

Exploring the role of copepods as hosts of ascetosporean parasites using PCR probing and metagenomics

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Class Ascetosporea (Rhizaria; Endomyxa) comprises many parasites of invertebrates. Group-specific environmental DNA (eDNA) studies of ascetosporean orders have contributed to the establishment of the new order Mikrocytida, a new phylogeny and characterisation of Paramyxida, and illuminated the diversity and distribution of Haplosporida. Little is known about the lifecycles of ascetosporean parasites, though transmission experiments between hosts suggest many species may have complex lifecycles involving at least one alternative host. The abundance of haplosporidian sequence types in environmental samples may implicate planktonic metazoans such as copepods as potential hosts, and oyster parasite *Marteilia refringens* has been observed infecting copepods in areas where the disease is endemic. Most recently, general and lineage-specific PCR approaches have revealed significant diversity in the phylogenetic “gap” between Haplosporida and their closest known free-living relatives, the testate amoeba *Gromia* and the reticulate amoeba *Filoreta*. Within this gap is a robustly supported radiation of parasites, ENDO-3 comprised of *Paradinium* spp. parasites of copepods, and three further uncharacterised clades (ENDO-3a, ENDO-3b, SPP). In this study, we use lineage-specific PCR and metagenomic approaches to screen planktonic copepods collected from littoral, coastal and deep-sea sites for ascetosporean diversity. We also identify a novel haplosporidian parasite infecting copepods parasitising mussels *Mytilus edulis* in the Tamar estuary, UK.