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Evaluation of some microsatellite markers variability in the study of genetic structure of vendace (*Coregonus albula* (L.)) populations from Latvian Lakes

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ABSTRACT

Vendace (*Coregonus albula* (L.)) is a very plastic species of freshwater whitefish which is widespread in Europe. But in Latvia this species is included into the list of specially protected fish species with limited use. We examined cross-species amplification of 14 microsatellite loci (*Cocl-Lav22, Cocl-Lav23, Cisco-59, Cisco-106, Cisco-90, Cisco-126, Cisco-157, Cisco-179, Cisco-181, Cisco-183, Cisco-200, BWF1, BWF2,* and *C4-183*) which were successfully used for genetic studies, monitoring, protection and management of different *Coregonus* species. Five microsatellite markers (*BWF1, Cisco-90, Cisco-126, Cisco-157, Cisco-200*) had a good representation in populations of vendace from five Latvian lakes (Sventes, Raznas, Nirzas, Dridzas, Stirnu) and were used for genetic analysis of these populations. It was shown that these 5 microsatellite loci were polymorphic and could differ among the investigated populations. The mean number of alleles per locus (from 4.4 to 6.2), the observed (from 0.53 to 0.70) and expected (from 0.49 to 0.70) heterozygosity, population structure (F_{ST} and R_{ST}) and gene flow (Nm) were also analysed in Latvian vendace populations.

Key words: *Coregonus albula,* microsatellites, Latvian lakes, polymorphism, heterozygosity, differentiation.

Because of their widespread distribution, commercial importance and high phenotypic diversity throughout the northern hemisphere, coregonids have been the subject of intensive research efforts for more than a century [Bernatchez, 2004]. The vendace (*Coregonus albula*) is a fish widely spread in Holarctic waters. It has reached North-western Europe after glaciations. The vendace is a polymorphic species of circumpolar distribution composed of several intraspecific forms. At the beginning of the 20th century, *Coregonus albula* was artificially introduced from lakes Peipus and Ladoga to more than 30 Latvian lakes. The vendace was detected in 30 Latvian lakes in the 1930s. In the 30s the industrial catch of vendace reached 13 tons per lake. At the present moment this species can be found only in some Latvian lakes and it is included in the list of specially protected species in Latvia (Regulation No 396 of the Cabinet of Ministers of the Republic of Latvia, 14.11.2000). The lack of basic data on

biology and population status of the local vendace population hinders sustainable utilization of this fish and efforts to manage its reproduction in Latvian lakes.

Microsatellites are more revealing over shorter geographical distances, where a few cases of panmixia [Dannewitz et al., 2005] and numerous cases of isolation by distance patterns [O'Reilly et al., 2004], clinal variation [Nielsen et al., 2004], fragmentation [Lemaire et al., 2005], and hybridization [Gum et al., 2005] have been identified. Microsatellite genotypes are particularly useful for detecting structure in closely related populations, regardless of whether they are in evolutionary equilibrium or not. But microsatellite markers that are used to study vendace population are not developed well enough. Therefore the aim of this work was to evaluate the variability of some microsatellite markers and use them to study the genetic structure of vendace populations in Latvian lakes.

MATERIALS AND METHODS

The fish samples were collected in Latvia in 2007, with the help of specialists of the Latvian Fish Resources Agency, from sampling catches according to Latvian Fish Resources Agency monitoring plan from seven Latvian lakes: Sventes, Raznas, Nirzas, Dridzas, Alūksnes and Ežezers. The lake characteristics are shown in Table 1. The location of lakes can be seen in Fig. 1. Sample tissues were stored at −20 °C. DNA was extracted according to the salt extraction method of S. M. Aljanabi, I. Martinez [1997].

