Massively Parallel Sequencing of Forensic Markers on the MiSeq FGx Forensic Genomics System

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The recent introduction of massively parallel sequencing (MPS) has revolutionized DNA typing in forensic science. We evaluated the ForenSeq™ DNA Signature Prep Kit that is designed to detect 231 forensically relevant STR and SNP markers in a single reaction on the MiSeq FGx™ Forensic Genomics System [1]. Full profiles were obtained from ≥ 100 pg input DNA for STRs and ≥ 200 pg for SNPs. A sample with ≥ 5% minor contributors was considered as a mixture, and full profiles from minor contributors were easily detected between 9:1 and 1:9 mixtures with known reference profiles. The ForenSeq Kit tolerated considerable concentrations of inhibitors like ≤ 200 μM hematin and ≤ 50 μg/ml humic acid, and > 56% STR profiles and > 88% SNP profiles were obtained from ≥ 200-bp degraded samples. Likewise, this kit demonstrated robust performance with case-type samples. Also, sensitive QC indicator and automated sample comparison function in the ForenSeq Universal Analysis Software (UAS) were quite helpful, enabling us to concentrate on questionable genotypes and avoid tedious and time-consuming labor to maximum the time spent in data analysis. Further, Xibe population (STR000107) was successfully genotyped using the ForenSeq Kit, which is the first MPS-STR and MPS-SNP dataset contributed to the STRidER from an East Asian population [2]. Most importantly, we developed an MPS whole mitochondrial genome panel to detect heavily degraded samples using the Nextera® XT DNA Library Preparation Kit with the MiSeq FGx System in RUO mode [3], and this dataset (EMP00726) was evaluated by the EMPOP. In conclusion, the MiSeq FGx System can universally detect forensic markers and fully meet requirements for human identification and DNA databasing.

Key Words: MPS, MiSeq FGx, STR, SNP, mtGenome

References

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