

Development of Polymorphic Microsatellite Markers from AFLP Products in the Xinjiang Arctic Grayling (*Thymallus arcticus grubei*) and a Test of Cross-Species Amplification

Yun-Guo Liu^{1,2,*} , Ling-Xiao Liu², Wen-Juan Shan¹, Jun Li¹, Wei Meng¹, Yao-Yao Li¹, Qing-Dian Han^{2,*}, Xiao-Ming Qu³

¹Xinjiang University, College of Life Sciences and Technology, Urumqi 830046, China;

²Linyi University, College of Life Sciences, Linyi 276000, China

³Liaoning Center for Disease Control and Prevention, Shenyang 110005, China

Article History

Received 12 November 2017

Accepted 24 April 2018

First Online 14 May 2018

Corresponding Author

Tel.: +086.9918582554

E-mail: yguoliu@163.com

Keywords

Thymallus arcticus grubei

Microsatellite markers

Cross-species amplification

Abstract

The population of Xinjiang arctic graylings (*Thymallus arcticus grubei*) has dramatically declined in China. A total of 22 polymorphic microsatellite loci were isolated and characterized from AFLP products in the Xinjiang arctic grayling. The number of alleles (Na) per locus varied from 3 to 13. Observed (H_o) and expected (H_e) heterozygosities ranged from 0.60 to 0.97, and from 0.58 to 0.89, respectively. These new microsatellite markers are a helpful tool for genetic analyses, stock management, and resource conservation efforts for *T. arcticus grubei*. According to the total number of alleles, the total effective number of alleles, and the total number of genotypes, the Fuyun population showed the highest diversity among all the populations while the Fuyun sample was the lowest. Five additional fish species: Red seam bream (*Pagrus major*), Lenok (*Brachymystax lenok*), Sea perch (*Lateolabrax japonicus*), Taimen (*Hucho taimen*), and Amur grayling (*Thymallus grubii*) were assessed for cross-species amplification. Three out of the five species showed at least two polymorphic loci. In addition, six loci were found to be polymorphic in at least one species.

Introduction

The Xinjiang arctic grayling, *Thymallus arcticus grubei*, one of the salmonid fishes, naturally occurs in the Xinjiang Irtysh River basin, China (Liu, Liu, & Wang, 2016). However, fisheries have reported heavily declined populations in China, due mainly to human activities, such as, but not limited to overfishing, coastal development, and environmental pollution (Liu *et al.*, 2016). Thus, it's key to protect the natural resources of *T. arcticus grubei*. In the long run, a comprehensive understanding of the genetic diversity, population structure, and genetic differentiation of *T. arcticus grubei* is required to create management plans for conservation (Liu *et al.*, 2016). Microsatellites, or simple sequences repeats (SSR), are widely distributed throughout the genomes of animals, plants, and microbes (Zeng *et al.*, 2013; Zhao, Zhao, & Peng, 2014;

Xin *et al.*, 2016). Microsatellites are highly variable and most are thought to be selectively neutral. Therefore, microsatellites have become the marker of choice for gene studies and genome evolution for all taxa. Many studies have examined the genetics of salmonid fishes using microsatellite markers in recent years (Kordichevaet *al.*, 2010; Khrustaleva, Volkov, Stocklitskaya, Mogue, & Zelenina, 2010; Afanasiev, Rubtsova, Shitova, Shaikhaev, & Zhivotovskii, 2011; Shaikhaev & Zhivotovsky, 2014; Rubtsovaet *al.*, 2016); however, many microsatellite sequences in GenBank for *T. arcticus grubei* are still unknown. We must screen for more polymorphic microsatellite markers in *T. arcticus grubei* in order to improve fine-scale population structure, stock management and enhancement, genetic linkage map construction, and molecular marker-assisted breeding. In this study, we isolated 22 polymorphic microsatellite markers derived

from *T. arcticus grubei* to develop a batch of microsatellite markers and to assess the genetic variability of natural populations of *T. arcticus grubei*.

Materials and Methods

Fish Sampling

The Xinjiang arctic grayling samples were collected from Fuhai county (Fuh), Habahe county (Hab), and Fuyun county (Fuy) in Xinjiang Irtysh River basin, Aletai, China in August, 2015. Geographic locations and sample sizes are shown in Figure 1. The samples of *Pagrus major*, *Brachymystax lenok*, *Lateolabrax japonicus*, *Hucho taimen*, and *Thymallus grubii* were collected from Qingdao in the Shandong province, Linjiang in the Jilin province, Rizhao in the Shandong province, Tumen in the Jilin province, and Mohe in the Heilongjiang province in China, respectively.

