

Table S2. Variations in *Pgβglu-1* amino acid sequence of resistant (R) and non-resistant (N-R) trees. Sites are considered variable if two or more variants are observed among the 14 sequences.

Test trees	Variable sites ¹																		
	14	98 ²	117	176	212	251 ²	268	309	310	312	342 ²	344	365 ²	377	384	385	412	417	439
NR-1	L	K	Q	I/L	I	T	L	S	M	S	A/E/P/Q	Y/D	Q/R	V	S	S	T	G	H/Y
NR-2	L	K	Q	I/L	I/L	I/L/S/T	L	F/S	M	S	A/E/P/Q	Y/D	Q/R	I/V	S	A/S	T	G	H/Y
NR-3	L	K	Q	I/L	I/L	T	L	S	M	S	P/Q/S/*	Y/D	Q	I/V	G/S	A/S	T	A/G	H/Y
NR-4	L/F	K	Q	I/L	I/L	I/L/S/T	L	F/S	M/L	S	A/E/P/Q	Y/D	Q/R	I/V	G/S	A/S	T	G	Y
NR-5	L	K	Q	I/L	I	I/S	L	S	M	S	P/Q	Y	Q/R	V	S	A/S	T	G	H/Y
NR-6	L	K	Q	I/L	I	T	F/L	F/S	M/L	R/S	E/Q	Y	Q	I/V	S	S	T	G	H/Y
NR-7	L	K	Q	I	I	T	L	S	M	S	Q	Y	Q	V	S	S	N/T	G	Y
R-1	L	K/R	Q	I/L	I/L	I/L/S/T	L	F/S	M	R/S	S	D	Q/R	I/V	S	A/S	T	A/G	Y
R-2	L	K	Q	I/L	I/L	I/L/S/T	L	S	M	S	P/Q/S/*	Y/D	Q/R	I/V	S	A/S	T	G	Y
R-3	L/F	K	Q/E	I/L	I/L	I/L/S/T	L	S	M	S	A/E/P/Q	Y/D	Q/R	I/V	S	S	T	G	H/Y
R-4	L	K	Q	I/L	I/L	I/L/S/T	L	S	M	S	A/E/P/Q/S/*	Y/D	Q/R	I/V	S	S	T	A/G	H/Y
R-5	L	K	Q	I/M	I/L	I/L/S/T	L	S	M	S	P/Q/S/*	Y/D	L/Q/R	I/V	S	S	T	A/G	H/Y
R-6	L	K/R/T	Q/E	I/M	I/L	T	F/L	S	M	S	S/*	Y/D	Q	I/V	S	S	N/T	G	H
R-7	L	K	Q	L/V	I	T	L	S	M	S	E/Q	Y/D	Q	I/V	S	S	T	G	Y

¹ The number above each site indicates their position in the coding sequence (see Fig. S2). Amino acid sequences were obtained by translating exons of the genomic sequence.

² Sites containing two variable DNA nucleotides resulting in more than two different codons and predicted amino acids. A stop codon was observed at site 342 in five of the trees but none of the trees were homozygous for a stop.