

Table 2. General characteristics of PAMPs (pathogen-associated molecular patterns) and the PRRs (pathogen recognition receptors) responsible for their recognition as opposed to the features of Avr (avirulence) proteins and their corresponding PRRs (characteristics of AvrXa21 and XA21 are shown in bold if they appear to be unique compared with other known systems)

PAMP • PRR General Characteristics	AvrXa21 • XA21 Characteristics	Avr • PRR General Characteristics
PAMP (e.g., flagellin) <ul style="list-style-type: none"> - Conserved among diverse species - Required for lifecycle - Not typically actively secreted 	AvrXa21 <ul style="list-style-type: none"> - Strain specific, but core molecule appears to be conserved among species - Activity is regulated in a cell-density-dependent manner by a two-component system - Synthesized in absence of plant host (thus part of lifecycle) - Absence compromises virulence in field - Secreted by TOSS 	Avr (e.g., AvrRpt2) <ul style="list-style-type: none"> - Strain specific - Many synthesized only in presence of host - Absence compromises virulence - From bacteria, secreted by TTSS
PRR (e.g., FLS2) <ul style="list-style-type: none"> - Extracellular (intracellular recognition only shown in animals) - Recognition and response does not lead to resistance in most cases 	XA21 <ul style="list-style-type: none"> - Recognition likely extracellular - Confers dominant resistance 	PRR (e.g., RPS2) <ul style="list-style-type: none"> - In dicots, recognition mostly intracellular (characterized RLPs are an important exception) - Confers dominant resistance

Supplemental Table 2. Primer sets for this study

Gene	Primer	Primer sequence	Amplification region, length
<i>raxST</i>	<i>raxST1-F</i>	5'-ACCATTTTCATTTCCGGGCT-3'	62 to 291 st , 230 bp
	<i>raxST1-R</i>	5'-CAGCTCCTGGCGATTCTGG-3'	
	<i>raxST2-F</i>	5'-GGGCACGGTGTTCGACACCA-3'	292 to 520 th , 229 bp
	<i>raxST2-R</i>	5'-CACGCCCCGCGGCGGTCA-3'	
	<i>raxST3-F</i>	5'-CTGCGCCAGGCGTTCTACGG-3'	601 to 838 th , 238 bp
	<i>raxST3-R</i>	5'-GCGAAGGCGCGCTTTCCAG-3'	
<i>raxP</i>	<i>raxP1-F</i>	5'-GACCCTGCCGCGCTGTCCC-3'	3 to 286 th , 284 bp
	<i>raxP1-R</i>	5'-CGCCATCAGGATTGATGTGC-3'	
	<i>raxP2-F</i>	5'-ATCGACACACGCTGGAAGTT-3'	187 to 523 rd , 337 bp
	<i>raxP2-R</i>	5'-TGCGCGCGTTGTAGAGAT-3'	
	<i>raxP3-F</i>	5'-GTGGAATCTCTACAACGCGC-3'	501 to 800 th , 300 bp
	<i>raxP3-R</i>	5'-GCTTCCAGCGTGTGCGCACTG-3'	
<i>raxC</i>	<i>raxC1-F</i>	5'-GCCACCGACCTGCTGCAGGT-3'	61 to 409 th , 349 bp
	<i>raxC1-R</i>	5'-GAAATACGCCGCCGAGGTAC-3'	
	<i>raxC2-F</i>	5'-CCAACAACGATCTGATGACG-3'	368 to 654 th , 287 bp
	<i>raxC2-R</i>	5'-CAATGCACGCAAACCAACTA-3'	
	<i>raxC3-F</i>	5'-TACGAGCAGCAGAAGCGCGC-3'	1021 to 1306 th , 285 bp
	<i>raxC3-R</i>	5'-CGGTGATGTCGAGCTTGCCG-3'	
<i>raxR</i>	<i>raxR1-F</i>	5'-CGGCTGCTGGTCATTGAAGAC-3'	4 to 337 th , 334 bp
	<i>raxR1-R</i>	5'-CTCGGGCAGTGCAAAGGG-3'	
	<i>raxR2-F</i>	5'-GCGCCGGCTGCGCGAACAGCAC-3'	195 to 515 th , 321 bp
	<i>raxR2-R</i>	5'-GCATCAGCACTTCGAGCAAC-3'	
	<i>raxR3-F</i>	5'-GCCGCAAGTTGCTCGAAGT-3'	488 to 707 th , 220 bp
	<i>raxR3-R</i>	5'-CATACAGCTGCGCCGGTAG-3'	
16S rRNA	rRNA-F	5'-TAGCTCAGGTGGTTAGAGCGC-3'	
	rRNA-R	5'-CAACGCGAACATACGACTCAA-3'	