Supplementary Information

Development of Molecular Marker linked with Bacterial Fruit Blotch resistance in Melon (*Cucumis melo* L.)

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Table S1: Details of 22 melon accessions used and their disease response, as determined by bioassay and PCR-based assay using polymorphic InDel marker MB157-2.

Sl.	Genotype	Taxonomy	Origin	Bioassay		Genotype (InDel marker MB157-2)
				Percent infected area per leaf	Phenotype	
1	PI 353814	*Cucumis melo* subsp. *melo*	Israel	0	Resistant (Control)	+
2	PI 614596	*Cucumis melo* subsp. *melo*	Madhya Pradesh, India	93	Susceptible (Control)	-
3	PI 140471	*Cucumis melo*	USA	3	Resistant	+
4	PI 420145	*Cucumis melo*	USA	5	Resistant	+
5	PI 614525	*Cucumis melo* subsp. *agrestis*	Madhya Pradesh, India	86	Susceptible	-
6	PI 482398	*Cucumis melo* subsp. *melo*	Zimbabwe	54	Susceptible	-
7	PI482399	*Cucumis melo* subsp. *melo*	USA	48	Susceptible	-
8	PI 536473	*Cucumis melo* subsp. *agrestis*	Maldives	39	Susceptible	-
9	PI 504558	*Cucumis ficifolius*	India	47	Susceptible	-
10	PI 343701	*Cucumis pustulatus* (Wild)	Nigeria	35	Susceptible	-
11	PI 614401	*Cucumis melo* subsp. *melo*	Rajasthan, India	24	Susceptible	-
12	PI 614601	*Cucumis melo* subsp. *melo*	Rajasthan, India	49	Susceptible	-
13	PI 147065	*Cucumis anguria var. longaculeatus* (Wild)	Amazonas, Brazil	28	Susceptible	-
14	PI 157076	*Cucumis melo* subsp. *melo*	China	44	Susceptible	-
15	PI 157082	*Cucumis melo* subsp. *melo*	Cornell University, USA	37	Susceptible	-
16	CornellZPPM	*Cucumis melo*	Cornel University, USA	48	Susceptible	-
17	PI 357152	*Cucumis melo* subsp. *melo*	Peru, Tacna	36	Susceptible	-
18	PI 378171	*Cucumis melo* subsp. *melo*	Israel	55	Susceptible	-
19	PI 381763	*Cucumis melo* subsp. *melo*	India, Rajasthan	50	Susceptible	-
20	PI 422164	*Cucumis melo* subsp. *melo*	Czech Republic	72	Susceptible	-

21	PI 504531	*Cucumis melo* subsp. *melo*	Korea, South	39	Susceptible	-
22	PI 512417	*Cucumis melo* subsp. *melo*	Spain, Cordoba	31	Susceptible	-
23	PI 512568	*Cucumis melo*	Spain, Castellon de Plana	64	Susceptible	-
24	SCNU1154	*Cucumis melo*	SCNU, South Korea	48	Susceptible	-

Resistant (PI 353814) and susceptible parent (PI 614596) were included as control in both bioassay and PCR based assay. All landraces/inbred were collected form USDA, USA, except SCNU1154 which was collected from South Korea. '+' and '-' indicate resistant and susceptible bands for the InDel marker BM157-2.

Table S2: Comparison of *Acidovorax citrulli* bioassay results and InDel marker BM157-2 bands for the putative R-gene MELO3C022157 in a population of 491 F2 melon individuals raised from resistant and susceptible parental accessions PI 353814 and PI 614596, respectively. "+", "и" and "-" indicate resistant, heterozygous and susceptible bands for the InDel marker BM157-2.

Sl.	PIA/L	P	G	Sl.	PIA/L	P	G	Sl.	PIA/L	P	G	Sl.	PIA/L	P	G	Sl.	PIA/L	P	G
1	46	S	-	45	97	S	-	89	45	S	-	133	8	R	и	177	0	R	и
2	0	R	+	46	10	R	+	90	5	R	и	134	0	R	+	178	42	S	-
3	2	R	и	47	5	R	+	91	3	R	+	135	0	R	и	179	77	S	-
4	39	S	-	48	0	R	+	92	9	R	+	136	3	R	и	180	0	R	и
5	31	S	-	49	100	S	-	93	6	R	и	137	4	R	и	181	38	S	-
6	53	S	-	50	2	R	+	94	14	R	и	138	0	R	+	182	7	R	и
7	1	R	и	51	8	R	и	95	5	R	и	139	44	S	и	183	41	S	-
8	3	R	и	52	29	S	и	96	4	R	и	140	0	R	и	184	3	R	+
9	6	R	+	53	4	R	и	97	11	R	и	141	6	R	+	185	5	R	и
10	4	R	+	54	16	R	и	98	74	S	-	142	0	R	и	186	0	R	+
11	9	R	+	55	43	S	-	99	7	R	и	143	3	R	+	187	0	R	и
12	44	S	-	56	5	R	и	100	38	S	-	144	32	S	и	188	53	S	-
13	17	R	и	57	12	R	+	101	45	S	-	145	2	R	и	189	3	R	и
14	5	R	и	58	24	S	-	102	0	R	и	146	0	R	и	190	64	S	и
15	7	R	+	59	5	R	+	103	33	S	-	147	5	R	+	191	6	R	и
16	3	R	+	60	9	R	и	104	2	R	и	148	7	R	и	192	3	R	и
17	11	R	и	61	4	R	и	105	0	R	+	149	4	R	+	193	0	R	+
18	29	S	-	62	0	R	и	106	27	S	-	150	9	R	+	194	0	R	и
19	5	R	и	63	27	S	-	107	4	R	и	151	0	R	и	195	56	S	-
20	14	R	и	64	3	R	и	108	3	R	+	152	10	R	и	196	28	S	-
21	33	S	-	65	5	R	и	109	15	R	+	153	13	R	и	197	23	S	-
22	3	R	и	66	59	S	-	110	61	S	-	154	18	R	и	198	41	S	-
23	2	R	+	67	15	R	+	111	25	S	-	155	4	R	и	199	50	S	-
24	6	R	и	68	7	R	и	112	0	R	и	156	0	R	+	200	0	R	и
25	10	R	и	69	12	R	и	113	2	R	и	157	6	R	и	201	4	R	+
26	52	S	-	70	6	R	и	114	46	S	-	158	30	S	-	202	22	S	-
27	0	R	+	71	11	R	и	115	7	R	+	159	0	R	и	203	29	S	-
28	4	R	и	72	38	S	-	116	23	S	-	160	73	S	-	204	33	S	-
29	71	S	-	73	52	S	-	117	9	R	и	161	0	R	и	205	46	S	-
30	5	R	и	74	32	S	-	118	3	R	+	162	0	R	и	206	5	R	+
31	3	R	и	75	0	R	и	119	0	R	+	163	5	R	и	207	26	S	-
32	49	S	+	76	6	R	и	120	4	R	и	164	0	R	+	208	4	R	и
33	10	R	+	77	2	R	+	121	75	S	-	165	2	R	и	209	3	R	+
34	3	R	+	78	5	R	+	122	5	R	+	166	4	R	+	210	12	R	и
35	5	R	+	79	9	R	+	123	83	S	-	167	0	R	и	211	5	R	и
36	13	R	+	80	4	R	+	124	0	R	+	168	3	R	и	212	30	S	-
37	2	R	+	81	30	S	-	125	0	R	и	169	0	R	и	213	0	R	и
38	0	R	и	82	7	R	и	126	8	R	и	170	4	R	+	214	24	S	-
39	7	R	и	83	3	R	и	127	2	R	+	171	62	S	-	215	6	R	и
40	53	S	-	84	0	R	+	128	3	R	и	172	43	S	-	216	10	R	и
41	64	S	-	85	13	R	и	129	0	R	+	173	8	R	и	217	8	R	+
42	76	S	-	86	98	S	-	130	6	R	+	174	34	S	-	218	5	R	и
43	3	R	и	87	39	S	-	131	8	R	и	175	47	S	-	219	27	S	-
44	61	S	-	88	9	R	+	132	0	R	+	176	3	R	и	220	3	R	и

