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FOR THE RECORD

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A New Allele of the Short Tandem Repeat Locus D21S11 in a Venezuelan Population*

POPULATION: Venezuelan, Caracas City, 255 individuals.

KEYWORDS: forensic science, DNA typing, short tandem repeats, D21S11, new alleles, single base mutation, population genetics

The proband was a 35-year-old female, who voluntarily donated a blood sample for the construction of the population database (1). Eight other members of the family contributed to the study, and except for the father, who was dead, all of them donated blood samples.

A single blood drop was obtained by piercing the index finger and spotted on FTA® cards (GIBCO-BRL, Life Technologies, Ltd., Paisley, Scotland). 2 mm^2 circles of the blood spots were cut and treated with the FTA™ Purification Reagent (GIBCO-BRL) following the manufacturer's recommendations.

Short tandem repeat (STR) amplification was performed according to the AmpF*ℓ*STR® Identifiler™ kit (Applied Biosystems, Warrington, U.K.) protocol using a PTC-200 thermocycler device (MJ Research® Inc., Waltham, MA). Short tandem repeat analysis was carried out on an ABI Prism™ 310 Genetic Analyzer, and automated allele sizing was performed using Genotyper® Software v. 3.7. Sequence edition was performed with Sequencing Analysis v. 3.7 Software. Sequences were analyzed using DNAMAN v. 5.2.2 Software. Primer sequences for allele amplification and cloning were reported by Sharma and Litt (2) and modified by adding restriction sites *Hin*dIII (forward) and *Bam*HI (reverse) to their 5′ ends, resulting in the following sequences: Forward primer: *5′- CGT AAG CTT GTG AGT CAA TTC CCC AAG -3′*; Reverse primer: *5′- CTA GGA TCC TTG TAT TAG TCA ATG TTC TCC -3′*.

A study of this individual's family revealed that the defunct family's father, who also passed it onto one illegitimate son, contributed the new allele. A history record of the father's ancestors confirmed that they all came from Venezuela.

Polymerase chain reaction amplification and dye terminator sequence analysis allowed us to confirm the sequence of this new allele. Except for a T deletion, it had a sequence identical to 33.2 allele; therefore, we propose that the new allele originated by a single T deletion in allele 33.2. Following international recommendations (3), we designated this new D21S11 allele as 33.1.

Quality Control was performed according to proficiency testing of the GEP-ISFG WG (4). All protocols used herein were approved by FONACIT Venezuelan Government Bioethical Committee. Original data are available to any interested researcher upon request; figures are available at: www.idea.org.ve/jfs

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