17) Logistic regressions between continuous morphological characters and prey type presences. Ntaxa = number of taxa used in the analyses after removing taxa with missing diet data and inapplicable character states. phyloGLM = Phylogenetic generalized logistic regression model. GLM = Generalized logistic regression model. P = p-value. b = slope. Only cases with significant GLM fits were retained. Cells colored blue indicate phyloGLM p-value < 0.05. Cells colored green indicate GLM p-value < 0.05

Character	Prey type	Ntaxa	phyloGLM AIC	phyloGLM P	phyloglm b	GLM AIC	GLM P	GLM b
Cnidoband coiledness	Decapod diet	21	23.701	0.029	2.327	21.762	0.016	3.227
Haploneme surface area:volume	Copepod diet	21	19.143	0.017	3.246	17.355	0.017	4.631
Haploneme width μm	Copepod diet	21	18.844	0.017	-3.098	16.997	0.019	-4.417
Pedicle width μm	Copepod diet	21	22.182	0.032	-1.16	23.723	0.024	-1.437
Tentacle width μm	Copepod diet	22	22.038	0.026	-1.543	23.634	0.025	-1.505
Cnidoband length μm	Copepod diet	21	23.431	0.042	-0.864	24.178	0.025	-1.131
Cnidoband width μm	Copepod diet	21	22.887	0.035	-1.545	23.658	0.027	-1.89
Heteroneme number	Copepod diet	17	20.52	0.059	-0.718	19.615	0.03	-0.973
Total haploneme volume	Copepod diet	21	23.507	0.03	-0.581	25.232	0.031	-0.578
Total heteroneme volume	Copepod diet	17	17.156	0.032	-0.533	16.369	0.031	-0.758
Pedicle width μm	Ostracod diet	21	17.523	0.041	-1.43	15.165	0.035	-1.97
Heteroneme shaft free length μm	Copepod diet	19	23.955	0.076	-1.53	23.378	0.04	-2.16
Haploneme width μm	Fish diet	21	28.118	0.091	1.268	27.551	0.043	1.642
Tentacle width μm	Fish diet	22	28.927	0.058	0.804	28.771	0.044	0.874
Haploneme surface area:volume	Fish diet	21	28.258	0.098	-1.329	27.596	0.044	-1.768
Total haploneme volume	Ostracod diet	21	20.028	0.043	-0.619	17.733	0.046	-0.681
Heteroneme volume μm3	Copepod diet	19	24.282	0.091	-0.521	24.297	0.046	-0.72
Pedicle width μm	Fish diet	21	28.21	0.074	0.815	27.839	0.049	0.918