Sl.	PIA/L	P	G
221	6	R	и
222	0	R	+
223	5	R	+
224	9	R	+
225	5	R	и
226	6	R	+
227	3	R	и
228	4	R	+
229	0	R	+
230	13	R	+
231	4	R	и
232	0	R	+
233	33	S	и
234	0	R	и
235	7	R	+
236	9	R	+
237	10	R	и
238	0	R	и
239	11	R	+
240	14	S	-
241	8	R	и
242	5	R	+
243	9	R	и
244	5	R	+
245	2	R	+
246	14	R	и
247	0	R	+
248	8	R	и
249	12	R	и
250	5	R	и
251	0	R	+
252	34	S	+
253	3	R	и
254	6	R	+
255	0	R	+
256	4	R	и
257	3	R	и
258	4	R	и
259	24	R	и
260	0	R	+
261	24	S	-
262	51	S	-
263	62	S	-
264	43	S	-
265	6	R	+
266	22	S	-
267	25	S	-
268	30	S	-
269	43	S	-
270	7	R	+
271	11	R	и
272	28	S	-
273	10	R	и
274	0	R	+
275	4	R	и
276	0	R	и

Sl.	PIA/L	P	G
277	0	R	+
278	9	R	+
279	36	S	-
280	6	R	и
281	4	R	+
282	12	R	и
283	84	S	-
284	0	R	+
285	5	R	и
286	0	R	+
287	31	S	-
288	24	S	-
289	5	R	и
290	8	R	+
291	3	R	и
292	0	R	+
293	6	R	и
294	78	S	-
295	4	R	и
296	0	R	+
297	24	S	-
298	73	S	-
299	0	R	и
300	6	R	и
301	35	S	-
302	5	R	и
303	57	S	-
304	10	R	и
305	46	S	-
306	74	S	-
307	0	R	и
308	0	R	+
309	0	R	и
310	62	S	-
311	6	R	+
312	0	R	и
313	31	S	-
314	0	R	и
315	48	S	-
316	8	R	+
317	26	S	-
318	39	S	-
319	22	S	-
320	15	R	+
321	36	S	-
322	82	S	-
323	12	R	и
324	10	R	и
325	3	R	+
326	5	R	+
327	34	S	-
328	0	R	и
329	3	R	+
330	7	R	и
331	9	R	и
332	32	S	-

Sl.	PIA/L	P	G
333	5	R	и
334	51	R	+
335	25	S	-
336	3	R	и
337	65	S	-
338	77	S	-
339	27	S	-
340	6	R	+
341	3	R	и
342	34	S	-
343	0	R	и
344	23	S	-
345	35	S	-
346	2	R	и
347	25	S	-
348	0	R	и
349	23	S	-
350	0	R	и
351	5	R	+
352	7	R	и
353	0	R	+
354	9	R	и
355	39	S	+
356	0	R	+
357	0	R	и
358	4	R	+
359	6	H	+
360	2	R	и
361	0	R	+
362	10	R	и
363	5	R	и
364	13	R	и
365	4	R	+
366	37	S	+
367	0	R	и
368	6	R	и
369	0	R	+
370	7	R	+
371	5	R	и
372	6	R	+
373	7	R	и
374	5	R	+
375	0	R	и
376	9	R	+
377	0	R	+
378	0	R	и
379	4	R	+
380	0	R	и
381	4	R	+
382	0	R	+
383	6	R	и
384	3	R	и
385	8	R	+
386	0	R	и
387	0	R	+
388	5	R	и

Sl.	PIA/L	P	G
389	5	R	и
390	0	R	и
391	0	R	+
392	0	R	и
393	0	R	и
394	6	R	+
395	37	S	+
396	4	R	+
397	0	R	и
398	0	R	и
399	4	R	и
400	0	R	+
401	0	R	и
402	0	R	и
403	0	R	и
404	0	R	+
405	5	R	+
406	7	R	и
407	0	R	и
408	11	R	и
409	5	R	+
410	0	R	и
411	0	R	и
412	5	R	и
413	3	R	и
414	0	R	и
415	47	S	-
416	0	R	и
417	3	R	и
418	0	R	и
419	4	R	+
420	0	R	и
421	0	R	и
422	5	R	и
423	40	S	-
424	0	R	-
425	35	S	-
426	30	S	-
427	7	R	и
428	6	R	+
429	0	R	и
430	8	R	и
431	4	R	и
432	31	S	-
433	35	S	-
434	3	R	и
435	6	R	и
436	0	R	и
437	9	R	и
438	0	R	+
439	2	R	и
440	0	R	и
441	0	R	и
442	0	R	+
443	4	R	+
444	5	R	и

Sl.	PIA/L	P	G
445	2	R	и
446	29	S	-
447	50	S	-
448	27	S	-
449	53	S	-
450	0	R	и
451	4	R	и
452	0	R	+
453	0	R	и
454	24	S	-
455	66	S	-
456	4	R	и
457	38	S	-
458	31	S	-
459	0	R	и
460	35	S	-
461	24	S	-
462	0	R	и
463	0	R	и
464	36	S	-
465	56	S	-
466	2	R	+
467	24	S	-
468	47	S	-
469	0	R	и
470	5	R	и
471	0	R	и
472	0	R	и
473	0	R	+
474	0	R	и
475	0	R	и
476	3	R	и
477	0	R	и
478	5	R	+
479	8	R	+
480	69	S	-
481	0	R	и
482	72	S	-
483	0	R	+
484	3	R	+
485	0	R	+
486	0	R	+
487	0	R	+
488	33	S	-
489	5	R	+
490	8	R	и
491	54	S	-

PIA/L. Percent infected Area per leaf, P. phenotype and G. Genotype. Red text indicate mismatch between bioassay phenotype and marker assisted genotype.

