

# Identification of cryptic species using both phylogenetic and population genetics approaches

Jean-Dominique Durand, UMR 5119 ECOLAG, IRD Dakar

In systematics, morphometric characters are used to identify species and highlight phylogenetic relationships among them. However, morphometric variability often does not correspond with the evolutionary processes underlying the divergence within a group of organisms. With the development of molecular techniques and population genetic statistics, new species have been described in organisms that don't present obvious morphometric differences.

Mugilidea is a fish family with a worldwide distribution that constitutes an important fishery resource for numerous developing countries. However, due to its high morphological similarities, nomenclature and taxonomy of this family is still not stable, and taxonomic status of wide range species such as *Mugil cephalus* is still questioned. To address these issues, we used both phylogenetic and population genetics approaches.

All molecular phylogenetic trees stress the low phylogenetic utility of morphometric characters used so far in the Mugilidae taxonomy. However, all samples of *M. cephalus* collected worldwide belong to a unique phylogenetic unit that harbors numerous mitochondrial lineages each with a clear geographic structure. Among 12 mitochondrial lineages described along the distribution range of *M. cephalus*, only one is observed in West Africa, from Mauritania to Angola. If most of these lineages appear strongly allopatric, in the North West Pacific, 3 mitochondrial lineages are present sometime in sympatry. The level of divergence among these mitochondrial lineages questioned the taxonomic status (up to 2% with the COI), but genetic isolation of these lineages and thus the presence of cryptic species in *M. cephalus* is still to be demonstrated. To provide some answers, we investigated the level of genetic isolation among *M. cephalus* samples in NW Pacific using a set of 8 microsatellite loci and by considering mitochondrial lineage (COI) of each genotyped individual. Using assignment test on microsatellites data, 3 cryptic species were identified in NW Pacific *M. cephalus* each specie being characterized by one of the 3 mtDNA lineage highlighted in the COI phylogenetic tree. The genetic architecture of the *M. cephalus* species in NW Pacific probably results from the complex interaction of contemporary and evolutionary time-scale factors.