	22	7	1	7	65	6	0	5	19	132	99.5 **	11.0 ± 2.1
XNpb368 - XNpb147	12	15	4	11	46	20	2	13	9	132	10.0 *	34.4 ± 3.8
XNpb368 - XNpb130	11	11	8	15	36	27	4	12	8	132	4.3	44.3 ± 4.3
XNpb368 - XNpb174	12	11	8	14	36	27	3	13	8	132	6.5	42.7 ± 4.2
XNpb368 - spl-6	11	13	7	17	35	26	4	13	7	133	3.9	44.5 ± 4.3
XNpb368 - XNpb97	11	-	20	16	-	62	7	-	17	133	2.8	45.6 ± 5.3
XNpb368 - eg	11	16	4	15	42	21	7	10	7	133	5.0	43.1 ± 4.2
XNpb368 - XNpb346	8	15	7	14	41	21	9	7	6	128	4.5	>50
XNpb314 - XNpb147	14	13	1	11	50	17	0	11	15	132	30.0 **	23.8 ± 3.1
XNpb314 - XNpb130	13	8	8	14	38	26	3	13	10	133	9.3	40.0 ± 4.1
XNpb314 - XNpb174	12	9	8	14	37	26	2	14	10	132	8.2	40.1 ± 4.1
XNpb314 - spl-6	12	10	7	16	37	25	4	13	9	133	5.6	41.8 ± 4.2
XNpb314 - XNpb97	10	-	19	17	-	61	6	-	20	133	1.8	43.8 ± 5.2
XNpb314 - eg	10	14	5	17	41	20	6	12	8	133	2.4	43.3 ± 4.2
XNpb314 - XNpb346	4	19	5	17	36	22	9	8	8	128	6.3	>50
XNpb147 - XNpb130	18	6	1	10	42	22	1	11	21	132	51.5 **	22.6 ± 3.0
XNpb147 - XNpb174	18	6	1	10	42	22	1	11	21	132	51.5 **	22.6 ± 3.0
XNpb147 - spl-6	18	7	0	12	41	22	2	12	19	133	44.2 **	24.3 ± 3.1
XNpb147 - XNpb97	16	-	9	15	-	60	3	-	30	133	20.8 **	24.9 ± 4.2
XNpb147 - eg	14	10	1	14	45	16	5	13	15	133	21.8 **	29.5 ± 3.5
XNpb147 - XNpb346	5	14	4	18	38	18	8	10	13	128	5.9	44.3 ± 4.3
XNpb130 - XNpb174	28	2	0	0	58	0	0	0	44	132	290.0 **	0.8 ± 0.5
XNpb130 - spl-6	27	3	0	4	53	2	1	4	39	133	217.9 **	5.8 ± 1.5
XNpb130 - XNpb97	25	0	5	7	0	52	1	0	43	133	70.0 **	11.5 ± 2.9
XNpb130 - eg	23	6	1	8	47	4	2	14	28	133	106.1 **	15.4 ± 2.4

to be continued

chromosome 1 continued

XNpb130 - XNpb346	13	15	1	14	30	13	3	18	21	128	30.2 **	30.3 ± 3.6
XNpb174 - spl-6	27	2	0	4	54	2	1	4	39	133	220.8 **	5.4 ± 1.4
XNpb174 - XNpb97	26	-	3	6	-	54	1	-	43	133	78.9 **	9.1 ± 2.6
XNpb174 - eg	23	6	0	8	47	5	2	14	28	133	106.5 **	15.0 ± 2.4
XNpb174 - XNpb346	14	14	0	14	31	14	3	18	21	129	33.2 **	29.0 ± 3.5
spl-6 - XNpb97	27	-	5	7	-	54	0	-	41	134	79.6 **	9.5 ± 2.6
spl-6 - eg	27	6	0	7	55	4	1	10	32	142	150.0 **	10.8 ± 2.0
spl-6 - XNpb346	15	16	0	14	32	13	2	15	22	129	41.4 **	27.0 ± 3.4
XNpb97 - eg	30	4	0	-	-	-	3	64	33	134	99.6 **	5.3 ± 2.0
XNpb97 - XNpb346	21	12	0	-	-	-	10	51	35	129	42.8 **	17.9 ± 3.7
eg - XNpb346	21	12	0	10	42	11	0	9	24	129	79.1 **	17.7 ± 2.7

\* and \*\* significant at 5% and 1% levels, respectively

## Chromosome 2

Gene pair A(a) — B(b)	Segregation mode									Total	$\chi^2$ (linkage)	Recombination value (%)
	AABB	AABb	AAbb	AaBB	AaBb	Aabb	aaBB	aaBb	aabb			
<i>tri</i> — <i>XNpb250</i>	38	49	10	-	-	-	0	5	13	115	27.8 **	16.1 ± 3.7
<i>tri</i> — <i>b1-1</i>	104	0	6	-	-	-	7	0	14	131	30.9 **	12.4 ± 3.1
<i>tri</i> — <i>XNpb57</i>	52	45	5	-	-	-	6	6	3	117	8.3 *	29.8 ± 4.9
<i>tri</i> — <i>XNpb42</i>	42	44	18	-	-	-	5	4	7	120	5.2	35.7 ± 5.2
<i>tri</i> — <i>XNpb45</i>	32	44	25	-	-	-	6	4	6	117	0.6	46.5 ± 5.6
<i>tri</i> — <i>XNpb132</i>	31	45	25	-	-	-	5	6	5	117	0.2	46.9 ± 5.6
<i>tri</i> — <i>XNpb227</i>	27	43	29	-	-	-	4	8	5	116	0.3	49.5 ± 5.7
<i>tri</i> — <i>XNpb223</i>	29	45	31	-	-	-	4	12	3	124	2.6	>50
<i>tri</i> — <i>XNpb349</i>	28	49	29	-	-	-	5	9	4	124	0.3	>50
<i>XNpb250</i> — <i>b1-1</i>	38	-	0	52	-	2	7	-	13	112	33.9 **	10.2 ± 3.0
<i>XNpb250</i> — <i>XNpb57</i>	28	10	0	17	31	4	6	7	4	107	43.9 **	26.8 ± 3.7
<i>XNpb250</i> — <i>XNpb42</i>	23	13	2	16	25	12	2	6	11	110	36.7 **	28.0 ± 3.7
<i>XNpb250</i> — <i>XNpb45</i>	16	19	3	14	23	15	5	3	11	109	18.0 **	35.7 ± 4.3
<i>XNpb250</i> — <i>XNpb132</i>	16	16	6	14	25	14	5	6	8	110	8.0	39.5 ± 4.5
<i>XNpb250</i> — <i>XNpb227</i>	12	16	9	12	26	15	5	7	7	109	2.0	45.6 ± 4.7
<i>XNpb250</i> — <i>XNpb223</i>	11	17	10	14	26	13	4	10	7	112	1.0	46.7 ± 4.7
<i>XNpb250</i> — <i>XNpb349</i>	12	15	11	12	27	15	5	11	5	113	2.2	49.2 ± 4.7
<i>b1-1</i> — <i>XNpb57</i>	54	47	3	-	-	-	3	3	5	115	18.9 **	16.6 ± 3.8
<i>b1-1</i> — <i>XNpb42</i>	45	47	14	-	-	-	1	0	11	118	22.6 **	18.4 ± 3.9
<i>b1-1</i> — <i>XNpb45</i>	35	46	22	-	-	-	1	2	9	115	8.4 *	29.6 ± 4.9
<i>b1-1</i> — <i>XNpb132</i>	33	44	26	-	-	-	1	7	4	115	2.8	41.2 ± 5.6
<i>b1-1</i> — <i>XNpb227</i>	27	44	30	-	-	-	2	6	4	113	0.6	48.3 ± 5.8
<i>b1-1</i> — <i>XNpb223</i>	30	47	30	-	-	-	1	9	4	121	2.2	45.3 ± 5.5
<i>b1-1</i> — <i>XNpb349</i>	29	50	28	-	-	-	2	8	5	122	0.8	44.5 ± 5.5
<i>XNpb57</i> — <i>XNpb42</i>	44	11	2	3	36	11	0	0	8	115	167.1 **	13.3 ± 2.4
<i>XNpb57</i> — <i>XNpb45</i>	31	18	5	7	27	16	0	2	6	112	61.1 **	26.4 ± 3.6
<i>XNpb57</i> — <i>XNpb132</i>	24	24	7	12	22	16	0	4	4	113	21.6 **	35.5 ± 4.2
<i>XNpb57</i> — <i>XNpb227</i>	18	27	9	11	20	20	2	2	4	113	9.5 *	42.6 ± 4.6
<i>XNpb57</i> — <i>XNpb223</i>	21	25	12	11	22	18	1	4	3	117	8.6	42.6 ± 4.5
<i>XNpb57</i> — <i>XNpb349</i>	19	26	13	12	26	13	1	3	4	117	4.0	43.2 ± 4.5
<i>XNpb42</i> — <i>XNpb45</i>	34	11	0	4	34	9	0	3	22	117	146.4 **	12.1 ± 2.3
<i>XNpb42</i> — <i>XNpb132</i>	25	16	3	9	26	12	0	9	15	115	54.6 **	24.8 ± 3.4
<i>XNpb42</i> — <i>XNpb227</i>	18	20	5	10	21	17	2	8	12	113	20.7 **	34.6 ± 4.1
<i>XNpb42</i> — <i>XNpb223</i>	21	20	6	8	21	19	3	12	8	118	22.1 **	37.3 ± 4.2
<i>XNpb42</i> — <i>XNpb349</i>	19	20	8	10	24	14	2	13	10	120	14.2 **	37.3 ± 4.2
<i>XNpb45</i> — <i>XNpb132</i>	26	10	1	7	34	7	0	7	22	114	101.5 **	15.4 ± 2.6
<i>XNpb45</i> — <i>XNpb227</i>	19	14	3	9	26	13	1	9	18	112	43.4 **	26.3 ± 3.6
<i>XNpb45</i> — <i>XNpb223</i>	16	19	3	11	23	14	3	10	16	115	25.5 **	32.4 ± 4.0
<i>XNpb45</i> — <i>XNpb349</i>	15	19	4	10	23	15	4	15	12	117	13.5 **	37.1 ± 4.2
<i>XNpb132</i> — <i>XNpb227</i>	39	8	3	9	67	14	1	13	28	182	141.5 **	15.5 ± 2.1
<i>XNpb132</i> — <i>XNpb223</i>	26	22	3	14	54	18	5	17	20	179	41.5 **	28.4 ± 2.9
<i>XNpb132</i> — <i>XNpb349</i>	27	17	7	19	55	16	7	22	16	186	29.3 **	33.3 ± 3.2

to be continued

chromosome 2 continued

<i>XNpb132 - spl-2</i>	12	-	3	33	-	6	15	-	0	69	1.4	>50
<i>XNpb227 - XNpb223</i>	32	16	2	15	63	8	0	13	33	182	121.8 **	16.7 ± 2.2
<i>XNpb227 - XNpb349</i>	29	13	7	22	59	7	2	20	25	184	69.2 **	24.9 ± 2.7
<i>XNpb227 - spl-2</i>	16	-	3	35	-	5	10	-	3	72	1.0	42.8 ± 7.1
<i>XNpb223 - XNpb349</i>	41	6	0	10	73	11	2	15	27	185	157.2 **	13.3 ± 1.9
<i>XNpb223 - spl-2</i>	16	-	0	35	-	5	6	-	5	67	7.1 *	20.5 ± 5.4
<i>XNpb349 - spl-2</i>	23	-	0	35	-	3	2	-	7	70	19.1 **	9.1 ± 3.6

