MASSIVELY PARALLEL SEQUENCING OF FORENSIC STRS USING THE ION CHEF^{TM} AND THE ION S5^{TM} XL SYSTEM

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STR data yielded with several NGS platforms has been published, but forensic application trials on the Ion S5^{TM} XL system has not been reported. In this work, we report our preliminary data on the Ion Chef^{TM} and the Ion S5^{TM} XL systems using an early access panel multiplexing 24 STR markers and the sex-determining locus Amelogenin. Sensitivity experiments showed that sequencing data with 62 pg of genomic DNA was still acceptable. Mixture studies demonstrated that alleles from the minor contributor could be correctly assigned at 1:9 and 9:1 ratios. In the parallel experiments using simulated degradation samples, NGS proved to be advantageous over capillary electrophoresis (CE) in genotyping the severely degraded samples (DI=8.947). Notably, NGS successfully reported 12 full genotype results in 13 challenging casework samples, compared with 5 full results on the CE platform. Interestingly, discordant STR genotypes were observed when using different softwares (NextGENe, STRait Razor and Ion Torrent Suite) in analyzing the same FASTQ data suggesting that computer programing and bioinformatic parameters could impact NGS-based STR results substantially.