

LETTER TO THE EDITOR

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Allele frequencies of F13A01, FESFPS, and vWA in a group of cohorts of the Dusun population from Borneo, Malaysia

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Dear Editor,

Short tandem repeats (STR), or repeated DNA sequences, are microsatellite markers that are often used for human identification, particularly in forensic and paternity analyses. STR polymorphisms refer to differing numbers of copies of the repeated DNA sequences, and these polymorphisms can occur within a population of individuals, allowing for their unique identification (Kristmundsdóttir et al., 2016). In our study, three STRs (F13A01, FESFPS, and vWA) were analyzed to generate frequency data for the Dusun population from Borneo, Malaysia. This population contributes to the multiracial population of the country (Reid, 1997). Dusun communities are also present in countries such as Brunei and the Central Kalimantan, Indonesia. According to the Department of Statistics Malaysia, the Dusun population makes up 24.5% of the 3.12 million people in Sabah, Borneo. The use of STR regional frequency data will be essential for population and human identity testing for the Dusun population.

After obtaining informed consent, saliva samples were collected using sterile cotton buds from 100 unrelated Dusun individuals born in the Sabah State. All subjects were confirmed to have lived in Sabah for three consecutive generations. Samples were amplified using the Promega Geneprint™ STR system (Madison, WI, USA) following the manual method described in the user's guide. The polymerase chain reaction products were separated by vertical denaturing polyacrylamide gel electrophoresis (6% for silver STRIII and 4% for FFv triplex) followed by silver staining of the gels according to the published method (Budowle et al., 1995). Allele designation was performed by side to side comparison with

known allelic ladders. Allelic frequencies for each locus in the Dusun population were then compared with other major populations in Malaysia: Malay, Chinese, and Iban (Iban is the largest ethnic group in Borneo). Pairwise genetic distances were calculated between these populations using Mega software version 7.0.26 (Pennsylvania State University, USA) (Zhang et al., 2017). This study was approved by the Research and Ethics Committee, Universiti Sains Malaysia.

Allele nomenclatures of F13A01, FESFPS, and vWA were determined by the number of STR repeats and described based on the International Society for Forensic Haemogenetics guidelines (Gusmão et al., 2006). The three alleles chosen represent the individual microsatellite markers that have unique characteristics in the Dusun population. The power of discrimination values for the markers F13A01, FESFPS, and vWA were high at 0.8496, 0.8112, and 0.9173, respectively. The power of exclusion values were 0.4767, 0.4524, and 0.6074, respectively (Table 1). The highest frequency allele for these microsatellites differed: for F13A01, it was allele 6 (0.545); for FESFPS, it was allele 11 (0.405); and for vWA, it was allele 17 (0.31) (Table 1). This is the first report of the distribution of F13A01 and FESFPS in Malaysia Dusun population. The allele frequency of vWA in the Malaysian Dusun population was previously published by (Kee et al., 2011), and our results were in agreement with theirs.

The genetic distance analysis showed significant differences between the Dusun population and the Malay, Chinese, and Iban populations (Table 2). Although the number of STR alleles investigated in the study was small, this short study illustrates the importance of DNA profiling for this minority group.

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Table 1 Allele frequencies and forensic parameters of the three STR loci for the Dusun population from Borneo, Malaysia

Allele	F13A01	FESFPS	vWA
3.2	0.095	–	–
4	0.115	–	–
5	0.225	–	–
6	0.545	–	–
7	ND	–	–
8	0.015	0.04	–
9	0.005	0.02	–
10	–	0.065	–
11	–	0.405	–
12	–	0.31	–
13	–	0.145	0.02
14	–	0.015	0.13
15	–	–	0.07
16	–	–	0.12
17	–	–	0.31
18	–	–	0.25
19	–	–	0.09
20	–	–	0.01
Chi	7.815	9.48	9.488
H	0.8313	0.756	0.9093
PE	0.4767	0.4524	0.6074
PD	0.8496	0.8112	0.9173

H: Heterozygosity; PD: Power of discrimination; PE: Power of exclusion; Chi: Chi-square; –: Non-detectable

Overall, the microsatellite vWA had the highest power of discrimination for the Dusun population, and F13A01 showed the greatest genetic distance among the populations. The three STR loci described herein have useful discriminatory power for genetic analysis for forensic purposes. Profiling additional STR loci will enhance the unique profile that represents individuals from Malaysia Dusun population.

Table 2 Comparison of allele frequencies for F13A01, FESFPS, and vWA loci between the Dusun population and other populations in Malaysia

Microsatellite markers	Dusun × Iban (Ishara et al., n.d.)	Dusun × Malay (Panneerchelvam et al., 2003)	Dusun × Chinese (Panneerchelvam et al., 2004)
F13A01	0.0876	0.445	NA
FESFPS	0.0255	0.0225	0.00524
vWA	0.0199	NA	0.1305

NA data not available

Abbreviations

DNA: Deoxyribonucleic acid; STR: Short tandem repeats; Chi: Chi-square; H: Heterozygosity; PE: Power of exclusion; PD: Power of discrimination

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Authors' contributions

MYA did the laboratory work and wrote up the letter. SP collected the samples and supervised the laboratory work. ARI helped to analyze the data. All authors read and approved the final manuscript.

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Availability of data and materials

The datasets used and/or analyzed during the current study are available from the corresponding author on reasonable request.

Ethics approval and consent to participate

Research and Ethics Committee, Universiti Sains Malaysia.

Consent for publication

Not applicable

Competing interests

The authors declare that they have no competing interests.

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