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## ABSORBING HYBRIDIZATION OF *COBITIS TAENIA* AND *SABANEJEWIA AURATA* (CYPRINIFORMES, COBITIDAE) IN WATER RESERVOIRS OF NORTHERN UKRAINE CONNECTED WITH DIPLOID-POLYPLOID COMPLEX FORMATION

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**Absorbing Hybridization of *Cobitis taenia* and *Sabanejewia aurata* (Cypriniformes, Cobitidae) in Water Reservoirs of Northern Ukraine Connected with Diploid-Polyploid Complex Formation.** Mezhzherin, S. V., Pukhtayevych, P. P., Tsyba, A. A. — In the rivers of the Northern Ukraine by means of karyological and allozyme analysis obtained extensive natural hybridization between *Cobitis taenia* and *Sabanejewia aurata*, initially leading to the formation of diploid hybrids. Besides that certain water bodies are predominantly populated by triploids of the *C. taenia* — *C. tanaitica* — *S. aurata* biotypes. Since the share of this kind of hybrid biotypes significantly exceeds the number of individuals of *S. aurata*, it is concluded that the hybridization of a common and eurybiontic *C. taenia* with rarer stenobiontic *S. aurata*, is of absorbing character.

**Key words:** hybridization, *Sabanejewia aurata*, *Cobitis taenia*, karyotypes, allozymes.

**Поглощающая гибридизация обыкновенной (*Cobitis taenia*) и золотистой (*Sabanejewia aurata*) щиповок (Cypriniformes, Cobitidae) в водоёмах севера Украины, связанная с образованием диплоидно-полиплоидного комплекса.** Межжерин С. В., Пухтаевич П. П., Цыба А. А. — В реках северной Украины путём кариологического и аллозимного анализа установлена естественная гибридизация обыкновенной *Cobitis taenia* (Linnaeus, 1758) и золотистой *Sabanejewia aurata* (De Filippi, 1863) щиповок, первично приводящая к образованию диплоидных гибридов. Кроме того, некоторые водоёмы населены преимущественно триплоидами *C. taenia* — *C. tanaitica* — *S. aurata* биотипов. Поскольку доля подобного рода гибридных биотипов существенно превышает численность особей *S. aurata*, сделан вывод о том, что гибридизация достаточно обычного и эврибионтного вида *C. taenia* с явно более редким стенобионтным, каким и является *S. aurata*, носит поглощающий характер.

**Ключевые слова:** гибридизация, *Sabanejewia aurata*, *Cobitis taenia*, кариотипы, аллозимы.

### Introduction

Interspecies hybridization of fishes in Holarctic region is widely distributed and has evolutionary meaning. Suffice it to remember that all Holarctic endemic fish families, which are rich in species, are represented only with allopolyploids. Fish hybridization often takes place amongst far species of the same genus and even amongst representatives of different genera. In such situations the hybridization has mainly accidental character as it takes place spontaneously and is stimulated with unfavorable ecological factors or species invasion.

One of the interspecies hybridization consequences may be the absorption of one hybridizing species with another one. The absorbing species is everybiontic which is characterized with numerous populations and its habitat conditions are favourable. The oppressed species is stenobiontic not numerous, habited factors are unfavourable far it. Similar situation in european waters is typical for *Carassius carassius* Linnaeus, 1758, which freely hybridize with adventive species *C. auratus* (Linnaeus, 1758 (Mezhzherin et al., 2012). The analysis of these species mutual habitats shows that the part of hybrids *C. auratus* × *C. carassius* is the same as in *C. carassius* which is considered disappearing species and is included into the 3rd edition of Ukrainian Red Book.

