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MORPHOMETRIC ANALYSIS USING TRUSS NETWORK SYSTEM IN ORANGE FIN BARB, *HYPSELOBARBUS JERDONI* (DAY 1870) FROM THE NETRAVATHI RIVER

Shamima Nasren[1]*, Nagappa Basavaraja[1], Malathi Shekar[1], Md. Abdullah Al-Mamun[1], Sanjay Singh Rathore[1], Shobha Rawat[2], Kevin Dsouza Ronald[3] and Aswhin Rai[4]

[1]College of Fisheries, Mangaluru, Karnataka Veterinary, Animal Fisheries Science University, Mangaluru- 575 002, India.
[2]Fisheries KVK, Muzaffarpur, India.
[3]Mangalore University, Mangaluru, India.
[4]Aquatic Biosystems, Mangaluru, India.
*e-mail : s.nasren2013@gmail.com

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ABSTRACT : The truss network system was used to investigate the morphometric differences among three different life stages (Juvenile, sub-adult and adult) of Orange fin barb,*Hypselobarbus jerdoni* (Day 1870) from the Netravathi river.Truss network system of 14 landmarkswas interconnected to yield 91 distance variables. The principal component analysis (PCA) was employed for determining the morphometric variations. Four principal components were extracted through PCA explaining 99.864% of the total variance in samples. Again, the factor analysis of the transformed variables explained 98.24% of the total morphometric variation with percentage contribution of 93.543% and 4.70% on the first and second factor, respectively. The results acquired from Factor analysis (FA) and truss network system was that the maximum variations were dependent on the distance from i) anterior attachment of dorsal membrane from caudal fin to end of anal fin, ii) anterior attachment of dorsal membrane from caudal fin to insertion of pelvic fin, iii) anterior attachment of dorsal membrane from caudal fin to insertion of pectoral fin, iv) anterior attachment of dorsal membrane from caudal fin to end of operculum. The present study providesa useful insight on the application of truss analysis in the shape variationamong three different life stages of *H. jerdoni*.

Key words : *Hypselobarbus jerdoni*, truss network analysis, principal component analysis, factor analysis, shape variation.

INTRODUCTION

Cyprinidae is a taxonomic family, within the superfamily Cyprinoidea that belongs to order Cypriniformes. The medium sized barbs of genus *Hypselobarbus* are endemic to India (Arunachala *et al*, 2016). *Hypselobarbus* has been familiar as a "catch-all" genus and encompasses morethan 26 species found in India and new species are continuously being discovered (Knight *et al*, 2013a; Knight *et al*, 2013b). The members of the genus *Hypselobarbus* are an economically important ornamental, as well as a food fish and locally sold fresh inmarkets (Jayaram, 2010). These fishes are highly valued in recreational fisheries and constitute a major component of thetropical fish trade and the juvenile *Hypselobarbus jerdoni* (Day, 1870) plays a significant economicrole in aquarium trade (Knight *et al*, 2013a). In spite of its economic significance, comprehensive knowledgeon its systematics/taxonomy is still incomplete. Further, generic placement/status of several species of *Hypselobarbus* remains questionable.

Morphometric characters have been efficiently employed for taxonomic related problems (Barriga-Sosa *et al*, 2004; Erguden and Turan, 2005). The traditional morphometric method involves direct quantification of a range of morphological characters that are subsequently analyzed via multivariate methods (Marcus, 1990; Mutanen and Pretorius, 2007). This method is remarkably useful in identification of closely related species and provides preliminary insights on fish taxonomy and shape variation (Stiasny *et al*, 1996). Meristic characters were also found to be valid in the race and species identification (Mekkawy, 1997; Turan, 2004). The traditional morphometric methods have some limitations in describing the fish shape and therefore this has overlooked (Turan, 1999; Sajina *et al*, 2011). Consequently, a stronglandmark-supported tool based on statistical analysis called 'truss network technique' was testedfor distinguishing species and this technique was

