



Common origin of the Austronesian and Daic Populations

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Abstract: Molecular anthropology has become a multidisciplinary field cross-linked by both natural science and social science. In the studies of molecular anthropology, human DNA is used as a tool for analyzing the population structures and relationships. These analyses result in genetic distances among the populations, which, together with findings from other anthropologic fields, is used to reconstruct phylogenetic trees of various populations. In this paper, we found a close relationship between the Austronesian and Daic populations in the south of East Asia, and reconstructed the phylogenesis of the two population groups using paternal Y-chromosomes and maternal mitochondrial DNA. We argued that an Austro-Tai super-family is reasonable based on the close relationship between the two families.

Key words: Molecular Anthropology, Austro-Tai, Y chromosome haplogroups, mtDNA haplogroups, Bai Yue, Ethnic history

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侗台语与南岛语人群的遗传同源性

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摘要: 由于学科领域的自然哲学的发展,特别是方法论的发展,分子人类学已经脱离了遗传学的范畴,真正地成为了一门独立的融会自然科学和人文科学为一体的交叉科学。在分子人类学的研究中,人体的DNA材料被作为工具,以分析群体中的各种结构关系,获得群体的遗传结构,以此与其它各种领域的人类学研究结果结合判断群体的系统发生历史。本项研究就是以这种方法来探索澳泰族群的系统发生和发展。本研究用的DNA材料主要是目前分子人类学中最为有效的Y染色体单倍群结构和线粒体单倍群结构,分别代表着群体的父系和母系结构。

关键词: 分子人类学; 澳泰族群; Y染色体单倍群; 线粒体单倍群; 百越; 民族史

The Austro-Tai populations include three groups, the Dai (Tai-Kadai) family on the South China and Indo-China Peninsular, the aboriginal group on Taiwan Island, and the Malay-Polynesian family found throughout the Pacific Ocean, India Ocean, and Southeast Asia. To determine the phylogenetic tree within the Austro-Tai populations, we examined the Y chromosomal and mitochondrial DNA (mtDNA) diversity of 1,325 individual samples, covering most of the Austro-Tai population from Taiwan, Hainan, mainland China, Vietnam, Thailand, and Indonesia. Our findings show that the

Austro-Tai populations are a unity not only in culture but also in genetic structure. The most frequent Y-SNP marker of Austro-Tai is the O1 haplogroup, which is very rare out of the Austro-Tai family. By analyzing the structure within the O1 haplogroup, we can learn the expansion history of the Austro-Tai populations. Aside from the Y-chromosome, we also studied the maternal lineages by examining the mtDNA. We found that B4a, B4b, M7b etc of mtDNA are also concentrated in the Austro-Tai populations. By these analyses, the early history of the peopling of the southern East

Asia will be clearer.

Austro-Tai populations were one of the Mongoloid branches of modern humans that emerged out of Africa around 50 thousand years ago. Mongoloid people branched off along the migration path from East Africa to the Far East. About 30 thousand years ago, the early Mongoloid population divided into two groups in Southeast Asia. Some went northward into East Asia along a west route from Myanmar into Yunnan, and others went along the east route from Vietnam into Guangxi. These two migrations were the origin of most of the East Asians today.

The ancestors of Austro-Asiatic, Hmong-Mien, and Sino-Tibetan were in the west route, while Austro-Tai was in the east route. The Austro-Tai populations resided and developed for many thousand years around the Gulf of Tonkin, and it is assumed that the Y chromosome O1 haplogroup originated there about 20 thousand years ago.

