Figure S2: Phylogeny of Cyprinidae

50% majority rule consensus tree from 1,000 independent Maximum Likelihood analyses using the GTR+I+G model, with 1000 bootstrap replications, Consensus is based on five mitochondrial genes (COI, Cyt *b*, 16S, ND4, ND5), using 103 species of Cypriniformes, of which 74 species represent Cyprininae. Clades of non-Cyprininae species are in black (other subfamilies of Cyprinidae and other families of Cypriniformes). The seven clades that are part of Cyprininae are in blue. Numbers beside nodes are bootstrap values (shown in percentage). Bootstrap values lower than 50% are not shown.

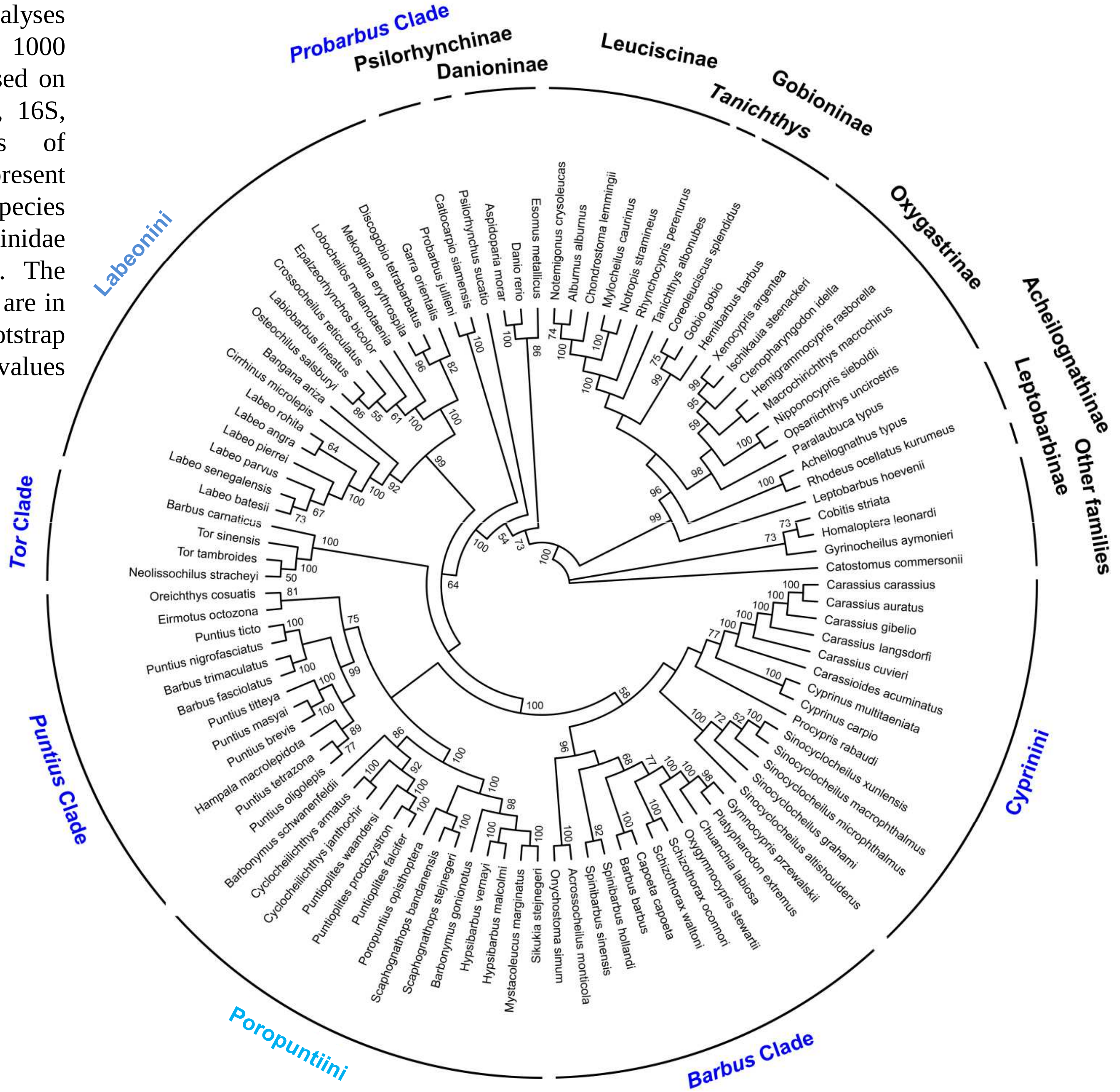
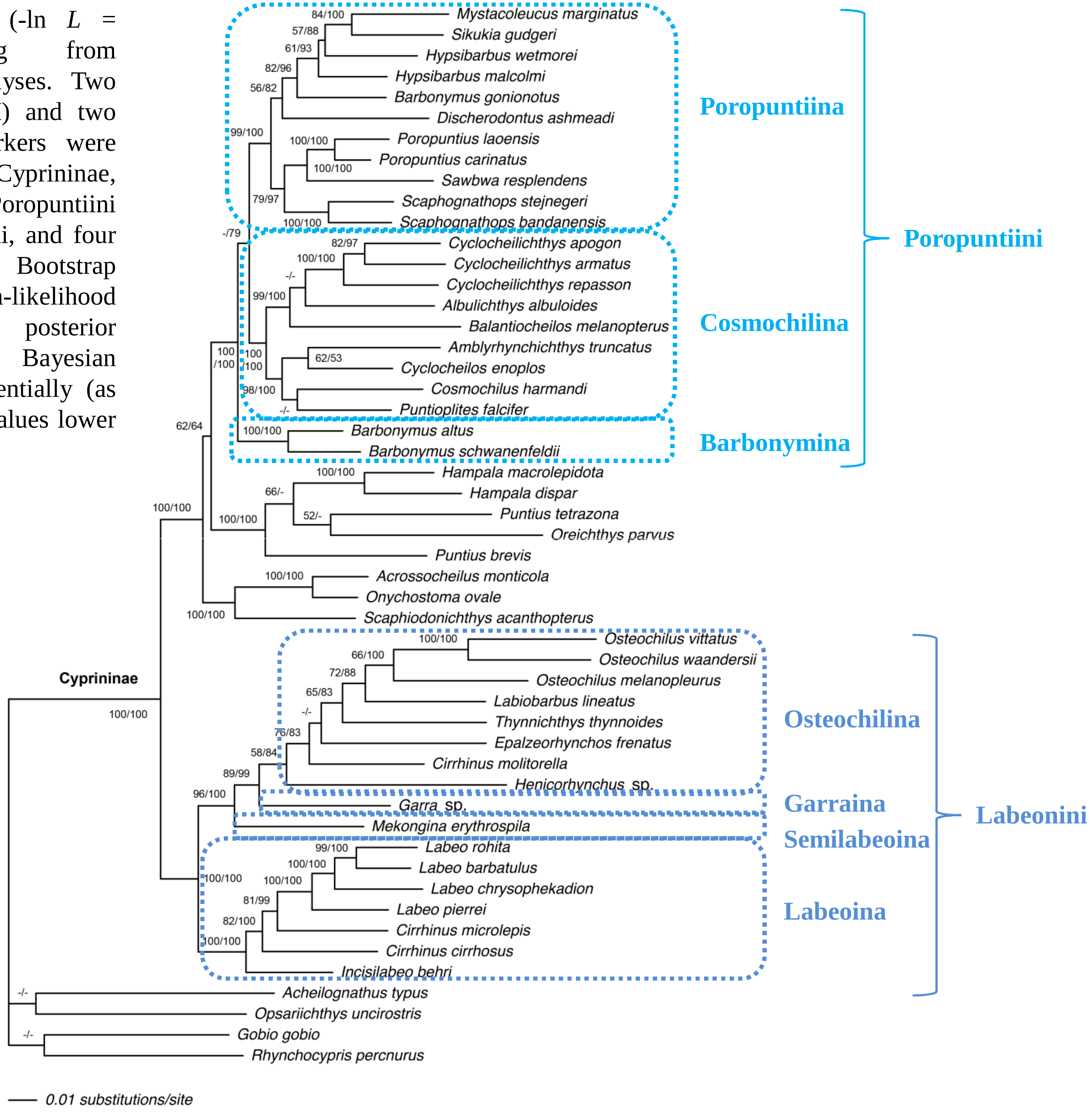