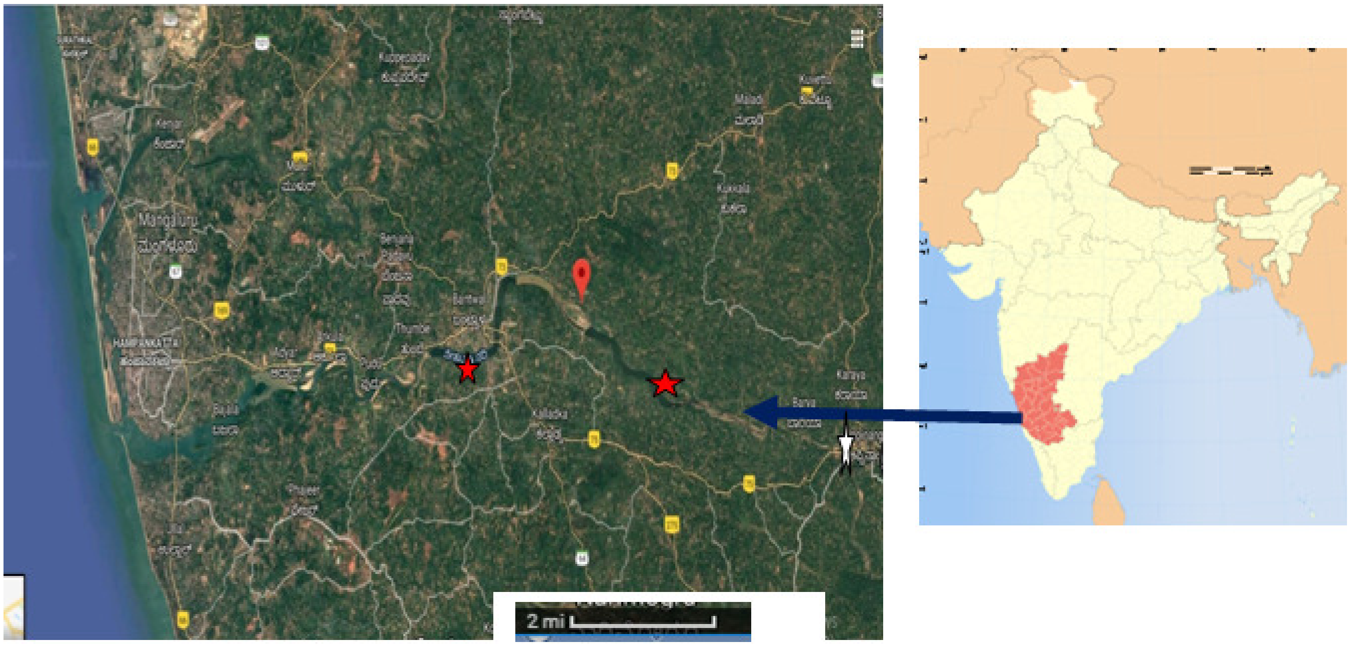

Fig. 1 : Netravathi river in southern India. The mark-ups indicate the locations from where fish samples were collected for this study.

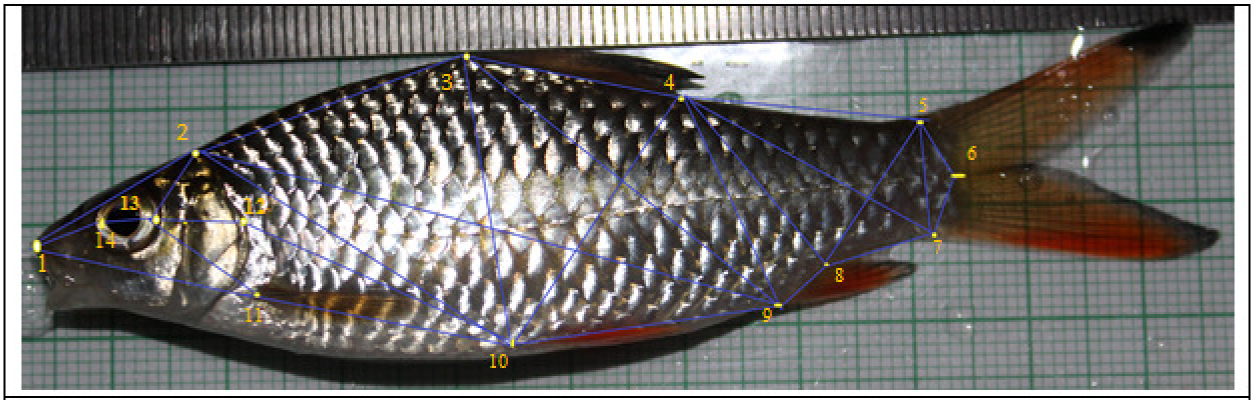

Fig. 2 : *H. jerdoni* (juvenile stages) representing locations of 14 landmarks and the distances measured which were used for morphological variations. Landmarks refer to: (1) anterior tip of snout at upper jaw (2) most posterior aspect of neurocranium (beginning of scaled nape) (3) origin of dorsal fin (4) end of dorsal fin (5) anterior attachment of dorsal membrane from caudal fin (6) posterior end of vertebrae column (7) anterior attachment of ventral membrane from caudal fin (8) end of anal fin(9) origin of anal fin (10) insertion of pelvic fin (11) insertion of pectoral fin (12) end of operculum (13) posterior end of eye (14) anterior end of eye.

