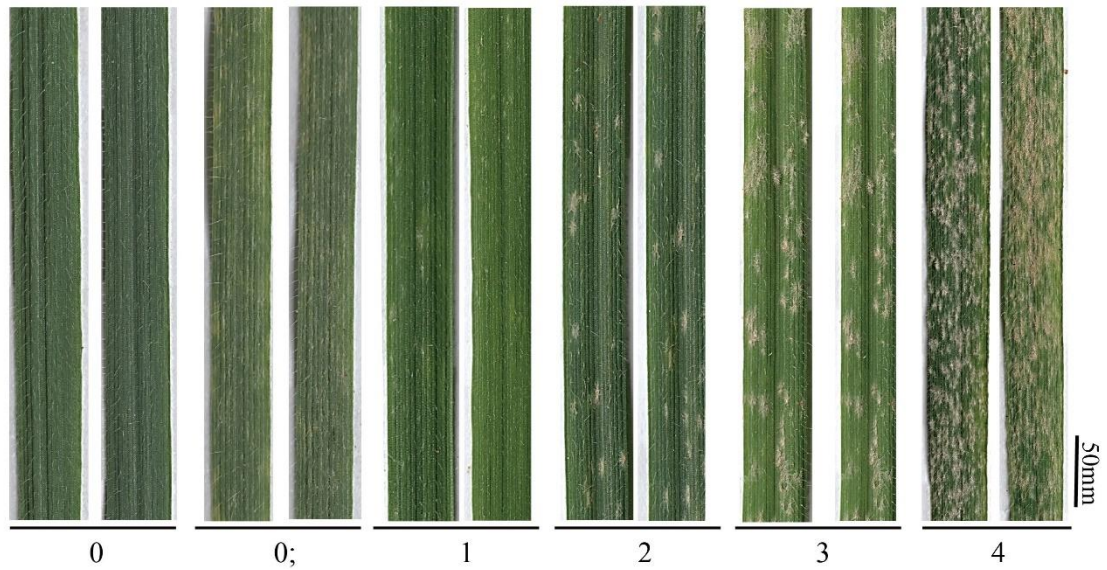
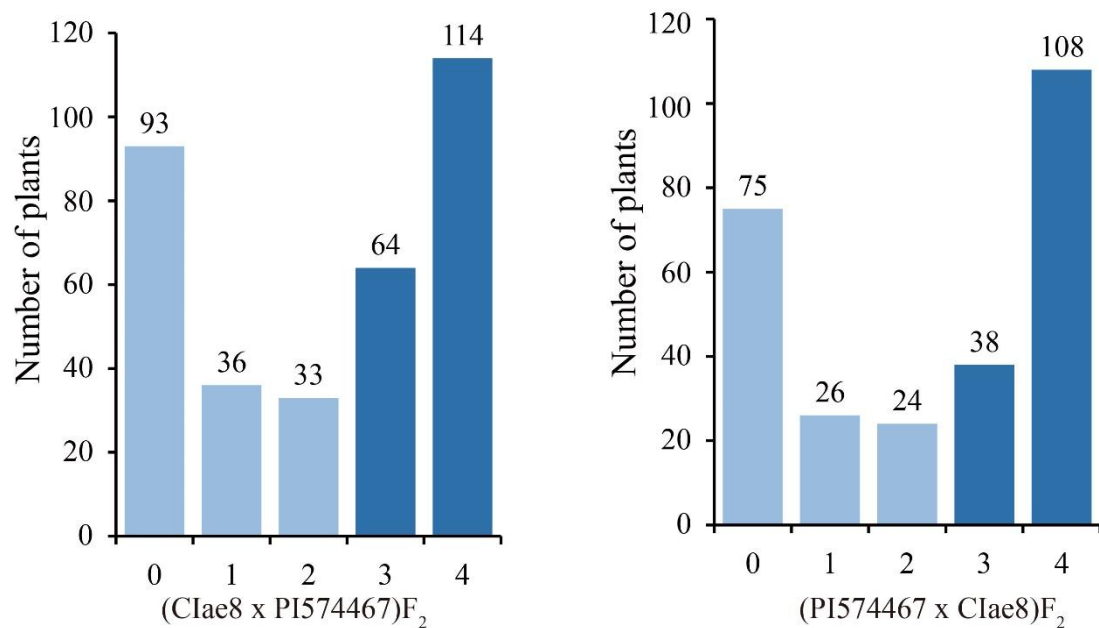




