A Big Earth Data Platform for Three Poles

**Post-processing products for typical year ice bacteria distribution in the Tripolar regions (2010-2018)**

1、Description

The microbial reprocessing products of polar ice and snow in typical years collected the analysis results of bacteria sampled from glaciers, Glacial Snow and ice in the polar regions and the Qinghai Tibet Plateau from 2010 to 2018. Through sorting, summarizing and summarizing, the post-processing data products of soil microorganisms in the three pole region are obtained, and the data format is excel, which is convenient for users to view. Among them, the prokaryotes of Glacial Snow and ice in the polar regions and Qinghai Tibet Plateau are the sequences of bacterial 16S ribosomal RNA gene collected by teacher Liu Yongqin's experimental group from NCBI database from 2010 to 2018. The collected sequences calculate the similarity between sequences by using dotour software. Sequences with a similarity of more than 97% are clustered into an OTU, and OTU representative sequences are defined. OTU representative sequences were compared with RDP database through "Classifier" software, and were identified to the first level when the reliability was greater than >80%; The glaciers on the Qinghai Tibet Plateau were collected from 2010 to 2018, including the bacterial 16S ribosomal RNA gene sequence of seven glaciers on the Qinghai Tibet Plateau (East Rongbu glacier on Mount Everest, Tianshan No. 1 glacier, Guliya glacier, Laohugou glacier, muzitang glacier, July 1st glacier and yuzhufeng glacier) isolated by teacher Liu Yongqin's experimental group, Malan glacier isolated by teacher Xiang Shurong and ruogangri glacier isolated by teacher Zhang Xinfang. Glacier samples were collected and brought back to the ecological Laboratory of the Institute of Qinghai Tibet Plateau Research in Beijing and the Lanzhou cryosphere National Laboratory. After coating the plate, it was cultured at different temperatures (4-25 ℃) for 20-90 days, and a single colony was picked for purification. The isolated bacteria extracted DNA, amplified 16S ribosomal RNA gene fragments with 27f/1492r primers, and sequenced with Sanger method. 16S ribosomal RNA gene sequence was compared with RDP database through "Classifier" software, and was identified to the first level when the reliability was greater than >80%.

2、Keywords

Theme：RiverIce,River Ice
Discipline：Cryosphere
Places：Arctic, Tibetan Plateau, Antarctic
Time：2010-2018

3、Data details

1.Scale：None

2.Projection：WGS84

3.Filesize：0.08MB

4.Data format：None

4、Space scope

|  |  |  |
| --- | --- | --- |
| - | north：90.0 | - |
| west：0.5 | - | east：0.5 |
| - | south：90.0 | - |

5、Time frame:2010-06-29 16:00:00+00:00--2018-06-29 16:00:00+00:00

6、Reference method

References to data:

YE Aizhong. Post-processing products for typical year ice bacteria distribution in the Tripolar regions (2010-2018). A Big Earth Data Platform for Three Poles, doi:10.11888/Cryos.tpdc.2727522022

References to articles:

7、Supporting project information

CASEarth:Big Earth Data for Three Poles（grant No. XDA19070000）

8、Data resource provider

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