Microsatellite amplification was performed using the ABI 9700 biocycler. PCR was performed in 12 μkl. PCR mixture components were: a DNA sample, 10 × Taq Buffer with KCl, 1.5 mM $MgCl_2$, 2mM dNTP mix, 0.06 U/μl Taq DNA polymerase, 0.4 μmol/μl of each primers of 14 microsatellite loci (*Cocl-Lav22, Cocl-Lav23, Cisco-59, Cisco-106, Cisco-90, Cisco-126, Cisco-157, Cisco-179, Cisco-181, Cisco-183, Cisco-200, BWF1, BWF2,* and *C4-157*). PCR were performed using the thermal cycling programme, following an initial denaturation at 94 °C for 5 min, 25 cycles were run with 94 °C for 30 s, 56 °C for 30 s, and 72 °C for 60 s followed by 7-min extension at 72 °C and cooling at 4 °C. PCR products were fractioned by analytic electrophoresis in polyacrylamide gel (PAAG) according to the general recommendations [Paulauskas, Tubelyte-Kirdiene, 2002], using TBE (0.045M Tris, 0,001M EDTA, 0,045M H_3BO_3, pH 8.3−8,4) buffer in a vertical electrophoresis device. Amplified microsatellites were being electrophoreticaly separated for one hour using the following mode: 10 V · cm 20 min^{-1} and 16−17 V · cm^{-1}. The DNA marker (pUC19 DNA/Msp l (Hpa II) marker (34−50 bp), (MBI "Fermentas", Vilnius, Lithuania)) was used. PCR products were

Table 1

The characteristics of Latvian lakes in which the vendace was collected

Lake	Location	Area, ha	Mean depth, m	Max depth, m
Rāznas	56°19′ N	5760	7	17
	27°27′ E			
Nirzas	56°23′ N	550	8	21
	27°54′ E			
Sventes	55°51′ N	740	8	38
	26°21′ E			
Drīdzis	55°58′ N	750	13	65
	27°18′ E			
Stirnu	56°33′ N	150	8	26
	26°01′ E			
Alūksnes	57°27′ N	1540	7	15
	27°5′ E			
Ežezers	56°10′ N	990	6	21
	27°35′ E			

