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Phylogenetic Diversity and Antibiotic Resistance in Sediments of Aegean Sea

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Abstract : The studies in bacterial diversity and antimicrobial resistance in coastal areas are important to understand the variability in the community structures and metabolic activities. In the present study, antimicrobial susceptibility and phylogenetic analysis of bacteria isolated from stations with different depths and influenced by terrestrial and marine fluxes in eastern Aegean Sea were illustrated. 51% of the isolates were found as resistant and 14% showed high MAR index indicating the high-risk sources of contamination in the environment. The resistance and the intermediate levels and high MAR index of the study area were 38–60%, 11–38% and 0–40%, respectively. According to 16S rRNA gene analysis, it was found that the isolates belonged to two phyla Firmicutes and Gammaproteobacteria with the genera Bacillus, Halomonas, Oceanobacillus, Photobacterium, Pseudoalteromonas, Psychrobacter, and Vibrio. 47% of Bacillus strains which were dominant among all isolates were resistant. In addition to phylogenetically diverse bacteria, the variability in resistance, intermediate and high MAR index levels of the study area indicated the effect of geographical differences.

Keywords : bacterial diversity, multiple antibiotic resistance, 16S rRNA genes, Aegean Sea
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