SUPPLEMENTARY MATERIALS
to the article by O.S. Afanasenko, N.V. Mironenko, N.M. Lashina, I.V. Rozanova, E.I. Kyrova, Yu.S. Nikolskaya, A.A. Zubkovich "Validation of markers for resistance to *Pyrenophora teres* f. *teres* loci on barley chromosomes 3H, 4H, and 6H in the polygenic inheritance of the trait"

Table S1. Origin of *P. teres* f. *teres* isolates

Isolate	Origin	Barley cultivar	Year
F18	Belarus, Zhodino	Fest	2017
S18	Russia, Rrasnodar Region	Sprinter	2017
B18	Russia, Leningradskaya oblast	Tausen	2016
V13	Russia, Leningradskaya oblast	Suzdalets	2015
Pr2	Russia, Far East	Primorski 207	2015
Ger7	Germany, Quedlinburg	Unknown	2011
Cz11.1	Czech Republic, Lisice	Unknown	2011
Can11	Canada, Alberta	Harrington	2010
SA7	South Africa, Bredasdorp	Unknown	2017

Table S2. Response of barley differentials to inoculation with *P. teres* f. *teres* isolates

No.	Differentials	Infection responses (IRs) to isolates (score 1–10)								
		Vol13	SA7	Can11	Ger7	Pr2	Cz11.1	F18	S18	B18
1	Tatum	7.0	8.8	9.7	7.0	10	9.3	10	10	9.5
2	Canadian Lake Shore (3H - *qPttCLS*)	3.3	2.3	2.5	5.5	3.2	1.3	2.2	4.5	6.0
3	Skiff	8.8	10	7.0	8.5	10	10	6.0	10	9.0
4	Prior	7.8	5.8	6.0	7.3	4.5	3.8	4.2	3.0	7.5
5	k-20019	2.5	4.6	5.0	3.0	2.5	3.3	5.0	2.9	6.0
6	C.I. 4929 (3H - *qPttCLS*)	2.1	2.3	2.5	7.0	4.3	1.8	6.0	2.0	6.2
7	C.I. 9825	2.1	7.0	5.3	5.3	8.7	6.8	5.0	3.8	7.1
8	C.I. 5791 (6H, 3H)	5.0	1.8	2.0	2.3	3.0	2.5	1.4	4.0	2.3
9	k-8755 (3HL)	3.3	2.4	2.3	5.5	4.5	2.7	5.0	3.9	5.3
	Virulence formula: Virulent/ Avirulent	1,3,4,8/ 2,5,6,7,9	1,3,4,7/ 2,5,6,8,9	1,3,4,5,7/ 2,6,8,9	1,2,3,4,6,7,9/ 5,8	1,3,7/ 2,4,5,6,8,9	1,3,7/ 2,4,5,6,8, 9	1,3,5,6,7,9/ 2,4,8	1,3/ 2,4,5,6,7,8,9	1,2,3,4,5,6,7,9/ 8

Note. Scores 1.0–4.9 correspond to resistance (R); 5.0–5.9 – intermediate reaction type (MR-MS); 6.0–10 – susceptibility (S).

Table S3. Primers for markers associated with resistance to *P. teres* f. *teres* on chromosome 4H

