# Genetic and morphological analyses of 50 -chromosome spined loaches (Cobitis, Cobitidae, Pisces) from the Black Sea basin that are morphologically similar to C. taenia, with the description of a new species 

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#### Abstract

Karyotyped specimens from three populations of spined loaches, genus Cobitis, that occurred in the Veleka (Bulgaria), Chernaya (Crimean Peninsula) and Southern Bug (Ukraine) Rivers in north-western Pontic region were subjected to enzyme electrophoresis (for 5 loci), comparative morphological studies, and phylogenetic analysis (based on PCR of a 1230 bp fragment of mtDNA and the cytochrome $b$ gene). These studies resulted in the description of loaches from the Crimean Peninsula as a new species Cobitis taurica, while the taxonomic status of populations from the Veleka and S. Bug rivers appeared to be controversial and in need of further investigation.


Key words: "Cobitis taenia complex", karyotype, nuclear and mtDNA markers, biogeography

## Introduction

Several species of European spined loaches of the genus Cobitis correspond to the May r, (1969) concept of sibling species (Vasil'eva \& Vasil'ev 1998, Vasil'eva 2000). One group of such loaches, "the C. taenia complex", contains diploid as well as hybrid polyploid forms, which differ significantly at the genetic level, but are nearly indistinguishable from C. taenia Linnaeus, 1758 by all major diagnostic morphological characters. For example, the presence of only one elongated dark spot at the base of a caudal fin, broad axe-shaped lamina Canestrini in males and more or less rounded scales with a relatively small central part devoid of cross furrows (see Vasil'eva 2000). One of these forms has been discovered in the Chernaya River, the south-western part of the Crimean Peninsula, the Black Sea basin, in 1981 (see V a sil'e va 1984). Loaches from this river displayed external morphological characters that were quite similar to those of C. taenia (see V a s il'e v a 1984, 2000), but their karyotype was entirely different ( $2 \mathrm{n}=50$ with chromosome arms, $\mathrm{NF}=96$; V a s i l'e v 1985, 1995, Vasil'ev \& Vasil'eva 1994, Rábová et al. 2004) from any other European Cobitis species studied to date (see Vasil'ev \& Vasil'eva 1982, Ráb \& Slavík 1996, Boroń 2003). Vasil’ev (1995) therefore hypothesized the separate specific status for loaches from the Chernaya River.

[^0]Further extensive genetic screening of loach populations from south-eastern Europe using karyotyping, flow cytometry ( FC ), mtDNA and nuclear markers revealed other populations of spined loaches with $2 \mathrm{n}=50$ chromosomes and very similar karyotype structure in the Southern Bug R. (Ukraine) and the Veleka R. (southern Bulgaria). This discovery stimulated our research into this new form with such an unusual karyotype and the comparison of all three populations with other members of "the C. taenia complex" based on morphological characters as well as genetic diagnostic markers. The present paper deals with the formal description of the spined loach from the Chernaya River as a new species and discusses mutual relationships among populations of loaches with 50 chromosomes and the unusual karyotype in the north-western Pontic region.

## Materials and Methods

## Materials

50-chromosome spined loaches were collected during expeditions in 2002-2003 at three localities (Table 1, Fig.1): the Chernaya River, the Crimean Peninsula (5), 10 ), the Veleka R., southern Bulgaria ( $49,3 \sigma^{\prime}$ ), and the mouth of the Southern Bug R., Ukraine ( 9 , $100^{\prime}$ ). All these specimens were subsequently identified genetically and all but 8 individuals, from the latter locality, were morphologically examined. For morphological investigation, we further used loach samples collected in the Chernaya R. in 1985 ( 37 spec.) and in 2004 (1 spec.). All these voucher specimens are kept in the Zoological Museum of the Moscow State University (ZMMU), and detailed information about samples used for the description of a new species are given below. Karyological, morphological and genetic data from our previous studies on European loaches (Vasil'eva 1984, Vasil'ev 1995, Vasil'eva \& Vasil'ev 1998 , Ráb et al. 2000, J a n ko et al. 2003, 2005, Rábová et al. 2004, Culling et al. 2005) were also used as a comparative data-set, as well as partially described (V a s il'e v 1985, 1995) karyological data obtained in 1981 (20 karyotyped specimens) and in 1985 (69 karyotyped specimens) from spined loaches occurring in the Chernaya R.

