Table S1. Evolution of venom in ancient and evolutionarily young animal lineages

	PAML	MEME	Reference
Cnidaria			
Type I and Type II sodium channel toxins	**PS:** 0 **ω:** 0.58	8	(Jouiaei, et al. 2015)
Type I potassium channel toxins	**PS:** 1 0.66	5	
Type III potassium channel toxins	**PS:** 6 **ω:** 1.33	5	
Actinoporins	**PS:** 0 **ω:** 0.39	25	
Sea Anemone aerolyin-related toxins	**PS:** 0 **ω:** 0.27	41	
Hydralysins	**PS:** 0 **ω:** 0.21	9	
Jellyfish toxins	**PS:** 0 **ω:** 0.39	17	
Small cysteine-rich proteins (SCRiPs) in corals	**PS:** 0 **ω:** 0.72	7	
Coleoids			
Cysteine-rich secretory proteins, antigen 5, and pathogenesis-related 1 (CAP)	**PS:** 0 **ω:** 0.22	1	(Ruder, et al. 2013)
Phospholipase A2 (PLA2)	**PS:** 0 **ω:** 0.52	1	
Pacifastin	**PS:** 0 **ω:** 0.36	3	
Serine proteases	**PS:** 1 **ω:** 0.29	26	
Scorpions			
α-sodium channel toxins	**PS:** 5 **ω:** 0.54	19	(Sunagar, et al. 2013c)
β-sodium channel toxins	**PS:** 4 **ω:** 0.53	18	
Long potassium channel toxins	**PS:** 1 **ω:** 0.30	10	
Short potassium channel toxins	**PS:** 0 **ω:** 0.42	4	
Chloride channel toxins	**PS:** 2 **ω:** 0.6	5	
Inhibitor cystine knot (ICK)	**PS:** 0	0	

	ω: 0.34		
Disulphide-directed beta-hairpin (DDH)	**PS:** 0 **ω:** 0.32	1	
Antimicrobial peptides (AMP)	**PS:** 1 **ω:** 0.33	2	
Linear peptides	**PS:** 0 **ω:** 0.27	3	
Bradykinin	**PS:** 0 **ω:** 0.20	2	
Anionic peptides	**PS:** 0 **ω:** 0.22	0	
Glycine-rich peptides	**PS:** 0 **ω:** 0.14	1	
Spiders			
Family E ICK	**PS:** 3 **ω:** 0.64	6	
Funnel-web spider ω toxins	**PS:** 0 **ω:** 0.69	7	(Pineda, et al. 2014)
Funnel-web spider κ toxins	**PS:** 0 **ω:** 1.06	0	
Funnel-web spider ω/κ hexatoxins	**PS:** 1 **ω:** 0.78	8	
Tarantula Huwentoxin-1 Family	**PS:** 1 **ω:** 0.72	19	
***Loxosceles* Sphingomyelinase D**	**PS:** 0 **ω:** 0.19	22	
Kunitz-type Serine Protease Inhibitors	**PS:** 4 **ω:** 1.58	2	
Magi-1 Family toxins	**PS:** 0 **ω:** 0.72	17	
α-Latrotoxins	**PS:** 3 **ω:** 0.25	47	
U1-lycotoxin family	**PS:** 0 **ω:** 0.80	2	
Toxicofera Lizards			
Kallikreins	**PS:** 14 **ω:** 0.86	30	
CRiSPs	**PS:** 13 **ω:** 1.0	11	(Sunagar, et al. 2012)
Crotamine	**PS:** 0 **ω:** 1.31	1	

Phospholipase A2	**PS:** 0 **ω:** 0.50	2	
Natriuretic peptides	**PS:** 0 **ω:** 0.57	3	
Nerve Growth Factor	**PS:** 0 **ω:** 0.33	1	(Sunagar, et al. 2013a)

	PAML	MEME	Reference
Advanced Snakes			
Cysteine-rich Secretory Proteins (CRISPs)	**PS:** 35 **ω:** 1.18	35	(Sunagar, et al. 2012)
Group I Phospholipase A_2	**PS:** 49 **ω:** 1.23	55	
Group II Phospholipase A_2	**PS:** 14 **ω:** 0.76	39	
Type I α-neurotoxins	**PS:** 19 **ω:** 1.72	13	(Sunagar, et al. 2013b)
Type II α-neurotoxins	**PS:** 21 **ω:** 1.45	30	
Type III α-neurotoxins	**PS:** 30 **ω:** 2.61	24	
Cytotoxins	**PS:** 2 **ω:** 0.53	0	
κ-neurotoxins	**PS:** 5 **ω:** 2.11	2	
Snake venom metalloproteinases (SVMPs)	**PS:** 160 **ω:** 1.14	168	File S1
SVMPs in *Psammophis mossambicus*	**PS:** 2 **ω:** 1.23	1	(Brust, et al. 2013)
SVMPs in *Echis coloratus*	**PS:** 34 **ω:** 1.15	28	
PII Disintegrins	**PS:** 14 **ω:** 1.49	9	File S1 and (Juarez, et al. 2008)
Crotamines	**PS:** 11 **ω:** 1.18	4	(Sunagar, et al. 2014)
Kallikreins	**PS:** 36 **ω:** 1.36	45	
Lectins	**PS:** 48 **ω:** 1.29	51	
Serine Proteases	**PS:** 51	69	

	ω: 1.18		
Cone snails (Dutertre, et al. 2014)			
Con-ikot-ikot in *Conus geographus*	**PS:** 23	7	(Dutertre, et al. 2014)
	ω: 2.38		
Conantokin in *C. geographus*	**PS:** 17	31	
	ω: 1.26		
Conkunitzin in *C. geographus*	**PS:** 26	0	
	ω: 4.39		
Superfamily A in *C. geographus*	**PS:** 6	5	
	ω: 1.57		
Superfamily M in *C. geographus*	**PS:** 14	6	
	ω: 2.80		
Superfamily O1 in *C. geographus*	**PS:** 25	4	
	ω: 7.0		
Superfamily O2 in *C. geographus*	**PS:** 0	0	
	ω: 1.46		
Superfamily O1 in *C. marmoreus*	**PS:** 9	6	
	ω: 2.23		
Superfamily O2 in *C. marmoreus*	**PS:** 13	4	
	ω: 2.76		
Superfamily T in *C. marmoreus*	**PS:** 7	1	
	ω: 4.97		
Superfamily I2 in *C. marmoreus*	**PS:** 16	6	
	ω: 2.40		
Superfamily M in *C. marmoreus*	**PS:** 10		
	ω: 2.43	4	

Note: For details regarding datasets and analyses, please see the cited papers where they were reported. Results of analyses conducted in this study are colored in green.

Legend:
PS: Positively selected sites detected by the Bayes Empirical Bayes approach implemented in model 8 of PAML.
MEME: episodically diversifying sites identified by the mixed effects model of evolution
ω: mean dN/dS

Table S1 References

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