DNA Extraction

DNA extraction was performed as described by Liu, Chen, and Li (2005a) and Liu, Chen, Li, Wang and Liu (2005b) with minor modifications. DNA was collected after brief centrifugation and was washed twice with 70% ethanol, air-dried, and redissolved in double distilled water. The concentrations were measured with a GENEQUANT Pro (Pharmacia Biotech Ltd, Cambridge, England) RNA/DNA spectrophotometer for absorption at 260 nm.

Microsatellite Sequence Screening

Procedures of AFLP analysis were based on Voset *al.* (1995) with some modifications. About 120 ng of total DNA was digested with 5U of EcoRI and MseI in 1× NE buffer 2 at 37°C for 3 h. To generate the DNA template for subsequent PCR amplification, the digested DNA fragments were ligated with 2.5 pmol of EcoRI and 25 pmolMseI adapters in a reaction mixture containing 0.25 mg BSA, 5 pmol ATP, 0.05 U T4Dnase, and 10 × NE buffer 2 at 37°C for 8 h. The sequences for the EcoRI primer were 5'-GACTGCGTACCAATTC-3', and for the MseI primer, the sequences were 5'-GATGAGTCCTGAGTAA-3'. Co-dominant AFLP bands were hand selected, excised from the dried gel, and placed individually into tubes containing 0.25 ml of TE buffer as described by Liu, Liu, Li, and Li (2009) with minor modifications. The gel pieces were then incubated for 3 h at 57°C to elute the DNA fragments. Then, the incubation buffer was stored at 5°C before being used as a template for PCR re-amplification of the AFLP bands. The re-amplified PCR products were then checked with agarose gel (1.2%) electrophoresis and purified with a purification kit (Qiagen, Germany). The purified PCR products were ligated into T-vectors and then transformed to *E. coli* of DH5α for the next sequencing (Lunt, Hutchinson, & Carvalho, 1999; Yokota & Oishi, 1990). We sequenced 160 randomly selected clones of recombinant *E. coli* of DH5α. Microsatellite sequences were screened using Tandem Repeats Finder (version: 2.02) (Benson, 1999). Tandem Repeats Finder's standardized identification of

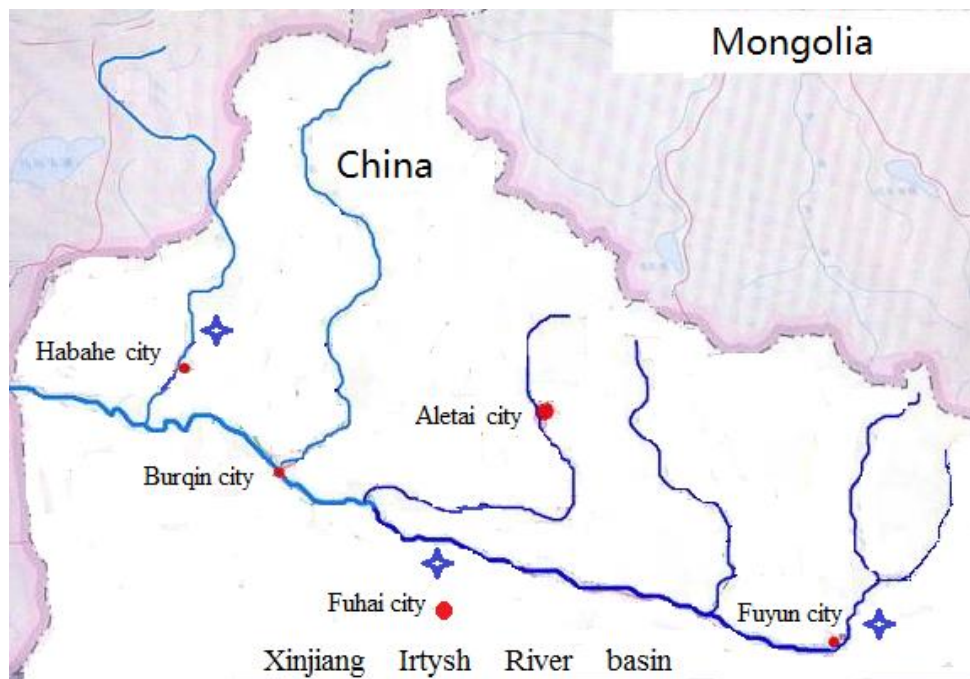


Figure 1. Geographic origin of Xinjiang arctic grayling (*Thymallus arcticus grubei*) samples. Fuh, Fuhai county (n=30); Hab, Habahe county (n=30); Fuy, Fuyun county (n=30).

