DNA barcoding of meat species.

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Abstract:

DNA barcoding is a novel technique in molecular taxonomy that identifies animals and their body parts with at most accuracy. DNA sequences to be aligned for the taxonomic study are aligned in the alignment software MEGA 5.2. Alignment of different sequences is done using the ClustalW parameters. The maximum likelihood tree of the DNA sequences was drawn in the software and a cladogram was obtained. The cladogram clearly depicted the efficacy of COI gene in identifying the meat species and its possible aid in food adulteration.

Keywords: Molecular taxonomy, cladogram, COI gene.

Introduction:

Precise and exact information about the origin, methods of production, transformation technologies, authentication and traceability of foodstuffs is a prime demand of globalization of the food trade. DNA barcoding using COI gene is one of the robust methods in molecular taxonomy to identify food adulteration along with rbcL and ITS (Nehal Nazish et al. 2021). DNA barcoding using COI gene has helped in identifying individuals up to the species level (Hebert et al. 2003, Ward et al. 2005). Many times food of meat species is adulterated with many other closely related animals. Identifying the same at exact level using naked eye is almost impossible. COI gene barcodes can identify various life stages at fish species at exact level (Ahrens D. et al. 2007). DNA barcoding can also help in population level variation occurring among the individuals (Hajibabaei et al. 2007). Present paper adds to the knowledge of world with COI gene barcodes that can identify meat species individuals, their life stages and their body parts exactly.
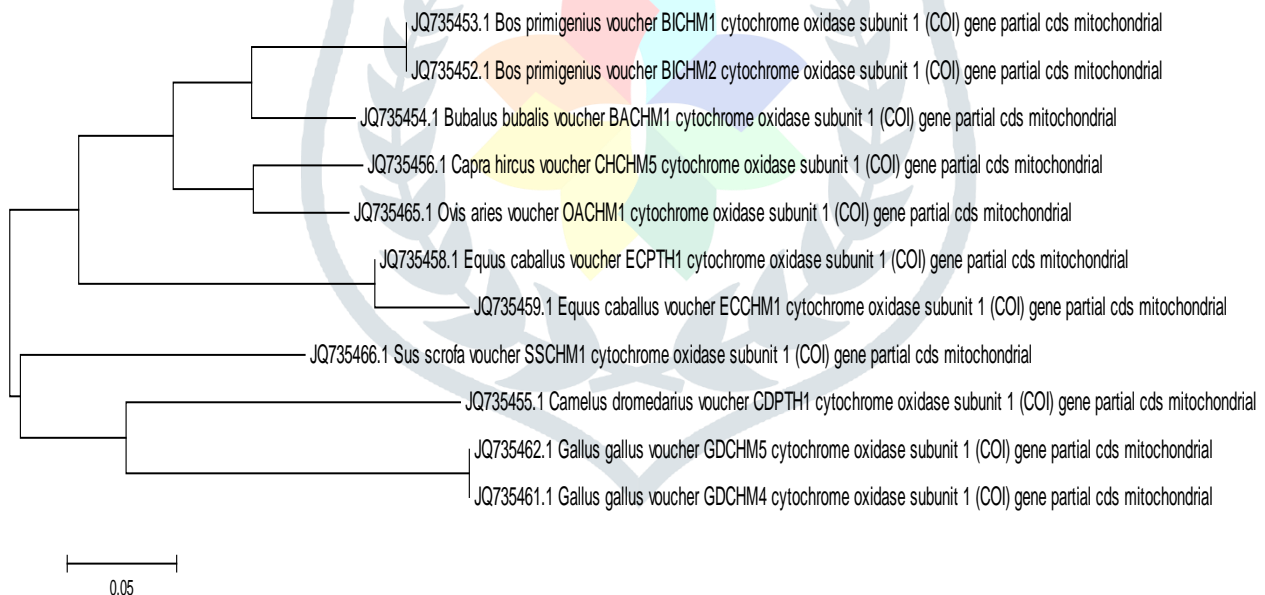
Material methods:

The COI gene sequences considered in the present work were trimmed to 500 bases as to reach full length of 650 bases in not an easy task (Hajibabaei et al. 2006). The COI gene sequences of mainly available meat species in Maharashtra state were aligned in software MEGA (Molecular Evolutionary Genetic Analysis) 5.02. (Tamara et al. 2011). ClustalW was the alignment method used for COI gene sequence alignment. The accession numbers of meat species individual's COI gene sequence are as follows:

Number	Individual's biological name	NCBI Accession number
1	*Bos primigenius*	JQ735452
2	*Bos primigenius*	JQ735453
3	*Bubalus bubalis*	JQ735454
4	*Camelus dromedarius*	JQ735455
5	*Capra hircus*	JQ735456
6	*Equus caballus*	JQ735458
7	*Equus caballus*	JQ735459
8	*Gallus gallus*	JQ735461
9	*Gallus gallus*	JQ735462
10	*Ovis aries*	JQ735465
11	*Sus scrofa*	JQ735465

Result:

The maximum likelihood tree was drawn using these sequences as most taxa were taxonomically unrelated. The different individuals belonging to same species were placed together. The individual's of species *Bos primigenius* were placed together in a Clade. The individuals of *Gallus gallus* were found share a common Clade.

JQ735453.1 Bos primigenius voucher BICHM1 cytochrome oxidase subunit 1 (COI) gene partial cds mitochondrial
JQ735452.1 Bos primigenius voucher BICHM2 cytochrome oxidase subunit 1 (COI) gene partial cds mitochondrial
JQ735454.1 Bubalus bubalis voucher BACHM1 cytochrome oxidase subunit 1 (COI) gene partial cds mitochondrial
JQ735456.1 Capra hircus voucher CHCHM5 cytochrome oxidase subunit 1 (COI) gene partial cds mitochondrial
JQ735465.1 Ovis aries voucher OACHM1 cytochrome oxidase subunit 1 (COI) gene partial cds mitochondrial
JQ735458.1 Equus caballus voucher ECPTH1 cytochrome oxidase subunit 1 (COI) gene partial cds mitochondrial
JQ735459.1 Equus caballus voucher ECCHM1 cytochrome oxidase subunit 1 (COI) gene partial cds mitochondrial
JQ735466.1 Sus scrofa voucher SSCHM1 cytochrome oxidase subunit 1 (COI) gene partial cds mitochondrial
JQ735455.1 Camelus dromedarius voucher CDPTH1 cytochrome oxidase subunit 1 (COI) gene partial cds mitochondrial
JQ735462.1 Gallus gallus voucher GDCHM5 cytochrome oxidase subunit 1 (COI) gene partial cds mitochondrial
JQ735461.1 Gallus gallus voucher GDCHM4 cytochrome oxidase subunit 1 (COI) gene partial cds mitochondrial

0.05

Discussion:

Placement of similar individuals in a similar Clade implied the success of COI gene related DNA barcoding in differentiating dissimilar taxa and placement together of similar taxa in the cladogram (maximum likelyhood tree). Two different Clades formed by mammals and aves (*Gallus gallus*) implied the success of cladogram separating two different taxa.

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