

Sequence of specific mitochondrial 16S rRNA gene fragment from Egyptian buffalo is used as a pattern for discrimination between river buffaloes, cattle, sheep and goats

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Abstract Characterization of molecular markers and the development of better assays for precise and rapid detection of domestic species are always in demand. This is particularly due to recent food scares and the crisis of biodiversity resulting from the huge ongoing illegal traffic of endangered species. The aim of this study was to develop a new and easy method for domestic species identification (river buffalo, cattle, sheep and goat) based on the analysis of a specific mitochondrial nucleotide sequence. For this reason, a specific fragment of Egyptian buffalo mitochondrial 16S rRNA gene (422 bp) was amplified by PCR using two universal primers. The sequence of this specific fragment is completely conserved between all tested Egyptian buffaloes and other river buffaloes in different places in the world. Also, the lengths of the homologous fragments were less by one nucleotide (421 bp) in case of goats and two nucleotides (420 bp) in case of both cattle and sheep. The detection of specific variable sites between investigated species within this fragment was sufficient to identify the biological origin of the samples. This was achieved by alignment between the unknown homologous sequence and the ref-

erence sequences deposited in GenBank database (accession numbers, FJ748599–FJ748607). Considering multiple alignment results between 16S rRNA homologous sequences obtained from GenBank database with the reference sequence, it was shown that definite nucleotides are specific for each of the four studied species of the family Bovidae. In addition, other nucleotides are detected which can allow discrimination between two groups of animals belonging to two subfamilies of family Bovidae, Group one (closely related species like cattle and buffalo, Subfamily Bovinae) and Group two (closely related species like sheep and goat, Subfamily Caprinae). This 16S DNA barcode character-based approach could be used to complement cytochrome c oxidase I (COI) in DNA barcoding. Also, it is a good tool for identification of unknown sample belonging to one of the four domestic animal species of family Bovidae quickly and easily.

Keywords Sequence analysis · Bovidae · Species identification · Mitochondrial DNA · 16S rRNA gene

Introduction

Species identification is essential in food quality control procedures or for the detection and identification of animal material in food samples. Recent food scares e.g. avian flu and swine flu, malpractices of some food producers and religious reasons have tremendously reinforced public awareness regarding the composition of food products. However, because labels do not provide sufficient guarantee about the true contents of a product, it is necessary to identify and/or authenticate the components of processed food, thus protecting both consumers and

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