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MITOGENOME ANNOUNCEMENT

Complete mitochondrial genomes of the Northern (*Salvelinus malma*) and Southern (*Salvelinus curilus*) Dolly Varden chars (Salmoniformes, Salmonidae)

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Abstract

The complete mitochondrial genomes were sequenced from the Northern and Southern Dolly Varden chars, *Salvelinus malma* and *S. curilus*. The genome sequences are 16,654 bp in size in both species, and the gene arrangement, composition, and size are very similar to the salmonid fish genomes published previously. The level of sequence divergence between *S. malma* and *S. curilus* inferred from the complete mitochondrial genomes is relatively low (1.88%) indicating recent divergence of the species and/or historical hybridization.

Keywords

Arctic char *S. alpinus*, complete mitochondrial genome, hybridization, mtDNA introgression, northern dolly varden char *Salvelinus malma*, salmonids, southern dolly varden char *Salvelinus curilus*

History

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The Dolly Varden chars *Salvelinus malma* Walbaum and *S. curilus* Pallas (or *S. malma kraschenninnikovi* Taranetz) have wide distribution in coastal marine and freshwaters of the Arctic and Pacific (details for species range see in Behnke, 1980; Chereshnev et al., 2002). The taxonomic status of the Dolly Varden chars was investigated intensively using different types of genetic markers (review in Salmenkova & Omelchenko, 2013). There were no fixed differences detected between the Southern and Northern forms with allozyme (Omelchenko et al., 2002) and microsatellite (Gordeeva et al., 2010) markers. However, using PCR-RFLP mtDNA analysis, Oleinik et al. (2007) detected a significant level of divergence between the forms (4%). The last authors included the *ND6* gene in their analysis that has quite different evolutionary properties from those of the other 12 protein genes, making it an inappropriate mix with model-based methods (e.g. Zardoya & Meyer, 1996).

We have sequenced the complete mitochondrial genomes of *S. malma* (GenBank accession number KJ746618) from the Bystraya river (Kamchatka, Russia) and *S. curilus* (GenBank accession number KJ746619) from the Tumen River (Khabarovsk region, Russia) to increase the power of phylogenetic analysis of this complex salmonid group. We used primers previously developed for *S. alpinus* (Doiron et al., 2002) and primers designed for *S. malma* and *S. curilus* with the program mitoPrimer_V1 (Yang et al., 2011). Both approaches yielded identical sequences. The sizes of the genomes are the same (16,654 bp) in both species (Table 1) and the gene arrangement,

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Table 1. Characteristics of the mitochondrial genome of *Salvelinus malma* (isolate SMM208) and *S. curilus* (isolate SMK33).

	Salvelinus malma			*Salvelinus curilus*		
Gene	Strand*	Position	Size	Strand*	Position	Size
D-loop	H	1–995	995	H	1–994	994
tRNA-Phe	H	996–1063	68	H	995–1062	68
12S rRNA	H	1064–2010	947	H	1063–2009	947
tRNA-Val	H	2011–2082	72	H	2010–2081	72
16S rRNA	H	2083–3761	1679	H	2082–3760	1679
tRNA-Leu	H	3762–3836	75	H	3761–3835	75
nad1	H	3837–4811	975	H	3836–4810	975
tRNA-Ile	H	4818–4889	72	H	4817–4888	72
tRNA-Gln	L	4887–4957	71	L	4886–4956	71
tRNA-Met2	H	4957–5025	69	H	4956–5024	69
nad2	H	5026–6075	1050	H	5025–6074	1050
tRNA-Trp	H	6076–6147	72	H	6075–6146	72
tRNA-Ala	L	6149–6217	69	L	6148–6216	69
tRNA-Asn	L	6219–6291	73	L	6218–6290	73
Oril	L	6292–6327	36	L	6291–6326	36
tRNA-Cys	L	6328–6394	67	L	6327–6393	67
tRNA-Tyr	L	6395–6465	71	L	6394–6464	71
cox1	H	6467–8017	1551	H	6466–8016	1551
tRNA-Ser	L	8018–8088	71	L	8017–8087	71
tRNA-Asp	H	8093–8166	74	H	8092–8165	74
cox2	H	8180–8870	691	H	8180–8870	691
tRNA-Leu	H	8871–8944	74	H	8871–8944	74
atp8	H	8946–9113	168	H	8946–9113	168
atp6	H	9104–9787	684	H	9104–9787	684
cox3	H	9787–10,572	786	H	9787–10,572	786
tRNA-Gly	H	10,572–10,641	70	H	10,572–10,641	70
nad3	H	10,642–10,990	349	H	10,642–10,990	349
tRNA-Arg	H	10,991–11,060	70	H	10,991–11,060	70

(*continued*)

Table 1. Continued

	Salvelinus malma			*Salvelinus curilus*		
Gene	Strand*	Position	Size	Strand*	Position	Size
nad4l	H	11,061–11,357	297	H	11,061–11,357	297
nad4	H	11,351–12,731	1381	H	11,351–12,731	1381
tRNA-His	H	12,732–12,800	69	H	12,732–12,800	69
tRNA-Ser	H	12,801–12,869	69	H	12,801–12,869	69
tRNA-Leu	H	12,871–12,943	73	H	12,871–12,943	73
nad5	H	12,944–14,782	1839	H	12,944–14,782	1839
nad6	L	14,779–15,300	522	L	14,779–15,300	522
tRNA-Glu	L	15,301–15,369	69	L	15,301–15,369	69
Cob	H	15,373–16,513	1141	H	15,373–16,513	1141
tRNA-Thr	H	16,514–16,585	72	H	16,514–16,585	72
tRNA-Pro	L	16,585–16,654	70	L	16,585–16,654	70

*H and L refer to genes located in the heavy strand and light strand, respectively.

composition, and size are very similar to the salmonid fish genomes published previously. The A+T base composition, 54.5% and 54.4% was higher than G+C, 45.5 and 45.6% in *S. malma* and *S. curilus*, respectively. The level of divergence between *S. malma* and *S. curilus* inferred from the complete mitochondrial genomes was relatively low, 1.88%. However, the level of divergence inferred from the 12 protein-coding genes (excluding *ND6*) was higher, 2.24%, supporting their status as valid biological species, despite recent divergence and/or historical hybridization (review in Salmenkova & Omelchenko, 2013). A low level of sequence divergence ($D_{xy} = 0.0074 \pm 0.0005$) was also detected between the genome of *S. malma* and the GenBank complete mitochondrial genome of the Arctic char *S. alpinus* (AF154851), but significantly higher between *S. curilus* and *S. alpinus* ($D_{xy} = 0.0196 \pm 0.0010$). The observed gradient of sequence divergence between *S. malma*, *S. curilus*, and *S. alpinus* could be explained by interspecific replacement of mtDNA and gene introgression (Shedko et al., 2007), as it has been found for *S. alpinus* and *S. fontinalis* (e.g. Bernatchez et al., 1995).

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Declaration of interest

The authors report no conflict of interest. The authors alone are responsible for the content and writing of the paper.

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