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Mapping Human Genetic Diversity on the Japanese Archipelago

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ABSTRACT

The Japanese people are one of the most important populations for studying the origin and diversification of East Asian populations. As an island population, the Japanese's path of migration is a long-standing controversy. Archeological evidence suggests that there were at least two waves of migration to the Japanese archipelago in prehistory: the Paleolithic and Neolithic Jomonese as well as the Aeneolithic Yayoiese. However, the contributions of these Jomonese and Yayoiese to the contemporary Japanese population remain unclear. In this article, we provide evidence from human genetics as a new approach to addressing this topic. At the beginning, we introduce the history of human migration to the Japanese archipelago, as well as materials and methods human geneticists use. Subsequently, we tested three distinct population expansion models using evidences from recent human genetic studies on the Japanese, East Asian, and Serbian populations. Finally, we conclude that the contemporary main island Japanese are the result of population admixture of Jomonese, Yayoiese, and Han Chinese, which consists with the Admixture model.

KEYWORDS

Japanese Archipelago, Population Genetic Structure, Jomonese, Yayoiese, Admixture Model

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