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Commentary on: Coble MD, Butler JM. Characterization of New miniSTR Loci to Aid Analysis of Degraded DNA. J Forensic Sci 2005;50:43–53.

Sir:

In the above-mentioned article by Coble and Butler, STR loci were described that allow the generation of amplicons less than 125 bp in size and, therefore, particularly may be suitable for the forensic analysis of degraded DNA. In this regard, the development and evaluation of two multiplex assays are presented, including the construction of allelic ladders (1).

Based on the published data, an STR PCR-assay for the locus D10S1248 was established in our laboratory. For the creation of an allelic ladder, the DNA of a total of 98 blood samples was extracted and amplified. After separation on polyacrylamide gels, different allele types were cloned into an M13 vector system and subsequently sequenced. The assignment of alleles was performed in consideration of the recommendations of the International Society of Forensic Genetics (2). For any further allelic typing, the DNA 9947A (Promega, Madison, WI) was used as a control. Although the genotype of this DNA is supposed to be 14/16 (3), our typing revealed the genotype 13/15. The same effect was observed for another control DNA (007, Applied Biosystems, Foster City, CA). Here, the genotype seemed to be 12/15 instead of 13/16, as given in Coble (3). For further clarification, the 9947A control DNA was directly sequenced. Using the above-mentioned nomenclature, the genotype consequently turned out to be 13/15.

The observation of a possibly erroneous allele designation by Coble and Butler is supported by population data, which apparently have been surveyed with allelic ladders from these authors (1,4,5). Comparing different data on several population subgroups, a noticeable step in the frequency of occurrence of short alleles could be observed between allele 13 (published frequency: 0.02–0.12) and 14 (published frequency: 0.19–0.36). However, in concordance with sequencing results, this significant frequency shift was noticed between alleles 12 and 13 in our population sample.

For many STR loci, the increase in information about sequence and substructure has repeatedly raised questions affecting nomenclature rules in the past. However, a uniform allelic assignment is required for interlaboratory data comparison and exchange, particularly in consideration of international databases. As the repeat structure of D10S1248 locus seems to be quite unambiguous on the bases of published sequence information (GenBank® accession number AL391869), a revision of the allelic classification by Coble and Butler and, hence, a verification of population data published so far would be highly preferable.

References

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Thomas Lederer, Ph.D.
Institute of Legal Medicine
University of Erlangen/Nuremberg
Universitätsstr. 22
D-91054 Erlangen
Germany
E-mail: thomas.lederer@recht.med.uni-erlangen.de

Günther Braunschweiger, Ph.D.
GenFOR GmbH
Altenahrer-Str. 9
D-53501 Grafschaft-Gelsdorf
Germany
E-mail: gbraunschweiger@gmx.de