Marker	Primer name forward (F) and reverse (R)	Primers 5′ – 3′
SCRI_RS_153184	4H184F	CGGCACGAGTAGCGGCACG
	4H184R	CGAGGTCCTATCCATCTACAGATTG
SCRI_RS_181886	4H886F	GTGCTTGAAAGTGTTCTGGAGGACG
	4H886R	CCATGACTTCACTGGTGGTGGC
SCRI_RS_170494	4H494F	CATTCGGCTCAAACTCCATCTCGC
	4H494R	GATGTAGAACCAATTATATTGCTGAAATCCT
SCRI_RS_154517	4H517F	GGACTTTGCGGTTGGTCGCCACT
	4H517R	GCTTGTTGTGCCTGCAGAGAGG
JHI-Hv50k-2016-237347	4H-347 F-in1	TCCCCTGGTTGATATCATTCACC
	4H-347 F-in2	TCCCCTGGTTGATATCATTCACA
	4H-347 R-out	CGACATAGAGATGGAGGTGCA
	4H-347 F-out	GCTGGGTAGCAGTTGGATG
	4H-347 R-in1	CATCGGATTGTCCAGGTGTG
	4H-347 R-in2	CATCGGATTGTCCAGGTGTT
JHI-Hv50k-2016-237471	4H-471 F-in1	CCTGGAACGTCTATCTTTTGCC
	4H-471 F-in2	CCTGGAACGTCTATCTTTTGCG
	4H-471 R-out	AGGGTAAGAAGTTCTGCATCTGA
	4H-471 F-out	TAGGTGCCTGAGGATGAACC
	4H-471 R-in1	CCTGAAACTGATTGGTACGCG
	4H-471 R-in2	CCTGAAACTGATTGGTACGCC
JHI-Hv50k-2016-237684	primer F-in1	CAGAATAAAATCTGCTTTTCAGTGGAATAATATC
	primer F-in2	CAGAATAAAATCTGCTTTTCAGTGGAATAATATT
	R-out	GGGTGTGCTCATATAAACAGGTTG
	F-out	GGCTGTGATTGTTACTCGTGAC
	R-in1	CCCATTATGACTTGTGTCGCA
	R-in2	CCCATTATGACTTGTGTCGCG
JHI-Hv50k-2016-237839	primer F-in1	GGGCTGCAGTTGCCG
	primer F-in2	GGGCTGCAGTTGCCA
	R-out	CTATACTGGTCAATTTCATCAAACAGC
	F-out	GGGGAAAGAAGCAGTTTAGAAAGG
	R-in1	CAAGCGAATTTATTGTGAAGGATACC
	R-in2	CAAGCGAATTTATTGTGAAGGATACT
JHI-Hv50k-2016-241935	primer F-in1	CAAAATGGACATTTTGGAGAGCG
	primer F-in2	CAAAATGGACATTTTGGAGAGCA
	R-out	GGCGGCGAGGAACGTG
	F-out	CCAAATCCCTGACGAACACC
	R-in1	CTCTCGGAAGTTAGACATTCAGTTTC
	R-in2	CTCTCGGAAGTTAGACATTCAGTTTT
JHI-Hv50k-2016-237924	primer F-in1	GTCTGAAAGTTCAGGCGATGTAC
	primer F-in2	GTCTGAAAGTTCAGGCGATGTAG
	R-out	CTGAGTGAAACGTCTACCAACTAC
	F-out	CAATGTATGCTGCTGCTGCT
	R-in1	CGGTGAAAACAGAAAGCACAG
	R-in2	CGGTGAAAACAGAAAGCACAC

Table S4. SNP markers on chromosome 4H converted to KASP marker format

Sequence including SNP markers
JHI-Hv50k-2016-237471
GGTATGACGAAGAATTTATCCCTGGGCTCCTGGAACGTCTATCTTTTGC[C/G] GCGTACCAATCAGTTTCAGGTGACAAAAGATCATTCCATTTTCACCTCTG
JHI-Hv50k-2016-237839
ATCGAACCTGATTCATGGTGCAACGCATCAAACGGGGGCTGCAGTTGCC[G/A] GTATCCTTCACAATAAATTCGCTTGATGCAGCCTACAATCAGCAGCAATG
JHI-Hv50k-2016-241935
CCAGCAGCAAAACCAAATTTAACTCAACAAAATGGACATTTTGGAGAGC[G/A] AAACTGAATGTCTAACTTCCGAGAGCAGAGGATTAAGGCTTGTCGGACCTG
JHI-Hv50k-2016-237347
TGTATGATGGCCGAGTGAGGACCTCCTGTCCCCTGGTTGATATCATTCAC[C/A] ACACCTGGACAATCCGATGCCACCTTCATCTCTTTTACATGGAGGTCTTCC

Table S5. Results of identifying polymorphism for the presence/absence of markers of the locus of resistance to *P. teres* f. *teres* on chromosome 4H in the parental accessions

Markers	Primers	Resistant barley varieties						Tatum (S)
		k-5900	k-8829	k-8877	k-14936	k-18552	k-30341	
4H-924	Fin1/Rout	–	+	+	+	–	+	–
	Fin2/Rout	+	–	–	–	+	–	+
	Fout/Rin1	+	+	+	+	+	+	+
	Fout/Rin2	+	–	–	–	+	–	+
4H-886	Fin1/Rout	+	+	+	+	+	+	+
	Fin2/Rout	+	+	+	+	+	+	+
	Fout/Rin1	–	–	–	–	+	+	+
	Fout/Rin2	+	+	+	+	+	+	+
4H-184	F/R	+	+	+	+	+	+	–

Note. «+» – presence of amplification products, «–» – absence; primers for which polymorphism of the resistant and susceptible parents was determined are highlighted.

