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AME 79:209-219 (2017) - DOI: <https://doi.org/10.3354/ame01829>

Diversity and abundance of sulfate-reducing microorganisms in a Mediterranean lagoonal complex (Amvrakikos Gulf, Ionian Sea) derived from *dsrB* gene

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ABSTRACT: Sulfate-reducing microorganisms (SRMs) are a phylogenetically and physiologically diverse group of microorganisms, responsible for the dissimilatory reduction of sulfate. SRMs thrive under anaerobic conditions with high availability of organic matter. Such conditions characterize lagoonal ecosystems which experience regular dystrophic crises. The aim of the present study was to explore the biodiversity patterns of SRMs and to examine the extent to which these patterns are associated with biogeographic and environmental factors. Sediment samples were collected from 5 lagoons in the Amvrakikos Gulf (Ionian Sea, western Greece). DNA was extracted from the sediment and was further processed through pyrosequencing of a region of the dissimilatory sulfite reductase β -subunit (*dsrB*). The results of this exploratory study show that the majority of the observed operational taxonomic units (OTUs) belong to the *Deltaproteobacteria* supercluster and more specifically, to the *Desulfobacteraceae* family. Salinity and ammonium ions are the environmental factors that best correlated with the SRM community pattern. Furthermore, the SRM community of the brackish lagoons is differentiated from that of the brackish-marine lagoons and the studied lagoons have distinct SRM communities.

KEY WORDS: *dsrB* gene · Amvrakikos Gulf · Lagoon · Pyrosequencing · Sediment · Sulfate-reducing microorganisms

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Cite this article as: Pavlou C, Oulas A, Vasileiadou K, Kotoulas G, De Troch M, Friedrich MW, Arvanitidis C (2017) Diversity and abundance of sulfate-reducing microorganisms in a Mediterranean lagoonal complex (Amvrakikos Gulf, Ionian Sea) derived from *dsrB* gene. *Aquat Microb Ecol* 79:209-219. <https://doi.org/10.3354/ame01829>

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Published in *AME* Vol. 79, No. 3. Online publication date: June 12, 2017

Print ISSN: 0948-3055; Online ISSN: 1616-1564

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