1 Supplementary Materials

Figure 1: SIMMAP Tentilla presence/absence.

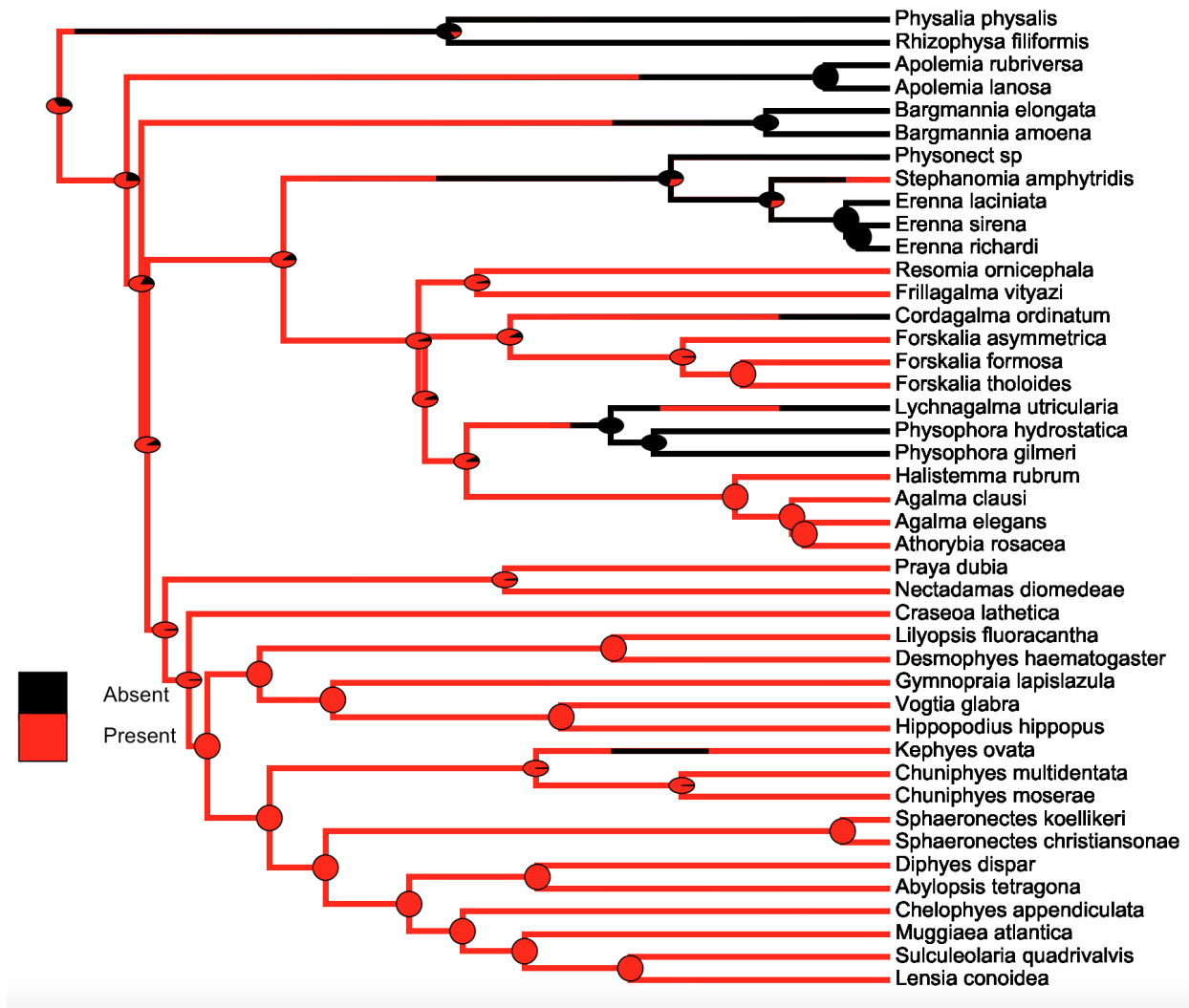Figure 2: SIMMAP Cnidoband proximal heteroneme presence/absence.

