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Variant allele 6.2 at locus D19S433 in Syrian family samples

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ABSTRACT

Variant allele 6.2 at locus D19S433 was found in an immigration case involving Syrian family samples where 2 out of 4 children inherited this variant allele from their parents. This variant allele has not been reported previously in the Syrian population since locus D19S433 was not studied. However, records showed the presence of the variant allele 6.2 in Middle Eastern samples of Iraqi, Lebanese, Kuwaiti and Turkish origins. These findings indicate that variant allele 6.2 at locus D19S433 could be specific for the Middle Eastern populations and could be useful in forensic investigation for suspect search.

1. Introduction

Anglia DNA Services uses the AmpFℓSTR® Identifiler® PCR Amplification Kit for paternity and relationship testing [1,2]. This kit contains 15 short tandem repeat loci including locus D19S433 which has tetranucleotide repeat of AAGG [3,4] and covers 15 alleles ranging from 9 to 17.2 [5]. Variant allele 6.2 out of this marker range was found in the Syrian family samples submitted for an immigration case consisting a mother, 4 children and an alleged father.

2. Materials and methods

2.1. Sample collection and DNA extraction

Buccal swabs from each individual involved in this immigration case were collected in duplicate with informed consent. Samples were extracted using the QIAamp® DNA Mini Kit (Qiagen®) following the manufacturer's protocol.

2.2. PCR amplification

Extracted DNA samples were normalised based on the in-house dilution factors and amplified with the AmpFℓSTR® Identifiler® PCR Amplification Kit (Applied Biosystems™) together with the extraction blank and PCR controls.

2.3. Electrophoresis and analysis

Capillary electrophoresis was performed on the ABI Prism® 3500xL Genetic Analyzer (Applied Biosystems™) and alleles were determined using the GeneMapper® ID-X v1.3 software (Applied Biosystems™). Variant alleles were manually assigned based on the amplicon size using the allelic ladder provided by the manufacturer.

2.4. Quality controls

Control DNA and allelic ladders were used for quality assurance. The second buccal swab for all the samples with the variant allele were re-extracted, re-amplified and re-analysed for confirmation.

3. Results and discussion

Out of the 6 family samples in this study, variant allele 6.2 was observed in 4 samples; mother, 2 children and alleged father. Mother has alleles 6.2 and 12 at locus D19S433 while the alleged father has alleles 6.2 and 14. Child 1 inherited variant allele 6.2 from the alleged father, while child 2 inherited it from the mother (Fig. 1). Variant allele 6.2 was not inherited by child 3 and child 4, where both have alleles 12 and 14 at locus D19S433 (data not shown). The sequence of this variant allele has been reported to be $(AAGG)_1AA(AAGG)_1(TAGG)_1(AAGG)_5$ [3,6], but no sequence data was obtained in this study due to limited resources. However, second buccal swab for the mother, child 1, child 2 and the alleged father were re-extracted, re-amplified and re-analysed for the confirmation of this variant allele. Also, there is no risk of mistyping this variant allele since no other marker range was available at the location where it appeared.

Variant allele 6.2 has not been reported in the Syrian population samples since locus D19S433 was not studied in the previous population genetics study [7]. Among the Middle Eastern populations, variant allele 6.2 was observed in the Iraqi Arab population with an allele