Supplementary Figure 1 Pm symptom of *Ae. tauschii* leaves representing the 0-4 infection type (IT) scales when inoculated by *Bgt* isolate E26

0 = no visible symptoms; 0₊ = necrotic flecks; 1 = low sporulation; 2 = medium sporulation; 3 = medium to high sporulation; and 4 = full sporulation. The plants having disease scales of ITs 0, 0₊, 1 and 2 were classified as resistant, and those having ITs 3 and 4 were classified as susceptible.



Supplementary Figure 2 Disease severity distribution of individuals of two F₂ segregation population. Plants having disease scales of ITs 0, 1 and 2 were classified as resistant (light blue) and those having disease scales of ITs 3 and 4 were classified as susceptible (blue).

Supplementary Table 1 The powdery mildew resistance level of 35 *Ae. tauschii* accessions from

Accession No	Origin	Infection type ^a (Pm resistance)
Clae 8	Iran	0(R)
Clae 9	Iran	0 (R)
Clae 21	Iran	1 (R)
Clae 26	Iran	2 (R)
PI 511362	Pakistan	0 (R)
PI 220326	Afghanistan	1 (R)
PI 452131	China	0 (R)
PI 499262	China	0 (R)
PI 276980	Soviet Union	0 (R)
PI 428564	Azerbaijan	0 (R)
PI 603242	Turkmenistan	0 (R)
PI 662053	Turkmenistan	0 (R)
PI 662055	Turkmenistan	1 (R)
PI 603246	Portuga	0 (R)
PI 662112	Tajikistan	0 (R)
PI 603226	Iran	4 (S)
Clae 1	Pakistan	4 (S)
Clae 4	Afghanistan	3 (S)
PI 452130	China	4 (S)
PI 508262	China	4 (S)
PI 508263	China	4 (S)
PI 486265	Turkey	3 (S)
PI 486270	Turkey	3 (S)
PI 486271	Turkey	4 (S)
PI 486275	Turkey	4 (S)
PI 554319	Turkey	4 (S)
PI 574466	Georgia	3 (S)
PI 574467	Russian Federation	4 (S)
PI 603235	Azerbaijan	3 (S)
PI 603245	Western Asia	3 (S)
PI 662062	Turkmenistan	3 (S)
PI 662065	Turkmenistan	3 (S)
PI 662067	Turkmenistan	4 (S)
PI 662078	Turkmenistan	4 (S)
PI 662111	Tajikistan	4 (S)

different origins against *Bgt* isolates E26

^aInfection types (ITs) 0, 1 and 2 were classified as resistant (R), while ITs 3 and 4 were classified as susceptible (S) . The two accessions used for constructing the mapping populations were highlighted dark grey.

Supplementary Table 2 Chromosomal distribution of SNPs in *Ae. tauschii* genotyped using the wheat

Chromosome	Total SNPs commonly present in the two parents	Polymorphic SNPs between Bulk-R/Clae8 and Bulk-S/PI574467
1D	1036	9
2D	1180	39
3D	871	8
4D	303	5
5D	902	4
6D	848	10
7D	1248	69
Total	6388	144

55 K array

Supplementary Table 3 Physical interval distribution of polymorphic SNPs on chromosomes 2D and 7D referring to the *Ae. tauschii* reference genome sequence

