

Table 3 Genetic Distances Within and Between Effector Homology Family Subgroups

Effector	Old Effector Name	Genetic Distance (amino acid, gamma model $\alpha=2.25$)						
		Total	Within Group			Between Group		
			Group1	Group2	Group3	Group1- Group2	Group1- Group3	Group2- Group3
<i>Effector families that were not divided into subgroups</i>								
AvrD	AvrD	0.80	0.08	0.01	-	0.14	-	-
AvrRpm1	AvrRpm1, AvrPpiA	0.23	0.03	na	-	0.54	-	-
HopD	AvrPphD, HopPtoD	0.10	0.04	na	-	0.20	-	-
HopH	HopPtoH	0.08	0.01	na	-	0.10	-	-
HopI	HopPmaI	0.39	0.21	na	-	0.55	-	-
HopJ	HopPmaJ	0.17	0.15	na	-	0.19	-	-
HopM	HopPtoM, HolPtoX	0.55	0.29	na	-	0.68	-	-
HopO	HopPtoO, HopPtoS	0.50	0.30	na	-	0.61	-	-
HopQ	HolPtoQ	0.08	0.01	na	-	0.12	-	-
HopW	HopPmaA	0.23	0.00	0.08	-	0.34	-	-
HrpK	HrpK	0.14	0.04	na	-	0.30	-	-
HrpW	HrpW	0.40	0.31	na	-	0.51	-	-
HrpZ	HrpZ	0.23	0.03	0.04	0.01	0.26	0.52	0.52
HopAA	HopPtoA	0.32	0.22	0.26	-	0.37	-	-
HopAF	HopPtoJ, HolPtoN	0.11	0.05	na	-	0.15	-	-
HopAK	HopPmaH	0.28	0.26	0.17	-	0.31	-	-
HopAN	AvrE	0.35	0.16	0.40	-	0.44	-	-
HopAQ	Ipx53	0.03	0.02	na	-	0.03	-	-
<i>Effector families that were divided into subgroups</i>								
AvrB	AvrB, AvrC	1.00	0.004	0.19	-	1.17	-	-
HopA	HopPsyA, HopPsyB, HrmA	0.56	0.02	0.50	-	1.26	-	-
HopB	HopPtoB, HopPsyG	0.51	0.03	na	-	0.75	-	-
HopF	AvrPphF	0.93	0.73	na	-	1.13	-	-
HopT	HolPtoU, HopPtoT	0.68	0.36	na	-	0.84	-	-
HopX	AvrPphE, HopPmaB, HopPsyE	0.58	0.29	na	-	2.30	-	-
HopZ	AvrPpiG HopPmaD, HopPsyH	2.04	0.37	na	na	2.45	2.52	2.24
HopAB	VirPphA HopPmaL, HolPmaN	0.52	0.16	0.52	-	0.76	-	-
HopAH	HolPsyAH	0.63	0.19	0.27	-	0.83	-	-
HopAJ	HopPmaG	0.54	0.02	0.03	-	0.88	-	-

na = not applicable because of only a single sequence within the subgroup