

Table S1. Bacterial leaf blight resistance genes in IRBB60 and blast resistance genes in Putra-1 and their linked markers.

s/n	Gene	Chromo-Some	Linked marker	Primer sequence	Reference
BLB					
1.	<i>Xa5</i>	5	RM122	F: GAGTCGATGTAATGTCATCAGTGC R: GAAGGAGGTATCGCTTTGTTGGAC	[59,60]
2.	<i>Xa13</i>	8	Xa-13prom	F: GGCCATGGCTCAGTGTAT R: GAGCTCCAGCTCTCCAAATG	[61–63]
3.	<i>Xa5</i>	5	RM13	F: TCCAACATGGCAAGAGAGAG R: GGTGGCATTTCGATTCCAG	[64,65]
4.	<i>Xa5</i>	5	RG556	F: TAG CTG CTG CCG TGC TGT GC R: AAT ATT TCA GTG TGC ATC TC	[63,66]
5.	<i>Xa13</i>	8	RG136	F: TCCCAGAAAGCTACTACAGC R: GCAGACTCCAGTTTGACTTC	[61]
6.	<i>Xa21</i>	11	pTA248	F: AGACGCGGAAGGGTGGTTCCCGGA R: AGACGCGGAATCGAAGATGAAA	[63,67]
7.	<i>Xa5</i>	11	RM21	F: ACAGTATTCCGTAGGCACGG R: GCTCCATGAGGGTGGTAGAG	[68]
8.	<i>Xa13</i>	8	RM230	F: GCCAGACCGTGGATGTTC R: CACCGCAGTCACTTTTCAAG	[68]
9.	<i>Xa5</i>	5	RM390	F: CCCTTGTTTCAGTGGCTCAG R: CCAAGATCAAGAACAGCAGGAATC	[68]
10.	<i>Xa5</i>	5	Xa5S	F: GTCTGGAATTTGCTCGCGTTCG R: TGGTAAAGTAGATACCTTATCAAACCTGGA	[69,70]
11.	<i>Xa5</i>	5	Xa5R	F: AGCTCGCCATTCAAGTTCTTGAG R: TGACTTGGTTCTCCAAGGCTT	[69]
12.	<i>Xa21</i>	12	Xa21FR	F: TCCAACATGGCAAGAGAGAG R: GGTGGCATTTCGATTCCAG	[69]
13.	<i>Xa4</i>	11	RM224	F: ATCGATCGATCTTCACGAGG R: TGCTATAAAAGGCATTTCGGG	[64]
14.	<i>Xa13</i>	8	STS-RG136	F: TCCCAGAAAGCTACTACAGC R: GCAGACTCCAGTTTGACTTC	[71,72]
15.	<i>Xa4</i>	4	MP1, MP2	F: ATCGATCGATCTTCACGAGG R: TCGTATAAAAGGCATTTCGGG	[73]
Blast					
16.	<i>Piz</i>	6	RM8255	ATGCGTGTTTCAGAAATTAGG TTGTTGTATACCTCATCGACAG	[74]
17.	<i>Pi2, Pi9</i>	6	RM6836	TGTTGCATATGGTGCTATTGA GATACGGCTTCTAGGCCAAA	[74]

Table S2. Polymorphic background markers and their SSR details.

