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EVOLUTIONARY TRAJECTORIES OF THE REPRODUCTIVE SYSTEM OF THE GASTROTRICH GENUS *URODASYIS* (MACRODASYIDA, GASTROTRICHA) INFERRED FROM MORPHOLOGICAL AND MOLECULAR DATA

Macrodasyidan gastrotrichs are mostly hermaphrodites with complex accessory reproductive organs whose organization remains in most circumstances constant within individual genera. *Urodasyis* is a special case because it includes members presenting a range of different reproductive system organizations. With 16 known species, the genus includes individuals with (i) paired ovaries, which belong to exclusively parthenogenetic species, (ii) paired ovaries and paired testes but no accessory sex organs, (iii) paired ovaries, a single testis, and a copulatory organ furnished with a cuticularized stylet, or (iv) according to recent findings, individuals with two ovaries, the one stylet but two testes. Molecular data are still limited in this genus, as only partial rDNA 18S sequence data are currently available for only six species, and mtCOI sequence data for only three species, which is an obstacle to understanding the true evolutionary history of the group.

We used an integrative approach comprising detailed morphology and expanded rDNA 18S gene datasets to calculate evolutionary relationships among members of the genus, using Maximum Parsimony, Maximum Likelihood and Bayesian methods to investigate the evolutionary pathways of reproductive system development and adaptations in this group of organisms.

The most supported topology was based on molecular traits and obtained by ML and Bayesian approaches, which produced trees showing two robustly supported clades: Clade I that is grouping “two testes no stylet” and “two testes with stylet” taxa and Clade II that is grouping the “one testis, stylet-bearing” and “parthenogenetic” taxa. This relationship is in contradiction with the results of the molecular MP tree, which is weakly supported and of the MP tree based on morphological characters, where stylet-bearing taxa form a separate clade, calling for further expanded taxonomic and molecular sampling.

We will discuss the possible scenarios for trait gain and loss in the evolution of the reproductive system of these organisms and bridge the gap between their molecular and morphological data sets.