Figure S3: Phylogeny of Cyprininae
The best likelihood tree (-ln *L* = 38084.613690) resulting from Maximum Likelihood analyses. Two mitochondrial (Cyt *b*, COI) and two nuclear (RAG1, RH) markers were employed. 47 species of Cyprininae, including 22 species of Poropuntiini and 17 species of Labeonini, and four outgroups, were analyzed. Bootstrap values from the maximum-likelihood bootstrap analysis and posterior probability values of the Bayesian analyses were shown sequentially (as percentage) beside nodes. Values lower than 50% were shown as "-".



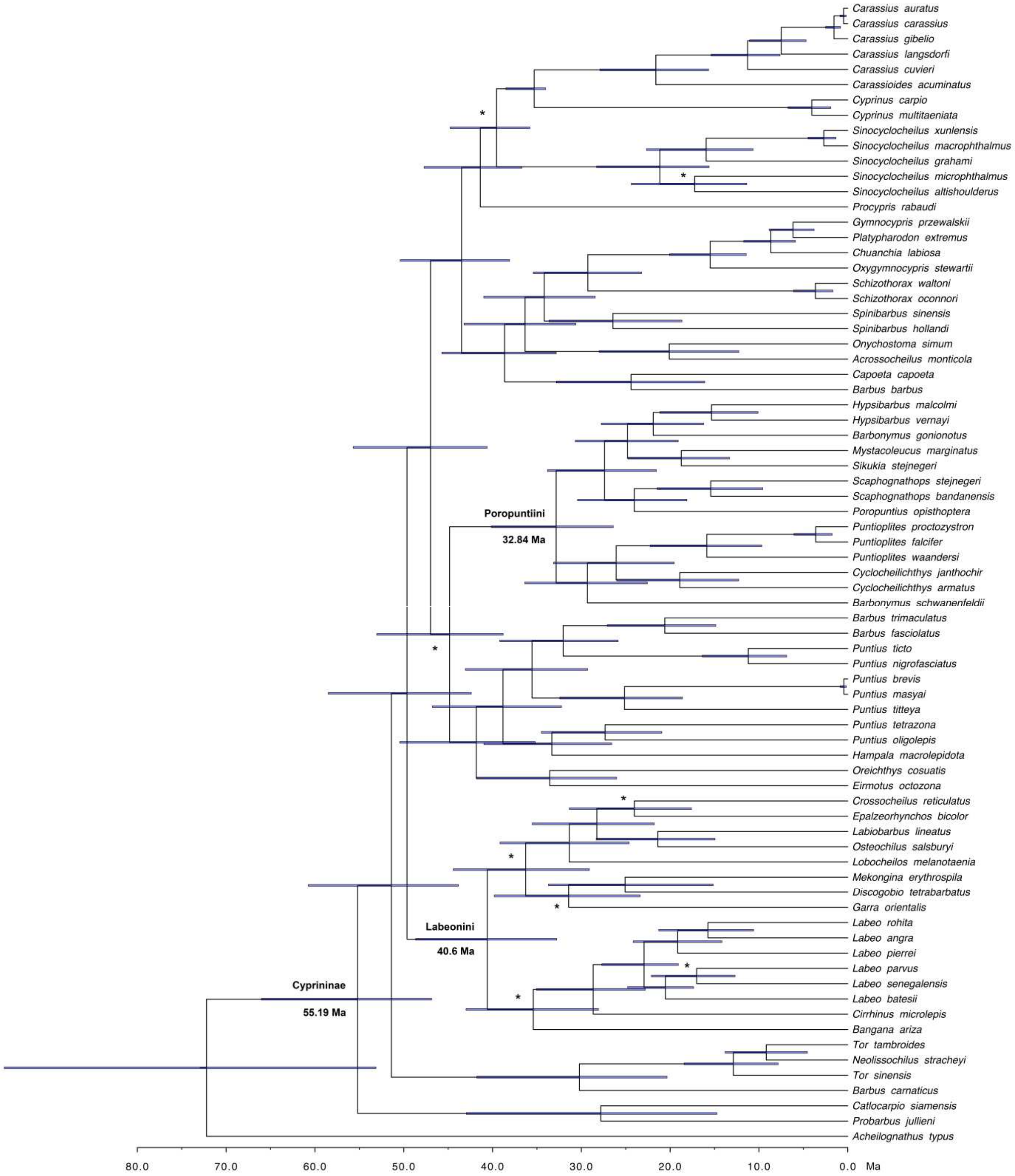


Figure S4: Molecular dating of Cyprininae Maximum Clade Credibility (MCC) tree of the subfamily Cyprininae derived from a Bayesian analysis employing a relaxed molecular clock. Branch lengths are drawn proportional to time. Horizontal bars denote 95% Highest Posterior Density (HPD) intervals of node ages. Nodes with posterior probabilities < 0.95 are indicated with asterisks. The outgroup used (*Acheilognathus typus*) is not shown. Four fossils were used as calibration priors: the oldest African *Labeo*-like fossil (17.0 Ma), the oldest *Cyprinus*-like fossil (33.9 Ma), an Asian *Puntius* fossil (28.4 to 37.2 Ma) and the oldest cyprinid fossil (*Parabarbus*, 48.6 Ma).

Figure S6: Morphometric analyses of pharyngeal bones in Cyprinidae

For 20 species of Poropuntiini and 15 species of Labeonini as well as eight species of other Cyprininae tribes, two species of Cultrinae and five species of Danioninae, all coming from South-East Asia, we performed a morphometric analysis of the fifth ceratobranchial, which bears the pharyngeal teeth. For each species, we extracted the fifth ceratobranchial from 3D volumes obtained by microtomography. Pharyngeal bones were then pictured from the posterior view without teeth in order to obtain the best contour to characterize the shape of the fifth ceratobranchial. Five views were taken independently for each bone. Contours were then transformed into Fourier coefficients with an automated function based on R, with 10 harmonics. PCA on Fourier coefficients was performed with Past. The first principal component (PC1), on the abscissa represents 66,9% of the total variation. The second principal component (PC2), on the ordinate, represents 13,8% of the total variation. PC1 corresponds to the difference in shape of the fifth ceratobranchial between Labeonini and other clades within Cyprinidae. It is interesting to note that two Labeonini genera (*Mekongina* and *Garra*) plot with the other clades.

