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Quantifying the evolution of a globally distributed deep marine sediment-hosted microbial lineage

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Deep marine sediment is one of the largest biomes on earth and contains a large fraction of global microbial biomass, but this ecosystem relies on scant available energy. Additionally, this environment is undersampled and understudied, particularly with regards to our understanding of microbial processes. The development of foundational concepts in biogeography and evolutionary processes such as dispersal barriers, genetic drift, and speciation is needed for a description of life at the lowest possible energy threshold. Most of our current understanding of evolutionary processes is based on "live fast, die young" microbial cultures, which do not represent a majority of life on Earth. Using single-cell genomes constructed from North Atlantic marine sediment we discovered a bacterial species within Phylum Aerophobota, that despite occupying depths separated by over 2 million years of sedimentation, showed no depth-specific genetic subpopulations. This suggests that there is connectivity between discrete sediment depths or very little evolutionary pressure over the time scales between when sediment was deposited. We also identified this species in multiple other deep marine sediment datasets from public sequencing archives. With this archived data, we constructed metagenome-assembled genomes from seven different sampling sites distributed over the globe, with some spanning multiple depths at these other sites. Despite the cosmopolitan distribution of this species, we only identified weak evidence for biogeographically driven genetic subpopulations of this lineage. Loci within genomes that show evolutionary differentiation across sites do display some evidence of location-based allele segregation. We interpret this as evidence that evolution is acting within this species, though not at a strength or speed that produces differentiation. The static, low-energy characteristics of deep marine sediment with limited sources of reducing or oxidizing power where this species inhabits may help explain the lack of genetically differentiated subpopulations over such large geographic distances. Our results demonstrate the opportunity that deep marine sediments provide for the study of evolution at the extreme low-end of its potential range as a process that shapes life and biomes, governed by environmental chemistry.