

Mitochondrial phylogeny of the european cyprinids : implications for their systematics, reticulate evolution and colonisation time.

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Two different mitochondrial genes, the cytochrome b and the 16S rDNA, support the same European cyprinid molecular phylogeny : the most basal subfamily is the paraphyletic Rasborinae, the cyprininae are monophyletic, the Tincinae and Gobioninae are close to the Cyprininae or more basal lineages but not close to Leuciscinae or Alburninae, and the Leuciscinae are paraphyletic but can become monophyletic if we include the biphyletic alburninae and exclude the Phoxinini. The relationship of the Acheilognathinae remains obscure. Natural intergeneric and interspecific hybridizations are clearly demonstrated within the Leuciscinae, both from high bootstrap proportions and intermediate morphological features : *Chondrostoma toxostoma* and *Rutilus rutilus*, *Scardinius erythrophthalmus* and *R. rutilus*, and *Leuciscus multicellus* and *Leuciscus soufia*. Finally, the use of the nonsaturated and clockwise 16S mtDNA sequences have been used to infer from nonintra-specific taxa the time of the first European cyprinid cladogeneses. The estimation confirms the hypothesis of Almaça and Banareescu that European cyprinids subfamilies started to diversify 35 mya and confirms the hypothesis of Bianco on the diversification of European leuciscines in the Mediterranean area during the late Messinian (6.5 to 5.3 mya).