A Big Earth Data Platform for Three Poles

**Mitochondrial genome sequencing data of Tibetan population in Lhasa**

1、Description

The whole mitochondrial genomes of 68 Tibetan samples were sequenced by high-throughput second-generation sequencing. The average depth of sequencing was 1000 ×, ensuring that the mitochondrial genome of each sample was completely covered (100%). Based on the phylogenetic analysis, we control the quality of these data to ensure that there is no sample pollution and other quality problems. According to the phylogenetic tree, each individual was allocated into haplogroups. The results showed that in Lhasa Tibetan population, M9a1c1b1a was the highest (19.12%), followed by G2 (13.23%), M13a (11.76%), C4a (7.35%), D4 (7.35%), A11a1a (5.88%), M9a1b (5.88%), and F1c, F1g, B4, F1d, M62b, F1a, F1b, G1, M11, M8a, U7a, Z3a. These haplogroups have different originations, including Paleolithic components (M13a, M62b, M9a1b, etc.), northern China millet farmers’ components (M9a1c1b1a and A11a1a), components distributed mainly in southern East Asia (F1a, etc.), northern East Asian haplogroups (C4a, D4, etc.). It is worth noting that the maternal component of Lhasa Tibetans is mainly composed of millet agricultural population in northern China, indicating the important impact of genetic input of millet agricultural population in northern China on the genetic structure of the population in this area. Taken together, the maternal genetic structure of Lhasa Tibetan population exhibits time stratification, which may represent the genetic imprint of different population entering the region in different periods.

2、Keywords

Theme：Population,Tibetan ethnic group
Discipline：Human-nature Relationship
Places：Lhasa
Time：2019-2020

3、Data details

1.Scale：None

2.Projection：

3.Filesize：1.08MB

4.Data format：None

4、Space scope

|  |  |  |
| --- | --- | --- |
| - | north：30.18 | - |
| west：92.09 | - | east：90.22 |
| - | south：29.25 | - |

5、Time frame:2018-12-31 16:00:00+00:00--2019-12-31 16:00:00+00:00

6、Reference method

References to data:

KONG Qingpeng. Mitochondrial genome sequencing data of Tibetan population in Lhasa. A Big Earth Data Platform for Three Poles, doi:10.1093/nsr/nwz0802021

References to articles:

Li, Y.C., Tian, J.Y., Liu, F.W., Yang, B.Y., Gu, K.S.Y., Rahman, Z.U., Yang, L.Q., Chen, F.H., Dong, G.H., Kong, Q.P. (2019). Neolithic millet farmers contributed to the permanent settlement of the Tibetan Plateau by adopting barley agriculture, National Science Review, Volume 6, Issue 5, September 2019, Pages 1005–1013, https://doi.org/10.1093/nsr/nwz080

7、Supporting project information

Second Tibetan Plateau Scientific Expedition Program

8、Data resource provider

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