Population genetic structure of chum salmon populations in the Pacific Rim inferred from the mitochondrial and microsatellite DNA analysis

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Chum salmon

- Most widely distributed species among all the Pacific salmon

- High commercial important species as food resources in North Pacific fisheries

Stock identification has become a matter of scientific and management interest!!!

Aims of the present study

- To clarify population structure among and within the Pacific Rim populations of chum salmon using mitochondrial and microsatellite DNA analyses

mtDNA analysis

  - Maternal inheritance genetic history

Microsatellite DNA

  - Both parental inheritance

Previous studies to estimate genetic variation

- Allozyme

  (Kondzela et al 1994, Phelps et al. 1994, Winans et al. 1994, Seeb 1999, Wilmot et al. 1979)

- mtDNA

  (Park et al. 1993 – RFLP analysis)

- Remains mostly at the regional- to continental levels of resolution

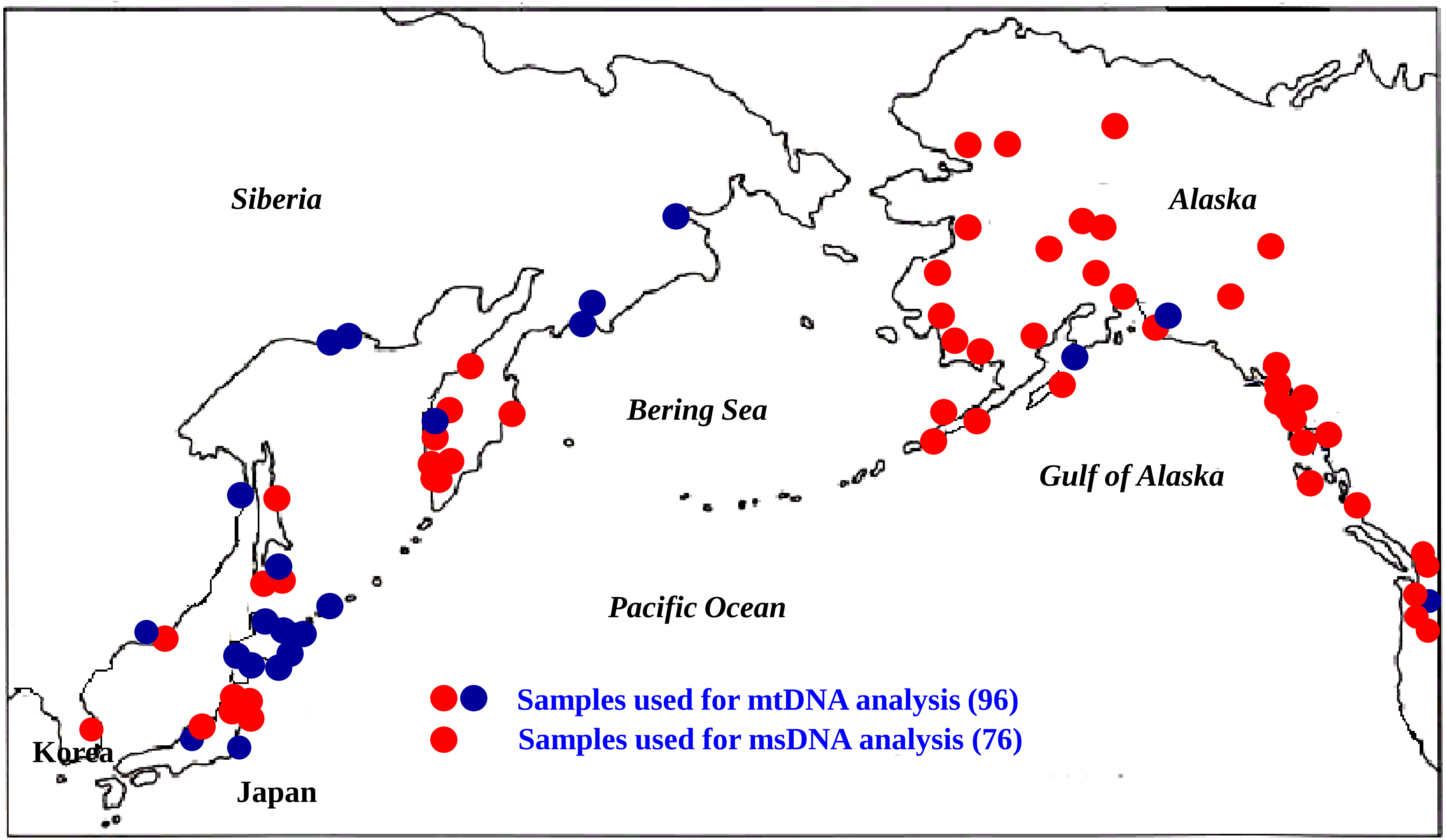
- mtDNA sequence analysis

  (Sato et al. 2001, 2004)

  -Increased power to detect genetic variation

  -Clear geographic structuring

Geographical position of sampling site



🟥 🟦 Samples used for mtDNA analysis (96)

🟥 Samples used for msDNA analysis (76)

Structure of the chum salmon mtDNA control region

(Sato et al, 2001,2004)