## Karyological analysis

We followed standard procedures described earlier (Vasil'e v 1978, Ráb \& Roth 1988). Chromosomes were classified according to Levan et al. (1964).

Table 1. Allozyme alleles found in studied samples of spined loaches (for the new form, the numbers of samples are given in parentheses; data for C. taenia, C. elongatoides and C. tanaitica are taken from Sk e chtová et al. 2000).

|  | Loci | Gpi-A* | s-Aat* | s-Mdh-A* | Ldh-B* |
| :--- | :---: | :---: | :---: | :---: | :---: |
| Species or morph |  | Sod* |  |  |  |
| Cobitis taenia | 87 | 71 | 60,100 | 100,117 | 60 |
| C. elongatoides | 100,113 | 100 | $100,70,40$ | 100,117 | 100 |
| 50-chromosome morph from <br> the Chernaya River (N=6) | 87 | 71 | 100,60 | 100 | 60 |
| 50-chromosome morph from the <br> Southern Bug (N=19) and Veleka <br> (N=7) rivers | 87 | 71 | 60 | 100 | 60 |
| "C. tanaitica" | 87 | 71 | 100,60 | 100,117 | 60 |



Fig. 1. Map of distribution of the C. taurica sp. nova and similar forms used for this study.
Allozyme analysis
The skeletal muscles of the examined specimens were stored at $-40^{\circ}$ before being electrophoretically analysed. The five diagnostic loci (i.e. glucosephosphate isomerase A, GpiA*; superoxide dismutase, Sod*; s-aspartate amino transferase, sAat*; malate dehydrogenase, Mdh*; and lactate dehydrogenase, $\mathrm{Ldh}^{*}$ ) were scored, using the same analyses protocols and enzyme nomenclature as in Šlechtová et al. (2000). Allele homologies were determined by comparing electrophoretic mobility of the studied samples to specimens analysed previously. Presence / absence of alleles were put into a matrix and overlaid on a data matrix from Š le chtová et al. (2000).

Morphological analysis
We included characters consistently used in the taxonomy of spined loaches that have been previously described (Vasil'eva 1984, 1988, Vasil'eva et al. 1989, Vasil'eva \& Vasil'ev 1998). All morphometric data were subject to standard statistic univariate analysis.

Phylogenetic relationships
Relationships between 50-chromosome specimens with peculiar karyotype examined in this study and some other European loaches were assessed using sequences of mitochondrial cytochrome b gene (cyt b) from Culling et al. (2005) and Janko et al. (2005) (Accesion numbers: AY706159- AY706203, AF263083 \& AF263084), which included the sequences from three specimens from the Chernaya R., one specimen from the S. Bug R. and three specimens from the Veleka R.

Nucleotide divergences between haplotypes were estimated with the PAUP* software package, version 4.0 b 10 (Swofford 1999) using the HKY 85 + Gamma model of DNA substitution (H a segawa et al. 1985). The HKY $85+$ Gamma model was selected as an
appropriate model for our dataset using the hierarchical likelihood ratio test implemented in the MODELTEST program, version 3.06 ( Pos ada \& Crandall 1998). Phylogenetic relationships among haplotypes were reconstructed by the neighbour-joining algorithm (NJ) using the corrected distance matrix, and by the maximum likelihood (ML) criterion using heuristic search and parameter settings as calculated with MODELTEST (base frequencies: $\mathrm{A}=0.2608, \mathrm{C}=0.2397, \mathrm{G}=0.1612, \mathrm{~T}=0.3383$, transition: transversion ratio $=7.1405$ ). Both analyses were performed with PAUP*. To infer statistical support for the internal branches of the NJ tree, nonparametric bootstrap resampling with 1000 replicates was performed. We used a sequence of C. albicoloris Chichkoff, 1932 as an outgroup which was justified by the phylogenetic relationships within the genus (Perdices \& Doadrio 2001).