extensively used by many workers in discrimination of species (Corti *et al*, 1998; Akyol and Kinacigil, 2002; Simon *et al*, 2010; Fernando and Amarasinghe, 2011; Rahman *et al*, 2014; Lal *et al*, 2015). Geometric morphometrics analysis of landmarks from digital images is highly effective in capturing information about the shape of an organism (Cavalcanti *et al*, 1999; Adams *et al*, 2013).

Locally known as Cha-meen, *H. jerdoni*, is categorized as Least Concern (IUCN), but the populations are declining (M. Arunachalam pers. comm., 2010). There was a need to study morphological variations among different age groups of *H. jerdoni* of the Netravati river for proper conservation and management. Hence, this study was aimed at investigating variations in different life stages, such as juvenile, sub adult and adult of *H. jerdoni* with truss network measurements.

MATERIALS AND METHODS

Sample collection

Thirty fishes of *H. jerdoni* were collected from different fishing sites of the Netravathi river (12°51’31"N 75°07’54"E to 12°55’40"N 75°21’55"E) in southern India (Fig. 1), with the assistance of local fishermen during February, 2018 -December, 2018.

Landmark-based morphometrics

Sampled specimens were placed on a flat surface with a plastic-coated graph paper, which was used for standardizing the coordinates of the digital images. Each fish was given a specific code for identification. A digital

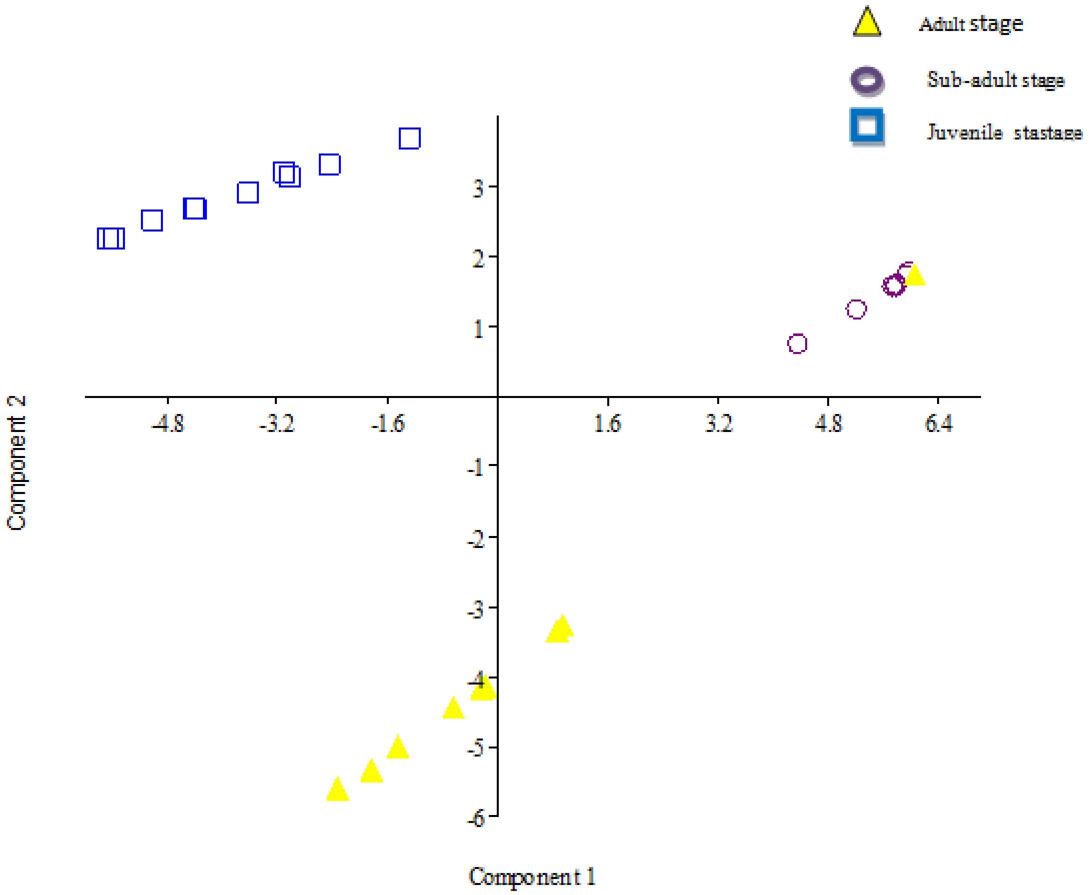

Fig. 3 : PCA scatter diagram.

