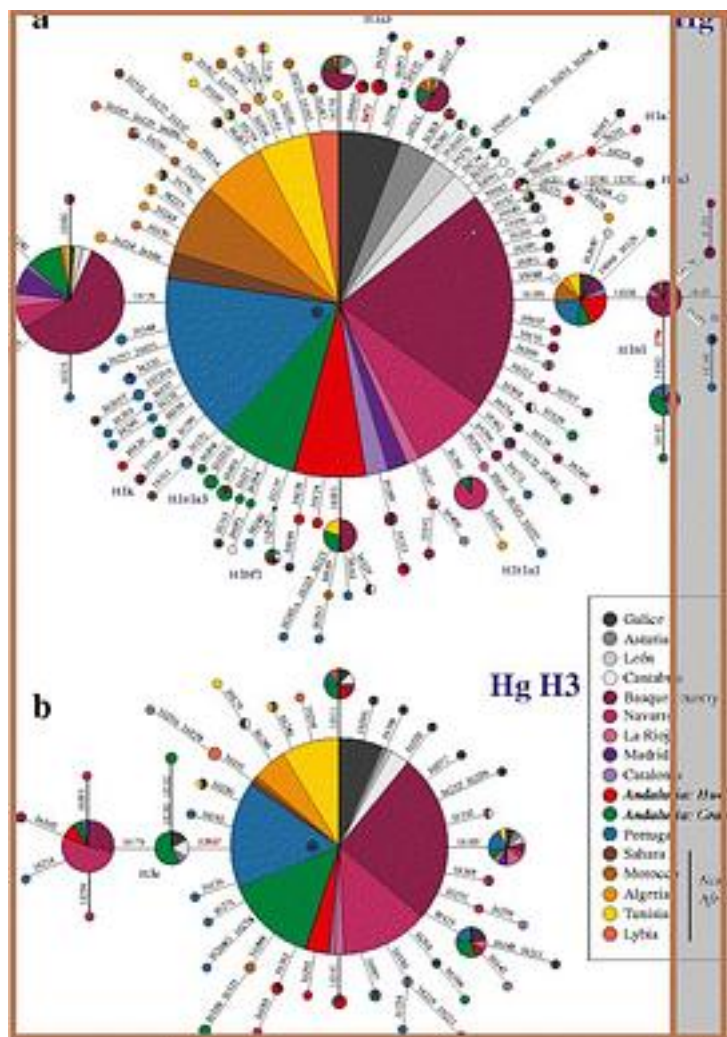# Origin and Expansion of the Dominant MitDNA in West Eurasia

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著者:U Roostalu

出版者:

出版时间:2007-2

装帧:Hardcover

isbn:9780674332751

More than a third of the European pool of human mitochondrial DNA (mtDNA) is fragmented into a number of subclades of haplogroup (hg) H, the most frequent hg throughout western Eurasia. Although there has been considerable recent progress in studying mitochondrial genome variation in Europe at the complete sequence resolution, little data of comparable resolution is so far available for regions like the Caucasus and the Near and Middle East—areas where most of European genetic lineages, including hg H, have likely emerged. This gap in our knowledge causes a serious hindrance for progress in understanding the demographic prehistory of Europe and western Eurasia in general. Here we describe the phylogeography of hg H in the populations of the Near East and the Caucasus. We have analyzed 545 samples of hg H at high resolution, including 15 novel complete mtDNA sequences. As in Europe, most of the present-day Near Eastern–Caucasus area variants of hg H started to expand after the last glacial maximum (LGM) and presumably before the Holocene. Yet importantly, several hg H subclades in Near East and Southern Caucasus region coalesce to the pre-LGM period. Furthermore, irrespective of their common origin, significant differences between the distribution of hg H sub-hgs in Europe and in the Near East and South Caucasus imply limited post-LGM maternal gene flow between these regions. In a contrast, the North Caucasus mitochondrial gene pool has received an influx of hg H variants, arriving from the Ponto-Caspian/East European area.

作者介绍:

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标签

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评论

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