

A multiplex PCR method to identify bushmeat species in wildlife forensics

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Abstract

Airports are important hubs for bushmeat trade, that is, the illegal commercialization of wildlife meat, often from endangered species. While the identification of bushmeat species is sometimes possible morphologically, in most cases genetic characterization would be necessary for precise taxonomic identification. We validated a mtDNA-based species identification method for its application to bushmeat species imported into Switzerland. This method consists of a multiplex-PCR-setup with 8 primers varying in their specificity to amplify a region of the mitochondrial cytochrome b (cytb) gene in different animal classes (mammals, fishes and birds). We tested the method on meat (cooked, dried, smoked or raw) and blood samples from 24 different species, obtained from museums and butchers. Following successful PCR and sequencing, we identified the species of origin using BLAST alignments to the cytb entries in the NCBI nucleotide database. Our method also passed all validation criteria, including repeatability, reproducibility, and robustness. We then applied this method to identify the taxonomic origin of 250 samples of putative bushmeat confiscated at the airports of Zurich and Geneva between September 2011 and January 2013. For 224 samples, there was sufficient DNA to allow successful sequencing. The samples belonged to one of four vertebrate groups (mammals, birds, reptiles and fishes): approximately two thirds of the analyzed samples originated from wild animals, one third of which are listed in the CITES appendices. Our validated DNA method offers a practical and easy approach for the identification of bushmeat at airports and in general in wildlife forensics.

Keywords

Species identification; Bushmeat; Cytochrome b; Validation; CITES

Figures and tables from this article:

Table 1.

Primers and Primer mix (PM) used in a multiplex-PCR-setup to amplify a region of the cytb.



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