Physical interval (Mb) on 2D	No. of polymorphic SNPs	Percentage of polymorphic SNPs	Physical interval (Mb) on 7D	No. of polymorphic SNPs	Percentage of polymorphic SNPs
0-20	13	33.33%	0-20	38	55.07%
20-40	2	5.13%	20-40	0	0.00%
40-60	0	0.00%	40-60	2	2.90%
60-80	15	38.46%	60-80	0	0.00%
80-100	2	5.13%	80-100	4	5.80%
100-120	0	0.00%	100-120	1	1.45%
120-140	2	5.13%	120-140	1	1.45%
140-160	0	0.00%	140-160	0	0.00%
160-180	1	2.56%	160-180	1	1.45%
180-200	0	0.00%	180-200	1	1.45%
200-220	0	0.00%	200-220	0	0.00%
220-240	0	0.00%	220-240	0	0.00%
240-260	1	2.56%	240-260	1	1.45%
260-280	0	0.00%	260-280	0	0.00%
280-300	0	0.00%	280-300	1	1.45%
300-320	0	0.00%	300-320	0	0.00%
320-340	0	0.00%	320-340	1	1.45%
340-360	0	0.00%	340-360	3	4.35%
360-380	0	0.00%	360-380	0	0.00%
380-400	0	0.00%	380-400	0	0.00%
400-420	0	0.00%	400-420	0	0.00%
420-440	0	0.00%	420-440	0	0.00%
440-460	0	0.00%	440-460	0	0.00%
460-480	1	2.56%	460-480	1	1.45%
480-500	0	0.00%	480-500	0	0.00%
500-520	0	0.00%	500-520	1	1.45%
520-540	0	0.00%	520-540	6	8.70%
540-560	1	2.56%	540-560	4	5.80%
560-580	0	0.00%	560-580	0	0.00%
580-600	1	2.56%	580-600	2	2.90%
600-620	0	0.00%	600-620	1	1.45%
620-640	0	0.00%	620-640	0	0.00%
640-660	0	0.00%	640-660	0	0.00%
Total	39		Total	69	

Supplementary Table 4 Information of the molecular markers used for genetic mapping of *pmAet-2DS* and *pmAet-7DS*

