PhD Course in "Models and Methods for Material and Environmental Sciences" – XVIII Cycle

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"Multi-gene phylogeny for a new approach to Gastrotrich taxonomy"

ABSTRACT:

This project aims to investigate the biodiversity and phylogeny of the phylum Gastrotricha using a combination of classical morphological techniques and phylogenetic analysis based on the commonly used molecular markers, implemented by the state of the art genomics and bioinformatics to provide complete mitochondrial genome sequences useful for the task.
Gastrotrichs are meiobenthic invertebrates, among the least studied representatives of the meiofauna; they constitute a highly diverse phylum, and their taxonomy has often been debated [1]. They also include many cosmopolitan species while being very poor at dispersing. In this framework, gastrotrichs are a good example of the puzzling "Meiofaunal paradox" [2].
So far, molecular phylogenetic studies, mainly based on the sequence of the 18S ribosomal unit (18S rDNA gene), have shown the limits of the traditional morphological taxonomy [3]. Still, they, too, have often failed to produce sufficiently robust phylogenetic trees, mainly because they are based on a single gene sequence. The necessity of improving gene sampling to increase the phylogenetic signal embedded in the molecular traits is now apparent. The 28S rDNA, Cox1, and Histon genes are all established markers in phylogenetic studies and can simultaneously be used in conjunction with the 18S rDNA gene to solve evolutionary issues within Gastrotricha at a relatively low cost [4]. The mitochondrial genome (mtDNA) is a promising new source of information. Recent technological developments have cut the costs linked to its sequencing, and mitophylogeny is rapidly gaining popularity since it allows the use/comparison of multiple genes [4]. During my doctorate, I plan to acquire experience in obtaining mitogenome sequences and the bioinformatics skills necessary to analyze them. This project also aims to contribute to international genome databases to facilitate worldwide studies on the phylum.
Phylogenetic analyses will be carried out with a cost-effective, scalable approach, i.e., first using the single nuclear and mitochondrial genes (alone or combined) and if results are inconclusive then using the whole mitochondrial genome. Nucleotide sequences will be aligned using software such as Muscle or Clustal X, while phylogenetic trees will be obtained using the Maximum Parsimony, Maximum Likelihood, and Bayesian Inference methods.
By applying these techniques and building up from work conducted during my master's thesis, I will investigate several lines of research on select taxa to solve the deep phylogenetic and biogeographical issues of Gastrotricha.

Literature cited
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