Occurrence of Alvinocaris muricola in whale bones from the SW Atlantic: molecular proximity with the Atlantic Equatorial Belt population

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The shrimp genus Alvinocaris is exclusively associated with deep-sea chemosynthetic communities. A. muricola and its sister species A. markensis have been reported on seeps from East Atlantic (EA) and Gulf of Mexico (GoM) and vents from the Mid-Atlantic Ridge (MAR). In the present work, we report the first A. muricola individuals associated with whale bones implanted in the Southwest Atlantic (SWA). We examined COI and 16S genes and constructed haplotype networks to infer genetic connectivity in order to evaluate how whale falls may contribute to the biogeography of chemosynthetic habitats. Both ML and BI trees based on alvinocaridid COI gene supported a robust clade of A. muricola/A. markensis across the Atlantic, with a specific branch in the SWA. We recovered 57 COI and one 16S haplotypes from 113 sequences of A. muricola/A. markensis. Haplotype diversity was high for all populations ranging from 0.67 (SWA) to 0.92 (GoM), but nucleotide diversity was low (i.e., from 0.002 in SWA to 0.006 in GoM). The same pattern was observed across all sites. The COI haplotype network formed a starlike topography with the most common haplotype, present in vent and seeps, in the center. SWA haplotypes were separated from those of the center by a node formed by a still unknown haplotype. Our analysis could indicate that whale falls work as stepping-stone habitats facilitating large scale dispersal across the Atlantic Ocean. Alternatively, they could be end members for taxa inhabiting vents and seeps as suggested by the present haplotype network. The search for possible populations of A. muricola/A. markensis in SWA cold seeps and in vents of South MAR would be highly relevant to answer a possible stepping stone role of carcasses for this group of shrimps.