

VALIDATION OF THE PROMEGA POWERPLEX® FUSION SYSTEM USING APPLIED BIOSYSTEMS' 3730XL DNA ANALYZER

Victoria L. Vance, MS, Donna J. Housley, PhD, Lars Mouritsen, BS, Sorenson Genomics

In 2011, the FBI Laboratory announced the proposed additional loci under consideration to expand the current set of CODIS core loci. According to the CODIS Core Loci Working Group, an expansion of the CODIS core loci would facilitate greater discrimination, assist in missing person investigation and encourage international data sharing efforts. In response, Promega developed the PowerPlex® Fusion System of 24 loci which includes both the current core loci for CODIS and the European Standard Set as well as all but one of the loci proposed for the CODIS expansion. The PowerPlex® Fusion System includes the following 24 short tandem repeat (STR) loci plus Amelogenin; D18S51, FGA, D21S11, D8S1179, vWA, D13S317, D16S539, D7S820, TH01, D3S1358, D5S818, CSF1PO, D2S1338, D19S433, D1S1656, D12S391, D2S441, D10S1248, TPOX, D22S1045, Penta D, Penta E, and DYS391. The PowerPlex® Fusion System does not require any new equipment or additional instrument upgrades for use in the laboratory which was a motivating factor in the decision to implement its use in the Sorenson Genomics-Identigene laboratory for improved paternity and extended relationship testing. In-house laboratory testing was performed using the protocol for extracted DNA from Promega's technical manual for the PowerPlex® Fusion System with the genetic analysis being done on an Applied Biosystems 3730xl DNA analyzer. Since the majority of specimens received by Sorenson Genomics-Identigene are buccal swabs, we chose to use them as the primary specimen type for this study although other specimen types were tested as well, including amniotic fluid, blood, abortus, filter paper-blood, hair shaft, Q-tip, toothbrush, Kleenex tissue, undergarment, and FFPE tissues. Reproducibility tests were performed and were 100% concordant. Sensitivity studies indicated that the optimal range for DNA concentration was between 0.05ng/µL and 0.5ng/µL. Samples below this concentration range displayed more stochastic effects such as allelic dropout while those above this concentration exhibited quality issues associated with pull-up (i.e. shifting, split peaks, size standard failure, extra peaks). Mixture studies showed that a minor profile could be detected at DNA concentration levels around 0.01ng/µL. These studies showed that PowerPlex® Fusion is an acceptable method for obtaining STR genotypes used in paternity and extended relationship testing.