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Whole-Y Sequencing Provided Clearer O Haplogroup Subclade Determinations Than Traditional Techniques Among Male Hans in Henan (Central China)

Hao Wang^{1,2,#}, Lu Yu^{1,3,#}, Ning Wang^{1,#}, Ruixue Peng^{1,4}, Zhongqian Guo^{1,5},
Lulu Wang¹, Lanhai Wei^{6,7,*}, Hong'en Xu^{8,*} and Zhaoshu Zeng^{1,*}

¹*Department of Forensic Medicine, School of Basic Medical Sciences,
Zhengzhou University, Zhengzhou 450001, Henan, China*

²*Material Evidence Identification Center,*

Public Security Bureau of Xizang Autonomous Region, Lasa 850000, Xizang Autonomous Region, China

³*Judicial Expertise Center, The 2nd People's Hospital of Zhengzhou City, Zhengzhou 450052,
Henan, China*

⁴*Department of Forensic Sciences, Public Security Bureau of Pingdingshan City,
Pingdingshan 467036, Henan, China*

⁵*Judicial Expertise Center, Henan No.3 Provincial People's Hospital,
Zhengzhou 450006, Henan, China*

⁶*School of Ethnology and Anthropology, Inner Mongolia Normal University,
Hohhot 010028, Inner Mongolia Autonomous Region, China*

⁷*Department of Anthropology and Ethnology, Institute of Anthropology,
Xiamen University, Xiamen 361005, Fujian, China*

⁸*Precision Medicine Center, Academy of Medical Science, Zhengzhou University,
Zhengzhou 450052, Henan, China*

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ABSTRACT Binary polymorphisms in the non-recombinant portion of Y chromosome are useful on many occasions and have been investigated using traditional techniques, such as enzyme cleavage, sequence-specific PCR, and SNaPshot. However, Y haplogroup reports may not be sufficiently accurate compared to next-generation sequencing (NGS) data. Here, the researchers first analysed 205 samples from male Henan Han people using traditional methods and found 75.11 percent O and 11.71 percent C. Subsequently, the researchers analysed 55 samples via NGS. A comparison of each haplogroup of the same sample by traditional methods and by NGS showed consistency in main clade determination. However, in O subclade determinations, only one sample was identical between the two techniques (1/55=1.82%), two samples were absolutely different in subclades (2/55 = 3.64%), and the remaining 52 samples yielded clearer subclades by NGS/Yleaf than by traditional methods (52/55 = 94.54%). Overall, the study suggested that NGS/Yleaf was much clearer in Y haplogroup O subclade determinations.