Dam construction as an important anthropogenic modification triggers abrupt shifts in microbial community assembly in freshwater lake sediments

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Microbial communities in freshwater lake sediments play a crucial role in regulating geochemical cycles and controlling greenhouse gas emissions. Many of them exhibit a highly ordered structure along depth profile. Besides redox effect, sediment stratification could also reflect historical transition. Dam construction dramatically increased in the mid-20th century and is considered one of the most far-reaching anthropogenic modifications of aquatic ecosystems. Here we attempted to identify the effect of historical dam construction on sediment microbial zonation in Lake Chaohu, one of the major freshwater lakes in China. The damming event in AD 1962 was coincidentally labeled by the $^{137}\text{Cs}$ peak. Physiochemical and sequencing analyses (16S amplicon and shotgun metagenomics) jointly showed a sharp transition occurred at the damming-labeled horizon which overlapped with the nitrate-methane transition zone (NMTZ) and controlled the depth of methane sequestration. At the transition zone, we observed significant taxonomic differentiation. Random forest algorithm identified Bathyarchaeota, Spirochaetes, and Patescibacteria as the damming-sensitive phyla, and Dehalococcoidia, Bathyarchaeia, Marine Benthic Group A, Spirochaetia, and Holophagae as the damming-sensitive classes. Phylogenetic null model analysis also revealed a pronounced shift in microbial community assembly process, from a selection-oriented deterministic community assembly down to a more stochastic, dispersal-limited one. These findings delineate a picture in which dam-induced changes to the lake trophic level and sedimentation rate generate great changes in sediment microbial community structure, energy metabolism, and assembly process.