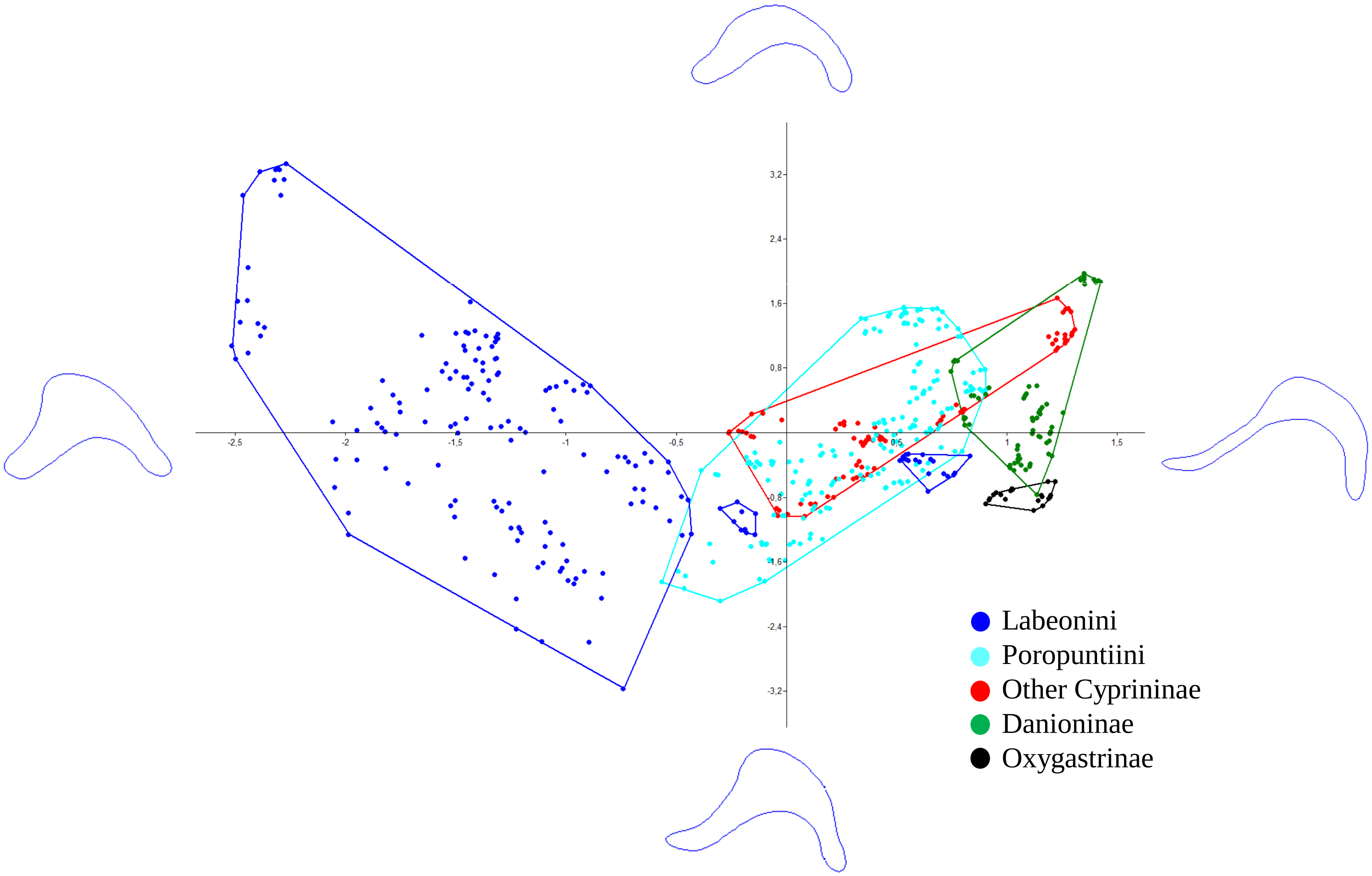


Figure S7: Comparison of the opening of the pharyngeal cavity in Poropuntiini and Labeonini.

For 20 species of Poropuntiini and 15 species of Labeonini, the following ratio was calculated: the pch/(pch+pdh) ratio between pharyngeal cavity height (pch) and pharyngeal dentition height (pdh), giving the relative size of the pharyngeal cavity height. This ratio is 0.30 for Poropuntiini and 0.17 for Labeonini (p <0.001).

