

Supplementary Table 1. Molecular evolution of Australian elapid 3FTx

		SLAC ^a	FEL ^b	REL ^c	FUBAR ^d	Integrative analyses	MEME Sites ^e	BSR ^f	PAML ^g	
						SLAC + FEL + REL + MEME + FUBAR			M8	M2a
<i>Acanthophis wellsi</i>										
	$\omega > 1^h$	0	0	17	8	17			8	3
Type II	$\omega < 1^i$	0	2	0	1	2	2	2	(3+5)	(2+1)
	$\omega =$	1.47	–	dN>>dS	–	–			1.76	1.76
<i>Brachyurophis roperi</i>										
	$\omega > 1^h$	0	0	10	12	12			25	25
Type I	$\omega < 1^i$	0	1	1	1	1	0	2	(13+12)	(12+13)
	$\omega =$	14.12	–	dN>>dS	–	–			18.95	18.95
	$\omega > 1^h$	0	0	2	12	13			17	16
Type II	$\omega < 1^i$	0	2	3	2	4	2	2	(13+4)	(11+5)
	$\omega =$	2.42	–	dN>>dS	–	–			3.52	3.54
<i>Cacophis squamulosus</i>										
	$\omega > 1^h$	0	0	2	1				3	3
Type I	$\omega < 1^i$	0	1	3	1			1	(0+3)	(0+3)
	$\omega =$	1.20	–	dN>>dS	–	–			2.51	2.50
<i>Drysdalia coronoides</i>										
	$\omega > 1^h$	0	0	1	2	3			10	10
Type I	$\omega < 1^i$	0	0	0	0	0	0	2	(6+4)	(6+4)
	$\omega =$	1.21	–	1.38	–	–			4.45	4.46
	$\omega > 1^h$	0		25	9	25			8	7
Type II	$\omega < 1^i$	0		0	1	2	3	5	(6+2)	(6+1)
	$\omega =$	2.97	–	dN>>dS	–	–			2.79	2.37
<i>Echiopsis curta</i>										
	$\omega > 1^h$	0	0	2	7	8			6	3
Type II	$\omega < 1^i$	0	2	0	2	2	0	3	(2+4)	(1+2)
	$\omega =$	4.92	–	dN>>dS	–	–			2.43	2.43
<i>Furina ornata</i>										
	$\omega > 1^h$	0	0	5	3	5			6	6
Type II	$\omega < 1^i$	2	1	0	1	2	0	0	(5+1)	(3+3)
	$\omega =$	1.16	–	3.07	–	–			1.63	1.67
	$\omega > 1^h$	0	0	4	5	6			9	7
Type III	$\omega < 1^i$	0	1	0	1	1	2	3	(3+6)	(1+6)
	$\omega =$	1.28	–	20.7	–	–			1.81	1.82

		SLAC ^a	FEL ^b	REL ^c	FUBAR ^d	Integrative analyses	MEME Sites ^e	BSR ^f	PAML ^g	
<i>Hemiaspis signata</i>										
Type I	$\omega>1^h$	0	0	3	2	3			0	0
	$\omega<1^i$	0	1	0	4	4	0	0		
	$\omega=$	1.19	—	1.33	—	—			1.18	1.18
Type II	$\omega>1^h$	0	0	3	12	14			14	13
	$\omega<1^i$	0	2	4	2	4	2	5	(10+4)	(9+4)
	$\omega=$	2.74	—	dN>>dS	—	—			4.26	4.26
<i>Parasuta nigriceps</i>										
Type I	$\omega>1^h$	0	0	5	2	5			5	3
	$\omega<1^i$	0	2	0	1	2	0	1	(1+4)	(1+2)
	$\omega=$	1.78	—	dN>>dS	—	—			3.0	3.0
Type II	$\omega>1^h$	0	0	1	2	3			8	5
	$\omega<1^i$	0	3	0	2	3	1	1	(2+6)	(2+3)
	$\omega=$	1.27	—	2.59	—	—			5.97	5.97
<i>Pseudonaja modesta</i>										
Type II	$\omega>1^h$	0	4	0	14	15			18	13
	$\omega<1^i$	2	3	6	21	7	3	6	(13+5)	(11+2)
	$\omega=$	2.65	—	dN>>dS	—	—			3.28	2.73
Type III	$\omega>1^h$	2	10	19	25	27			25	22
	$\omega<1^i$	2	4	24	3	24	16	10	(22+3)	(18+4)
	$\omega=$	2.69	—	11.22	—	—			2.82	2.78
<i>Suta nigriceps</i>										
Type I	$\omega>1^h$	0	0	5	2	5			5	3
	$\omega<1^i$	0	2	0	1	2	0	1	(1+4)	(1+2)
	$\omega=$	1.78	—	dN>>dS	—	—			3.0	3.0
Type II	$\omega>1^h$	0	0	1	2	3			8	5
	$\omega<1^i$	0	3	0	2	3	1	1	(2+6)	(2+3)
	$\omega=$	1.27	—	2.59	—	—			5.97	5.97
<i>Vermicella annulata</i>										
Type I	$\omega>1^h$	0	0	0	0	1			0	0
	$\omega<1^i$	0	1	1	1	4	1	1		
	$\omega=$	1.05	—	16.17	—	—			0.63	0.63
Type II	$\omega>1^h$	0	0	6	5	9			14	11
	$\omega<1^i$	0	1	0	2	2	1	3	(6+8)	(5+6)
	$\omega=$	1.66	—	2.99	—	—			3.89	3.89
Type III	$\omega>1^h$	0	3	4	13	13			20	19
	$\omega<1^i$	0	2	2	3	3	3	7	(18+2)	(14+5)
	$\omega=$	3.02	—	dN>>dS	—	—			6.84	5.66

Legend:

a: Single Likelihood Ancestor Counting

b: Fixed-effects likelihood

c: Random-effects likelihood

d: Fast Unconstrained Bayesian AppRoximation

e: Sites detected as experiencing episodic diversifying selection (0.05 significance) by the Mixed Effects Model Evolution

f: #of branches detected as episodically diversifying by Branch-site REL

g: Positively-selected sites detected using the Bayes Empirical Bayes approach implemented in M8 and M2a. Sites detected at 0.99 and 0.95 significance are indicated in the parenthesis

h: Number of positively selected sites at 0.05 significance (for SLAC, FEL) or 50 Bayes factor (for REL) / number of sites under pervasive diversifying selection at the posterior probability ≥ 0.9 (FUBAR)

i: Number of negatively selected sites at 0.05 significance (for SLAC, FEL) or 50 Bayes factor (for REL) / number of sites under pervasive purifying selection at the posterior probability ≥ 0.9 (FUBAR)

dN>>dS: Extremely large dN, as dS is nearly 0

ω : mean dN/dS