microsatellites was 8 or more repeats for dinucleotide repeat sequences, 5 or more repeats for trinucleotide repeat sequences, and 4 or more repeats for tetranucleotide repeat sequences.

Microsatellite Amplification and Polymorphism Detection

Microsatellite amplification was performed as described by Liu, Guo, Hao, and Liu (2012). PCR was performed in a 25- μ l reaction mixture composed of 10 pmol of each primer set, 100 μ M of dNTPs, 10 mM Tris-HCl (pH 8.3), 50 mM KCl, 2.0 mM MgCl₂, about 1.2 unit of Taq polymerase (Sangon Corp.), and approximately 150 ng of template DNA. PCR cycles were performed according to procedure described by Liu *et al.* (2012). Microsatellite polymorphism was detected using ABI 377 automated DNA sequencer.

Data Analysis

ARLEQUIN 3.0 (Excoffier, Laval, & Schneider, 2005) and POPGENE 1.3.1 (Yeh, Yang, & Boyle, 1999) were used to calculate observed (H_o) and expected (H_e) heterozygosities and linkage disequilibrium, respectively. Significance values for all tests were corrected following Sequential Bonferroni procedure (Rice, 1989). The Hardy-Weinberg equilibrium (HWE) at each locus was assessed by a test analogous to the Fisher's exact test using the Markov-chain method (the Markov-chain parameters used were: steps, 100,000; dememorization, 10,000).

Results

A total of 95 microsatellites were found of which 62 pairs of primers were designed and tested. A total of 22 microsatellite markers were found to be polymorphic among 30 individuals of *T. arcticus grubei* collected from the Xinjiang Irtysh River in China. The number of alleles per locus ranged from 3 (XBJH02) to 13 (XBJH17), and the observed and expected heterozygosity ranged from 0.60 to 0.97 and from 0.58 to 0.89, respectively (Table 1). All the loci conformed to Hardy-Weinberg equilibrium (HWE) was determined with the Markov-Chain method. Out of 231 possible pairwise comparisons between the 22 loci applied to *T. arcticus grubei*, none showed significant linkage disequilibrium. Considerable differences were found among Fuh, Hab, and Fuy populations in the number of alleles, effective number of alleles, and number of genotypes at all loci (Table 2). In regard to total number of alleles, total effective number of alleles, and total number of genotypes, the Fuh population showed the highest diversity among all the samples while the Fuy sample was the lowest. These new microsatellite markers are a helpful tool for genetic analyses of and resources conservation efforts for *T. arcticus grubei*.

The method is also practically efficient in rapid screening of polymorphic microsatellite markers based on AFLP products from aquaculture resources.

Cross-species PCR amplification was tested on five other fishes using the same methodology like for *T. arcticus grubei*. All primer pairs were tested on 30 individuals from each of the five species: Red seabream (*Pagrus major*), Lenok (*Brachymystax lenok*), Sea perch (*Lateolabrax japonicus*), Taimen (*Hucho taimen*), and Amur grayling (*Thymallus grubii*). In traditional taxonomy, each represents five different species from distant species to interrelated species. Three out of the five species (*Brachymystax lenok*, *Hucho taimen*, and *Thymallus grubii*) showed at least two polymorphic loci. In addition, six loci were found to be polymorphic in at least one species. The results, summarized in Table 3, highlight the potential of some microsatellite markers of *T. arcticus grubei* being used in studies on other fish species. Eleven microsatellite loci have amplification products, and five are polymorphic in the Amur grayling. Thus, the Xinjiang arctic grayling may have a closer phylogenetic relationship with the Amur grayling and a more distant ancestry, as denoted by no polymorphic amplification, to Red seam bream and Sea perch.

