

Table S3 (a) Results of CODEML analyses of selective constraint for CP gene of OrMV. (b) Codon positions under positive selection

OrMV group	Model	Parameter estimates (Frequency, f and ω Values)	χ^2	Ln L	LRT p -value
(a)					
Clade A	One-ratio 0 ($\omega_0=\omega_1$)	$\omega_0=\omega_1=0.152$	7.332	-6778.939	<0.001
	Two-ratio 2 (ω_0, ω_1)	$\omega_0=0.159, \omega_1=0.055$		-6775.272	
Clade B	One-ratio 0 ($\omega_0=\omega_1$)	$\omega_0=\omega_1=0.152$	8.437	-6778.939	<0.001
	Two-ratio 2 (ω_0, ω_1)	$\omega_0=0.159, \omega_1=0.028$		-6774.720	
OrMV Group	Model (np)	Parameter estimates	Positive sites	Ln L	LRT p -value
(b)					
All	M3 (74)	$p: 0.558, 0.442, 0.000$ $\omega: 0.050, 0.330, 46.913$	n/a	-6115.413	<0.001
	M0 (70)	$\omega_0: 0.161$	Not Allowed	-6169.647	
	M2a (73)	$p: 0.926, 0.047, 0.028$ $\omega: 0.143, 1.000, 1.000$	n/a	-6154.614	1.000
	M1a (71)	$p: 0.926, 0.074,$ $\omega: 0.143, 1.000,$	Not Allowed	-6154.614	
	M8 (73)	$p_0=0.999, p=0.728, q=3.136 (p_1= 0.00001), \omega= 1.000$	n/a	-6116.037	0.999
	M7 (71)	$p= 0.723, q=3.136$	Not Allowed	-6116.036	
Clade A	M3 (48)	$p: 0.513, 0.487, 0.000$ $\omega: 0.080, 0.464, 34.976$	n/a	-4289.288	<0.001
	M0 (44)	$\omega_0: 0.251$	Not Allowed	-4311.891	
	M2a (47)	$p: 0.865, 0.084, 0.050$ $\omega: 0.195, 1.000, 1.000$	n/a	-4298.504	1.000
	M1a (45)	$p: 0.865, 0.135$ $\omega: 0.195, 1.000$	Not Allowed	-4298.504	
	M8 (47)	$p_0=0.999, p=0.799, q=2.060 (p_1= 0.00001), \omega= 1.000$	n/a	-4289.356	0.999

Clade B	M7 (45)	$p=0.799, q=2.060$	Not Allowed	-4289.356	
	M3 (30)	$p: 0.807, 0.193, 0.000$ $\omega: 0.022, 0.317, 36.191$	n/a	-2470.915	<0.001
	M0 (26)	$\omega_0: 0.072$	Not Allowed	-2488.257	
	M2a (29)	$p: 0.955, 0.03314, 0.012$ $\omega: 0.052, 1.000, 1.000$	n/a	-2476.363	1.000
	M1a (27)	$p: 0.955, 0.045$ $\omega: 0.052, 1.000$	Not Allowed	-2476.363	
	M8 (29)	$p_0=0.993, p=0.196, q=1.883 (p_1=0.007), \omega=1.694$	15S, 30S, 36Q	-2469.270	0.107
	M7 (27)	$p=0.176, q=1.494$	Not Allowed	-2471.507	
