

## SHORT COMMUNICATION

# No association between Y chromosomal haplogroups and severe acne in the Han Chinese population

Mei-Hua Guo<sup>1,20</sup>, Wen-Juan Wu<sup>1,20</sup>, Long Fan<sup>2,20</sup>, Min-Sheng Peng<sup>2,3,20</sup>, Jian-Kang Yang<sup>3,4</sup>, Wen Zhang<sup>2,5</sup>, Fei Hao<sup>6</sup>, Hong-Fu Xie<sup>7</sup>, Lei-Hong Xiang<sup>8</sup>, Min Zheng<sup>9</sup>, Yan-Ni Guo<sup>10</sup>, Qing-Hua Song<sup>11</sup>, Cai-Xia Tu<sup>12</sup>, Hua Zhong<sup>13</sup>, Wen-Ge Fan<sup>14</sup>, Yue-Jun Shi<sup>15</sup>, Ping Cao<sup>16</sup>, Lian-Yuan Feng<sup>17</sup>, Meng Na<sup>18</sup>, Qin Pang<sup>19</sup>, Xiao-Yan Yang<sup>19</sup>, Cheng Yang<sup>19</sup>, Xi Zou<sup>19</sup>, Li He<sup>1</sup> and Ya-Ping Zhang<sup>2,3,4</sup>

**Severe acne presents sexual dimorphism in its incidence in Chinese population. It is more prevalent in males. To assess the possible Y chromosomal contribution to severe acne risk in Han Chinese males, we analyzed 2041 Y chromosomal SNPs (Y-SNPs) in 725 severe acne cases and 651 controls retrieved from our recent genome-wide association study data. After data filtering, we assigned 585 cases and 494 controls into 12 Y chromosomal haplogroups based on 307 high-confidence Y-SNPs. No statistically significant difference in the distribution of Y chromosomal haplogroup frequencies was observed between the case and control groups. Our results showed a lack of association between the incidence of severe acne and the different Y chromosomal haplogroup in the Han Chinese population.**

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Acne is a common human skin disease, and globally affects ~650 million people.<sup>1</sup> It can be graded into 1–4 levels based on clinical examination and photographic documentation.<sup>2</sup> Severe acne (grade IV acne of Pillsbury Grade) is characterized by widespread inflammatory lesions, such as nodules, cysts and potential scarring.<sup>2</sup> In a recent community-based study performed in China, 5.6% of subjects were found to have severe acne, and it was more prevalent in males (7.1%) than in females (3.4%).<sup>3</sup> The male-biased pattern was also observed in coronary artery disease, and it was linked to Y chromosome.<sup>4,5</sup> Some early epidemiological studies have suggested that severe acne appeared to be present more frequently in males with XYY syndrome,<sup>6</sup> implying a potential association between Y chromosome and severe acne.<sup>7</sup> Nevertheless, at least to our knowledge, few efforts have been carried out to explore the role of the Y chromosome in severe acne.

Recently, we conducted a genome-wide association study (GWAS) to identify two susceptibility loci, 1q24.2 and 11p11.2, as the genetic

risk factors to severe acne in the Han Chinese population.<sup>8</sup> As GWASs generally disregard Y chromosomal SNPs (Y-SNPs), we developed a pipeline for retrieving and analyzing Y-SNPs from GWAS data.<sup>9</sup> It provides us an opportunity to investigate the Y chromosomal variation in Han Chinese males with severe acne.

We extracted 2041 Y-SNPs of 1376 males (that is, 725 cases and 651 controls) with PLINK 1.07<sup>10</sup> from our previous GWAS data referring to 1031 cases and 1031 controls.<sup>8</sup> The well-matched case–control study showed minimal evidence of population stratification.<sup>8</sup> The GWAS SNPs were genotyped by HumanOmniZhongHua-8 BeadChip (Illumina, San Diego, CA, USA). A series of efforts of quality control were performed for Y-SNP data as suggested before.<sup>9,11</sup> First, 297 males were removed due to high proportions of missing genotypes (>66%; Supplementary Material 1), and 1079 male samples (that is, 585 cases and 494 controls) with a call rate >85% were used in analyses. Second, 244 Y-SNPs genotyped with heterozygous alleles in the 1079 male samples were

