A Big Earth Data Platform for Three Poles

**Whole genome microarray data of 150 Tibetan populations in the Qinghai Tibet Plateau (2019-2021)**

1、Description

The Qinghai Tibet Plateau is one of the most challenging environments for human survival, known as the "third pole" of the earth. The average altitude is above 4000 meters, and the oxygen partial pressure at 4000 meters is only about 60% of sea level. High altitude hypoxia is a strong selective pressure for human survival. Exposure to high altitude hypoxia will increase the number of red blood cells (polycythemia) and the level of hematocrit (HCT). The genetic background of plateau Tibetans is single, and the long-term high-altitude environment has a positive selection effect on the genes related to plateau adaptation, resulting in stable linkage genetic differences in the related single nucleotide polymorphisms (SNPs) in different altitude gradients, which is suitable for studying the association between high-altitude adaptive phenotypes and genotypes. In this study, DNA microarray was used to compare the male whole genome microarray data of 150 Tibetan and non Tibetan East Asians in plateau. About 700000 loci (including nuclear genome, mitochondrial DNA and Y chromosome) were genotyped for each sample, and the differential SNPs, genes and signal pathways were analyzed, The molecular adaptive evolution characteristics of Tibetan men in plateau to adapt to high altitude hypoxic environment were detected. This data is helpful to analyze the genetic adaptability of Tibetan population from the perspective of nuclear genome. By comparing with the data of people around the plateau, we can comprehensively understand the adaptive evolution of plateau indigenous men. It provides basic genetic reference data for studying human and biological evolution, exploring the molecular differences between high and low altitude populations, the homologous relationship between populations in different geographical environments, and the role of hypoxia in gene selection.

2、Keywords

Theme：人口, 生物资源
Discipline：Others
Places：Tibet
Time：2019-2021

3、Data details

1.Scale：None

2.Projection：

3.Filesize：1607.68MB

4.Data format：None

4、Space scope

|  |  |  |
| --- | --- | --- |
| - | north：32.26 | - |
| west：84.03 | - | east：94.05 |
| - | south：28.56 | - |

5、Time frame:2018-12-31 16:00:00+00:00--2021-12-31 03:59:59+00:00

6、Reference method

References to data:

KONG Qingpeng. Whole genome microarray data of 150 Tibetan populations in the Qinghai Tibet Plateau (2019-2021). A Big Earth Data Platform for Three Poles, doi:10.11888/Others.tpdc.2718812021

References to articles:

7、Supporting project information

Pan-Third Pole Environment Study for a Green Silk Road-A CAS Strategic Priority A Program

8、Data resource provider

name: KONG Qingpeng
unit: Kunming Institute of Zoology, Chinese Academy of Sciences
email: kongqp@mail.kiz.ac.cn