Another hybridizing group of European fishes — *Cobitis* Linnaeus, 1758 genus. In Central European water systems allopolyploid hybrids *C. melanoleuca* × *Cobitis taenia* (Mezhzherin, Lisetskaya, 2004), *C. elongatoides* × *C. tanaitica* (Mezhzherin, Pavlenko, 2007 a; Janko et al., 2007), *C. elongatoides* × *C. taenia* (Janko et al., 2007), are found as well as the zone of gene introgressions within *C. taenia* and *C. tanaitica* (Mezhzherin, Pavlenko, 2009). And as the result of these species sequential hybridization, a series of triploid and tetraploid biotypes (Janko et al., 2007; Mezhzherin, Pavlenko, 2010) is formed in Europe. At the same time intergenera hybridization can not be excluded and diploid hybrid amongst *C. taenia* and probably, *Sabanejewia aurata* from the Desna River confirms it (Mezhzherin, Lisetskaya, 2004). This fact was preliminary confirmed with multi-loci allozymic analysis. The small number of these hybrids makes possible to consider the hybridization amongst the above mentioned species to be very rare. But in the rivers of Northern Ukraine sometimes specimens of unidentified triploid biotype formed with *S. aurata* are found (Mezhzherin, Pavlenko, 2010). Judging from fixed allele in constant heterozygote of some enzyme systems, this biotype is formed with *C. taenia* and / or *C. tanaitica* and the third species with *Ldh-B<sup>90</sup>* allele making product with low electrophoretic mobility. This allele is absent in *C. elongatoides* from the Danube which is considered the ancestor of all known triploid biotypes (Janko et al., 2007; Mezhzherin, Pavlenko, 2010) and is found only in *S. aurata* in river systems of Northern Ukraine. It means that the hybridization amongst *C. taenia* and *S. aurata* with the following recurrent hybridization with *C. taenia* and *C. tanaitica* can also be the reason for another diploid-polyploid complex formation. To confirm this statement the hybridization between *C. taenia* and *S. aurata* should be proved using besides allozyme analysis some other methods, karyological analysis in particular.

### Material and methods

Nine series of spined loaches from some rivers of the Northern Ukraine, where *S. aurata* or hybrids of this species were found were taken for the research: 1 — Desna River, near Letochky Village (50°45'25" N, 30°46'11" E); 2 — Irpen River, near Irpen River (50°31'0" N, 30°15'0" E); 3 — Huyva River, near Pryazhev Village (50 11'7" N, 28°40'34" E) October, 2012; 4 — ibid, June, 2013; 5 — ibid, June, 2014; 6 — the channel, the basin of the Sluch River, Virlya Village (50°20'52" N, 27°43'43" E); 7 — the channel, the tributary of the Sluch River, Ostrozhok Village (50°23'38" N, 27°44'16" E); 8 — the tributary of the Sluch River, Nova Romanivka Village (E50°34'31" N, 27°43'05" E); 9 — Styr River, Lutsk (50°44'52" N, 25°19'28" E); 10 — Sobok River, Illintsi (49°6'0" N, 29°12'0" E).

The biotype of spined loaches was determined with allozymic markers (Mezhzherin, Pavlenko, 2007 a), using electrophoresis in polyacrylamide gel (Peacock et al., 1965).

Chromosome mitotic preparations were taken from epithelial cells of kidney tissue with air-drying (Boroń, 1994; Ráb, et al., 1988; Cucchi, Baruffaldi, 1990).  $\text{CoCl}_2$  as the stimulant of cell division was injected into fish bodies with following. The modification of this method was described in details earlier (Pukhtayevych, 2014).

### Results and discussion

**Karyotyping. Diploid biotypes.** The analysis of mitotic preparations from metaphase plates of *C. taenia* and *S. aurata* and supposed hybrid *C. taenia* × *S. aurata* definitely testifies to the hybridization of these species in the River Teteriv tributaries. Researched *C. taenia* have 48 chromosomes (Vasil'ev, Vasil'eva, 1982; Rab et al., 2000; Boroń, 2003 a) diploid set including two metacentric chromosomes which are larger than others and are markers for this species (fig. 1, a). *C. taenia* characterized with 12 metacentrics, 18 submetacentrics and 18 acrocentrics.

