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### **B7 Maximize Information From Your Mixture Samples Using a Combined Autosomal STR and Y-STR Multiplex System**

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After attending this presentation, attendees will be able to evaluate the potential benefit of using a combined autosomal Short Tandem Repeat (STR) and Y-chromosomal Short Tandem Repeat (Y-STR) marker set for analyzing mixture samples.

This presentation will impact the forensic science community by describing a less expensive and quicker STR method for analyzing casework samples.

The PowerPlex® Fusion™ 6C System is a six-color STR system for simultaneously amplifying 23 autosomal loci, three Y-STR loci, and amelogenin. The 20 required (amelogenin, D18S51, FGA, D21S11, D8S1179, vWA, D13S317, D16S539, D7S820, TH01, D3S1358, D5S818, CSF1PO, D2S1338, D19S433, D1S1656, D12S391, D2S441, D10S1248, and DYS391) and three recommended (TPOX, D22S1045, and SE33) proposed expanded Combined DNA Index System (CODIS) core loci are combined with Penta D, Penta E, DYS570, and DYS576 to give this system a discriminatory power ( $PI=1.80 \times 10^{-32}$ ) that is more than  $10^8$ -fold higher than that for the 20 required expanded CODIS core loci ( $PI=9.35 \times 10^{-24}$ ). With DYS391 and nine autosomal loci being less than 250bp, the additional genetic information obtained with this 27-loci STR system will be extremely useful for analyzing degraded samples, where even a partial profile would be informative.

The DYS391 locus is included in the proposed expanded CODIS core loci for verification of gender in amelogenin null samples; however, it has one of the lowest locus variability values and does not significantly increase discriminatory power. In contrast, DYS570 and DYS576 have two of the highest locus variability values within American subpopulations and contribute more to the system's discriminatory power than DYS391. Additionally, because they are rapidly mutating Y-STRs, DYS570 and DYS576 provide the potential for separating close male relatives and further improving useful information from a single STR analysis. These three Y-STR loci will allow more confident determination of the number of male contributors in complex mixtures without the need for a separate Y-STR analysis, thus saving time and money.

This system is designed for 1ng of optimal input DNA template. The average peak height ratio is over 90% with one ng DNA template and remains high (80%) with as low as 100pg DNA template. It is very sensitive and is capable of calling  $98 \pm 21\%$  (average  $\pm$ SD) of alleles with 100pg DNA template. Even with as low as 50pg DNA template,  $77 \pm 17\%$  (average  $\pm$ SD) of alleles are called. The system is also resistant to very high concentrations of PCR inhibitors. In reactions containing up to 0.5mM hematin, 100% of alleles are called with this system. Improved resistance to humic acid and tannic acid is also observed.

To improve laboratory workflow efficiency, this system is designed for use with both casework samples as well as with reference and database samples. Direct amplification of blood or buccal samples on multiple substrate types such as FTA® card, non-FTA® cards, and swabs eliminates the extraction process, which saves time and money. To further save time and improve efficiency, automation methods are available for multiple liquid-handling platforms which minimize potential cross-contamination and result in more than a 95% first-pass success rate.

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#### **STR, Y-STR, Casework**