## Results

Karyological analysis
We revealed 50 -chromosome spined loaches from the Chernaya, Veleka and S. Bug rivers to have the same karyotype composed of 5 pairs of meta-, 15 pairs of submeta-, 4 pairs of subteloand 1 pair of acrocentric chromosomes, $\mathrm{NF}=90^{1}$ (Fig. 2). There were no polyploid specimens among the karyotyped loaches collected in the Chernaya R. in 1981 and in 1985 (89 adult and juvenile specimens), and both males ( 47 adult specimens) and females ( 23 adult specimens) had the same karyotype structure. This karyotype differs remarkably from the karyotypes of other diploid bisexual species from "the Cobitis taenia complex": the karyotype of C. taenia s. stricto consists of 48 chromosomes with NF=76 (V a sil'ev \& Vasil'e va 1982, V a s il'e v 1985, Ráb et al. 2000, B o ron ń 2003); the karyotype of C.elongatoides Băcescu in Băcescu et Maier, $1969^{2}$ includes 50 chromosomes with NF=96 (R á b et al. 2000, Lusk et al. 2003, B or o ń 2003); the so called "C. tanaitica Băcescu et Maier, 1969" from Central Europe has $2 \mathrm{n}=50$ chromosomes and $\mathrm{NF}=82-84$ (R áb et al. 2000, Lusk et al. 2003), while East European C. rossomeridionalis Vasil'eva et Vasil'ev, 1998 is characterized by the presence of fixed Y-autosome translocation (centric fusion) resulting in $2 \mathrm{n}=50$ and $\mathrm{NF}=86$ in females and $2 \mathrm{n}=49$ and $\mathrm{NF}=86$ in males (Vasil'ev 1995, Vasil'eva \& Vasil'ev 1998).

## Allozyme analysis

For three (Gpi-A*, s-Aat*, Sod*) out of the five studied loci, the alleles found in 50-chromosome specimens from the Chernaya, Veleka and S. Bug rivers were identical to those found in

[^1]A




m-




Fig. 2. Karyotypes of Cobitis taurica sp. nova from the Chernaya River (a) and the similar forms from the Veleka (b) and the Southern Bug (c) rivers.
C. taenia and "C. tanaitica", while C. elongatoides was characterized by fixation of alternative alleles (Table 1). For locus Ldh-B* all of the compared species and populations possessed allele $* 100$, but populations from the Chernaya, Veleka and S. Bug rivers missed the allele *117, although it is relatively frequent among other species described previously. All three populations of the 50 -chromosome form possessed allele $* 60$ at the s-Mdh-A* locus, which
was otherwise characteristic for $C$. taenia, but we also encountered allele $* 100$ fixed in $C$. elongatoides and C. tanaitica and also found in a single C. taenia specimen from the Alma R. in Crimean Peninsula (Š le chtová et al. 2000, 2003).

## Phylogenetic analysis

The 1088 bp sequences of the cyt $b$ gene were determined for 7 individuals from the three studied populations. A total of 191 sites were variable. All observed polymorphisms were single nucleotide substitutions. The combination of nucleotide states at variable positions defined 4 distinct haplotypes encountered among the individuals of the studied 50 -chromosome form, designated as T6-T8, E22 according to J a n k o et al. (2005; accession numbers: AY706162,


Fig. 3. ML tree topology of phylogenetic relationships among analysed individuals from the C. taenia hybrid complex. Two major clades referred in the text are denoted by boxes A and B, respectively. Light grey lines indicate the positions of haplotypes encountered either in C. taenia or in asexual hybrids with taenia-type mtDNA, dark grey denotes haplotypes of C. elongatoides or hybrids with elongatoides-type mtDNA, stripped barrs indicate the haplotypes of $C$. tanaitica and black symbols indicate the haplotypes encountered in the new 50-chromosome form.