*S. aurata* karyotype is characterized with diploid set of 50 chromosomes (Vasil'eva, Vasil'ev, 1988; Rab et al., 1991; Boroń, 2000; Janko et al., 2007) (table 1). In this case (fig. 1, b) the karyotype is represented with 4 metacentric chromosomes, two of which are some that larger and are noted by other researchers in *S. aurata* from river basins of the Central Europe (Rab et al., 1991; Boroń, 2000). But *S. aurata* karyotype from the River Teteriv basin is unique (4 m + 14 sm + 32 sta) although it is close to this species karyotypes described earlier by A. Boron for *S. aurata* from the River Visla (Poland) basin (4 m + 16 sm + 30 sta) and by P. Rab for *S. aurata* balcanica (4 m + 12 sm + 34 sta) from the Tisa River (the Danube tributary) basin. This polymorphism may be caused variability of heterochromatin sections. And the spined loaches karyotype in the River Guiva and the Sluch River basin differs more from karyotypes of *S. aurata* from the Rivers Kuban and Kura (table 1).

In supposed clue to allozymic data *C. taenia* × *S. aurata* hybrid 49 chromosomes were found. This specimen has not only strict transitional state in chromosome number but in



Fig. 1. Karyograms of spined loach species and biotypes studied: *a* — *C. taenia*, the channel, the basin of the Sluch River; *b* — *S. aurata*, Guiva River, the basin of the Teteriv River; *c* — *C. taenia* × *S. aurata*, Guiva River, the basin of the Teteriv River; *d* — *C. elongatoides* — 2. *taenia*, Guiva River, the basin of the Teteriv River; *e* — *C. elongatoides* — *tanaitica* — *taenia*, Guiva River, the basin of the Teteriv River; *f* — *C. taenia* — *C. tanaitica* — *S. aurata*, Guiva River, the basin of the Teteriv River, the channel, the basin of the Sluch River; *g* — *C. 2 elongatoides* — *tanaitica*, the channel, the basin of the Sluch River (m — metacentric; sm — submetacentric; sta — subtelo- and acrocentric chromosomes).

Рис. 1. Кариограммы исследованных видов щиповок и их биотипов: *a* — *C. taenia*, канал, бассейн р. Случь; *b* — *S. aurata*, р. Гуйва, бассейн р. Тетерев; *c* — *C. taenia* × *S. aurata*, р. Гуйва, бассейн р. Тетерев; *d* — *C. elongatoides* — 2. *taenia*, р. Гуйва, бассейн р. Тетерев; *e* — *C. elongatoides* — *tanaitica* — *taenia*, р. Гуйва, бассейн р. Тетерев; *f* — *C. taenia* — *C. tanaitica* — *S. aurata*, р. Гуйва, бассейн р. Тетерев, канал, бассейн р. Случь; *g* — *C. 2 elongatoides* — *tanaitica*, канал, бассейн р. Случь (m — метацентрические; sm — субметацентрические; sta — субтело- и акроцентрические хромосомы).

Table 1. The Karyotypes of *Sabanejewia* genus representativesТаблица 1. Кариотипы представителей рода *Sabanejewia*

The taxonomic status	2n	Karyotype	NF	References
<i>S. larvata</i> (canal near Turin, the basin of the Po River, Italy)	50	4 m + 6 sm + 40 sta	60	Lodi, Marchionni, 1980
<i>S. caspia</i> (Ghizil-Agaj gulf of the Caspian Sea, Azerbaijan)	50	4 m + 6 sm + 40 sta	60	Vasil'ev, 1985
<i>S. aurata aurata</i> (River Kuban, Russia)	50	6 m + 14 sm + 30 sta	70	Vasil'ev, 1985
(Kura River, Azerbaijan)		6 m + 12 sm + 32 sta	68	Vasil'eva, Vasil'ev, 1994
<i>S. aurata kubanica</i> (River Kuban, Russia)	50	6 m + 14 sm + 30 sta	70	Vasil'eva, Vasil'ev, 1988
<i>S. aurata balcanica</i> (Laborets River, Danube basin, Slovakia)	50	4 m + 12 sm + 34 sta	66	Rab et al., 1991
<i>S. aurata</i> (Bug River, Vistula basin, Poland)	50	4 m + 16 sm + 30 sta	70	Boroń, 2000
<i>S. aurata</i> (Guiva River, the basin of the Teteriv River, Ukraine)	50	4 m + 14 sm + 32 sta	68	Present study

their set too. This *C. taenia* × *S. aurata* hybrid has 8 metacentrics, 19 submetacentrics and 25 acrocentrics (fig. 2, c).

