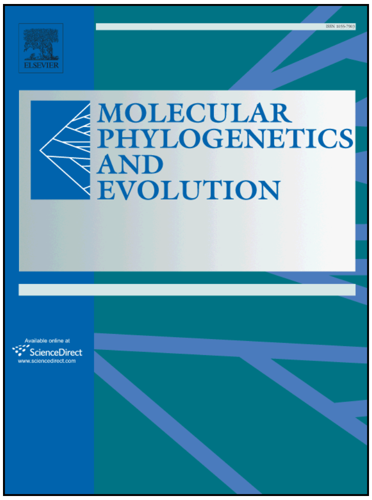

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Are ocean currents to slow to counteract SAR11 evolution? A next-generation sequencing, phylogeographic analysis

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Abstract

This work set out to shed light on the phylogeography of the SAR11 clade of Alphaproteobacteria, which is probably the most abundant group of heterotrophic bacteria on Earth. In particular, we assessed the degree to which empirical evidence (environmental DNA sequences) supports the concept that SAR11 lineages evolve faster than they are dispersed thus generating vicariant distributions, as predicted by recent simulation efforts. We generated 16S rRNA gene sequences from surface seawater collected at the South West Atlantic Ocean and combined these data with previously published sequences from similar environments from elsewhere. Altogether, these data consisted in about 1e6 reads, from which we generated 355,306 high quality sequences of which 95,318 corresponded to SAR11. Quantitative phylogeographic analyses supported the existence of a spatially explicit distribution of SAR11 species and provided evidence in favor of the idea that dispersal limitations significantly contribute to SAR11 radiation throughout the world's oceans. Likewise, pairwise phylogenetic distances between the communities studied here were significantly correlated with the genetic divergences predicted by a previously proposed neutral model. As discussed in the paper, these findings are compatible with the concept that the ocean surface constitutes a homogeneous environment for SAR11, in agreement with previous experimental data. We discuss the implications of this hypothesis in a global change scenario. This is the first study combining high throughput sequencing and phylogenic analysis to study bacterial phylogeography and reporting a distance decay pattern of phylogenetic distances for bacteria.

Keywords. Bacteria, SAR11, phylogeography, biogeography, phylogenetic, 16S.