IDENTIFICATION OF MARINE NEMATODE COMMUNITIES THROUGH DNA BARCODING: DO MITOCHONDRIAL COI SEQUENCES OUTPERFORM THE RIBOSOMAL 18S GENE? (Ît oral)

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Free-living nematodes are the most abundant metazoan organisms in marine sediments. They are important in many ecological processes and are used as bioindicators. Yet, they remain the least described taxon, because morphological diagnostic features are difficult to observe due to their small body size. DNA barcoding may overcome the problems associated with morphology and may lead to a guicker identification of marine nematodes. The nuclear ribosomal 18S gene has been the preferred locus for barcoding nematodes because it is easily amplified throughout the phylum. This fragment lacks however resolution at the species level. In contrast, only few studies have addressed the applicability of the mitochondrial COI gene for nematode identification. In this study, the amplification and sequencing success of both gene fragments were compared in a wide range of marine nematodes. We used 73 species belonging to 56 genera that were sampled from Paulina Polder (the Netherlands). Our results demonstrate that 18S is more easily amplified in marine nematodes compared to COI (57% vs 43% amplification success). The production of aspecific bands was more common in 18S than in COI, but sequencing success remained higher for 18S than for COI (61% vs 39%). Neighbor joining analysis using the K2P-model showed that both genetic markers cluster into well defined clades congruent with known taxonomic families and orders that have been delineated based on morphology. Pairwise genetic distance for the 18S sequences showed that $\approx 74\%$ of intraspecific comparisons showed a genetic divergence <3% while about 77% of interspecific comparisons were above 3%. For COI sequences, 98% of intraspecific comparisons showed a genetic divergence of ≤8% and >8% was observed for about 94% of all interspecific comparisons. This study shows that COI sequences qualitatively outperforms the 18S gene in the delineation of marine nematode species.