**Triploid biotypes.** The karyotypic analysis resulted in revealing 4 triploid biotypes with different numbers of chromosomes (table 2).

*C. elongatoides* — 2 *taenia*. Consists of 73 chromosomes. One haploid set *C. elongatoides* ( $n = 25$ ) and two chromosome sets of *C. taenia* ( $2n = 48$ ). Previously described from Poland (Boroń et al., 2003 a) as 24 m + 27 sm + 22 sta. In the 73 chromosome spined loach of the Teteriv River basin this chromosomal formula is somewhat different, but nevertheless fairly close (fig. 2, d).

*C. elongatoides* — *taenia* — *tanaitica*. Individuals of this biotype have 74 chromosomes: *C. elongatoides* ( $n = 25$ ), *C. taenia* ( $n = 24$ ), *C. tanaitica* ( $n = 25$ ). According to various researchers (Boroń, Kotusz, 2000; Boroń et al., 2003 a; Vasil'ev, 1990) the number of metacentric chromosomes varies from 21 to 24, submetacentric — from 25 to 35, and subteloacrocentric ones vary in number from 10 to 14. Individuals of this biotype of the Teteriv River basin have a similar formula (fig. 2, e).

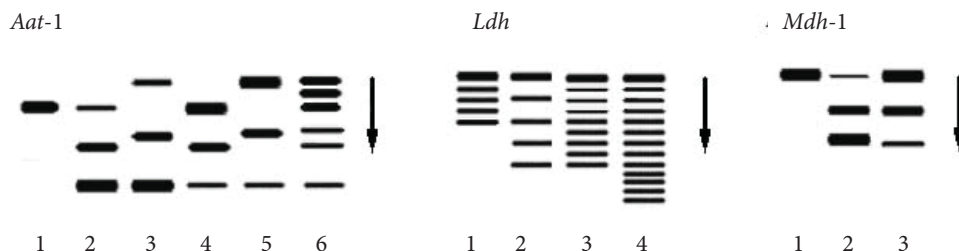


Fig. 2. Electrophoretic spectra of enzymes coding by allozymic loci: aspartate aminotransferase (1 — *Aat-1*<sup>100/100</sup>, 2 — *Aat-1*<sup>100/110-110</sup>, 3 — *Aat-1*<sup>95/110-110</sup>, 4 — *Aat-1*<sup>100-100/110</sup>, 5 — *Aat-1*<sup>95-95/110</sup>, 6 — *Aat-1*<sup>95-100/110</sup>), lactate dehydrogenase (1 — *Ldh-B*<sup>90/90</sup>, 2 — *Ldh-B*<sup>100/100</sup>, 3 — *Ldh-B*<sup>90/100-100</sup>, 4 — *Ldh-B*<sup>90/100/110</sup>), malate dehydrogenase (1 — *Mdh-1A*<sup>100/100</sup>, 2 — *Mdh-1A*<sup>100/110-110</sup>, 3 — *Mdh-1A*<sup>100-100/110</sup>).

