

## Species Identification in Forensic Casework Analysis: Validation Studies on the Sequence Analysis of the Cytochrome B Gene.

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The determination of the origin of a biological stain is a critical aspect in forensic casework analysis. It bridges the gap between the DNA-based result and the knowledge of the donor of a stain. Short Tandem Repeats (STR) are widely used in the forensic community. They are generally known to give human-specific results, due to the fact, that their primers usually do not amplify non-human DNA or at least do not produce results in an expected range. Thus, the need for additional species determination is decreasing, because the STR profile obtained itself indicates the human origin of the sample. In some cases, however, a more detailed information on the species of a stain can be of particular importance.

It has been demonstrated that the nucleotide sequence of the mitochondrial gene cytochrome b contains species-specific information, not only allowing for the discrimination between human and non-human samples. It has also been shown that, due to its rate of evolution, the cytochrome b gene enables the differentiation of even closely related species. The major advantage of this technique is the particularly high sensitivity of mtDNA typing, rendering species determination of micro-stains and/or degraded DNA samples feasible.

In this study, homologous segments of a cytochrome b gene fragment were amplified from different biological specimens of more than 50 vertebrate species. Two different approaches - PAUP (Phylogenetic Analysis Under Parsimony) and BLAST (Basic Local Alignment Search Tool) - were applied to identify a species by their cytochrome b sequence. Finally, an unexpected result in a casework example is presented, demonstrating for the usefulness of this method.