AY706165, AY706166 and AY706184). NJ and ML phylogenetic methods resulted in slightly differing tree topologies, however the positioning of the T6-T8, E22 among haplotypes, found in C. taenia, C. elongatoides, "C. tanaitica" and the clonal hybrids, didn't differ. The sequences, in the NJ tree, clustered in two major clades (Fig. 3), corresponding to clades A and B from Janko et al. (2003) with high bootstrap support (100\%). The average pairwise sequence divergence between the clades is $5.2 \%$. Sequences of the studied 50 -chromosome form did not represent a monophyletic lineage, but specimens from the Veleka R. (haplotype E22) clustered in clade A composed of haplotypes found in C. elongatoides, and "C. tanaitica" (and also polyploids and hybrids with elongatoides-type mtDNA). Whereas, haplotypes from the Crimean Peninsula (T7 and T8) and the Southern Bug R. (T6) clustered in clade B consisting of haplotypes encountered in C. taenia specimens (and also polyploids with taenia-type mtDNA). Neither of the two Ukrainian populations form a monophyletic lineage within clade
(a)

(b)

(c)


Fig. 4. Holotype of Cobitis taurica sp. nova, male, SL 60.0 mm , the Chernaya River, ZMMU P-21358 (a); spined loach male, SL 62.6 mm , from the Veleka River, ZMMU P-21363 (b); spined loach male, SL 62.6 mm , from the Southern Bug River, ZMMU P-21365 (c).
Table 2. Several morphometric characters of different spined loach species.

