CODIS Bulletin



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UPDATE ON THE AMENDMENT OF THE 1999 AND 2001 FBI STR POPULATION DATA

As reported in the CODIS Bulletin BT050815, the FBI Laboratory has identified some errors in the data published in the Journal of Forensic Sciences *Population data on the thirteen CODIS core short tandem repeat loci in African Americans, U.S. Caucasians, Hispanics, Bahamians, Jamaicans and Trinidadians*, Journal of Forensic Sciences 1999 44(6):1277-86. The FBI Laboratory has now been advised by the publisher of the Journal of Forensic Science (JFS) that the electronic version of the JFS, July 2015, Volume 60, Issue 4 containing the erratum notice containing the empirical data demonstrating their nominal effect on profile probabilities will be published as a Letter to the Editor in electronic form on July 1, 2015 and with the print version to follow on July 7, 2015.

Because this timeframe is substantially different than that originally provided by John Wiley and Sons, Inc. (<u>http://onlinelibrary.wiley.com/</u>), please see the table provided for more information regarding the changes in allele frequencies between the original and amended 1999 and 2001 FBI data sets. All alleles with incorrect allele counts derived from the original data are shown with the difference in frequency between the original and amended values. Negative and positive values reflect a decrease and increase, respectively, in allele frequency.

If you have any questions, please contact Anthony J. Onorato of the FBI's DNA Support Unit at Anthony.Onorato@ic.fbi.gov or 703-632-7572.

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TABLE 1—The effect of change in allele counts and/or sample size (N) on allele frequencies. All alleles with incorrect allele counts derived from the original data are shown with the difference in frequency between the original and amended values. Negative and positive values reflect a decrease and increase, respectively, in allele frequency.

EXPANSION OF FBI STR POPULATION DATA

Allele distributions for the autosomal short tandem repeat (STR) loci D1S1656, D2S441, D2S1338, D3S1358, D5S818, D7S820, D8S1179, D10S1248, D12S391, D13S317, D16S539, D18S51, D19S433, D21S11, D22S1045, CSF1PO, FGA, Penta D, Penta E, SE33 TH01, TPOX and vWA have been determined in the following FBI populations: Caucasians, Southwestern Hispanics, Southeastern Hispanics, African Americans, Bahamians, Jamaicans, Trinidadians, Chamorros, Filipinos, Apaches, and Navajos. An announcement of population data will be submitted for publication under the title "*Population data on the expanded CODIS core STR loci for eleven populations of significance for forensic DNA analyses in the United States.*" The Expanded FBI STR files contain all the corrections made to the recent Amended FBI STR data of the original 1999 population database files. The new expanded FBI population data will be made available immediately on the CJIS WAN (Expanded FBI STR) and then via publication and in a future update to Popstats.

The FBI Laboratory recently announced an expansion of the original thirteen short tandem repeat (STR) loci that have been the core of the National DNA Index System (NDIS) since 1997 (D.R. Hares (2015) Selection and Implementation of Expanded CODIS Core Loci in the Unites States. Forensic Sci. Int. Genet. http://dx.doi.org/10.1016/j.fsigen.2015.03.006 page 33 – page 34). Seven additional STR loci were selected by the CODIS Core Loci Working Group and, following an implementation phase concluding on January 1, 2017, will also be required for upload and searching of DNA profiles at NDIS. Collectively, these loci provide greater discrimination potential for human identification applications and enhance kinship analyses typically used in missing person inquiries. Since many of these loci are included in databases globally, the expanded STR locus set facilitates international law enforcement and counterterrorism endeavours.

The twenty STR loci (the original set: D3S1358, D5S818, D7S820, D8S1179, D13S317, D16S539, D18S51, D21S11, CSF1PO, FGA, TH01, TPOX and vWA; and the additional set: D1S1656, D2S441, D2S1338, D10S1248, D12S391, D19S433 and D22S1045) can be simultaneously genotyped with either the AmpFISTR® GlobalFiler® (GlobalFiler, Life Technologies, Inc., Carlsbad, CA) or PowerPlex® Fusion[™] (Fusion, Promega Corporation, Madison, WI) multiplex amplification systems. These kits also enable the genotyping of SE33

and a Y indel locus (GlobalFiler), Penta D and Penta E (Fusion), and DYS391 (GlobalFiler and Fusion), as well as Amelogenin for sex determination.

The FBI Laboratory has generated allele frequencies for the autosomal STR loci with both the GlobalFiler and Fusion kits in the following FBI population groups: African Americans, Caucasians, Southeast Hispanics, Southwestern Hispanics, Bahamians, Jamaicans, Trinidadians, Apaches, Navajos, Chamorros and Filipinos. Concordance studies on these populations demonstrate genotyping accuracy and identified instances of non-concordance due to rare kit-specific primer binding site variants. Additionally, the results of population genetic analyses support the usage of these loci and the associated allele frequencies for estimating match statistics in human identity testing. All of these studies will be described in an announcement of population data that will be submitted for publication under the title "*Population data on the expanded CODIS core STR loci for eleven populations of significance for forensic DNA analyses in the United States.*"

If you have any questions, please contact Anthony J. Onorato of the FBI's DNA Support Unit at Anthony.Onorato@ic.fbi.gov or 703-632-7572.