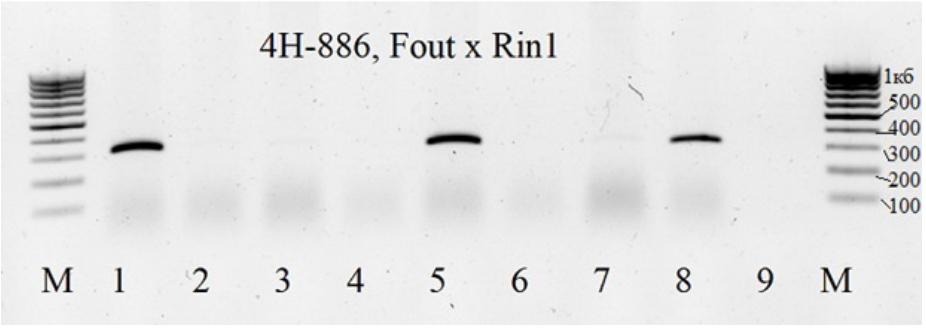

Fig. S1. Polymorphism of parental accessions by marker 4H-886 (Fout × Rin1). Designations: M – molecular weight marker (100 bp), 1 – Morex, 2 – k-30341, 3 – k-8877, 4 – k-8829, 5 – k-18552, 6 – k-14936, 7 – k-5900, 8 – Tatum, 9 – control (water).

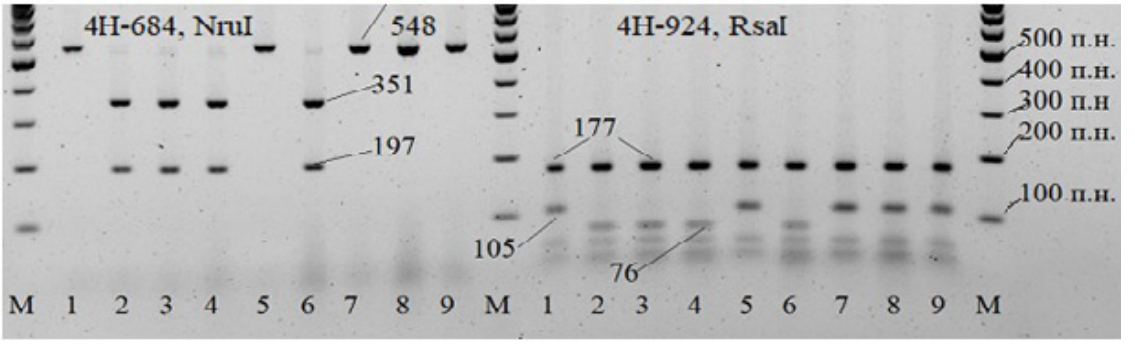

Fig. S2. Restriction fragment polymorphism of the amplification products of markers 4H-684 and 4H-924, obtained by treatment with restriction enzymes NruI and RsaI, in parental barley accessions. Key: M – molecular weight marker (100 bp), 1 – k-5900, 2 – k-8829, 3 – k-8877, 4 – k-14936, 5 – k-18552, 6 – k-30341, 7-9 – Tatum. The numbers indicate the molecular weights of the markers and restriction fragments.

Table S6. SNPs on chromosome 3H converted to KASP markers

Sequence including SNP markers
JHI-Hv50k-2016-183463
TATCCATGGACCTGAAAGTGCCAAATTGTATAAGCCATATCATGTTTTTT [T/C]AGTACAAGCCAGATCATGCTTACAATGCTCACTTTATTCTTTCAAACATA
JHI-Hv50k-2016-183207
TTGCCACCAAAAGTGCTCTTGAGTTGACATGTTTATATATTGTTCTCGCC [A/T]ACTTGCTCCAGCATTTGCATAATAATCTGTAAACAGCTCGGACACTTCTT
JHI-Hv50k-2016-165152
TGACATTGAGCTGCTTTGCTTTGGTTCATCTCCGTTCTTCTTTTCTTTTA [C/G]TTTGAGCGGCAGCAGCACTGATGATGATGACGACGACGATGATGGACGGG
JHI-Hv50k-2016-166392
AAGACGGTTGGGTCTCCGGCTCTCCGACGCACACACGCCGCGCCGTCCAG[T/C]TGGTGGTTT CGTTGCTTTTTCTTTGAACTGCCCACCTTGTATAATCAATC

Table S7. Primers for markers associated with resistance to *P. teres* f. *teres* on chromosome 3H for fragment analysis of amplification products

