Karyotypic Features of *Chironomus entis* and *Chironomus borokensis* (Diptera, Chironomidae) from Lake Kotokel (Lake Baikal Basin)

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Received March 15, 2011

Abstract—Karyotypes and chromosomal polymorphism of sympatric sibling species *Chironomus entis* and *Chironomus borokensis* from Lake Kotokel were studied. Five inversion banding sequences were found in *C. entis*, including p'*ent*A16, p'*ent*B9, and p'*ent*F6 that are new for the species; in *C. borokensis*, four inversion banding sequences were revealed, *bor*A4 being new for the species. The level of chromosome polymorphism in *C. entis* and *C. borokensis* can be considered similar: 54.2 and 53.8% heterozygosity, 0.67 and 0.73 inversions per individual, respectively. The new data are compared with those on *C. entis* population from Lake Kotokel obtained in 1981 and those of *C. borokensis* from Lake Dukhovoe (Lake Baikal basin) obtained in 1983.

DOI: 10.1134/S0013873813010065

Chironomus entis Shobanov, 1989 and Chironomus borokensis Kerkis, Filippova, Shobanov, Gunderina et Kiknadze, 1988 (Diptera, Chironomidae) are wellstudied sibling species from the group *plumosus* which now includes 14 species (Golygina et al., 2007). At the larval stage the species differ in the degree of development of ventral processes on abdominal segment VIII, the ventral coloration of the head capsule, the morphology of denticles on the mentum, and the shape and proportions of antennal segments (Shobanov, 1989, 2000); however, their reliable identification requires examination of species-specific characters of the polytene chromosomes from their salivary glands. C. entis has a vast geographic range. Its karyotypes and chromosome polymorphism have been studied in many Palaearctic and Nearctic (North American) populations, revealing specific banding sequences and specific regional traits in karyotype divergence (Demin and Shobanov, 1990; Belvanina et al., 1992; Kiknadze et al., 1991, 1996, 2000, 2004; Golygina, 1999; Kiknadze and Istomina, 2000; Petrova and Klishko, 2005; Golygina et al., 2007). C. borokensis is presently known only from Russia, where it occurs in Yaroslavl, Novosibirsk, Irkutsk, Chita Provinces, Khabarovsk and Primorye Territories, and Yakutia; populations from different parts of its range also demonstrate specificity of karyotype structure and chromosome polymorphism (Kerkis et al., 1988; Kiknadze

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et al., 1991, 1996, 2004; Proviz, 1993; Kiknadze and Istomina, 2000; Siirin et al., 2003; Petrova and Klishko, 2005; Golygina et al., 2003, 2007).

Karyological studies of chironomid midges in the Baikal region were started by Bukhteeva (1974) who described the karyotype and inversion polymorphism of Chironomus plumosus from Iskrinskii pond in the environs of Irkutsk. This population consisted of the larval form C. plumosus f. l. semireductus; in the recent taxonomy, this form corresponds to the distinct species C. entis (Shobanov, 1989). In our previous research carried out in the 1980s in some reservoirs of the Baikal region and in the shallow nearshore zone of Lake Baikal proper, the species C. entis (Lake Kotokel, Chivyrkui Bay of Baikal, Lake Rangatui) and C. borokensis (Dukhovoe and Shantalyk lakes) were also differentiated by their larvae, as C. plumosus f. l. semireductus and C. plumosus f. l. plumosus (Linevich and Proviz, 1987; Proviz, 1988, 1989). Earlier studies of East Siberian waters showed that in most cases, only one species of the group *plumosus* was found in each of the typical habitats, this situation being stable for many years in large eutrophic lakes with a distinct profundal zone. In particular, only C. plumosus f. l. semireductus (=C. entis) was recorded in 1935-1981 in Lake Kotokel, the largest lake in the Baikal shore area (70 km²). Examination of a smaller Lake Dukhovoe (6.16 km²), also located on the east Baikal shore, revealed only *C. plumosus* f. l. *semireductus* (=*C. entis*) in 1932–1937, and only *C. plumosus* f. l. *plumosus* (=*C. borokensis*) in 1983 (Linevich, 1981; Linevich and Proviz, 1987).

