

Table S3 Comparison of pNS and pS ratios for *ROP18* alleles

Strains	<i>ROP18</i>		
	pNS	pS	pNS/pS
^a Type I vs. Type II	0.02497	0.00536	4.660258
Type I vs. Type III	0.06049	0.03473	1.742024
Type II vs. Type III	0.05415	0.04036	1.341758
^b Type I* vs. Type II*	0.02323	0.00675	3.535183
Type I* vs. Type III*	0.06741	0.04565	1.476658
Type II* vs. Type III*	0.05665	0.04895	1.159953
^c Type I*a vs. Type I*b	0.00238	0.00252	0.944776
Type I*a vs. Type I*c	0.00383	0.00251	1.527424
Type I*a vs. Type I*c	0.00621	0.00503	1.236186

pN, Estimate of the proportion of nonsynonymous differences; $pNS = NSd/NS$,

NS, The number of nonsynonymous sites for each codon

NSd, The number of synonymous differences per codon

pS, Estimate of the proportion of synonymous differences; $pS = Sd/S$,

S, The number of synonymous sites for each codon

Sd, The number of synonymous differences per codon

^a Includes only North American and European clonal lineages, based on 2 strains each.

^b ROP18I* (17) II* (3) and III* (5) groups were defined based on the phylogeny shown in Fig 2C and the numbers of strains are given in parentheses.

^c ROP18Ia* (5), ROP18I*b (5) and ROP18I*c (6) are defined in Figure 4A and the numbers of strains are given in parentheses.