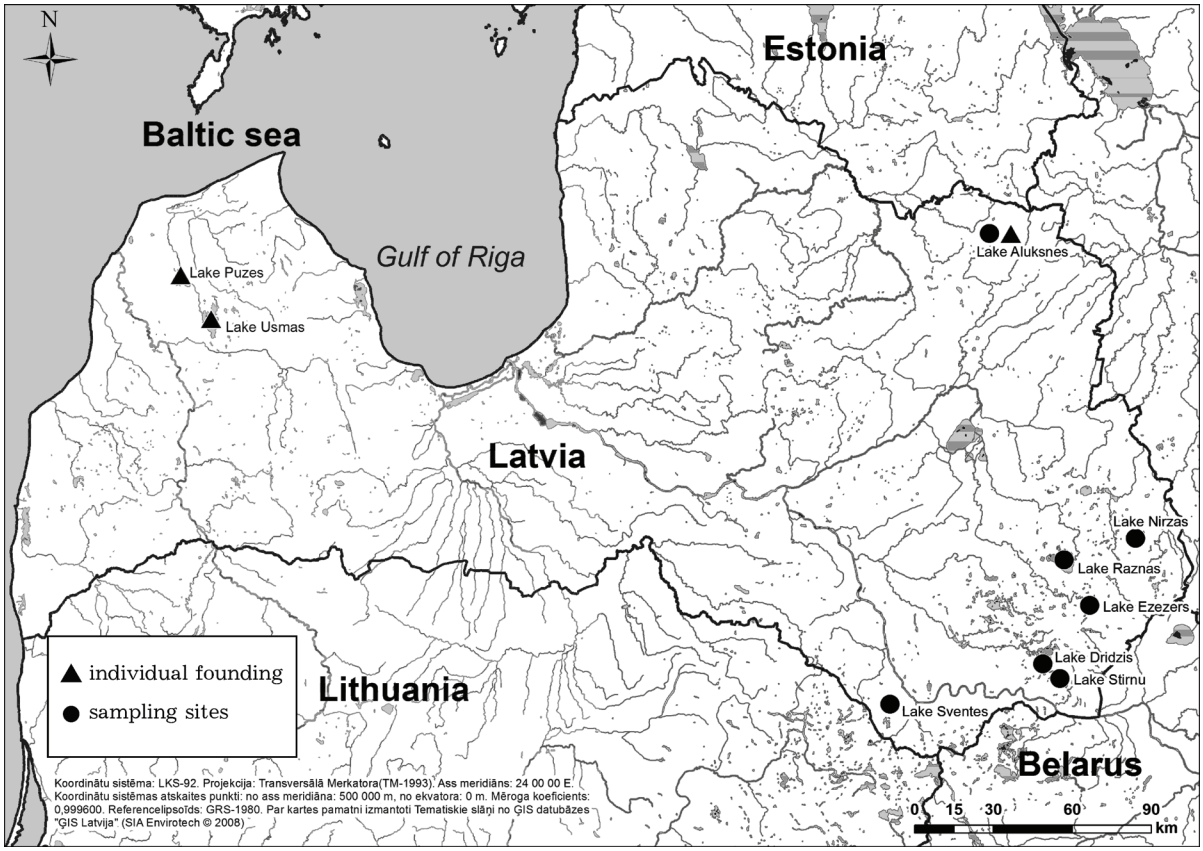

Fig. 1. Location of lakes in Latvia, in which the vendace was collected

visualized in UV light (302 nm) with EtBr (5 μkg/ml), using the UVP visualization system. The size of microsatellites was determined by comparing them to the marker using VisionWorksLS software ("Ultra-Violet Products Ltd", UK). Amplification was repeated three times with each primer, including a positive and negative control.

The six microsatellite primers (*Cisco-90, Cisco-106, Cisco-126, Cisco-157, Cisco-200* and *BWF1*), which gave repeatable and informative responds in testing, were selected for analysis. For genotyping the PCR products, which were obtained with fluorescently-marked primers TMR, HEX, FAM, were subjected on ABI 310 automated sequencer using Genescan LIZ 500 (Applied Biosystem) as international size standard. Number of alleles in a locus, frequency, private alleles in each population, observed and expected heterozygosity level in polymorph loci were measured, their differences and significance with χ criteria were calculated using POPGENE 1.32 and GeneAlex 6.41 software. The MICRO-CHECKER program was used to identify the null allele [Oosterhout et al., 2004]. The MICRO-CHECKER program helped to identify genotyping errors due to non-amplified alleles (null alleles), short allele dominance (large allele dropout) and scoring of stutter peaks. It was also used to detect typographic errors.

RESULTS AND DISCUSSION

Microsatellites are successfully used for genetic studies of different *Coregonus* species, as well as for monitoring, protection and management of this species. But microsatellite markers that are used to study vendace population are not developed well enough. Since the development of specific microsatellites primers requires time and material investments, it may be used to study the primers designed for related species. For example, Rogers et al. [2004] identified 31 microsatellite loci for the Canadian whitefish (*Coregonus clupeaformiss*, Mitchill). The authors tested the developed mar-

kers for six related fish species (*Prosopium coulteri, Coregonus lavaretus, Oncorhynchus mykiss, Salvelinus alpinus, C. artedi* и *Salmo salar*), which showed the applicability of these markers for these species. Many researchers [e. g. Patton et al., 1997; Turgeon et al., 1999] widely used the microsatellites markers designed for *Coregonus clupeaformiss* and *C. nasus* in the study of population genetic of different species of whitefish. The cross-species amplification of microsatellite loci on *Coregonus albula* was shown [Huuskonen et al., 2004; Schulz et al., 2006; Praebel et al., 2013]. We examined the amplification of 14 microsatellite loci (*Cocl-Lav22, Cocl-Lav23, Cisco-59, Cisco-106, Cisco-90, Cisco-126, Cisco-157, Cisco-179, Cisco-181, Cisco-183, Cisco-200, BWF1, BWF2, C4-157*) which were developed by J. Turgeon et al. [1999] and J. C. Patton et al. [1997]. These markers were successfully used for genetic studies of different *Coregonus* species (e. g. *C. nasus*, *C. artedi C. clupeaformis, C. hoyi* and others) [Huuskonen et al., 2002, Schulz et al., 2006]. Five microsatellite markers (*BWF1, Cisco-90, Cisco-126, Cisco-157* and *Cisco-200*) had a good representation in populations of vendace from the following Latvian lakes: Sventes, Rāznas, Nirzas, Drīzis, Stirnu, Alūksnes, Ežezers. General characterization of these five microsatellites primer pairs is described in Table 2. These loci (*BWF1, Cisco-90, Cisco-126, Cisco-157* and *Cisco-200*) were polymorphic in the investigated vendace population and the level of polymorphism was very high. The number of alleles in each locus in the investigated population of vendace from some Latvian lakes was different (Table 3). The number of alleles in each microsatellite locus was also different. The greatest number of alleles (12) was found in the locus *Cisco-200* of the vendace population from the lakes Drīdzis and Sventes. The minimum number of alleles (7) was found in the locus *Cisco-200* in the vendace *population* from Lake Rāznas (data are not shown). On the whole, the largest number of alleles (29) was found in *Cisco-200* in Latvian Lakes. In German lakes the maximum number of alleles (30–33) was also found in *Cisco-200*, with an average of 12–15 alleles per locus in different populations of *Coregonus albula* [Schulz et al., 2006]. The longest alleles (159–323) were also found in *Cisco-200* in Latvian lakes and the