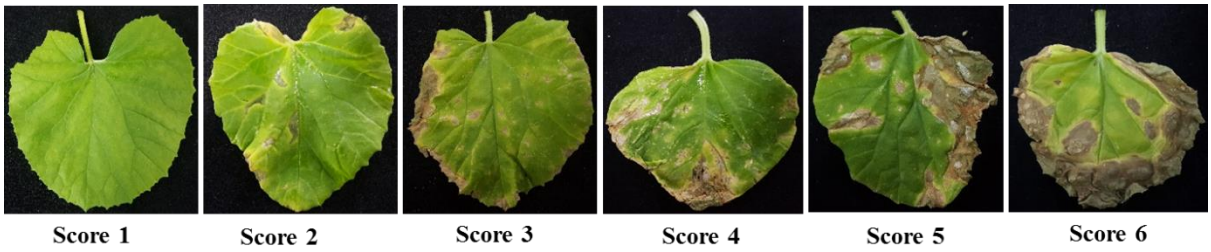

Figure S1: Disease scores used to assess the severity of bacterial fruit blotch (BFB) caused by *A. citrulli* at 12 days after inoculation. Scores range from 1 to 6, with 1 representing leaves with no damage and 6 representing maximum damage. All leaves were detached just before photographs were taken.

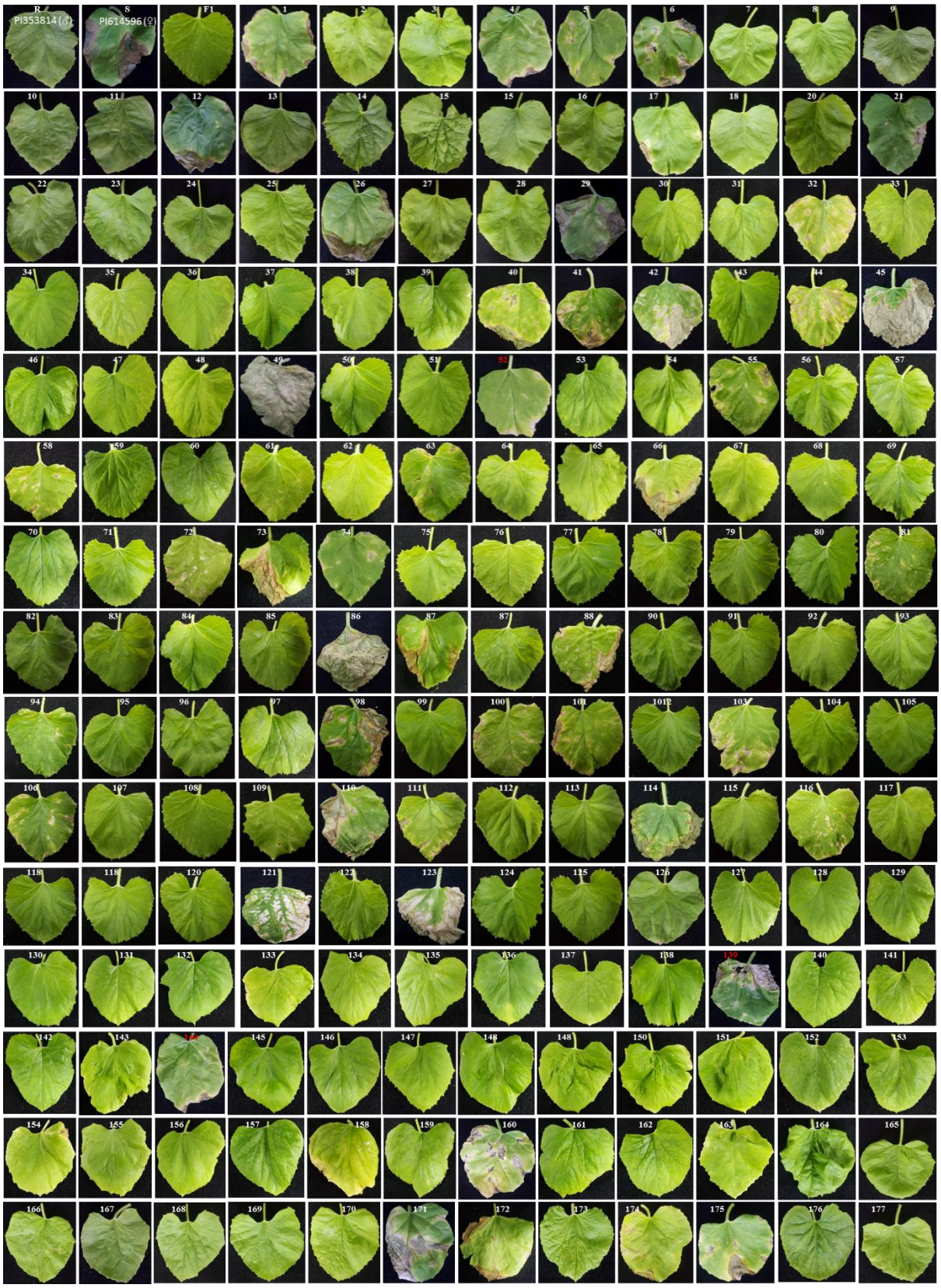

Fig. S1. Continued