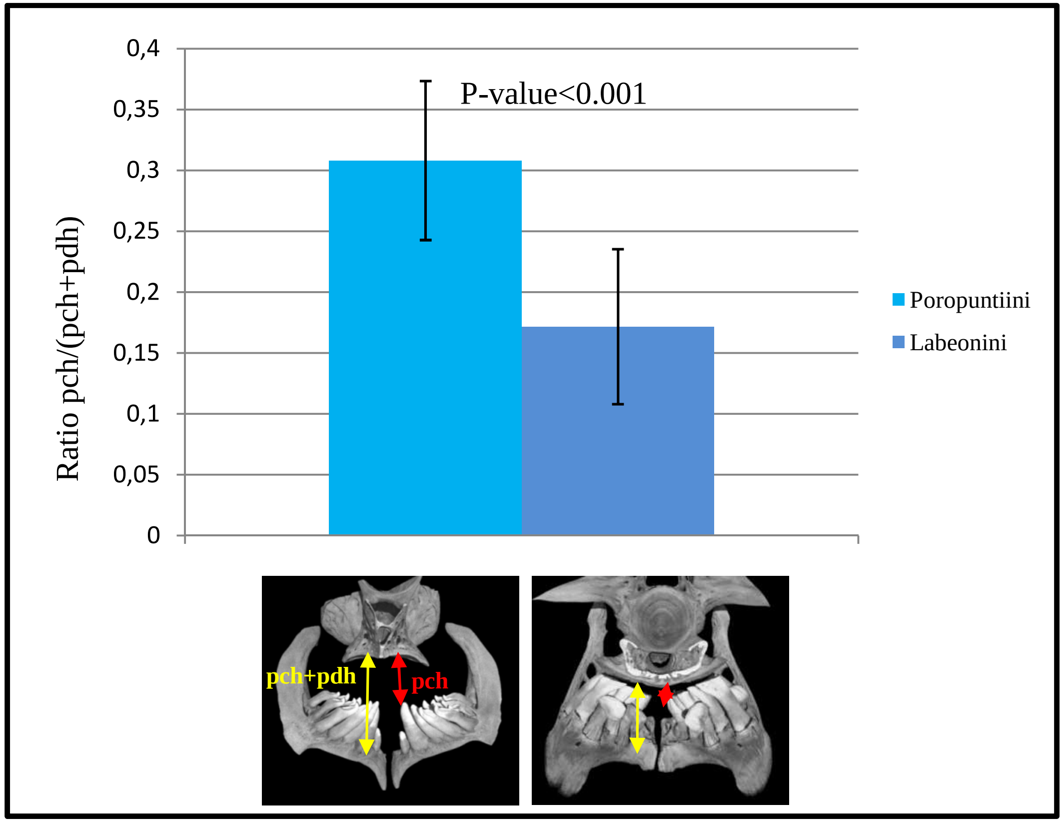


Figure S8: Carbon and Nitrogen isotopic analyses for Poropuntiini and Labeonini.

For 14 species of Poropuntiini and 12 species of Labeonini, we performed isotopic analyses for both Carbon and Nitrogen. For each species, based on one to three samples per species, we plotted $\delta^{15}N$ against $\delta^{13}C$ values. The range of values is similar for both tribes, suggesting that there are species feeding more on plant matters and species feeding more on animal matters in both tribes.