In 2008, Lake Kotokel attracted the attention of researchers due to cases of human and animal poisoning with fish from this lake. Hydrobiological studies demonstrated prolonged depression of the bottom biocenoses of the lake, which was first noticed in the 1990–2000s (Sokolova, 2001). Studies carried out in 2007–2008 showed that the depression continued while the diversity and quantitative parameters of the zoobenthos also declined (Bazova et al., 2010). The lake was described as a hypertrophic reservoir at the extreme dystrophic stage.

One of the possible factors which determined the catastrophic changes in the lake ecosystem was the presence of the introduced waterweed *Elodea canadensis* Michx which appeared in the lake in 1986, proliferated greatly in 1992, and died off en masse in 2000. According to the recent studies, the phytoplankton species composition shows clear signs of eutrophication, which is largely manifested in mass development of cyanobacteria, including toxic ones of the genus *Microcystis* (Belykh et al., 2010, 2011). Similar conclusions were made based on most parameters of the zooplankton (Sheveleva and Krivenkova, 2010).

Studies of the chironomid species composition have also revealed some differences during the period in question. Besides C. entis, one more dominant species of the plumosus group, C. borokensis, has appeared in Lake Kotokel. Now the two species occur sympatrically in black and gray clay-sand bottom areas. Morphologically, their larvae can be easily distinguished by the length of the ventral processes, allowing their relative abundance (%) to be determined. Our analysis of quantitative samples of zoobenthos taken in 2009 showed C. entis to be the dominant species in the central part of the lake. On average for the entire season, this species outnumbered C. borokensis at the depths 4.0-4.4 m, comprising about 70% of the total abundance. The fraction of C. entis was still greater at a depth of 14 m, reaching 96%. On the contrary, larvae of C. borokensis prevailed in the southern hollow of the lake at the depth 4.1 m, comprising 65%.

This communication reports the results of comparative karyological analysis of *C. entis* and *C. borokensis* populations from Lake Kotokel during the period of drastic changes in the lake ecosystem, and also describes their karyological specificity in the Baikal region in the 1980s and at present.

MATERIALS AND METHODS

Our material included IV instar larvae of C. entis (1981, 2009) and C. borokensis (2009) collected in Lake Kotokel from depths of 4-5 m: 47 larvae of C. entis in 1981, 24 larvae of C. entis and 26 larvae of C. borokensis in 2009. For comparison we also used the data of 1983 on 30 larvae of C. borokensis collected in Lake Dukhovoe from the depths 2-3 m (Proviz, 1989). The larvae were fixed in the mixture of 96% ethanol and glacial acetic acid (3:1). The preparations were made using the ethyl-orcein technique (Demin and Il'inskaya, 1988; Demin and Shobanov, 1990). The polytene chromosomes were documented at 90× lens magnification using the MKU-1 microfilm attachment (in 1981-1983) or at 100× lens magnification using the Carl Zeiss Axiostar Plus microscope (The Electron Microscopy Equipment Center, the Limnological Institute of the Siberian Branch of the Russian Academy of Sciences) and AxioVision Rel. 4.7.1 software. Chromosome arms A, C, D, E, and F of C. entis were mapped following the piger standard (Keyl, 1962; Devai et al., 1989), and arm B, after Maksimova (1976). The banding sequences are designated as follows: the first symbol refers to the geographic distribution (p' for the Palaearctic, n' for the Nearctic, h' for the Holarctic) (Golygina, 1999); it is followed by the abbreviated species name (ent), the arm (A), and the sequence number, for example, p'entA1 (in the homozygous state, p'entA1.1). Chromosomes of C. borokensis were mapped according to the standard of Maksimova (1976); since the range of C. borokensis is limited to the Palaearctic, the geographic symbols are not needed. The level of chromosome polymorphism of the populations was estimated by the fraction of heterozygous individuals in the sample (%) and the number of heterozygous inversions per individual

RESULTS AND DISCUSSION

Karyotype of *C. entis* (Kerkis et al., 1988; Demin and Shobanov, 1990; Kiknadze et al., 1991, 2000; Golygina, 1999). 2n = 8 (Fig. 1), chromosome arm combination AB, CD, EF, G (*thummi* cytocomplex). Chromosomes I (AB) and II (CD) are metacentric, chromosome III (EF) is submetacentric, and the short chromosome IV (G) is acrocentric. The nucleolus is



Fig. 1. Karyotype of *Chironomus entis* from Lake Kotokel. A, B, C, D, E, F, and G are chromosome arms; 1–25 are chromosome segments; a, b, c, d ... are bands; 1.1, 2.2, 11.11 are banding sequences; N is the nucleolar organizer, BR is the Balbiani ring; *arrows* mark centromeres, *bracket* marks the homozygous inversion.

located in arm G near the centromere; there are two Balbiani rings in arm G and one in arm B. The banding sequences in arms A, C, D, E, and F are designated according to Kiknadze and co-authors (2000, 2004), those in arm B, according to Kerkis and co-authors (1988).

