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## Authors' Response

Sir:

The letter by Lederer and Braunschweiger correctly points out that a nomenclature error was made for the STR locus D10S1248 in our paper on new miniSTR loci (1). We agree that the original D10S1248 nomenclature should be reduced by one repeat unit. Thus, the allelic ladder shown in Fig. 3 of Coble and Butler (1) should contain 9–19 repeats rather than the 10–20 repeats reported previously. We independently noted this error based on further sequencing conducted in our laboratory and have made attempts to correct it through contacting collaborating laboratories that we know are using these loci and posting information on the National Institute of Standards and Technology STRBase website: http://www.cstl.nist.gov/biotech/strbase/miniSTR.htm#Nomenclature_Errata.

Furthermore, in a forthcoming publication providing additional characterization and sequencing of these miniSTR loci, we have adjusted the D1S1677 nomenclature by +1 repeat, D452364 by −1 repeat, and D14S1434 by −4 repeats from what was originally published in Coble and Butles (1).

In addition, we have also changed our original D22S1045 nomenclature by +3 repeats from what was originally published (1) in an effort to include additional flanking sequence. This change was described in a poster presentation at the 17th International Symposium on Human Identification held in Nashville, TN, in October 2006 (2). Thus, the adjusted allele range for D22S1045 is 8–19 repeats rather than the 5–16 repeats reported previously (1). Forthcoming publications from our laboratory regarding these miniSTR loci will reflect these nomenclature changes.

It is also worth noting that the GenBank accession numbers in Table 1 of Coble and Butler (1) will not always correspond to the reference allele listed in the same table for the following reason. In the initial building of a database of potential miniSTR markers, we used the forward and reverse primer information for each marker taken from the Genome Database (GDB) website (http://www.gdb.org/). For each marker on the GDB website is a "Nucleic Acid Sequence Links" with locus information linked to GenBank. These GenBank numbers, based upon information from the Cooperative Human Linkage Center (http://lpgws.nci.nih.gov/CHLC/index.html), were also added to the marker information in our database. During the process of identifying miniSTR primer sequences, we utilized BLAST (http://www.ncbi.nlm.nih.gov/BLAST/Blast.cgi) and "dropped" the original primers from GDB to search for each marker in GenBank. The BLAST search brought us to the most recent version of the human genome, where we downloaded the locus DNA sequence into a text file. It was not until after the publication of (1) that we realized the GenBank numbers list in Table 1 utilized information from older versions of the human genome, and do not necessarily reflect the true repeat structure that we determined using the most recent version of human genome DNA sequence information. The following GenBank accessions are correct, and were used to determine our miniSTR primer sequences: D1S1677 (AL513307), D2S441 (AC079112), D4S2364 (AC022317), D10S1248 (AL391869), D14S1434 (AL121612), and D22S1045 (AL022314). We apologize for any confusion that these nomenclature errors may have caused laboratories using these loci. Feel free to contact us if there are any further questions.

The 10 genomic DNA components in the NIST Standard Reference Material 2391b have been sequenced (3) for the D10S1248, D2S441, and D22S1045 loci (1) that have been recommended by leaders in the European DNA typing community (4). Having this sequence information on available standard DNA samples should enable calibration of future typing results.

## References

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