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Peopling of Eurasia viewed from Y chromosomes

YAN Shi

CAS-MPG Partner Institute for Computational Biology, SIBS, CAS, Shanghai 200013, China

ABSTRACT: To understand the history of the world population is one of the main interests of anthropologists, historians, archaeologists and linguists. Since the 1990s, along with the development of biological science and techniques, molecular genetics has become a powerful tool for unveiling the origin and migration of the populations in the world, and gave birth to molecular anthropology. Especially, we can reconstruct a patrilineal tree of all males using the sequences of Y chromosome. Through phylogenetic investigations, we can trace back to the nearest common paternal ancestor of all the living human beings (Y-chromosomal Adam) in Africa at no more than 200ky BP, and to the ancestors of all the modern Eurasian people went out of Africa at less than 100ky BP. The distribution of haplogroups of Y chromosome is associated to geographical regions and highly related to language families, e.g., Haplogroups O, N, C, and D are concentrated in eastern and southeastern Asia, and the ancestor of Indo-Europeans are believed to have high frequency of Haplogroups R1a. Moreover, by detecting ancient DNA, we can compare and link modern and ancient peoples and reconstruct the migration routes.

通过 Y 染色体了解欧亚大陆的人群演化

严实

中国科学院-德国马普学会计算生物学伙伴研究所, 上海 200433

摘要: 了解世界各族群的历史是人类学、历史学、考古学和语言学的主要兴趣之一。自 1990 年代以来, 随着生物科学和技术的发展, 分子遗传学成为揭示世界上族群起源和迁徙的强有力工具, 并由此产生了分子人类学。其中最好的例子是通过 Y 染色体序列建立所有男性的父系系统树。藉此研究, 我们发现所有现存人类的父系最晚共同祖先 (Y 染色体亚当) 出现在非洲的时间不到 20 万年, 而欧亚大陆人群的共同祖先走出非洲的时间不到 10 万年。Y 染色体单倍群的分布有地区特异性, 且和语言分类高度相关。例如 O、N、C、D 单倍群集中在东亚和东南亚, 而印欧语系的祖先被认为具有高频的 R1a 单倍群。此外, 通过检测古代 DNA, 我们能够建立现代和古代人群间的联系, 并重构迁徙途经。