

Amelogenin Gene and Enamel Structure and Morphological Anthropology

ZHAO Lingxia

(Institute of Vertebrate Paleontology and Paleoanthropology, Academia Sinica, Beijing 100044)

Morphological anthropology and bio-molecular anthropology are two very different disciplines. At present it is still a great challenge for both sides in exploring the common interesting questions, such as origin of anatomically modern human, relationships between different human races. The fact is that we don't know so clearly about the inner relationships between characteristics (which are analyzed in human evolution research by morphologists) and genes (which are analyzed in molecular phenogeny by molecular biologists). Therefore the heating debates on some topics between them are unavoidable in recent years. However it is still possible for them to join each other in some way. This trend has been showed in tooth study.

Tooth enamel is the hardest tissue of human body, and consists of the main part of the tooth crown. Because of its durability and invulnerability, teeth are the most common fossil records. From dental morphology and histological structure, paleoanthropologists can get important information on individual identification and ontogeny and phylogeny. In last two decades, anthropologists pay a great attention to enamel structure and development and its application in hominid evolution and taxonomy. A series of enamel structure researching have been done among Miocene hominoids such as *Proconsul* and *Lufengpithecus* (Zhao Lingxia, et al, 1999; 2000; 2001; 2002), and Pliocene and Pleistocene hominids such as *Australopithecus* and *Homo*, as well as extant hominoids. The results from enamel structure cast some doubt on previous conclusions and suggests from classical morphological study, for example dental development in Plio-Pleistocene hominids was closer to that in extant great apes than to that in modern humans.

Amelogenin is the major extra-cellular matrix protein in the developing tooth bud, and is directly related to enamel structure. The results of cloning and sequencing of genomic sequences indicate the homologous amelogenin gene on the short arms of both X and Y chromosomes encodes amelogenin and this gene is highly conserved in primate. Single copy X-Y homologous amelogenin gene can be amplified by PCR technique. In recent years, amplifying segments of this gene is widely used in gender identification of modern human samples. Ancient DNA has also been extracted and a pair of 106-112bp amelogenin gene segments (used for sex test) have been amplified successfully from Chinese Neolithic human bones and teeth (about 6000-9000 years ago) (Zhao Lingxia, et al, 1996), and the molecular result is identical to the morphological sex judgment.

The analysis by amelogenin gene and enamel structure and morphology together is possibly applied to physical anthropological questions in future. As the undertaking Human Genome Project (HGP) develops expansively and deeply, it helps anthropologists to understand human diversity and helps morphological anthropologists and molecular biologists go closely on common interesting questions.