T a b l e 2

Microsatellite markers: description and amplification conditions

Name	Primer sequence 5′–3′	Repeat motif	Label	PCR conditions		Heterozygosity		
				T_a (°C)	number of cycles	H_{obs}	H_{exp}	p-value
Cisco-90	F: CAG ACA TGC TCA GGA ACT AG R: CTC AAG TAT TGT AAT TGG GTA C	$(AC)_{10}$ ATAT$(AC)_3$	TMR	55	30	0.65	0.89	***
Cisco-126	F: GCC AGA GGG GTA CTA GGA GTA TG R: GCA GAG AAA GAG CCT GAT TGA AC	$(TC)_{10}N_{84}(GT)_8$	HEX	53	27	0.61	0.70	ns
Cisco-157	F: CTT AGA TGA TGG CTT GGC TCC R: GGT GCA ATC ACT CTT ACA ACA CC	$(GC)_{17}$	TMR	53	27	0.43	0.51	*
Cisco-200	F: GGT TAG GAG TTA GGG AAA ATA TG R: GTT GTG AGG TAG GCC TGG	$(GT)_{45}$	HEX	53	27	0.89	0.95	ns
BWF1	F: GAT CAG AGA AAT ACA CAC AAC GCA TCA A R: CAG AGG TTC CAT TAC TGA GCA C	$(GA)_{25}$	FAM	55	30	0.66	0.76	***

N o t e. * – $p < 0.05$; ** – $p < 0.01$; *** – $p < 0.001$, ns – not significant differences.

Table 3

Parameters of alleles in each locus

Locus	*BWF1*	*Cisco-90*	*Cisco-157*	*Cisco-126*	*Cisco-200*
A. mean	4.86	5.14	3.14	4.00	9.86
Min	4	5	2	3	8
Max	7	7	5	5	12
A	13	15	8	8	29
Ad (bp)	206–240	112–152	122–166	191–211	159–323

N o t e. A. mean – average number of alleles per population; min – minimum number of alleles in population; max – maximum number of alleles in population; *A* – total number of alleles in locus; *ad (bp)* – range of allele size.

shortest alleles (112–152) were in *Cisco-90*. The same tendency was noticed in the investigation of vendace in Canadian lakes [Turgeon et al., 1999; Turgeon, Bernatchez, 2001]: the longest alleles were found in the locus *Cisco-200* and the shortest alleles were in *Cisco-90*. It was assumed that these alleles may play an important role in *Cisco* genome function and may be under strong selective constraints. It may also be assumed that this is a case of a size homoplasy.

We examined the utility of microsatellites *BWF1, Cisco-90, Cisco-126, Cisco-157* and *Cisco-200* for the genetic study of vendace in population. We also studied the occurrence of alleles, observed and expected heterozigosity (H_{obs} and H_{exp}) population structuring (F_{ST} and R_{ST}) and gene flow (Nm).

The abundance of alleles in investigated loci is shown in Fig. 2. It can be seen that the abundance of alleles in loci varies a lot among the studied populations. Private alleles were found in each of *BWF1, Cisco-90, Cisco-126, Cisco-157,* and *Cisco-200* loci for the vendace from all Latvian lakes. The maximum number of private alleles (8) was found in locus *Cisco-200*. But the number of private alleles varied between 1 and 2 in the vendace populations from the seven investigated lakes. The abundance and frequency of alleles in investigated loci can be seen in Fig. 3. The most variable allele was observed in this locus and dominant alleles 253 and 247 (frequency 0.20 and 0.30). The common alleles for seven vendace populations were found in the loci: *Cisco-126* (205), *Cisco-157* (122) and *BWF1* (214). The occurrence of alleles 214