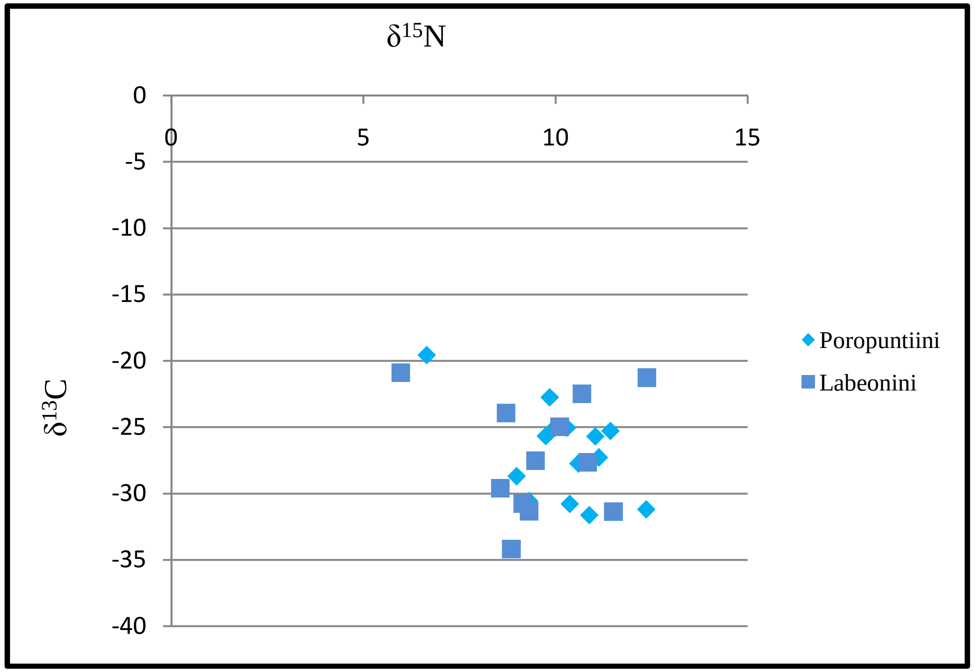
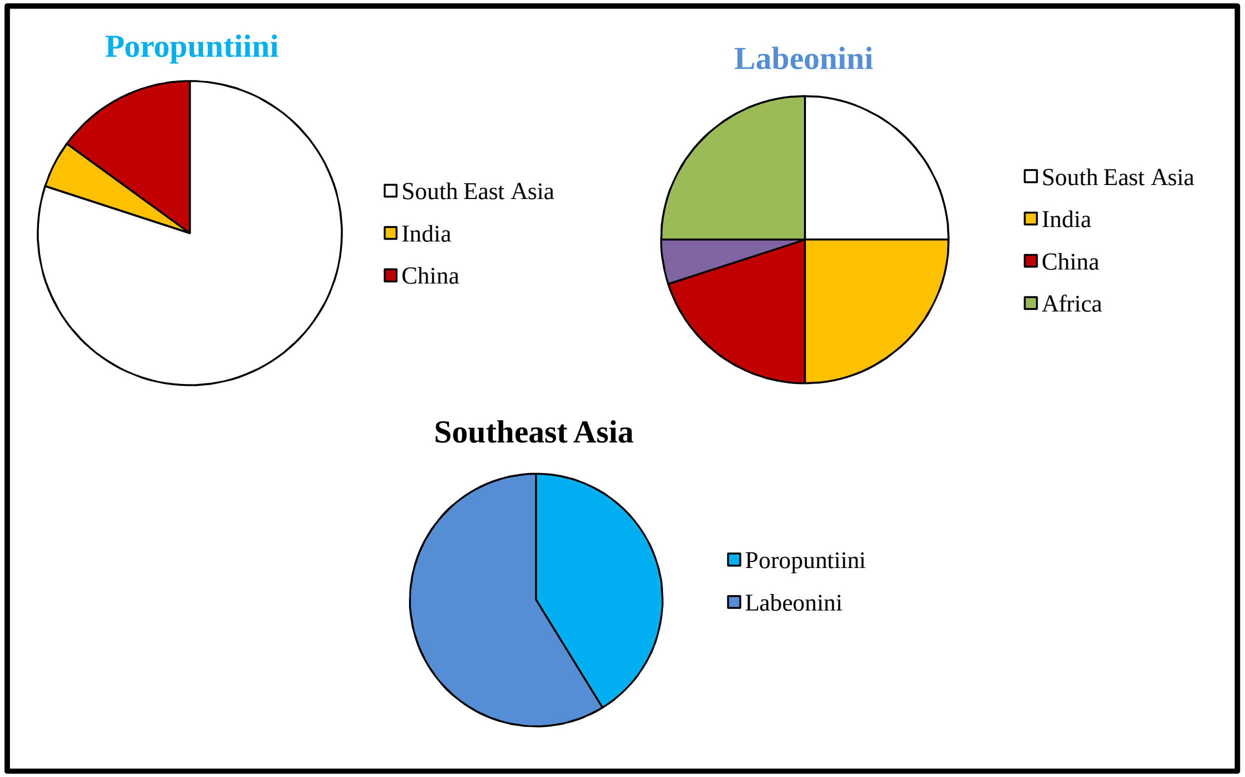


Figure S9: Geographical extension and species diversity in Poropuntiini and Labeonini

Based on (23, 51), this figure shows the number of species in Poropuntiini and Labeonini in each of the main geographical regions: Southeast Asia, India, China, West Asia, Africa. For Southeast Asia, we show the number of species for both clades. The total number of species is 100 for Poropuntiini and 400 for Labeonini. The number of species in Southeast Asia is 75 for Poropuntiini, 107 for Labeonini.



Froese R, Pauly D. 2013 FishBase. See www.fishbase.org.