\* and \*\* significant at 5% and 1% levels, respectively

## Chromosome 3

Gene pair		Segregation mode									Total	$\chi^2$ (linkage)	Recombination value (%)
A(a)	B(b)	AABB	AABb	AAbb	AaBB	AaBb	Aabb	aaBB	aaBb	aabb			
<i>chl-1</i>	— <i>XNpb164</i>	23	0	0	2	55	13	0	1	24	118	139.3 **	7.0 ± 1.7
<i>chl-1</i>	— <i>XNpb249</i>	14	8	0	6	50	14	3	9	14	118	39.7 **	21.0 ± 3.1
<i>chl-1</i>	— <i>fc</i>	11	—	14	7	—	69	0	—	29	130	15.5 **	19.9 ± 3.9
<i>chl-1</i>	— <i>XNpb51</i>	3	13	6	9	34	27	1	14	11	118	2.7	43.2 ± 4.5
<i>chl-1</i>	— <i>XNpb15</i>	4	12	7	8	37	25	1	15	10	119	1.8	43.5 ± 4.5
<i>chl-1</i>	— <i>XNpb182</i>	4	12	6	12	32	24	3	13	9	115	1.3	46.1 ± 4.6
<i>chl-1</i>	— <i>XNpb348</i>	3	11	9	13	39	18	3	13	9	118	1.4	50.0
<i>chl-1</i>	— <i>spl-3</i>	4	—	21	21	—	55	3	—	25	129	3.1	46.7 ± 5.4
<i>chl-1</i>	— <i>XNpb173</i>	3	10	10	19	34	17	6	15	5	119	4.1	>50
<i>XNpb164</i>	— <i>XNpb249</i>	14	10	0	8	47	12	3	18	28	140	59.1 **	21.7 ± 2.9
<i>XNpb164</i>	— <i>fc</i>	11	—	14	5	—	62	0	—	49	141	22.5 **	18.0 ± 3.5
<i>XNpb164</i>	— <i>XNpb51</i>	3	15	6	8	28	30	5	28	16	139	6.6	45.2 ± 4.2
<i>XNpb164</i>	— <i>XNpb15</i>	4	14	7	6	34	27	7	28	14	141	3.0	47.3 ± 4.2
<i>XNpb164</i>	— <i>XNpb182</i>	4	13	7	11	28	26	7	29	13	138	4.4	48.2 ± 4.2
<i>XNpb164</i>	— <i>XNpb348</i>	3	12	10	12	35	20	7	28	14	141	1.5	50.0
<i>XNpb164</i>	— <i>spl-3</i>	5	—	20	14	—	53	9	—	39	140	0.3	47.3 ± 5.2
<i>XNpb164</i>	— <i>XNpb173</i>	4	10	11	13	31	23	13	27	9	141	5.7	>50
<i>XNpb249</i>	— <i>fc</i>	14	—	11	1	—	74	0	—	41	141	33.3 **	10.8 ± 2.7
<i>XNpb249</i>	— <i>st</i> <sup>11</sup>	33	—	1	51	—	9	15	—	2	111	3.3	34.6 ± 5.3
<i>XNpb249</i>	— <i>XNpb51</i>	30	39	6	48	66	20	10	29	3	251	7.8	43.0 ± 3.1
<i>XNpb249</i>	— <i>XNpb15</i>	26	42	7	49	66	20	10	27	5	252	5.7	44.2 ± 3.1
<i>XNpb249</i>	— <i>XNpb182</i>	26	40	7	47	60	27	9	27	6	249	8.7	43.9 ± 3.1
<i>XNpb249</i>	— <i>XNpb348</i>	22	42	10	43	64	28	10	22	10	251	4.3	45.2 ± 3.1
<i>XNpb249</i>	— <i>spl-3</i>	3	—	22	16	—	59	8	—	32	140	0.4	>50
<i>XNpb249</i>	— <i>XNpb173</i>	1	17	7	17	34	24	12	17	12	141	5.2	>50
<i>fc</i>	— <i>XNpb51</i>	3	11	1	—	—	—	13	61	51	140	10.6 **	27.2 ± 4.3
<i>fc</i>	— <i>XNpb15</i>	3	11	2	—	—	—	14	66	46	142	6.1 *	30.1 ± 4.5
<i>fc</i>	— <i>XNpb182</i>	3	10	2	—	—	—	19	60	44	138	4.6	34.9 ± 4.8
<i>fc</i>	— <i>XNpb348</i>	5	7	4	—	—	—	17	68	40	141	3.9	33.7 ± 4.7
<i>fc</i>	— <i>spl-3</i>	6	—	16	—	—	—	24	—	113	159	1.5	39.0 ± 5.2
<i>fc</i>	— <i>XNpb173</i>	2	7	7	—	—	—	29	61	36	142	0.3	>50
<i>st</i> <sup>11</sup>	— <i>XNpb51</i>	36	57	6	—	—	—	0	5	7	111	16.9 **	13.4 ± 3.4
<i>st</i> <sup>11</sup>	— <i>XNpb15</i>	36	52	11	—	—	—	1	7	4	111	6.9 *	25.8 ± 4.7
<i>st</i> <sup>11</sup>	— <i>XNpb182</i>	35	50	14	—	—	—	1	7	4	111	5.5	29.5 ± 5.0
<i>st</i> <sup>11</sup>	— <i>XNpb348</i>	29	45	25	—	—	—	2	9	1	111	2.2	49.4 ± 5.8
<i>st</i> <sup>11</sup>	— <i>d1</i>	76	—	24	—	—	—	12	—	1	113	0.5	>50
<i>st</i> <sup>11</sup>	— <i>XNpb173</i>	18	45	36	—	—	—	3	7	2	111	3.3	>50
<i>XNpb51</i>	— <i>XNpb15</i>	70	17	1	13	110	11	1	8	20	251	248.4 **	11.3 ± 1.5
<i>XNpb51</i>	— <i>XNpb182</i>	54	31	3	25	87	20	2	9	17	248	104.6 **	21.6 ± 2.1
<i>XNpb51</i>	— <i>XNpb348</i>	40	40	8	31	73	29	4	14	11	250	30.9 **	33.5 ± 2.7
<i>XNpb51</i>	— <i>d1</i>	33	—	3	45	—	17	8	—	5	111	7.4 *	34.5 ± 5.3
<i>XNpb51</i>	— <i>spl-3</i>	3	—	13	17	—	55	7	—	44	139	3.0	42.1 ± 5.1

to be continued

chromosome 3 continued

<i>XNpb51</i> - <i>XNpb173</i>	5	8	3	19	32	21	6	27	19	140	8.4	40.4 ± 4.0
<i>XNpb15</i> - <i>XNpb182</i>	64	20	1	18	102	12	0	5	27	249	219.2 **	12.2 ± 1.6
<i>XNpb15</i> - <i>XNpb348</i>	47	32	6	26	87	22	2	10	20	252	79.3 **	24.2 ± 2.3
<i>XNpb15</i> - <i>d1</i>	34	-	3	46	-	13	6	-	9	111	12.7 **	27.1 ± 4.8
<i>XNpb15</i> - <i>spl-3</i>	8	-	9	16	-	60	4	-	44	141	10.5 **	29.9 ± 4.5
<i>XNpb15</i> - <i>XNpb173</i>	6	7	4	20	33	24	5	28	15	142	7.8	42.3 ± 4.1
<i>XNpb182</i> - <i>XNpb348</i>	58	24	0	14	92	21	3	10	27	249	172.6 **	16.4 ± 1.8
<i>XNpb182</i> - <i>d1</i>	36	-	0	45	-	12	5	-	13	111	29.6 **	17.7 ± 3.9
<i>XNpb182</i> - <i>spl-3</i>	10	-	12	16	-	53	1	-	45	137	18.4 **	26.6 ± 4.3
<i>XNpb182</i> - <i>XNpb173</i>	8	9	5	17	31	22	4	27	15	138	8.9	41.0 ± 4.1
<i>XNpb348</i> - <i>d1</i>	31	-	0	54	-	0	1	-	25	111	94.5 **	1.0 ± 0.9
<i>XNpb348</i> - <i>spl-3</i>	15	-	7	12	-	62	1	-	43	140	30.3 **	17.9 ± 3.5
<i>XNpb348</i> - <i>XNpb173</i>	10	8	4	17	39	19	3	21	20	141	17.2 **	33.7 ± 3.6
<i>d1</i> - <i>XNpb173</i>	21	46	19	-	-	-	0	6	19	111	27.0 **	23.1 ± 4.5
<i>spl-3</i> - <i>XNpb173</i>	22	3	3	-	-	-	9	64	40	141	52.1 **	14.6 ± 3.2

<sup>1)</sup> *st* (t) (CM120)