tRNA^{Thr} tRNA^{Pro} tRNA^{Phe}

5’ **3’**

Control Region

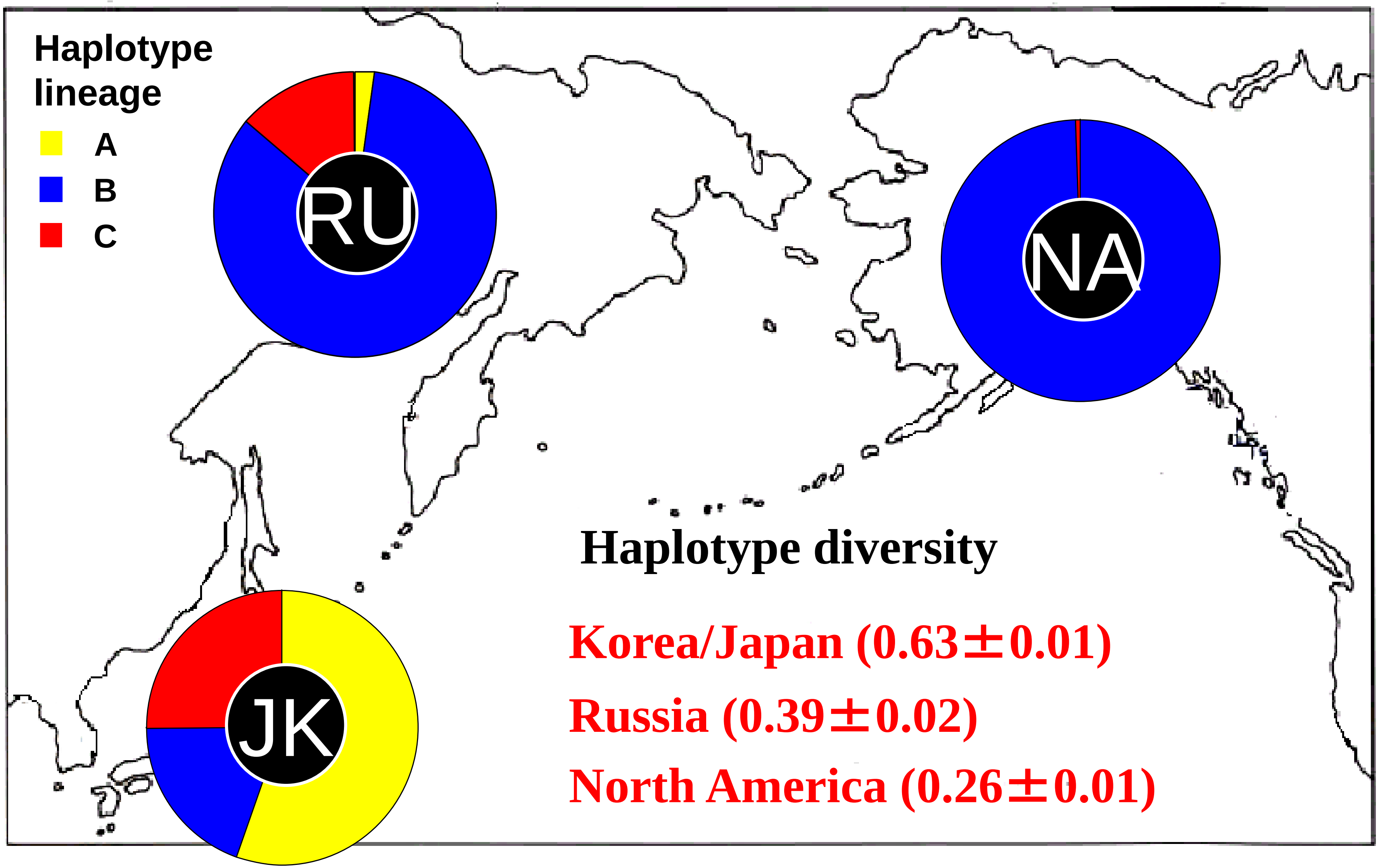
500bp

- Control region
  - -higher variability than coding region

Variable nucleotide sites in the 5'half of the chum salmon mtDNA control region

Haplo type	10	30	42	57	70	78	96	108	154	194	231	242	244	250	260	339	340	386	395	401	428	471
A-1	T	T	A	A	T	T	-	A	C	A	T	C	C	T	A	T	C	G	C	T	A	A
A-2	C	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
A-3	.	.	G	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
A-4	.	.	.	.	.	.	.	C	.	.	.	.	.	.	.	.	.	.	.	.	.	.
A-5	.	.	.	.	.	.	.	.	.	T	.	.	.	.	.	.	.	.	.	.	.	.
A-6	.	.	.	.	.	.	.	.	.	.	C	.	.	.	.	.	.	.	.	.	.	.
A-7	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	C
A-8	.	.	.	.	.	.	A	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
B-1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	-	A	.	.	.
B-2	.	C	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	-	A	.	.	.
B-3	.	.	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.	-	A	.	.	.
B-4	.	.	.	.	.	.	.	.	.	.	C	.	.	.	.	.	.	-	A	.	.	.
B-5	C	.	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.	-	A	.	.	.