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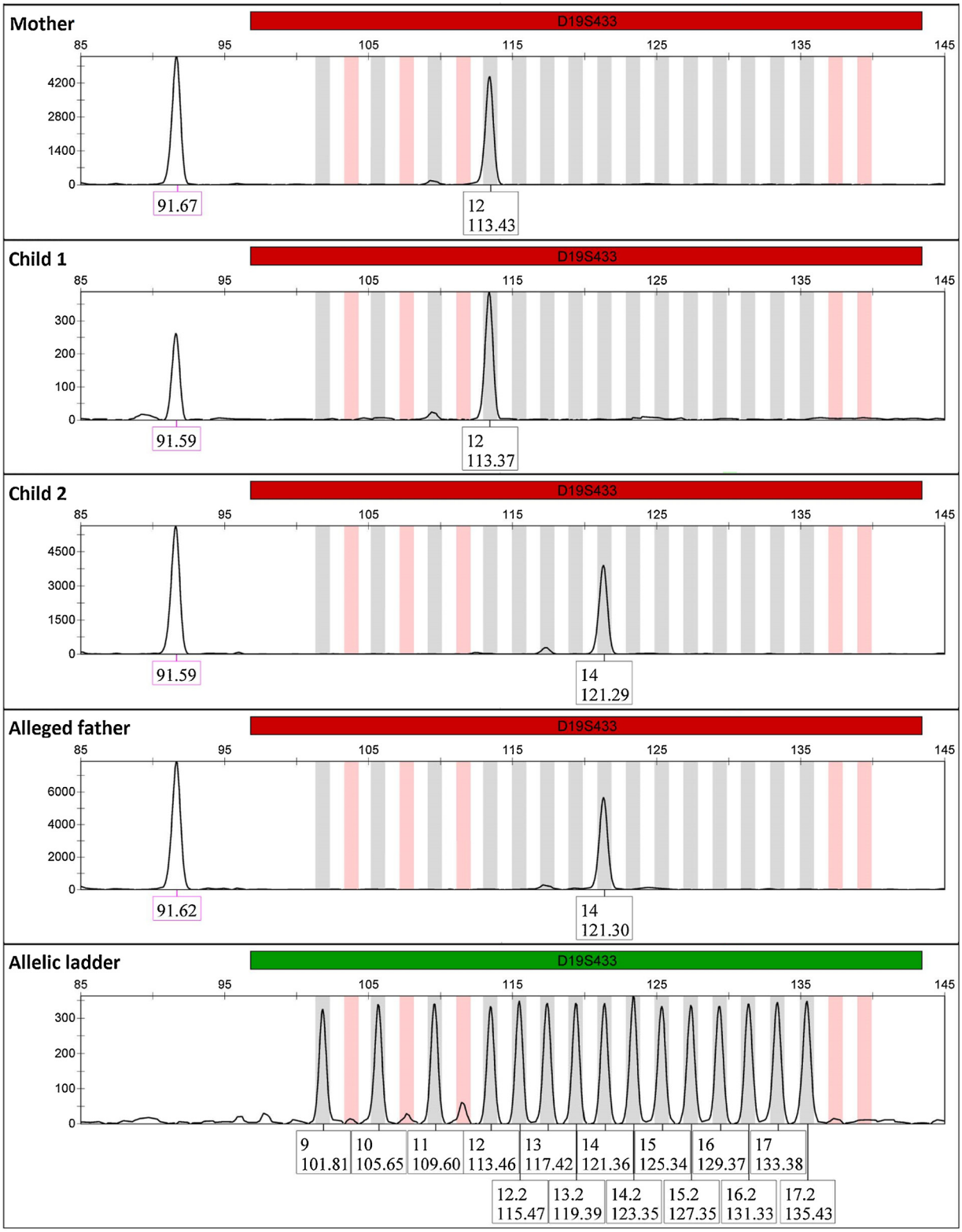

Fig. 1. Electropherograms of mother, child 1, child 2 and alleged father with the variant allele 6.2 at locus D19S433. Variant allele 6.2 was derived based on the amplicon size using the allelic ladder.

frequency of 0.005 (N = 1088) [8] and Lebanese population with an allele frequency of 0.003 (N = 1010) [9]. This variant allele was also found in another study where interestingly all four persons carrying it were known to have Turkish origin. Two additional samples tested in the same study also produced variant allele 6.2; one from Turkey and another with an unknown origin but with a Turkish forename [3].

Previously, this variant allele was found in another immigration case at Anglia DNA Services consisting a mother, 2 children and an alleged father where it was found in 1 of the children, inherited from the alleged father. The ethnic origin of this family was confirmed to be Kuwaiti, however the family surname is primarily found in Jordan and also in Egypt, northern Iraq and Syria (Fig. 2). This variant allele was

