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Title Page

Concordance of mitochondrial DNA sequencing method on bloodstains using Ion PGM™

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Concordance of mitochondrial DNA sequencing methods on bloodstains using Ion PGM™

ABSTRACT: In this study, the complete mitochondrial genome (mtGenome) of six samples from three forensic cases was sequenced using the Ion Torrent Personal Genome Machine (PGM). The analyzed samples from forensic cases included bloodstains from several materials, such as gauze, Flinder's Technology Associates (FTA) cards and swabs. The age of the samples ranged from two months to twelve years. The complete mtGenomes were amplified using the tiling sequencing strategy which divided the whole mtGenome into 162 amplicons. All amplicons were successfully recovered. A phylogenetic analysis was performed to determine the accuracy of the PGM data, and which were compared to partial Sanger-based sequencing data. The average coverage of the PGM data were above 4000× in all case samples, and 99.86% concordance was observed using both sequencing methods. In conclusion, we demonstrate the ability to recover the complete mtGenome from bloodstains with relatively poor DNA quality by PGM. Moreover, the results are concordant with Sanger sequencing data. This new method has potential use in forensic practice.

Keywords: mtDNA; Forensic casework; Personal Genome Machine; Aged bloodstain; Degraded DNA;

1. Introduction

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