Discussion

Vos *et al.* (1995) proved that the AFLP technique is a PCR-based DNA fingerprinting that can rapidly identify thousands of band polymorphisms associated with restriction sites and has been successfully applied to a wide range of organisms. The AFLP polymorphisms usually include microsatellites: indels (insertions and deletions) and SNPs (Liu *et al.*, 2015; Bradeen & Simon, 1998). Therefore, polymorphic AFLP products contain many co-dominant bands caused by microsatellite sequences. Typically, microsatellite markers have been isolated from small insert size of genomic libraries of the species of interest, screening hundreds of clones through hybridization with repeat containing probes (Rassmann, Schlotterer, & Tautz, 1991). However, it requires southern hybridization, which is time-consuming. If sequenced randomly without hybridizing for microsatellite enrichment, the yield of microsatellite-containing sequences is low. We utilized a fast and effective protocol in this study for quick isolation of sequences containing microsatellite repeats from co-dominant AFLP bands of *T. arcticus grubei*. This method is very effective in amplifying large amounts of DNA in a suitable size for direct cloning and sequencing. Despite lacking library construction and hybridization screening, the method ended with a relative high microsatellite yield (Liu *et al.*, 2007). We sequenced a total of 160 clones from co-dominant AFLP bands of *T. arcticus grubei*, and 95 microsatellite-containing sequences were obtained. Nearly 60% of clones contained microsatellites. However, only 22

Table 1. Characterization of twenty twopolymorphic microsatellite lociderived from *Thymallus arcticus grubei*

Locus	Repeat sequence	Primer sequences (5'-3')	Ta (°C)	Na (size range, bp)	H _o	H _e	P	Accession no.
XJBH01	(AC) ₈	F: GGTGAAAGAAAGAGGGAGGG R: AGCCCTCACCAAGATGAGAA	58	4 (230-310)	0.73	0.70	0.663	KY471332
XJBH02	(TAGA) ₇	F: CCTTTTATGCATTTCTGTGGG R: TTTGTGCACTTTCGTCTGG	57	3 (130-180)	0.90	0.88	0.165	KY471333
XJBH03	(CA) ₉	F: TCACACATCTGGCTGTCAT R: TCCCAGATAGTCGTC AAGG	58	7(190-230)	0.67	0.58	0.231	KY471334
XJBH04	(GA) ₇	F: GATGACCAGCAGGGTCAAAT R: ATGACTCCTAGCTGTCCCA	56	5(200-240)	0.67	0.64	0.102	KY471335
XJBH05	(GA) ₁₅	F: ATTACAGAAAACCCCTCCG R: TCTCTCTCTCGCTCTGCC	59	9 (250-290)	0.60	0.59	0.376	KY471336
XJBH06	(CCAT) ₆	F: GCAAAGAAACCTGCTTGAG R: TCCGTTCTCAGAAACAGT	57	4(130-180)	0.77	0.68	0.089	KY471337
XJBH07	(GT) ₁₂	F: GCAATGATTTTGAGTGGTG R: ATCCCTCTGGTGTGTC AAA	58	6 (110-150)	0.97	0.89	0.192	KY471338
XJBH08	(TATC) ₇	F: TCGGGATTGCTAAGCTCT R: GCCAGCAAGGTTGATTGATT	57	6 (100-150)	0.90	0.86	0.410	KY471339
XJBH09	(ATAG) ₁₈	F: CTTTCGACCAATCACACCCT R: ACAAAGAAATTTCCCTCCG	56	12 (130-170)	0.83	0.75	0.225	KY471340
XJBH10	(GT) ₉	F: TTTTGACCAGGACCCATAGC R: CTTACACCTGGCTGGTCACA	58	8(250-290)	0.87	0.82	0.921	KY471341
XJBH11	(AG) ₁₀	F: CCAGCTGAGAGAGGGAGAGA R: AGTTGTCCCAGGTTCAAACG	56	5 (220-270)	0.67	0.63	0.476	KY471342
XJBH12	(GA) ₁₂	F: GCCATAACCAGCCTCTCAAA R: ACTGCAGTCCCAGAGATGCT	56	6 (230-270)	0.87	0.82	0.202	KY471343
XJBH13	(GT) ₁₃	F: TCACATCTTTAGTTGTGCATGTG R: TGAGGACCAAGGGAACAATC	55	8 (140-180)	0.80	0.75	0.305	KY471344
XJBH14	(CA) ₁₀	F: CCCAGGACAGTCATACCAC R: GTTCCCCTCCACTAATGGC	58	7(110-160)	0.77	0.71	0.166	KY471345
XJBH15	(TTAC) ₇	F: AGCTCATGAAACATGGGACC R: CGGGAGAGAGACTAGCCCTT	57	4(160-190)	0.90	0.85	0.094	KY471346
XJBH16	(GAT) ₁₄	F: GCACATTTTGATGTATGCC R: TGTGTTTTTGAAGCAGGCAC	56	5 (170-200)	0.87	0.79	0.361	KY471347
XJBH17	(TCAC) ₉	F: GAGTTTGAACCGATTGGGA R: CCAAGAATGCTGGAGGTGAT	58	3(230-270)	0.87	0.83	0.136	KY471348
XJBH18	(TATC) ₂₃	F: TGCTCTGGTAGTAGGACCTGG R: CAGCCAACGCACATTTATCA	55	13(190-230)	0.80	0.74	0.239	KY471349
XJBH19	(AG) ₁₀	F: ATGCCTTTTGCACCTCCTT R: AGAAATGTCTCTCGGGGAT	57	5(250-310)	0.80	0.76	0.702	KY471350
XJBH20	(AG) ₁₁	F: CCTGGACACTCAGCATCTCA R: GCACGTTATTGGAGGGAAGA	58	7(150-190)	0.87	0.73	0.094	KY471351
XJBH21	(AG) ₁₃	F: ACTGTGGGAGAGGAAGGGAT R: AGTAGGCTCTGGCTGTCTGG	57	7(120-160)	0.83	0.75	0.296	KY471352
XJBH22	(CA) ₁₀	F: CCGTTGTGAAAGTGAACCTT R: TGGACCTGCATGTGTCTGAT	59	9(170-210)	0.70	0.62	0.179	KY471353