S/n	Marker	Chro.	Genetic distance (cM)	Anneal. temp.	Repeat Motif	Genomic DNA	Primer Sequence (F)	Primer Sequence (R)	Exptd. band size
1	RM72	8,7	39.7	55	(TAT)5C(ATT) 15	AF344086	CCGGCGATAAAACAATGAG	GCATCGGTCCTAACTAAGG G	166
2	RM10	7	63.5	55	(GA)15	AF344012	TTGTCAAGAGGAGGCATCG	CAGAATGGGAAATGGGTCC	159
3	RM3761	8	112.6	50	(GA)18	AY02043	CCTCAACAATAGCACCACC	CTGCAAGTCTGCAAGCACA G	177
4	RM1261	12	61.6	50	(AG)16	AY01793	GTCCATGCCCAAGACACAA	GTTACATCATGGGTGACCC C	167
5	RM561	2	74.1	55	(GA)11	AQ91330	GAGCTGTTTTGGACTACGG	GAGTAGCTTTCTCCACCCC C	190
6	RM415	12	0.0	55	(AT)21	AQ15904	CTTCGATCCATCATCCATG	ATTGCTGTACGCAGTTTCGG G	227
7	RM333	10	110.4	55	(TAT)19(CTT) 19	AF344157	GTACGACTACGAGTGTAC	GTCTTCGCGATCACTCGC CAA	191
8	RM272	1	28.7	55	(GA)9	AF344098	AATTGGTAGAGAGGGGAG	ACATGCCATTAGAGTCAGG C	119
9	RM211	2	14.4	55	(TC)3A(TC)18	AF344032	CCGATCTCATCAACCAACT	CTTCACGAGGATCTCAAAG G	161
10	RM127	4	150.1	55	(AGG)8	D40108	GTGGGATAGCTGCGTCGCG	AGGCCAGGGTGTGGCATG TCG	223
11	RM6208	8	42.9	55	(CGG)8	AY02288	TCGAGCAGTACGTGGATCT	CACACGTACATCTGCAAGG G	143
12	RM410	9	79.3	55	(TA)13	AQ15644	GCTCAACGTTTCGTTCTG	GAAGATGCGTAAAGTGAAC GG	183
13	RM122	5	0.0		(GA)7A(GA)2 A (GA)11		GAGTCGATGTAATGTCATC	GAAGGAGGTATCGCTTTGT AGTGC	227
14	RM3750	10	22	61	(GA)17	AY02042	CCGACTTCGAAGTCCGAAC	TCCAGCTGTCTCTTCCGC 5	166
15	RM302	1	147.8	55	(GT)30(AT)8	AF344127	TCATGTCATCTACCATCAC	ATGGAGAAGATGGAATACT AC	156
16	RM547	8	27.3	55	(ATT)19	AQ86608	TAGGTTGGCAGACCTTTTC	GTCAAGATCATCCTCGTAG G	235
17	RM432	7	43.5	55	(CATC)9	AQ27373	TTCTGTCTCACGCTGGATTG	AGCTGCGTACGTGATGAAT G	187
18	RM3248	2	153.2	55	(CT)13	AY01992	AGAAGGTTGCTTTCTTGGC	CTTGCAAGGTCTGTTGCATC C	197

Table S2 Cont'd.

S/n	Marker	Chro.	Genetic distance (cM)	Anneal. temp.	Repeat Motif	Genomic DNA	Primer Sequence (F)	Primer Sequence (R)	Exptd. band size
19	RM3843	4	108.2	55	(GA)23	AY020518	ACCCTACTCCCAACAGTCC C	GGGGTCGTACGCTCATGTC	172
20	RM130	3	208.2	55	(GA)10	D40295	TGTTGCTTGCCCTCACGCG AAG	GGTCGCGTGCTTGGTTTGG TTC	85
21	RM309	12	73	55	(GT)13	AF344134	GTAGATCACGCACCTTTCT GG	AGAAGGCCTCCGGTGAAG	169
22	RM336	7	80	55	(CTT)18	AF344160	CTTACAGAGAAACGGCAT CG	GCTGGTTTGTTCAGGTTC G	154
23	RM573	2	131.8	55	(GA)11	AQ364937	CCAGCCTTTGCTCCAAGTA C	TCTTCTTCCCTGGACCACA C	201
24	RM342	8,9	63.6	55	(CAT)12	AF344166	CCATCCTCCTACTTCAATG AAG	ACTATGCAGTGGTGTCAAC C	141
25	RM117	12	28.1	55	(AG)7	D24346	CGATCCATTCTGCTGCTC GCG	CGCCCCATGCATGAGAA GACG	208
26	RM262	2	64.6	55	(CT)16	AF344081	CATTCCGTCTCGGCTCAAC T	CAGAGCAAGGTGGCTTGC	154
27	RM588	6	7.4	55	(TGC)9	AP000559	GTTGCTCTGCCTCACTCTT G	AACGAGCCAACGAAGCAG	126
28	RM1089	5	69.2	55	(AC)33	AY017760	CAGAAGGATTATCTCGAT ACC	AATAGGGCTTGAAATAAA TTG	239
29	RM447	8	100.4	55	(CTT)8	AQ290369	CCCTTGCTGTCTCCTCT C	ACGGGCTTCTTCTCCTTCT C	111
30	RM1237	5	67.5	55	(AG)15	AY017912	CTCCGCGAGCTTTAGAAG AG	CACATACTCTGGCTCTCCC G	144
31	RM25	8	23.5	55	(GA)18	AF343842	GGAAAGAATGATCTTTTCACTACCATCAAAACCAATGT TGG	TC	146
32	RM1134	7	25.4	50	(AG)12	AY017809	ACACCCAACTTTTCTCACG C	AGCTAGGGTTTCGATCTCC C	144
33	RM518	4	34.6	55	(TC)15	AQ690034	CTCTTCACTCACTCACCAT GG	ATCCATCTGGAGCAAGCA AC	171
34	RM1253	7	44.4	50	(AG)16	AY017928	CTGAACTTGCCTGAGAACT C	GACGACCTCTCCATGCTCG	175
35	RM525	2	143.7	55	(AAG)12	AQ794433	GGCCCGTCCAAGAAATAT TG	CGGTGAGACAGAATCCTTA CG	131
36	RM23865	9			(CT)10		TCATCCCATTCTCTCCTC ACC	CATACGGCCATACAAATG AACC	148