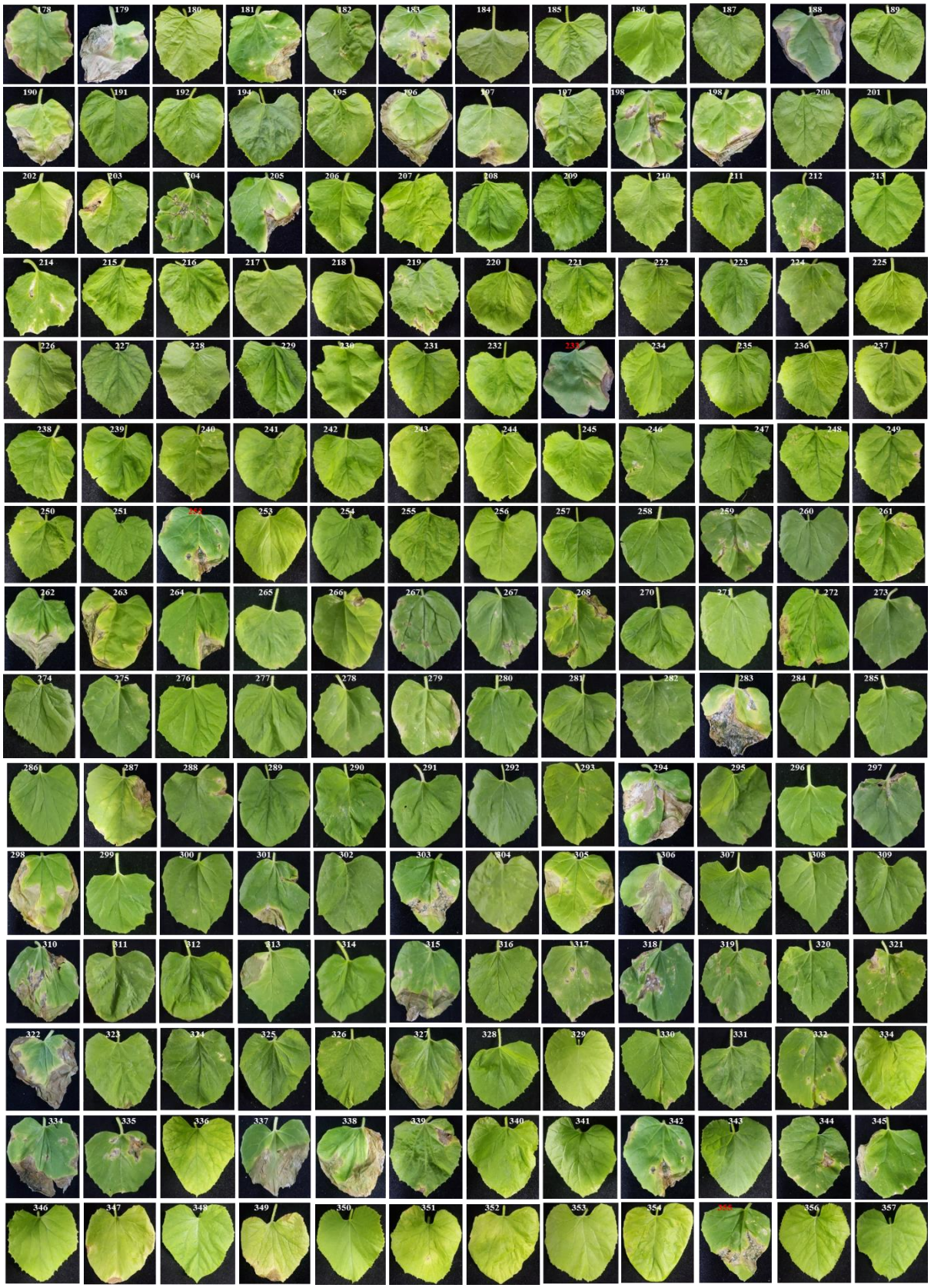

Fig S1. Continued

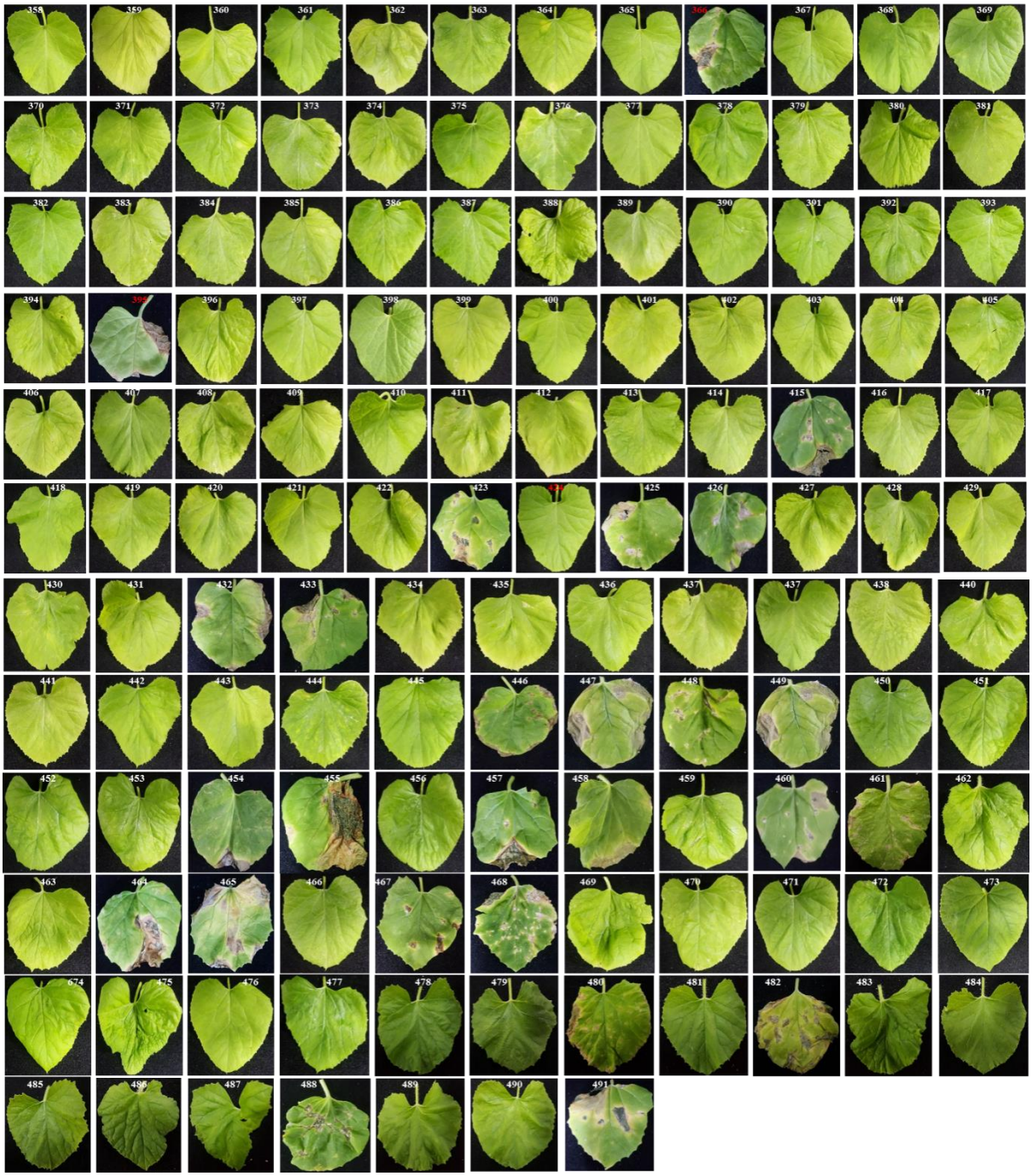

Figure S2: Disease symptoms on resistant (R) and susceptible (S) melon parental accessions PI 353814 and PI 614596, respectively, their F1 hybrid and 491 individuals of the F2 population at 12 days after inoculation with *A. citrulli*. All leaves were detached just before photographs were taken.

