A Big Earth Data Platform for Three Poles

**Post-processing products for typical year soil bacteria distribution in the Tripolar regions (2005, 2006, 2015)**

1、Description

The three pole soil microbial post-treatment products in typical years collected the distribution and analysis results of soil samples from the north and south polar regions from 2005 to 2006 and the distribution and analysis results of soil samples from the Qinghai Tibet Plateau in 2015. Through sorting and summarizing, the post-processing data products of soil microorganisms in the three pole region are obtained. The data format is excel, which is convenient for users to view. Among them, the collection time of samples from the north and south polar regions was from December 13, 2005 to December 8, 2006, including 52 samples from three regions in the Arctic (Spitsbergen slijeringa, Spitsbergen vestpynten, and Alexandra fjord Highlands), and 171 samples from five regions in the Antarctic (Mitchell Peninsula, Casey station main power house, Robinson ridge, herring Island, browning Peninsula); The Qinghai Tibet Plateau was collected from July 1 to July 15, 2015, including meadow, grassland and desert ecosystems. There were 18 sampling points in total, and the number of samples at each sampling point was 3-5. The precipitation, air temperature and drought degree of the sampling point are estimated from the meteorological information for reference. The soil surface samples were collected and stored in liquid nitrogen, then transported back to the Sydney Laboratory for extraction by fastprep DNA kit. The extracted DNA samples were amplified with the 16S rRNA gene fragment using 27F (5'-gagttttgatcntggctca-3') and 519r (5'-gtnttacngcgckctg-3'). The amplified fragments were sequenced by 454 method, and the original data were analyzed by mothur software. The sequences with poor sequencing quality were first removed, and then the chimeric sequences were sequenced and removed. After that, the similarity between sequences is calculated. Sequences with a similarity of more than 97% are clustered into one OTU, and OTU representative sequences are defined. The OTU representative sequences were aligned with the Silva database, and were identified to belong to the first level when the reliability was greater than 80%.

2、Keywords

Theme：Soil,Soil bacteria
Discipline：Terrestrial Surface
Places：Arctic, Tibetan Plateau, Antarctic
Time：2005, 2006, 2015

3、Data details

1.Scale：None

2.Projection：WGS84

3.Filesize：2.0MB

4.Data format：None

4、Space scope

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

5、Time frame:2005-12-30 16:00:00+00:00--2015-12-30 16:00:00+00:00

6、Reference method

References to data:

YE Aizhong. Post-processing products for typical year soil bacteria distribution in the Tripolar regions (2005, 2006, 2015). A Big Earth Data Platform for Three Poles, doi:10.11888/Terre.tpdc.2727262022

References to articles:

7、Supporting project information

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

8、Data resource provider

name: YE Aizhong
unit: Beijing Normal University
email: azye@bnu.edu.cn