



Figure S1. Phylogenetic reconstructions using the sequences of one nuclear marker (a) ITS-rDNA, and two mitochondrial markers (b) 16S-rDNA, and (c) COI-mtDNA (cytochrome c oxidase I). Values on branches represent bootstrap support > 50 from maximum likelihood analyses and black circles indicate Bayesian posterior probabilities > 95%. Note the clear monophyly formed by all sequences from *P. atlanticus* sp. n. in the phylogenetic reconstructions of ITS-rDNA and COI-mtDNA. Trees branches are presented as cladograms to facilitate the visualization of the species and clade relationships. CU53 = NSMT-Co 1706; CU54 = NSMT-Co 1707; CU60 = MISE JDR170613-10-60; CU61 = MISE JDR170613-10-61; CU76 = MISE JDR170616-13-76; CU2BH = RMNH.COEL.42433; CU6 = MISE JDR170609-2-6; CU32 = MISE JDR170610-4-32; CU94 = MISE JDR170619-20-94.