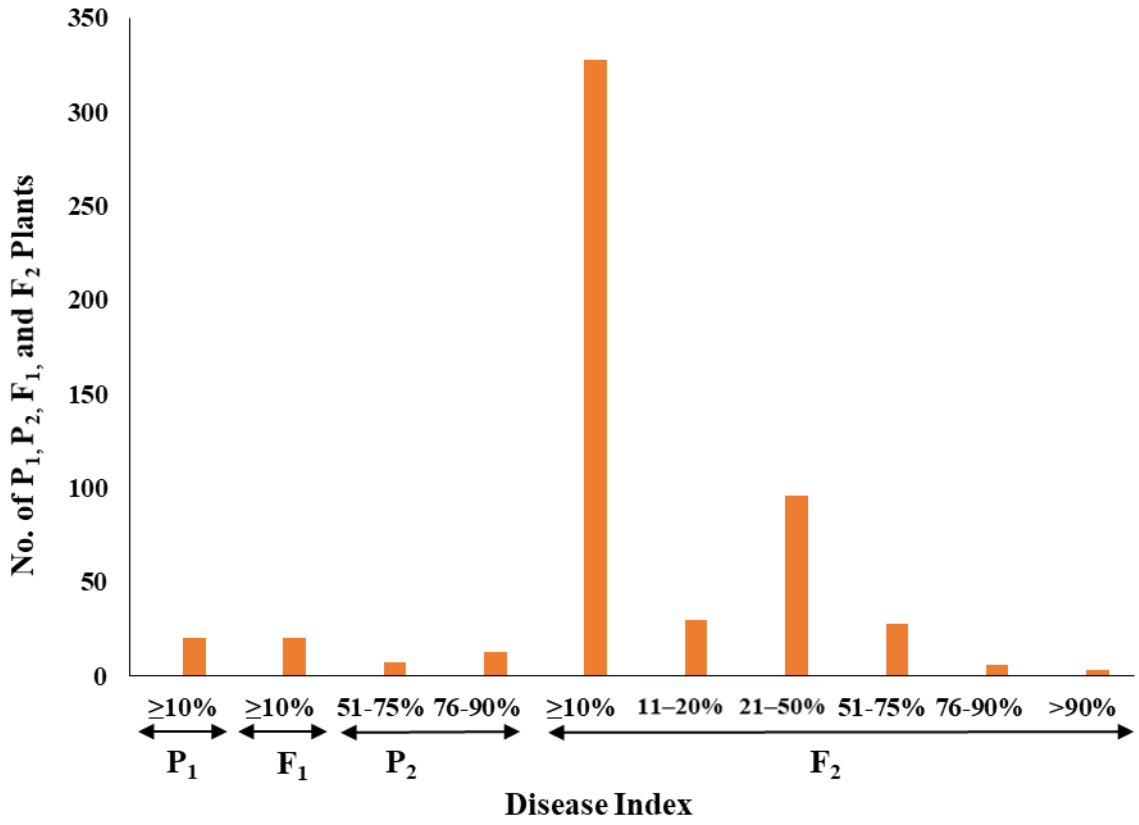

Figure S3: Frequency distribution of BFB scores in melon P_1, P_2, F_1 and F_2 populations.

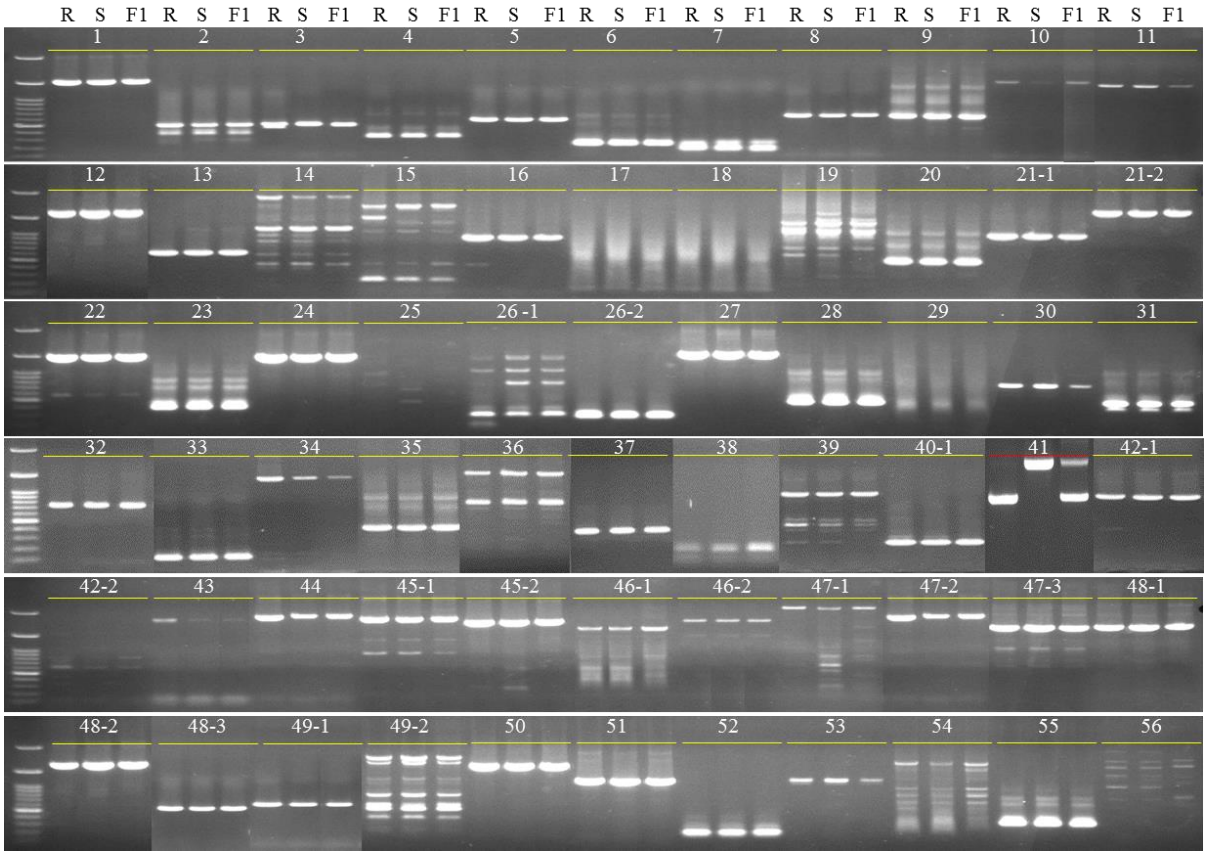

Figure S4: Detection of length polymorphism in 57 putative disease resistance genes containing NBS, LRR, CC and TIR domains by PCR-based assay. Details of the genes and corresponding primer specifications are presented in Table 1. Genes 40-2 and 57 were not amplified. Gene 41 (red underline) showed conspicuous length polymorphism. R—resistant parent PI 353814, S—susceptible parent PI 614596 and F1—hybrid (PI 614596 × PI 353814).

