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Whole gene sequences of three chromosomals of bonobo on variant maps**Huaxian Zheng and Jeffrey Zheng**
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Genetic information of human evolution could be determined by comparative analysis of the human genome and related species possible genetic variations in the Anthropoid. The lineages of chimpanzees and humans making them humanities closest living relative. It is detected that the chimpanzee's gene sequence is highly similar to the human gene sequence by 95%-99%, but the difference in the external traits is still quite large. The gain or loss of DNA from chromosomes can lead to a variety of genetic disorders. Therefore, it is necessary to analyze the distribution characteristics of the gene sequence of each chromosome of the species and analyze the expressed protein. One major development to come from the study of human genes and proteins has been the identification of potential new drugs for the treatment of disease. Along with the common chimpanzee, the bonobo is the closest extant relative to humans. Analysis of the sequence distribution characteristics of each chromosome of bonobos not only helps us to understand what changes in chromosomal DNA sequences during human evolution lead to the expression of different proteins, but also provides a theoretical basis for biopharmaceuticals. In this paper, Bonobo's three whole sequences of chromosomes(2, 17, X) are selected to be mapped into variant maps. A single chromosome gene sequence is corresponding to a 2D visual map, significant differences can be observed.

Biography

Huaxian Zheng has completed her Graduation from Qujing Normal University, China. She is currently pursuing her Masters degree in systems analysis at Yunnan University, China.

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