

# Molecular data support *Pharyngocirrus gabriellae* (Saccocirridae: Annelida) as an ampho-Atlantic and ampho-American species

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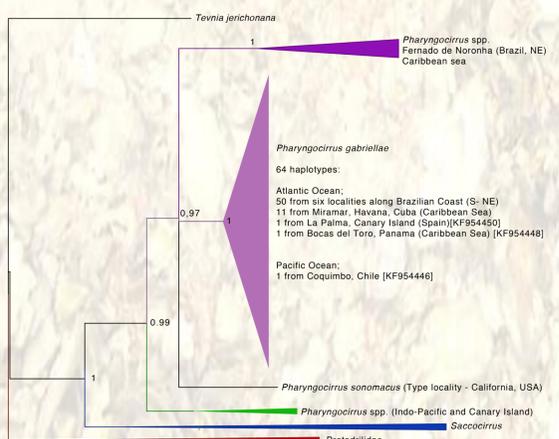
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The interstitial saccocirrid *Pharyngocirrus gabriellae* (Du Bois-Reymond Marcus, 1946), originally described from southeastern Brazil, has been reported from worldwide shallow waters. This reported distribution pattern could be masking a complex of cryptic species or in fact correspond to a single widespread species due to geological and oceanographic processes.

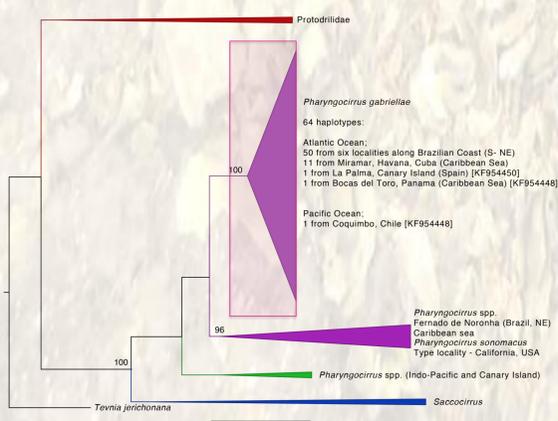


Anterior end and chaetae of *Pharyngocirrus gabriellae*

To assess these two explanatory hypotheses, we inferred the relationships among 95 terminals (5 species of Protodrilidae and 16 species of *Saccocirrus* as outgroups, and 74 specimens attributed to *Pharyngocirrus* and collected from worldwide locations) through maximum-likelihood and Bayesian methods and species delimitation analyses (ABGD, GMYC and PTP), using 16S rRNA sequencing.



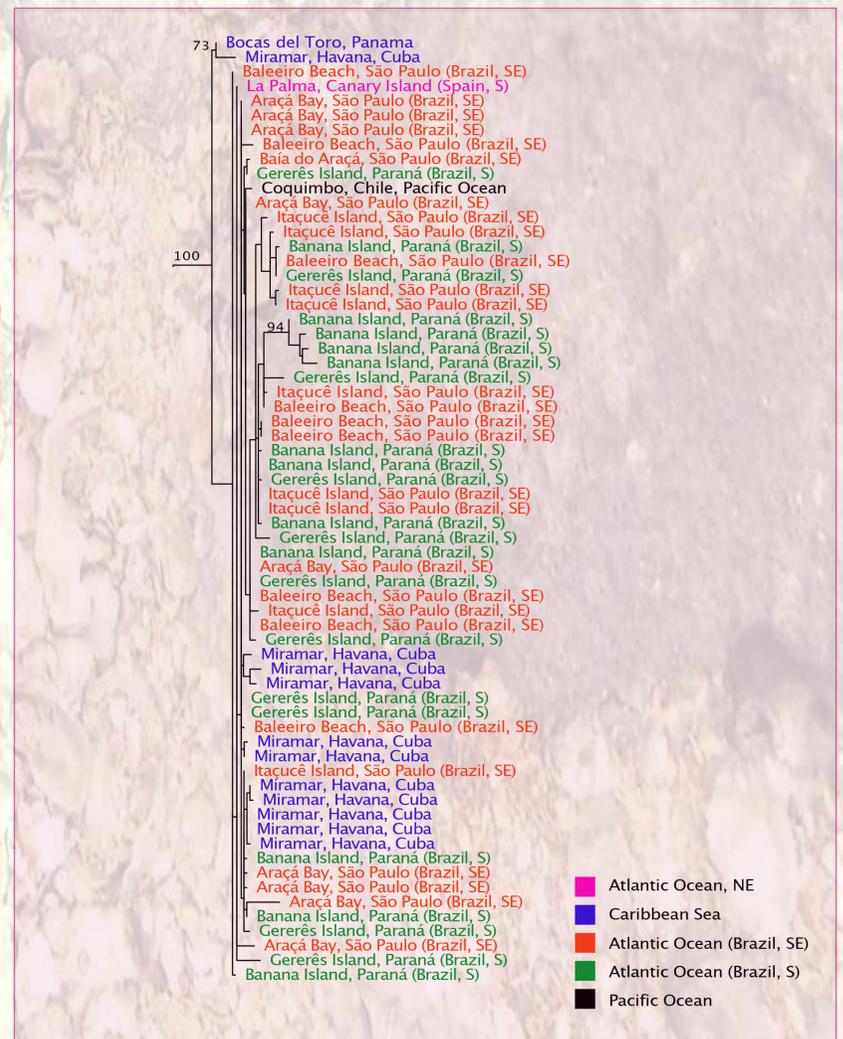
Phylogenetic relationships of Saccocirridae. Tree from the Bayesian analysis. Bayesian posterior probabilities with 16S rRNA data



Phylogenetic relationships of Saccocirridae. Maximum likelihood best tree. Maximum likelihood bootstrap (MLB) with 16S rRNA data

Both analyses resulted in a clade with 64 specimens referred to *Pharyngocirrus gabriellae*, including ampho-Atlantic and ampho-American populations (Chile, Brazil, Cuba, Panama, and Canary Islands). Surprisingly, individuals from each of these populations were not recovered as monophyletic groups but intermixed, and their sequences differed only from 0 to 14 based pairs.

In addition, our analyses revealed that the 16S sequences of *Pharyngocirrus sonomacrus* (KF954446), *Pharyngocirrus* sp. 3 (KF954448, from Panama) and *Pharyngocirrus* sp. 4 (KF954450, from Canary Islands) deposited in Genbank, match with sequences of *P. gabriellae*.



Phylogenetic relationships of *Pharyngocirrus gabriellae*. Maximum likelihood best tree. Maximum likelihood bootstrap (MLB) with 16S rRNA data

Our results highlight that at least some interstitial taxa may be true cosmopolitans or widespread animals, in contrast to previous studies, which showed high speciation rates for other meiofaunal groups. However, sequencing of additional genes, sampling of more regions, and calibration of a molecular clock are needed to better evaluate such widespread distribution patterns.