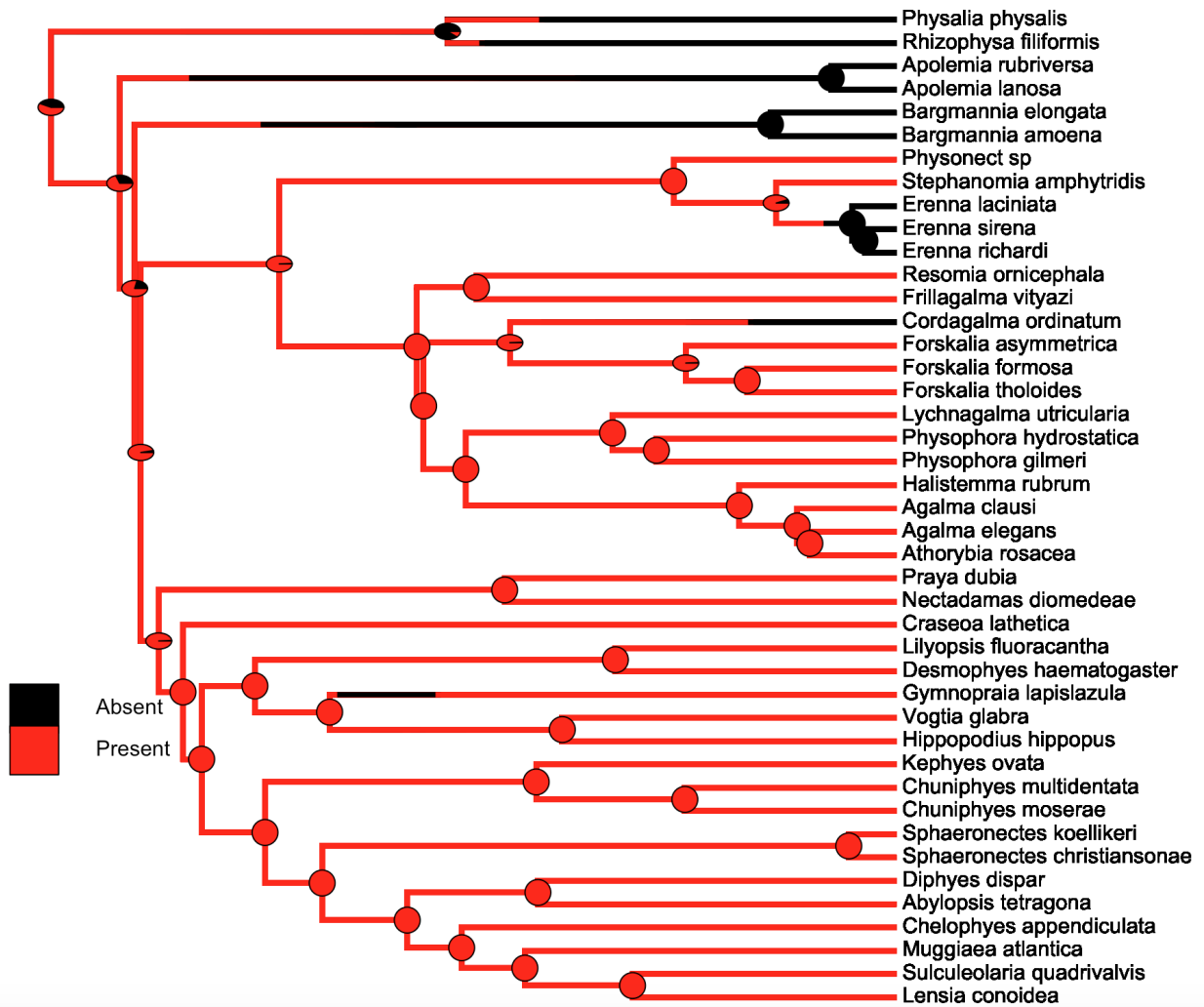Figure 3: SIMMAP Desmoneme+Rhopaloneme presence/absence.

Figure 4: SIMMAP Actively discharging cnidobands presence/absence.

