

Table S4. Comparison of evolutionary parameters of the *AvrPii* family among three *Mo* populations, of which parameters of the two populations previously reported were re-computed by the same approaches used in the current study

Population	<i>S</i> ^a	π ^b	<i>D</i> * ^c	<i>F</i> *	<i>Ka</i> ^d	<i>Ks</i> ^e	<i>Ka/Ks</i>
All <i>AvrPii</i> (the current study)							
Entire coding region	20	0.037	1.74 ^β	2.65 ^β	193.8	357.6	0.54
Non-signal peptide region	18	0.045	1.68 ^α	2.59 ^β	246.8	434.8	0.57
Signal peptide region	2	0.013	0.68	1.11	54.9	166.0	0.33
All <i>AvrPii</i> (Lu et al. 2019)							
Entire coding region	15	0.013	1.58 ^α	1.05	19.80	22.39	0.88
Non-signal peptide region	14	0.017	1.55 ^α	1.04	24.97	31.48	0.79
Signal peptide region	1	0.003	0.54	0.34	5.98	0	Ka>Ks
All <i>AvrPii</i> (Sirisathaworn et al. 2017)							
Entire coding region	11	0.003	-3.81 ^β	-3.92 ^β	3.71	0.88	4.23
Non-signal peptide region	5	0.002	-2.20	-2.48	3.07	0	Ka>Ks
Signal peptide region	6	0.004	-3.90 ^β	-3.90 ^β	5.49	3.33	1.65

^a Number of segregating sites.

^b Nei's nucleotide diversity based on silent site.

^c Fu and Li's *D** and *F**, and ^α, ^β represents statistical significance at *P* < 0.05, 0.02 level, respectively.

^d Nonsynonymous.

^e Synonymous.