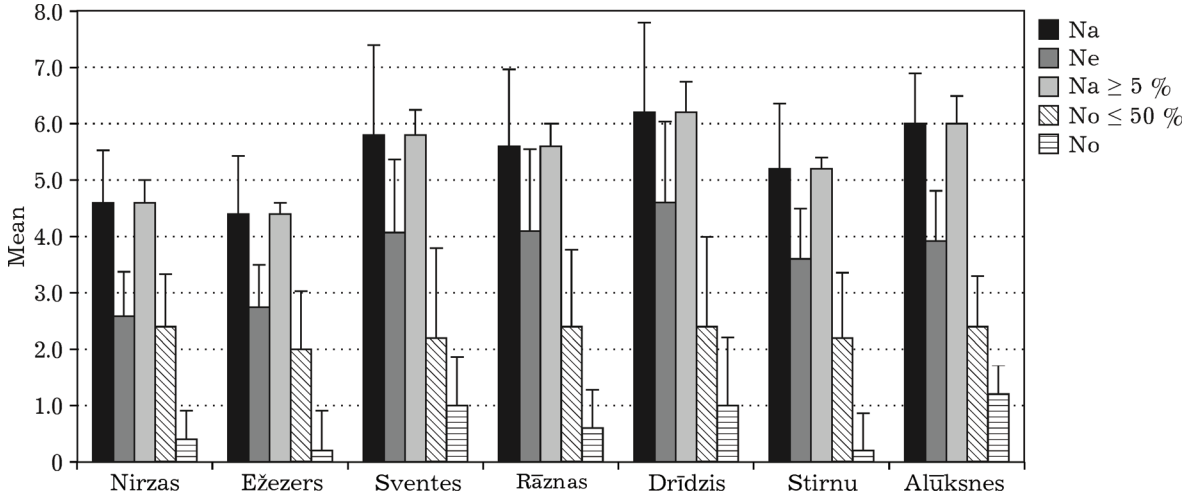

Fig. 2. Abundance of alleles in the investigated populations of vendace in Latvian lakes.

Na is an average number of allele on a locus; *Na* ≥ 5 % is an average number of allele with the abundance occurrence of more than 5 %; *Ne* is an average effective number of allele on a locus; *No* is an average number of private alleles; *No* ≤ 50 % is an average number of allele with the occurrence abundance of less than 50 % ± standard error