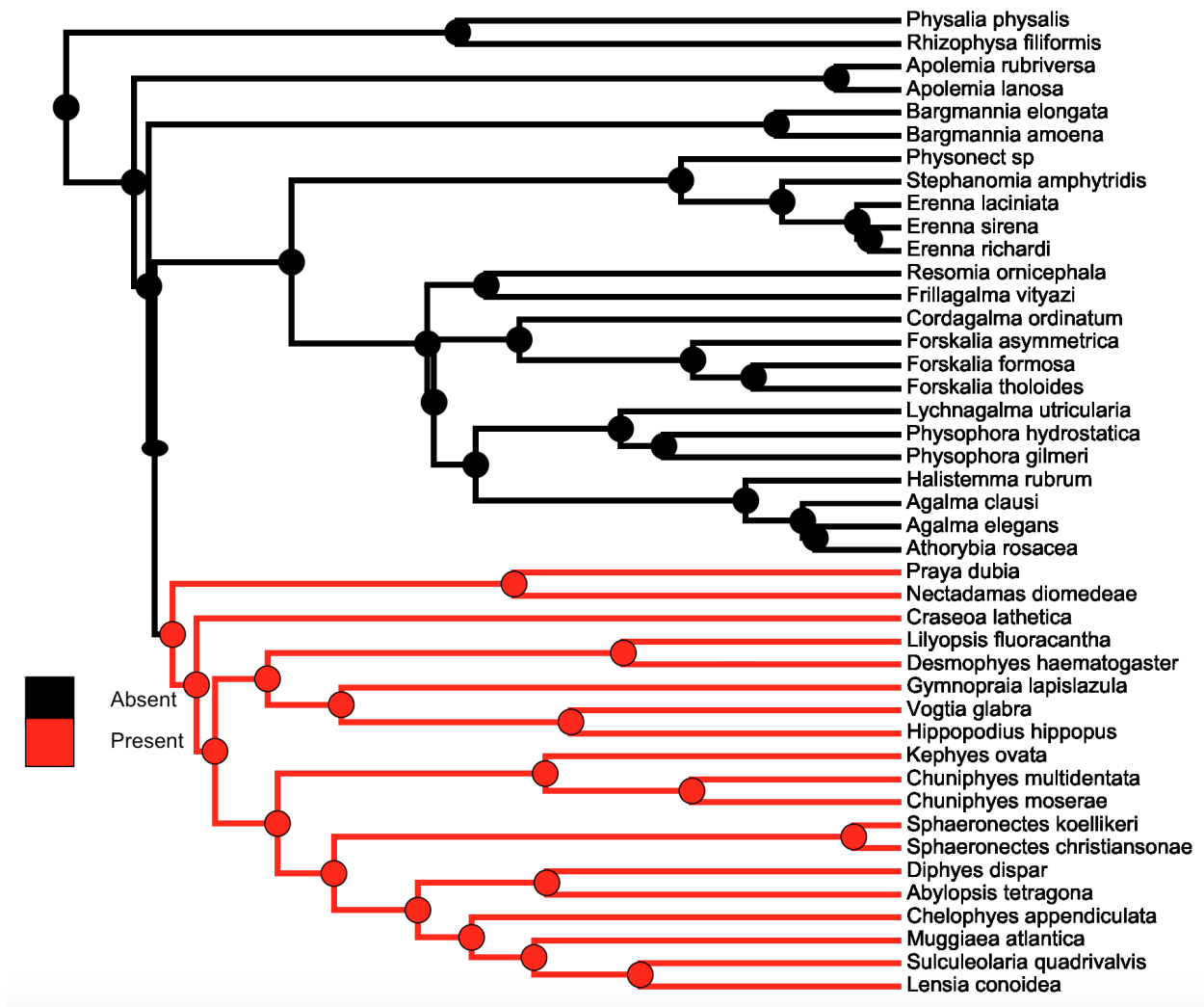Figure 5: SIMMAP Elastic strands presence/absence.

