A Big Earth Data Platform for Three Poles

**Genome sequencing data of cyanine de novo**

1、Description

In order to analyze how and when vines entered the Qinghai Tibet Plateau, and to explore the relationship between the spread and domestication of vines on the Qinghai Tibet Plateau and the plateau settlement and ancient Silk exchanges of early human activities, the research team conducted genome sequencing and de sequencing of the whole genome of self bred F1 varieties of Brassica rapa in Nangqian County of Qinghai Province in June 2018 The size of the assembled genome was 409.69 MB and contig N50 was 1.21 MB. This result can provide a genetic basis for studying the relationship between plant dispersal and human activities. At the same time, this study will help to reveal the effects of artificial domestication and human selection on the genetic differentiation of the plant and the adaptive mechanism of the plant to the plateau ecological environment.

2、Keywords

Theme：Biological Resources,Vegetation
Discipline：Terrestrial Surface,Human-nature Relationship
Places：Nanqian,Yushu,Qinghai
Time：2020

3、Data details

1.Scale：None

2.Projection：

3.Filesize：395.0MB

4.Data format：None

4、Space scope

|  |  |  |
| --- | --- | --- |
| - | north：32.0 | - |
| west：95.0 | - | east：97.0 |
| - | south：31.0 | - |

5、Time frame:None--None

6、Reference method

References to data:

DUAN Yuanwen. Genome sequencing data of cyanine de novo. A Big Earth Data Platform for Three Poles, doi:10.11888/Geogra.tpdc.2710702020

References to articles:

段元文，杨云强.蔓菁de novo基因组测序数据

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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