

14. Model support (delta AICc) for each morphological character analyzed on the feeding guild reconstruction regime tree. OU1 = Single-optimum Ornstein-Uhlenbeck. OUm = Multi-optima Ornstein-Uhlenbeck. Model adequacy scores calculated for the best supported model only. Msig = mean of squared contrasts. Cvar = coefficient of variation of the absolute value of the contrasts. Svar = Slope of a linear model fitted to the absolute value of the contrasts against their expected variances. Sasr = slope of the contrasts against the ancestral state inferred at each corresponding node. Shgt = slope of the contrasts against node depth. Dcfd = Kolmogorov-Smirnov D-statistic comparing contrasts to a normal distribution with SD equal to the root of the mean of squared contrasts.

Character	N	dAICc BM	dAICc OU1	dAICc OUm	Msig	Cvar	Svar	Sasr	Shgt	Dcfd
Haploneme elongation	21	0	0.953	713.671	0.801	0	0.038	0.156	0.362	0.098
Heteroneme shaft width µm	19	0	1.051	632.503	0.767	0.801	0.128	0.092	0.4	0.813
Cnidoband width µm	21	0	1.595	761.241	0.781	0.723	0.072	0.09	0.31	0.228
Heteroneme shaft free length µm	19	0	1.649	628.334	0.791	0.402	0.941	0.098	0.575	0.464
Heteroneme volume µm3	19	0	2.105	629.21	0.779	0.034	0.39	0.338	0.637	0.392
Haploneme width µm	21	0	2.452	766.546	0.779	0.599	0.316	0.791	0.995	0.288
Pedicle width µm	21	0	2.458	764.406	0.815	0.791	0.368	0.26	0.963	0.298
Heteroneme width µm	19	0	2.516	634.229	0.805	0.809	0.292	0.208	0.709	0.38
Tentacle width µm	22	0	2.702	383.12	0.835	0.496	0.344	0.867	0.096	0.444
Heteroneme to CB	19	0	0.127	NA	0.811	0.336	0.004	0.068	0.026	0.434
Haploneme surface area:volume	21	0	2.282	757.267	0.747	0.563	0.392	0.583	0.927	0.15
Heteroneme elongation	19	0.217	0	618.621	0.819	0.601	0.012	0.707	0.062	0.715
Total nematocyst volume	22	0.57	0	378.872	0.809	0.501	0.06	0.088	0.266	0.501
Heteroneme free length µm	19	0.746	0	627.372	0.811	0.885	0.593	0.156	0.368	0.679
Total haploneme volume	21	1.281	0	730.592	0.829	0.452	0.038	0.134	0.096	0.819
Cnidoband length µm	21	1.439	0	763.478	0.761	0.328	0.04	0.11	0.098	0.803
Cnidoband free length µm	21	2.219	0	760.518	0.843	0.35	0.012	0.066	0.05	0.911
Cnidoband coiledness	21	2.669	0	765.921	0.807	0.002	0.008	0.03	0.076	0.791
Haploneme row number	21	4.177	0	729.95	0.825	0.004	0.002	0.06	0.006	0.346
Haploneme free length µm	21	5.497	0	778.011	0.793	0.388	0.032	0	0.052	0.306
Heteroneme shaft extension	19	6.17	0	611.533	0.775	0	0.068	0.665	0.124	0.184
Rhopaloneme elongation	13	144.229	146.783	0	0.753	0.641	0.434	0.188	0.933	0.617
Desmoneme length µm	13	148.14	151.403	0	0.763	0.182	0.607	0.31	0.745	0.014
Rhopaloneme length µm	13	150.731	154.198	0	0.739	0.803	0.24	0.03	0.14	0.316
Rhopaloneme width µm	13	150.82	154.287	0	0.743	0.462	0.306	0.07	0.182	0.092
Desmoneme elongation	13	159.594	158.584	0	0.719	0.206	0.074	0.094	0.036	0.993
Desmoneme width µm	13	164.639	168.106	0	0.773	0.11	0.885	0.098	0.605	0.002
Involucrum length µm	14	148.672	151.078	0	0.779	0.126	0.17	0.25	0.418	0.671
Elastic strand width µm	15	473.984	477.156	0	0.827	0.921	0.184	0.064	0.953	0.785
Total heteroneme volume	17	619.03	619.932	0	0.797	0.803	0.078	0.172	0.35	0.697
Heteroneme number	17	620.836	620.193	0	0.777	0.39	0.008	0.074	0.056	0.054

Brownian Motion Supported

Single Optimum OU Supported

Multiple Optima OU Supported