

Coevolutionary dynamics of cymothoid isopods and their fish hosts

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The study of co-evolution between parasites and their hosts is a powerful approach for investigating a range of fundamental evolutionary patterns and processes, including diversification, specialisation, and whether particular evolutionary changes are irreversible. One of the single most extraordinary examples of host-parasite co-evolution is shown by cymothoid isopods, a highly diverse family (~400 species) which are all obligate parasites of fish - including many commercially important species. Superficially at least, within the suborder Cymothoidea, cymothoids represent the extreme of a continuum of 'trophic dependency' from free-living scavengers and predators, through temporary to obligatory parasitism. As parasites on highly labile hosts, Cymothoids have evolved striking parasitic strategies. Some species, for example, gruesomely supplant their host's tongues; the only natural example of functional, anatomical replacement by another organism. Other parasitic modes include external attachment to the dermis, within the opercular cavity, invagination within the body.

Due to their bizarre life-histories, large size relative to their hosts, and their economic impacts in fisheries and aquaculture, cymothoids have been studied for over a century and mostly using traditional taxonomical approaches. However, compared with their free-living relatives, evolution of morphological innovation in cymothoids has been largely constrained by their parasitic lifestyle. Early taxonomic work, for example, prioritised variable or inconsistent features with an emphasis on body shape - a convergent character influenced by location on the host: *Mothocya ihi* resembles other buccal-inhabiting species but is actually placed within a genus of mainly gill attaching species. Host species have also been important for classification of cymothoids due their seemingly high specificity but host range for most species remains unknown. Thus, intraspecific morphological variation in cymothoids is easily confounded with interspecific differences which obfuscate evolutionary relationships, makes identification problematic, and species boundaries unclear. Without a clear phylogenetic

The objective for this project is to establish the relationships within Cymothoidea and to apply this phylogenetic framework to answer whether cymothoids and their hosts have cospeciated, whether different parasitic modes have evolved 'progressively', and examine host specificity. Our approach sits at the interface between the historical and modern themes of this symposium, where we have used high-throughput DNA sequencing of museum specimens up to 100 years old, using novel ancient DNA techniques. This has allowed us to sample more broadly than traditional methods both taxonomically and biogeographically. We have recovered full, or nearly-complete mitogenomes, and high copy number loci for over forty cymothoid species from across the world, representing the different parasitic strategies and range of habitats including deep sea and riverine. Furthermore, for some species, we have also recovered the mitogenomes of the cymothoid host - some previously not sequenced - allowing us to confirm host identities. Additionally, geometric morphometrics have allowed us to quantify patterns of shape variation in important morphological traits and show that both ecology and phylogeny are influential. These data are important for understanding the evolutionary dynamics marine host-parasite systems, and identify novel hosts as climate induced range shifts introduce cymothoids to new environments.

Keywords: coevolution; ancient DNA; parasites