

Table 5. Positive selection detected in the highly similar paralogs groups

Paralog group*	Number of <i>Avh</i> genes	<i>Avh</i> genes belonging to the paralog group	dN [†]	dS [‡]	dN/dS	Number of positively selected sites [§]	Positively selected amino acid residues	Positively selected AA in signal peptides	Positively selected AA in RXLR-dEER domain	Positively selected AA in the C-terminal region
ParalogGroup_1	3	PsAvh_295 PsAvh_378 PsAvh_379	0.01	0.04	0.38	0	none			
ParalogGroup_2	3	PrAvh_229 PrAvh_248 PrAvh_90	0.01	0.01	1.68	2	W48 S71	0	2	0
ParalogGroup_3	3	PrAvh_18 PrAvh_84 PrAvh_9	0.00	0.00	nd	7	T138 N171 S176 R190 K192 S203 F216	0	0	7
ParalogGroup_4	3	PrAvh_165 PrAvh_281 PrAvh_67	0.02	0.02	1.08	3	N29 A63 V147	0	2	1
ParalogGroup_5	3	PrAvh_181 PrAvh_287 PrAvh_319	0.02	0.03	0.47	0	none			
ParalogGroup_6	3	PrAvh_305 PrAvh_308 PrAvh_309	0.01	0.01	1.64	0	none			
ParalogGroup_7	3	PrAvh_274 PrAvh_275 PrAvh_335	0.01	0.01	1.73	1	F136	0	0	1
ParalogGroup_8	3	PrAvh_213 PrAvh_218 PrAvh_220	0.00	0.00	nd	0	none			
ParalogGroup_9	3	PrAvh_109 PrAvh_110	0.02	0.03	0.50	0	none			

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9		PrAvh_111								
ParalogGroup_10	4	PsAvh_277 PsAvh_299 PsAvh_300 PsAvh_301	0.01	0.01	1.42	0	none			
ParalogGroup_11	4	PrAvh_240 PrAvh_262 PrAvh_265 PrAvh_286	0.01	0.02	0.91	0	none			
ParalogGroup_12	4	PrAvh_131 PrAvh_132 PrAvh_138 PrAvh_139	0.02	0.03	0.50	0	none			
ParalogGroup_13	4	PsAvh_7a PsAvh_7b1 PsAvh_7b2 PsAvh_7c	0.01	0.01	0.56	0	none			
ParalogGroup_14	4	PrAvh_131 PrAvh_132 PrAvh_138 PrAvh_139	0.02	0.03	0.50	0	none			
ParalogGroup_15	5	PrAvh_302 PrAvh_303 PrAvh_304 PrAvh_306 PrAvh_307	0.03	0.03	0.96	13	D145 T159 E209 G223 E228 L230 H231 G236 Y239 R240 M242 T249 K252	0	0	13
ParalogGroup_16	5	PrAvh_178 PrAvh_179 PrAvh_190 PrAvh_195 PrAvh_235	0.03	0.02	1.12	6	N105 L107 A130 H132 I133 E134	0	0	6
ParalogGroup_	6	PrAvh_148 PrAvh_187	0.02	0.06	0.36	0	none			

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17		PrAvh_361 PrAvh_364 PrAvh_65 PrAvh_85								
Avr1b [¶]	5	P6954 P7064 P7074 P7076 P7081	0.02	0.01	3.00	18	L3 V69 A77 K80 A87 K94 E97 K98 I G103 S105 D107 K108 N111 Q120 D125 N129 L135 S138		0	18
ELI ^{¶¶}	6	SOJ1A SOJ1B SOJ1C SOJ1D SOJ1E SOJ1F	0.51	4.91	0.10	0	None			

*Paralog groups sharing [mt]90% nucleotide sequence identity are grouped together.

[†]dN represents the rate of nonsynonymous nucleotide substitution per nonsynonymous sites estimated by the codeml program of the PAMLv3.14 package.

[‡]dS represents the rate of synonymous nucleotide substitution per synonymous sites estimated by the codeml program of the PAMLv3.14 package.

[§]Positively selected amino acid sites were assigned based on a probability >95% with Bayes empirical Bayes statistics.

[¶]The analysis of Avr1b was performed with the four alleles present in the *P. sojae* population (1).

^{¶¶}The analysis of ELI1 was performed with the close paralogs of *soj* genes (2).

1. Shan W, Cao M, Leung D, Tyler BM (2004) The Avr1b locus of *Phytophthora sojae* encodes an elicitor and a regulator required for avirulence on soybean plants carrying resistance gene Rps1b. *Mol Plant Microbe Interact* 17:394–403.

2. Jiang RHY, Tyler BM, Govers F (2006) Comparative analysis of *Phytophthora* genes encoding secreted proteins reveals conserved synteny and lineage-specific gene duplications and deletions. *Mol Plant-Microbe Interact* 19:1311-1321.