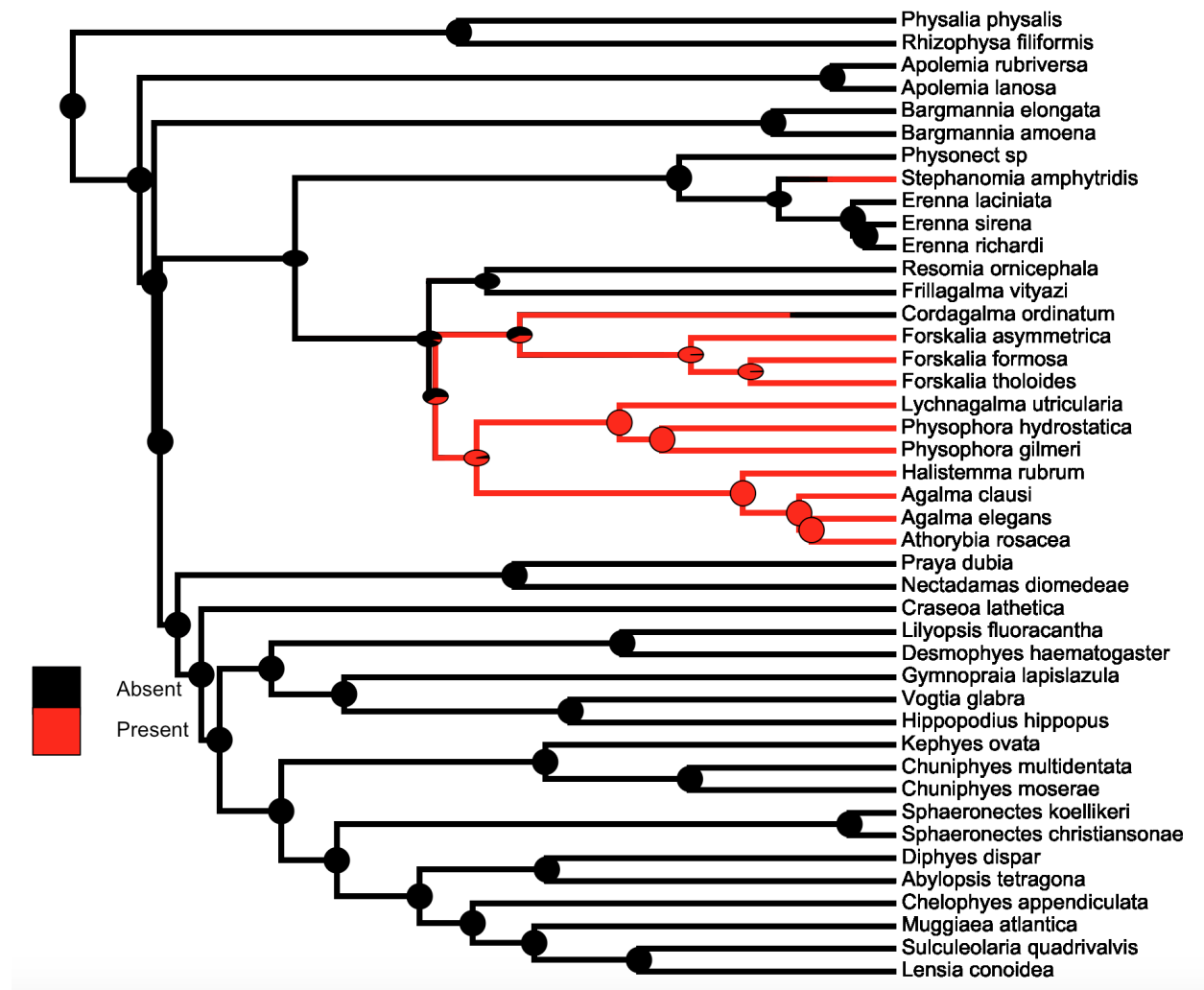Figure 6: SIMMAP Cnidoband distal desmonemes presence/absence.

Figure 7: SIMMAP Coiled cnidoaband phenotype presence/absence.

