

ABSTRACT

Nutritional Analysis and Metagenomics Study of Candidate Fish Species of Cyprinidae Family from *Hel* River, Assam

The *Hel* river is an important river of Kokrajhar of Assam, India, which is a great source of freshwater fish. Considering the availability of indigenous fish species in the *Hel* river and consumption of these species by the local people, the focused objectives of the present work were the collection of the fish species from the *Cyprinidae* family based on the abundance study, analysis of the nutritional composition of candidate fish species, and metagenomics study of *Barilius bendelisis*.

In the present work, the relative abundance study of fish diversity was conducted from August 2014 to July 2015 along with the evaluation of species richness and species evenness. The results show that a total of 181 species and 1313 individuals could be found from the *Hel* river. The relative abundance (%) study showed that the fish species belonging to the *Cyprinidae* family were found to be the highest in the *Hel* river. The highest relative abundance (%) occurrence of the fish species was *Barilius bendelisis* (15.31 %) followed by *Garra gotyla* (14.09 %) and *Barilius barna* (13.78 %). The study reveals that the selected *Hel* river is rich in fish species belonging to the family *Cyprinidae* along with other varying numbers of species. A total of nine fish species of the *Cyprinidae* family were selected for further studies based on the high relative abundance report. These nine fish species were morphologically identified as *Barilius bendelisis*, *Garra gotyla*, *Barilius barna*, *Chagunius chagunio*, *Cyprinion semiplotum*, *Tor putitora*, *Labeo pangusia*, *Raiamas bola* and *Neolissochilus hexagonolepis*.

In this study, nutritional composition, fatty acid composition, amino acid composition, cholesterol, triglyceride, and vitamin contents of the nine fish species were determined. The results showed that all the fish species have variable data of proximate composition and mineral contents. The fatty acid compositions determined by the GC-MS technique ranged from 51.20–89.47 % of SFAs, 0.27–19.68 % of MUFAs, and 1.75–30.75 % of PUFAs. EPA and DHA varied respectively from 0.54–22.30 % and 1.26–18.85 %. The fish species are found to be rich in ω -3 fatty acids such as EPA and DHA. The TEAA and other amino acids investigated by HPLC were found to vary among the nine fish species. The highest amount of

TEAA was detected in *C. chagunio* (43.88 %) followed by *L. pangusia* (42.79 %), and the lowest TEAA content was observed in *G. gotyla* (26.45 %). Valine (0.82 % to 10.35 %), threonine (0.41 % to 7.34 %), and lysine (0.55 % to 10.52 %) were the three EAA that were detected in all the nine fishes in varying amounts. Other EAAs like histidine, methionine, phenylalanine, isoleucine, etc. were also detected in some of the fish species in varying quantities. In this study, the nine fish species exhibited varying concentrations of lipid components. The vitamin A content found in the fish species varied from 15.85 to 1287.0 µg/100 g and the vitamin D content was found in the range of 45.0–593.83 µg/100 g.

In this study, *B. bendelisis* fish species belonging to the *Cyprinidae* family was found to be the highest (15.31 %) in the *Hel* river based on its relative abundance study, and hence, it was selected for the metagenomics study. The microbial diversity of fish gut flora was investigated using the 16S rRNA metagenomics Illumina platform and is showing the taxonomic distribution of the gut microbiome of *B. bendelisis*. The high abundant level of the taxonomic distribution of the phylum was *Firmicutes* (74.8 %), the class was *Clostridia* (74.8 %), the order was *Clostridiales* (74.8 %), the family was *Veillonellaceae* (74.6 %), the genus was *Citrobacter* (7.7 %) and the species was *morganii* (2.4 %). The result of the present study reveals that some of the bacterial community in the intestinal gut is similar to some of the reported research work. However, various types of bacterial microbiome were also detected in the gut sample and this variation may be due to fish habit, fish feed, and environmental conditions.

In conclusion, the nine fish species from the *Hel* river of Assam, India are good sources of fats, proteins, high nutritive values, minerals, vitamins, and lipid components. The fish species of this study have the potentials to be served as natural dietary supplements for ω-3 fatty acids and its consumption can fulfill malnutrition problems and can reduce the risk of various health diseases. The fish species have good sources of both EAA and NEAA, and these could be suggested for the natural supplementation of EAA for proper maintenance and the growth of human health. The metagenomics study gives an idea about the microbial diversity of the selected river, which is a freshwater river source of Kokrajhar that originated from the Indo-Bhutan river.