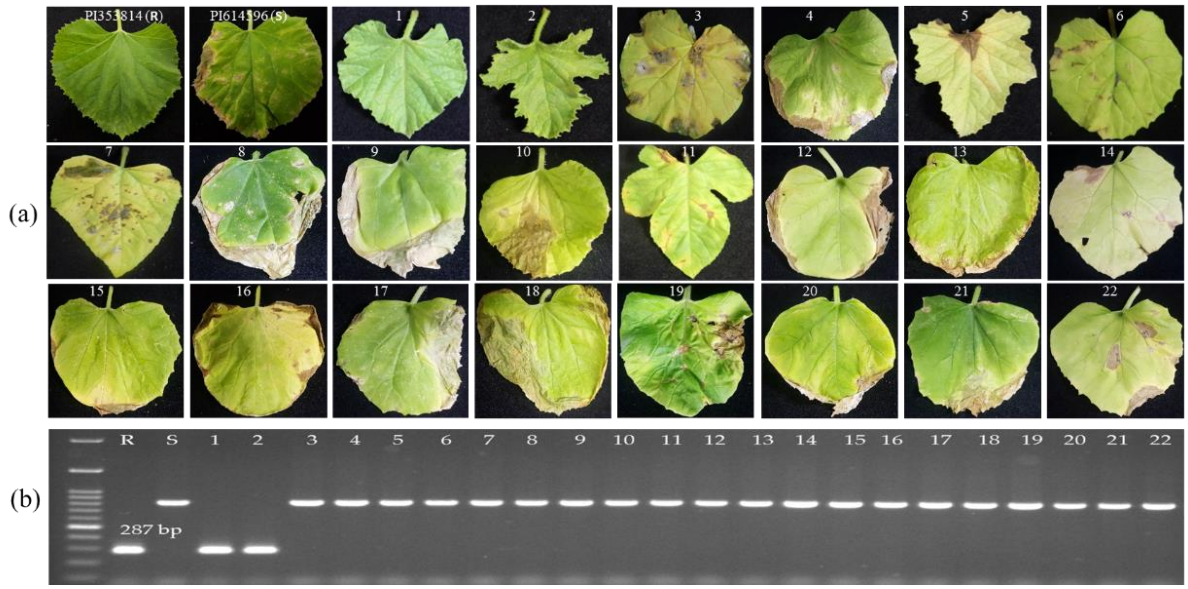

Figure S5: (a) Bacterial fruit blotch (BFB) disease symptoms on 22 melon accessions at 12 days after inoculation with *A. citrulli*. Details of these 22 melon accessions are shown in Supplementary Table S1. All leaves were detached just before photographs were taken. (b) Validation of resistance status to BFB using InDel marker MB157-2 in the 22 melon accessions. R—resistant (PI 353814) and S—susceptible (PI 614596) used as control.

a. Genomic DNA (gDNA) sequence (with intron)

>MELO3C022157Ref

ATGGAAGCAATTGAGGAATCAAGAACAGCTATTGTGGTTTTATCACAAAACTATTCTACTTCAAGATGGTGCT
TGAGAGAATTGGAGAAGATTATGGAATCCATGGACGACGGAACAAATCGAGTTCTTCCTGTGTTTTACCATGT
AGATCCTTCTCATGTTCGTCATCAATCTGGACCTTTTGAGAGAAGCTTTGTTGAATATGAAAATAATGGACAAG
ACTCACAAGAGCAGGTTCATCGGTGGAGGGATGCTTTCGCTAGAGTTGGCCATCTTGCAGGGGTCGTAGTAAA
CAAAAACAGGTAGGGTCTCACTCTTCTCATTATCATTTTCTTCTTTTTTTTTTTATATATAATTATTTCTTCGTATG
GTTAGATGTTAGGGAACAACAGACCTCCAAATATCTTCACAATAATATGATATTATCCACTTTAAACATACAT
CCTTCATGGTTTTCCTTTTGTTTTCACTCAAAAAACTATCTCATATATACCGTTTGAACCAAAAATCCATGGTCA
TCCCCTTAGTCTTATTTAACCGAAATGTGAAACTTTGATCGCTTTCTCACTTCGCATTAGACAAAATTGGGTGT
ACTCTAATACCATTTTTGAACCTAATAGTCTTTTGAGTTTTGTGCGTTCTGATACTATACGTTAGTGATAAACAT
CCTATTTTATCTCAAAAAACCAATTGACTAATGATCAGGAAGCTAGAGGGAGTACTAGGTCATTGTATCTTAT
CAAACATGCATTTATGAGGTCTCGAACTCCTTTGTTTTTTCCAATGTAGCACACAACCTAGCTCAACACACTTT
TATTTTTTAGCATTCAAGTACATAAAATAATATGCGAATAGAAGAAGTTAGAGATTCCTAAATTAATAGCCTA
ATAAATAGTACTTTAAAAAAATAATATTACACATAATTGTTTCTTTACATATTCCTAGAATCTCTGCTTGTTCTA
AAAAGTCTCATGGAATATATAGAAAGGAGCCCGACTAATTGAAGAATTAGATACACAAACTTTTTTAGAATTA
GGAAAATAACTCTCTTCATTGATGGTGTGGATTATATAGTGGGGATTCTGTTAATAGTCGTTCATTGTATACTA
TAGGAAGAAAGAAAGCGAATCCAAGCACACCATAAATTTTTTTTTGACATACTACTCTTTGGCCATGCAGCCC
TGAAGTGGACAGTATCAACCGAATCACCAATCAAATATTTGATAAGTTGCGAAGACCTATGTTAATAGGCCCT
AATCAATTGAATTACTTGGTTGATATGCGAAGTAAGCTAAGGGATATCAATAACCTACTTGACTTTGAATCAG
ATGAAGTACGATTTATAGGAATAGTTGGAATGGGTGGTATTGGTAAAACAACTATTGCAAAAGTTTTACACGA
CAGTATTGCATTTACATTATTTGGTGAAAATTCTTGCTTTGTCACTATGTCTGGGCGTGATATCGTCACGGTCC
AATGTCTACTACTCTCTCGACTTCTTGGAACTAGGGAGAATATTAACATTTTAGAAAAGAATGAAGGAGCAAA
CATGATTAAAGATTGTTTGAGTAGGAGAAAGGTTTTGATTATTTTTGATGGGGTGAATGATAGAGAGGAATTA
GGATACATAGCCGGAAGTTTTGATTGGTTTGGTCGAGGAAGTCGAGTCATCATTACCACTAGAAATAAAAATG
TTTTTTCTCACCCCAATCATGAACAAGTTCAACTCTACAATGTGAAACCACTTGATTACAACACTTCATTCTCA
CTTTTTTGGAAGCATGCATTTGATCAACAAAGTGGGGGTCCAAGTGAACAACAATTCATACAACTTAGTCAGA
ATATAGTGGAAAAGGTCGAAGGAAATCCACAAGCATTGGAACAAATTGGATCATTTTTGCGTGGTAAAGATA
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b. CLUSTALW multiple sequence alignment of gDNA sequence (with intron)

