INTEGRATION OF A EUROPEAN STR ASSAY ON THE RapidHIT™ 200 SYSTEM FOR INVESTIGATIVE SEARCHES

Lori K. Hennessy[1], Lesley Ives[2], Des Vanhinsbergh[2], Keith Elliott, Yuan Li[1], Richard Belcinski[1], Neelima Mehendale[1], Francesca Pearson[1], Bob McLaren[3], Doug Storts[3], Stephen Williams[1]
[1]IntegenX Inc.
[2]Key Forensic Services Ltd
[3]Promega Corporation

The forensic community is continually striving to improve the analysis of DNA, particularly in regards to decreasing turnaround time to obtain a DNA profile. Rapid profiling would provide intelligence information to identify or eliminate suspects at the start of police investigations increasing the probability of solving cases. IntegenX's RapidHIT™ 200 Human DNA Identification System is a fully integrated instrument that simplifies and streamlines the DNA workflow, allowing generation of a STR profile from buccal swabs in less than 90 minutes. Here we present initial development studies and preliminary validation results conducted on the RapidHIT 200 system using the PowerPlex® ESI 16 Fast System (Promega) chemistry, which contains the SGM Plus loci and the five new loci recommended by ENSFI. DNA extraction and PCR conditions for the ESI 16 Fast chemistry were optimized to generate full profiles from fresh to two-month old buccal samples collected on Omni swabs. From 13 runs on two different instruments, 95% of buccal swab samples yielded full, concordant profiles with average heterozygote peak height balance of 89% ± 7% (n=605, 59-100%). Samples with alleles at D1S1656 (226-273 nt), D12S391 (291-343 nt) and D2S441 (347-383 nt) differing by 1 nt were clearly resolved in electrophoresis separations.

Preliminary validation studies performed by Key Forensic Services comprised 10 runs using 50 buccal swabs from known donors. The results were assessed for concordance with donor profile, profile quality, and reproducibility. Full DNA profiles, containing all expected donor alleles, were obtained from 100% of samples analyzed (4 samples required manual amendment for pull-up peak and one low peak height) and results suitable for intelligence-led searching of the UK database were obtained from all analyzed samples. Average heterozygote peak height balance of buccal swab samples was 89% ± 7% (n=797, 49-100%). Five replicate swabs run for five different individuals were 100% concordant verifying reproducibility of the system.

These initial results demonstrate the ability of the RapidHIT 200 instrument to provide high quality DNA-based investigative leads in less than two hours. In addition, the simple, straightforward operation of the system requires less than five minutes of hands-on time and its user-friendly graphical interface enables operation of the instrument by non-scientists with minimal training.