\* and \*\* significant at 5% and 1% levels, respectively



## Chromosome 4

Gene pair		Segregation mode									Total	$\chi^2$ (linkage)	Recombination value (%)
A(a)	B(b)	AABB	AABb	AAbb	AaBB	AaBb	Aabb	aaBB	aaBb	aabb			
<i>XNpb203</i>	— <i>XNpb237</i>	25	7	1	5	48	7	0	8	24	125	114.3 **	12.3 ± 2.2
<i>XNpb203</i>	— <i>XNpb311</i>	14	14	5	11	34	16	1	15	17	127	21.6 **	31.4 ± 3.7
<i>XNpb203</i>	— <i>XNpb49</i>	12	15	4	14	28	14	3	15	13	118	11.1 *	36.3 ± 4.1
<i>XNpb203</i>	— <i>XNpb72</i>	12	17	4	13	31	17	4	18	11	127	7.6	39.0 ± 4.1
<i>XNpb203</i>	— <i>d-11</i>	29	—	4	48	—	13	25	—	8	127	1.6	43.2 ± 5.3
<i>XNpb203</i>	— <i>XNpb114</i>	10	18	5	17	30	14	9	17	7	127	0.8	47.8 ± 4.4
<i>XNpb203</i>	— <i>XNpb120</i>	10	16	7	18	31	12	9	18	6	127	0.3	50.0
<i>XNpb203</i>	— <i>Ph</i>	23	—	6	39	—	9	24	—	7	108	0.1	49.1 ± 5.9
<i>XNpb203</i>	— <i>lg</i>	27	—	6	52	—	9	26	—	7	127	0.4	48.0 ± 5.4
<i>XNpb237</i>	— <i>XNpb311</i>	18	11	1	7	42	17	1	12	20	129	50.7 **	22.2 ± 3.0
<i>XNpb237</i>	— <i>XNpb49</i>	16	11	1	10	33	15	3	14	14	117	27.1 **	28.7 ± 3.7
<i>XNpb237</i>	— <i>XNpb72</i>	16	13	1	10	38	18	3	18	12	129	22.6 **	30.9 ± 3.6
<i>XNpb237</i>	— <i>d-11</i>	29	—	1	53	—	13	23	—	10	129	5.7	35.0 ± 5.0
<i>XNpb237</i>	— <i>XNpb114</i>	13	13	4	14	39	13	9	16	8	129	5.6	42.4 ± 4.3
<i>XNpb237</i>	— <i>XNpb120</i>	10	15	5	17	35	14	10	17	6	129	0.7	49.2 ± 4.4
<i>XNpb237</i>	— <i>Ph</i>	22	—	5	42	—	12	24	—	5	110	0.3	>50
<i>XNpb237</i>	— <i>lg</i>	26	—	4	55	—	11	26	—	7	129	0.4	45.4 ± 5.4
<i>XNpb311</i>	— <i>XNpb49</i>	21	3	0	8	45	6	0	10	25	118	107.2 **	12.2 ± 2.3
<i>XNpb311</i>	— <i>XNpb72</i>	23	3	0	5	55	7	1	11	29	134	128.0 **	11.1 ± 2.0
<i>XNpb311</i>	— <i>d-11</i>	26	—	0	63	—	5	19	—	22	135	38.1 **	18.8 ± 3.7
<i>XNpb311</i>	— <i>XNpb114</i>	18	5	3	11	49	8	7	17	17	135	40.6 **	26.9 ± 3.3
<i>XNpb311</i>	— <i>XNpb120</i>	12	10	4	15	43	10	10	18	13	135	9.8 *	39.5 ± 4.0
<i>XNpb311</i>	— <i>Ph</i>	18	—	3	47	—	9	26	—	12	115	3.4	40.6 ± 5.5
<i>XNpb311</i>	— <i>lg</i>	22	—	4	61	—	7	28	—	13	135	6.3 *	39.3 ± 5.1
<i>XNpb49</i>	— <i>XNpb72</i>	25	4	0	2	53	3	0	4	27	118	163.5 **	5.7 ± 1.6
<i>XNpb49</i>	— <i>d-11</i>	29	—	0	55	—	3	9	—	22	118	57.3 **	10.8 ± 3.0
<i>XNpb49</i>	— <i>XNpb114</i>	21	7	1	8	41	9	4	11	16	118	56.2 **	21.5 ± 3.1
<i>XNpb49</i>	— <i>XNpb120</i>	16	10	3	9	36	13	8	15	8	118	16.6 **	37.1 ± 4.2
<i>XNpb49</i>	— <i>Ph</i>	22	—	3	39	—	10	19	—	7	100	1.5	41.7 ± 6.0
<i>XNpb49</i>	— <i>lg</i>	26	—	3	47	—	11	24	—	7	118	1.2	43.0 ± 5.5
<i>XNpb72</i>	— <i>d-11</i>	29	—	0	69	—	0	9	—	27	134	82.0 **	6.9 ± 2.3
<i>XNpb72</i>	— <i>XNpb114</i>	23	5	1	10	53	6	3	12	21	134	83.0 **	16.9 ± 2.5
<i>XNpb72</i>	— <i>XNpb120</i>	16	10	3	14	44	11	7	16	13	134	19.0 **	32.8 ± 3.7
<i>XNpb72</i>	— <i>Ph</i>	21	—	3	48	—	11	21	—	10	114	3.0	39.1 ± 5.5
<i>XNpb72</i>	— <i>lg</i>	25	—	4	60	—	9	25	—	11	134	4.1	39.3 ± 5.1
<i>d-11</i>	— <i>XNpb114</i>	36	65	8	—	—	—	0	6	21	136	51.3 **	11.4 ± 2.9
<i>d-11</i>	— <i>XNpb120</i>	34	62	14	—	—	—	3	11	13	137	14.2 **	27.2 ± 4.3
<i>d-11</i>	— <i>Ph</i>	84	—	20	—	—	—	14	—	10	128	4.5 *	35.2 ± 5.5
<i>d-11</i>	— <i>lg</i>	103	—	18	—	—	—	17	—	12	150	8.3 **	31.0 ± 4.7
<i>XNpb114</i>	— <i>XNpb120</i>	26	9	1	11	53	7	0	10	19	136	86.5 **	15.6 ± 2.4
<i>XNpb114</i>	— <i>Ph</i>	30	—	1	52	—	11	9	—	12	115	18.0 **	22.2 ± 4.3
<i>XNpb114</i>	— <i>lg</i>	33	—	3	64	—	7	15	—	14	136	17.9 **	25.0 ± 4.2

to be continued

chromosome 4 continued

<i>XNpb120 - Ph</i>	33	-	1	57	-	5	2	-	18	116	50.4 **	8.7 ± 2.7
<i>XNpb120 - lg</i>	37	-	0	69	-	4	7	-	20	137	52.4 **	9.1 ± 2.6
<i>Ph - lg</i>	95	-	3	-	-	-	9	-	21	128	53.4 **	10.5 ± 2.9

\* and \*\* significant at 5% and 1% levels, respectively

## Chromosome 5

Gene pair		Segregation mode										$\chi^2$ (linkage)	Recombination value (%)
A(a)	B(b)	AABB	AABb	AAbb	AaBB	AaBb	Aabb	aaBB	aaBb	aabb	Total		
<i>XNpb292</i>	— <i>XNpb139</i>	22	15	0	9	73	15	2	16	39	191	111.5 **	17.0 ± 2.1
<i>XNpb292</i>	— <i>XNpb387</i>	11	6	0	7	23	10	1	10	21	89	51.0 **	21.5 ± 3.6
<i>XNpb292</i>	— <i>d-1</i>	12	—	5	30	—	12	23	—	9	91	0.0	49.5 ± 6.4
<i>XNpb292</i>	— <i>st</i> <sup>11</sup>	15	—	5	43	—	12	17	—	8	100	1.0	45.9 ± 6.1
<i>XNpb292</i>	— <i>XNpb105</i>	9	19	9	23	55	19	15	22	20	191	6.7	46.9 ± 3.6
<i>XNpb292</i>	— <i>XNpb81</i>	10	15	12	22	50	25	20	28	9	191	6.1	>50
<i>XNpb292</i>	— <i>spl-7</i>	13	—	7	48	—	7	23	—	2	100	5.2	>50
<i>XNpb292</i>	— <i>n1-1</i>	14	—	6	41	—	14	19	—	6	100	0.2	>50
<i>XNpb292</i>	— <i>XNpb297</i>	10	16	11	24	50	23	20	23	14	191	3.5	>50
<i>XNpb139</i>	— <i>XNpb387</i>	17	0	0	3	37	4	0	2	27	90	146.9 **	5.1 ± 1.7
<i>XNpb139</i>	— <i>d-1</i>	16	—	1	34	—	13	17	—	16	97	13.9 **	31.1 ± 5.5
<i>XNpb139</i>	— <i>st</i> <sup>11</sup>	17	—	0	44	—	15	14	—	10	100	7.3 *	31.5 ± 5.4
<i>XNpb139</i>	— <i>XNpb105</i>	14	19	1	26	56	23	7	24	25	195	22.5 **	33.5 ± 3.1
<i>XNpb139</i>	— <i>XNpb81</i>	11	15	8	29	52	25	16	27	14	197	0.2	49.5 ± 3.6
<i>XNpb139</i>	— <i>spl-7</i>	13	—	4	49	—	10	22	—	2	100	1.5	>50
<i>XNpb139</i>	— <i>n1-1</i>	12	—	5	43	—	16	19	—	5	100	0.4	>50
<i>XNpb139</i>	— <i>XNpb297</i>	9	15	10	28	50	28	21	25	10	196	4.1	>50
<i>XNpb387</i>	— <i>d-1</i>	19	—	1	29	—	10	17	—	14	90	12.7 **	31.4 ± 5.7
<i>XNpb387</i>	— <i>st</i> <sup>11</sup>	15	—	0	50	—	13	10	—	12	100	12.8 **	24.5 ± 4.9
<i>XNpb387</i>	— <i>XNpb105</i>	8	12	0	6	21	12	4	14	13	90	14.5 **	33.7 ± 4.6
<i>XNpb387</i>	— <i>XNpb81</i>	6	9	5	8	20	11	6	14	11	90	2.0	44.1 ± 5.2
<i>XNpb387</i>	— <i>spl-7</i>	11	—	4	53	—	10	20	—	2	100	1.8	>50
<i>XNpb387</i>	— <i>n1-1</i>	10	—	5	48	—	15	16	—	6	100	0.4	>50
<i>XNpb387</i>	— <i>XNpb297</i>	5	10	5	10	18	11	9	16	6	90	1.0	>50
<i>d-1</i>	— <i>XNpb105</i>	18	41	7	—	—	—	0	9	20	95	43.8 **	16.0 ± 4.0
<i>d-1</i>	— <i>XNpb81</i>	19	35	13	—	—	—	4	10	16	97	15.9 **	31.4 ± 5.5
<i>d-1</i>	— <i>XNpb297</i>	19	33	15	—	—	—	8	14	7	96	0.0	49.5 ± 6.2
<i>st</i> <sup>11</sup>	— <i>XNpb105</i>	29	41	5	—	—	—	0	8	17	100	41.4 **	13.9 ± 3.7
<i>st</i> <sup>11</sup>	— <i>XNpb81</i>	28	37	10	—	—	—	5	12	8	100	4.9	36.8 ± 5.8
<i>st</i> <sup>11</sup>	— <i>spl-7</i>	64	—	11	—	—	—	20	—	5	100	0.3	45.1 ± 7.1
<i>st</i> <sup>11</sup>	— <i>n1-1</i>	58	—	17	—	—	—	16	—	9	100	1.8	41.0 ± 6.7
<i>st</i> <sup>11</sup>	— <i>XNpb297</i>	24	30	21	—	—	—	7	13	5	100	1.1	>50
<i>XNpb105</i>	— <i>XNpb81</i>	34	11	2	18	64	17	2	19	28	195	92.9 **	20.8 ± 2.4
<i>XNpb105</i>	— <i>spl-7</i>	27	—	2	42	—	7	15	—	7	100	5.0	33.0 ± 5.5
<i>XNpb105</i>	— <i>n1-1</i>	25	—	4	35	—	14	14	—	8	100	3.9	39.4 ± 5.9
<i>XNpb105</i>	— <i>XNpb297</i>	18	19	10	29	44	25	9	27	13	194	5.2	44.4 ± 3.5
<i>XNpb81</i>	— <i>spl-7</i>	33	—	0	46	—	3	5	—	13	100	34.7 **	9.8 ± 3.1
<i>XNpb81</i>	— <i>n1-1</i>	32	—	1	36	—	13	6	—	12	100	23.2 **	23.2 ± 4.7
<i>XNpb81</i>	— <i>XNpb297</i>	36	19	1	18	52	24	4	19	23	196	72.1 **	25.8 ± 2.7

to be continued

chromosome 5 continued

<i>spl-7 - nl-1</i>	72	-	12	-	-	-	2	-	14	100	27.0 **	16.3 ± 4.1
<i>spl-7 - XNpb297</i>	31	39	14	-	-	-	0	4	12	100	19.8 **	21.4 ± 4.5
<i>nl-1 - XNpb297</i>	30	39	5	-	-	-	1	4	21	100	59.4 **	11.6 ± 3.4

