Order Cypriniformes

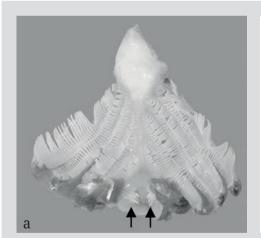
Carps and loaches

In West Asia, 434 species, 70 % of all freshwater fishes, belong to the order Cypriniformes. Cypriniforms represent the largest group of freshwater fish worldwide, with about 4300 species recognised, though about 10,000 species exist. The earliest fossil is Jianghanichthys from China's early Eocene (56-48 million years ago). Bayesian relaxed molecular clock analyses of Cypriniformes result in an average posterior crown age estimate of 97 million years ago, with the credible interval ranging between 85 and 115 million years ago. The origin of Cypriniformes is found in the Late Cretaceous, similar to the evolutionary roots of modern birds, mammals, and frogs, three other species-rich groups of vertebrates. As in modern birds, mammals, and frogs, major diversification events in Cypriniformes have likely started in the Paleogene after the collapse of ecosystems at the Cretaceous-Paleogene boundary.

Until the late 20th century, only two major families were recognised: Cyprinidae for all carps, barbels, and minnows, and Cobitidae for all loaches. Just three small families were excluded: Gyrinocheilidae for three Southeast Asian suckers; Psilorhynchidae for some South Asian

torrent minnows; and Catostomidae for one Chinese and many American suckers. Since Cobitidae has been split into 8 families and Cyprinidae into 12 families, not all of which are recognised by all authors, only the position of a few genera, such as *Sundadanio*, *Paedocypris*, *Tanichthys*, *Leptobarbus*, *Tinca*, and *Zacco* and some of their allies remain under discussion. Similarly, the phylogenetic relationships 'within' and 'among' the major groups have proved difficult to resolve across the entire order.

The phylogenetic position of a few genera is irrelevant compared to the benefits in communication associated with the erection of the former subfamilies of Cyprinidae into the range of families. We recognise monophyletic groups as their own families, different from Cyprinidae as Acheilognathidae, Leuciscidae, Danionidae, Gobionidae, Tincidae, and Xenocyprididae. These are the families found within the geographic coverage of this book. Further reading. Howes et al.1991; Cavender & Coburn 1992; Arai & Kato 2003; Saitoh et al. 2006; He et al. 2008; Mayden et al. 2008; Yang et al. 2012; Imoto et al. 2013; Liu et al. 2015 (Jianghanichthys); Stout et al. 2016 (phylogenetics); Feng et al. 2017 (phylogeny of frogs); Hughes et al. 2018 (molecular estimation of age); Tan & Armbruster 2018 (family placement of genera).



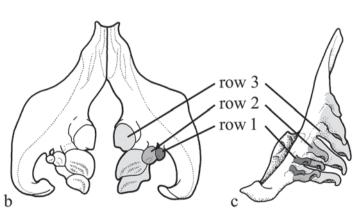


Figure 31. Dorsal view of branchial arches of *Carassius gibelio* **a**, showing four gill arches and one pharyngeal arch on each side; arrows point to pharyngeal teeth. **b**, Dorsal view of pharyngeal arches of *Cyprinus*, showing a way of counting pharyngeal teeth (1,1,3–3,1,1 teeth). **c**, Anteriordorsal view of left pharyngeal arch of *Barbus* (2,3,5–5,3,2 teeth) (from Kottelat & Freyhof 2007, after Holčík 1989).

Pharyngeal teeth in Cypriniformes. The pharyngeal teeth are located on the fifth gill arch or pharyngeal arch (gill arches 1–4 carry gill filaments and gill rakers). Their number, arrangement, and shape are useful characters to distinguish some species. To examine them, it is necessary to remove the pharyngeal arch. This dissection requires some experience and training, magnification, and good light. The standard procedure is to remove a single pharyngeal arch, usually the right one, to leave the other side of the head intact. To extract the pharyngeal arch, the opercle

is folded forward, and a small sharp tool (forceps, scalpel) is inserted between the arch and the anterior edge of the cleithrum. The tool is moved dorsally and ventrally along the cleithrum to cut the tissue surrounding the arch. The dorsal end of the bow is released first. The bow is grasped by its dorsal or ventral end and moved back and forth to release it. It should not be grasped in the middle as the tool will damage the bow or the teeth. The pharyngeal arches of small individuals are fragile, but firm handling is required to extract them. Remaining tissue is removed from the arch and between the teeth, either manually or by soaking the arch in dilute potassium hydroxide (KOH) solution (0.5-1.0 %) (this should be done carefully as teeth of small species are easily broken during handling or damaged by the chemical).