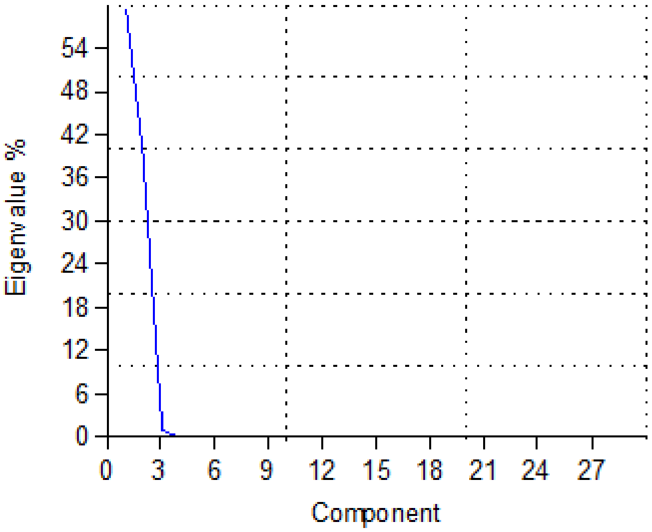

Fig. 4 : PCA scree plot between eigen values with their corresponding component.

camera (Canon 1300D digital camera) was used to capture the digital images. All the specimens were positioned laterally on their right side, with their body posture and fins into a natural position. Images of specimens were captured and transferred to acomputer for further analysis.

Truss-based morphometric analysis

The extraction of the truss distances from the digital images of specimens was carried out using a combination of the software platforms, tpsUtil, tpsDig 2 v2.1 (Rohlf, 2006) and PAST (Hammer *et al*, 2001). Software tpsUtil converts JPEG image into tps format. For covering entire shape of fish specimen, two dimensional Cartesian coordinates of 14 landmarks were recorded on the lateral view of each specimen (Fig. 2). The locations of the landmarks were selected following two criteria: reliability in terms of correspondence between specimens and the

Table 1 : Fish size, number of landmarks, latitude and longitude of the study area of *H. jerdoni* used in the present study.

H. jerdoni	Standard length (SL) range (mm)	Mean SL (mm)±SD	Sample size	Number of landmarks	Latitude and Longitude
Juvenile stage	83-93	90±2.89	10	14	12°51’31"N 75°07’54"E
Sub-adult stage	110-190	145±2.9	11	14	12°55’40"N 75°21’55"E
Adult stage	280-302	291±3.24	09	14	12°51’31"N 75°07’54"E

Table 2 : Summary of principal component analysis for the truss variables of Eigen value and percentage variance.

PCA	Eigen value	Percentage of Variance	Cumulative percentage
1	16.6546	59.481	59.481
2	11.0534	39.477	98.958
3	0.2346	0.83786	99.796
4	0.019208	0.068601	99.864

Table 3 : Factor loading based on eigenvalues on truss variables, rotated sum of square loading based truss variables based on factor analysis.

Factor number	Initial Eigenvalues			Rotation Sums of Squared Loadings		
	Total	Percentage of Variance	Cumulative percentage	Total	Percentage of Variance	Cumulative percentage
1	85.124	93.543	93.543	54.734	60.147	60.147
2	4.273	4.695	98.238	34.663	38.091	98.238
3	.415	.456	98.693			
4	.274	.301	98.994			
5	.233	.256	99.251			
6	.197	.217	99.468			
7	.133	.146	99.614			
8	.095	.104	99.718			
9	.067	.073	99.791			
10	.048	.052	99.844			
11	.039	.043	99.887			
12	.036	.040	99.927			
13	.018	.020	99.946			
14	.013	.014	99.960			
15	.011	.012	99.972			
16	.009	.010	99.982			
17	.005	.005	99.988			
18	.004	.004	99.992			
19	.003	.003	99.995			
20	.002	.002	99.997			
21	.001	.002	99.998			
22	.001	.001	99.999			
23	.000	.000	99.999			
24	.000	.000	100.000			
25	.000	.000	100.000			

Extraction Method: Maximum Likelihoood.

