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or less straight, (5) 1-5 more abdominal than caudal vertebrae, (6) absence of foramen on anterior wall of horizontal limb of the cleithrum, (7) presence of rasborin process on epibranchial 4, and (8) interhyal well ossified. *Rasbora* sensu stricto can be distinguished from all other rasborin genera by presence of the opercular canal.

To examine the phylogenetic significance of the rasborin process for rasborins, another phylogenetic analysis was conducted including 34 taxa of rasborins and representatives of the cyprinid subfamily Danioninae. Forty-three characters were coded, and the phylogenetic analysis confirms the rasborin process as a synapomorphy for the genus *Rasbora* and related genera.

Two species of trouts, resident and migratory, sympatric in streams of northern Anatolia (Salmoniformes: Salmonidae)

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Two species of trouts inhabit streams and rivers draining to the Black Sea in northern Anatolia (Turkey). One is restricted to the upper parts of streams and rivers and the other is migratory and found in the lower and middles parts. They are distinguished by their morphology, maximum size (250 mm vs. 500 mm SL), colour pattern, and life history. The two species occur in sympatry in several streams, and occasionally in syntopy. Preliminary molecular analyses show that they belong to distinct lineages, congruent with morphological and life history characters. In our study, the resident trouts of different drainages are more closely related to each other than to the migratory ones in the same drainages. This contradicts the credo that resident and migratory trouts in a given stream are only 'forms' of the same species with different life histories. We do not extrapolate this to be the case in other drainages and for other species, but this calls for a more cautious treatment of the taxonomy, diversity and conservation of trouts in southern Europe and the Middle East.

New data on the karyotype of the kaluga *Huso dauricus* (Acipenseridae, Pisces) and their applications for sturgeon phylogeny, taxonomy, and aquaculture

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Taxonomy and Systematics

The karyotype of the kaluga *Huso dauricus* has been studied at first by imperfect methods resulted in incorrect value of 60 chromosomes, and later it was transformed in 120-chromosome karyotype without any special analysis (Burtzev et al. 1973, 1976). The recent karyological analysis performed by using lymphoid organ cells revealed the karyotype of the kaluga to be represented by 268±4 chromosomes. The number of biarmed chromosome is 100, and the number of chromosome arms 368±4. These results prove the kaluga to be octoploid fish (according to evolutionary ploidy scale) for the first time and reject previous indirect inferences of its 120-chromosome state presented by the nuclear DNA content (Birstein et al. 1993, Yin et al. 2004) and the microsatellite (Ludwig et al. 2001) analyses.

Most authors traditionally combine the kaluga with the great sturgeon *Huso huso* and separate them in a special genus *Huso*. Newly obtained karyological data confirm polyphyletic origin of *Huso* previously demonstrated by molecular studies (Ludwig et al. 2000, 2001, Robles et al. 2004, Krieger et al. 2008), since the great sturgeon belongs to tetraploid species, while the kaluga is octoploid. Moreover, re-examination of the set of morphological characters diagnostic for genus *Huso* (Berg 1948, Sokolov 1989) revealed that only two morphological features combine the kaluga and the great sturgeon, namely the shape of a mouth and the joining manner of gill membranes and the isthmus in adult specimens, whereas four morphological characters (the number of dorsal fin rays, mouth size, barberls structure and size relations of dorsal scutes) differentiate them. Consequently, revealed phylogenetic relations of sturgeon species and their observed morphological divergence may result in two different taxonomic conclusions: 1) the division of both former *Acipenser* and *Huso* into several genera of phylogenetically related and morphologically similar species, 2) the recover of the initial system with all sturgeon species united in the same genus *Acipenser*. The last opinion seems the most constructive in different aspects. It presumes the restoration of the old name *Acipenser huso* for the great sturgeon and *A. dauricus* for the kaluga.

Since the kaluga was assumed as 120-chromosome species and the Far Eastern analog of the great sturgeon, its hybrid with *A. ruthenus* was believed to have the same success in sturgeon aquaculture as already employed bester

has. But revealed octoploid level of the kaluga presumes that its hybridization with 120-chromosome species will result in sterile progeny, while the hybrids between the kaluga and 260-chromosome sturgeon species, namely *A. schrenckii*, will be fertile.

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Discrimination of two picarel species (*Spicara flexuosa and Spicara maena,* Pisces: Centracanthidae) based on mitochondrial DNA sequences

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Introduction. Picarel (*Spicara flexuosa* Rafinesque, 1810) and blotched picarel, *Spicara maena* (Linnaeus, 1758) belong to Centracanthidae family. Due to the fact that both species are protogynous hermaphrodites, many systematic problems occurred in the family Centracanthidae. Nowdays, *S. flexuosa* appears as another scientific name of *S. maena*. In contrast, many researchers consider them as two different species. Some mtDNA segments, notably the rRNA genes, have been shown to be useful for determining relationships at different taxonomic levels. The aim of this study is the evaluation of the similarity/dissimilarity of *S. flexuosa* and *S. maena* species, using a mtDNA segment, i.e. a part of the 16S rDNA gene.

Materials and methods. In total, 39 individuals of *S. flexuosa* and 39 individuals of *S. maena* were analyzed. Total DNA was extracted from muscle according to the CTAB method. A universal primer set was used for the amplification of a part of the 16S rDNA gene, in both *S. flexuosa* and *S. maena*. A sequencing analysis on a 3730 x l DNA Analyzer (Applied Biosystems) was followed using both forward and reverse primers for crosschecking. The nucleotide sequences of all individuals were aligned using the Clustal X software and the BioEdit software, set to default parameters and corrected by eye.

Results. The size of the PCR products was approximately 600 bp for both species. In total 566 bp at the 5′ end of the mtDNA 16S rRNA gene for both species, were sequenced. All the 39 individuals of *S. flexuosa* revealed the same haplotype and all the individuals of *S. maena* revealed another haplotype, which was different in fifteen nucleotides compared to *S. flexuosa* as a reference sequence. DNA sequences were deposited in GenBank (accession numbers FJ62583; FJ625836). The average nucleotide compositions of A, C, G, T, was 21.38%, 24.03%, 26.33% and 28.27% for *S. flexuosa* and 22.26%, 23.85%, 25.44% and 28.45% for *S. maena*, respectively.

Discussion. There was only a single study dealing with the genetic discrimination between *S. flexuosa* and *S. maena*, using allozyme electrophoresis. According to this study *S. flexuosa* and *S. maena* are conspecific despite morphological differences, as no discriminating monomorphic locus was identified between the two species and genetic distance was only D = 0.006. Contrary to that, our results show that the two species (i.e. *S. flexuosa* and *S. maena*) are well discriminated using genetic data, as the 16S rDNA haplotype of *S. flexuosa* can be differentiated from the *S. maena* haplotype in 15 nucleotide differences. Considering that the 16S rDNA gene is a very good species – specific marker, our data could be a first indication for a probable identification of the two species. This study is being continued with the use of the multivariate analysis technique of morphomertic characteristics, in order to have more data for the discrimination of the species.

Populations of North-Eastern Europe with intermediate characteristics of vendace (*Coregonus albula)* and least cisco (*C. sardinella*)

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Northern Eurasia is traditionally considered to have *Coregonus albula* and *C. sardinella*. The habitats of the two species overlap in Pechora River area forming a wide hybridization zone (Reshetnikov, 1980; Sendek, 1998). However, our results allow reconsidering this point of view.