

**APPLICATION OF DEGENERATED PRIMERS IN SEQUENCE ANALYSIS OF THE CYTOCHROME B GENE**

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The alternate of species identification using sequence analysis of the cytochrome b gene has been previously described. The forensic application by aligning to cytb gene sequences entries in nucleotide databases is reliable in the great majority of cases, and the validation performed according to various specimens. However, the semi-conservative trait of flanking regions may result in ambiguous sequences as well, in spite of the advantage of universal pair of primers. Avoiding the challenge of the interpretation new degenerated primers and PCR conditions were reconstructed for dog, roe and deer investigation. The multiplied annealing which results in different amplicons as the putative background of occurrence of mixed sequence was indicated by comparative testing. The annealing insufficiency arising from sequence incomplementarity can be eliminated using these new degenerated primer pairs, and the results support the presence of the inserted mitochondrial segments in the nuclear genome, as well.