Рис. 2. Схемы электрофоретических спектров ферментных продуктов, кодируемых локусами: аспаратаминотрансферазы (1 — *Aat-1*<sup>100/100</sup>, 2 — *Aat-1*<sup>100/110-110</sup>, 3 — *Aat-1*<sup>95/110-110</sup>, 4 — *Aat-1*<sup>100-100/110</sup>, 5 — *Aat-1*<sup>95-95/110</sup>, 6 — *Aat-1*<sup>95-100/110</sup>), лактатдегидрогеназы (1 — *Ldh-B*<sup>90/90</sup>, 2 — *Ldh-B*<sup>100/100</sup>, 3 — *Ldh-B*<sup>90/100-100</sup>, 4 — *Ldh-B*<sup>90/100/110</sup>), малатдегидрогеназы (1 — *Mdh-1A*<sup>100/100</sup>, 2 — *Mdh-1A*<sup>100/110-110</sup>, 3 — *Mdh-1A*<sup>100-100/110</sup>).

Table 2. The Karyotypes of *Cobitis* species and biotypesТаблица 2. Карิโอотипы видов рода *Cobitis* и их биотипы

Species / biotype	Formula (m + sm + sta)	NF	Xn	References
<i>C. taenia</i>	48 (12 + 18 + 18)	78	2n	Present study
<i>C. taenia</i>	48 (12 + 18 + 18)	78	2n	Boron et al., 2003a
<i>C. taenia</i>	48 (10 + 18 + 20)	76	2n	Boron et al., 2003 a
<i>C. taenia</i>	48 (10 + 18 + 20)	76	2n	Boron et al., 2003 b
<i>C. taenia</i>	48 (10 + 18 + 20)	76	2n	Vasil'ev et al., 1989
<i>C. taenia</i>	48 (10 + 20 + 18)	78	2n	Janko et al., 2007
<i>C. tanaitica</i>	50 (10 + 22 + 18)	82	2n	Bohlen et al., 2002
<i>C. tanaitica</i>	50 (10 + 30 + 10)	90	2n	Janko et al., 2007
<i>C. tanaitica</i> (rosomeridionalis) ♀	50 (8 + 28 + 14)	86	2n	Vasil'ev, 1995
<i>C. tanaitica</i> (rosomeridionalis) ♂	49 (9 + 28 + 12)	86	2n	Vasil'ev, 1995
<i>C. taurica</i>	50 (10 + 30 + 10)	90	2n	Janko et al., 2005
<i>C. pontica</i>	50 (10 + 30 + 10)	90	2n	Vasil'ev, 1995
<i>C. elongatoides</i>	50 (30 + 16 + 4)	96	2n	Rab et al., 2000
?	50 (28 + 18 + 4)	96	2n	Boron, 2003a
<i>C. elongatoides</i>	50 (22 + 26 + 2)	98	2n	Janko et al., 2007
<i>C. melanoleuca</i>	50 (8 + 18 + 24)	76	2n	Vasil'ev et al., 1989
	50 (8 + 16 + 26)	74	2n	Vasil'ev, Vasil'eva, 2008
	50 (6 + 16 + 28)	72	2n	Vasil'ev, Vasil'eva, 2008
	50 (30 msm + 20 sta)	80	2n	Lee et al., 1983
	50 (24 msm + 26 sta)	74	2n	Kim et al., 1999
<i>C. taenia</i> × <i>S. aurata</i>	49 (8 + 16 + 25)	73	2n	Present study
<i>C. elongatoides</i> × <i>C. taenia</i>	49 (15 + 21 + 14)	86	2n	Boron et al., 2003 a
<i>C. elongatoides</i> — 2 <i>taenia</i>	73 (23 + 31 + 19)	127	3n	Present study
<i>C. elongatoides</i> — 2 <i>taenia</i>	73 (24 + 27 + 22)	124	3n	Boron et al., 2003 a
<i>C. elongatoides</i> — <i>taenia</i> — <i>tanaitica</i>	74 (22 + 33 + 19)	129	3n	Present study
?	74 (24 + 35 + 15)	133	3n	Boron, Kotusz, 2000
?	74 (21 + 31 + 22)	126	3n	Boron et al., 2003 a
?	74 (23 + 27 + 24)	124	3n	Vasil'ev, 1990
?	74 (23 + 25 + 26)	122	3n	Vasil'ev, 1990
<i>C. 2 elongatoides</i> — <i>taenia</i>	74 (35 + 25 + 14)	134	3n	Rab et al., 2000
?	74 (33 + 27 + 14)	134	3n	Boron et al., 2003 a
<i>C. taenia</i> — <i>C. tanaitica</i> — <i>S. aurata</i>	74 (13 + 27 + 34)	114	3n	Present study
	74 (16 + 36 + 22)	126	3n	Boron, Kotusz, 2000
<i>C. 2 elongatoides</i> — <i>tanaitica</i>	75 (27 + 37 + 11)	139	3n	Present study
?	75 (25 + 36 + 14)	136	3n	Boron, Kotusz, 2000
?	75 (38 + 31 + 6)	144	3n	Rab et al., 2000
?	75 (24 + 35 + 16)	134	3n	Boron et al., 2003 a
<i>C. elongatoides</i> — <i>taenia</i>	49 (16 + 23 + 10)	88	2n	Janko et al., 2007
<i>C. elongatoides</i> — <i>tanaitica</i>	50 (16 + 25 + 9)	91	2n	Janko et al., 2007

