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## Microbial community analysis of the hypersaline water of the Dead Sea using high-throughput amplicon sequencing.

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**Abstract:** Amplicon sequencing using next-generation technology (NGS) has been utilized in describing the diversity of Dead Sea microbiota. The investigated area is a well-known salt lake in the western part of Jordan found in the lowest geographical location in the world (more than 420 m below sea level) and characterized by extreme salinity (approximately, 34%) in addition to other extreme conditions (low pH, unique ionic composition different from sea water). DNA was extracted from Dead Sea water. A total of 314,310 small subunit RNA (SSU rRNA) sequences were parsed, and 288,452 sequences were then clustered. For alpha diversity analysis, sample was rarefied to 3,000 sequences. The Shannon-Wiener index curve plot reached a plateau at approximately 3,000 sequences indicating that sequencing depth was sufficient to capture the full scope of microbial diversity. Archaea was found to be dominating the sequences (52%), whereas Bacteria constitute 45% of the sequences. Altogether, prokaryotic sequences (which constitute 97% of all sequences) were found to predominate. The findings expand on previous studies by using high-throughput amplicon sequencing to describe the microbial community in an environment which in recent years has been shown to hide some interesting diversity.