Ta is annealing temperature (°C); Na is number of alleles; H_o is observed heterozygosity; H_e is expected heterozygosity.

microsatellite sequences, approximately 23%, showed polymorphic loci. The other microsatellites had inappropriate flanking regions on one or both sides of the simple sequence repeats or contained only a few repeats and thus, had less potential for polymorphism. The Fuh population showed the highest diversity among all the populations based on the analysis using the microsatellite markers. This phenomenon might be a result of the Fuh population that was sampled from Fuhai county, located at the middle place of the Irtysh River. The geographic proximity increased the chance of gene flow between the Hab population and Fuy population.

Microsatellite loci have ancient origins and show considerable evolutionary conservation, suggesting that microsatellite primers developed for any single locus may often be useful across a wide range of taxa (Liu *et al.*, 2009). For example, Liu *et al.* (2007) tested cross-species amplification of 68 existing microsatellite loci in 6 species of the Sparidae family: *Acanthopagrus butcheri*, *Sparus aurata*, *Pagrus auratus*, *Chrysophrys major*, *Pagellus bogaraveo*, *Pagellus erythrinus*, and one species of Bothidae, *Paralichthys olivaceus*. Of the 68 loci screened, sixteen were found to be polymorphic when tested in 20 individual black sea bream, or *Acanthopagrus schlegeli*. Cross-species amplification is

Table 2. Allelic variability at twenty two microsatellite loci in three different populations of *Thymallus arcticus grubei*

Microsatellite Loci	Populations								
	Fuh			Hab			Fuy		
	A	a _e	G	A	a _e	G	A	a _e	G
XJBH01	5	4.16	8	5	4.09	8	4	3.02	6
XJBH02	5	4.13	8	4	3.88	6	3	2.23	5
XJBH03	6	5.56	9	6	5.23	9	6	4.87	9
XJBH04	6	4.15	9	5	3.70	7	5	3.51	7
XJBH05	11	8.22	14	10	7.92	12	9	7.46	10
XJBH06	4	2.92	6	4	2.92	4	4	2.77	4
XJBH07	6	4.73	7	6	4.67	6	5	4.46	6
XJBH08	8	5.33	10	7	4.65	9	7	4.29	9
XJBH09	13	8.90	14	13	8.32	14	12	7.73	12
XJBH10	8	5.74	10	8	5.68	10	8	5.68	10
XJBH11	7	5.16	5	5	3.76	5	4	3.04	4
XJBH12	7	4.64	11	7	4.13	9	5	3.93	6
XJBH13	9	5.34	13	8	5.20	12	8	5.02	11
XJBH14	7	4.15	7	7	4.15	7	7	3.89	7
XJBH15	5	3.65	6	4	2.56	6	3	2.27	4
XJBH16	6	3.34	8	6	3.10	8	6	2.195	6
XJBH17	4	2.23	6	3	1.89	4	3	1.89	4
XJBH18	13	8.97	15	13	8.25	15	10	7.13	12
XJBH19	6	4.18	6	5	3.30	6	4	3.01	5
XJBH20	8	6.55	10	8	6.64	10	8	6.39	10
XJBH21	8	4.67	9	7	4.52	9	6	3.94	8
XJBH22	9	7.29	12	9	7.06	12	8	6.49	10
Total	161	101.46	203	150	97.3	188	135	87.49	165