<sup>1</sup>Kunming Medical University, and Institute of Dermatology & Venereology of Yunnan Province, Kunming, China; <sup>2</sup>KIZ/CUHK Joint Laboratory of Bioresources and Molecular Research in Common Diseases, Kunming, China; <sup>3</sup>State Key Laboratory of Genetic Resources and Evolution, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, China; <sup>4</sup>Laboratory for Conservation and Utilization of Bio-Resources & Key Laboratory for Microbial Resources of the Ministry of Education, Yunnan University, Kunming, China; <sup>5</sup>Key Laboratory of Animal Models and Human Disease Mechanisms, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, China; <sup>6</sup>Department of Dermatology, Southwest Hospital, Third Military Medical University, Chongqing, China; <sup>7</sup>Department of Dermatology, Xiangya Hospital Central South University, Changsha, China; <sup>8</sup>Department of Dermatology, Huashan Hospital, Fudan University, Shanghai, China; <sup>9</sup>Department of Dermatology, The Second Affiliated Hospital of Zhejiang University School of Medicine, Hangzhou, China; <sup>10</sup>Department of Dermatology, Second Affiliated Hospital of Fujian Medical University, Quanzhou, China; <sup>11</sup>Department of Dermatology, Peking University Third Hospital, Beijing, China; <sup>12</sup>Department of Dermatology, The Second Hospital of Dalian Medical University, Dalian, China; <sup>13</sup>Department of Dermatology, Qilu Hospital of Shandong University, Jinan, China; <sup>14</sup>Department of Dermatology, Changshu NO.1 People's Hospital, Changshu, China; <sup>15</sup>Department of Dermatology, Dalian Dermatoses Hospital, Dalian, China; <sup>16</sup>Department of Dermatology, First people's Hospital of Yunnan Province, Kunming, China; <sup>17</sup>Yuxi Lianyuan Hospital, Yuxi, China; <sup>18</sup>Department of Dermatology, Kaiyuan People's Hospital, Kaiyuan, China and <sup>19</sup>Winona Dermo-Cosmetology Center, Kunming, China

<sup>20</sup>These authors contributed equally to this work.

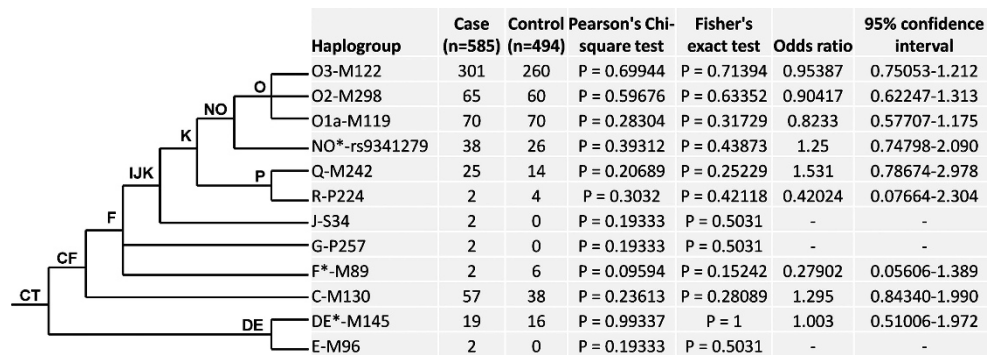
Correspondence: Professor L He, Kunming Medical University, and Institute of Dermatology & Venereology of Yunnan province, Kunming 650032, China.

E-mail: helikm2662@126.com

or Professor Y-P Zhang, State Key Laboratory of Genetic Resources and Evolution, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming 650223, China.

E-mail: zhangyp@mail.kiz.ac.cn

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**Figure 1** Y chromosomal haplogroup distribution in severe acne cases and controls in the Han Chinese population. The statistical analyses were performed by using MitoTool (<http://mitotool.org/>).<sup>17</sup>

disregarded (Supplementary Material 2). Third, 25 Y-SNPs with missing genotypes in >5% of the male samples were excluded (Supplementary Material 2). Fourth, 1450 Y-SNPs identified as invariant were filtered (Supplementary Material 2). Fifth, 15 Y-SNPs that occurred as recurrent mutations were not considered (Supplementary Material 3). All the above data filtering were done using the combination of PLINK 1.07 (<http://pngu.mgh.harvard.edu/~purcell/plink/>),<sup>10</sup> YTool 1.0 (<http://mitotool.org/ytool/>)<sup>9</sup> and NETWORK 4.611 (<http://www.fluxus-engineering.com/sharenet.htm>).<sup>12</sup>

For the 307 Y-SNPs obtained after data filtering (Supplementary Material 3), we constructed the Y chromosomal haplogroup tree for 1079 male samples (Supplementary Material 4). All samples were allocated into 12 Y chromosomal (sub-)haplogroups (paragroups) spread over East Asia.<sup>13,14</sup> The haplogroup distribution pattern in the case and control groups is concordant with previous results about Han Chinese.<sup>15,16</sup> We performed statistical analyses to address the distribution of the 12 (sub-)haplogroups (paragroups) between the case and control groups (Figure 1). No statistically significant difference ( $P < 0.05$ ) was observed. Thus, our study provides no support for the association between Y chromosomal haplogroups and severe acne in the Han Chinese population.

## CONFLICT OF INTEREST

The authors declare no conflict of interest.

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