Marker name	Chromosome	Forward primer sequence	Reverse primer sequence	Type of marker	Annealing temperature (°C)
<i>CINAU-AE60</i>	2D	TAGGTGCTGTGTGGGTATCG	GCTCAATGCGGGACTACATC	SSR	56
<i>gwm455</i>	2D	ATTCGGTTCGCTAGCTACCA	ACGGAGAGCAACCTGCC	SSR	56
<i>CINAU-AE240</i>	2D	TATCACTCACTGCGAGCAT	CTAGGCTGGGGAGCTTAT	STS	56
<i>wmc503</i>	2D	GCAATAGTTCCCGCAAGAAAAG	ATCAACTACCTCCAGATCCCGT	SSR	56
<i>CINAU-AE24</i>	2D	TGCATGTAATCTCAACCCCCT	GGGGAGCCTTGTGACGTTTA	SSR	56
<i>CINAU-AE17</i>	2D	TCAAGAATCAAGTCGGCCCC	TTGCTGCAAAGGCTGAGGAT	SSR	56
<i>CINAU-AE20</i>	2D	AGTCCGGAGTAGGTTGAGCT	CCCGGATGAGACCACAAACA	SSR	56
<i>CINAU-AE15</i>	2D	AGGGAAAACATCATGAGCCCA	CTGGGGAGCTTATATGGGCG	SSR	56
<i>CINAU-AE74</i>	2D	GAATGGCCAGTGTCTCCGAA	TAGCAAGATGGTTCGGCTCC	SSR	56
<i>CINAU-AE7800</i>	2D	CGTGTTGCTTGGGTCTTCAA	TTCCTGTCCCCGATAACATCC	SNP	58
		AGGCGGCGAGTCTAGTACTGAG	ACGCTCCATTTGTTGTCGTG		
<i>CINAU-AE50</i>	2D	GACTTGAGCAGCGGTGAGAT	GGAGGGAAACGAGTCCAAGG	SSR	50
<i>CINAU-AE38</i>	2D	AAAGACCGGGCAAAGGTAGG	TGCTCTATACAAGGCGCAGG	SSR	56
<i>CINAU-AE18</i>	2D	TGACCACACCAAGCCATAGT	GCGTCTGGATGGAGCTATCC	SSR	56
<i>CINAU-AE85</i>	2D	CTGAATTGTTGCTGGCAGGT	CCCAGCTGCAACAACCTAAA	SSR	56
<i>CINAU-AE7</i>	2D	CTGACTGGCGTGTCTTCCTT	AGCCTACTCCATCCGTCCTT	SSR	56
<i>CINAU-AE203</i>	2D	GGAAATGATCAAACCGGCGT	CCCCACACAACCTCAACAACA	STS	56
<i>gwm210-D</i>	2D	TGCATCAAGAATAGTGTGGAAG	TGAGAGGAAGGCTCACACCT	SSR	56
<i>Xcfd66</i>	7D	AGGTCTTGGTGGTTTTGGTG	TTTTCACATGCCACAGTTG	SSR	56
<i>Xgwm635b</i>	7D	TTCCTCACTGTAAGGGCGTT	CAGCCTTAGCCTTGGCG	SSR	56
<i>CINAU-AE15</i>	7D	TCTGAAGGTTTGTGCGCCAA	TGGAAGACTTGTGCTGCCAA	SSR	56
<i>CINAU-AE623</i>	7D	ACTTGGAAGAAGGCGGATT	AACCTTGTCTGAATGTGAA	STS	56
<i>CINAU-AE473</i>	7D	TGTGCCGATTGACGATGA	ACTGCGGCACGCTTGTAG	STS	56

<i>CINAU-AE4</i>	7D	AGTAAGCCCTTTAGAGCCACAA	AGAGTGCCCAATCAGAAAAC	SSR	56
<i>CINAU-AE362</i>	7D	GTCAAGCGGCTCGTCTAC	GCATTGGGGTCTTTAGGC	STS	56
<i>CINAU-AE66</i>	7D	TGGGCAGGATACCACCAAAC	GTGAAATTCCCCCTGGCTCA	SSR	56
<i>Xwmc506</i>	7D	CACTTCCTCAACATGCCAGA	CTTTCAATGTGGAAGGCGAC	SSR	56
<i>CINAU-AE314</i>	7D	GGAGCACGACAAGTTCAT	ATGCTTCGATCTTTCTCC	STS	56
<i>CINAU-AE28</i>	7D	GTCACCGATCATGCACATGC	ATAGGATGCCAAGTCCTCGC	SSR	58
<i>CINAU-AE25</i>	7D	CCTCCGTGATGGTCTCCAAC	GGCTTTGCTGATAATGGCGG	SSR	58
<i>CINAU-AE58</i>	7D	TGAGACTTTGGCGCCATCAT	CGGTCCGTAGTTTTGAACGA	SSR	58
<i>CINAU-AE13</i>	7D	GAAGTCATCACCGAGGGCAA	TTCCCGCTACAGCCTCAAAG	SSR	58
<i>CINAU-AE6</i>	7D	TGATCTTGTTGGTGGCCTGG	CAGGGGTCGCTTCAGATGTT	SSR	58
<i>CINAU-AE3</i>	7D	TGGCCACAGAAGAGTTCCAT	GGTGTATGGCTTCCTCACCC	SSR	58
<i>CINAU-AE301</i>	7D	TGAAAAGGTGCCGTATTCAAGT	ATCAGCGCATATCAGGAGGC	SSR	58
<i>CINAU-AE98</i>	7D	TGGTTTTGTTCCCGTAGCGA	AATTTCCGCCAGACCTAGCC	SSR	56