Number of alleles per locus (A), Effective number of alleles (a_e), Number of genotypes (G), are given for each population and locus.

Table 3. Cross-species amplification and PCR product size range of twenty two microsatellite loci from *T. arcticus grubei* in different fish species of the vertebrates including *Pagrus major*, *Brachymystax lenok*, *Lateolabrax japonicus*, *Hucho taimen*, *Thymallus grubii*

Locus	<i>Pagrus major</i>	<i>Brachymystax lenok</i>	<i>Lateolabrax japonicus</i>	<i>Hucho taimen</i>	<i>Thymallus grubii</i>
XJBH01	0	0	0	0	0
XJBH02	0	0	0	1	0
XJBH03	0	0	0	0	0
XJBH04	0	1	0	0	0
XJBH05	1*	1*	1*	3 (250-290)	1*
XJBH06	0	0	1†	1†	0
XJBH07	0	0	0	1	1
XJBH08	0	2(100-130)	0	0	2(100-130)
XJBH09	0	0	0	0	1
XJBH10	0	2 (270-280)	0	3(270-290)	2 (270-280)
XJBH11	0	0	0	0	0
XJBH12	1†	1	1†	0	3 (230-270)
XJBH13	0	1	0	0	0
XJBH14	0	0	0	0	0
XJBH15	0	0	0	0	5 (160-190)
XJBH16	0	0	0	0	0
XJBH17	0	0	0	1	1
XJBH18	0	1	0	0	0
XJBH19	0	2 (250-310)	0	3 (250-300)	5 (250-310)
XJBH20	0	0	0	0	1
XJBH21	0	0	0	0	0
XJBH22	0	0	0	0	1

The number in each cell indicates the number of observed alleles; "0" indicates no amplification or smear only; "*" indicates larger than expected size; "†" indicates smaller than expected size.

a practical method to extend the utilization of microsatellite markers. Although cross-species amplification is convenient, it may lead to low or incomplete amplification, since as little as a single dinucleotide mismatch between the primer and the target DNA sequences could lead to erroneous results (Zane, Bargelloni, & Patarnello, 2002). This problem can often be resolved by employing less stringent polymerase chain reaction (PCR) conditions such as lowering the annealing temperature or increasing the magnesium concentration in the reaction (Liu *et al.*, 2007). In this study, three microsatellite loci show polymorphism in Taimen and Lenok. Other studies have reported that they have a polymorphic amplification product in closely related species in cross-species amplification of microsatellite markers (Dallimer, 2015; Delghandiet *al.*, 2016).

In conclusion, the findings of this study prove the usefulness of co-dominant AFLP bands as a valuable source for the identification of microsatellite from the Xinjiang arctic grayling. The polymorphic microsatellite loci developed in this study for *T. arcticus grubei* should be used in the future studies of systematic and population genetics in this endangered species. Cross-species amplification on five other fishes indicates that some Xinjiang arctic grayling microsatellite loci are conservative in closely related species.

Acknowledgements

This work was supported by grants from the National Natural Science Foundation of China (31560719), the Natural Science Foundation of Xinjiang Uygur Autonomous Region (2015211C261), and the project of domestic visiting scholars for young College Backbone Teachers in Shandong province (SD2014).