<sup>1)</sup> *st* (t) (CM37)

\* and \*\* significant at 5% and 1% levels, respectively

## Chromosome 6

Gene pair		Segregation mode									Total	$\chi^2$ (linkage)	Recombination value (%)
A(a)	B(b)	AABB	AABb	AAbb	AaBB	AaBb	Aabb	aaBB	aaBb	aabb			
<i>dp-1</i>	— <i>spl-4</i>	73	-	1	-	-	-	7	-	15	96	39.2 **	9.5 ± 3.2
<i>dp-1</i>	— <i>XNpb209</i>	57	86	13	-	-	-	1	12	33	202	75.8 **	14.6 ± 2.7
<i>dp-1</i>	— <i>XNpb165-1</i>	61	94	5	-	-	-	3	29	14	206	25.7 **	23.7 ± 3.3
<i>dp-1</i>	— <i>XNpb233</i>	28	30	16	-	-	-	4	5	12	95	10.4 **	33.3 ± 5.7
<i>dp-1</i>	— <i>XNpb172</i>	25	50	11	-	-	-	4	14	7	111	3.3	36.9 ± 5.5
<i>dp-1</i>	— <i>C1</i>	27	-	60	-	-	-	2	-	24	113	5.5 *	27.6 ± 8.6
<i>dp-1</i>	— <i>XNpb386</i>	30	38	18	-	-	-	1	17	7	111	9.5 **	37.3 ± 5.5
<i>dp-1</i>	— <i>XNpb135</i>	23	31	16	-	-	-	5	7	7	89	1.4	42.9 ± 6.4
<i>dp-1</i>	— <i>XNpb170</i>	28	-	58	-	-	-	8	-	17	111	0.0	49.0 ± 7.2
<i>spl-4</i>	— <i>XNpb209</i>	30	46	4	-	-	-	0	0	15	95	46.8 **	5.0 ± 2.3
<i>spl-4</i>	— <i>XNpb165-1</i>	30	44	6	-	-	-	0	12	3	95	8.9 *	25.5 ± 5.1
<i>spl-4</i>	— <i>XNpb233</i>	30	30	20	-	-	-	2	5	8	95	5.6	35.9 ± 5.9
<i>XNpb209</i>	— <i>XNpb165-1</i>	43	15	0	17	74	7	2	32	12	202	99.6 **	21.0 ± 2.3
<i>XNpb209</i>	— <i>XNpb233</i>	12	13	5	17	15	14	3	7	9	95	7.7	40.2 ± 4.9
<i>XNpb209</i>	— <i>XNpb172</i>	7	14	7	12	34	6	7	16	4	107	2.1	>50
<i>XNpb209</i>	— <i>C1</i>	8	-	20	13	-	39	5	-	22	107	0.8	45.0 ± 5.9
<i>XNpb209</i>	— <i>XNpb386</i>	10	12	6	12	27	13	7	14	6	107	1.7	47.2 ± 4.8
<i>XNpb209</i>	— <i>XNpb135</i>	10	13	3	11	15	14	7	9	6	88	5.2	44.9 ± 5.2
<i>XNpb209</i>	— <i>XNpb170</i>	10	-	18	14	-	38	11	-	16	107	2.1	>50
<i>pb165-1</i>	— <i>XNpb233</i>	20	8	2	10	27	19	2	0	7	95	37.6 **	27.2 ± 3.9
<i>pb165-1</i>	— <i>XNpb172</i>	13	16	5	15	42	10	1	6	3	111	6.5	35.2 ± 4.2
<i>pb165-1</i>	— <i>C1</i>	10	-	24	17	-	50	1	-	9	111	0.9	43.4 ± 5.7
<i>pb165-1</i>	— <i>XNpb386</i>	12	16	6	17	34	16	2	5	3	111	2.2	42.2 ± 4.6
<i>pb165-1</i>	— <i>XNpb135</i>	9	12	4	16	21	17	3	5	2	89	3.2	45.8 ± 5.2
<i>pb165-1</i>	— <i>XNpb170</i>	10	-	24	21	-	46	5	-	5	111	0.1	>50
<i>XNpb233</i>	— <i>XNpb172</i>	26	3	0	1	60	4	2	1	14	111	136.3 **	6.1 ± 1.7
<i>XNpb233</i>	— <i>C1</i>	19	-	10	7	-	58	2	-	15	111	35.7 **	19.2 ± 4.1
<i>XNpb233</i>	— <i>XNpb386</i>	17	12	0	12	37	16	2	6	9	111	27.5 **	26.3 ± 3.6
<i>XNpb233</i>	— <i>XNpb135</i>	7	9	3	16	23	17	5	6	3	89	1.9	47.7 ± 5.3
<i>XNpb233</i>	— <i>XNpb170</i>	9	-	20	20	-	45	7	-	10	111	0.1	>50
<i>XNpb172</i>	— <i>C1</i>	19	-	10	7	-	57	2	-	16	111	35.5 **	19.2 ± 4.1
<i>XNpb172</i>	— <i>XNpb386</i>	16	11	2	13	39	12	2	5	11	111	26.9 **	25.9 ± 3.5
<i>XNpb172</i>	— <i>XNpb135</i>	6	9	4	18	24	13	4	5	6	89	1.7	45.2 ± 5.2
<i>XNpb172</i>	— <i>XNpb170</i>	8	-	21	22	-	42	6	-	12	111	0.7	>50
<i>C1</i>	— <i>XNpb386</i>	23	5	0	-	-	-	8	50	25	111	59.6 **	11.7 ± 3.2
<i>C1</i>	— <i>XNpb135</i>	8	7	2	-	-	-	20	31	21	89	2.7	39.4 ± 6.2
<i>C1</i>	— <i>XNpb170</i>	12	-	16	-	-	-	24	-	59	111	2.2	41.7 ± 6.4
<i>XNpb386</i>	— <i>XNpb135</i>	15	6	0	12	26	10	1	6	13	89	37.8 **	22.5 ± 3.7
<i>XNpb386</i>	— <i>XNpb170</i>	19	-	12	15	-	40	2	-	23	111	24.7 **	26.8 ± 4.8
<i>XNpb135</i>	— <i>XNpb170</i>	26	-	2	5	-	33	0	-	23	89	92.3 **	7.3 ± 2.8

\* and \*\* significant at 5% and 1% levels, respectively

## Chromosome 7

Gene pair		Segregation mode									Total	$\chi^2$ (linkage)	Recombination value (%)
A(a)	B(b)	AABB	AABb	AAbb	AaBB	AaBb	Aabb	aaBB	aaBb	aabb			
<i>XNpb50</i>	<i>g-1</i>	24	-	0	49	-	7	5	-	15	100	33.8 **	13.0 ± 3.6
<i>XNpb50</i>	<i>d-6</i>	22	-	2	47	-	9	6	-	14	100	23.4 **	20.6 ± 4.5
<i>XNpb50</i>	<i>sp1-5</i>	22	-	2	43	-	13	15	-	5	100	2.2	40.0 ± 5.9
<i>XNpb50</i>	<i>v-11</i>	18	-	6	42	-	14	15	-	5	100	0.0	50.0
<i>XNpb50</i>	<i>XNpb85-1</i>	19	-	5	41	-	15	15	-	5	100	0.3	47.8 ± 6.1
<i>XNpb50</i>	<i>XNpb20</i>	7	10	7	14	27	15	5	12	3	100	1.7	>50
<i>XNpb50</i>	<i>XNpb117</i>	8	9	7	16	24	16	3	10	7	100	1.9	45.2 ± 4.9
<i>XNpb50</i>	<i>XNpb22</i>	10	12	2	18	22	16	4	12	4	100	6.2	43.0 ± 4.9
<i>g-1</i>	<i>d-6</i>	74	-	4	-	-	-	1	-	21	100	68.3 **	5.2 ± 2.3
<i>g-1</i>	<i>sp1-5</i>	67	-	11	-	-	-	13	-	9	100	6.4 *	30.9 ± 5.8
<i>g-1</i>	<i>v-11</i>	62	-	16	-	-	-	13	-	9	100	3.5	36.8 ± 6.3
<i>g-1</i>	<i>XNpb85-1</i>	62	-	16	-	-	-	13	-	9	100	3.5	36.8 ± 6.3
<i>g-1</i>	<i>XNpb20</i>	23	36	19	-	-	-	3	13	6	100	2.2	43.5 ± 6.0
<i>g-1</i>	<i>XNpb117</i>	24	32	22	-	-	-	3	11	8	100	2.6	42.4 ± 6.0
<i>g-1</i>	<i>XNpb22</i>	26	34	18	-	-	-	6	12	4	100	0.9	49.1 ± 6.1
<i>d-6</i>	<i>sp1-5</i>	65	-	10	-	-	-	15	-	10	100	7.1 **	31.2 ± 5.8
<i>d-6</i>	<i>v-11</i>	61	-	14	-	-	-	14	-	11	100	6.4 *	33.7 ± 6.0
<i>d-6</i>	<i>XNpb85-1</i>	61	-	14	-	-	-	14	-	11	100	6.4 *	33.7 ± 6.0
<i>d-6</i>	<i>XNpb20</i>	24	34	17	-	-	-	2	15	8	100	5.8	38.7 ± 5.9
<i>d-6</i>	<i>XNpb117</i>	25	31	19	-	-	-	2	12	11	100	7.6 *	36.2 ± 5.7
<i>d-6</i>	<i>XNpb22</i>	27	32	16	-	-	-	5	14	6	100	2.6	43.9 ± 6.0
<i>sp1-5</i>	<i>v-11</i>	74	-	6	-	-	-	1	-	19	100	55.8 **	7.6 ± 2.8
<i>sp1-5</i>	<i>XNpb85-1</i>	74	-	6	-	-	-	1	-	19	100	55.8 **	7.6 ± 2.8
<i>sp1-5</i>	<i>XNpb20</i>	26	42	12	-	-	-	0	7	13	100	20.3 **	21.3 ± 4.5
<i>sp1-5</i>	<i>XNpb117</i>	22	37	21	-	-	-	5	6	9	100	2.2	43.2 ± 6.0
<i>sp1-5</i>	<i>XNpb22</i>	24	38	18	-	-	-	8	8	4	100	0.5	>50
<i>v-11</i>	<i>XNpb85-1</i>	74	-	1	-	-	-	1	-	24	100	89.6 **	2.0 ± 1.4
<i>v-11</i>	<i>XNpb20</i>	26	42	7	-	-	-	0	7	18	100	41.4 **	14.6 ± 3.8
<i>v-11</i>	<i>XNpb117</i>	22	38	15	-	-	-	5	5	15	100	16.2 **	32.1 ± 5.5
<i>v-11</i>	<i>XNpb22</i>	24	35	16	-	-	-	8	11	6	100	0.1	49.1 ± 6.1
<i>XNpb85-1</i>	<i>XNpb20</i>	26	43	6	-	-	-	0	6	19	100	47.9 **	12.5 ± 3.5
<i>XNpb85-1</i>	<i>XNpb117</i>	22	37	16	-	-	-	5	6	14	100	12.1 **	34.2 ± 5.6
<i>XNpb85-1</i>	<i>XNpb22</i>	23	36	16	-	-	-	9	10	6	100	0.5	>50
<i>XNpb20</i>	<i>XNpb117</i>	17	6	3	7	32	10	3	5	17	100	50.9 **	22.5 ± 3.4
<i>XNpb20</i>	<i>XNpb22</i>	13	6	7	14	27	8	5	13	7	100	10.4 *	41.6 ± 4.8
<i>XNpb117</i>	<i>XNpb22</i>	20	5	2	11	24	8	1	17	12	100	46.0 **	26.2 ± 3.8

