Vampires in the oceans: predatory cercozoan amoebae in marine habitats.

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List of all Supplementary Files and Tables and Legends to the Supplementary Figures

Supplementary File 1

Provides detailed information about the *BioMarKs* sampling sites, DNA and RNA extraction, and PCR amplification protocols, the bioinformatic curation of the resulting sequence data, the procedure we used to identify the 2766 vampyrellid reads in these data, and our stringent clustering approach to reduce these 2766 reads to 461 vampyrellid SSU-types.

Supplementary File 2

Provides the 461 vampyrellid SSU-types obtained after clustering of the 2766 vampyrellid reads we identified in the *BioMarKs* V4 sequence data (in fasta format).

Supplementary Table S1

Primers used in this study.

Supplementary Table S2

List of the 62 vampyrellid SSU rDNA environmental clones identified in the GenBank database.

Supplementary Table S3

List of the chimeric environmental clone sequences detected in this study.

Supplementary Table S4

List of the 461 sequence clusters ("SSU-types") from the BioMarKs data.
Sequences are grouped according to the higher-level lineages defined in Figures 4 and 5. The sequence reads belonging to each cluster are listed (after dereplication, see Suppl. File 1), with the samples they originated from (the sampling IDs refer to the list provided in Suppl. Table S5). Numbers after the underscore in the sequence labels indicate how many exactly identical reads were present in that same sample, adding up to the total of 2766 reads that are available as a sequence read archive in the European Nucleotide Archive (project accession number PRJEB1843).

Supplementary Table S5

List of the samples containing vampyrellid V4 sequences in the *BioMarKs* data.

Supplementary Figure S1

Graphical representation of the diversity of *BioMarKs* SSU-types belonging to the two most diverse vampyrellid lineages, highlighting their habitat preferences. As for Figure 5, a maximum likelihood tree is used, based on the V4 region of the SSU rDNA. (**A**) Subclade T, containing *Thalassomyxa* sp. (**B**) Subclade P, containing *Penardia* sp. Sequence labels and ecological provenance of the sequences follow the conventions used in Figure 5.

Supplementary Figure S2

Maximum likelihood tree highlighting the fact that the depth of SSU rDNA diversity observed within the order Vampyrellida matches that of the whole of the kingdom Fungi. The dataset used for this figure was analysed using the RaxML BlackBox (v. 7.3.1) hosted on the Cipres Science Gateway (www.phylo.org/portal2/).