

POSTER

Sea-worms a new research avenue: A preliminary assessment using morphological and molecular markers

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During the past few years, efforts have been made to understand the deeper relationships within the Annelida phylum. Despite, marine polychaetes are responsible for the diversification of this phylum, the establishment of a stable phylogenetic representation still remains a controversial issue. Polychaetes worms classified as one of the best indicators of marine pollution are subjected to extensive research for medical applications. Morphological and molecular tools were used to determine the diversity of marine worms in Mauritius. A total of fifteen marine worms were collected, belonging to three different phyla, Annelida (Polychaetes), Nemertea and Echiura. A phenetic analysis based on morphological markers separated the species into two major clusters. Group 1 contained all the segmented worms while the unsegmented worms were clustered into Group 2. Genetic variation was investigated among the marine species using a total of 23 arbitrary primers. Of these, IRAP-4, IRAP-5, URP 2F, OPAS 13, OPAS 14 and GEN 2 showed 100% polymorphism. Moreover, the efficiency of the mitochondrial gene, Cytochrome Oxidase Subunit 1 (CO1) was assessed and successfully amplified for 12 marine sea-worms. DNA sequencing further revealed the presence of nine new marine worms in Mauritius. A phylogenetic analysis was conducted based on 18 sequences of mitochondrial genomes including the unpublished sequences of the nine marine worms. The data was processed using maximum parsimony and pair-wise distance methods and clade robustness was strengthened by bootstrapping at 1000 replicates. This resulted in paraphyletic clades between marine worms with strong support to a close relationship between Echiura and Syllidae. In conclusion, molecular tools have, once more, evolved as a more reliable and fast technique to deal with taxonomic classification of marine worms in Mauritius. However, the phylogeny of polychaetes needs to be revised with a greater taxon sampling and more studies are yet to be carried out