



## First genetic data for species of the genus *Haploniscus* Richardson, 1908 (Isopoda: Asellota: Haploniscidae) from neighbouring deep-sea basins in the South Atlantic

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### Abstract

The phylogenetic analysis in this study, based on a fragment of the CO1 mtDNA gene, provides first evidence in favour of Brökeland's (2010) conclusion of recent or ongoing gene flow in *Haploniscus rostratus* (Menzies, 1962) across the Walvis ridge. It adds the first evidence for the presence of either restricted gene flow or potential cryptic species in the Guinea Basin. The data suggest furthermore that distinct species within the *H. unicornis* complex occur sympatrically in the East Atlantic deep-sea basin north of the Walvis Ridge. However, without more specimens (males in particular) and more markers, other processes that may have generated this pattern cannot be excluded.

**Key words:** Isopoda, Haploniscidae, deep sea, CO1, DNA barcoding

### Introduction

The abyss is of extensive dimension and difficult and expensive to access. Hence, only a small fraction of the deep sea has been studied (Rex & Etter 2010). Results of biological studies have shown that the deep-sea benthos comprises an enormous, though mostly unstudied, diversity (Hessler & Sanders 1967; Wilson 1998, Brandt *et al.* 2007; Ramirez-Llodra *et al.* 2010). Isopods are among the better known groups in the deep sea, especially with respect to their origin and evolution (Raupach *et al.* 2004; Rex & Etter 2010). Several new species have been described based on morphological characters; however, genetic analyses were and still are hampered due to the difficulty to obtain sufficient high-quality DNA from abyssal isopods. Thus, molecular studies on deep-sea isopods are scarce and the existing ones often used different DNA fragments. The only previous molecular study on Haploniscidae Hansen, 1916 used 16S and 18S rRNA genes besides morphology for an integrative approach to unravel a species complex (Brökeland & Raupach 2008). Overall, we found 47 CO1 sequences for four distinct asellote families in GenBank (34 of them for Munnopsidae Lilljeborg, 1864; Osborn 2009), but none for Haploniscidae.

Haploniscid isopods are among the more common taxa in the deep-sea macrofauna. Brökeland (2010a, b) re-described *Haploniscus rostratus* (Menzies, 1962), added information to *H. unicornis* Menzies, 1956 and described four new species of the *H. unicornis* complex (Brökeland 2010b), which now contains six species. The specimens used by Brökeland (2010a, b) were sampled during the DIVA and ANDEEP expeditions to the South Atlantic abyss (DIVA: Latitudinal Gradients of Deep-Sea Biodiversity in the Atlantic Ocean; ANDEEP: Antarctic benthic deep sea biodiversity: colonization history and recent community patterns). For a subset of this material we were able to retrieve DNA for phylogenetic analyses. The dataset comprises specimens from the Cape, Angola and Guinea Basins (Table 1) and adds the first genetic data to the morphology-based results by Brökeland (2010a, b).