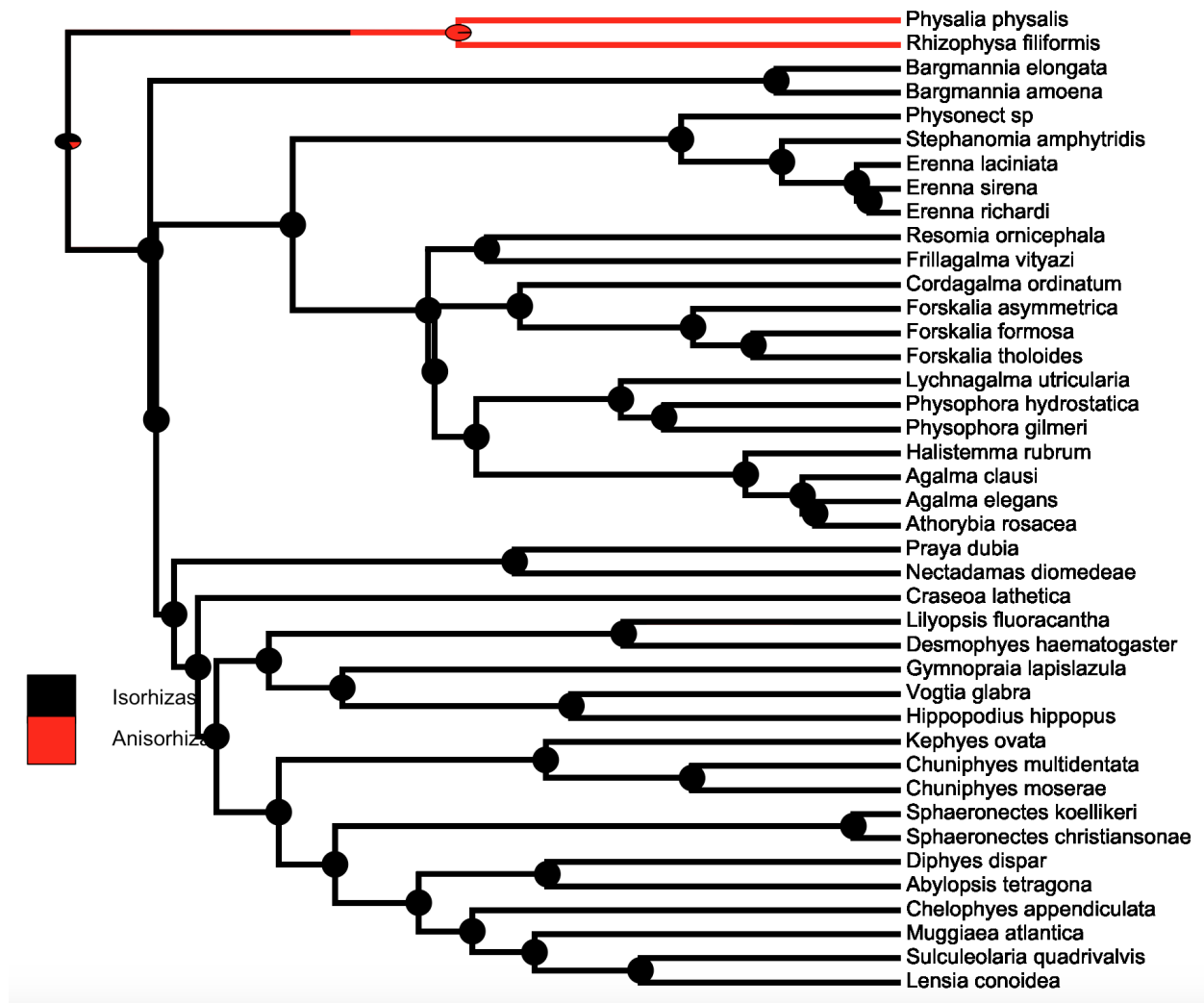Figure 8: SIMMAP Heteroneme type.

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Figure 9: SIMMAP Haploneme type.

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 (rows 1–4)

Brownian Motion model supported (rows 5–29)

Early Burst model supported (last 2 rows)

Figure 10: 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.

Variable	Best model	Msig	Cvar	Svar	Sasr	Shgt	Dcfd
Desmoneme length µm	WN	0.889	0.224	0.084	0.32	0.146	0
Heteroneme shaft extension	WN	0.861	0	0.577	0	0.533	0.042
Total heteroneme volume	WN	0.895	0.577	0.006	0.026	0.078	0.603
Rhopaloneme width µm	WN	0.823	0.42	0.182	0.014	0.531	0.006
Haploneme free length µm	EB	0.841	0.052	0.036	0.168	0.226	0.843
Heteroneme volume µm3	BM	0.855	0.731	0.228	0.897	0.775	0.104
Involucrum length µm	BM	0.839	0.01	0.018	0.116	0.09	0.987
Tentacle width µm	BM	0.817	0.841	0.402	0.386	0.785	0.48
Cnidoband coiledness	BM	0.873	0	0.028	0.016	0.144	0.41
Total haploneme volume	BM	0.807	0.228	0.004	0.006	0.024	0.398
Cnidoband free length µm	BM	0.825	0.076	0.002	0	0.006	0.681
Heteroneme free length µm	BM	0.859	0.392	0.386	0.056	0.591	0.284
Rhopaloneme elongation	BM	0.873	0.022	0.006	0.004	0.048	0.104
Desmoneme width µm	BM	0.813	0.877	0.531	0.014	0.941	0.014
Cnidoband length µm	BM	0.829	0.096	0	0	0.004	0.901
Heteroneme number	BM	0.823	0.312	0	0.004	0.02	0.869
Heteroneme shaft free length µm	BM	0.877	0.468	0.565	0.034	0.841	0.851
Rhopaloneme length µm	BM	0.829	0.525	0.547	0.01	0.917	0.08
Heteroneme/cnidoband length	BM	0.839	0.01	0	0.004	0.008	0.715
Cnidoband width µm	BM	0.907	0.977	0	0.002	0.01	0.11
Pedicle width µm	BM	0.817	0.931	0.476	0.088	0.969	0.813
Haploneme width µm	BM	0.881	0.805	0.12	0.294	0.511	0.15
Heteroneme width µm	BM	0.849	0.142	0.156	0.356	0.819	0.278
Heteroneme elongation	BM	0.933	0.094	0.07	0.681	0.791	0.777
Haploneme row number	BM	0.863	0	0.002	0.004	0.008	0.012