Arm A is represented by two sequences in the population examined: h'*ent*A11 and p'*ent*A16, the latter being found for the first time in this species. Sequence A11 was found both in the homozygous state (Fig. 1) and in heterozygotes with A16 (Fig. 2*a*), while A16 was found only in heterozygotes with A11. Sequence A16, as well as A11, differs from h'*ent*A1 in a simple inversion:

h'*ent*A1 1a-2c 10a-12c 14f-13a 3i-2h 4a-4c 2g-2d 9e-4d 14g-16d 17a-19f

h'*ent*A11 1a-2c 10a-12c 14f-13a 3i-2h <u>4d-9e 2d-2g</u> <u>4c-4a</u> 14g-16d 17a-19f p'*ent*A16 1a-2c 10a-12c 14f-13a <u>16d-14g 4a-4c 2g-</u> <u>2d 9e-4d 2h-3i</u> 17a-19f

Sequence A11 was originally described from the Nearctic populations (Golygina, 1999) and later discovered in Finland (Michailova, 2001) and in two lakes in Chita Province where it existed only in the homozygous state (Petrova and Klishko, 2005).

Arm B is usually monomorphic; only one larva collected in 1981 had a previously unknown heterozygous inversion with a sequence resembling h'*plu*B1; here it is designated as p'*ent*B9 (Fig. 2*b*). Using the mapping system of Maksimova (1976), this sequence can be described as follows:

h'*plu*B1 12-25 h'*ent*B1 12-15b 22-15c 24 23 25 p'*ent*B9 12-22 24 23 25 37

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Fig. 2. Chromosome polymorphism in the population of *Chironomus entis* from Lake Kotokel: heterozygotes h'*ent*A11.p'*ent*A16 (*a*), h'*plu*B1.p'*ent*B9 (*b*), h'*ent*D1.h'*ent*D4 (*c*), h'*ent*E1.p'*ent*E1 (*d*), h'*ent*F1.p'*ent*F6 (*e*) and disrupted conjugation of homologs in arms F and E (*f*, *g*). *Brackets* mark the segments with inversions; other designations as in Fig. 1.

Arm C is represented by only one sequence, p'*ent*C2, which is common in the Palaearctic populations but has not been found in the Nearctic ones (Golygina, 1999; Kiknadze et al., 2000):

p'*ent*C2 1a 11h-11d 6g-6h 17a-16a 7d-7a 6f-6c 2c-1b 12a-15e 8a-11c 6b-2d 17b-22g

Arm D revealed two sequences: h'entD1 and h'entD4; the latter was found only in heterozygotes with D1 (Fig. 2c)¹ and differs from D1 in a simple inversion of the greater part of the arm:

h'*ent*D1 1a-2d 15e-16c 18d 8a-8d 9a-10a 13a-12a 18c-18a 7g-4a 10e-10b 13b-15d 2e-3g 11a-11c 16d-17f 18e-18g 19a-19h 20a-24g

h'*ent*D4 1a-2d 15e-16c 18d 8a-8d <u>19h-19a 18g-18e</u> <u>17f-16d 11c-11a 3g-2e 15d-13b 10b-10e 4a-7g 18a-</u> <u>18c 12a-13a 10a-9a</u> 20a-24g

Sequence D4 was previously known only from the Nearctic and designated as "n'*ent*D4" (Kiknadze et al., 2000). The finding of this sequence in East Siberia suggests a Holarctic distribution: h'*ent*D4.

Arm E revealed two sequences: h'entE1 and p'entE2. Of these, E1 was found only in heterozygotes E1.2 (Fig. 2*d*), whereas E2 was found both in heteroand homozygotes E2.2 (Fig. 1).

¹ Sequence h'*ent*D4 was found only in one larva characterized by compact chromosomes, hence the indistinct banding pattern of arm D fragment containing the inversion in Fig. 2*c*.