The diversification and diffusion of Austro-Tai can be divided into three periods. The first period is the population differentiation in the Paleolithic Age. In this period, difference appeared between the mountain populations in Guangxi backland and the seashore populations around Gulf of Tonkin. While the mountain population developed into Daic-Kloc (Luo-Yue), the O1 haplogroup originated in the seashore populations and subsequently spread along the seashore, kept in the Hlai populations as the oldest layer in Hainan. By 14 thousand years ago, the seashore population had spread along the seashore of Guangdong to Taiwan. The Taiwan Island was connected to the mainland of Guangdong at that time, and the migration of that time became the earliest part of the present Taiwan aboriginal populations. Around 12 thousand years ago, other populations began to go southward from Gulf of Tonkin along the Vietnam seashore, which developed into Malaysians later. Genetic

structural analysis on Y chromosome O1 haplogroup shows that Taiwan aborigines and Malaysians were on opposite sides of Daic. About 10 thousand years ago, Tai and Kadai populations were polarized. Populations in the west of Guangdong became Kadai, the ancestors of the present Gao people, and those in the east of Guangdong became Tai, the ancestor of Kam-Tai. Geographically, the Kam-Sui population is closest neighbor of the Gao, which resulted in frequent gene flow subsequently.

The second period is the further diversification of Daic and migration of Austronesian populations in the Neolithic Age. About eight thousand years ago, Neolith culture and agriculture germinated in the east of Guangdong, making this area a core region of the Daic expansion. These cultures spread out rapidly, branching off into three groups, Yue, Klam, and Lowland Taiwanese. The Yue group arrived in Zhejiang and later developed into the famous Hemudu and Liangzhu Neolithic culture. The core group of Klam, which spread in Guangdong and Fujian, Nan-Yue and Min-Yue subsequently, became the second stratum of the Kam-Tai structure. The Lowland Taiwanese mostly came from Min-Yue. Time estimate of the O1 haplogroup indicates that paternal lineages of the Yue, Kam-Tai, and Taiwan aborigines were mostly founded about eight thousand years ago. This time point was supported by archaeological discoveries.

During the time from five to three thousand years ago, Min-Yue in Fujian and Nan-Yue in Guangdong were polarized, and gave birth to some new groups migrating out of the core region. These new populations were usually called Ou, which meant the outside people. Eventually, the Eastern-Ou migrated northward out of Min-Yue to south Zhejiang, and the Western-Ou traveled westward out of Nan-Yue to Guangxi. The Western-Ou mixed with the Luo-Yue and became the ancestors of

the Zhuang-Tai. At about the same time period, the Kadai went northwest to Guizhou and founded several Kingdoms such as Yerong (Ye-Lang). They assimilated a large number of Phu aboriginal populations there, whose mother tongues were Proto-Austro-Asiatic. These findings were determined based on the duality of the Kadai genetic structure.

The third period of Austro-Tai population history is the scattering and migration of the Kam-Tai. About two thousand years ago, the Han people began to migrate into the area of the Kam-Tai, and the Kam-Tai populations left the southeast coast zone in succession. The largest migration was the exile of the Min-Yue. It was a coercive migration by the Han Empire, resulting in almost all of the Min-Yue populations leaving Fujian. Thus, Austro-Tai markers can hardly be found in today's Fujian population.

Some Min-Yue populations escaped to Guangdong and then went further west to Guizhou, forming today's Sui people. Others moved to Taiwan. We found that the Sui is the population with the most genetic connections to the Taiwan aborigines among world populations. Most of the Guangdong populations also migrated northwest, turning into Kam people. Subsequently, a part of the Zhuang-Tai people also left Guangxi and migrated to the Indo-China peninsular, becoming Tai-Thai populations.

A comprehensive investigation in Laos and Thailand revealed that present Tai-Thai populations mostly came from the indigenous Austro-Asiatic populations, with only very low proportion of the Daic ancestry. And the proportion of Daic ancestry also varies among the Tai-Thai populations, with higher proportions in the larger populations, such as Lao, Phutai, Thai, Tai-Lue, etc. Whereas in the small populations, such as Saek and Rien, show no genetic resemblance to the Daic populations in China. Therefore, the small Daic populations

in Southeast Asia most probably came from the Austro-Asiatic populations and accepted the language and culture of Daic migrants in the recent two thousand years.

The Austro-Tai populations are very large in East and Southeast Asia. Many details about migration routes and ancient populations are yet unclear, requiring more genetic study on more populations. By now, at least we are able to reconstruct a compendious phylogenetic tree of the Austro-Tai, which helps greatly in accessing the early history of the peopling in Far East.