Figure 11: Model adequacy scores for the best model supported for each morphological character. 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 = Kolmolgorov-Smirnov D-statistic comparing contrasts to a normal distribution with SD equal to the root of the mean of squared contrasts.
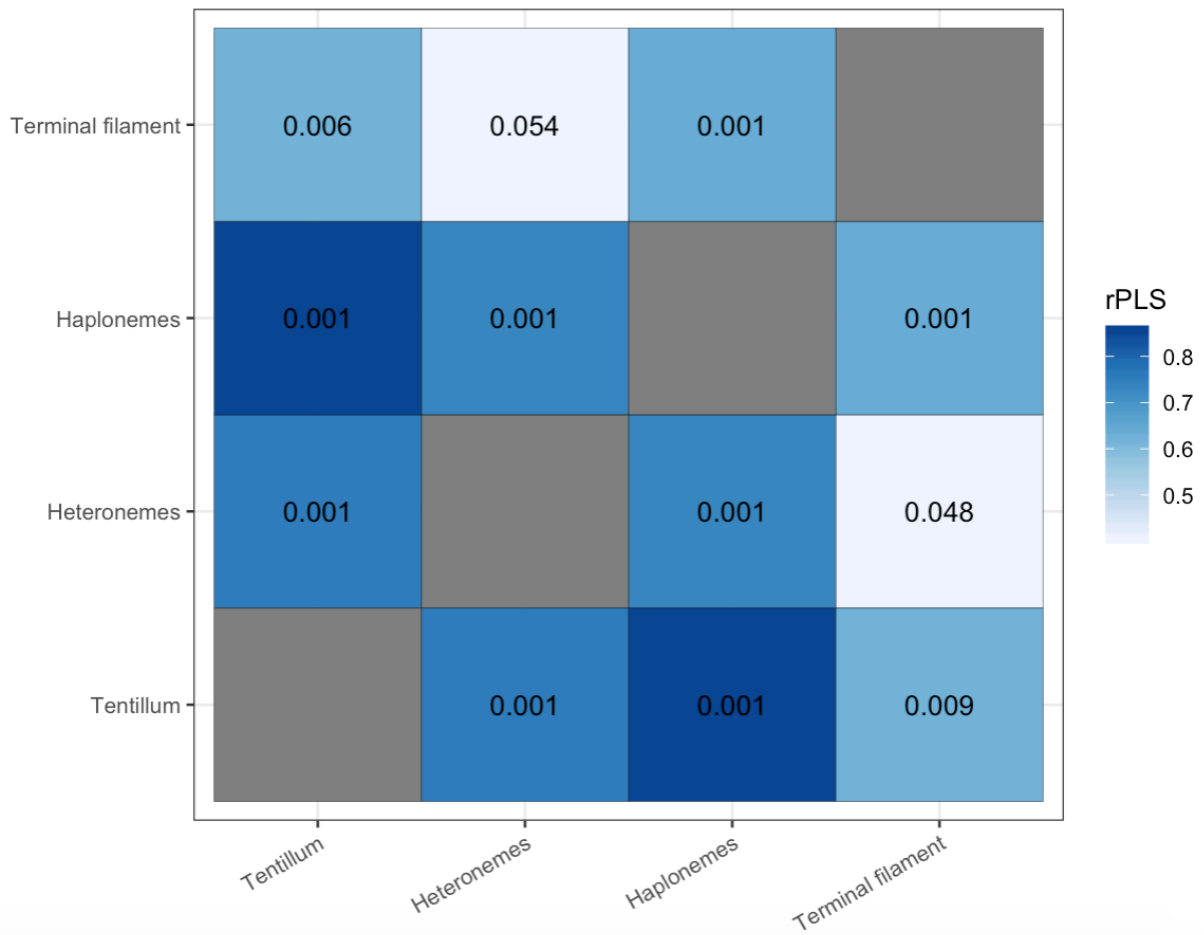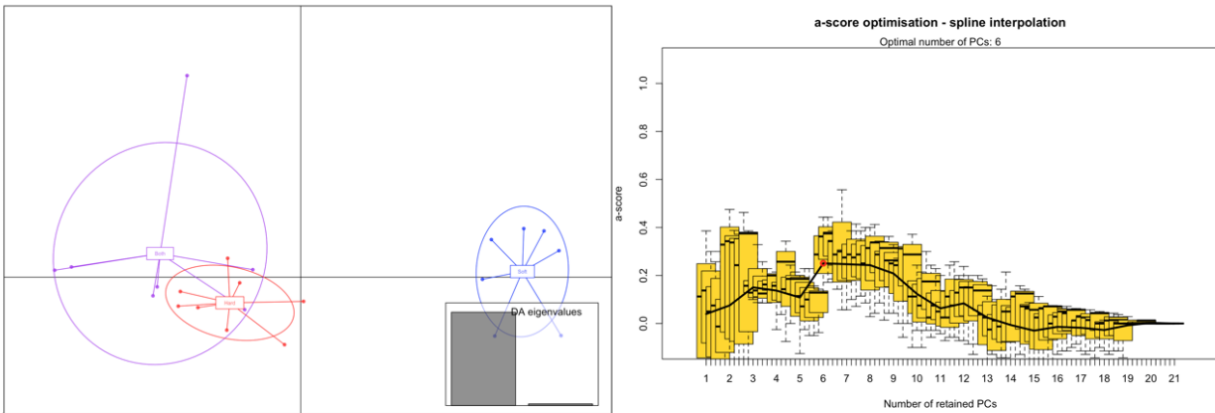
Figure 12: Heatmap showing the phenotypic integration between character modules accounting for phylogeny. Text in cells shows p-values. Color indicates the partial least squares (PLS) multivariate correlation coefficients.