Table 2 Cont'd.

S/n	Marker	Chro.	Genetic distance (cM)	Anneal. temp.	Repeat Motif	Genomic DNA	Primer Sequence (F)	Primer Sequence (R)	Exptd. band size
37	RM8213	4	0	55	(TC)10	AL442113	AGCCCAGTGATACAAAGA TG	GCGAGGAGATACCAAGA AAG	177
38	RM508	6	0	55	(AG)17	AQ577547	GGATAGATCATGTGTGGG GG	ACCCGTGAACCACAAAGA AC	235
39	RM313	12	65.5	55	(GT)6CA(CG) 5-6-(GT)8	AF344138	TGCTACAAGTGTCTTCA GGAC	GCTCACCTTTTGTGTTCCA C	111
40	RM310	8	110.4	55	(GT)19	AF344135	CCAAAACATTTAAAATAT CATG	GCTTGTGTCATTACCAT TC	105
41	RM7376	12	23	50	(GAAA)6	AY024051	TCACCGTCACCTCTTAAG TC	GGTGGTTGTGTTCTGTTG G	195
42	RM431	1	166.7	55	(AG)16	AQ272944	TCCTGCGAACTGAAGAGT TG	AGAGCAAAACCCTGGTTC AC	251
43	RM1375	10	80.8	50	(AG)31	AY018050	CTACACGCGCAAACCTCTG TC	ATGAAGGTCTAGGCTGCA CC	180
44	RM6293	11	117.3	55	(CTT)8	AY022968	GGCTCGATCGATTGGATT C	TCACTAAAACGCGTTACG GG	198
45	RM241	4	102.3	55	(CT)31	AF344061	GAGCCAAATAAGATCGCT GA	TGCAAGCAGCAGATTTAG TG	158
46	RM452	2	56.3	55	(GTC)9	AQ326476	CTGATCGAGAGCGTTAAG GG	GGGATCAAACCACGTTTC TG	209
47	RM305	5	95.1	55	(GT)4+degene r	AF344130	TACTGCCAAAGGCGAGCT TC	GTGAGAGGCTACAGCTAA CC	203
48	RM1	1,3	79.4	55	(GA)26		GCGAAAACACAATGCAA AAA	GCGTTGGTTGGACCTGAC	113
49	RM6836	6	54.1	55	(TCT)14	AY023511	TGTTGCATATGGTGCTAT TTGA	GATACGGCTTCTAGGCCA AA	240
50	RM8225	6	54.1	55	A11N(AAG)1 4				221
51	RM520	3	170.4	55	(AG)10	AQ690961	AGGAGCAAGAAAAGTTC CCC	GCCAATGTGTGACGCAAT AG	247
52	OSR28	9	0	55	(AGA)n	D40471	AGCAGCTATAGCTTAGCT GG	ACTGCACATGAGCAGAGA CA	0
53	RM28076	12	135		(CT)13		GGGACTTGGGACCAGTTT ATGG	TCAGGTCTGTTGGATTCC ATGC	289
54	RM219	9	108.6	55	(CT)17	AF344040	CGTCGGATGATGTAAAGC CT	CATATCGGCATTGCGCTG	202

Table 2 Cont'd.

