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A new genus and species of Serpulidae (Annelida, Polychaeta, Sabellida) from the Caribbean Sea

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Abstract

A new genus and species of Serpulidae (Annelida, Polychaeta) from the Caribbean Sea. *Turbocavus secretus* (**gen. nov.** and **sp. nov.**) is described from shallow hard substrates (0.5–3 m) in wind-sheltered bays of St. John, U.S. Virgin Islands and Curaçao, as well as from diving depths (46–49 m) around Bonaire (Leeward Antilles), Caribbean Sea. The new taxon, which has from 7 to 19 thoracic chaetigers and up to 335 abdominal chaetigers, bears a unique type of thoracic chaeta which is multifolded at the base and continues with a groove tapering to the capillary tip. The new serpulid has unique 18S rRNA sequences and genetic analysis of the 18S rRNA gene situates the new genus at the basis of the serpulid cladogram, well separated from other genera, and close to *Filograna/Salmacina* and *Protula*.

Key words: U.S. Virgin Islands, Bonaire, Curaçao, grooved chaetae, multifolded chaetae

Introduction

The Serpulidae (Rafinesque, 1815) are a large family of annelid polychaete worms, which secrete and live within calcareous tubes affixed to hard surfaces. Common to all oceans, they exist from intertidal habitats to deep-sea zones (Rouse & Pleijel 2001; ten Hove & Kupriyanova 2009; Kupriyanova *et al.* 2014). The most recent review of the family, which does not include the spirorbin taxa (ten Hove & Kupriyanova 2009), lists 350 species within 46 genera. However, these authors acknowledge that much work needs to be done to examine the validity of 19 monophyletic genera, which may eventually be synonymized with other genera.

While the Serpulidae are easily recognized, their genera are considered as difficult to classify, since there are few taxonomic characters to clearly separate them. Frequently, genera and species are classified based on "negative traits", or the lack of specific characters, rather than for presenting combinations of unique characters (e.g. generic diagnoses in Fauchald 1977; ten Hove & Kupriyanova 2009). An analysis of thoracic blood vessel pattern was used to discern between the genera *Apomatus* and *Protula* (ten Hove & Pantus 1985), but blood vessel patterns can only be studied in fresh material. However the patterns of other genera are not known, and as a consequence the character has not been used in subsequent taxonomic literature. Taxonomists now routinely use scanning electron microscopy to identify unique characters, which cannot be detected with a light microscope.

Comparisons of DNA sequences also provide a powerful tool for taxon identification at genus and species level. The 18S rRNA nuclear gene has widely been employed for screening Serpulidae taxa and has been a valuable character for hypothesizing phylogenetic relationships within the family (Kupriyanova *et al.* 2006; Lehrke *et al.* 2007).

In this paper, a new serpulid genus, *Turbocavus*, is described on the basis of unique morphological characters and 18S rRNA gene sequence data.

Knight-Jones, Oliver & Mackie, 1997, which might have adapted to low oxygen conditions of the deep sea by losing its operculum, which would hinder respiration. However, reading Kupriyanova *et al.* (2014), operculate taxa appear to be more common than non-operculate ones in the deep sea. Ecological selection (fewer predators and/or lower oxygen levels) could perhaps account for the absence of an operculum in *Turbocavus secretus* **sp. nov.** Individuals were found subtidally under rocks, where the colonies would not only be safeguarded from water loss, but also be relatively protected from predators. *Turbocavus secretus* **sp. nov.** seems to inhabit an oxic-anoxic interface. Their tubes are underneath rocks firmly embedded in fine sediment and appear to be stained orange by iron oxyhydroxides.

The importance of chaetal characters for the classification within the Serpulidae was stressed by ten Hove (1984). This might, in part, be reflected in the molecular results of the present study: *Turbocavus secretus* **sp. nov.** forms a distinct clade, a result which concurs with the unique thoracic chaetae observed.

It is not the intention of the present paper to discuss the phylogeny of serpulids in depth, only to illustrate the genetic basis, if any, for our morphology initiated decision to attribute generic rank to the new taxon. Although different genes and analyses have been used by Kupriyanova *et al.* (2006, Fig. 5B; 2009, Fig. 5; 2010, Fig. 4), Lehrke *et al.* (2007, Fig. 2) and Kupriyanova & Nishi (2010, Fig. 7), and the used number of taxa varies between these papers, some general trends can be discerned. For example, all show clades with *Spirobranchus-Ficopomatus-Galeolaria*, *Serpula-Crucigera-Hydroides* on the one hand, *Salmacina/Filograna*, *Protis*, as well as a *Protula* clade on the other. Relationships between the clades, however, are unclear, with recurrent polytomies. Differences in topology of the cladograms, for instance the position of the Spirorbinae and of the *Vermiliopsis*-like genera, indicate that a relatively stable phylogeny reconstruction on the basis of a single gene is not to be expected. Nevertheless, in both our maximum-likelihood and Bayesian analysis, *Turbocavus* clearly stands out as a well-supported separate clade with a jackknife value respectively posterior probability of 100, substantiating a generic status for the taxon.

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