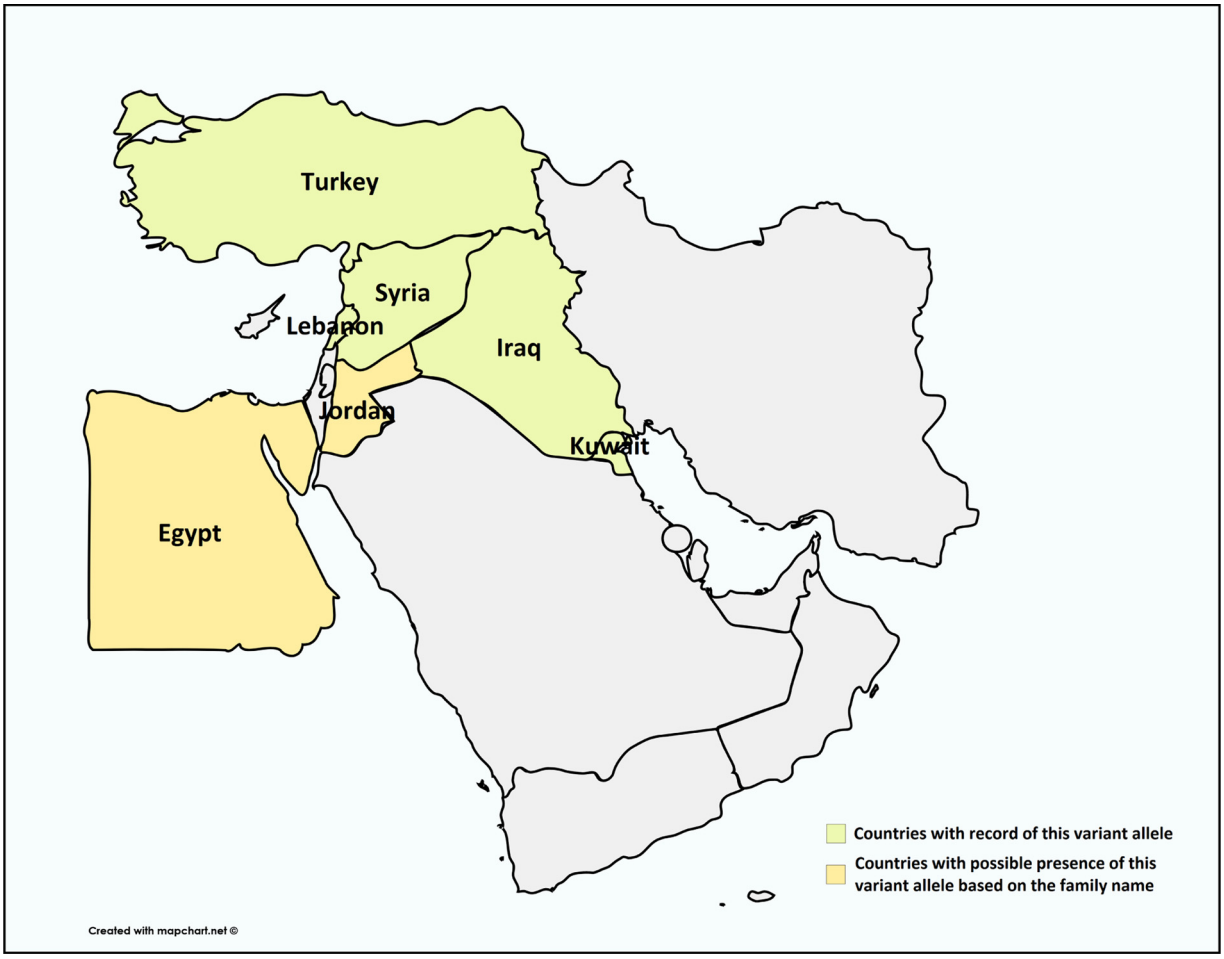

Fig. 2. Countries with the record of the variant allele 6.2 at locus D19S433 on Middle Eastern map. Countries with possible presence of this variant allele based on the family name are also indicated.

also reported by Institute of Legal Medicine, University of Cologne, Germany on the National Institute of Standards and Technology (NIST) website (D19S433 variants; https://strbase.nist.gov//var_D19S433.htm) where they mentioned it was inherited from mother to a child in a Middle Eastern family (accessed on 13th September 2019). They profiled these samples using the AmpFℓSTR® SEfiler™ PCR Amplification Kit (Applied Biosystems™) and the AmpFℓSTR® NGM SElect™ PCR Amplification Kit (Applied Biosystems™) to confirm the presence of this variant allele.

4. Conclusion

All the findings indicate that the variant allele 6.2 at locus D19S433 could be specific to the Middle Eastern populations. This can be useful in forensic cases where the suspect search could be narrowed down to a specific ethnic origin based on the DNA profiles developed from the crime scene samples.

Declaration of Competing Interest

None.

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