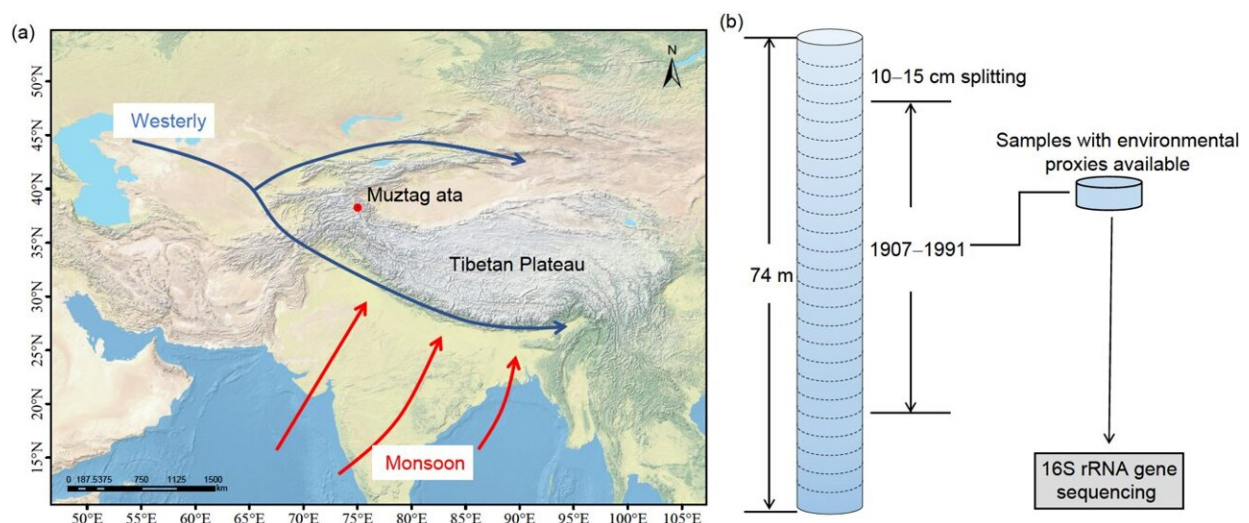


Research finds human activity over natural inputs determines the bacterial community in an ice core

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The location of Muztag ata glacier on the Tibetan Plateau and the influence of Westerly jet and Indian monsoon are shown in panel a. The ice core sampling strategy is illustrated in panel (b). Briefly, the 74 m ice core was cut into 10 to 15 cm sections and dated, then sections with environmental proxies available are used for DNA extraction and bacterial 16S rRNA gene amplicon sequencing. Credit: Science China Press

The Tibetan Plateau (TP) has the third-largest number of glaciers after the Antarctic and Greenland. Bacteria, deposited on glacier surfaces through dry and wet deposition, undergo in-situ growth and are

subsequently preserved in ice cores following environmental selection pressures such as UV radiation and low temperatures.

Since glacier bacteria are largely transported from distant or local sources by atmospheric circulation, changes in source ecosystems can also affect the composition of surface glacier bacteria. Therefore, the characteristics of bacterial communities in ice cores can serve as indicators of past climates and human activities.

