

PUSHING THE LIMITS OF TrueAllele®

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In 2012, the Virginia Department of Forensic Science (VDFS) began to independently validate the expert system software, TrueAllele® (TA), for casework sample analysis. As a result of this validation work, 52 mock casework samples were analyzed. These consisted of 17 degraded or stochastic single source, 18 two person, 10 three person and 7 four person mixture profiles. These samples were chosen to assess the limits of the TA process since they contained low level contributors which exhibited stochastic artifacts. Criteria such as the quality of the Markov chain Monte Carlo analysis, convergence, genotype concordance and match statistic reproducibility were assessed and scored. The TA process correctly excluded all non-contributors tested for the two, three and four person mixtures, except for one non-contributor to a complex four person mixture which provided inconclusive results. The accuracy with which the TA process defines the mixture weights of contributors to two person mixtures was independently confirmed. The extent to which the software can successfully eliminate non-contributors to two, three and four person mixtures was confirmed by interrogating the mixtures with 100 synthetic reference STR profiles. The degree to which the TA process could eliminate “sons” of the contributors to the two, three and four person mixtures was assessed; there were two observations of a small positive match statistic for the three person mixtures and one for the four person mixtures which was not unexpected. Finally, the use of assumed knowns was explored for the three person mixtures; generally, the use of an assumed known who was a contributor to the mixture enhanced the match statistics whereas the use of an assumed known who was not a contributor to the mixture reduced the match statistics but did not result in the false inclusion of other non-contributors. This study dovetails nicely with validation work performed by Cybergenetics using 72 Virginia criminal cases and demonstrates the analysis power and accuracy of the TrueAllele® software.