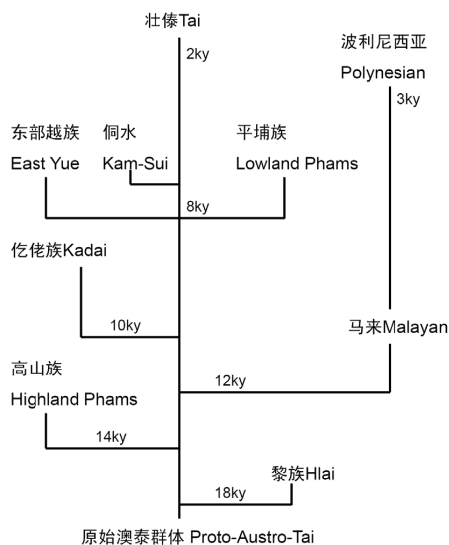


图1 澳泰族群演化的父系遗传谱系树
Fig.1. A paternal phylogenetic tree of Austro-Tai populations.

澳泰族群包括分布于中国大陆和东南亚各国的侗傣、黎仡族群, 中国台湾岛的原住民, 分布于东南亚、太平洋、印度洋岛屿的马来-波利尼西亚族群。本项研究采集的样本量有 1,325 例, 包括了大陆和台湾几乎所有的澳泰群体, 以及越南、泰国、印尼的大量处, 遗传结构上也有非常明显的共性。澳泰族群最明显的特征性标记是 Y 染色体 SNP 单倍群 O1。整个澳泰族群的演变过程基本上可以根据对 O1 单倍群的内部结构观察得到。另外, 线粒体单倍群 B4a、B4b、M7b 等等也具

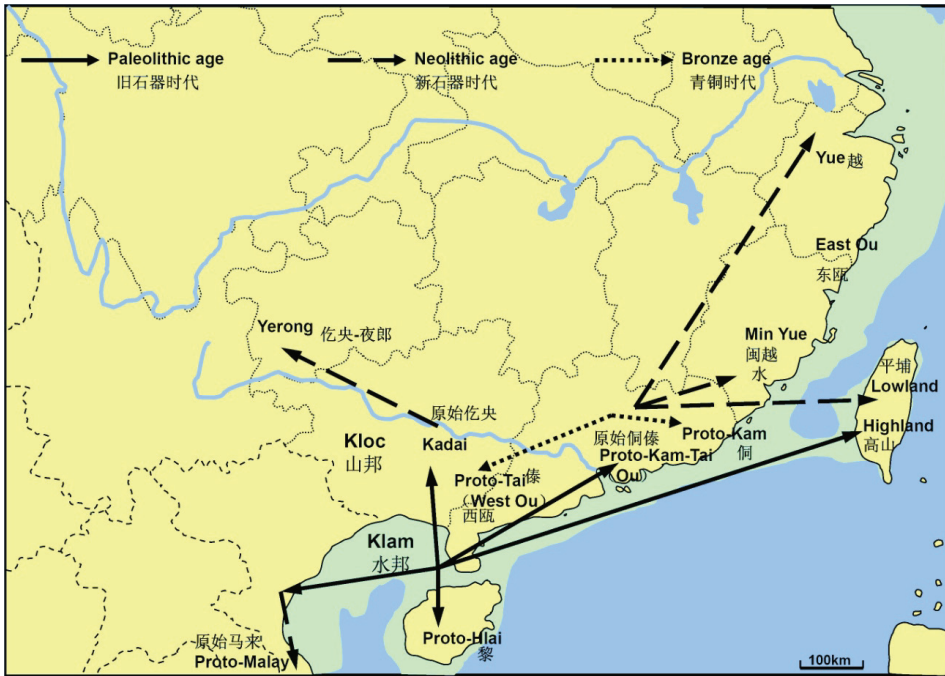


图 2 从 Y 染色体分析推测的澳泰族群演化线路和过程

Fig.2. Diversification history and migration routes of Austro-Tai populations inferred from the Y chromosome diversity