Species, locality, and collection date		Hetero- zygosity, %	Inversions per ind.	Number of heterozygous inversions in chromosome arms, %						
				А	В	С	D	Е	F	G
C. entis, Lake Kotokel, 25.V.1981	47	83.3	1.27	60.0	3.3	1	—	63.3	Ι	_
C. entis, Lake Kotokel, 15.VI.2009		54.2	0.67	25.0	_	_	4.2	20.8	4.2	_
C. borokensis, Lake Dukhovoe, 26.V.1983		43.3	0.47	16.7	20.0	_	10.0	_	_	_
C. borokensis, Lake Kotokel, 15.VI.2009		53.8	0.73	19.2	46.2	-	7.7	_	—	_

Table 1. Parameters of chromosome polymorphism in the populations of *C. entis* and *C. borokensis* from Kotokel and Dukhovoe lakes

Table 2. Genomic combinations of banding sequences in the populations of *C. entis* and *C. borokensis* from Kotokel and Dukhovoe lakes

Genomic combinations						Frequency of genomic combinations in different samples, %					
А	В	С	D	Е	F	G	1e	2e	1b	2b	
11.11	1.1	1.1	1.1	1.2	1.1	1.1	23.3	8.3			
11.11	1.1	1.1	1.1	2.2	1.1	1.1	16.7	45.8			
11.11	1.1	1.1	1.4	2.2	1.1	1.1		4.2			
11.11	1.1	1.1	1.1	2.2	1.6	1.1		4.2			
11.16	1.1	1.1	1.1	1.2	1.1	1.1	40.0				
11.16	1.1	1.1	1.1	2.2	1.1	1.1		25.0			
11.16	1.1	1.1	1.1	1.2	1.1	1.1		12.5			
11.16	1.1	1.1	1.1	2.2	1.1	1.1	16.7				
11.16	1.4	1.1	1.1	2.2	1.1	1.1	3.3				
1.1	1.1	1.1	1.1	1.1	1.1	1.1			56.6	46.2	
1.1	1.1	1.1	1.2	1.1	1.1	1.1			6.7		
1.1	1.2	1.1	1.1	1.1	1.1	1.1			16.7	34.6	
1.1	1.2	1.1	1.2	1.1	1.1	1.1			3.3		
1.2	1.1	1.1	1.1	1.1	1.1	1.1			10.0		
1.4	1.1	1.1	1.1	1.1	1.1	1.1			6.7		
1.4	1.1	1.1	1.2	1.1	1.1	1.1				7.7	
1.4	1.2	1.1	1.1	1.1	1.1	1.1				11.5	

Notes: 1e, C. entis from Lake Kotokel, 25.V.1981; 2e, C. entis from Lake Kotokel, 15.VI.2009; 1b, C. borokensis from Lake Dukhovoe, 26.V.1983; 2b, C. borokensis from Lake Kotokel, 15.VI.2009.

h'*ent*E1 1a-2e 10g-10c 3f-4h 10b-5a 3e-3a 11a-13g

p'entE2 1a-2e <u>3a-3e 5a-10b 4h-3f 10c-10g</u> 11a-13g

It should be noted that sequence p'*ent*E2, occurring in many regions of the Palaearctic, was found only in the heterozygous state in Chita Province; this sequence was not found in the Nearctic (Belyanina et al., 1992; Kiknadze et al., 2000; Petrova and Klishko, 2005).

Besides the heterozygous inversions E1.E2, many larvae (one-third of the samples in 2009) revealed disrupted conjugation of homologs at the terminal segments (Fig. 2g), probably due to an inversion whose exact position remains unknown.

Arm F revealed sequence p'entF6 which was new for the species in question. This sequence, found in heterozygotes F1.F6 (Fig. 2e), differs from F1 in a simple inversion:

h'*ent*F1 1a-1d 6e-1e 7a-10d 17d-16a 15i-11a 18a-19d 20a-23f

p'*ent*F6 1a-1d 6e-1e 7a-10d 17d-16a <u>19d-18a 11a-</u> <u>15i</u> 20a-23f



Fig. 3. Karyotype of *Chironomus borokensis* from Lake Kotokel: 1.1, 1.2 are banding sequences of chromosome arms; other designations as in Fig. 1.

In the material of 2009, a single case of mosaicism with respect to conjugation of arm F homologs was observed: in one cell of the salivary gland the homologs were not conjugated along nearly the entire arm (Fig. 2f), whereas in the other nuclei conjugation was normal.