SNP	Allele	Primers
Clone ID 3272635 (635)	G/C	Clone ID 3272635-F 5′CGGGAGCCTAAGAAGAGGGTATAACC - 3′ Clone ID 3272635-R 5′ GGCATAATGGGTTTTGCTTATTTTTTAGACGAC 3′
JHI-Hv50k-2016-165152 (152)	G/C	JHI-Hv50k-2016-165152 F 5′ - GGTTCATCTCCGTTCTTCTTTTCTTTTAC 3′ JHI-Hv50k-2016-165152-R 5′ CCATCAGTTCAGGCAGCAGTGAC - 3′
JHI-Hv50k-2016-166356 (356)	A/C	JHI-Hv50k-2016-166356-F 5′ GCAGACTCCATTGCTTGTGATTTGTGAG 3′ JHI-Hv50k-2016-166356-R 5′ CCAGGCACGGATCTTTTTAGTAGTCAA 3′
JHI-Hv50k-2016-183207 (207)	A/T	JHI-Hv50k-2016-183207-F 5′ CAAAGAAAGTATTATTTCCATTGGTGGTGC 3′ JHI-Hv50k-2016-183207-R 5′ CAGATTATTATGCAAATGCTGGAGCAAGTT 3′
JHI-Hv50k-2016-183478 (478)	C/A	JHI-Hv50k-2016-183478-F 5′ GGTTCTTCTGATGTGTTTGTTTCTACCAC 3′ JHI-Hv50k-2016-183478-R 5′ GTATTCCTGCCTCTATAACAGTTCTGG 3′
JHI-Hv50k-2016-183463 (463)	T/C	JHI-Hv50k-2016-183463-F 5′GTGCCAAATTGTATAAGCCATATCATGTTTTTTT3′ 5′GTGCCAAATTGTATAAGCCATATCATGTTTTTTC3′ JHI-Hv50k-2016-183463-R 5′TACACAACACGGGAGGGAGGG 3′

Table S8. Allelic polymorphism of parental accessions for four markers on chromosome 3H

Barley accessions	SNP-haplotypes of markers			
	3H-152	166392	183463	183207
k-5900	C:C	T:C	T:C	A:T
k-8829	C:C	T:C	T:C	A:T
k-8877	C:C	T:C	T:C	A:T
k-14936	G:G	C:C	T:C	A:T
k-18552 Zolo	C:C	T:C	T:C	T:T
k-30341	C:C	T:C	T:C	T:T
Tatum	C:C	T:C	T:C	A:T

Table S9. Primers for markers associated with resistance to *P. teres* f. *teres* on chromosome 6H

Marker	Primer name forward (F) and reverse (R)	Primers 5'– 3'
JHI-Hv50k-2016-391380	6H-380 Fout	CGGCACGAGTAGCGGCACG
	6H-380 Rout	CGAGGTCCTATCCATCTACAGATTG
SCRI_RS_181886	6H-178 F	GTGCTTGAAAGTGTTCTGGAGGACG
	6H-178 R	CCATGACTTCACTGGTGGTGGC

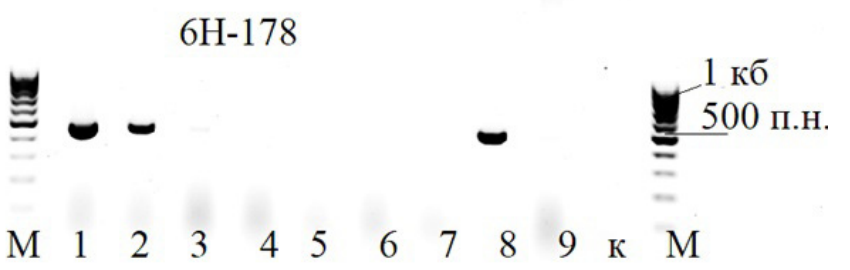

Fig. S3. Polymorphism of parental accessions by marker 6H-178. Designations: M – molecular weight marker (100 bp), 1 – k-5900, 2 – k-8829, 3 – k-8877, 4 – k-14936, 5 – k-18552, 6 – k-30341, 7 – k-26959, 8 – Fox, 9 – Tatum, k – water.

