A Big Earth Data Platform for Three Poles

**Mitochondrial DNA genome sequencing dataset of populations from the southeastern Tibetan Plateau**

1、Description

Based on Sanger sequencing technology, we sequenced Hypervariable segments (HVS) of mitochondrial genomes of 258 individuals from the southeastern Tibetan Plateau (Northwestern Yunnan). Quality control was conducted based on phylogenetic analysis, which has been proven to be of great help in distilling potential problems such as artificial recombination. By combining mitogenome data from literature, we analyzed the genetic landscape of populations in this region, with special attempts to unravel what kind of factors played the most important roles in this process. Results indicated substantial genetic components that could be traced back to Paleolithic period, likely representing the genetic legacy of initial settlers in southern East Asia. More components, which are prevalent in East Asians, especially in northern China, could also be observed, probably related to the migration of millet farmers from northern China into southwestern China.

2、Keywords

Theme：Biological Resources,Mammals
Discipline：Human-nature Relationship
Places：Southeastern Tibetan Plateau
Time：2019

3、Data details

1.Scale：None

2.Projection：

3.Filesize：0.27MB

4.Data format：None

4、Space scope

|  |  |  |
| --- | --- | --- |
| - | north：29.09 | - |
| west：97.16 | - | east：100.21 |
| - | south：24.05 | - |

5、Time frame:2019-03-15 08:00:00+00:00--2019-05-23 19:59:59+00:00

6、Reference method

References to data:

KONG Qingpeng. Mitochondrial DNA genome sequencing dataset of populations from the southeastern Tibetan Plateau. A Big Earth Data Platform for Three Poles, doi:10.11888/Ecolo.tpdc.2703622019

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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