Teeth are arranged in 1-3 rows. All teeth in each row are counted, including broken and missing teeth. Some teeth may be missing due to breakage during preparation or as part of the replacement process. An empty socket indicates the position of a missing tooth. Teeth counts are given as a formula, with the left arch count given first, separated from the right by a hyphen. For each side, the tooth counts on the different rows are separated by commas, from the outermost to the innermost row of the left arch, then from the innermost to the outermost row of the right arch. For example, the formula 2,3,5-5,2,2 means that there are three rows of teeth on each arch, that the left arch has two teeth on the outer row, 3 on the middle row, and 5 on the inner row, that the right arch has two teeth on the outer row, 2 on the middle row and 5 on the inner row (Figure. 31c).

The number of teeth may differ between the two sides of an individual (usually by one unit), with the left arch generally having more teeth. Within a species, the number of pharyngeal teeth usually shows little variability.

The formula of the pharyngeal teeth, especially the number of rows, has often been used as a character to distinguish genera. The loss of tooth rows from 3 to 2 or 1 occurred independently in different lineages, especially during the evolution of small-sized species and genera, so this character cannot be used alone to define genera.

Pharyngeal teeth are regularly replaced, and empty sockets in the pharyngeal arch may result from lost teeth. New teeth develop next to the pharyngeal arch, embedded in tissue and without contact with bone. As the new tooth grows, it will attach to the part of the pharyngeal arch occupied by the lost tooth. Further reading. Chu 1935; Jenkins & Burkhead 1993.

Key to families of Cypriniformes based on species native and introduced to West Asia 1a - Three pairs of barbels2 1b - No, one or two pairs of barbels3
2a - An erectable suborbital spineCobitidae 2b - No suborbital spine, lacrimal bone elevated with a suborbital flap or groove in males of some speciesNemacheilidae
3a - Female with long ovipositor; a prominent dark-grey midlateral stripe on posterior part of flankAcheilognathidae 3b - Female without long ovipositor; if a stripe is present, then running from head or anterior body to caudal base4
4a - Usually 5½ branched anal rays and two pairs of barbels (rarely one pair or no barbels); if 6–7½ branched anal rays, then always two pairs of barbels (<i>Cyprinion, Carasobarbus</i>)

4b - 6–48½ branched anal rays; usually no or one pair of barbels5
5a - One pair of barbels (except in <i>Pseudorasbora</i>)6 5b - No Barbels7
6a - 8½ branched dorsal rays; 6–8½ branched anal rays; scales deeply embedded, body compressed; belly flattened; no lateral blotches or stripeTincidae 6b - 7½ branched dorsal rays; 6½ branched anal rays; scales not embedded on flank; in all but one species (<i>Pseudorasbora</i>), body cylindrical or slightly depressed, belly flattened; mouth inferior; a row of dark-brown or grey blotches on body; in <i>Pseudorasbora</i> mouth superior; a dark-grey stripe from eye to caudal base
7a - Last unbranched dorsal ray spinous, rigid; belly keeled from pectoral base to anusXenocyprididae (<i>Hemiculter</i> , <i>Hypophthalmichthys</i>) 7b - Last unbranched dorsal ray neither spinous nor rigid; belly rounded or with a keel starting behind pelvic origin (except <i>Pelecus cultratus</i> , which has very large pectoral, reaching beyond pelvic base)8
8a - Distance from anal origin to caudal base shorter than distance from anal origin to pelvic originXenocyprididae (<i>Ctenopharyngodon</i> , <i>Mylopharyngodon</i>) 8b - Distance from anal origin to caudal base greater than or equal to distance from anal origin to pelvic originLeuciscidae



Despite being only distantly related, young Ctenopharyngodon (upper) might challenge identification as being quite similar to Squalius species (lower).