Bacterial communities association with distribution characteristics of n-alkanesin in lacustrine sediments of Linxia Basin, NE Tibetan Plateau, NW China

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The study on lacustrine sediments in the marginal basins of Tibetan Plateau is of great significance for global climate change and paleoclimate reconstruction. What's more, sediments can record past vegetation changes, the analysis of lacustrine sedimentary bacteria communities in Linxia Basin could help elucidate bacterial responses to environmental change. However, the profiles of the bacterial communities in the Linxia basin remain largely unknown. In this study, the characteristic bimodal distribution of n-alkanes, this was observed in the investigated samples. The distributions of the nC27/nC31 and nC21-/nC22+ ratio in different thicknesses were carried out. More, based on the 16S rRNA high-throughput sequencing method, the changes of bacterial community structure and diversity were also studied to display any systematic change along the geological change. In these sediments, bacterial communities were dominated by Bacilli (25.08%), Gammaproteobacteria (15.50%), Alphaproteobacteria (13.93%), Betaproteobacteria (14.06%) and Actinobacteria (8.34%), accounting for more than 76.92% of the bacterial sequences. The integration analysis of distribution characteristics of normal paraffins and sedimentary bacterial diversity was detected to infer important climate change events, especially the arid-cold conditions at ~8 Ma responded to the uplift of the Tibetan Plateau. Our data provide a better microbial ecology understanding for climate change and paleoclimate reconstruction in arid region Linxia Basin, NE Tibetan Plateau, NW China.