Optimizing Storage and Handling of DNA Extracts

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ABSTRACT: Nucleic acid sample storage is of paramount importance in forensic science as well as in epidemiological, clinical, and genetic laboratories. Millions of biological samples, including cells, viruses, and DNA/RNA, are stored every year for diagnostics, research, and forensic science. PCR has permitted the analysis of minute sample quantities. Samples such as bone, teeth, touch samples, and some sexual assault evidence may yield only low-quality and low-quantity DNA/RNA. Efficient storage of the extracted DNA/RNA is needed to ensure the stability of the sample over time for retesting of the CODIS STRs, mtDNA, YSTRs, mRNA, and other future marker-typing systems.

Amplification of some or all of these markers may fail because the biological material has been highly degraded, contains inhibitors, is too low in quantity, or is contaminated with contemporary DNA. Reduction in recovery has been observed with refrigerated liquid DNA extracts and also those exposed to multiple freeze-thaw cycles. Therefore, the development of optimal storage and amplification methods is critical for successful recovery of profiles from these types of samples since, in many cases, retesting is necessary.

This review is divided into three sections. The Introduction and Background covers forensic DNA storage, factors that influence DNA stability, and a brief review of molecular strategies to type non-optimal DNA. Section I covers the importance of DNA extract storage in forensic and non-forensic DNA databanks and the mechanisms responsible for loss during storage. Finally, Section II covers strategies and technologies being utilized to store DNA.

KEY WORDS: DNA storage, FTA, SampleMatrix, trehalose.