Table 1. Pathotypes of *Phytophthora sojae* isolates determined on Harosoy and Williams differential sets, and as predicted by a molecular assay.

| Isolate | Reported pathotype[a] | Haro 7[b] | Sloan[c] | Rps genes in lines exhibiting virulence to the indicated isolate | | Pathotype predicted by molecular assay[z] |
				Harosoy differentials[d,x]	Williams differentials[d,y]	
R1-AD	Avirulent	-	-	-	-	-
R1-BT	7	-	+	-	-	1a,1d,(1k,3a)
R25-AD	7	+	+	1a,1b,1c,1d,1k	1a,1b,1c,1k	(1a)
IV 13-4A	Avirulent	-	-	-	-	1a,1d
V 13	1a,7	-	+	1a,1c	1a,1c	1a,1d
P6497	1b,7	+	+	1b,1d	1b	-
S5-5	1d,7	-	+	-	-	1a,1d
IV 12-2A	1k,7	-	+	1a	-	1a,1d
P7361	6,7	-	+	-	6	1a,(1d)
RM-15	1a,1c,7	+	+	1a,1b,1c,1d,1k	1a,1c	1a
P7375	1a,1c,7	-	+	1a,1c,1k	1a,1c,1k	1a,1d,(1k)
NE-1	1a,1c,7	+	+	1a,1b,1c,1d,1k	1a,1b,1c,1d,1k,3a,6	1a,(1b),1d,(1k)
NE-144	1a,1c,7	+	+	1a,1b,1c,1d,1k,6	1a,1b,1c,1d,1k,3a,6	1a,1d
P7360	1b,6,7	+	+	1b,1d	1b	(1a,1k,1d)
NE-20	1a,1b,1k,7	+	+	1a,1b,1d,1k	1b,1d,1k,3a	1a,1b,1d,1k
NE-33	1a,1b,1k,7	+	+	1k	1c	1d,1k
NE-53	1a,1b,1k,7	+	+	1a,1b,1d,1k	1b,1d,1k,3a	1a,1b,(1d),1k,(3a)
NE-58	1a,1b,1k,7	+	+	1a,1b,1d,1k	1b, 1k,3a	1a,1b,1d,1k
P7064	1a,3a,6,7	-	+	1a,1c,6	3a,6	1a,3a,6
NE-80	1b,1k,6,7	+	+	1b,1c,1d,1k,6	1a,1b,1c,1d,1k,6	1a,1b,1d
P7081	1a,1b,1c,1k,7	+	+	1a,1b,1c,1d,1k	1a,1b,1c,1d,1k,3a,6	1a,(1b),1d,(1k)
P9073	1a,1b,1c,1k,7	+	+	1a,1b,1d,1k	1a,1b,1c,1k	1a,(1d),(1k)
NE-4	1a,1b,1c,1k,7	+	+	1a,1k	1a,1b,1c,1k	1a,1d
P7063	1a,1d,3a,6,7	-	+	1a,6	1c,3a,6	1a,3a,6
R26	1b,1d,3a,6,7	+	+	1b,1d,6	1b,1d,3a,6	1a,1b,1d,3a
P7074	1b,1d,3a,6,7	+	+	1b,1d,6	3a,6	1a,1b,1d,3a
P7076	1a,1b,1c,1d,7	+	+	1a,1b,1c,1d,1k	1a,1b,1c,1d,1k,3a	1a,1b,1d,1k
PT2004	1a,1b,1c,1d,1k,6,7	+	+	1a,1b,1c,1d,1k,6	1a,1b,1c,1k,6	1a,1b,1k,(3a),6

[a] Determined from current publications

[b] Haro susceptible control, + indicates virulence, - indicates avirulence

[c] Williams susceptible control, + indicates virulence, - indicates avirulence

[d] Virulence on a differential was determined as a mean greater than 70% death of inoculated seedlings in 2-4 repetitions (appendix I). Although the Harosoy differentials were used in the study that developed the molecular markers (Dussault-Benoit 2020), the current study used stem inoculation, whereas the prior study used root inoculation to determine virulence on those differential lines.

[x] Haro differential lines; 1a Haro 12, 1b Haro 13, 1c Haro 14, 1d Haro 16, 1k Haro 15, 6 Haro 6272

[y] Williams differential lines; 1a L88-8470, 1b L77-1863, 1c Williams 79, 1d PI103091, 1k Williams 82, 3a L83-570, 6 L89-1581

[z] Pathotype predicted based on the absence of the cognate avirulence genes to target *Rps* genes. This assay excluded *Avr1c* due to poor performance. () indicates lack of agreement between 2 runs of the experiment.