

Table S6A. Selection pressures acting on Hp0519 : ML parameter estimates

Model Code	κ	Tree Length	ln L ^a	dN / dS ^b	Estimates of Parameters	LRT [d.f.] ^c	χ^2	P	Positively Selected Sites ($\omega > 1$); Reference Sequence 26695
Site-Specific Models									
M0 (one-ratio)	4.325	2.203	-4359.719	0.406	$\omega = 0.406$				None
M1 (neutral)	4.258	2.275	-4232.698	0.435	$p0 = 0.564, \omega_0 = 0;$ $p1 = 0.435, \omega_1 = 1$				Not Allowed
M2 (selection)	4.881	2.442	-4204.934	0.652	$p0 = 0.553, p1 = 0.385, (p2 = 0.061),$ $\omega_2 = 4.408$	M0 vs M2 [2] M1 vs M2 [2]	309.57 55.528	<0.000 <0.000	44*, 81R, 82L, 87S, 114F, 117E, 132L, 136R, 171A, 189S, 216*, 220S, 221T, 230W, 264T, 269D, 279A, 290L
M3 (discrete)	4.613	2.458	-4199.613	0.541	$p0 = 0.589, \omega_0 = 0.023; p1 = 0.336,$ $\omega_1 = 0.796;$ $p2 = 0.073,$ $\omega_2 = 3.515$	M0 vs M3 [4] M1 vs M3 [4] M2 vs M3 [2]	320.21 66.17 10.642	<0.000 <0.000 <0.004	44*, 81R, 82L, 87S, 114F, 117E, 132L, 136R, 171A, 189S, 216*, 220S, 221T, 230W, 264T, 269D, 279A, 290L
M7 (β)	3.967	2.321	-4225.387	0.351	$p = 0.093,$ $q = 0.174$				Not Allowed
M8 (β & ω)	4.619	2.461	-4199.561	0.542	$p0 = 0.932, p = 0.116, q = 0.251,$ $p2 = 0.067,$ $\omega_2 = 3.645$	M7 vs M8 [2]	51.652	<0.000	44*, 81R, 82L, 87S, 114F, 117E, 132L, 136R, 171A, 189S, 216*, 220S, 221T, 230W, 264T, 269D, 279A, 290L

a, lnL, Log-likelihood score; b, dN/dS, rate ratio of non-synonymous to synonymous changes averaged over all lineages and all sites
c, likelihood ratio test [degrees of freedom];

Table S6B. Episodic adaptive evolution in the Japanese HP0519 lineage

Model Code	κ	Tree Length	ln L ^a	Estimates of Parameters	LRT [d.f.] ^b	χ^2	P	Positively Selected Sites Foreground lineage (Reference Sequence 26695)	Positively Selected Sites Background lineage (Reference Sequence 26695)
A. Lineage-Specific Models [LSMs]									
FR (Free-Ratio)	4.344	2.191	-4313.6	one ω for each of 51 lineages	vs M0 [50]	92.2	<0.000	Not Applicable	Not Applicable
M2J (Two-ratio)	4.336	2.191	-4348.9	ω_0 (Background lineage) = 0.354; ω_1 (Foreground lineage, Japan) = 1.581	vs M0 [1]	21.7	<0.000	Not Applicable	Not Applicable
B. Lineage-Site Specific Models [LSSMs]									
M2JM2	4.563	2.516	-4188.1	$p0 = 0.551, \omega_0 = 0;$ $p1 = 0.326, \omega_1 = 1;$ $(p2 + p3) = 0.121,$ $\omega_2 = 21.581$	vs M1 [2]	89.2	<0.000	39D, 40D, 44*, 56H, 82L, 153K, 162F, 166S, 171A, 181E, 182F, 184S, 185M, 186L, 209G, 210L, 213K, 219K, 221T, 222Q, 223I, 224K, 225D, 227T	Not Allowed
M2JM3	4.834	2.571	-4177.6	$p0 = 0.636, \omega_0 = 0.043; p1 = 0.242,$ $\omega_1 = 1.497;$ $(p2 + p3) = 0.121,$ $\omega_2 = 25.184$	vs M3 [2]	44.1	<0.000	39D, 40D, 44*, 56H, 82L, 153K, 162F, 166S, 171A, 181E, 182F, 184S, 185M, 186L, 209G, 210L, 212V, 213K, 219K, 221T, 222Q, 223I, 224K, 225D, 227T, 231E	12F, 14K, 15P, 16L, 21V, 25P, 33E, 38S, 54R, 79D, 81R, 87S, 102G, 107V, 114F, 122G, 131A, 132L, 136R, 140E, 144M, 157H, 161M, 173N, 176L, 177P, 178N, 180A, 183T, 190R, 199A, 206K, 220S, 226K, 229L, 230W, 241T, 267K, 269D, 270R, 279A

* Sites listed in bold, >95% probability, sites in Italics, > 75% < 95%, sites in plain letters > 50% < 75% probability; sites listed in blue and red are those that are restricted to Region I and Region II of Hp0519 as shown in Figure 3b.

a, lnL, log likelihood score; b, likelihood ratio test [degrees of freedom].

Table 6C: Selection pressures acting on Hp0519: ML parameter estimates assuming a 'Star' phylogeny

Model Code	ln L ^a	dN / dS ^b	Estimates of Parameters	LRT [d.f.] ^c	χ^2	P	Positively Selected Sites ($\omega > 1$); Reference Sequence 26695
Site-Specific Models							
M0 (one-ratio)	-6320.0002	0.4816	$\omega = 0.481$				None
M1 (nearly neutral)	-5769.2927	0.313	$p0 = 0.703, \omega_0 = 0.02;$ $p1 = 0.293, \omega_1 = 1$				Not Allowed
M2 (selection)	-5610.7626	0.718	$p0 = 0.661, \omega_0 = 0.02$ $p1 = 0.261, \omega_1 = 1$ $p2 = 0.061, \omega_2 = 5.74$	M0 vs M2 [2] M1 vs M2 [2]	1101.415 317.0602	<0.000 <0.000	10L, 44*, 82L, 87S, 114F, 117E, 132 L, 136 R, 171 A, 176 L, 177 P, 182F, 220S, 221T, 222Q, 223 I, 267 K, 269 D, 288E, 290 L
M3 (discrete)	-5609.5942	0.766	$p0 = 0.672, \omega_0 = 0.023;$ $p1 = 0.256, \omega_1 = 1.1;$ $p2 = 0.073, \omega_2 = 6.34$	M0 vs M3 [4] M1 vs M3 [4]	1420.81 319.39	<0.000 <0.000	10L, 44*, 82L, 87S, 114F, 117E, 132 L, 136 R, 171 A, 176 L, 177 P, 182F, 220S, 221T, 222Q, 223 I, 267 K, 269 D, 288E, 290 L + 23 more sites (because of two ws under positive selection)
M7 (β)	-5757.4825	0.2955	$p = 0.073, q = 0.174$				Not Allowed
M8 (β & ω)	-5608.7399	0.64	$p0 = 0.922,$ $p = 0.068, q = 0.201,$ $p1 = 0.077, \omega_2 = 5.262$	M7 vs M8 [2]	297.48	<0.000	10L, 44*, 82L, 87S, 114F, 117E, 132 L, 136 R, 171 A, 176 L, 177 P, 182F, 220S, 221T, 222Q, 223 I, 267 K, 269 D, 288E, 290 L

See footnotes to Table 6a for explanation.