有澳泰族群的特征。

研究发现，澳泰族群是 5 万年前走出非洲的现代人类的一个分支。现代人类来到远东地区以后，形成了蒙古人种的群体，并由东南亚向东亚大陆进发。大约 3 万年前，群体在云贵高原两侧分为两条路线北上，南亚-苗瑶-汉藏祖先群从西线走缅甸-云南路线；澳泰族群从东线走越南-广西路线。在北部湾一带，澳泰群体孕育了很长时间，O1 单倍群就是 2 万多年前在此出现的。

澳泰族群的分化和扩张分为三个阶段。第一个阶段是旧石器时代的分化，首先是广西内陆的山地群体和北部湾沿岸的群体发生了差异。山地群体后来发展成为雒越。O1 出现在沿海群体中，并随后者沿海岸的迁徙而扩张开来，在海南岛的黎族中保存了最古老的结构。一万四千多年前，沿海群体向东迁徙，散布到了整个广东和台湾的海岸线上。台湾的原住民就是从那个时期开始形成遗传基础。稍后，北部湾的沿海群体又有部分沿着越南海岸南下，后来发展成马来族群。所

以我们观察到，澳泰遗传结构中台湾和马来族群相隔距离明显，两者都联结在大陆的侗傣族群上。在大约一万年以前，广东西部的群体和东部的群体发生了差异，西部群体后来大部分演化成仡佬族，而东部是侗傣族群的祖先。我们发现与仡佬族遗传关系最密切的是现代的侗水族群。

第二个阶段是新石器时代的扩张和分化。大约 8000 多年前，广东东部的某一个部族中开始萌发新石器文化和农业文明，并迅速扩张开来。这次扩张先是形成了三个族群，向浙江的迁徙形成了江浙的越族祖先，并发展出了辉煌的河姆渡文化和良渚文化；向台湾的渡海迁徙形成了台湾平埔族的一部分；在广东和福建的内部扩张形成了侗傣族群的第二个遗传层次。对 O1 的年代估算确实发现，江浙的越裔人群、侗水族群、台湾原住民的这一部分年代都是 8000 多年。到了 5000 年到 3000 年期间，闽越和南越发生了分化，闽越向北分出了东瓯，南越向西分出了西瓯。西瓯和雒越融合形成了壮傣族群的祖先。而

仡佬族的祖先向西北迁徙到了贵州，建立了夜郎诸国，同化了当地的许多南亚语百濮族群，使得我们现在观察仡央族群遗传结构的时候可以看到明显的二元性。

第三个阶段是历史时期的流散和迁徙。2000 千多年前，在汉族的扩张压力下，澳泰族群百越民族纷纷离开东南沿海。特别是闽越在强制移民政策下，几乎完全离开了福建。故而在福建几乎看不到澳泰遗传特征了。部分闽越群体逃亡到了广东，并渐渐向西迁徙到贵州，演化成了今天的水族类民族。我们可以观察到，大陆的民族中与台湾遗传联系最多的是水族。广东的南越群体也大规模地向西北迁徙，形成了今天的侗族类群体。壮傣族群中有一部分人向中南半岛迁徙，渐渐分化成了现在的傣泰族群。

在对老挝和泰国进行了大规模的人群调查以后，我们发现傣泰族群的遗传结构中来自中国侗傣族群的成分普遍较少，而且这种成分比例在不同群体中有明显的差异。在较大的群体中，比如老族、泰族、普泰族、傣泐族等群体中，来自中国的成分(Y 染色体 O1 为代表)明显较高。而在一些小群体中，比如老挝的傣族和仡族，就完全不含有明确的中国成分。这说明，这些中南半岛的傣泰族群小民族很可能是当地原来的孟高棉族群被侗傣移民同化的结果。

我们通过分子人类学的遗传结构分析，大致了解了澳泰族群源头的发生历史。但是还有大量的向外流散过程还没有调查分析。对古代族群的研究推断还没有足够的实证。所以澳泰族群的遗传结构研究还任重道远。