

12) Model support (delta AICc), phylogenetic signal (Blomberg’s K), and phylogenetic signal permutation test p-value for each continuous character. Ntaxa = Number of taxa used in the analyses after removing those where the character sate is inapplicable or the data is missing.

Character	Non-Phylogenetic dAIC	BM dAIC	EB dAIC	OU dAIC	K	K p-value	Ntaxa
Haploneme elongation	0	2.017	4.332	2.38	0.583	0.001	43
Desmoneme elongation	0	3.232	5.693	3.183	0.018	0.864	31
Heteroneme shaft width µm	0	5.346	7.67	2.581	0.45	0.005	42
Elastic strand width µm	0	1526	3.938	1.296	0.706	0.001	34
Desmoneme length µm	0.518	0	2.46	0.578	0.566	0.002	31
Heteroneme shaft extension	0.589	0	2.324	1.965	0.041	0.970	42
Haploneme SA/V	0.91	0	2.315	2.291	0.156	0.132	43
Total heteroneme volume µm3	0.961	0	2.352	2.328	0.248	0.046	39
Rhopaloneme width µm	1.205	0	2.46	1.321	0.308	0.123	31
Heteroneme volume µm3	2.002	0	2.153	2.324	0.196	0.117	42
Involucrum length µm	2.479	0	2.498	2.492	0.529	0.001	29
Tentacle width µm	2.939	0	2.307	1.974	0.367	0.044	44
Cnidoband coiledness	3.077	0	2.315	1.786	0.174	0.043	43
Total haploneme volume µm3	3.641	0	1.852	2.296	0.198	0.267	43
Cnidoband free length µm	3.801	0	2.132	2.315	0.325	0.007	43
Heteroneme free length µm	3.82	0	2.01	1.325	0.301	0.080	42
Rhopaloneme elongation	3.852	0	2.145	2.46	0.062	0.827	31
Desmoneme width µm	3.96	0	2.46	2.121	0.553	0.004	31
Cnidoband length µm	4.094	0	1.911	2.315	0.321	0.015	43
Heteroneme number	4.262	0	2.352	2.219	0.866	0.001	39
Heteroneme shaft free length µm	4.553	0	2.324	2.321	0.331	0.126	42
Rhopaloneme length µm	5.599	0	2.46	2.457	0.589	0.001	31
Heteroneme/Cnidoband length	5.671	0	1.862	2.342	1.068	0.001	42
Pedicle width µm	6.566	0	2.253	2.315	0.541	0.001	43
Haploneme width µm	7.495	0	2.218	2.304	0.553	0.001	43
Heteroneme width µm	7.53	0	2.324	1.647	0.502	0.001	42
Heteroneme elongation	14.169	0	0.819	2.23	0.508	0.001	42
Haploneme row number	19.566	0	2.114	2.315	0.442	0.001	43
Total nematocyst volume µm3	21.007	0	2.213	2.292	1.3	0.001	45
Cnidoband width µm	5.69	0.307	0	2.623	0.374	0.001	43
Haploneme free length µm	12.337	7.125	0	9.439	1.079	0.001	43

Non-phylogenetic model supported

Brownian Motion model supported

Early Burst model supported