

DNA barcodes for fish identification: To believe or not to believe

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A popular FISH-BOL-program is actively developing as a global effort to coordinate an assembly of a standardized reference sequence library for all fish species, one that is derived from voucher specimens with authoritative taxonomic identifications (www.fishbol.org). As a result, many authors conclude that the identifications of specimens that remain problematic for the researcher or observer after consulting the photographic guide and descriptive accounts will in most cases be enabled by DNA barcoding (Mecklenburg et al. 2016). However, there are known cases of controversial results obtained by DNA barcoding and other genetic markers, for example for the taxonomy of cods *Gadus macrocephalus* and *G. ogac* (Stroganov et al. 2011; Mecklenburg, Steinke 2015). Other types of problems are situations where barcode sequences from samples of morphologically different species exhibit little variability (0-hypothesis is not rejected), for example, in cases of Arctic cods *Arctogadus borisovi* and *A. glacialis* (Møller et al. 2002; Jordan et al. 2003) or flatfishes *Hippoglossoides robustus* and *H. elassodon* (Kartavtsev et al. 2007) and *Pseudopleuronectes yokohamae* and *P. schrenki* (Kartavtsev et al. 2007). In turn, when the 0-hypothesis is rejected and polyphyletic origins of genera are revealed, the problem of the levels of taxonomic division arises: to separate numerous independent genera/species or to unite branches in the same genus/species and accept them as subgenera (groups of related species)/subspecies. The first way, for example, is accepted for minnows of *Abramis* – *Ballerus* – *Blicca* – *Vimba* species group, and the second one for *Alburnus* – *Chalcalburnus* (Eschmeyer et al. 2018). And in the case of *Huso* and *Acipenser* (family Acipenseridae) even the third unique way to ignore both polyphyletic origins of these nominal genera and morphological evidence (Vasil'eva et al. 2009) is accepted (Eschmeyer et al. 2018).

Our common studies on genetic variation and differentiation within Ponto-Caspian shads (*Alosa*) based on a single mtDNA gene and 11 microsatellite loci suggest the lack of support for most of previously described and morphologically diverged taxa (Sotelo et al. 2012). And only more complex sequencing analyses of both mitochondrial and nuclear markers succeeded in detecting various Eurasian phylogenetic lineages in spirlins (*Alburnoides*) and gudgeons (*Gobio*) (Mendel et al. 2008; Stierandová et al. 2016). Our recent studies are related with some taxonomic problems in Ponto-Caspian gobies (family Gobiidae) and spined loaches (fam. Cobitidae). We are trying to select the most appropriate genetic markers and out-groups, and in some cases we are faced with the need to check voucher specimens for samples from GenBank dataset, but for samples that are devoid of a voucher fund it is completely impossible. And so we should collect new materials for DNA researches with voucher samples available for any verification.

Keywords: molecular genetic studies; taxonomic problems; limited resolution; voucher specimens