The results of studies of chromosome polymorphism are shown in Tables 1 and 2. Comparative analysis of chromosome polymorphism parameters of *C. entis* from Lake Kotokel reveals both qualitative and quantitative changes in the genetic structure of the population that have occurred since the first karyological examination in 1981. The mean number of inversions per individual has decreased considerably by 2009: from 1.27 to 0.67 (Table 1), due to a smaller number of heterozygous inversions in arms A and E. The general index of heterozygosity has also decreased from 83.3 to 54.2%. The frequency of se-

quence p'*ent*A16, which was found in Lake Kotokel only in the heterozygous state in 1981 and 2009, has decreased nearly twofold: from 60.0 to 25.0%. The frequency of heterozygotes with sequence p'*ent*E2, widespread in the Palaearctic, has decreased from 63.3 to 20.8% due to stabilization of this inversion sequence in the homozygous state (Table 2). The increasing frequency of homozygotes *ent*E2.2 indicates that this sequence may have a higher adaptive value during the period in question.

The inversion spectrum observed in 2009 lacked the rare sequence p'*ent*B9 but included two new ones, h'*ent*D4 and p'*ent*F6. The sample of 1981 included 5 genotypic combinations of banding sequences, of which the combination of h'*ent*A11.p'*ent*A16 and p'*ent*E1.2 was the most common (40.0%; see Table 2). The material of 2009 included 6 genotypic combinations, the prevalent ones being h'*ent*A11 and p'*ent*E2.2



Fig. 4. Chromosome polymorphism in the populations of *Chironomus borokensis* from Kotokel and Dukhovoe lakes: heterozygotes *bor*A1.2 (*a*), borA1.4 (*b*), borD1.2 (*c*) and disrupted conjugation of homologs in arms B, C, A, and E (d–g). *Brackets* mark the segments with inversions; other designations as in Fig. 1.

(45.8%), and also h'*ent*A11.p'*ent*A16 and p'*ent*E2.2 (25.0%).

In general, the present level of chromosome polymorphism of *C. entis* in the Baikal region resembles that of most Palaearctic and Nearctic populations but differs from that in Lake Shaksha (Chita Province). The latter population is characterized by a high heterozygosity level (100%) and a large mean number of inversions per individual (1.6) (Belyanina et al., 1992; Golygina, 1999; Kiknadze et al., 2000; Petrova and Klishko, 2005).

Karyotype of *C. borokensis* (Kerkis et al., 1988; Kiknadze et al., 1991, 1996). 2n = 8 (Fig. 3), chromosome arm combination AB, CD, EF, G (thummi cytocomplex). The long chromosomes I (AB) and II (CD) are metacentric, chromosome III (EF) is submetacentric, and the short chromosome IV (G) is telocentric. The centromeres are large and heterochromatic, this feature differentiating *C. borokensis* from the rest of *Chironomus* species of the group *plumosus*. The nucleolar organizer (N) and two Balbiani rings (BR) are located in arm G, one more BR is located at segment 16 of arm B. The banding sequences are designated according to Kerkis and co-authors (1988).

The population of Lake Kotokel revealed two sequences in arm A: *bor*A1 in the homozygote A1.1 (Fig. 3) and in the heterozygote A1.4 (Fig. 4b). Three sequences were found in the larvae from Lake Dukhovoe: *bor*A1 in the homozygote A1.1 and in the heterozygotes A1.2 (Fig. 4a) and A1.4, and also *bor*A2 and *bor*A4 which were found only in the heterozygous state.

Sequence *bor*A2 was found in all the previously studied populations (Kerkis et al., 1988; Kiknadze et al., 1991, 1996; Golygina et al., 2003) except for those from Chita Province (Petrova and Klishko, 2005); sequence *bor*A4, involving segments 6, 5, and partly 10, was recorded for the first time. In Lake Ivan (Chita Province), one more sequence, *bor*A3, was found in the same arm (Petrova and Klishko, 2005); it differs from *bor*A1 in a simple inversion:

borA1 1-4 10a-5 10b-12

*bor*A2 1-12

borA3 1-4 10a-7b 10bc 5-7c 11 12

*bor*A4 1-4 10a-7 <u>5 6</u> 10bc 11 12

Arm B is represented by sequences *bor*B1 (Fig. 4*d*) and *bor*B2 (Fig. 3), differing in an inversion in the median part of the arm:

borB1 25-23 15c 21-16 22 15b-13

borB2 25-23 15c 16-21 22 15b-13

The former sequence was recorded in the homozygote B1.1 and in the heterozygote B1.2 in the material from both lakes, the latter, only in the above heterozygote.