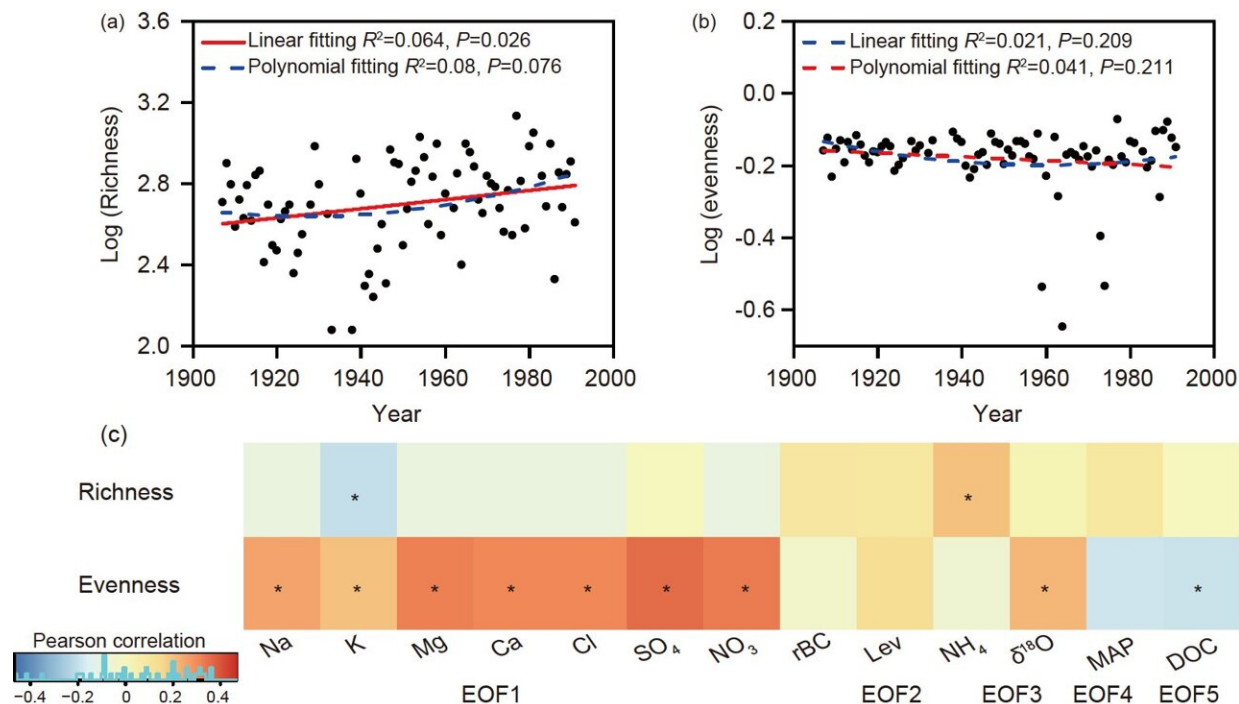
A research team investigated the [bacterial community](#) from a 74 m ice core of Muztag Ata glacier on the Tibetan Plateau to link biological indicators with past climate and anthropogenic activities. They observed an increase in bacterial richness throughout the ice core, which was associated with higher NH_4^+ , an indicator of agricultural development.

Meanwhile, the evenness demonstrated negative correlations with DOC and MAP, and positive correlation with $\delta^{18}\text{O}$, Na^+ , K^+ , Mg^{2+} , Ca^{2+} , Cl^- , SO_4^{2-} , and NO_3^- . These indicators collectively offer promising insights for inferring past climate and [environmental changes](#).

The researchers further investigated the composition of bacterial communities in ice cores. Cluster analysis at the bacterial family level indicates three distinct groupings of samples. Through [cluster analysis](#) at the bacterial family level, they uncovered three distinct groupings of samples.

Cluster A encompasses the years 1953 to 1991, Cluster B consists of 11 samples from 1933 to 1951, while the majority of samples in Cluster C are dated between 1907 and 1930. It was found that the bacterial community composition was shaped by a combination of human activity, natural inputs, and air temperature, with a pronounced human influence becoming evident after the 1950s.

Furthermore, the relative abundance of animal gut-associated bacteria, including Aerococcaceae, Nocardiaceae, Muribaculaceae, and Lachnospiraceae, was associated with livestock number changes in the Central Asian region. Together with other bacterial lineages, they jointly explained 59.8% of the livestock number changes.



The linear regression between bacterial richness (a) and evenness (b) with the dated ice core age is shown. (c) shows the correlation between bacterial richness and evenness with the measured environmental proxies. Significant correlations (at P

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