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A comparison of theoretical and observed statistical data in paternity testing by DNA analysis

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One of the most important features of DNA typing is its ability to determine family relationships. This most often involves the determination of the identity of the biological father of a child, which is known as paternity testing. When a man cannot be excluded from paternity after several STR loci are considered, the question then arises as to the certainty of the conclusion that he is the biological father. A probability value known as the probability of paternity is calculated using population allelic frequency data. This data was derived from a previous population genetics study of the Sri Lankan human population. Two statistical parameters generated from this study were the Power of Exclusion, and the Typical Paternity Index. These two statistics are derived from the allele frequency data of a random population. These are theoretical values, which are not derived from actual observations of mother-child-putative father trios. It is of practical utility to first test the STR loci with high Power of Exclusion and high Typical Paternity Index when screening several individuals for paternity of a child, thereby reducing the cost and the time involved in identifying the father of the child

After having performed 191 paternity tests at Genetech Molecular Diagnostics, a considerable amount of practical data has been derived. The objective of this study was to compare the trends derived from the theoretical values for the Power of Exclusion and Typical Paternity index with that of the observed data. Of the 191 tests for paternity, 51 tested negative. The power of exclusion data derived from the previous study was compared with the percentage of exclusionary events in each STR locus for paternity trios that tested negative. A total of 140 tests for paternity tested positive. In each case, the observed Paternity Index was calculated for each STR locus. The mean value for the Paternity Index for each locus was calculated over all 140 tests, and these values were compared with the theoretical Typical Paternity Index derived from the population genetics study.

Power of Exclusion data derived from the previous study compared broadly with the percentage of exclusionary events derived practically from paternity tests. The Typical Paternity Index data derived from the previous study showed a similar trend with the average Paternity Index derived from paternity tests. Both theoretical and observed indicators showed that STR loci TH01, D16S539, D7S820 and vWA were the most likely to exclude a non-father from paternity, and was therefore the most useful in mass screening. Similarly STR locus CSF1PO, TPOX and FESFPS were the least efficient at excluding the non-father.

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