

Taxonomical review of French Freshwater Ichthyological fauna : molecular validation of the determination guide and definition of species distribution area

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Abstracts

An update of the taxonomic reference table for fish is currently in progress. The elaboration of a determination guide will notably help French fish resources management policies. To correctly answer to the scientific requirements and management projects, two objectives were fixed: the use of molecular tools (mtDNA and microsatellites) to validate the species identification of dace (*Leuciscus*), minnows (*Phoxinus*) and gudgeons (*Gobio*) made by the agents of the ONEMA, and a description of their distribution areas. This work completes the convention established between the MNHN and the ONEMA " Taxonomical review of French Freshwater Ichthyological fauna: adaptation of management tools ".

We analyzed 1043 daces, 1594 minnows and 1280 gudgeons (instead of 500 individuals by groups initially planned) to answer at best these objectives. The complementarity of the molecular approaches (mtDNA and microsatellites) allowed us to establish the evolutionary history of these groups and to identify the geographical structuring of their genetic diversity.

Considering daces, the obtained genetic results are in favour of the definition of three species : *L. leuciscus* / *L. burdigalensis* and *L. bearnensis*, for which we highlight an ongoing speciation process. However, our data did not allow validating *L. oxyrrhis*. Globally, an important structuring was identified and definition of conservation units was made. We also confirm the possibility of hybridization between *L. leuciscus* and *Leuciscus idus*.

The study of minnows allowed us to highlight an unsuspected and considerable genetic diversity. The obtained genetic data validate the description of *P. bigerri* and *P. septimaniae* (with a reevaluation of their areas of distribution), but the message is more difficult for *P. phoxinus*. Indeed nine mitochondrial lineages have been detected under the *P. phoxinus* appellation and a reflection is proposed for the definition of this species as well as associated conservation units.

Previous conclusions done by the MNHN convention concerning the potential presence of hybridization and introgression on their studied minnows were confirmed in most of the cases and tend to explain the difficulties encountered for morphological identification. All of this illustrates the presence of a cryptic diversity.

As for the two other species complex, we found a geographical structuring of the genetic diversity of the gudgeons. Nevertheless, this genetic diversity is clearly lower. The current mitochondrial data seem to be in favour of the definition of *G. gobio*, *G. occitaniae* and *G. lozanoi* but does not allow validating *G. alverniae*. We do not found any genetic trace of *Romanogobio belingi* on the mitochondrial data set.

The level of translocation highly varies in regards of the considered species. The combined use of the two types of genetic markers allowed us to identify some of the populations sources.

In conclusion we discuss about the potential consequences in term of managing and conservation of all this cryptic genetic diversity.

KEY WORDS (THEMATIC AND GEOGRAPHICAL AREA)

***Phoxinus*, *Leuciscus*, *Gobio*, species, phylogeography, mitochondrial DNA, microsatellites, French catchments, distribution area, identification, conservation unit, ESU**