Genetic diversity, population structure and phylogeography of Pacific salmon inferred from molecular genetic analyses

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Distribution of chum and masu salmon in the North Pacific

OBJECTIVES
◆ To analyze the genetic population structure and phylogeography
◆ To understand evolutionary process of two species using mtDNA and msDNA markers

Life history of two species:
Chum salmon – anadromous only
Masu salmon – anadromous (♀ > ♂)
non-anadromous (♀ < ♂)
(♀ ≒ ♂ in north)

From Kato (1991)

From Salo (1991)
Detection of genetic polymorphisms

DNA extraction

liver blood adipose fin

Nucleotide sequencing

Nuclear DNA Mitochondrial DNA PCR amplification

Microsatellite DNA

PCR-RFLP

Allozyme
Geographical hierarchy in genetic population structure of Pacific Rim chum salmon based on mtDNA data

ca. 450bp 5’ portion of the control region: 32 haplotypes

AMOVA
(96 populations; >4,200 fish)

Russia
28.97% (p<0.001)

Japan
7.83% (p<0.001)

North America
2.05% (p<0.001)

Among three regions
68.7% (p<0.001)

Haplotype diversity: JAP: 0.59 > RUS: 0.36 > NAM: 0.24

(Yoon et al. 2008)
Geographic structure of Pacific Rim chum salmon populations based on msDNA data from 5 loci

Among three regions:
- North America: 5.27% (p < 0.001)
- Japan: 0.59% (p < 0.01)
- Russia: 4.29% (p < 0.001)

Gene diversity:
- Japan: 0.71
- Russia: 0.48
- North America: 0.43

AMOVA (75 populations) (Yoon et al. 2009)
AMOVA and pairwise $F_{ST}$ estimates for genetic differentiation of chum salmon populations

- Sea of Okhotsk: $-0.0$~$0.24$
- Bering Sea: $0.0$~$0.2$
- Gulf of Alaska: $0.0$~$0.35$
- Sea of Japan: $0.0$~$0.43$

Among 4 regions: $68.0\%$

(Yoon et al. 2008)
Genetic differentiation of chum salmon within the Yurappu River

Egg introduction from indicated rivers

1952~1995

(Yokotani et al. 2009)

mtDNA

msDNA
AMOVA with 21 mtDNA haplotypes (ca. 560bp of ND5) and 6 msDNA loci in masu salmon (24 populations)

- Japan vs. Korea vs. Russia
- Sea of Japan vs. Sea of Okhotsk vs. Pacific Ocean

(Yu et al. 2010a)

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<td>1.65%</td>
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<td>(P&lt;0.001)</td>
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Large geographical population groups besides traditional grouping by country
Genetic diversity of masu salmon in the Far East

A) Haplotype diversity - mtDNA ND5

Japan

Russia

Korea

B) Expected (he) and observed heterozygosity (ho) – msDNA
Genetic diversity in hatchery stocks and mother populations of masu salmon

Haplotype diversity (mtDNA)
Gene diversity (msDNA)

River populations
Hatchery stocks
**Genetic differentiation among hatchery stocks and spawning populations ($F_{ST}$)**

Below diagonal: msDNA  
Above diagonal: mtDNA

*P<0.05, **P<0.001 (Bonferroni correction)

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Comparison with mother populations

Between hatchery stocks

Genetic differentiation among hatchery stocks and spawning populations ($F_{ST}$)
Neighbor-joining population tree by mtDNA and msDNA

A) mtDNA

B) msDNA

Sea of Okhotsk  Sea of Japan  Hatchery stocks
Pairwise genetic and geographical distance measures in chum salmon

mtDNA

Japan; \( r=0.307, P<0.01 \)

Russia; \( r=0.478, P<0.001 \)

North America; \( r=0.302, P<0.001 \)

msDNA

Japan; \( r=0.128, P>0.1 \)

Russia; \( r=-0.120, P=0.89 \)

North America; \( r=0.243, P<0.001 \)

(Yoon et al. 2008)
Pairwise genetic and geographical distance measures in anadromous masu salmon

mtDNA: $r = 0.0081, P > 0.05$

No significant correlation between genetic and geographical distance

msDNA: $r = 0.439, P < 0.001$

Significant correlation between genetic and geographical distance

Restricted gene flow with isolation by distance

(Yu et al. 2010a)
 Nested clade phylogeographical analysis (NCPA)

A: crude nested design

B: haplotype distribution

C: geographic distance

Speculation of historical event in population structure
Nested clade phylogeographical analysis on geographical association of 32 mtDNA haplotypes in chum salmon

CRE: contiguous range expansion, clades 1-2, 2-1, & 3-1
IBD: restricted gene flow with isolation by distance, clades 1-1, 1-4, & 2-2
LDC: long distance colonization, clades 1-2, 1-4, & 2-2

(Sato et al., in preparation)
Nested clade phylogeographical analysis on geographical association of 21 mtDNA haplotypes in masu salmon

Clade 2-1(RGF-IBD): restricted gene flow with IBD
Clade 2-2(CRE): contiguous range expansion
Clade 2-3(CRE): contiguous range expansion

(Yu et al. 2010a)
Mismatch distribution analysis and Neutrality tests for demographic history in chum salmon (mtDNA)

**Rim of the Sea of Japan (RSJ)**
- $F_s: S$
- $D: NS$
- $SSD: NS$
- $T: 0.11\text{~}1.16\text{Mya}$

**Rim of the Sea of Okhotsk and Western Bering Sea (RSOWB)**
- $F_s: S$
- $D: NS$
- $SSD: S$
- $T: 0.07\text{~}0.72\text{Mya}$

**Northwest Alaska (NWA)**
- $F_s: S$
- $D: S$
- $SSD: S$
- $T: 0.08\text{~}0.61\text{Mya}$

**RSJ**: multiple population expansion in the middle to late Pleistocene

**RSOWB**: multiple population expansion in the late Pleistocene

**NWA**: most recent sudden population expansion in the late Pleistocene

*similar to the Gulf of Alaska

(Sato et al., in preparation)
Mismatch distribution analysis and Neutrality tests for demographic history in masu salmon (mtDNA)

Late Pleistocene multiple population expansion in the Sea of Okhotsk followed by recent sudden expansion in the Sea of Japan

Yu et al. 2010a

Sea of Okhotsk

Sea of Japan

Entire

Frequency (%)
Conclusions:

♦ Distinct geographical structure of populations in chum and masu salmon

♦ Population genetic structure mostly reflecting the past glacial history in two species

♦ Contemporary gene flow likely having a little influence on the population genetic structure in two species

♦ Current molecular population genetic data useful for management of two species at lower hierarchical level of population structure
Our salmon research is an international collaboration with

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Alaska Department of Fish and Game, Anchorage, Alaska, USA
Auke Bay Laboratory, NOAA, Juneau, Alaska, USA
US Fish and Wildlife Service, Anchorage, Alaska, USA
Washington Department of Fish and Wildlife, Olympia, WA, USA
Gangneung National University, Gangneung, Korea
Institute of Marine Biology, Vladivostok, Russia
Kamchatka Research Institute of Fisheries and Oceanography, Russia
Nissinbo Research and Development Center, Chiba, Japan

Thank you!