

## Session 2 (October 9<sup>th</sup>, 2010)

### Biologic evolution and Human Paleobiology

#### Table 2.1: Taxonomy and phylogeny of the Eurasian peopling

## Are Neanderthals challenging the “out-of-Africa” model for modern human origins?

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There has been a debate on the origin of anatomically modern humans. One side, supported by the Geneticists and now more from other fields, suggested an “out-of-Africa” replacement model, assuming that ancestors of modern humans evolved in Africa, and spread and replaced all other hominids subsequently. The other side, which has been insisted by some paleoanthropologists, suggested the multiregional model claims that a gradual transition from *Homo erectus* to modern humans took place on different continents in the Old World. There are also some intermediate models, acknowledging an African origin of modern humans but with some contribution from other archaic hominids outside Africa.

The debate is now focusing on whether other archaic hominids could breed with anatomically modern humans and then contributed to the current modern human gene pool.

One of the hominids is the “Neanderthals” (*Homo neanderthalensis*), an extinct member of the *Homo* genus, populated Europe and parts of western and central Asia before their disappearance 25 kya ago. Fossil evidences suggest that Neanderthals had probably coexisted with early modern humans for 20 kya. This long period of coexistence, including cohabitation in the Middle East and Europe, raises the possibility of genetic admixture between Neanderthals and modern humans.

One approach to this question is to make a direct comparison of DNA sequences from both Neanderthals and modern populations. Analysis of mitochondrial DNA data from multiple Neanderthals has been interpreted as evidence against a genetic contribution by the Neanderthals to the modern human gene pool. But it was argued that even if some Neanderthals could interbreed with anatomically modern humans, their genes probably have been lost through genetic drift.

The development of high-throughput DNA sequencing technologies has led to the large-scale sequencing of nuclear DNA from fossil bones and teeth. Svante Pääbo’s team has presented a draft sequence of the Neanderthal genome composed of more than four billion nucleotides from three individuals. Their data suggest that 1-4% of the genomes of Eurasians are derived from the Neanderthals. Neanderthals shared more genetic variants with modern humans in Eurasia than with modern humans in sub-Saharan Africa, suggesting that gene flow from the Neanderthals into the ancestors of Eurasians occurred before the divergence of Eurasians. The team detected gene flow from the Neanderthals into modern humans but no reciprocal gene flow from modern humans into the Neanderthals.

However, this result, especially the direction of the assumed gene flow, is quite doubtful. The

comparison of only three Neanderthal genomes with few modern human genomes can not immediately answer questions about the evolutionary fate of the Neanderthals. Further analyses of the Neanderthal sequences and multiple modern human genomes, as well as the genomes of other archaic hominids, have the potential to be much more informative. And as regard of the direction of gene flow, we can first figure out the mutations that might have been inherited from Neanderthals, and then see whether Africans and non-Africans carry these same mutations. Improved computational and statistical methods are needed.

What about the situation in Asia? Fossils from Java suggest that Asian *Homo erectus* and anatomically modern humans might also have overlapped in time and space. We expect that more analyses will provide further insights into the origins of modern humans.

## 尼安德特人挑战现代人“出非洲”学说?

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现代人的起源是学术界长期争论的问题。“出非洲”学说认为现代人的祖先起源于非洲而迁徙扩散到其他大陆, 并取代了当地的古人种。然而, 多地区起源说则认为不同大陆上的古人类独立、连续地进化成了现代人。还有一些中间学说, 既承认现代人起源于非洲, 又认为非洲外的古人类对其有遗传贡献。

争论的焦点就在于其他古人种能否与解剖学上的现代人杂交及他们对现代人的基因库是否有贡献。

尼安德特人(尼人)为解决上述问题提供了线索。尼人是已经灭绝了的古人种, 他们 2 万 5 千年前生活在欧洲以及中亚和西亚的部分地区。化石证据显示尼人与早期现代人极可能共存了 2 万年。如此长时间的共存, 在中东和欧洲, 尼人与现代人的栖居地甚至还有重叠, 这就极大增加了尼人和现代人基因交流的可能性。解决这个问题的一条途径是直接比较尼人和现代人的 DNA 序列进行比对。已有的众多尼人的线粒体 DNA 数据无一例外均证明尼人对现代人的基因库没有贡献。但也可能尼人可与现代人杂交, 只不过他们的线粒体基因经漂变而逐渐丢失了。

高通量测序技术的不断发展使得古 DNA 基因组的大规模测序成为可能。斯万特·派博领导的研究组对 3 个尼人进行基因组全测序, 得到了 40 亿碱基, 做出了尼人的基因组草图。他们的数据显示现代人有约 1-4% 的 DNA 源自尼人, 且尼人与欧亚地区的现代人所共享的基因突变比其与撒哈拉以南非洲的现代人要多, 既就是说现代人与尼人非常可能在小范围内发生过基因交流, 时间是现代人走出非洲后在中东遇到尼安德特人之时。他们声称基因是由尼人流入现代人的, 且并未观察到反向基因流。

然而, 这一结论非常可疑, 特别是基因的流向。仅用 3 个尼人的基因组草图与极少数的现代人比对仍难以回答尼人的进化速率等问题。若将尼人基因组与更多的现代人的及其他古人种的进行比对, 则可使问题变得更清楚。对于基因流向问题, 我们可以利用计算和统计的方法对现代人基因组里那些可能来自尼人的突变进一步分析, 看非洲人和其他大陆的人是否也有相同的突变。

那么, 亚洲的情形会如何呢? 爪哇的化石证据显示亚洲的直立人与现代人也可能在生活时间和空间上有重叠。我们期待更进一步的研究可以为我们揭开现代人起源的迷团。