\* and \*\* significant at 5% and 1% levels, respectively

## Chromosome 8

Gene pair		Segregation mode									Total	$\chi^2$ (linkage)	Recombination value (%)
A(a)	B(b)	AABB	AABb	AAbb	AaBB	AaBb	Aabb	aaBB	aaBb	aabb			
<i>v-8</i>	— <i>XNpb278</i>	15	46	21	—	—	—	0	6	11	99	7.0 *	31.6 ± 5.5
<i>v-8</i>	— <i>XNpb369</i>	13	50	19	—	—	—	3	8	6	99	1.5	47.3 ± 6.1
<i>v-8</i>	— <i>XNpb126</i>	12	51	19	—	—	—	6	6	5	99	4.8	>50
<i>v-8</i>	— <i>XNpb187</i>	12	48	22	—	—	—	7	5	5	99	5.8	>50
<i>v-8</i>	— <i>XNpb397</i>	20	42	20	—	—	—	9	6	2	99	3.9	>50
<i>v-8</i>	— <i>sug</i>	70	—	12	—	—	—	15	—	3	100	0.3	43.6 ± 6.9
<i>XNpb278</i>	— <i>XNpb369</i>	10	5	0	4	40	8	2	13	17	99	40.7 **	19.4 ± 3.2
<i>XNpb278</i>	— <i>XNpb126</i>	7	7	1	8	31	13	3	19	10	99	8.4	34.6 ± 4.4
<i>XNpb278</i>	— <i>XNpb187</i>	7	7	1	8	28	16	4	18	10	99	7.6	37.1 ± 4.6
<i>XNpb278</i>	— <i>XNpb397</i>	5	6	4	14	25	13	10	17	5	99	1.7	>50
<i>XNpb278</i>	— <i>sug</i>	14	—	1	43	—	9	27	—	5	99	0.2	>50
<i>XNpb369</i>	— <i>XNpb126</i>	10	6	0	8	42	8	0	9	16	99	42.1 **	17.5 ± 3.0
<i>XNpb369</i>	— <i>XNpb187</i>	10	6	0	8	40	10	1	7	17	99	42.5 **	18.7 ± 3.1
<i>XNpb369</i>	— <i>XNpb397</i>	8	4	4	17	27	14	4	17	4	99	6.8	45.6 ± 5.0
<i>XNpb369</i>	— <i>sug</i>	15	—	1	49	—	9	20	—	5	99	0.4	43.7 ± 6.1
<i>XNpb126</i>	— <i>XNpb187</i>	18	0	0	1	52	4	0	1	23	99	144.8 **	3.1 ± 1.2
<i>XNpb126</i>	— <i>XNpb397</i>	14	3	1	11	33	13	4	12	8	99	21.5 **	29.9 ± 4.1
<i>XNpb126</i>	— <i>sug</i>	18	—	0	49	—	8	17	—	7	99	3.7	32.1 ± 5.5
<i>XNpb187</i>	— <i>XNpb397</i>	15	3	1	11	32	10	3	13	11	99	29.3 **	26.4 ± 3.8
<i>XNpb187</i>	— <i>sug</i>	19	—	0	47	—	6	18	—	9	99	6.5 *	29.6 ± 5.3
<i>XNpb397</i>	— <i>sug</i>	28	—	1	46	—	2	10	—	12	99	23.2 **	17.1 ± 4.1

\* and \*\* significant at 5% and 1% levels, respectively

Gene pair A(a) — B(b)		Segregation mode									Total	$\chi^2$ (linkage)	Recombination value (%)
		AABB	AABb	AAbb	AaBB	AaBb	Aabb	aaBB	aaBb	aabb			
<i>I-Bf</i> — <i>XNpb36</i>		19	0	0	—	—	—	13	71	38	141	45.8 **	10.9 ± 2.8
<i>I-Bf</i> — <i>XNpb47</i>		11	6	2	—	—	—	19	69	34	141	11.6 **	26.7 ± 4.2
<i>I-Bf</i> — <i>XNpb385</i>		10	5	4	—	—	—	21	67	34	141	8.1 *	32.6 ± 4.6
<i>I-Bf</i> — <i>XNpb108</i>		6	7	6	—	—	—	30	64	28	141	1.1	>50
<i>I-Bf</i> — <i>XNpb293</i>		12	—	7	—	—	—	96	—	25	140	1.8	>50
<i>XNpb36</i> — <i>XNpb47</i>		61	20	0	25	100	24	4	27	46	307	185.5 **	18.5 ± 1.8
<i>XNpb36</i> — <i>dp-2</i>		40	—	2	60	—	18	25	—	19	164	17.7 **	30.9 ± 4.2
<i>XNpb36</i> — <i>drp-2</i>		40	—	3	61	—	18	25	—	19	166	16.1 **	31.9 ± 4.2
<i>XNpb36</i> — <i>XNpb385</i>		36	38	7	40	78	32	12	31	34	308	36.6 **	34.6 ± 2.5
<i>XNpb36</i> — <i>Dn-1</i>		5	—	13	9	—	33	4	—	21	85	1.0	42.9 ± 6.5
<i>XNpb36</i> — <i>XNpb404</i>		7	28	8	21	35	23	5	20	19	166	11.5 *	43.3 ± 3.8
<i>XNpb36</i> — <i>XNpb108</i>		22	42	17	30	77	41	19	34	24	306	3.5	46.7 ± 2.8
<i>XNpb36</i> — <i>XNpb293</i>		19	—	62	29	—	120	23	—	54	307	2.9	>50
<i>XNpb47</i> — <i>dp-2</i>		51	—	2	65	—	6	8	—	31	163	84.6 **	12.1 ± 2.7
<i>XNpb47</i> — <i>drp-2</i>		50	—	4	67	—	5	8	—	31	165	80.9 **	13.9 ± 2.9
<i>XNpb47</i> — <i>XNpb385</i>		57	28	5	30	101	16	1	17	52	307	190.3 **	18.4 ± 1.8
<i>XNpb47</i> — <i>Dn-1</i>		12	—	12	6	—	30	0	—	24	84	18.9 **	23.3 ± 5.2
<i>XNpb47</i> — <i>XNpb404</i>		15	30	9	17	42	13	0	11	28	165	45.8 **	31.4 ± 3.2
<i>XNpb47</i> — <i>XNpb108</i>		28	46	16	35	79	33	8	28	33	306	22.4 **	38.2 ± 2.6
<i>XNpb47</i> — <i>XNpb293</i>		21	—	69	38	—	108	11	—	59	306	2.4	46.8 ± 3.5
<i>dp-2</i> — <i>drp-2</i>		123	—	3	—	—	—	2	—	39	167	140.2 **	3.0 ± 1.4
<i>dp-2</i> — <i>XNpb385</i>		48	72	5	—	—	—	0	3	36	164	121.0 **	5.2 ± 1.8
<i>dp-2</i> — <i>Dn-1</i>		18	—	47	—	—	—	0	—	20	85	5.9 *	0.0
<i>dp-2</i> — <i>XNpb404</i>		32	73	20	—	—	—	0	9	30	164	56.6 **	17.9 ± 3.3
<i>dp-2</i> — <i>XNpb108</i>		23	19	12	—	—	—	0	9	7	70	12.1 **	31.8 ± 6.5
<i>dp-2</i> — <i>XNpb293</i>		35	—	90	—	—	—	3	—	36	164	6.2 *	29.4 ± 7.0
<i>drp-2</i> — <i>XNpb385</i>		50	74	2	—	—	—	0	1	39	166	146.5 **	1.9 ± 1.1
<i>drp-2</i> — <i>Dn-1</i>		18	—	45	—	—	—	0	—	22	85	7.4 **	0.0
<i>drp-2</i> — <i>XNpb404</i>		33	75	18	—	—	—	0	8	32	166	68.0 **	15.7 ± 3.0
<i>drp-2</i> — <i>XNpb108</i>		23	20	11	—	—	—	0	8	8	70	13.3 **	29.0 ± 6.3
<i>drp-2</i> — <i>XNpb293</i>		36	—	90	—	—	—	3	—	37	166	7.0 **	28.7 ± 7.0
<i>XNpb385</i> — <i>Dn-1</i>		15	—	5	3	—	39	0	—	23	85	39.8 **	10.2 ± 3.4
<i>XNpb385</i> — <i>XNpb404</i>		27	23	0	6	52	17	0	8	33	166	112.6 **	17.6 ± 2.3
<i>XNpb385</i> — <i>XNpb108</i>		44	40	4	25	85	36	2	28	42	306	92.4 **	26.1 ± 2.1
<i>XNpb385</i> — <i>XNpb293</i>		37	—	51	29	—	117	5	—	68	307	29.2 **	31.7 ± 3.1
<i>Dn-1</i> — <i>XNpb404</i>		10	7	1	—	—	—	5	37	25	85	18.7 **	19.1 ± 4.7
<i>Dn-1</i> — <i>XNpb108</i>		4	13	1	—	—	—	7	35	23	83	6.5 *	32.5 ± 6.0
<i>Dn-1</i> — <i>XNpb293</i>		3	—	15	—	—	—	10	—	57	85	0.1	46.1 ± 7.8
<i>XNpb404</i> — <i>XNpb108</i>		8	9	0	6	36	7	0	8	20	94	51.8 **	17.6 ± 3.1
<i>XNpb404</i> — <i>XNpb293</i>		9	—	9	7	—	42	2	—	27	96	11.7 **	25.4 ± 5.0
<i>XNpb108</i> — <i>XNpb293</i>		55	—	16	14	—	138	1	—	81	305	143.1 **	11.2 ± 1.9