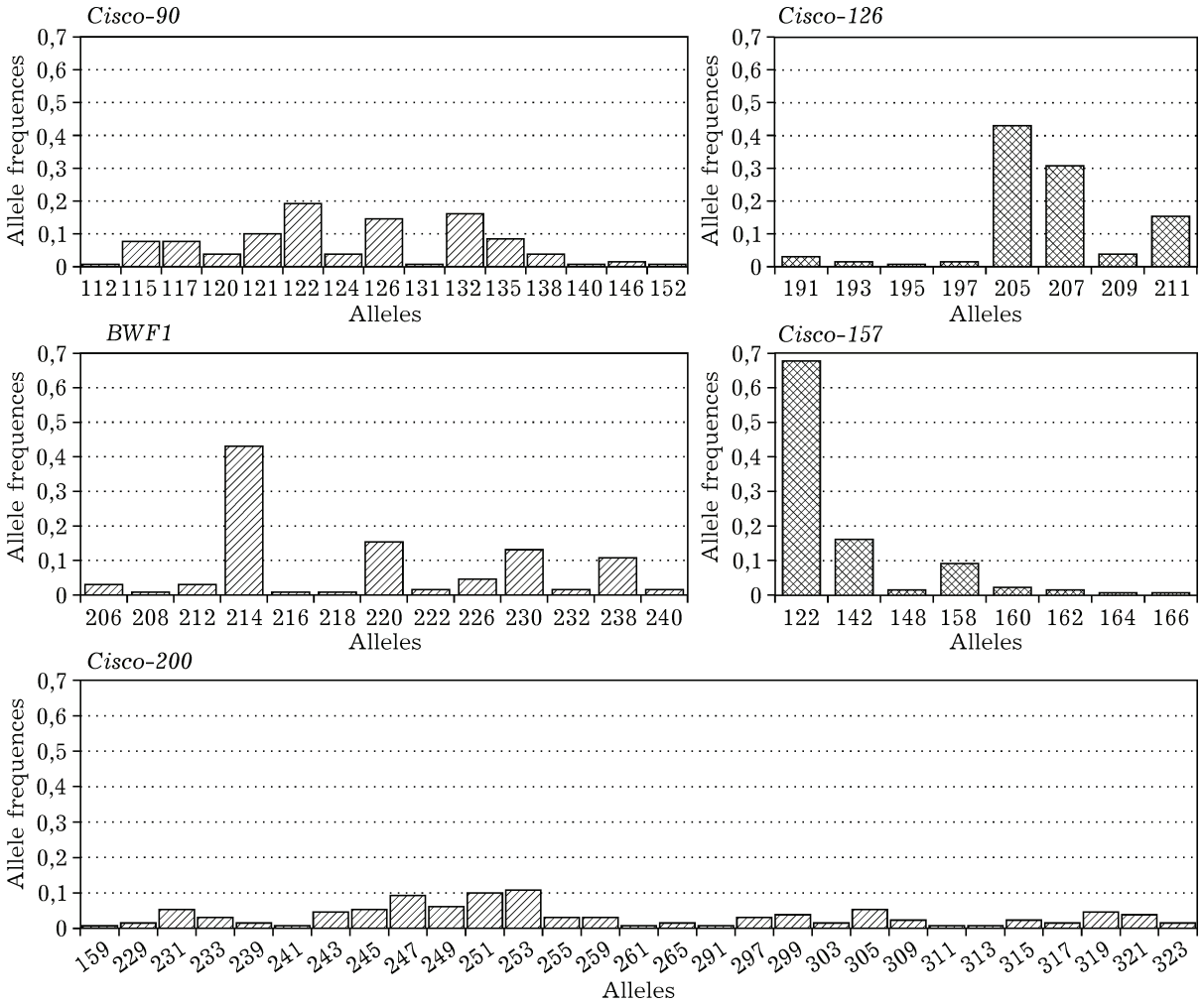

Fig. 3. The common abundance of alleles in microsatellite loci *BWF1, Cisco-90, Cisco-126, Cisco-157* and *Cisco-200* for the vendace

in locus *BWF1* was high: from 0.40 to 0.55 (except for the vendace population from the Lake Rāznas). The occurrence of alleles 214 in locus *BWF1* was also high: from 0.40 to 0.55 (except for the vendace population from the Lake Rāznas). The occurrence of the common alleles *Cisco-126* (205), *Cisco-157* (122) *v*aried considerably in the studied Latvian lakes. For example, the occurrence of alleles 205 in locus *Cisco-126* varied from 0.15 (Lake Drīdzis) to 0.81 (Lake Nirzas) and the occurrence of alleles 122 in locus *Cisco-157*: from 0.2 (Lake Aluksne) to 0.88 (Lake Nirzas). The Fig. 3 reflects the common diversity of alleles in five investigated microsatellite loci: *BWF1, Cisco-90, Cisco-126, Cisco-157* and *Cisco-200*.

As can be seen from Fig. 2 the average value of alleles in a locus (*Na*) is different in the investigated populations. The greatest amount of alleles per locus was found in the Dzīdzis vendace population (6.2) and the smallest amount of alleles per locus was found in the Nirzas and Ežerers vendace populations. Frequencies of alleles in five microsatellites loci *BWF1, Cisco-90, Cisco-126, Cisco-157* and *Cisco-200* from vendace populations in seven Latvian lakes are represented in Fig. 3. It can be seen that locus *Cisco-200* is represented by the largest number of alleles in the studied vendace populations. The highest frequency was found in 22 allele of locus *Cisco-157*.

Observed heterozigosity (H_{obs}) ranged from 0.43 to 0.89 in five microsatellite loci (Table 4). H_{obs} reached its maximum value in locus *Cisco-200* in each lake. H_{obs} was minimal in locus *Cisco-157* in each lake. The maximum value of

Table 4

Observed and expected heterozigosity (H_{obs} and H_{exp}) in vendace population

Locus	*BWF1*	*Cisco-90*	*Cisco-157*	*Cisco-126*	*Cisco-200*
			Sventes		
H_{obs}	0.600	0.700	0.600	0.700	0.900
H_{exp}	0.595	0.675	0.460	0.740	0.890
P-value	ns	ns	ns	ns	ns
			Rāznas		
H_{obs}	0.571	0.571	0.429	0.571	0.857
H_{exp}	0.653	0.673	0.367	0.684	0.898
p-value	ns	ns	ns	ns	ns
			Nirzas		
H_{obs}	0.625	0.500	0.250	0.375	0.875
H_{exp}	0.648	0.422	0.227	0.320	0.820
p-value	ns	ns	ns	ns	ns
			Drīdzis		
H_{obs}	1.000	0.600	0.400	0.900	0.900
H_{exp}	0.745	0.780	0.395	0.655	0.900
p-value	ns	ns	ns	ns	ns
			Stirnu		
H_{obs}	0.700	0.800	0.200	0.600	0.900
H_{exp}	0.645	0.750	0.500	0.565	0.855
p-value	ns	ns	ns	ns	ns
			Alūksnes		
H_{obs}	0.500	0.400	1.000	0.700	0.900
H_{exp}	0.765	0.480	0.700	0.660	0.860
p-value	**	ns	ns	ns	ns
			Ežezers		
H_{obs}	0.600	0.900	0.100	0.400	0.900
H_{exp}	0.585	0.630	0.095	0.485	0.820
p-value	ns	ns	ns	ns	ns
H_{obs}	0.66	0.65	0.43	0.61	0.89
H_{exp}	0.76	0.89	0.51	0.70	0.95
p-value	***	***	ns	ns	ns