| Species, sample | Cobitis taurica sp. nova, Chernaya R., type specimens |  | C. taurica sp. nova, Chernaya R. (from Vasil'e va, 1984) |  | Spined loaches from the Veleka R. <br> (ZMMU P-21363, P-21364) |  | Spined loaches from the Southern Bug R. (ZMMU P-21365, P21366) |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| Character | Females ( $\mathrm{n}=6$ ) | Males ( $\mathrm{n}=5$ ) | Females ( $\mathrm{n}=7$ ) | Males ( $\mathrm{n}=7$ ) | Females ( $\mathrm{n}=4$ ) | Males ( $\mathrm{n}=3$ ) | Females ( $\mathrm{n}=4$ ) | Males ( $\mathrm{n}=4$ ) |
|  | Ranges / M | Ranges / M | Ranges / M | Ranges / M | Ranges / M | Ranges / M | Ranges / M | Ranges / M |
| TL (mm) | $\frac{89.3-120.0}{102.8}$ | $\frac{60.5-70.5}{66.2}$ | $\frac{46.0-84.2}{67.7}$ | $\frac{49.5-66.0}{59.3}$ | $\frac{83.2-114.3}{95.8}$ | $\frac{67.0-74.0}{69.8}$ | $\frac{79.3-92.5}{85.3}$ | $\frac{63.0-79.3}{70.9}$ |
| SL (mm) | $\frac{78.6-94.0}{87.1}$ | $\frac{51.5-60.0}{56.6}$ | $\frac{40.0-71.2}{57.7}$ | $\frac{42.3-56.0}{50.3}$ | $\frac{71.5-100.5}{83.4}$ | $\frac{58.2-62.6}{59.7}$ | $\frac{69.0-81.0}{74.3}$ | $\frac{54.2-69.5}{61.5}$ |
| In \% of SL |  |  |  |  |  |  |  |  |
| aD | $\frac{49.9-53.6}{51.0}$ | $\frac{50.3-53.0}{51.9}$ | $\frac{49.5-53.9}{51.6}$ | $\frac{50.0-55.3}{52.0}$ | $\frac{50.8-52.7}{51.5}$ | $\frac{49.5-51.1}{50.5}$ | $\frac{50.6-52.5}{51.9}$ | $\frac{49.8-52.8}{51.1}$ |
| pD | $\frac{39.3-42.1}{40.2}$ | $\frac{37.3-40.3}{39.0}$ | $\frac{36.8-43.1}{40.8}$ | $\frac{37.5-42.1}{40.3}$ | $\frac{39.7-41.5}{40.7}$ | $\frac{39.5-41.9}{40.4}$ | $\frac{39.8-42.0}{40.8}$ | $\frac{39.4-41.6}{40.6}$ |
| aV | $\frac{48.9-50.8}{49.9}$ | $\frac{50.0-52.7}{51.5}$ | $\frac{49.5-54.8}{52.7}$ | $\frac{51.3-57.0}{54.2}$ | $\frac{49.6-51.1}{50.6}$ | $\frac{51.4-52.9}{52.2}$ | $\frac{48.0-50.4}{49.5}$ | $\frac{49.7-50.8}{50.4}$ |
| aA | $\frac{70.4-76.4}{73.5}$ | $\frac{73.5-76.3}{75.3}$ | $\frac{73.8-78.7}{76.8}$ | $\frac{74.6-78.9}{77.3}$ | $\frac{73.5-76.5}{74.6}$ | $\frac{74.6-80.8}{77.0}$ | $\frac{70.6-75.4}{73.8}$ | $\frac{70.1-73.1}{71.8}$ |
| pl | $\frac{15.3-18.5}{16.4}$ | $\frac{14.9-17.1}{15.9}$ | $\frac{15.7-19.7}{17.6}$ | $\frac{12.2-18.9}{15.8}$ | $\frac{15.7-16.8}{16.1}$ | $\frac{15.8-16.5}{16.2}$ | $\frac{15.2-18.8}{17.2}$ | $\frac{17.0-18.6}{17.8}$ |
| H | $\frac{14.2-15.5}{14.9}$ | $\frac{12.5-15.5}{13.6}$ | $\frac{12.6-17.1}{15.1}$ | $\frac{11.3-16.4}{14.7}$ | $\frac{15.8-17.4}{16.3}$ | $\frac{13.6-14.1}{13.8}$ | $\frac{12.6-15.6}{14.2}$ | $\frac{12.4-13.1}{12.9}$ |
| h | $\frac{7.5-8.9}{8.2}$ | $\frac{8.3-9.9}{9.1}$ | $\frac{6.9-9.1}{8.2}$ | $\frac{7.4-10.5}{9.1}$ | $\frac{8.3-9.8}{9.0}$ | $\frac{9.3-9.8}{9.6}$ | $\frac{8.2-8.7}{8.6}$ | $\frac{8.8-9.7}{9.3}$ |
| Cr | $\frac{6.6-8.1}{7.4}$ | $\frac{6.1-9.1}{7.0}$ | $\frac{6.5-9.3}{8.0}$ | $\frac{6.9-8.0}{7.3}$ | $\frac{7.6-8.2}{7.8}$ | 7.4 | $\frac{7.0-8.3}{7.7}$ | $\frac{6.7-7.2}{7.0}$ |
| Crm | $\frac{6.4-7.0}{6.8}$ | $\frac{5.2-8.4}{6.4}$ | $\frac{7.4-9.3}{8.2}$ | $\frac{6.0-8.0}{6.9}$ | $\frac{7.2-8.1}{7.6}$ | 7.4 | $\frac{6.2-7.5}{6.8}$ | $\frac{6.6-6.9}{6.7}$ |






 - in ventral fin, C - in caudal fin, sp - spots in the forth Gambetta's zone; n - number of specimens.

B, since the haplotype from the S. Bug R. (T6) clustered together with local populations of C. taenia, whereas haplotypes from the Chernaya R. (T7 and T8) clustered with C. taenia populations occurring in the Dnieper R.

Morphological analysis
Spined loaches from the Chernaya River diverged from populations occurring in the Veleka and S. Bug rivers by the size and number of spots in the fourth Gambetta's zone of pigmentation (spots along the side midline) and by the position of the tip of suborbital spine, as well as the tip of its outer branch. The fourth Gambetta's zone of specimens from the Chernaya River consists of relatively small and low $15-28$, usually more than 18 , spots whose depth is about two times smaller than the horizontal eye diameter (Fig. 4a), their suborbital spine always reaches the posterior edge of the pupil and usually beyond, and its outer branch usually goes as far as the centre of the eye and often even further (see description). At the same time, the fourth Gambetta's zone of the specimens from the Veleka and S. Bug rivers consists of relatively large 13-18, more often $15-18$, spots whose depth is about equal to the horizontal eye diameter (Fig. 4b,c). Their suborbital spine usually does not reach the posterior edge of the pupil (it goes as far as the posterior edge of the pupil or further in small males from the Veleka River only), and its outer branch usually ( $85.7 \%$ in the Veleka R. and $100 \%$ in the S. Bug R.) does not reach the centre of the eye. The diagnostic characters differentiating between spined loaches of the Chernaya River and other European species are given below.

