

Massively Parallel Sequencing Improved Resolution for Paternity Testing

Authors : Xueying Zhao, Ke Ma, Hui Li, Yu Cao, Fan Yang, Qingwen Xu, Wenbin Liu

Abstract : Massively parallel sequencing (MPS) technologies allow high-throughput sequencing analyses with a relatively affordable price and have gradually been applied to forensic casework. MPS technology identifies short tandem repeat (STR) loci based on sequence so that repeat motif variation within STRs can be detected, which may help one to infer the origin of the mutation in some cases. Here, we report on one case with one three-step mismatch (D18S51) in family trios based on both capillary electrophoresis (CE) and MPS typing. The alleles of the alleged father (AF) are [AGAA]₁₇AGAG[AGAA]₃ and [AGAA]₁₅. The mother's alleles are [AGAA]₁₉ and [AGAA]₉AGGA[AGAA]₃. The questioned child's (QC) alleles are [AGAA]₁₉ and [AGAA]₁₂. Given that the sequence variants in repeat regions of AF and mother are not observed in QC's alleles, the QC's allele [AGAA]₁₂ was likely inherited from the AF's allele [AGAA]₁₅ by loss of three repeat [AGAA]. Besides, two new alleles of D18S51 in this study, [AGAA]₁₇AGAG[AGAA]₃ and [AGAA]₉AGGA[AGAA]₃, have not been reported before. All the results in this study were verified using Sanger-type sequencing. In summary, the MPS typing method can offer valuable information for forensic genetics research and play a promising role in paternity testing.

Keywords : family trios analysis, forensic casework, ion torrent personal genome machine (PGM), massively parallel sequencing (MPS)

Conference Title : ICFST 2017 : International Conference on Forensic Science and Technology

Conference Location : Tokyo, Japan

Conference Dates : November 13-14, 2017