Note. * – $p < 0.05$; ** – $p < 0.01$; *** – $p < 0.001$, ns – not significant differences.

H_{obs} was observed in *Cisco-157* (1.00) in Alūksnes Lake. The overage expected heterozigosity (H_{exp}) varied from 0.51 (in locus *Cisco-157*) to 0.95 (in loci *Cisco-200*). The significant deviation of the observed heterozigosity from the expected value ($p < 0.001$) was observed in Alūksnes Lake in loci *BWF1*. The reason for this may be the presence of non-amplified alleles. The MICRO-CHECKER program estimates the frequency of null alleles and can adjust the allele and genotype frequencies of the amplified alleles, permitting their use in further population genetic analysis. But the presence of null allele was not identified.

The data of F_{ST} and R_{ST} statistics in total and in each investigated microsatellite locus (the level of significance is given in brackets) are shown in Table 5. For the interpretation of F_{ST} and R_{ST}, it was suggested that a value lying in the range between 0 and 0.05 indicates little genetic differentiation; a value between 0.05 and 0.15 – moderate differentiation; a value between 0.15 and 0.25 – great differentiation; and values above 0.25 – very great genetic diffe-

Table 5

F_{ST} and R_{ST} statistics total and in each investigated microsatellites locus (the level of significance is given in brackets)

Locus	F_{ST}	Nm	R_{ST}
Cisco-90	0.272 (0.001)	0.67	0.189 (0.001)
Cisco-126	0.120 (0.001)	1.83	0.082 (0.024)
Cisco-157	0.198 (0.001)	1.01	0.294 (0.001)
Cisco-200	0.046 (0.001)	5.22	−0.023 (0.73)
BWF1	0.09 (0.001)	2.52	0.119 (0.004)
Total	0.143 (0.001)	1.50	0.043 (0.03)

rentiation [Hartl, Clark, 1997; Wright, 1978]. The estimation and comparison of both *F*- and *R*-statistics is relevant particularly when important variations in levels of differentiation are expected among sets of subpopulations. Two loci (*Cisco-126* and *BWF1*) had a moderate differentiation. Two loci (*Cisco-90* and *Cisco-157*) had a very great genetic differentiation. Locus *Cisco-200* had a little genetic differentiation. It should be noted that the values of F_{ST} and R_{ST} were similar in these loci and, in most part, authentic (see Table. 5).

Given the practically complete geographic isolation of investigated populations of vendace, it may be assumed that the four loci (*Cisco-126* and *BWF1*; *Cisco-90* and *Cisco-157*) possess most accurate information about the differentiation of the studied populations.

The main problem affecting *F*-statistics when working with microsatellites, is their sensitivity to the mutation rate when migration is low [Balloux, Lugon-Moulin, 2002], e. g. the effect of polymorphism (due to mutations) drastically deflates F_{ST} expectations [Wright, 1978; Charlesworth, 1998; Nagylaki, 1998; Hedrick, 1999], although R_{ST} does not depend on the mutation rate. It should be noted that certain loci may be unsuitable for the study of differentiation of populations because they have a high rate of mutation.

In particular, high mutation rate is characteristic of the loci which have many alleles. The maximum amount of alleles was found in *Cisco-200* (29) (see Fig. 3), which may influence the values of the differential statistics. The separate data of differential statistics (F_{ST} and R_{ST}) for each locus showed a similar level of genetic differentiation of populations. The generalized data, which was based on five microsatellite loci, showed radically different genetic differentiation with different levels of reliability (see Table 5). We assume that, at this moment, to identify the genetic differentiation of populations of vendace, it is advisable to use the data for the four loci: *Cisco-126* and *BWF1; Cisco-90* and *Cisco-157*. The level of genetic differentiation of populations, which was based on combination of these data of four loci, was sufficiently high (F_{ST} (0.174) and R_{ST} (0.227)) with a high level of significance ($p < 0.001$).