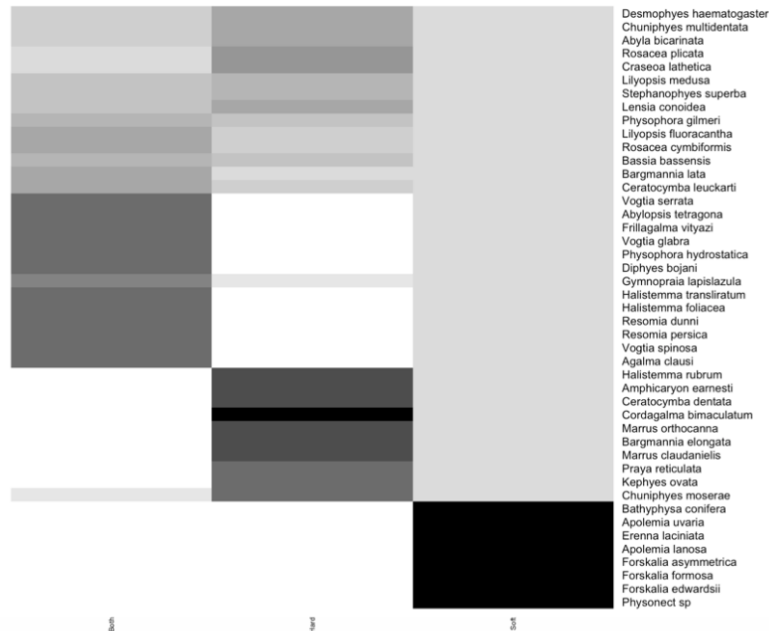| Variable contribution	
Involucrum.length..um.	24.425696
Heteroneme.number	18.129947
Heteroneme.volume..um3.	6.849738
Tentacle.width..um.	6.587487
Total_nematocyst_volume	5.606488
total_haploneme_volume	4.185115
Elastic.strand.width..um.	3.584917
Heteroneme.free.length..um.	3.014292

Figure 13: DAPC for soft-bodied vs. hard bodied prey specialization. Six PCs retained after a-score optimization (100 iterations). Two LDA functions used. Discriminant power on training set: 90.9%. Grayscale heat map shows the posterior probability distribution of the predictions. Variable contribution (top quartile) calculated by the sum of the LDA variable loadings weighted by the eigenvalue of each LDA.