Supplementary Table 5 Genotyping and Pm resistance evaluation of the 40 recombinants for the *pmAet-2DS* region flanked by markers *CINAU-AE38* and *CINAU-AE17*

Line No. of the recombinant	Recombinant screening by genotyping using seven markers ^a							Recombination type	Infection type ^b
	<i>CINAU-AE3</i>	<i>CINAU-AE5</i>	<i>CINAU-AE780</i>	<i>CINAU-AE7</i>	<i>CINAU-AE1</i>	<i>CINAU-AE2</i>	<i>CINAU-AE1</i>		
	8	0	0	4	5	0	7		
TX2-83	A	A	A	A	A	A	H	1	0 (R)
TX2-21	A	A	A	A	A	A	H		0 (R)
TX2-191	A	A	A	A	A	A	H		0 (R)
TX2-131	A	A	A	A	A	H	H	2	0 (R)
TX2-60	A	A	A	A	A	H	H		0 (R)
TX2-243	A	A	A	H	H	H	H	3	4 (S)
TX2-87	A	A	A	H	H	H	H		4 (S)
TX2-73	A	A	H	H	H	H	H		3 (S)
TX2-273	A	A	H	H	H	H	H	4	4 (S)
TX2-24	A	A	H	H	H	H	H		4 (S)
TX2-123	A	A	H	H	H	H	H		3 (S)
TX2-267	A	A	H	H	H	H	H	5	4 (S)
TX2-326	A	H	H	H	H	H	H		4 (S)
TX2-36	A	H	H	H	H	H	H		4 (S)
TX2-40	A	H	H	H	H	H	H	6	4 (S)
TX2-164	H	H	H	H	H	H	A		3 (S)
TX2-193	H	H	H	H	H	H	A		4 (S)
TX2-218	H	H	H	H	H	H	A		4 (S)
TX2-253	H	H	H	H	H	H	A		4 (S)
TX2-311	H	H	H	H	H	H	A		4 (S)
TX2-238	H	H	H	H	H	H	A		4 (S)
TX2-216	H	H	H	H	H	H	A		4 (S)

TX2-282	H	H	H	H	H	H	A	7	4 (S)
TX2-89	H	H	H	H	H	H	A		4 (S)
TX2-95	H	H	H	H	H	H	A		3 (S)
TX2-291	H	H	H	H	H	A	A		4 (S)
TX2-31	H	H	H	H	H	A	A		4 (S)
TX2-222	H	H	H	A	A	A	A		1 (R)
TX2-116	H	H	H	A	A	A	A		1 (R)
TX2-125	H	H	H	A	A	A	A	8	0 (R)
TX2-255	B	B	B	A	A	A	A		0 (R)
TX2-130	B	B	B	A	A	A	A		0 (R)
TX2-86	B	B	B	A	A	A	A		0 (R)
TX2-135	B	B	B	A	A	A	A	9	0 (R)
TX2-259	H	H	A	A	A	A	A		0 (R)
TX2-292	H	H	A	A	A	A	A		0 (R)
TX2-232	H	A	A	A	A	A	A	10	0 (R)
TX2-241	H	A	A	A	A	A	A		0 (R)
TX2-167	H	A	A	A	A	A	A		0 (R)
TX2-54	H	A	A	A	A	A	A		0 (R)

^aA: Clae8 genotype, B: PI574467 genotype, H: heterozygous genotype.

^bInfection types (ITs) 0, 1 and 2 were classified as resistant (R), while ITs 3 and 4 were classified as susceptible (S).

