A Big Earth Data Platform for Three Poles

**Sequencing of intestinal microorganisms of domestic animals in QTP (2019)**

1、Description

In order to describe the disease situation of the main domesticated animals in and around the Qinghai Tibet Plateau, the epidemic situation of the main domestic animals in the Qinghai Tibet Plateau was investigated, and the genetic samples and intestinal microbial samples of the main epidemic diseases of the main domestic animals were collected. We collected Camel dung at Mohe camel farm, Ulan County, Haixi Mongolian and Tibetan Autonomous Prefecture, Qinghai Province. This data set is the 16S rRNA sequencing data of camel's intestinal microorganism in Qinghai Province. By extracting the total DNA of camel faeces, we designed primers to amplify the v3-v4 region gene fragment of bacteria, and then sequenced the corresponding data with high-throughput of the second generation. 44 samples were sequenced. This data set can be used to mine genetic resources of disease resistant individuals and find corresponding candidate genes.

2、Keywords

Theme：Biological Resources,Enteric microorganism  
Discipline：Human-nature Relationship  
Places：Qinghai-Tibetan Plateau  
Time：2019

3、Data details

1.Scale：None

2.Projection：

3.Filesize：1200.0MB

4.Data format：None

4、Space scope

|  |  |  |
| --- | --- | --- |
| - | north：37.121979 | - |
| west：98.896655 | - | east：98.202157 |
| - | south：36.793462 | - |

5、Time frame:2018-07-07 08:00:00+00:00--2020-07-05 19:59:59+00:00

6、Reference method

References to data:

DUAN Ziyuan. Sequencing of intestinal microorganisms of domestic animals in QTP (2019). A Big Earth Data Platform for Three Poles, doi:10.11888/Ecolo.tpdc.2704622020

References to articles:

7、Supporting project information

Pan-Third Pole Environment Study for a Green Silk Road-A CAS Strategic Priority A Program

8、Data resource provider

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