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## GENETIC LINK BETWEEN CHAOSHANESE AND OTHER CHINESE Populations: Evidence from Mitochondrial DNA

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Various variations of mitochondiral DNA (mtDNA) were determined in 256 Chaoshan individuals by direct sequencing two hypervariable segments (HVS-I and HVS-II) and some coding fragments, and by genotyping 9-bp deletion and some haplogroup-specific regions using PCR-polyacrylamide gel electrophoresis (PCR-PAGE) and PCR-restriction fragment length polymorphism (PCR-RFLP) assays, respectively. The matrilineal genetic composition of Chaoshan population and its maternal relationship with other Chinese populations were investigated by comparing mtDNA data of our Chaoshan population with those of other 84 Chinese populations involving 4289 individuals from seven linguistic families and subfamilies. Principal component and neighbour-joining phylogenetic tree analyses showed a clear demarcation between populations from Northern and Southern China, and Chaoshan population clustered closely with Southern Han group, which was separated distinctively from Northern Han. Furthermore, admixture analysis by using Northern China Han and Southern China natives as two parental populations revealed about equal contribution of these parental populations to the matrilineal gene pool of Chaoshan population, indicating that the maternal origin of Chaoshan population was derived from both Northern China Han and Southern natives. Social factors such as virilocal paternal inheritance, gender ratio of migrants, mate choice, and cultural assimilation, might have also played significant roles in shaping the matrilineal genetic landscape of Chaoshan population during the blending of Northern China Han migrants with Southern natives. In conjoining of the results from this work with those from our previous studies, it once again confirmed the Southern Han characteristics of Chaoshan population.

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