ONE COMPLETE VERSUS TRIPLICATE ANALYSES IN LOW TEMPLATE DNA TYPING

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There are generally two strategies for Low template DNA typing, the complete strategy, which uses all available DNA in a single PCR and subsequent typing, and the consensus strategy, in which the biological sample is divided into two or more aliquots and the genotype profile is determined by consensus from these "replicates." In this study, the consensus and complete strategies are compared by a statistical approach in terms of the accuracy of obtaining the correct genotype at a single locus for single source samples. Logistic models were employed to describe the allele drop-out and drop-in events. The parameters of the models were estimated with empirical or hypothetical data. The probabilities of obtaining the true genotype and the chances to observe drop-out and drop-in alleles were estimated and compared for both strategies. Consistent with a previous experimental study, this study found that, with relatively high input DNA (e.g., ≥100pg), the complete strategy performs better than the consensus strategy to obtain the true genotype and the complete strategy will display less dropped out alleles. The consensus strategy had less drop-in alleles for ≤100pg DNA samples. Moreover, the limitations of the logistic models were discussed. Ideal models with better fit of empirical data approximating casework conditions were proposed for future studies.