The differences between populations from the Veleka and the S. Bug rivers are not so prominent being revealed mainly in the head shape. The head of specimens from the Veleka R. is somewhat shortened and deep, with a more or less straight profile. While specimens from the S. Bug R. have a some what elongated head that is not so deep, with an obviously hooked and overhanging nose; Fig. 4b,c). Significant differences between these populations (slight overlap between the ranges of characters) were also revealed for 5 morphometric characters, namely maximum body depth, distance between paired fins, preorbital distance, head depth and the relationship between ventral fin length and the distance between paired fins. Some characters demonstrated prominent differences between the two species in males only (Table 2).

## Discussion

Three newly discovered populations of 50 -chromosome spined loaches from the north-western Pontic region studied by combined comparative morphological and genetic analyses turned out to differ from all other known forms of European loaches of the genus Cobitis s. stricto. The population of this form dwelling in the Chernaya R. apparently represents a bisexual diploid species, since we have recorded individuals of both sexes ( 23 males among 34 adult specimens collected in 1981-20 of them were used for karyology and osteology and 14 for external morphology, and 46 males among 73 adult specimens collected in 1985 - 36 specimens karyotyped and 37 specimens kept in ZMMU; sex-ratio 1.7: 1 in favor of males). The loaches inhabiting these locations share a common karyotype not observed in any other loach species studied to-date.

The hypothesized ancestral karyotype for Cobitis species is characterized by $2 \mathrm{n}=50$ with 32-34 acrocentric chromosomes and $\mathrm{NF}=66-68$ because this karyotype is the least structured (the most simple from a cytogenetic point of view) and is observed in species occurring in the Far East, Korea and Japan as well as in European species (Hit ot s u machi et al. 1969,

Ueno \& Ojima 1976, Cataudella et al. 1977, Ueno et al. 1985, Vasil'eva et al. 1992, K i m et al. 1999). Thus, the karyotypes of European Cobitis species are represented by at least two different evolutionary lineages: 1) "the C. taenia" lineage with karyotype ( $2 \mathrm{n}=48, \mathrm{NF}=76$ ) arose by centric fusion resulting in the origin of large metacentric pair and several pericentric inversions and 2) one or several lineages with karyotypes characterized by high NF that arose by pericentric inversions. The newly discovered 50 -chromosome form of loaches belongs to the second lineage.

Our results suggest some differences between unique 50 -chromosome populations and other members of "the C. taenia complex" in s-Mdh-A* and Ldh-B* loci, but this must be considered with caution since a restricted number of samples were studied (Table 1). Similarly, divergences in several enzyme and nonenzyme protein systems including malate dehydrogenase were found by the isoelectric focusing analysis between the loaches from the Veleka R. and Middle Danubian specimens (D a nailov et al. 1998, Ivanova et al. 2003). These fishes were determined by the authors as C. taenia, but recent investigations confirm the Danube River basin to be inhabited by C. elongatoides and "C. tanaitica", while C. taenia is apparently absent in this river system (see Janko et al. 2005, Culling et al. 2005). Based on the presence of the same allele in the superoxide dismutase locus in the Veleka R. and Danubian samples (I vanova et al. 2003) we suggest the latter population was represented by "C. tanaitica" and not C. elongatoides, which is fixed for a different allele at this locus (Šlechtová et al. 2000).

Our results also suggest genetic heterogeneity among populations of the unique 50 -chromosome form themselves: the Chernaya River population harbours an Mdh* allele (*100) missing in the other populations and the results of mtDNA analysis placed all three populations into different lineages; the haplotype of the Bulgarian population even being derived from C. elongatoides.