CLUSTAL 2.1 multiple sequence alignment

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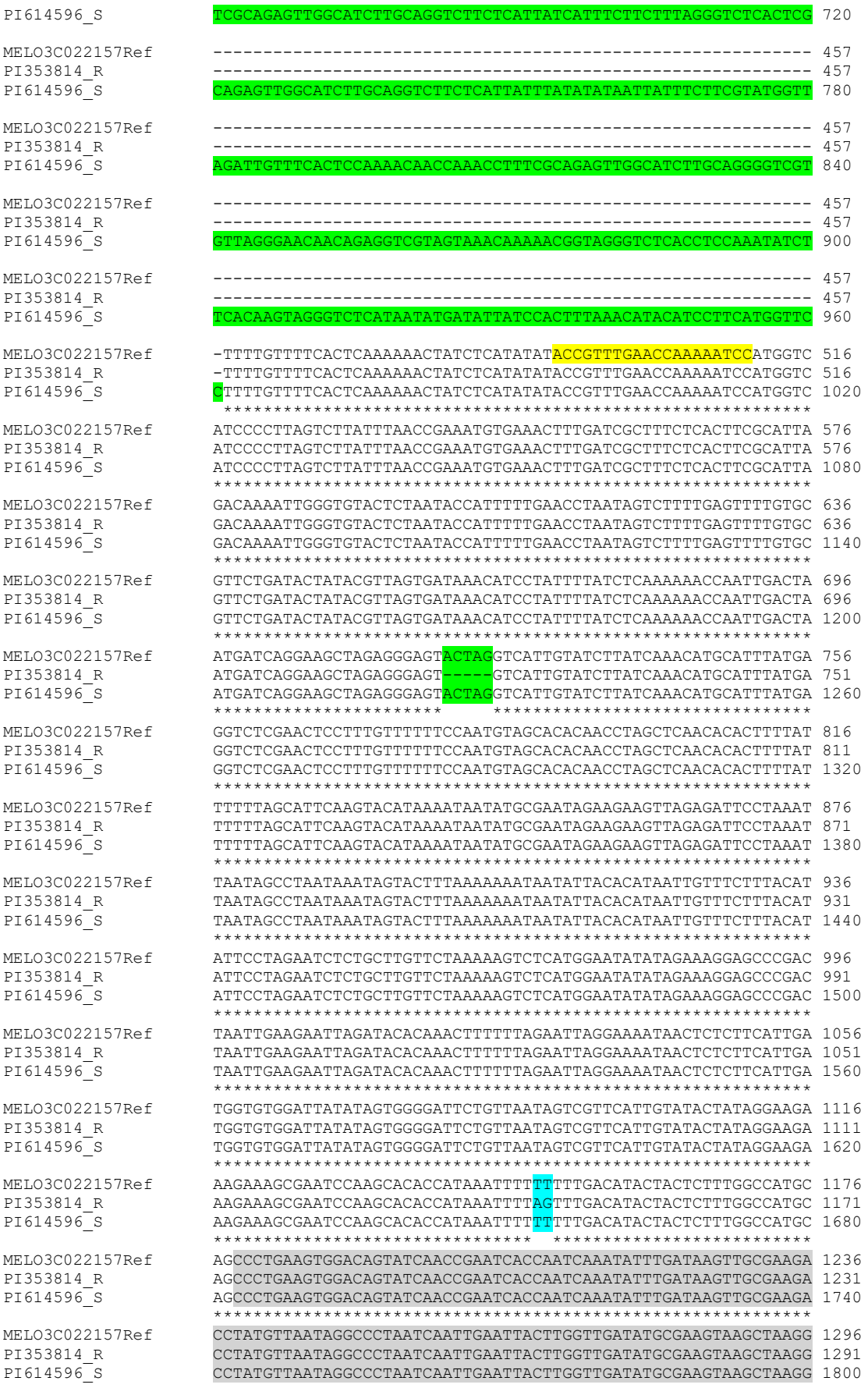
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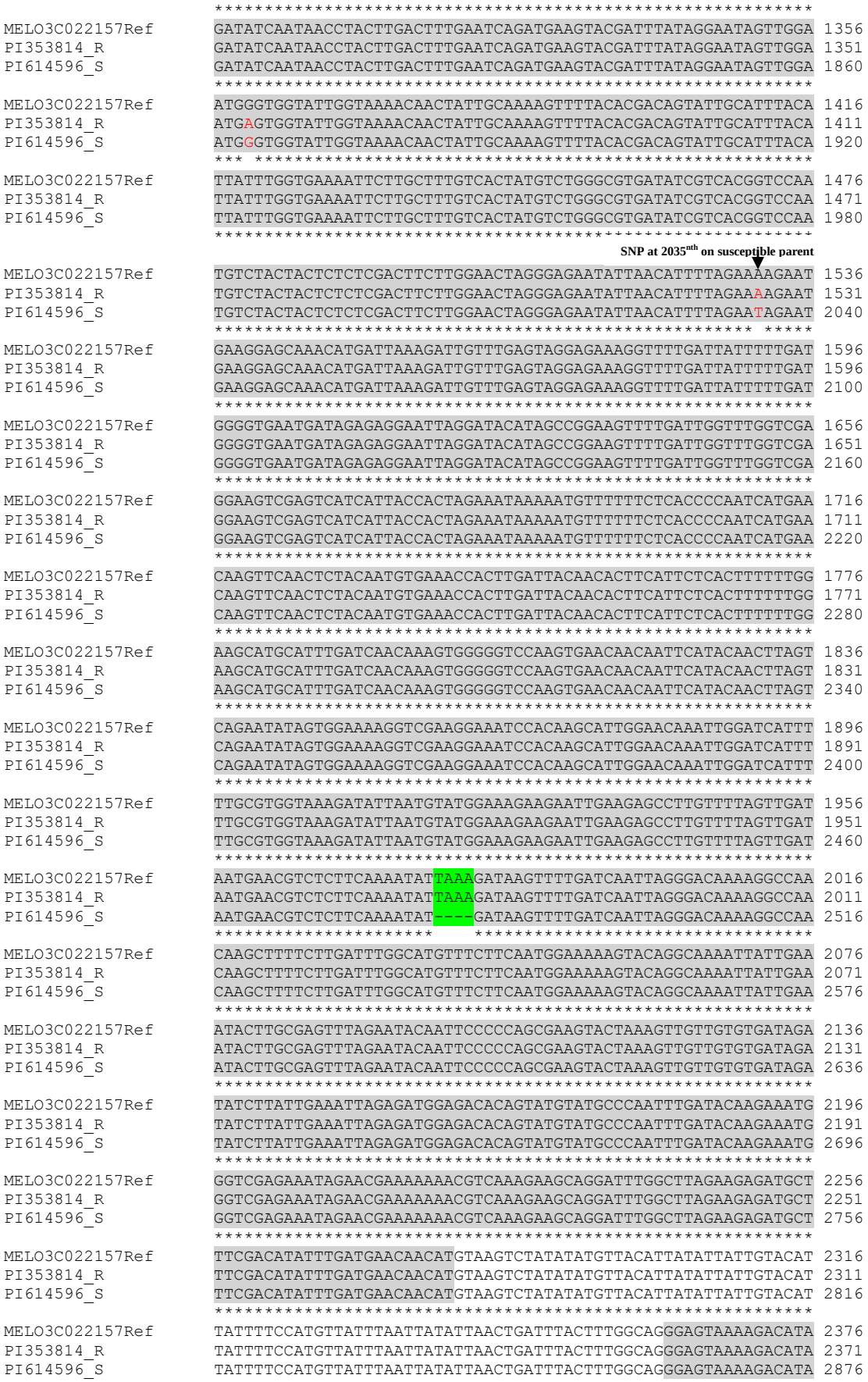
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MELO3C022157Ref   CTAGAAAGATTGATTCTATGTAATTGTACAAGATTGAAGAAAATTGATAATTCAATTACA 2916
PI353814_R        CTAGAAAGATTGATTCTATGTAATTGTACAAGATTGAAGAAAATTGATAATTCAATTACA 2911
PI614596_S        CTAGAAAGATTGATTCTATGTAATTGTACAAGATTGAAGAATATTGATAATTCAATTACA 3416
                  ****************************************** ******************

