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POPULATION DATA

Allele frequencies of 20 autosomal STR loci for 207 unrelated individuals of the Blang people in China

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Abstract

The Blang is a minority living in the mountainous areas of Xishuangbanna Dai Autonomous Prefecture, and they also scatter in the neighboring cities of Lincang and Simao. This population is investigated in this study through PowerPlex® 21 System. The frequency distribution of allele, forensic, and population parameters of 20 autosomal short tandem repeat loci were evaluated based on 207 non-related individuals from Blang minority; meanwhile, the genetic relationships between Blang and 11 related populations were also assessed.

Keywords Short tandem repeats (STRs) · Blang · Forensic applications · Southwestern China

With a population of 119,639 (in 2010), the Blang people (also known as Bulang) live mainly in the mountainous areas of Menghai County and Xishuangbanna Dai Autonomous Prefecture ("Banna" for short), in the southwestern region of Yunnan Province. Some of them scatter in the neighboring cities like Lincang and Simao, as well. As identified by Chinese ethnographers, the Blang people are descendants of a tribe known as the "Pu", who lived in the Lancang river valley during the ancient times. The Blang people are the oldest tea farmers in China [1].

Buccal swabs (obtained after informed consent) were collected from a total of 207 unrelated healthy donors from Menghai County, whose ancestry can be traced back to at least two generations. Chelex extraction method was adopted to extract DNA. Based on the user's manual recommendations, simultaneous amplifications for 20 autosomal short tandem repeat (STR) loci were performed by virtue of the PowerPlex® 21 System (Promega, Madison, USA), and subsequently the amplified products and reference ladders provided in the kit were analyzed in ABIPrism 3130 Genetic Analyzer (Thermo Scientific, Madison, USA). The GeneMapper software Version 3.5 was employed to analyze the electrophoresis results. The laboratory procedure was accredited according to ISO/IEC 17025:2005.

Several forensic and population parameters, such as the power of discrimination (PD), the power of exclusion (PE),

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and the polymorphism information content (PIC) of the 20 loci were estimated by using the statistical power state; moreover, the Hardy–Weinberg equilibrium analysis and marker's observed and expected heterozygosity (Ho and He, respectively) were performed for each locus through the Arlequin 3.5 [2].

A set of inter-population comparisons in terms of allele frequencies obtained from this study, and 9 additionally published population data sets were implemented. Data from the Blang (from Shuangjiang [3]), Dai, Hani, Yi, Nakhi, Lisu, Va, Achang (unpublished data), Pulang (unpublished data), Indian, and Filipino were compared in this analysis, where the same loci studied were shared. The genetic distance matrix of Nei was computed by using the computer package DISPAN, and a neighbor-joining (NJ) phylogenetic tree was constructed via the MEGA 6.0 software [4].

Table s1 lists the allele frequency and population parameter statistic. No deviation from Hardy–Weinberg equilibrium was observed after the Bonferroni correction. For all of the STR loci, the PD value was > 0.7159, and the PE values ranged from 0.1731 (TPOX) to 0.7434 (D8S1179). The combined power of discrimination and that of exclusion for the 20 STR loci tested were greater than 0.999999.

According to the NJ tree (Fig s2), the minority in the South China can be categorized into two groups, namely, the Austroasiatic-speaking group and the Tibeto-Burman – speaking group. By comparing the two sets of data about the Blang, it can be found that the Shuangjiang Blang clusters with the Va, who come from the same settlement place; however, the Blang in our study and the Va still cluster together, which corresponds with the historical record that the Blang was one branch of population collectively referred to as the "Baipu" (Va and Palaung) by the ancient Chinese. It is interesting that the Blang is genetically more distant to the Dai, even though the settlements of the Blang people overlap with the residential locations of the Dai people, which seems to provide more opportunities for gene exchange.

Data about the Blang obtained from these statistical parameters might be useful for researches on population genetics, individual identification, and paternity testing in forensic science.

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Compliance with ethical standards

Conflict of interest The authors declare that they have no conflict of interest.

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