The Chernaya River belongs to the territory of so called Mountain Crimea representing the northern remains of the hypothetical large Pontic Land supposed to exist at the site of the contemporary deep Black Sea hollow until the end of Tertiary period and to be the most developed of the Sarmat age. The Dobrudzha region in the west (coastal part of Roumania and northern Bulgaria), the coastal zone of Anatolia in the south and the Meskhi plateau in Transcaucasia in the east are considered to be the other remains of this Land (see P u z a n o v 1929, 1949). According to biogeographic data, the hydrofauna of the Chernaya River is of ancient origin from this Pontic Land fauna and thus is the most related to its remains in Balkan and Minor Asia (Puzanov 1949). After the Pontic Land dipped into the sea at the beginning of the first glacial period, the Mountain Crimea island is supposed to have been connected with Roumania, southern Ukraine and the Novorossiysk coast of the Caucasus by a broad land strip (see Puzanov 1929, 1949). Furthermore, the main immigration wave of Pleistocene fauna from the southern Ukraine and Russia were given the possibility to survive in the refuge of the so-called Steppe Crimea. This immigration wave, however, did not affect the Chernaya R. that was supposed to be isolated from the recent fauna of the northern coast of the Black Sea basin since the Paleocene period ( Puzanov 1949 ).), about 60 My ., and is represented by several endemic species (see Vasil'e va et al. 2005). Such processes may explain the disjointed distribution of the studied form of loaches, which have also been observed in other freshwater fishes (e.g. Barbus escherichii lineage II from K o t lík et al. (2004).

At the moment, since the present results of genetic, morphological and biogeographic analyses yield controversial solutions to the relationship of the 50 -chromosome spined loaches from the Chernaya, Southern Bug and Veleka Rivers, we consider further comprehensive investigations
of the spined loaches from the Black Sea basin crucial for more advanced taxonomic conclusions. In any case, the description of the spined loaches from the Crimean Peninsula as a separate species should be considered as an essential procedure for the taxonomic resolution of diploid spined loach species as well as for further studies of polyploid hybrid loaches possessing haploid chromosome sets of such diploids. We therefore present formal a description here.

## Cobitis taurica Vasil'eva, Vasil'ev, Janko, Ráb et Rábová sp. nova (Fig. 4a).

Cobitis taenia (not of Linnaeus, 1758): Puzanov 1929: 19; T s e e b 1929: 115; B e rg 1949: 890 (part.: Chernaya R. in Crimea); Delyamure 1964: 45; V a s i l ' e v 1985: 172 (part.: Crimea); Prokopov 2004: 165.
Cobitis taenia taenia (not of Linnaeus, 1758): M o v c h a n 1988: (part.: Crimea).
Holotype - ZMMU P-21358, male TL 70.5 mm , SL 60.0 mm , Chernaya River, Crimean Peninsula, 14.06.2002, collector K. J a n k o (karyotyped, electrophoretically and DNA-studied). Paratypes: ZMMU P-21359, 1 female TL 96.1 mm , SL 82.5 mm and 3 males TL 63.7-69.2 mm, SL 27.4-31.4 mm, Chernaya R., 5.07.1985, collector V. V a s il'ev; P-21360, 5 females TL 89.3-120.0 mm, SL 78.6-91.5 mm, collected together with holotype; P-21361, male TL 60.5 mm , SL 51.5 mm , Chernaya R., 11.07.2004, collectors V. Vasil'ev \& E. Vasil'eva. Additional materials: P-21362, 33 specimens ( 21 males), collected together with P-21359.