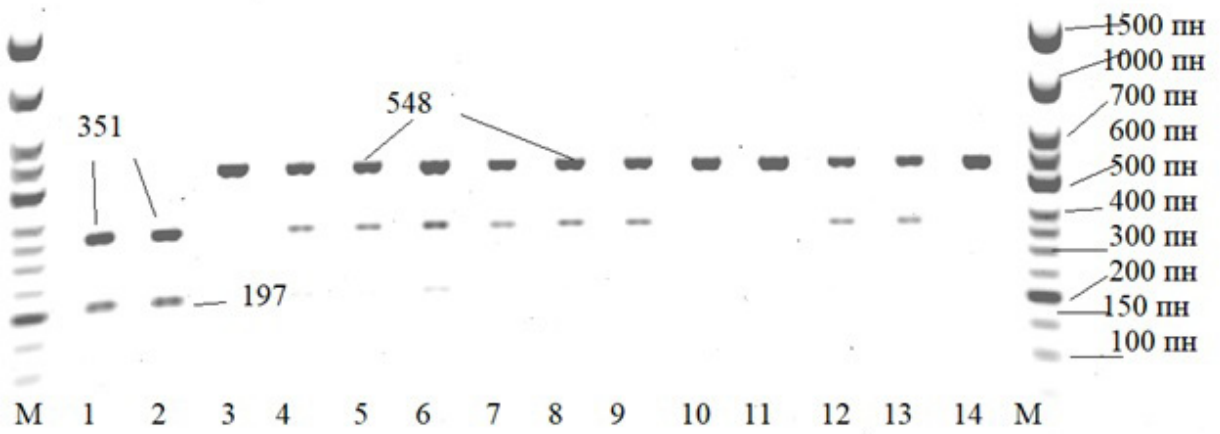

Fig. S4. Polymorphism of the progeny from the Tatum × k-8829 cross at the 4H-684 marker restricted by NruI endonuclease. For each lane (No. 1–14), the DNA sample number* is indicated, and the plant response score to Ptt infection is given in brackets. Designations: 1 – k-8829, 2 – 17* (4), 3 – 18* (4), 4- 42* (4), 5 – 58* (4), 6 – 3* (10), 7 – 4* (10), 8 – 38* (10), 9 – 39* (10), 10 – 2* (10), 11 – 6* (10), 12 – 26* (10), 13 – 27* (10), 14 – Tatum. M – Step50 plus DNA length markers. The sizes of restriction fragments in bp are indicated on the gel.

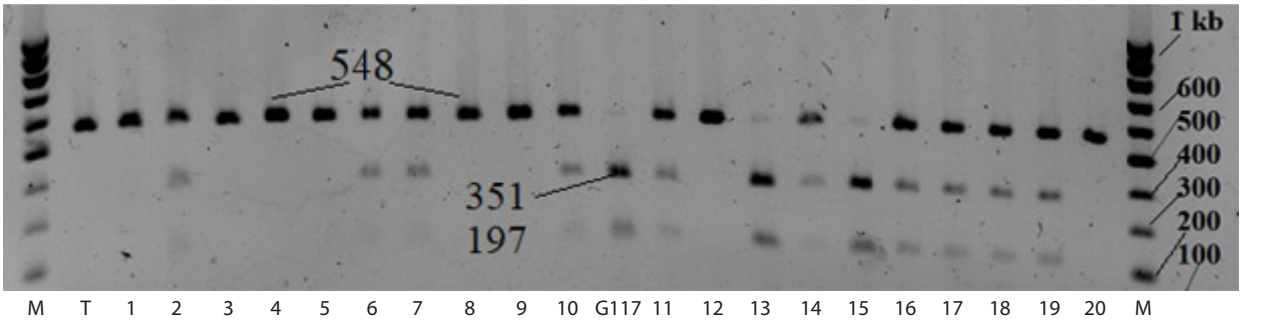

Fig. S5. Polymorphism of the progeny from the Tatum × k-8877 cross at marker 4H-684, restricted by the NruI endonuclease. For each lane (No. 1–20), the DNA sample number* is indicated, and the plant response score to Ptt infection is shown in brackets. Designations: T – Tatum, 1 – 4* (8), 2 – 7* (8), 3 – 12* (8), 4 – 22* (8), 5 – 23* (8), 6 – 26* (8), 7 – 31* (9), 8 – 33* (9), 9 – 39* (9), 10 – 46* (10), G117 – k-8877, 11 – 3* (1), 12 – 5* (2), 13 – 11* (1), 14 – 27* (2), 15 – 34* 9), 16 – 38* (2), 17 – 43* (4), 18 – 47* (2), 19 – 50* (4), 20 – 58* (3). M – molecular weight marker 100 bp.

Table S10. Correspondence between phenotypic resistance and restriction products of CAPS markers 4H-684 (NruI) and 4H-924 (RsaI) in populations obtained from crossing resistant accessions and the susceptible cv. Tatum

A combination of crossing the susceptible cv. Tatum with resistant accessions	Restriction marker product size, bp.	Genotype	Resistant	Susceptible	Minimum table value (χ^2) at significance level (α) = 0.05	Calculated chi-square χ^2
		4H-684 (Nrul restriction enzyme)				
k-8877	351+197	CC (R)	3	1	5.99	4.78
	548/351+197	CT	6	3		
	548	TT (S)	2	7		
k-14936	351+197	CC (R)	4	2	5.99	1.66
	548/351+197	CT	3	5		
	548	TT (S)	4	4		
k-8829	351+197	CC (R)	1	0	5.99	3.61
	548/351+197	CT	2	6		
	548	TT (S)	1	3		
k-30341	351+197	CC (R)	2	3	5.99	1.17
	548/351+197	CT	7	4		
	548	TT (S)	2	3		
		4H-924 (Rsal restriction enzyme)				
k-8877	76	CC (R)	3	9	3.84	3.16
		CG	0	0		
	105	GG (S)	0	11		
k-14936	76	CC (R)	2	9	3.84	3.16
		CG	0	0		
	105	GG (S)	1	10		
k-8829	76	CC (R)	1	0	3.84	2.44
		CG	0	0		
	105	GG (S)	3	9		

