A57 Impact of Additional STR Loci on Random Match Probability Calculations and Kinship Analysis

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After attending this presentation, attendees will understand the value of additional autosomal STR loci in performing random match probability calculations, DNA database searches, and kinship analysis involving close relatives.

This presentation will impact the forensic science community by showing how DNA database searches and kinship analysis can be benefitted by additional STR loci.

Since their selection in November 1997, genetic information from a core set of 13 autosomal short tandem repeat (STR) loci have been required by the FBI for upload of DNA profiles to the national DNA database.[1,2] Unfortunately, only eight of the current 13 United States core loci overlap with data being gathered in the United Kingdom and most other European nations. Thus, international DNA comparisons can be hindered by lack of information overlap. As the United States considers expansion to additional core loci, recently adopted and previously used European STR markers should be considered to provide greater capabilities for international comparisons where needed. The European forensic DNA community has expanded the number of core loci for the same reason that the United States must do the same in the very near future– concern over potential adventitious matches between DNA profiles when trillions of comparisons are being performed with DNA database searches involving millions of profiles.

In November 2009, the European Union adopted five new autosomal short tandem repeat (STR) loci as part of their expanded European Standard Set (ESS). These new ESS STR loci, which include D12S391, D1S1656, D2S441, D10S1248, and D22S1045, were selected based on discussion over the past few years within the European Network of Forensic Science Institutes (ENFSI).[3,4] In the past year, Promega Corporation and Applied Biosystems have released new STR kits to enable coverage of these additional loci as well as the highly polymorphic locus SE33.

The probability of identity with different sets of loci will be illustrated in order to help assess the benefits of adding additional loci to the current 13 CODIS core loci. In addition, likelihood ratio calculations with parent-offspring, full siblings, and half-siblings will be shown.

References:

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2. Butler, J.M. (2006). Genetics and genomics of core short tandem repeat loci used in human identity testing. *J. Forensic Sci., 51*, 253-265.

3. Gill, P., et al. (2006) The evolution of DNA databases- Recommendations for new European STR loci. *Forensic Sci. Int.* 156: 242-244.

4. Gill, P., et al. (2006) New multiplexes for Europe-amendments and clarification of strategic development. *Forensic Sci. Int.* 163: 155-157.

Forensic DNA, New STR Loci, Kinship Analysis

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