Diagnosis: One elongated narrow dark spot in the upper part of the base of the caudal fin; males with one lamina Canestrini in the pectoral fin, usually broad, axe-shaped; more or less rounded scales with a relatively small central part devoid of cross furrows; Gambetta's zones of pigmentation are well developed, the fourth zone consists of relatively small and low 15-28, usually more than 18 spots whose depth is about two times smaller than the horizontal eye diameter (the largest spots on the caudal peduncle are also noticeably smaller than the horizontal eye diameter); the suborbital spine always reaches the posterior edge of the pupil and usually goes further and in small specimens (with TL less than 65 mm ), usually reaches the posterior edge of the eye; the outer branch of this spine usually $(95.5 \%, n=44)$ goes as far as centre of eye and often further; the head is moderately long and deep with a more or less straight profile; $2 \mathrm{n}=50$ ( 5 pairs of meta-, 15 pairs of submeta-, 4 pairs of subtelo- and 1 pair of acrocentrics), NF=90.

Description. ${ }^{4}$ D II-III 6-8 (more often 7), A (II) III 5-6 (more often 6), P I (5) $6-8$ (more often 7), V I-II (5) 6, C I 13-14 I. Morphometric characters are presented in Table 2. Head without overhanging nose; dorsal fin begins at the level of the origin of the pelvic fin or somewhat anteriorly (pelvic fins are situated at the level of the last unbranched dorsal ray); barbels short: the mandibular barbels never reach the anterior edge of the eye, more often they do not go as far as the posterior edge of the nostrils, samples collected in 2002 included fishes with completely or noticeably reduced rostral barbels; descriptions of some other morphological characters, as well as some craniological features and drawings of specimens, lips, lamina Canistrini and bones were presented earlier (V a s il'e va 1984). Maximum body length (TL) comprises 109 mm in females and 73 mm (V a s il' e va 1984) in males; the smallest male with developed lamina Canestrini was 49 mm in length.

Distribution. Recently we consider this species to be endemic of the Chernaya River in the Crimean Peninsula. But we can't completely reject its possible conspecificity with spined loach populations from the Veleka and S. Bug rivers and thus its wider distribution within the Black Sea basin.

[^2]Etymology. The species name taurica is derived from Tauris-Taurida, the ancient Greek and Latin name of the Crimean Peninsula.

Comparative remarks. As mentioned above, C. taurica belongs to "the C. taenia complex", but it differs (as well as spined loaches from the Veleka and S. Bug rivers) from all other members of this group by the unique karyotype structure. Furthermore, this species can be distinguished from every other diploid bisexual species (including the populations from the Veleka and S. Bug rivers with the same karyotype), as well as from polyploids attributed to this complex, by the smaller and more abundant spots in the fourth Gambetta's zone of pigmentation. This last character, as well as the position of the suborbital spine separate C. taurica from C. taenia also found in the Crimean Peninsula (the Alma River): C. taenia usually has less than 15 large spots in the fourth Gambetta's zone, its suborbital spine usually (about $70 \%$ ) does not reach the posterior edge of the pupil, and the outer branch of the spine usually (about $80 \%$ ) does not reach the centre of the eye.

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[^1]:    ${ }^{1}$ In this work we used a chromosome classification that differed from those presented for loaches from the Chernaya River in a previous study (V a sil'e v 1995) to compare the data with that obtained later for different European loaches.
    ${ }^{2}$ Some authors (Frey hof et al. 2000, Nalbant et al. 2001) believe Băcescu \& Maier to be authors of the name elongatoides because this name was available from their publication (B ăcescu \& Maier 1969). But Băcescu \& Maier (1969) undoubtedly considered only B_cescu to be responsible for the name elongatoides (pp. 39, 40, 43). Other nomenclature problems for this species were discussed in Frey h of et al. 2000.
    ${ }^{3}$ The name " $C$. tanaitica" is usually applied to species with $2 \mathrm{n}=50$ and $\mathrm{NF}=82-84$ (L u sk et al. 2003, Š l e c h t o v á et al. 2003, Janko et al. 2003, 2005). But nomenclature problems remain in discussion (see Vasil'eva \& Vasil'ev 1998, Freyhof et al. 2000, Bohlen \& Ráb 2001), and the taxonomic relationship between populations from the Don River (typical locality) and Central European fresh waters seem to be unresolved.

[^2]:    ${ }^{4}$ In our paper we present very short descriptions of the new species due to their external resemblance with the well-known C. taenia.

