SUPPORTING INFORMATION

A Proposed Timescale for the Evolution of Armophorean Ciliates: Clevelandellids Diversify More Rapidly Than Metopids by Peter Vďačný, Ľubomír Rajter, Thorsten Stoeck & Wilhelm Foissner

Table S1. Number of species described in the class Armophorea and proportion of the taxa sampled.

Table S2. Characters, character states and their coding used for ancestral state reconstruction.

Table S3. Parametrization and fitting of constant-rate diversification models to the phylogeny of metopids and clevelandellids.

Table S4. Pagel's test of correlated character evolution performed on the BEAST maximum credibility tree.

Table S1. Number of species described in the class Armophorea and proportion of the taxa sampled.

Family	Total No. of taxa	No. of taxa sampled	Proportion of taxa sampled[a]	Reference[b]
Caenomorphidae	13	2	15%	Kahl (1932)
Metopidae	81	23	28%	Kahl (1932), Biggar and Wenrich (1932), Villeneuve-Brachon (1940), Jankowski (1964a, b), Dragesco (1968), Esteban et al. (1995), Foissner (2016a, b), Omar et al. (2017), Vďačný and Foissner (2017a, b)
Nyctotheridae	186	10	5%	Earl (1972), Albaret (1972, 1973), Lalpotu (1980a, b, c), Shete (1982a, b), Affa'a (1986, 1991), Galavíz-Silva and Jiménez-Guzmán (1986), Kalavati et al. (1991), Grim (1992), Li et al. (1998), Senler and Yildiz (2000), Grim et al. (2002), Li et al. (2002), Xiao et al. (2002), Fokam et al. (2013, 2014)
Clevelandellidae	11	4	35%	Kidder (1937), Uttangi and Desai (1963), Mandal and Nair (1974)

[a] Taking into account the 20% synonymy rate in ciliates (Foissner et al. 2008) and the proportion of undescribed and cryptic species in armophoreans, we consider the proportion of sampled taxa as a reasonable estimate for diversification analyses.

[b] Kahl (1932) summarized all described free-living metopids known at that time, while Earl (1972) summarized all described endosymbiotic nyctotherids and clevelandellids known at that time.

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Table S2. Characters, character states and their coding used for ancestral state reconstruction.

Taxon	LS[a]	PM[b]	PS[c]	Taxon	LS[a]	PM[b]	PS[c]
Atopospira galeata	0	1	0	*Nyctotheroides hubeiensis*	1	1	1
Atopospira violacea	0	1	0	*Nyctotheroides parvus*	1	1	1
Brachonella contorta	0	0	0	*Nyctotheroides pyriformis*	1	1	1
Caenomorpha medusula	0	1	0	*Nyctotheroides* sp. AF147882	1	1	1
Caenomorpha uniserialis	0	1	0	*Nyctotherus cordiformis*	1	1	1
Clevelandella constricta	1	1	1	*Nyctotherus ovalis*	1	1	1
Clevelandella nipponensis	1	1	1	*Nyctotherus* sp1. KC139720	1	1	1
Clevelandella panesthiae	1	1	1	*Nyctotherus* sp2. KC139721	1	1	1
Clevelandella parapanesthiae	1	1	1	*Nyctotherus velox*	1	1	1
Metopus es	0	0	0	*Palmarella lata*	0	0	0
Metopus fuscus	0	0	0	*Parametopidium circumlabens*	1	1	0
Metopus hasei	0	0	0	*Urostomides bacillatus*	0	0	0
Metopus laminarius	0	0	0	*Urostomides caducus*	0	0	0
Metopus minor	0	0	0	*Urostomides campanula*	0	0	0
Metopus palaeformis	0	0	0	*Urostomides darwini*	0	0	0
Metopus setosus	0	0	0	*Urostomides denarius*	0	0	0
Metopus sp.	0	0	0	*Urostomides pullus*	0	0	0
Metopus yantaiensis	0	0	0	*Urostomides striatus*	0	0	0
Nyctotheroides deslierresae	1	1	1				

[a] Lifestyle (LS): free-living coded 0, endosymbiotic coded 1.

[b] Paroral membrane (PM): single-rowed coded 0, double-rowed coded 1.

[c] Perizonal stripe (PS): present coded 0, absent coded 1.

Table S3. Parametrization and fitting of constant-rate diversification models to the phylogeny of metopids and clevelandellids.

Model	Group	logLik[a]	BF[b]	λ	μ	R	ε
Pure-birth	Armophorea	–285.15		0.0168 [0.0058, 0.0283]	–	0.0168 [0.0058, 0.0283]	–
Birth-death	Armophorea	–273.82	22.66	0.0589 [0.0165, 0.1101]	0.0499 [0.0070, 0.1020]	0.0090 [0.0012, 0.0181]	0.8204 [0.5686, 0.9871]
Group-specific rates under the birth-death model							
	Metopida			0.0207 [0.0050, 0.0421]	0.0127 [6.2e–7, 0.0337]	0.0080 [0.0014, 0.0158]	0.5492 [0.0772, 0.9295]
	Clevelandellida			0.1351 [0.0218, 0.3412]	0.1069 [1.5e–5, 0.3145]	0.0282 [0.0055, 0.0518]	0.6738 [0.1576, 0.9909]

Tabulated are mean rates of speciation (λ) and extinction (μ) as well as net diversification rate (r) and extinction fraction (ε) estimated over 100 trees from the posterior distribution of the BEAST analysis. Square brackets represent the 95% credibility interval.

[a]logLik: log likelihoods are marginal likelihoods estimated across the sample of 100 trees in BayesRate using thermodynamic integration.

[b]BF: BayesFactor is expressed relative to the model of highest marginal likelihood. BF = $2(\log Lik_1 - \log Lik_2)$. The higher BayesFactor, the stronger the support for the best model. BF > 10 is interpreted as very strong support.

Table S4. Pagel's test of correlated character evolution performed on the BEAST maximum credibility tree.

Character evolution	$\ln Lik_4$	$\ln Lik_8$	$\Delta \ln Lik$	χ^2	*p*
Lifestyle vs. Paroral membrane	–23.9665	–17.2328	6.73	13.46	< 0.001
Lifestyle vs. Perizonal stripe	–15.4970	–8.9853	6.51	13.02	< 0.001
Perizonal stripe vs. Paroral membrane	–19.8839	–15.6179	4.26	8.52	0.01

$\ln Lik_4$: log likelihood of four parameter model without correlation, $\ln Lik_8$: log likelihood of eight parameter model with correlation, $\Delta \ln Lik$: difference in log likelihoods of four and eight parameter models, χ^2: chi–square, *p*: probability.