A Big Earth Data Platform for Three Poles

**Genome resequencing data of equine (2019)**

1、Description

In order to study the population evolution history and local adaptive genetic mechanism of the main domesticated equine animals in the Qinghai Tibet Plateau and its surrounding areas, and to establish the corresponding germplasm genetic resource bank. We sequenced the whole genome of 100 horse species collected in Qinghai Province, Tibet Autonomous Region and Xinjiang Autonomous Region, including Tibetan horses, Tibetan donkeys, Pingyuan donkeys and local breeds of Jiama plain. A lot of genomic data were generated by sequencing, which provided data for tracing the historical events of domestication, migration and expansion of the main domesticated equine animals in this area, and further exploring the adaptation mechanism of equine animals to the poor environment such as hypoxia, high cold and dry.

2、Keywords

Theme：Forest
Discipline：Terrestrial Surface
Places：Tibetan Plateau
Time：2019

3、Data details

1.Scale：None

2.Projection：

3.Filesize：212000.0MB

4.Data format：None

4、Space scope

|  |  |  |
| --- | --- | --- |
| - | north：36.930877 | - |
| west：101.680463 | - | east：106.637811 |
| - | south：23.91083 | - |

5、Time frame:2019-01-05 08:00:00+00:00--2020-01-04 19:59:59+00:00

6、Reference method

References to data:

LI Yan. Genome resequencing data of equine (2019). A Big Earth Data Platform for Three Poles, doi:10.11888/Ecolo.tpdc.2708932020

References to articles:

7、Supporting project information

Pan-Third Pole Environment Study for a Green Silk Road-A CAS Strategic Priority A Program
Second Tibetan Plateau Scientific Expedition Program

8、Data resource provider

name: LI Yan
unit: Yunnan University
email: liyan0910@ynu.edu.cn