Validation of SGM and PowerPlex™ STR Systems for Paternity Testing

J.A. Thomson[1] V. Pilotti[1] , P. Stevens[1], K.L. Ayres[2] and P.G. Debenham[1]
[1] Life Sciences Group, LGC, Teddington, UK
[2] Dept. of Applied Statistics, University of Reading, Reading, UK

DNA profiling by analysis of Short Tandem Repeat (STR) loci has been widely used in forensic casework for several years. STR analysis offers significant benefits in sensitivity, broader range of suitable samples and speed of analysis. These benefits are also pertinent to parentage testing and other kinship analysis but the adoption of STR typing in these areas has lagged significantly behind the forensic applications.

This is primarily because the overall reduction in discriminating power with respect to previously used SLP systems has a more profound effect in parentage testing, where only one allele at each locus is informative. However, the continuing development and validation of STR systems for use in identity testing has now resulted in twenty or more highly suitable systems available either commercially or via published primer sequences, with many more available for development.

This study details validation of two separate multiplex STR systems for use in paternity investigations. These are the SGM multiplex developed by the UK Forensic Science Service and the PowerPlex™ multiplex commercially available from Promega. These multiplexes contain 12 different STR systems (2 are duplicated in the two systems). An empirical approach has been taken to validate these systems. Samples from 121 cases of disputed paternity, routinely submitted to this laboratory, were analyzed using the established SLP tests currently in use, and also using the two multiplex STR systems. Results of all three test systems were compared and any anomalies identified and investigated. The data was then analyzed to give information on expected paternity indices and exclusion rates for these STR systems.

For the six SGM loci, 96% of cases where the putative father had not been excluded had Relative Chance of Paternity (RCP) values of >99% (59% of cases >99.9%). For the six PowerPlex™ loci (discounting the two loci present in SGM), these figures were 61% of cases >99% , 20% of cases >99.9%. In combination, 100% of cases had RCP > 99%, 99% of cases > 99.9% and 89% of cases > 99.99%.

Exclusion rates for the combined SGM/PowerPlex™ system was calculated at 99.998% of wrongly named men excluded from paternity on at least one STR system.

Five presumed mutations were identified in approximately 2800 meiosis, an overall rate of 1.8×10^{-3}. Three of these mutations were in the D16S539 system which therefore demonstrates an unusually high mutation rate in this data set of 1.2×10^{-2}.

In addition, population frequency databases have been constructed for the three major ethnic groups in the UK; British Caucasians, Afro-Caribbean and Asians. These databases were compared to published data and were used in the calculation of paternity indices and in other analysis carried out on the data.