\* and \*\* significant at 5% and 1% levels, respectively



## Chromosome 10

Gene pair A(a) — B(b)		Segregation mode									Total	$\chi^2$ (linkage)	Recombination value (%)
		AABB	AABb	AAbb	AaBB	AaBb	Aabb	aaBB	aaBb	aabb			
<i>XNpb333</i> — <i>XNpb37</i>		9	7	4	10	24	5	1	6	12	78	22.5 **	28.6 ± 4.5
<i>XNpb333</i> — <i>XNpb133</i>		10	6	4	8	23	8	1	5	13	78	24.9 **	27.4 ± 4.4
<i>XNpb333</i> — <i>XNpb291</i>		6	10	4	11	19	9	1	9	9	78	6.8	38.1 ± 5.2
<i>XNpb333</i> — <i>sp1-10</i>		14	—	6	27	—	12	14	—	5	78	0.1	>50
<i>XNpb333</i> — <i>pg1</i>		13	—	7	26	—	13	15	—	4	78	1.3	>50
<i>XNpb333</i> — <i>XNpb127</i>		4	9	7	5	21	13	5	10	4	78	2.2	>50
<i>XNpb37</i> — <i>XNpb133</i>		18	2	0	1	32	4	0	0	21	78	131.2 **	4.6 ± 1.7
<i>XNpb37</i> — <i>XNpb291</i>		26	6	0	2	52	8	0	6	29	129	150.1 **	8.9 ± 1.9
<i>XNpb37</i> — <i>sp1-10</i>		29	—	3	46	—	16	15	—	20	129	23.2 **	28.5 ± 4.6
<i>XNpb37</i> — <i>pg1</i>		27	—	5	45	—	17	19	—	16	129	9.0 *	36.2 ± 5.0
<i>XNpb37</i> — <i>XNpb127</i>		12	17	3	10	34	17	3	16	16	128	16.2 **	33.5 ± 3.8
<i>XNpb133</i> — <i>XNpb291</i>		15	4	0	3	28	3	0	6	19	78	86.9 **	10.8 ± 2.6
<i>XNpb133</i> — <i>sp1-10</i>		18	—	1	26	—	8	11	—	14	78	19.5 **	26.1 ± 5.7
<i>XNpb133</i> — <i>pg1</i>		15	—	4	26	—	8	13	—	12	78	7.8 *	36.3 ± 6.5
<i>XNpb133</i> — <i>XNpb127</i>		5	10	4	7	19	8	2	11	12	78	8.7	37.0 ± 5.2
<i>XNpb291</i> — <i>sp1-10</i>		27	—	2	56	—	10	9	—	28	132	62.7 **	16.8 ± 3.5
<i>XNpb291</i> — <i>pg1</i>		25	—	4	55	—	11	14	—	23	132	33.7 **	25.1 ± 4.3
<i>XNpb291</i> — <i>XNpb127</i>		13	14	2	10	44	11	2	12	23	131	45.2 **	24.1 ± 3.1
<i>sp1-10</i> — <i>pg1</i>		106	—	5	—	—	—	7	—	40	158	130.0 **	7.4 ± 2.2
<i>sp1-10</i> — <i>XNpb127</i>		24	62	5	—	—	—	1	8	31	131	88.5 **	10.7 ± 2.8
<i>pg1</i> — <i>XNpb127</i>		24	68	1	—	—	—	1	2	35	131	133.0 **	3.5 ± 1.6

\* and \*\* significant at 5% and 1% levels, respectively

Gene pair A(a) — B(b)	Segregation mode										Total	$\chi^2$ (linkage)	Recombination value (%)
	AABB	AABb	AAbb	AaBB	AaBb	Aabb	aaBB	aaBb	aabb				
XNpb181 — XNpb389	32	1	0	-	-	-	1	52	13	99	136.3 **	1.7 ± 1.3	
XNpb181 — XNpb78	32	1	0	-	-	-	1	51	14	99	136.0 **	1.7 ± 1.3	
XNpb181 — z-2	33	-	0	-	-	-	59	-	7	99	4.2 *	0.0	
XNpb181 — gmZ410	14	17	2	-	-	-	20	38	8	99	4.0	39.2 ± 5.9	
XNpb181 — XNpb202	8	18	7	-	-	-	21	35	10	99	0.5	>50	
XNpb181 — XNpb44	7	18	8	-	-	-	21	35	10	99	1.4	>50	
XNpb181 — XNpb183	7	18	8	-	-	-	21	38	7	99	1.9	>50	
XNpb181 — v-9	24	-	9	-	-	-	59	-	7	99	2.5	>50	
XNpb181 — XNpb189	9	15	9	-	-	-	21	32	13	99	0.6	>50	
XNpb181 — XNpb52	11	18	4	-	-	-	23	27	16	99	2.8	44.9 ± 6.1	
XNpb389 — XNpb78	33	0	0	0	51	2	0	1	12	99	189.6 **	1.5 ± 0.9	
XNpb389 — z-2	33	-	0	52	-	1	7	-	6	99	15.5 **	11.3 ± 3.3	
XNpb389 — gmZ410	15	16	2	18	34	1	1	5	7	99	20.3 **	27.6 ± 3.9	
XNpb389 — XNpb202	9	17	7	18	31	4	2	5	6	99	8.2	42.2 ± 4.8	
XNpb389 — XNpb44	8	17	8	16	31	6	4	5	4	99	3.6	50.0	
XNpb389 — XNpb183	8	17	8	15	33	5	5	6	2	99	3.1	>50	
XNpb389 — v-9	24	-	9	49	-	4	10	-	3	99	5.2	>50	
XNpb389 — XNpb189	9	15	9	17	25	11	4	7	2	99	0.8	>50	
XNpb389 — XNpb52	11	18	4	19	21	13	4	6	3	99	3.6	44.8 ± 4.9	
XNpb78 — z-2	33	-	0	51	-	1	8	-	6	99	14.6 **	12.8 ± 3.6	
XNpb78 — gmZ410	15	16	2	18	33	1	1	6	7	99	19.5 **	28.2 ± 3.9	
XNpb78 — XNpb202	9	17	7	18	30	4	2	6	6	99	7.6	42.6 ± 4.9	
XNpb78 — XNpb44	8	17	8	16	30	6	4	6	4	99	3.0	50.0	
XNpb78 — XNpb183	8	17	8	15	32	5	5	7	2	99	2.6	>50	
XNpb78 — v-9	24	-	9	48	-	4	11	-	3	99	4.8	>50	
XNpb78 — XNpb189	9	15	9	16	26	10	5	6	3	99	0.8	>50	
XNpb78 — XNpb52	11	18	4	18	22	12	5	5	4	99	3.0	44.6 ± 4.9	
z-2 — gmZ410	34	55	3	-	-	-	0	0	7	99	23.3 **	4.2 ± 2.0	
z-2 — XNpb202	28	53	11	-	-	-	1	0	6	99	11.0 **	18.3 ± 4.2	
z-2 — XNpb44	27	52	13	-	-	-	1	1	5	99	7.0 *	23.2 ± 4.8	
z-2 — XNpb183	28	51	13	-	-	-	0	5	2	99	3.0	27.6 ± 5.1	
z-2 — v-9	78	-	14	-	-	-	6	-	5	103	4.3	28.5 ± 5.4	
z-2 — XNpb189	29	42	21	-	-	-	1	5	1	99	1.4	43.6 ± 6.1	
z-2 — XNpb52	33	40	19	-	-	-	1	5	1	99	2.8	39.7 ± 5.9	
gmZ410 — XNpb202	22	11	1	6	42	7	1	0	9	99	64.3 **	15.5 ± 2.8	
gmZ410 — XNpb44	21	12	1	6	39	10	1	2	7	99	49.5 **	19.3 ± 3.2	
gmZ410 — XNpb183	16	16	2	11	35	9	1	5	4	99	16.3 **	28.6 ± 4.0	
gmZ410 — v-9	32	-	2	45	-	10	6	-	4	99	7.0 *	27.5 ± 5.1	
gmZ410 — XNpb189	10	19	5	19	22	14	1	6	3	99	5.1	43.7 ± 4.9	
gmZ410 — XNpb52	9	19	6	24	19	12	1	7	2	99	9.0	46.7 ± 5.0	
XNpb202 — XNpb44	26	3	0	2	48	3	0	2	15	99	135.9 **	5.2 ± 1.6	
XNpb202 — XNpb183	20	8	1	7	44	2	1	4	12	99	69.7 **	13.7 ± 2.7	

to be continued

chromosome 11 continued

<i>XNpb202</i> - <i>v-9</i>	27	-	2	47	-	6	9	-	8	99	10.5 **	24.4 ± 4.9
<i>XNpb202</i> - <i>XNpb189</i>	13	11	5	14	27	12	3	9	5	99	6.2	39.4 ± 4.7
<i>XNpb202</i> - <i>XNpb52</i>	12	10	7	19	24	10	3	11	3	99	5.3	45.1 ± 5.0
<i>XNpb44</i> - <i>XNpb183</i>	22	5	1	6	47	0	0	4	14	99	98.9 **	9.1 ± 2.1
<i>XNpb44</i> - <i>v-9</i>	26	-	2	49	-	4	8	-	10	99	17.0 **	19.9 ± 4.4
<i>XNpb44</i> - <i>XNpb189</i>	13	11	4	14	28	11	3	8	7	99	8.5	36.2 ± 4.5
<i>XNpb44</i> - <i>XNpb52</i>	12	10	6	19	25	9	3	10	5	99	5.4	42.0 ± 4.8
<i>XNpb183</i> - <i>v-9</i>	28	-	0	51	-	5	4	-	11	99	26.5 **	10.9 ± 3.3
<i>XNpb183</i> - <i>XNpb189</i>	16	8	4	12	33	11	2	6	7	99	20.4 **	29.9 ± 4.1
<i>XNpb183</i> - <i>XNpb52</i>	15	6	7	17	30	9	2	9	4	99	14.3 **	38.1 ± 4.6
<i>v-9</i> - <i>XNpb189</i>	29	43	11	-	-	-	1	4	11	99	18.0 **	20.8 ± 4.5
<i>v-9</i> - <i>XNpb52</i>	32	38	13	-	-	-	2	7	7	99	7.8 *	30.7 ± 5.4
<i>XNpb189</i> - <i>XNpb52</i>	29	1	0	5	37	5	0	7	15	99	130.4 **	9.5 ± 2.2