The important factor is not the mutation rate *per se*, but the magnitude of the ratio of mutation over migration. When gene flow is reduced, as can be expected across hybrid zones, or when known barriers to dispersal exist, the effect of mutation may become important relative to migration and has to be accounted for. On the other hand, mutation is unlikely to matter when the level of gene flow is high. This situation can be encountered at restricted geographical scales, as well as over much wider areas for species with high dispersal abilities, such as many marine organisms [Waples, 1998] or flying animals like bats [Petit et al., 2001]. Summarizing all this, as the relative performance of these two statistics depends on many factors that cannot generally be quantified, it is the use, critical comparison and careful interpretation of both statistics which may give the most valuable information about the genetic structure of populations.

The estimated gene flow (*Nm*) value was greater than 1 in loci *Cisco-126* (1.83) and *Cisco-157* (1.01) and greater than 2 in loci *Cisco-200* (5.22) and *BWF* (2.52). It can be assumed that the number of immigrants to these popu-

lations is sufficient, populations are stable. The same result was obtained in the study of these vendace populations with the RAPD method [Oreha, Škute, 2013]. The potential for migrants from other lakes was limited due to the geographic isolation of the populations in this study. We consider that in the present case, despite the geographical isolation, the value of the estimated gene flow shows that genetic differences between populations are not great and populations retain the similarities of the mother population.

Therefore, we examined cross-species amplification of microsatellites loci but the presence of null allele was not identified in investigated populations, although it was found in analogical investigation. *I*t was found that the four loci *Cisco-126*, *BWF1, Cisco-90* and *Cisco-157* may be used to identify the genetic differentiation of vendace populations, and the level of genetic differentiation of populations which is based on combination of the data of these loci, is sufficiently high. Microsatellites loci *BWF1, Cisco-90, Cisco-126, Cisco-157* and *Cisco-200* can be successfully used for investigation of the genetic structure of vendace populations in Latvian lakes. It was shown, that vendace populations have a sufficiently high level of heterozygosity, the number of alleles on each microsatellite locus is very different, and frequency of alleles in these microsatellite loci is also different in each investigated vendace population.

CONCLUSIONS

The vendace (*Coregonus albula* (L.)) is a fish widely spread in Holarctic waters. At the beginning of the last century, *Coregonus albula* was artificially introduced from lakes Peipus and Ladoga to more than 30 Latvian lakes. At the present moment it can be found only in some Latvian lakes. The lack of basic data on biology and population status of the local vendace populations hinders sustainable utilization of this fish and efforts to manage its reproduction in Latvian lakes. Microsatellites are successfully used for genetic studies of different *Coregonus* species, as well as for the monitoring, protection and management of these species. The cross-species amplification of 14 microsatellites loci (*Cocl-Lav22, Cocl-Lav23, Cisco-59, Cisco-106, Cisco-90, Cisco-126, Cisco-157, Cisco-179, Cisco-181, Cisco-183, Cisco-200, BWF1, BWF2, C4-183*) which was successfully used for genetic studies of different *Coregonus* species, was examined. Five microsatellite markers (*BWF1, Cisco-90, Cisco-126, Cisco-157* and *Cisco-200*) had a good representation in populations of vendace from these Latvian lakes: Sventes, Rāznas, Nirzas, Drizis, Stirnu, Alūksnes, Ežezers. The investigation of polymorphism of microsatellites in seven Latvian lakes showed the variability of microsatellites in different lakes and an analogical trend of these loci in Canadian and German cisco. It was assumed that these alleles may play an important role in the genome function and evolution of cisco. The utility of microsatellites *BWF1, Cisco-90, Cisco-126, Cisco-157* and *Cisco-200* for the genetic study of vendace in population from Latvian lakes was examined. The observed and expected heterozigosity (H_{obs} and H_{exp}), population structuring (F_{ST} and R_{ST}), gene flow (Nm) in Latvian vendace populations was studied. It was shown that vendace populations have a sufficiently high level of heterozygosity and the level of genetic differentiation of vendace populations in Latvian lakes is also quite high.

The four loci (*Cisco-126*, *BWF1, Cisco-90* and *Cisco-157*) may be used to identify the genetic differentiation of vendace populations.

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