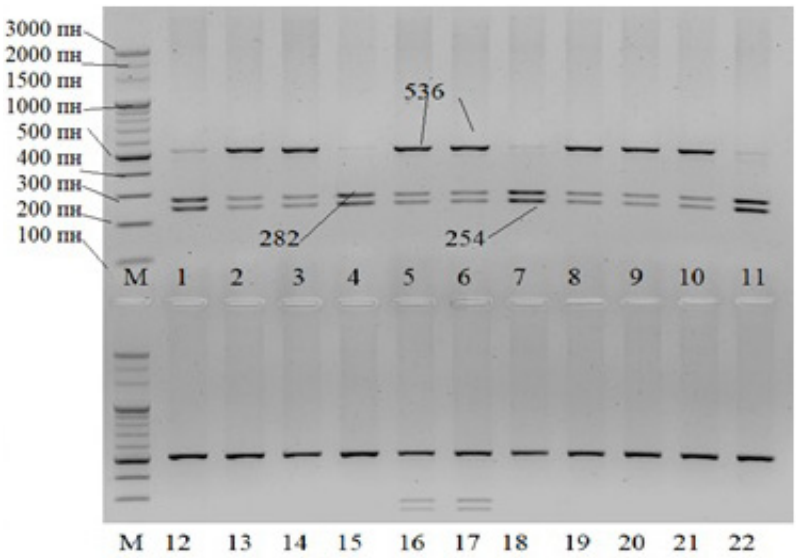

Fig. S6. Polymorphism of the progeny from the Tatum × k-8877 cross at the 6H-380 marker, restricted by the HindIII endonuclease. For each lane (No. 1–22), the DNA sample number* is indicated, and the plant response score to *Ptt* is shown in parentheses. Designations: 1– Tatum, 2 – 4* (8), 3 – 7* (8), 4 – 12* (8), 5 – 22* (8), 6 – 23* (8), 7 – 26* (8), 8 – 31* (9), 9 – 33* (9), 10 – 39* (9), 11 – 46* (10), 12 – k-8877, 13 – 3* (1), 14 – 5* (2), 15 – 11* (1), 16 – 27* (2), 17 – 34* (9), 18 – 38* (2), 19 – 43* (4), 20 – 47* (2), 21 – 50* (4), 22 – 58* (3). M - DNA length marker GeneRuler 100 bp Plus (Dia-M, Moscow, Russia).

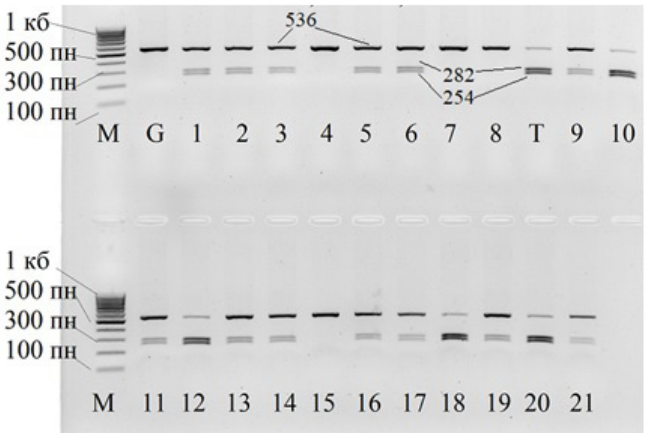

Fig. S7. Polymorphism of the progeny from the Tatum × k-5900 cross at the 6H-380 marker, restricted by the HindIII endonuclease. For each lane (No. 1–21), the DNA sample number* is indicated, and the plant response score to *Ptt* infection is shown in brackets. Designations: G – k-5900, 1 – 32* (score 5), 2 – 31* (4), 3 – 21* (3), 4 – 11* (3), 5 – 3* (4), 6 – 36* (4), 7 – 33* (4), 8 – 54* (4), T – Tatum, 9 – 4* (9), 10 – 5* (9), 11 – 3* (10), 12 – 15* (10), 13 – 17* (8), 14 – 19* (9), 15 – 20* (9), 16 – 24* (9), 17 – 58* (8), 18 – 65* (8), 19 – 47* (8), 20 – 40* (8), 21 – 37* (8). M – molecular weight marker 100 bp.