References

- Afanasiev, P.K., Rubtsova, G.A., Shitova, M.V., Shaikhaev, E.G., & Zhivotovskii, L.A. (2011). Extension of a set of microsatellite markers for more precise identification of chum salmon *Oncorhynchus keta* Walbaum. *Russian Journal of Genetics*, 47(11), 1307-1313. <http://dx.doi.org/10.1134/S1022795411110020>
- Benson, G. (1999). Tandem repeats finder: a program to analyze DNA sequences. *Nucleic Acids Research*, 27, 573-580. <http://dx.doi.org/10.1093/nar/27.2.573>
- Bradeen, J.M., & Simon, P.W. (1998). Conversion of an AFLP fragment linked to the carrot Y2 locus to a simple codominant PCR-based marker form. *Theoretical and Applied Genetics*, 97, 960-967. <http://dx.doi.org/10.1007/s001220050977>
- Dallimer, M. (2015). Cross-species amplification success of avian microsatellites in the redbilled quelea *Quelea quelea*. *Molecular Ecology*, 8(4): 695-698. <http://dx.doi.org/10.1046/j.1365-294x.1999.00877.x>
- Delghandi, M., Hasifa, A., Manal Saif Nasser, A.H., Rafaida Dhuai Gharib, A.B., Dean R.J., & Hoc Tan, D. (2016). Novel Polymorphic Microsatellite Markers for *Panulirus ornatus* and their Cross-species Primer Amplification in *Panulirus homarus*. *Animal Biotechnology*, 27(4), 310-314. <http://dx.doi.org/10.1080/10495398.2016.1190372>
- Excoffier, L., Laval, G., & Schneider, S. (2005). Arlequin (version3.0): an integrated software package for population genetics data analysis. *Evolutionary Bioinformatics Online*, 1, 47-50. <http://creativecommons.org/licenses/by/3.0/>
- Khrustaleva, A.M., Volkov, A.A., Stocklitskaya, D.S., Mugue, N.S., & Zelenina, D.A. (2010). Comparative analysis of STR and SNP polymorphism in the populations of sockeye salmon (*Oncorhynchus nerka*) from Eastern and Western Kamchatka. *Russian Journal of Genetics*, 46(11), 1362-1372. <http://dx.doi.org/10.1134/S1022795410110128>
- Kordicheva, S.Y., Rubtsova, G.A., Shitova, M.A., Shaikhaev, G.O., Afanasiev, K.I., & Zhivotovsky, L.A. (2010). A search for null alleles at the microsatellite locus of chum salmon (*Oncorhynchus keta* Walbaum). *Russian Journal of Genetics*, 46(8), 1019-1022. <http://dx.doi.org/10.1134/S1022795410080168>
- Liu, J., Qu, J., Yang, C. Tang, D., Li, J., Lan, H., & Rong, T. (2015). Development of genome-wide insertion and deletion markers for maize, based on next-generation sequencing data. *BMC Genomics*, 16, 601. <http://dx.doi.org/10.1186/s12864-015-1797-5>
- Liu, Y.G., Chen, S.L., & Li, B.F. (2005a). Assessing the genetic structure of three Japanese flounder (*Paralichthys olivaceus*) stocks by microsatellite markers. *Aquaculture*, 243, 103-111. <http://dx.doi.org/10.1016/j.aquaculture.2004.10.024>
- Liu, Y.G., Chen, S.L., Li, B.F., Wang, Z. J., & Liu, Z.J. (2005b). Analysis of genetic variation in selected stocks of hatchery flounder, *Paralichthys olivaceus*, using AFLP markers. *Biochemical Systematics and Ecology*, 33, 993-1005. <http://dx.doi.org/10.1016/j.bse.2005.02.008>
- Liu, Y.G., Guo, Y.G., Hao, J., & Liu, L.X (2012). Genetic diversity of swimming crab (*Portunus trituberculatus*) populations from Shandong peninsula as assessed by microsatellite markers. *Biochemical Systematics and Ecology*, 41, 91-97. <http://dx.doi.org/10.1016/j.bse.2011.12.024>
- Liu, Y.G., Liu, C.Y., Li, F.Z., & Li, Z.X. (2009). Development of Microsatellite Markers in Sea Perch, Lateolabrax japonicus, from Codominant Amplified Fragment Length Polymorphism Bands. *Journal of the World Aquaculture Society*, 40(4), 522-530. <http://dx.doi.org/10.1111/j.1749-7345.2009.00277.x>
- Liu, Y.G., Liu, L.X., & Wang, Y.X. (2016). A review: research progress of development of microsatellite markers and conservation genetics in Graying. *Fisheries Science*, 35(1), 87-92. in Chinese with English abstract. <http://dx.doi.org/10.16378/j.cnki.1003-1111>
- Liu, Y.G., Liu, L.X., Wu, Z.X., Lin, H., Li, B.F., & Sun, X.Q. (2007). Isolation and characterization of polymorphic microsatellite loci in black sea bream (*Acanthopagrus schlegelii*) by cross-species amplification with six species of the Sparidae family. *Aquatic Living Resources*, 20(3): 257-262. <http://dx.doi.org/10.1051/alr:2007038>
- Lunt, D.H., Hutchinson, W.F., & Carvalho G.R. (1999). An efficient method for PCR-based isolation of microsatellite arrays (PIMA). *Molecular Ecology*, 8, 891-894. <http://dx.doi.org/10.1046/j.1365-294X.1999.00636.x>