\* and \*\* significant at 5% and 1% levels, respectively

## Chromosome 12

Gene pair		Segregation mode									Total	$\chi^2$ (linkage)	Recombination value (%)
A(a)	B(b)	AABB	AABb	AAbb	AaBB	AaBb	Aabb	aaBB	aaBb	aabb			
<i>XNpb193</i>	— <i>XNpb124-1</i>	32	23	7	14	46	16	3	13	14	168	43.3 **	29.8 ± 3.1
<i>XNpb193</i>	— <i>spl-1</i>	21	—	5	26	—	5	13	—	7	77	2.4	41.5 ± 6.8
<i>XNpb193</i>	— <i>XNpb88</i>	25	27	9	16	45	15	7	14	9	167	13.3 *	38.9 ± 3.6
<i>XNpb193</i>	— <i>XNpb402</i>	25	—	37	30	—	47	9	—	22	170	4.3	43.3 ± 4.6
<i>XNpb193</i>	— <i>r1-1</i>	30	—	6	40	—	6	9	—	2	93	0.8	43.2 ± 6.2
<i>XNpb193</i>	— <i>XNpb148</i>	7	17	2	13	14	4	6	12	2	77	3.4	49.0 ± 5.7
<i>XNpb193</i>	— <i>XNpb198</i>	29	21	12	28	33	16	8	20	3	170	14.5 **	44.3 ± 3.8
<i>pb124-1</i>	— <i>spl-1</i>	18	—	0	39	—	3	6	—	17	83	44.9 **	10.9 ± 3.6
<i>pb124-1</i>	— <i>XNpb88</i>	40	8	1	7	71	7	1	10	28	173	173.3 **	11.0 ± 1.8
<i>pb124-1</i>	— <i>XNpb402</i>	36	—	14	23	—	64	5	—	34	176	57.6 **	24.5 ± 3.7
<i>pb124-1</i>	— <i>r1-1</i>	31	—	1	38	—	7	10	—	6	93	9.3 **	26.6 ± 5.2
<i>pb124-1</i>	— <i>XNpb148</i>	11	7	0	14	23	5	3	16	4	83	11.0 *	35.3 ± 4.9
<i>pb124-1</i>	— <i>XNpb198</i>	20	19	11	33	38	16	14	21	4	176	2.6	>50
<i>spl-1</i>	— <i>XNpb88</i>	17	43	2	—	—	—	0	1	19	82	66.9 **	3.6 ± 2.1
<i>spl-1</i>	— <i>XNpb402</i>	24	—	41	—	—	—	5	—	15	85	1.3	41.9 ± 8.8
<i>spl-1</i>	— <i>XNpb148</i>	26	34	5	—	—	—	3	13	4	85	5.4	34.7 ± 6.1
<i>spl-1</i>	— <i>XNpb198</i>	25	25	15	—	—	—	8	9	3	85	0.5	>50
<i>XNpb88</i>	— <i>XNpb402</i>	39	—	10	20	—	71	6	—	30	176	74.9 **	21.8 ± 3.5
<i>XNpb88</i>	— <i>r1-1</i>	31	0	1	41	0	6	8	0	7	94	12.1 *	22.2 ± 4.8
<i>XNpb88</i>	— <i>XNpb148</i>	11	6	0	15	24	5	3	14	4	82	10.6 *	34.3 ± 4.8
<i>XNpb88</i>	— <i>XNpb198</i>	17	24	8	37	34	19	13	19	4	175	3.1	50.0
<i>XNpb402</i>	— <i>r1-1</i>	37	—	0	—	—	—	43	—	14	94	14.3 **	0.0
<i>XNpb402</i>	— <i>XNpb148</i>	20	9	0	—	—	—	9	38	9	85	39.3 **	18.6 ± 4.6
<i>XNpb402</i>	— <i>XNpb198</i>	36	22	7	—	—	—	31	57	25	178	32.2 **	33.1 ± 4.1
<i>r1-1</i>	— <i>XNpb148</i>	46	31	2	—	—	—	1	4	9	93	33.2 **	12.5 ± 3.6
<i>r1-1</i>	— <i>XNpb198</i>	34	35	10	—	—	—	0	10	4	93	11.9 **	28.2 ± 5.4
<i>XNpb148</i>	— <i>XNpb198</i>	31	13	3	3	27	5	0	5	6	93	88.8 **	18.7 ± 3.2

\* and \*\* significant at 5% and 1% levels, respectively

Appendix 5. Segregation of marker genes and RFLP markers

Chromosome 1

Gene	Allele <sup>1)</sup>			Total	J/J (%)	$\chi^2$ (3:1 or 1:2:1)	No. of cross
	I/I	I/J	J/J				
<i>fs-2</i>	136	-	17	153	11.1	15.7 ***	1
<i>XNpb216</i>	33	82	23	138	16.7	6.3 *	1
<i>XNpb96</i>	77	159	36	272	13.2	20.1 ***	2
<i>d-18</i>	131	-	23	154	14.9	8.3 **	1
<i>XNpb269</i>	78	151	42	271	15.5	13.1 **	2
<i>XNpb359</i>	77	145	35	257	13.6	18.0 ***	2
<i>d-2</i>	112	-	23	135	17.0	4.6 *	1
<i>XNpb252</i>	118	202	81	401	20.2	6.9 *	3
<i>r1-2</i>	29	75	32	136	23.5	1.6	1
<i>XNpb368</i>	31	78	24	133	18.0	4.7	1
<i>XNpb314</i>	107	210	89	406	21.9	2.1	3
<i>XNpb147</i>	25	75	33	133	24.8	3.1	1
<i>XNpb130</i>	30	59	44	133	33.1	4.6	1
<i>XNpb174</i>	29	60	44	133	33.1	4.7	1
<i>spl-6</i>	33	66	43	142	30.3	2.1	1
<i>XNpb97</i>	34	-	100	134	74.6	0.0	1
<i>eg</i>	35	72	36	143	25.2	0.0	1
<i>XNpb346</i>	31	63	35	129	27.1	0.3	1
<i>d-10</i>	139	-	37	176	21.0	1.5	2
<i>lax</i>	139	-	36	175	20.6	1.8	2

<sup>1)</sup> I/I homozygous for Indica allele

I/J heterozygous for Indica and Japonica alleles

J/J homozygous for Japonica allele

\*, \*\* and \*\*\* significant at 5%, 1% and 0.1% levels, respectively

## Chromosome 2

Gene	Allele <sup>1)</sup>			Total	J/J (%)	$\chi^2$ (3:1 or 1:2:1)	No. of cross
	I/I	I/J	J/J				
<i>tri</i>	110	-	24	134	17.9	3.6	1
<i>XNpb250</i>	38	54	23	115	20.0	4.3	1
<i>bl-1</i>	111	-	20	131	15.3	6.6 *	1
<i>XNpb57</i>	58	51	8	117	6.8	44.7 ***	1
<i>XNpb42</i>	47	48	25	120	20.8	12.9 **	1
<i>XNpb45</i>	38	48	31	117	26.5	4.6	1
<i>XNpb132</i>	51	90	45	186	24.2	0.6	2
<i>XNpb227</i>	50	91	47	188	25.0	0.3	2
<i>XNpb223</i>	49	97	45	191	23.6	0.2	2
<i>XNpb349</i>	56	96	42	194	21.6	2.0	2
<i>spl-2</i>	68	-	12	80	15.0	4.3 *	1

- <sup>1)</sup> I/I homozygous for Indica allele  
 I/J heterozygous for Indica and Japonica alleles  
 J/J homozygous for Japonica allele

\*, \*\* and \*\*\* significant at 5%, 1% and 0.1% levels, respectively

## Chromosome 3

Gene	Allele <sup>1)</sup>			Total	J/J (%)	$\chi^2$ (3:1 or 1:2:1)	No. of cross
	I/I	I/J	J/J				
<i>chl-1</i>	29	76	25	130	19.2	4.0	1
<i>XNpb164</i>	49	67	25	141	17.7	8.5 *	1
<i>XNpb249</i>	75	135	42	252	16.7	9.9 **	2
<i>fc-1</i>	138	-	22	160	13.8	10.8 ***	1
<i>st</i> <sup>2)</sup>	100	-	13	113	11.5	11.0 ***	1
<i>XNpb51</i>	88	134	29	251	11.6	28.9 ***	2
<i>XNpb15</i>	85	136	32	253	12.6	23.6 ***	2
<i>XNpb182</i>	82	127	40	249	16.1	14.3 ***	2
<i>XNpb348</i>	75	129	48	252	19.0	5.9	2
<i>d1</i>	88	-	25	113	22.1	0.5	1
<i>sp1-3</i>	129	-	30	159	18.9	3.2	1
<i>XNpb173</i>	43	68	31	142	21.8	2.3	1

- <sup>1)</sup> I/I homozygous for Indica allele  
I/J heterozygous for Indica and Japonica alleles  
J/J homozygous for Japonica allele

<sup>2)</sup> *st* (t) (CM120)

\*, \*\* and \*\*\* significant at 5%, 1% and 0.1% levels, respectively

## Chromosome 4

Gene	Allele <sup>1)</sup>			Total	J/J (%)	$\chi^2$ (3:1 or 1:2:1)	No. of cross
	I/I	I/J	J/J				
<i>XNpb203</i>	33	61	33	127	26.0	0.2	1
<i>XNpb237</i>	30	66	33	129	25.6	0.2	1
<i>XNpb311</i>	26	68	41	135	30.4	3.3	1
<i>XNpb49</i>	29	58	31	118	26.3	0.1	1
<i>XNpb72</i>	29	69	36	134	26.9	0.9	1
<i>d-11</i>	121	-	29	150	19.3	2.6	1
<i>XNpb114</i>	36	71	29	136	21.3	1.0	1
<i>XNpb120</i>	37	73	27	137	19.7	2.1	1
<i>Ph</i>	98	-	30	128	23.4	0.2	1
<i>lg</i>	120	-	30	150	20.0	2.0	1
<i>lg</i>	304	-	77	381	20.2	4.7 *	3
<i>nal-1</i>	297	-	84	381	22.0	1.8	3

- <sup>1)</sup> I/I homozygous for Indica allele  
 I/J heterozygous for Indica and Japonica alleles  
 J/J homozygous for Japonica allele

\* significant at 5% level



## Chromosome 5

Gene	Allele <sup>1)</sup>			Total	J/J (%)	$\chi^2$ (3:1 or 1:2:1)	No. of cross
	I/I	I/J	J/J				
<i>XNpb292</i>	37	97	57	191	29.8	4.2	2
<i>XNpb139</i>	34	106	57	197	28.9	6.5 *	2
<i>XNpb387</i>	35	102	53	190	27.9	4.4	2
<i>d-1</i>	67	-	30	97	30.9	1.8	1
<i>st</i> <sup>2)</sup>	75	-	25	100	25.0	0.0	1
<i>XNpb105</i>	47	99	49	195	25.1	0.1	2
<i>XNpb81</i>	56	94	47	197	23.9	1.2	2
<i>sp1-7</i>	84	0	16	100	16.0	4.3 *	1
<i>n1-1</i>	74	0	26	100	26.0	0.1	1
<i>XNpb297</i>	58	90	48	196	24.5	2.3	2
<i>v-10</i>	135	-	46	181	25.4	0.0	1
<i>sp1-7</i>	151	-	30	181	16.6	6.9 **	1

- <sup>1)</sup> I/I homozygous for Indica allele  
I/J heterozygous for Indica and Japonica alleles  
J/J homozygous for Japonica allele

<sup>2)</sup> *st* (t) (CM37)

\* and \*\* significant at 5% and 1% levels, respectively

## Chromosome 6

Gene	Allele <sup>1)</sup>			Total	J/J (%)	$\chi^2$ (3:1 or 1:2:1)	No. of cross
	I/I	I/J	J/J				
<i>dp-1</i>	161	-	48	209	23.0	0.5	2
<i>spl-4</i>	80	-	16	96	16.7	3.6	1
<i>XNpb209</i>	58	98	46	202	22.8	1.6	2
<i>XNpb165-1</i>	64	123	19	206	9.2	27.4 ***	2
<i>XNpb233</i>	29	65	17	111	15.3	5.8	1
<i>XNpb172</i>	29	64	18	111	16.2	4.8	1
<i>C1</i>	29	-	84	113	74.3	0.0	1
<i>XNpb386</i>	31	55	25	111	22.5	0.7	1
<i>XNpb135</i>	28	38	23	89	25.8	2.5	1
<i>XNpb170</i>	36	-	75	111	67.6	3.3	1
<i>v-3</i>	91	-	16	107	15.0	5.8 *	1

- <sup>1)</sup> I/I homozygous for Indica allele  
 I/J heterozygous for Indica and Japonica alleles  
 J/J homozygous for Japonica allele

\* and \*\*\* significant at 5% and 0.1% levels, respectively .