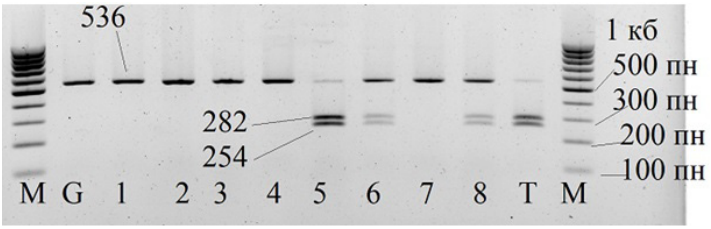

Fig. S8. Polymorphism of the progeny from the Tatum × k-8829 cross at the 6H-380 marker, restricted by the HindIII endonuclease. For each lane (No. 1–8), the DNA sample number is indicated, and the plant response score to *Ptt* infection is shown in brackets. Legend: G – k-8829, 1 – 17 (4), 2 – 18 (4), 3 – 42 (4), 4 – 58 (4), 5 – 3 (10), 6 – 4 (10), 7 – 38 (10), 8 – 39 (10), T – Tatum. M – 100 bp length markers. The sizes of restriction fragments in bp are indicated on the gel.

Table S11. Results of KASP genotyping using polymorphic markers on chromosomes 4H and 3H in F_2 populations (susceptible variety Tatum × resistant samples)

Marker and parental haplotypes	Allele	Resistant (R)	Susceptible	Minimum table value of χ^2 at significance level (α) = 0.05	Calculated value of χ^2	Diagnostic efficiency of the marker
	F_2 Tatum × k-8829					
4H-471	CC	2	1	5.99	3.14	0.60*
Tatum - CC	CG	1	4			
k-8829 - GG	GG	2	0			
4H-839	GG	1	0	5.99	0.12	< 0.5
Tatum - GG	GA	4	2			
k-8829 - AA	AA	2	0			
4H-935	GG	1	0	5.99	0.12	< 0.5
Tatum - GG	GA	2	4			
k-8829 - AA	AA	1	0			
4H-347	CC	1	0	5.99	0.12	< 0.5
Tatum - CC	CA	2	4			
k-8829 - AA	AA	1	0			
3H-152	C:C	5	5	5.99	–	< 0.5
Tatum - CC	C:G	0	0			
k-8829 - G:G	G:G	0	0			
	F_2 Tatum × k-14936					
4H-471	CC	4	4	3.84	1.15	< 0.5
Tatum - CC	CG	6	6			
k-14936 - GG	GG	0	0			
4H-839	GG	4	3	3.84	1.07	< 0.5
Tatum - GG	GA	5	6			
k-14936 - AA	AA	1	0			
4H-935	GG	3	1	3.84	1.53	< 0.5
Tatum - GG	GA	7	9			
k-14936 - AA	AA	0	0			
4H-347	CC	4	4	3.84	0.02	<0.5
Tatum - CC	CA	6	7			
k-14936 - AA	AA	0	0			
3H-152	C:C	3	2	3.84	0,15	<0.5
Tatum - CC	C:G	6	6			
k-14936 - G:G	G:G	2	2			
	F_2 Tatum × k-8877					
4H-471	CC	5	6	3.84	2.29	0.71
Tatum - CC	CG	8	1			
k-8877 - GG	GG	2	0			
4H-839	GG	4	4	3.84	1.11	0.75
Tatum - GG	GA	8	1			
k-8877 - AA	AA	3	0			
4H-935	GG	4	4	3.84	3.81	0.73
Tatum - GG	GA	11	1			
k-8877 - AA	AA	0	0			
4H-347	CC	4	4	3.84	3.81	0.73
Tatum - CC	CA	11	1			
k-8877 - AA	AA	0	0			
3H-152	C:C	11	10	–	–	–
Tatum - CC	C:G	0	0			
k-8877 - G:G	G:G	0	0			

* Under the hypothesis of recessive inheritance of resistance.