- Rassmann, K., Schlotterer C., & Tautz, D. (1991). Isolation of simple sequence loci for use in polymerase chain reaction-based DNA fingerprinting. *Electrophoresis*, 12, 113-118. <http://dx.doi.org/10.1002/elps.1150120205>
- Rice, W.R. (1989). Analyzing tables of statistical tests. *Evolution*, 43, 223-225. <http://dx.doi.org/10.1111/j.1558-5646.1989.tb04220.x>
- Rubtsova, G.A., Ponomareva, E.V., Afanasiev, K.I., Shaikhaev, E.G., Kholodova M.V., Pavlov, S.D., & Zhivotovsky L.A. (2016). A detection of allelic variants at microsatellite markers by using capillary and traditional electrophoresis. *Russian Journal of Genetics*, 52(4), 423-427. [http:// dx.doi.org/10.1134/S1022795416040086](http://dx.doi.org/10.1134/S1022795416040086)
- Shaikhaev, E.G., & Zhivotovsky, L.A. (2014). The evolution of microsatellite loci in salmonid fishes. *Russian Journal of Genetics*, 50(8), 853-859. <http://dx.doi.org/10.1134/S1022795414080079>
- Vos, P., Hogers, R., Bleeker, M., Reijans, M., van de Lee, T., Hornes, M., Frijters, A., Pot, J., Peleman, J., & Kuiper, M. (1995). AFLP: a new technique for DNA fingerprinting. *Nucleic Acids Research*, 23, 4407-4414. <https://dx.doi.org/10.1093/nar/23.21.4407>
- Xin, M.M., Zhang, S.H., Wang, D.Q., Li, C.J., Yue, H.M., & Wei, Q.W. (2016). Twenty-four novel microsatellites for the endangered Chinese sturgeon (*Acipenser sinensis* Gray, 1835). *Journal of Applied Ichthyology*, 32, 405-408. <https:// dx.doi.org/10.1111/jai.13071>
- Yeh, F.C., Yang, R.C., & Boyle, T. (1990). POPGENE version 1.3.1. Microsoft window-bases freeware for population genetic analysis. University of Alberta and the Centre for International Forestry Research. <http://www.ualberta.ca/~fyeh/>
- Yokota, H., & Oishi, M. (1990). Differential cloning of genomic DNA: Cloning of DNA with an altered primary structure by in-gel competitive reassociation. *Proceedings of the National Academy of Science*, 87, 6398-6402. <http://dx.doi.org/10.1073/pnas.87.16.6398>
- Zane L., Bargelloni L., & Patarnello, T., (2002). Strategies for microsatellite isolation: a review. *Molecular Ecology*, 11, 1-16. <http://dx.doi.org/10.1046/j.0962-1083.2001.01418.x>
- Zeng, Q., Ye, H., Ludwig, A., Wang, Z., Zhang, Y., & Peng, Z. (2013). Microsatellite development for the endangered Yangtze sturgeon (*Acipenser dabryanus* Dumeril, 1869) using 454 sequencing. *Journal of Applied Ichthyology*, 29, 1219-1221. <http://dx.doi.org/10.1111/jai.12278>
- Zhao, J., Zhao, K., & Peng, Z. (2014). Development and characterization of eleven microsatellite markers for an endangered cavefish (*Triplophysarosa* Chen and Yang, 2005) using 454 sequencing. *Journal of Applied Ichthyology*, 30, 1056-1058. <http://dx.doi.org/10.1111/jai.12474>