S/n	Marker	Chro.	Genetic distance (cM)	Anneal temp.	Repeat Motif	Genomic DNA	Primer Sequence (F)	Primer Sequence (R)	Exptd. band size
55	RM544	8	34.2	55	(TC)9	AQ863302	TGTGAGCCTGAGCAATAACG	GAAGCGTGTGATATCGCAT G	248
56	RM261	4	0	55	C9(CT)8	AF344080	CTACTTCTCCCCTTGTGTCG	TGTACCATCGCCAAATCTC C	125
57	RM5556	8	26	55	(TG)15	AY022231	ATCTCCCTCCCTCTCCTCAC	TCCACACCTTCACAGTTGA C	102
58	RM206	11	74.1	55	(CT)21	AF344027	CCCATGCGTTTAACTATTCT	CGTTCCATCGATCCGTATGG	147
59	RM294A	1,10,8	95.9	55	{{(GT)3T2AG GGACA}2	AF344120	TTGGCCTAGTGCCTCCAATC	GAGGGTACAACCTTAGGACG CA	173
60	RM250	2	158.6	55	(CT)17	AF344070	GGTTCAAACCAAGCTGATCA	GATGAAGGCCTTCCACGCA G	153
61	RM402	6	44.4	55	(ATA)7	AQ050029	GAGCCATGGAAAGATGCATG	TCAGCTGGCCTATGACAAT G	133
62	RM5390	2	50.3	55	(TC)14				148
63	RM232	3	28.1	55	(CT)24	AF344052	CCGGTATCCTTCGATATTGC	CCGACTTTTCCTCCTGACG	158
64	RM160	9	88.3	55	(GAA)23				131
65	RM463	12	104.8	55	(TTAT)5	AQ328446	TTCCCCTCCTTTTATGGTGC	TGTTCTCCTCAGTCACTGCG	192
66	RM1973	7	70.8	55	(AT)19	AY018648	GAGTTGCAAGGATATTTTAA	TGGAGCCTAGAGAATACAT A	143
67	RM10025	1	395		(CTTT)5		GCTTGAAGCATTTCATCTCCT CTTCC	CGTGCATTGATTCCAAGAA GATCC	82
68	RM6308	3	180	55	(CTT)9	AY022983	TCGACCTGGCTCTCCTCTAG	TATCAACCTGCTCCTCCTGG	104
69	RM233A	2,5	16.3	55	(CT)20	AF344053	CCAAATGAACCTACATGTTG	GCATTGCAGACAGCTATTG A	162
70	SSR21	3	144.5	55	(CT)9	AC091494	GTCCCACATGTCAGGATG	ATCTGCTACTTGTGGAGGA G	224

Table 2 Cont'd.

S/n	Marker	Chro.	Genetic distance (cM)	Anneal. temp.	Repeat Motif	Genomic DNA	Primer Sequence (F)	Primer Sequence (R)	Exptd. band size
71	SSR23	1		55	(TC)22	AP003227	GCGTAAGATCTCCCTACCA C	CAACACATGATAGCACATG G	211
72	SSR13	1	103.4	55	(GT)31(AT)3 0	AP002839	GCAGAAAATTTCATTAG CATCT	GGATATGACTTACTACTGC AACAAATCT	291
73	SSR26	1	25	55	(TAT)5	AP004317	AATCTAACGTTTGACTATC CATC	TCTACCAGTACTCCCTTCAC C	192
74	RM13	5	28.6	55	(GA)6- (GA)16	AF344014	TCCAACATGGCAAGAGAGA G	GGTGGCATTTCGATTCCAG	141
75	Xa- 13prom	8			-	-	GGCCATGGCTCAGTGT T	GAGCTCCAGCTCTCCAAAT G	
76	RM21	11	85.7	55	(GA)18	AF344021	ACAGTATTCCGTAGGCACG G	GCTCCATGAGGGTGGTAGA G	157
77	Xa21FR	12			-		TCCAACATGGCAAGAGAGA G	GGTGGCATTTCGATTCCAG	
78	pTA248	11	95.8		-		AGACGCGGAAGGGTGGTTC CCGGA	AGACGCGGTAATCGAAGAT GAAA	
79	MP	4			-		ATCGATCGATCTTCACGAG G	TCGTATAAAAGGCATTCCG G	

