

Phylogenetic position and description of a novel unicellular holozoan parasite isolated from the amphipod *Echinogammarus marinus*

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We developed a workflow to generate high genome sequencing coverage of a novel holozoan parasite of the amphipod *Echinogammarus marinus* from a low-complexity eukaryotic metagenomic dataset. Phylogenomic analyses show the parasite to be an early-diverging filasterean – the first truly parasitic member of this group. So far it has only been detected in only two amphipod host species, sampled from the southern coast of England. It was not detected, even when using highly specific PCR primers, in proximally sampled environmental samples or those from similar habitats. The parasite peaks in prevalence in May and has not been detected at other times of the year. Infections are most prominent in the gonads, and appear to subsequently infect surrounding connective tissue and the haemolymph, via which it reaches other parts of the body. The parasite is variable in size (c. 1-7 µm), with uni- and trinucleate cells. TEM analyses show that the cells have mitochondria and distinctive electro-dense bodies of variable size.