A 700-year record of accumulation rates at Dome A, Antarctica

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Dome A, located along the dividing line of East Antarctica, has the highest altitude in Antarctica. Preliminary evidence indicates that Dome A holds high potential for 'oldest ice' cores [1].

During the 21st Chinese Antarctic Research Expedition in 2004/2005 austral summer, a 109.91 m ice core (hereafter DA2005 ice core) was recovered at the site about 300 m away from the summit of Dome A. Chemical analysis of the DA2005 core has been used to construct continuous, detailed glaciochemical record. And time stratigraphic horizons from known volcanic eruptions were used for dating. Several clearly visible sulfate peaks in the top 35 m part of DA2005 were identified by comparison with common volcanic chronologies from Antarctica [2, 3]. These include the well-known volcanic events in the last millennium: Agung 1963, Krakatoa 1883, Tambora 1815 and an unknown eruption 1809, Unknown 1693, Kuwae 1453 and Unknown 1259. A mean accumulation rate was calculated according to the time stratigraphic horizons between two adjacent events and was assumued constant to date the intervening snow layers. Results show that the mean accumulation rates during different time periods are quite constant, ranging from 21.5 to 24.5 $mmH_2O \cdot yr^{-1}$. And the resulting dates for other volcanic events during the period of 1259-1963 A.D. are in good agreement with those in previous Antarctic ice core volcanic records. The mean accumulation rate between Agung and 1259 A.D. is 23.2 $mmH_2O \cdot yr^{-1}$, which is the same as the value between 1966 and 2004 A.D. measured from snow blocks collected at Dome A [4]. It seems that there is neither an indication of a change nor a trend in the accumulation rate apparent during the period of 1259-1963 A.D. which may indicate no drastic change in deposition has occurred at Dome A within this time period.

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Analysis of microbial molecular ecology techniques in constructed rapid infiltration system

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The microbial molecular ecology techniques, which were developed on the basis of molecular, were applied in studying the bacteria in Constructed Rapid Infiltration system (CRI). These techniques are very efficient in better describing the bacterial diversity, microbial community distribution and the relations between microbial group structure and nitrogen contamination through the analysis of microbial nucleic acid sequence fragment in CRI. The results further revealed the removal mechanism of contamination, which are essentially for the improvement of wastewater treatment in CRI.

In this study, a series of microbial molecular ecology techniques were applied in studying the bacteria in CRI. The microbial community distribution of bacteria was analyzed by PCR-DGGE qualitatively and a bacterial 16S rDNA gene clone library was constructed to analyze the bacterial diversity quantitatively. The anaerobic ammonium oxidation bacteria were proved to exist in CRI by phylogenetic analysis with a DNA sequence similarity of 97 %. The relations between microbial groups' structure and nitrogen contamination, and the removal mechanism of contamination were revealed.