*C. 2 elongatoides* — *tanaitica*. The number of chromosomes — 75 (Boron, Kotusz, 2000; Rab et al., 2000; Boroń et al., 2003 a). Two sets from *C. elongatoides* (2n = 50) and one from *C. tanaitica* (2n = 25). It is featured by an unusually large number of metacentrics and chromosome arms, respectively. Parameters of the chromosomal formula of specimens of this biotype of the Teteriv River basin (fig. 2, f), in general, meet the peculiarities of the chromosomal formula of this biotype recorded for the Danube River Basin.

*C. taenia* — *C. tanaitica* — *S. aurata*. The number of chromosomes — 74 together with a small number of arms NF = 114 (fig. 2, g). The genomic structure is as follows: *C. taenia* (n = 24), *C. tanaitica* (n = 25), *S. aurata* (n = 25). Symptomatic is a very small number of metacentrics — 13, though other triploid biotypes of the spined loach with 74 chromosomes have at the very least 21 metacentric chromosomes. The only exception is a series of individuals from Olawa (Odra River basin) (Boroń, Kotusz, 2000). There amongst triploids of unidentified hybrid structure a record was made of significantly lower than usual numbers of metacentric chromosomes.

Allozyme analysis. Gene marking allozymic loci level helped determine 9 species and biotypes of spined loaches (table 3), amongst which both *S. aurata* specimens as well as

**Table 3. The distribution of spined loaches according to species and biotypes in each of the researched samples**

**Таблица 3. Распределение щиповок по видам и биотипам в каждой из исследованных выборок**

Samples	TT	AA	AT	ETT	EET	EET <sup>95</sup>	ATT	ATT <sup>95</sup>	AT <sup>95</sup> T <sup>95</sup>
1	6	1	1	89					
2	1	1		8		54			
3	4						20	3	3
4	18						18	1	2
5	6						17		
6	2	1				16			
7				1		23			
8			1		1	20			
9	4					73		3	
10	40					1		7	
All in all	81	3	3	172	62	54	72	4	5

Biotypes: TT — *C. taenia*; AA — *S. aurata*; AT — *C. taenia* × *S. aurata*; ETT — *C. elongatoides* — *taenia*, *C. elongatoides* — *taenia* — *tanaitica*; EET — *C. 2 elongatoides* — *tanaitica*; EET<sup>95</sup> — *C. 2 elongatoides* — *tanaitica* with modified allele *Aat-1*<sup>95</sup>. TTA — *C. taenia* — *C. tanaitica* — *S. aurata*; AT<sup>95</sup>T<sup>95</sup> — *C. 2 elongatoides* — *tanaitica* with modified products; ATT<sup>95</sup> — *C. 2 elongatoides* — *tanaitica* with modified products allele.

hybrids of this species with different ploidy level were found in samples *C. taenia* specimens and polyploid unisex forms with definite genome combinations were found *C. elongatoides* on one side and *C. taenia* and *C. tanaitica* on the other (table 4).

