A Big Earth Data Platform for Three Poles

**Genome sequencing data of equine (2020)**

1、Description

In order to study the population evolution history and local adaptive genetic mechanism of main domesticated equine animals in Qinghai Tibet Plateau and its surrounding areas, and to establish the corresponding germplasm genetic resource bank. We have sequenced 236 horse samples collected in Qinghai Province, Tibet Autonomous Region and Xinjiang Autonomous Region by the end of 2018, including Tibetan horse, Tibetan donkey, plain domestic donkey and Jiama plain local breed. Seventy five samples (including 73 donkey samples and two horse samples) were sequenced for mitochondrial genome and D-loop sequencing. A number of genomic data were generated by sequencing, which provided data for tracing the domestication, migration, expansion and other historical events of horse domesticated animals in this area, and further exploring the adaptation mechanism of equine animals to the harsh environment such as hypoxia, high temperature and dryness.

2、Keywords

Theme：Forest
Discipline：Terrestrial Surface
Places：Pan-third pole
Time：2020

3、Data details

1.Scale：None

2.Projection：

3.Filesize：3404000.0MB

4.Data format：None

4、Space scope

|  |  |  |
| --- | --- | --- |
| - | north：30.0 | - |
| west：94.0 | - | east：100.0 |
| - | south：28.0 | - |

5、Time frame:2019-12-31 16:00:00+00:00--2020-12-31 03:59:59+00:00

6、Reference method

References to data:

LI Yan. Genome sequencing data of equine (2020). A Big Earth Data Platform for Three Poles, doi:10.11888/Ecolo.tpdc.2710862020

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

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