MELO3C022157Ref   AAATTGAGACTTCTAGTTTTAGTAGACCTCACAGGCTGTGTTCGCCTCGAAACATCCGAG 2976
PI353814_R        AAATTGAGACTTCTAGTTTTAGTAGACCTCACAGGCTGTGTTCGCCTCGAAACATCCGAG 2971
PI614596_S        AAATTGAGACTTCTAGTTTTAGTAGACCTCACAGGCTGTGTTCGCCTCGAAACATCCGAG 3476
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MELO3C022157Ref   TGCATCGATATCTTGAAGAGTCGCCCAACAGTAGAACTTCGTGGCTTAGTTCTACAGTGT 3036
PI353814_R        TGCATCGATATCTTGAAGAGTCGCCCAACAGTAGAACTTCGTGGCTTAGTTCTACAGTGT 3031
PI614596_S        TGCATCGATATCTTGAAGAGTCGCCCAACAGTAGAACTTCGTGGCTTAGTTCTACAGTGT 3536
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MELO3C022157Ref   CGCCAATCATTGAAAGGTATTTGTTATATTCGTAAATTTTTTCACTTCTTTTTTAAAATT 3096
PI353814_R        CGCCAATCATTGAAAGGTATTTGTTATATTCGTAAATTTTTTCACTTCTTTTTTAAAATT 3091
PI614596_S        CGCCAATCATTGAAAGGTATTTGTTATATTCGTAAATTTTTTCACTTCTTTTTTAAAATT 3596
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MELO3C022157Ref   CAGGATCATTTTGTGTAA 3114
PI353814_R        CAGGATCATTTTGTGTAA 3109
PI614596_S        CAGGATCATTTTGTGTAA 3614
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(c)InterProScan (protein)

Reference (MELO3C022157)

5'3' Frame 1

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MEAIEESRTAIVVLSQNYSTSRWCLRELEKIMESMDDGTNRVLPVFYHVDPSHVRHQSGPFERSFVEYENNGQDSQEQVHRWRDAFARVGHLAGVVVNKNSPEVDSINRITNQIFDKLRRPMLIGPNQLNYLVDMRSKLRDINNLLDFESDE
VRFIGIVGMGGIGKTTIAKVLHDSIAFTLFGENSCFVTMSGRDIVTVQCLLLSRLLGTRENINILEKNEGANMIKDCLSRRKVLIIFDGVNDREELGYIAGSFDWFGRGSRVIITTRNKNVFSHPNHEQVQLYNVKPLDYNTSFSLFWKHAF
DQQSGGPSEQQFIQLSQNIVEKVEGNPQALEQIGSFLRGKDINVWKEELKSLVLVDNERLFKILKISFDQLGTKGQQAFLDLACFFNGKSTGKIIEILASLEYNSPSEVLKLLCDRYLIEIRDGDTVCMPNLIQEMGREIERKKRQRSRIWL
RRDAFDIFDEQHGVKDIKGVVLDKRDTEPNLKLKAKQLQDMSRLKILEIDNVQLSPRNQNDLSNQLRLLHWDGFPSDTLPLNFEAPYLFELLLPNAQTTHLWKELKGFKKLKVIDVSNSQTLVETPNLSAVPNLERLILCNCTRLKKIDNSI
TKLRLLVLVDLTGCVRLETSECIDILKSRPTVELRGLVLQCRQSLKGICYIRKFFHFFFKIQDHFV-
```

Resistant Parent

5'3' Frame 1

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MEAIEESRTAIVVLSQNYSTSRWCLRELEKIMESMDDGTNRVLPVFYHVDPSHVRHQSGPFERSFVEYENNGQDSQEQVHRWRDAFARVGHLAGVVVNKNSPEVDSINRITNQIFDKLRRPMLIGPNQLNYLVDMRSKLRDINNLLDFESDE
VRFIGIVGMGGIGKTTIAKVLHDSIAFTLFGENSCFVTMSGRDIVTVQCLLLSRLLGTRENINILEKNEGANMIKDCLSRRKVLIIFDGVNDREELGYIAGSFDWFGRGSRVIITTRNKNVFSHPNHEQVQLYNVKPLDYNTSFSLFWKHAF
DQQSGGPSEQQFIQLSQNIVEKVEGNPQALEQIGSFLRGKDINVWKEELKSLVLVDNERLFKILKISFDQLGTKGQQAFLDLACFFNGKSTGKIIEILASLEYNSPSEVLKLLCDRYLIEIRDGDTVCMPNLIQEMGREIERKKRQRSRIWL
RRDAFDIFDEQHGVKDIKGVVLDKRDTEPNLKLKAKQLQDMSRLKILEIDNVQLSPRNQNDLSNQLRLLHWDGFPSDTLPLNFEAPYLFELLLPNAQTTHLWKELKGFKKLKVIDVSNSQTLVETPNLSAVPNLERLILCNCTRLKKIDNSI
TKLRLLVLVDLTGCVRLETSECIDILKSRPTVELRGLVLQCRQSLKGICYIRKFFHFFFKIQDHFV-
```

Susceptible Parent

5'3' Frame 1

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MEAIEESRTAIVVLSQNYSTSRWCLRELEKIMESMDDGTNRVLPVFYHVDPSHVRHQSGPFERSFVEYENNGQDSQEQVHRWRDAFARVGHLAGVVVNKNSPEVDSINRITNQIFDKLRRPMLIGPNQLNYLVDMRSKLRDINNLLDFESDE
VRFIGIVGMGGIGKTTIAKVLHDSIAFTLFGENSCFVTMSGRDIVTVQCLLLSRLLGTRENINILE-NEGANMIKDCLSRRKVLIIFDGVNDREELGYIAGSFDWFGRGSRVIITTRNKNVFSHPNHEQVQLYNVKPLDYNTSFSLFWKHAF
DQQSGGPSEQQFIQLSQNIVEKVEGNPQALEQIGSFLRGKDINVWKEELKSLVLVDNERLFKI--VLIN-GQKANKLFLIWHVSSMEKVQAKLLKYLRV-NTIPPAKY-SCCVIDILLKLEMETQYVCPI-YKKWVEK-NEKNVKEAGFGLE
EMLSTYLMNNME-KT-KVLCWTRETQNQT-S-RLNNYKI-AV-EY-RLTMCS-VQEIKMISQISFDCSTGMAFLQTLCH-ISKHHIYLNFSCLMHKPLIFGKN-RDLRN-R-SMLAIPKLWWRHRI-VLFQI-KD-FYVIVQD-RILIIQLQ
N-DF-F--TSQAVFASKHPSASIS-RVAQQ-NFVA-FYSVANH-KVFVIFVNFFTSFLKFRIILC
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Figure S6: Sequences and alignments of cloned and sequenced TIR-NBS-LRR gene MELO3C022157 from resistant (PI353814) and susceptible (PI614596) melon accessions. (a) Genomic sequences of reference, resistant and susceptible accessions. (b) Their alignment with reference sequences retrieved from the Cucurbit Genomics database (http://cucurbitgenomics.org) considering DHL92 as the reference genome. In the sequence alignment, asterisks (*) indicate sequence similarity and absence of asterisks indicates sequence dissimilarity; em-dash (—) and green color designate insertion/deletion of nucleotides. In the gDNA sequences, grey highlights illustrate the position of exons, yellow highlights indicate InDel primer (MB157-2-F and MB157-2-R) sequences and light blue indicates the primer name and InDel position. (c) Translated protein sequences of reference gene, resistant and susceptible parent sequences determined using the "Translate Tool-ExPASy" (https://web.expasy.org/translate/) web-based database and showing amino acid alterations and truncated protein in the susceptible parent.