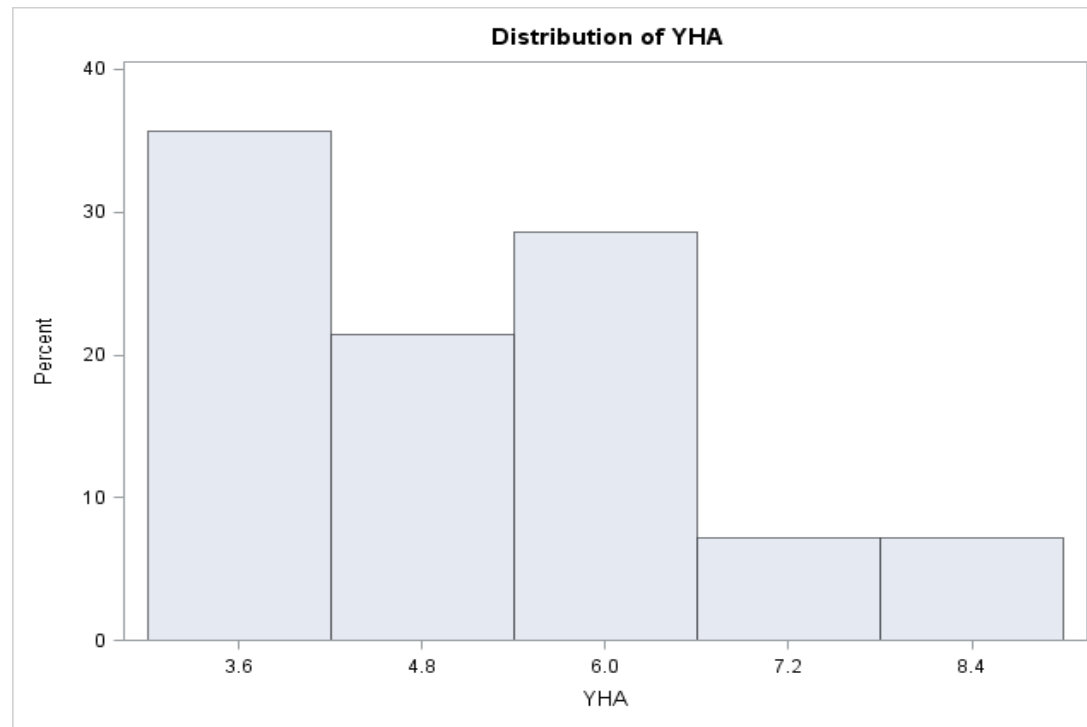


Figure S1. Histogram of yield/ha of the selected lines.

Note: YHA=yield per hectare (tons/ha)

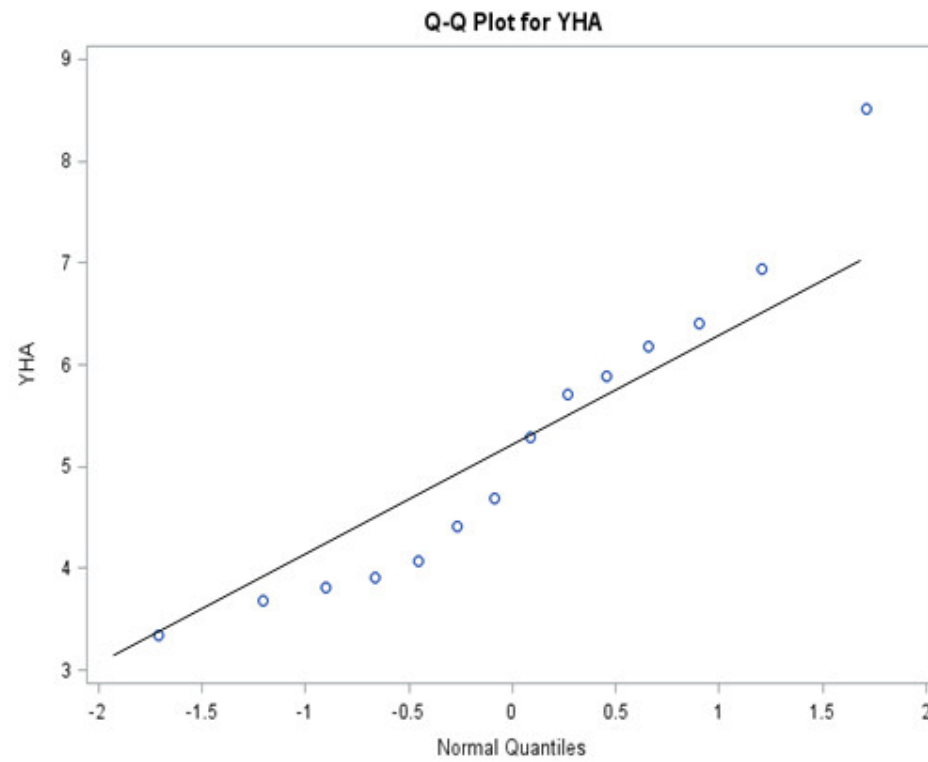


Figure S2. Normal quantile-quantile (Q-Q) plot for yield/ha of the selected lines.

Note: YHA=yield per hectare (tons/ha)