## Chromosome 7

Gene	Allele <sup>1)</sup>			Total	J/J (%)	$\chi^2$ (3:1 or 1:2:1)	No. of cross
	I/I	I/J	J/J				
<i>XNpb50</i>	24	56	20	100	20.0	1.8	1
<i>g-1</i>	78	-	22	100	22.0	0.5	1
<i>d-6</i>	75	-	25	100	25.0	0.0	1
<i>sp1-5</i>	80	-	20	100	20.0	1.3	1
<i>v-11</i>	75	-	25	100	25.0	0.0	1
<i>XNpb85-1</i>	75	-	25	100	25.0	0.0	1
<i>XNpb20</i>	26	49	25	100	25.0	0.1	1
<i>XNpb117</i>	27	43	30	100	30.0	2.1	1
<i>XNpb22</i>	32	46	22	100	22.0	2.6	1

- <sup>1)</sup> I/I homozygous for Indica allele  
 I/J heterozygous for Indica and Japonica alleles  
 J/J homozygous for Japonica allele

## Chromosome 8

Gene	Allele <sup>1)</sup>			Total	J/J (%)	$\chi^2$ (3:1 or 1:2:1)	No. of cross
	I/I	I/J	J/J				
<i>v-8</i>	82	-	18	100	18.0	2.6	1
<i>XNpb278</i>	15	52	32	99	32.3	6.1 *	1
<i>XNpb369</i>	16	58	25	99	25.3	4.6	1
<i>XNpb126</i>	18	57	24	99	24.2	3.0	1
<i>XNpb187</i>	19	53	27	99	27.3	1.8	1
<i>XNpb397</i>	29	48	22	99	22.2	1.1	1
<i>sug</i>	85	-	15	100	15.0	5.3 *	1

- <sup>1)</sup> I/I homozygous for Indica allele  
 I/J heterozygous for Indica and Japonica alleles  
 J/J homozygous for Japonica allele

\* significant at 5% level

## Chromosome 9

Gene	Allele <sup>1)</sup>			Total	J/J (%)	$\chi^2$ (3:1 or 1:2:1)	No. of cross
	I/I	I/J	J/J				
<i>I-Bf</i>	138	-	21	159	13.2	11.8 ***	1
<i>XNpb36</i>	81	150	77	308	25.0	0.3	3
<i>XNpb47</i>	90	147	70	307	22.8	3.2	3
<i>dp-2</i>	126	-	41	167	24.6	0.0	2
<i>drp-2</i>	127	-	42	169	24.9	0.0	2
<i>XNpb385</i>	88	147	73	308	23.7	2.1	3
<i>Dn-1</i>	18	-	67	85	78.8	0.7	1
<i>XNpb404</i>	33	83	50	166	30.1	3.5	2
<i>XNpb108</i>	71	153	82	306	26.8	0.8	3
<i>XNpb293</i>	71	-	236	307	76.9	0.6	3

- <sup>1)</sup> I/I homozygous for Indica allele  
 I/J heterozygous for Indica and Japonica alleles  
 J/J homozygous for Japonica allele  
 \*\*\* significant at 0.1% level

## Chromosome 10

Gene	Allele <sup>1)</sup>			Total	J/J (%)	$\chi^2$ (3:1 or 1:2:1)	No. of cross
	I/I	I/J	J/J				
<i>XNpb333</i>	20	39	19	78	24.4	0.0	1
<i>XNpb37</i>	32	62	35	129	27.1	0.3	1
<i>XNpb133</i>	19	34	25	78	32.1	2.2	1
<i>XNpb291</i>	29	66	37	132	28.0	1.0	1
<i>spl-10</i>	111	-	49	160	30.6	2.7	1
<i>pgl</i>	113	-	45	158	28.5	1.0	1
<i>XNpb127</i>	25	70	36	131	27.5	2.5	1

- <sup>1)</sup> I/I homozygous for Indica allele  
 I/J heterozygous for Indica and Japonica alleles  
 J/J homozygous for Japonica allele

## Chromosome 11

Gene	Allele <sup>1)</sup>			Total	J/J (%)	$\chi^2$ (3:1 or 1:2:1)	No. of cross
	I/I	I/J	J/J				
<i>XNpb181</i>	33	-	66	99	66.7	3.7 *	1
<i>XNpb389</i>	33	53	13	99	13.1	8.6 *	1
<i>XNpb78</i>	33	52	14	99	14.1	7.5 *	1
<i>z-2</i>	92	-	11	103	10.7	11.3 ***	1
<i>gmZ410</i>	34	55	10	99	10.1	12.9 **	1
<i>XNpb202</i>	29	53	17	99	17.2	3.4	1
<i>XNpb44</i>	28	53	18	99	18.2	2.5	1
<i>XNpb183</i>	28	56	15	99	15.2	5.1	1
<i>v-9</i>	84	-	19	103	18.4	2.4	1
<i>XNpb189</i>	30	47	22	99	22.2	1.5	1
<i>XNpb52</i>	34	45	20	99	20.2	4.8	1
<i>la</i>	199	-	42	241	17.4	7.4 **	2
<i>v-4</i>	198	-	43	241	17.8	6.6 *	2
<i>sp</i>	174	-	23	197	11.7	18.7 ***	2

- <sup>1)</sup> I/I homozygous for Indica allele  
 I/J heterozygous for Indica and Japonica alleles  
 J/J homozygous for Japonica allele

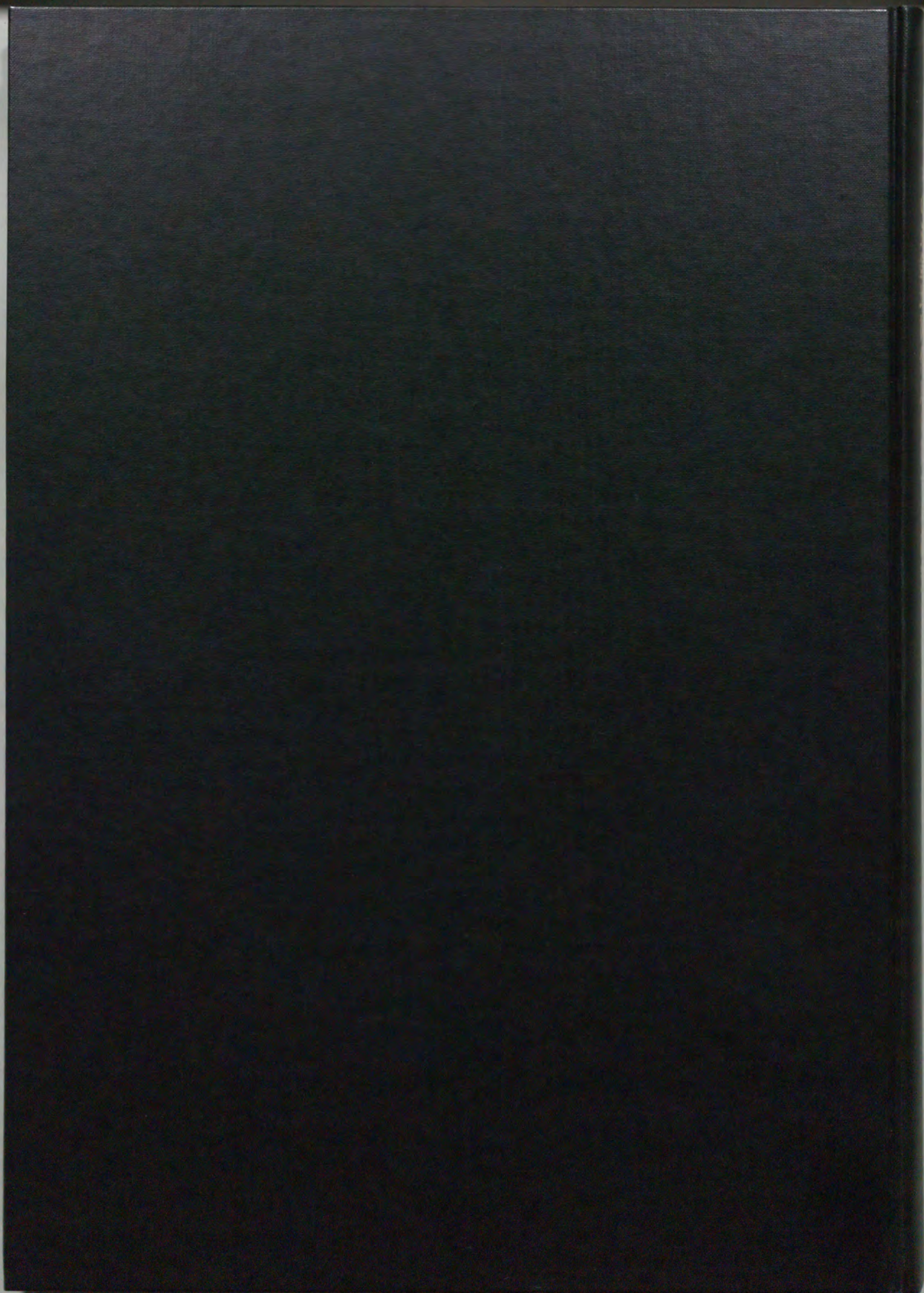
\*, \*\* and \*\*\* significant at 5%, 1% and 0.1% levels, respectively

## Chromosome 12

Gene	Allele <sup>1)</sup>			Total	J/J (%)	$\chi^2$ (3:1 or 1:2:1)	No. of cross
	I/I	I/J	J/J				
<i>XNpb193</i>	62	77	31	170	18.2	12.8 **	2
<i>XNpb124-1</i>	50	87	39	176	22.2	1.4	2
<i>sp1-1</i>	65	-	25	90	27.8	0.4	1
<i>XNpb88</i>	49	91	36	176	20.5	2.1	2
<i>XNpb402</i>	66	0	113	179	63.1	13.5 ***	2
<i>rl-1</i>	82	-	14	96	14.6	5.6 *	1
<i>XNpb148</i>	47	35	11	93	11.8	33.6 ***	1
<i>XNpb198</i>	67	79	32	178	18.0	16.0 ***	2

- <sup>1)</sup> I/I homozygous for Indica allele  
 I/J heterozygous for Indica and Japonica alleles  
 J/J homozygous for Japonica allele

\*, \*\* and \*\*\* significant at 5%, 1% and 0.1% levels, respectively



Inches 1 2 3 4 5 6 7 8  
cm 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19

# Kodak Color Control Patches

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# Kodak Gray Scale



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**A** 1 2 3 4 5 6 **M** 8 9 10 11 12 13 14 15 **B** 17 18 19

