A Big Earth Data Platform for Three Poles

**Genomic data of plant de novo (2019)**

1、Description

In order to analyze how and when it entered the Qinghai Tibet Plateau and explore the relationship between its spread and domestication in the Qinghai Tibet Plateau and the plateau settlement of early human activities and the ancient Silk Exchange, in June 2018, the research team used three generations of genome sequencing technology to sequence the whole genome and de novo assembly of F1 generation of its self bred varieties in Nangqian County, Qinghai Province, and got a genome size of 40 9.69 MB, contig N50 is 1.21 MB. This result can provide genetic basis for studying the relationship between plant diffusion and human activities. At the same time, this study is helpful to reveal the influence of artificial domestication and human selection on the genetic differentiation of cyanine, and the adaptive mechanism of cyanine to adapt to the plateau ecological environment.

2、Keywords

Theme：Biological Resources  
Discipline：Human-nature Relationship  
Places：Tibetan Plateau  
Time：2018

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:2018-06-07 08:00:00+00:00--2019-01-06 19:59:59+00:00

6、Reference method

References to data:

DUAN Yuanwen. Genomic data of plant de novo (2019). A Big Earth Data Platform for Three Poles, 2020

References to articles:

Yang, Y.Q., Sun, X.D., Kong, X.X., Wang, C.T., Yang, Y., Yin, X., Yang, D.N., Duan, Y.W., &   
 Yang, Y.P. (2019). The Turnip Genome Provides Insights into Independent Evolution of Glucosinolate Biosynthesis, Nature Communications, 34(4), 848-854.

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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