



A170 A 27-Locus STR Assay to Meet All United States and European Law Enforcement Agency Standards

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After attending this presentation, attendees will become familiar with a 27-locus, six-dye multiplex containing all STR loci recommended or proposed for use in national databases in the United States, Europe, and Asia, and with advanced instrumentation that permits separation and detection of up to eight separate dyes to support even more highly multiplexed assays.

This presentation will impact the forensic science community by introducing an STR multiplex containing all existing and proposed standard loci for database searches in United States, Europe, and Asia that will support cross-border searching of all existing and proposed databases.

Investigative and judicial agencies worldwide have developed DNA databases to store short tandem repeat (STR) profiles. These databases provide capabilities to match DNA profiles from crime scene samples to database entries, provide investigative leads, and permit familial searching. Recently the FBI proposed expansion of the CODIS core loci to include amelogenin plus 19 required STR loci and three recommended STR loci. This approach retains the current 13 CODIS core STR loci (with transfer of the locus TPOX from required to recommended status), while expanding the set to include STR loci popular in other parts of the world, notably Europe. Increasing the number of loci in multiplex sets will not only permit compatibility across borders, but will also diminish the chances of obtaining false hits in databases, and will enhance the ability to perform familial searching. It will also improve kinship analysis in support of immigration requests.

In this presentation, attendees will become familiar with the development of a multiplex STR set permitting co-amplification of 26 STR loci plus amelogenin to supporting expansion of database compatibility across national and international borders. The 27plex set includes all 15 loci in common between the proposed CODIS required core and the European standard, i.e., amelogenin, D1S1656, D2S441, D2S1338, D3S1358, D8S1179, D10S1248, D12S391, D16S539, D18S51, D19S433, D21S11, FGA, TH01, and vWA. In addition, the 27plex includes locus D22S1045 that is part of the European standard and is recommended in the proposed expanded CODIS core. It includes the proposed five additional required CODIS core loci CSF1PO, D5S818, D7S820, D13S317, and DYS391, and the remaining two proposed CODIS recommended loci SE33, and TPOX. Beyond these, the multiplex contains an additional locus commonly employed in Asia, D6S1043, and three other loci, Penta C, Penta D, and Penta E, respectively, that are commercially available and are used in many database searches.

To maintain the forensic preference for amplification products of less than 500 bases while incorporating so many highly polymorphic loci required expansion of previously described dye panels to six fluorescent dyes and modification of the existing NetBio GeneBench electrophoresis instrument to permit detection, separation, and display of amplified products containing each individual dye. In addition, the multiplex design generates amplified products of all alleles smaller than 400 bases except for the least commonly employed loci D6S1043, SE33, Penta C, Penta D, and Penta E. The authors propose the use of the 27-locus multiplex to permit laboratories in any jurisdiction to employ an expanded common global STR profiling set to permit full application of all data currently available in any of the national or international databases.

The multiplex has been optimized to generate all products in a 19.5 minute amplification reaction. The modified instrument used to evaluate the amplified products can simultaneously detect and employ software to separate eight or more different fluorescent dyes. These additional advances provide opportunity for adaptations to Rapid DNA Analysis and to multiple instrument platforms, and for the creation of a variety of amplification formats from higher order multiplexes to highly discriminating miniplexes.

Multiplex, CODIS, Database