Table S12. Correspondence between the responses of individual F_2 plants (isolate F18) in the combination of k-8877 × Tatum with the presence of MMs with proven and unproven efficacy

Parents and numbers of plants	Response score	CAPS-markers			KASP-markers		
		4H-684 NruI	4H-924 RsaI*	6H-380* HindIII	4H-471	4H-935	4H-347
k-8877	3	CC	CC	GG	GG	AA	AA
3	1	CT	GG	GG	CC	GA	CA
5	2	TT	GG	GG	CC	GG	CC
11	1	CC	CC	GG	CC	GA	CA
27	2	CT	GG	A/G	GG	GA	CA
34	4	CC	CC	A/G	GG	GA	CA
38	2	CT	GG	GG	CG	GA	CA
43	4	CT	GG	GG	CG	GA	CA
47	2	CT	GG	GG	CG	GA	CA
50	4	CT	GG	GG	CG	GA	CA
58	3	TT	GG	GG	CC	GG	CC
Tatum	9,10	TT	GG	AA	CC	GG	CC
4	8	TT	GG	A/G	CC	GG	CC
7	8	*CC	GG	A/G	CC	GG	CC
12	8	TT	GG	AA	CC	GA	CA
22	8	TT	GG	A/G	CG	GG	CC
23	8	TT	GG	A/G	CC	GG	CC
26	8	CT	GG	AA	CG	GA	CA
31	9	CT	GG	A/G	CG	GA	CA
33	9	TT	GG	A/G	CC	GG	CC
39	9	TT	GG	A/G	CC	GG	CC
46	10	CT	GG	AA	CG	GA	CA
Calculated value of χ^2		4.78	3.47 (df = 1)	15.78	3.82	5.11	5.11
Reliability (*p*)		> 0.05	> 0.05	**< 0.05**	> 0.05	> 0.05	> 0.05
Diagnostic efficiency		0.76	0.64	**0.91**	0.71	0.73	0.73

* The marker's effectiveness has been proven.

Table S13. Correspondence of responses of individual F_2 plants (isolate F18) in the combination of k-8829 × Tatum with the presence of MM with proven and unproven efficacy

Parents and numbers of plants F_2	Response score	4H-924 RsaI	4H-684 NruI	4H-347 FxR1	4H-184	6h-178	6H380 HindIII	3H-56	4H-471
k-8829	4,3	CC	CC	–	+	+	GG	+	GG
Tatum	10,10	GG	TT	+	–	–	AA	–	CC
17	4	CC	CC	+	+	+	GG	+	GG
18	4	GG	TT	–	+	+	GG	+	CC
42	4	GG	CT	+	+	+	GG	+	CC
58	4	GG	CT	+	+	+	GG	+	CG
3	10	GG	CT	+	–	–	AA	–	CG
4	10	GG	CT	+	+	+	AG	+	CG
38	10	GG	CT	+	+	+	GG	+	CG
39	10	GG	CT	+	+	+	AG	–	CG
2	10	n/a	TT	+	n/a	n/a	n/a	n/a	n/a
6	10	n/a	TT	+	n/a	n/a	n/a	n/a	n/a
26	10	n/a	CT	+	n/a	n/a	n/a	n/a	n/a
27	10	n/a	CT	+	n/a	n/a	n/a	n/a	n/a
32	10	n/a	TT	+	n/a	n/a	n/a	n/a	n/a
Calculated value of χ^2 5.99 for df=2 3.84 for df=1		2.04 (df = 1)	3.75 (df = 2)	**4.62** **(df = 1)**	2.50 (df = 1)	2.50 (df = 1)	**8** **(df = 2)**	2.06 (df=1)	4.13 (df = 2)
Reliability (*p*)		> 0.05	> 0.05	**< 0.05**	> 0.05	> 0.05	**< 0.05**	> 0.05	> 0.05

Note. n/a – no data available.

Table S14. Correspondence of responses of individual F_2 plants (isolate F18) in the combination of k-5900 × Tatum with MM with proven and unproven efficacy

Parents and numbers of plants F_2	Response score	6H-178	4H-886 F × Rin1	6H380 HindIII	3H-56
k-5900		+	–	GG	+
32	5	–	–	AG	+
31	4	+	+	AG	–
21	3	+	–	AG	+
11	3	+	+	GG	+
3	4	+	–	AG	+
36	4	+	+	AG	–
33	4	+	–	GG	+
54	4	+	+	GG	–
Tatum	10	–	+	AA	–
4	9	+	+	AG	–
5	9	–	+	AA	+
14	10	–	+	AG	–
15	10	–	+	AA	+
17	8	+	+	AG	+
19	9	+	+	AG	+
20	9	+	+	GG	+
24	9	+	+	AG	+
58	8	+	+	AG	–
65	8	–	+	AA	+
47	8	+	+	AG	+
40	8	–	–	AA	–
37	8	+	–	AG	+
Calculated value of χ^2 5.99 for df = 2 3.84 for df = 1		2.61 (df = 1)	2.58 (df = 1)	**6.72** **(df = 2)**	0.01 (df = 1)
Reliability (*p*)		> 0.05	> 0.05	**< 0.05**	> 0.05