PHYLOGENETIC RELATIONSHIP AMONG INTENSIVELY FARMED CARP SPECIES THROUGH DNA BARCODES

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DETERMINACIJA FILOGENETSKIH VEZA IZMEĐU INTEZIVNO GAJENIH ŠARANA UZ POMOĆ DNK BARKODINGA

Abstract

Many carp species have been domesticated and cultured as food all around Europe and Asia for thousands of years. Aquaculture of carp still exceeds the total amount of farmed fish volume of intensively farmed marine species, especially in Asia. In this study, mitochondrial cytochrome c oxidase subunit I gene (COI) sequences, known as DNA barcode, was used to clarify phylogenetic relationship among 7 cultured carp species.

Specimens of all species (Bighead carp (*Hypophthalmichthys nobilis*), Catla (*Gibelion catla*), Common carp (*Cyprinus carpio*), Grass Carp (*Ctenopharyngodon idella*), Mrigal carp (*Cirrhinus mrigala*), Rohu (*Labeo rohita*), Silver carp (*Hypophthalmichthys molitrix*)) were collected and tissue (muscle and liver) samples were taken from each specimen and stored at -20°C until DNA extraction. Mitochondrial COI gene was amplified using polymerase chain reaction (PCR), with universal fish DNA barcoding primer pairs (Fish F1-R1 and Fish F2-R2). Amplified DNA's were purified and DNA sequencing reactions were conducted on an automatic sequencing system. Alignment of sequences was performed using ClustalW. Phylogenetic analyses of the aligned sequences were conducted using MEGA 5.

Analyses of nucleotide composition, variable/conserved sites and parsimony informative sites were conducted on each species. Tamura-Nei model was used for pairwise distance calculation. Maximum likelihood (ML) and unweighted pair-group method of arithmetic average (UPGMA) methods were used in construction of consensus tree, with bootstrap tests of 1000 replicates for the reliability of the constructed tree.

Including all species studied, there were 76.0% conserved sites and 24.0% variable sites along with 16.1% of parsimony informative sites. Average of A-T contents was found as 55.2%. Rate of transitionsal pairs over transversional pairs (R) was calculated as 2.84. Estimates of evolutionary divergence between sequences were between 0.040-0.171 among the species with an average distance of 0.132. In conclusion, DNA barcode analysis of seven intensively farmed carp species provided us some useful information about effectiveness of using DNA barcodes in estimating phylogenetic relationship among these species, in congruence with the existing taxonomy.

Key words*: Carp, Cyprinidae, cytochrome c oxidase subunit I, DNA barcode, phylogeny.*