*S. aurata* specimens were not numerous — only one specimen in each of three samples. Diploid hybrids *S. aurata* × *C. taenia* were also rare — one hybrid in each of three samples. At the same time triploid hybrid biotypes, whose genome was formed with *S. aurata*, make a very significant part — about 16 % of all researched specimens. They all were females. The specimens of this biotype can be divided into two groups. The specimens of the first group have following genotypes: *Aat-1*<sup>100-100/110</sup>, *Mdh-1A*<sup>100-100/110</sup>, *Ldh-B*<sup>90/100-100</sup> and the size of erythrocytes corresponding to triploids. They are represented in series in samples from the Sobok River basin (sample N 9), the Styr River (sample N 8) and the Guiva River (samples N 3, 4). According to gene dose display they should be identified as complex hybrids *C. 2 taenia* — *S. aurata* or *C. taenia* — *C. tanaitica* — *S. aurata*.

The belonging to the latter biotype is confirmed by karyological analysis.

Specimens of the second group were found only in the Guiva River. They are also complex hybrids with *S. aurata*. Their part is not significant. All in all they make only 2 %.

**Table 4. The genotypes of three diagnostic loci used for identification of species and biotypes**

**Таблица 4. Генотипы трёх диагностических локусов, использованных для идентификации видов и биотипов**

Species and biotypes	<i>Aat-1</i>	<i>Mdh-1A</i>	<i>Ldh-B</i>
TT	100/100	100/100	100/100, 100/105
AA	110/110	110/110	90/90
AT	100/110	100/110	90/100
ETT	100-100/110	100-100/110	100/100, 100-100/105
EET	100/110-110	100/110-110	100/100
EET <sup>95</sup>	95/110-110	100/110-110	100/100
ATT	100-100/110	100-100/110	90/100-100
AT <sup>95</sup> T <sup>95</sup>	95-95/110	100-100/110	90/100-105
ATT <sup>95</sup>	95-100/110-110	100-100/110	90/100-105

Biotypes: TT — *C. taenia*; AA — *S. aurata*; AT — *C. taenia* × *S. aurata*; ETT — *C. elongatoides* — 2 *taenia*, *C. elongatoides* — *taenia* — *tanaitica*; EET — *C. 2 elongatoides* — *tanaitica*; EET<sup>95</sup> — *C. 2 elongatoides* — *tanaitica* with modified allele *Aat-1*<sup>95</sup>. TTA — *S. aurata* — *C. taenia* — *C. tanaitica*; AT<sup>95</sup>T<sup>95</sup> — *C. 2 elongatoides* — *tanaitica* with modified products; ATT<sup>95</sup> — *C. 2 elongatoides* — *tanaitica* with modified products allele.

This biotype specimens are characterized with electromorphs with *Aat-1*<sup>95</sup> allele and triheterozygotes *Ldh-B*<sup>90/100/105</sup> (table 2). Judging from erythrocytes size, they are also triploids, but their genome interpretation is not definite. The thing is that diploid loaches with *Aat-1*<sup>95</sup> allele in Ukrainian rivers are not known and mass emergence of complex electromorphs hybrid biotypes with supposed *Aat-1*<sup>95</sup> allele, is typical only for genetically unstable populations (Mezhzherin, Pavlenko, 2007 b). It can be assumed that in this case we have genetic instability in hybrids *C. taenia* — *C. species* — *S. aurata*. The presence of genome *Cobitis* species is certified with *Ldh-B*<sup>105</sup> allele fixation typical for underscribed species.

## Conclusion

Thus, the investigation definitely proves the fact of hybridization amongst different spined loach genera and also testifies to real existence of another diploid-polyploid fish complex, namely *C. 2 taenia* — *S. aurata*. The attention should be paid to the absorbing character of hybridization amongst *S. aurata* and *C. taenia*, resulting in the fact that rare and stenobiotic species *S. aurata* in river systems of Northern Ukraine is represented more this hybrid forms than with “pure” ones.

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