Supplementary Table 6 Genotyping and Pm resistance evaluation of the 32 recombinants for *pmAet-7DS* region flanked by markers *CINAU-AE6* and *CINAU-AE314*

Line No. of the recombinant	Recombinant screening by genotyping using six markers ^a						Recombination type	Infection type ^b
	<i>CINAU-AE6</i>	<i>CINAU-AE13</i>	<i>CINAU-AE58</i>	<i>CINAU-AE25</i>	<i>CINAU-AE28</i>	<i>CINAU-AE314</i>		
TX7-106	A	A	A	H	H	H	1	3 (S)
TX7-546	A	A	A	H	H	H		4 (S)
TX7-548	A	A	A	H	H	H		4 (S)
TX7-582	A	A	A	H	H	H		4 (S)
TX7-684	A	A	A	H	H	H		3 (S)
TX7-323	A	A	H	H	H	H	2	3 (S)
TX7-716	A	A	H	H	H	H		3 (S)
TX7-728	A	H	H	H	H	H		3 (S)
TX7-759	A	H	H	H	H	H		3 (S)
TX7-763	A	H	H	H	H	H		3 (S)
TX7-797	A	H	H	H	H	H	3	3 (S)
TX7-283	A	H	H	H	H	H		3 (S)
TX7-204	A	H	H	H	H	H		4 (S)
TX7-485	A	H	H	H	H	H		4 (S)
TX7-542	A	H	H	H	H	H		3 (S)
TX7-492	A	H	H	H	H	H		4 (S)
TX7-65	H	H	H	H	H	A	4	4 (S)
TX7-390	H	H	H	H	H	A		4 (S)
TX7-647	H	H	H	H	H	A		3 (S)
TX7-23	H	H	H	A	A	A		4 (S)
TX7-276	H	H	H	A	A	A		3 (S)
TX7-37	H	H	H	A	A	A	5	3 (S)

TX7-584	H	H	H	A	A	A	6	4 (S)
TX7-21	H	H	A	A	A	A		2 (R)
TX7-235	H	H	A	A	A	A		1 (R)
TX7-112	H	A	A	A	A	A		1 (R)
TX7-421	H	A	A	A	A	A		1 (R)
TX7-347	H	A	A	A	A	A		1 (R)
TX7-375	H	A	A	A	A	A	7	2 (R)
TX7-452	H	A	A	A	A	A		0 (R)
TX7-576	H	A	A	A	A	A		1 (R)
TX7-541	H	A	A	A	A	A		2 (R)

^aA: Clae8 genotype, B: PI574467 genotype, H: heterozygous genotype.

^bInfection types (ITs) 0, 1 and 2 were classified as resistant (R), while ITs 3 and 4 were classified as susceptible (S).

Supplementary Table 7 Annotated genes situated in the physical interval harboring *pmAet-2DS*

Gene ID in the reference genome of <i>Ae. tauschii</i> AL8/78	Gene annotation
AET2Gv20068200	NA
AET2Gv20068400	Horcolin
AET2Gv20068500	Disease resistance protein RGA2
AET2Gv20068600	Disease resistance protein Piks-2
AET2Gv20068700	NA
AET2Gv20068900	Putative disease resistance protein RGA1
AET2Gv20069100	Anthocyanidin reductase ((2S)-flavan-3-ol-forming)
AET2Gv20069200	NA
AET2Gv20069300	Uncharacterized acetyltransferase At3g50280
AET2Gv20069400	NA
AET2Gv20069500	Putative disease resistance protein RGA4

NA: not available.

Supplementary Table 8 Annotated genes situated in the physical interval harboring *pmAet-7DS*

Gene ID in the reference genome of <i>Ae. tauschii</i> AL8/78	Gene annotation
AET7Gv20022900	50S ribosomal protein L9
AET7Gv20023000	NA
AET7Gv20023100	Scarecrow-like protein 6
AET7Gv20023200	NA
AET7Gv20023300	NA
AET7Gv20023400	Dihydrolipoyllysine-residue acetyltransferase component 3 of pyruvate dehydrogenase complex, mitochondrial
AET7Gv20023600	Protein arginine N-methyltransferase 7
AET7Gv20023700	Putative cysteine-rich receptor-like protein kinase 35
AET7Gv20023800	Protein transport protein SEC16B homolog

NA: not available.