Arm D also revealed two sequences *bor*D1 and *bor*D2 that occurred in the heterozygote D1.1 and in the heterozygote D1.2 (Fig. 4c).

borD1 1-13

borD2 1 6-2 7-13

Sequences *bor*B2 and *bor*D2 are characterized by the same distribution as *bor*A2.

Arms C, E, F, and G in the examined populations were represented by the standard sequences only:

borC1 25-14

*bor*E1 1-10

borF1 22 19-21 18-11

borG1 1 2 8 3-8

A similar structure of these arms was found only in the population from Chita Province (Petrova and Klishko, 2005). In addition to the standard homozygotes, hetero- and homozygotes *bor*F1.2 and *bor*F2.2 were found in Yaroslavl Province (Kerkis et al., 1988), *bor*G1.2 and *bor*G2.2 in Yakutia (Kiknadze et al., 1996), *bor*F1.2, *bor*F2.2, and *bor*G1.2 in Primorye Territory (Golygina et al., 2003).

Besides large chromosome transformations, lack of conjugation in arms A, B, C, and E was observed in several cases in the populations examined, without any apparent changes in the banding patterns (Figs. 4d-4g).

Data on the chromosome polymorphism and genotypic combinations of banding sequences are presented in Tables 1 and 2. The heterozygosity level in C. borokensis populations from the Baikal region is 53.8 (Lake Kotokel) and 43.3% (Lake Dukhovoe), which is lower than in populations from Yakutia (100%) and Yaroslavl Province (68.0%) (Kerkis et al., 1988; Kiknadze et al., 1996) but much higher than in those from Chita Province (20.0%) (Petrova and Klishko, 2005). The mean number of inversions per individual is greater in Lake Kotokel (0.73) than in Lake Dukhovoe (0.47) but smaller than in Yaroslavl Province (0.90). The differences in these parameters between the two populations from the Baikal region are determined by the high frequency (46.2%) of heterozygotes borB1.2 in Lake Kotokel (Table 2). Such high frequency of this inversion was not recorded in C. borokensis populations from other regions, either. The greatest number of genotypic combinations of banding sequences (six), observed in the population from Lake Dukhovoe, is determined by the combination of the standard sequences and four inversion ones. As a rule, only one inversion sequence was present in an individual karyotype; two sequences, namely borB2 and borD2, were observed in only one case. Four genotypic combinations are present in Lake Kotokel, two of them including two inversion sequences: borA4 and borB2, borA4 and borD2. Individuals with standard sequences prevail in both lakes: 56.6% in Lake Dukhovoe and 46.2% in Lake Kotokel.

Thus, the results obtained have allowed us to characterize the karyotypic specificity of populations of two dominant chironomid species in Lake Kotokel. Changes in the genetic structure of C. entis population that have occurred since our first research, may be related to transformations in the lake ecosystem. The fraction of heterozygous individuals, reflecting the adaptive capacities of the population (Dobzhansky, 1970; White, 1977), has decreased by 1.5 times, and the number of inversions per individual, by almost 2 times. The appearance of C. borokensis, which has now colonized the medium depth zone (4 m) and has become dominant in the southern hollow of the lake, also appears to be related to the changes in the environment. The level of heterozygosity and the number of inversions per individual in the population of C. borokensis are now almost the same as in that of C. entis, and exceed the values previously observed in Lake Dukhovoe by 1.2 and 1.5 times, respectively.

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The demonstration of intraspecific microevolutionary processes in the populations of *C. entis* and *C. borokensis* shows that cytogenetic monitoring of the ecological condition of Lake Kotokel holds much promise and should be continued. The new banding sequences found in the Baikal region enrich our knowledge of the karyotypes of these species.

ACKNOWLEDGMENTS

The authors are sincerely grateful to N.A. Shobanov (Institute for Biology of Inland Waters, RAS) for valuable advice and discussion, and to D.V. Matafonov, N.M. Pronin (Institute of General and Experimental Biology, SB RAS), and N.G. Sheveleva (Limnological Institute, SB RAS) for help with material collection.

This work was carried out within the framework of National Research Project VII 62-1-4 "A Complex Study of the Supralittoral Zone as an Essential Component of the Littoral Zone in Lake Baikal" and partly supported by the Siberian Branch of RAS (Integration Project M-49).

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