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ABSTRACT

Progress in microbial ecology is confounded by problems when evaluating results generated by different sequencing methodologies due to inherent biases. Existing comparative studies of data generated by the different sequencing platforms are restricted to comparisons of sequencing performance, or reporting 16S phylogenetic profiling outcomes. Here, we demonstrate that the same biological conclusion is reached using different NGS technologies. We evaluated four different bioinformatics strategies that generated 16S amplicon profiles from two widely used NGS platforms. The bacterial and archaeal 16S rRNA genes were amplified from soil samples and sequenced using MiSeq and PGM high-throughput sequencing platforms. The same beta diversity trends between platforms were observed irrespective of the bioinformatic strategies. However, the analysis of alpha diversity varied among strategies. Satisfactory results were