ability to best describe the geometry of the form under study. All the landmarks were digitized and truss networks were constructed by interconnecting the landmarks using software tpsDig. Using the computerized Pythagorean theorem in software PAST, X–Y coordinate data was transformed into linear distances for subsequent analysis. Altogether, 91 morphometric characters were attained connecting these landmarks (Strauss and Bookstein, 1982). The truss data generated by PAST were log-transformed to conserve allometries and to standardize variances (Strauss, 1985). To eliminate size effect, data were M-transformed by employing formula given below (Poulet *et al*, 2005):

$$M - trans = \log M - b (\log SL - \log SL\ mean)$$

Where, M-trans is the transformed measurement, M is the original measurement, b is the within-group slope regression of the log M versus log SL, SL is the standard length of the fish and SL mean is the overall mean of the standard length.

RESULTS AND DISCUSSION

Data on fish size, number of landmarks, latitude and

Table 4 : Rotated Factor matrix of Factor 1 and 2 showing loading for truss variables.

Rotated Factor Matrix		
Truss variables	**Factor 1**	**Factor 2**
5 to 8	.916	
5 to 9	.963	
5 to 10	.923	
5 to11	.897	
5 to 12	.893	
6 to 9	.937	
6 to 10	.890	
7 to 9	.924	
8 to 9	.950	
4 to 12	.896	
4 to 11	.890	
1 to 11		.943
1 to 12		.929
1 to 13		.922
2 to 11		.858
2 to 12		.866
6 to 9		.928
6 to 10		.890
7 to 9		.924
8 to 9		.950
11 to 13		.845
11 to 14		.908
12 to 13		.851
12 to 13		.918
13 to 14		.914

Extraction Method: Maximum Likelihood
Rotation Method: Varimax with Kaiser Normalization

longitude of the study area of *H. jerdoni* used in the present study is given in Table 1.

The truss network distances were subjected to PCA, at Jolliffe's rule with eigenvalues of at least 0.7. In total, four principal components were extracted through PCA responsible for 99.864% variation. The first two components extracted, accounts for a total variance of 98.958%, in which the first principal component (PC1) accounts for 59.481, while second PC2 contributes 39.477% (Table 2, Figs 3 and 4). The PC1 is the axis that always accounts for the greatest amount of variation in the data and the PC2 accounts for the second-most amount of variation. In different biological contexts,the geometric method provides shape-related additional information present in the relativelocations of landmarks (Adams and Rohlf, 2000). Fish show more noteworthy variation in morphometric attributes both within and between species when compared to other vertebrates and are more disposed to ecological changes (Allendorf *et al*, 1987; Wimberger, 1992).

The factor analysis of the transformed variables explained 98.24% of the total morphometricvariation with a contribution of 93.543% and 4.70% on the first and second factor, respectively (Table 3). The 1st and 2nd factors were chosen for rotation based on eigenvalues. After rotating the1st and 2nd factors the characters belonging to the middle portion of the body (below the first dorsal fin) loaded heavily on the first factor (truss distances 5 to 8, 5 to 9, 5 to 10, 5 to 11, 5 to 12, 6 to 9, 6 to 10, 7 to 9, 8 to 9, 4 to 12 and 4 to 11), while the measurements associated with the region along the head region loaded significantly on the second factor; those were the truss distances from 1 to 11, 1 to 12 , 1 to 13, 2 to 11, 2 to 12, 6 to 10, 7 to 9, 8 to 9, 11 to 13, 11 to 14, 12 to 13 and 13 to 14 (Table 4).

Organisms are capable of making adaptations that enable them to survive and fishes, like other organisms exhibit similar characteristics (Nacua *et al*, 2010). During the developmental history or ontogeny of an organism, its morphology modeling is greatly influenced by its environment. Geometric morphometric (GM) analysis on differentiating the shape variation in fish specieswas successfully applied by Rohlf (2002) and Adams *et al* (2004). Conversely, Addis *et al* (2010) used truss distances in bluefin tuna.

CONCLUSION

In our study, we applied truss network analysis to identify differences in the body shape of three stages of *H. jerdoni*. In geometric morphometrics, the biological homology criteria limit the selection of landmarks that provide information on shape, so that one can obtain results that make inferences about shape. Using the truss network system, weobtained a visualization of morphological changes of *H. jerdoni*; the variations were maximum in the middle and end parts of the body. Thus, the present study offers a useful insight that the truss network analysis is the perfect tool to pointing out the changes in body shape.

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