B-6	.	.	.	.	C	.	.	.	G	.	.	.	.	.	.	.	.	-	A	.	.	.
B-7	.	.	.	.	.	C	.	.	G	.	.	.	.	.	.	.	.	-	A	.	.	.
B-8	.	.	.	.	.	.	.	C	G	.	.	.	.	.	.	.	.	-	A	.	.	.
B-9	.	.	.	.	.	.	.	.	G	.	C	.	.	.	.	.	.	-	A	.	.	.
B-10	.	.	.	.	.	.	.	.	G	.	.	.	T	.	.	.	.	-	A	.	.	.
B-11	.	.	.	.	.	.	.	.	G	.	.	.	.	C	.	.	.	-	A	.	.	.
B-12	.	.	.	.	.	.	.	.	G	.	.	.	.	.	G	.	.	-	A	.	.	.
B-13	.	.	.	.	.	.	.	.	G	.	.	.	.	.	.	A	.	-	A	.	.	.
B-14	.	.	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.	-	A	C	.	.
B-15	.	.	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.	-	A	.	.	C
B-16	.	.	.	.	.	.	.	.	G	.	.	.	.	.	.	A	T	-	A	.	.	.
B-17	.	.	.	.	.	.	.	.	G	.	.	.	.	.	.	A	.	-	A	C	.	.
B-18	.	.	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.	-	A	.	G	.
B-19	.	.	.	.	.	.	.	.	G	.	.	T	.	.	.	.	.	-	A	.	.	.
C-1	.	C	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
C-2	.	C	.	T	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
C-3	.	C	.	.	C	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
C-4	.	C	.	.	.	.	.	T	.	.	.	.	.	.	.	.	.	.	.	.	.	.
C-5	.	C	.	.	.	.	.	.	.	.	C	.	.	.	.	.	.	.	.	.	.	.

mtDNA haplotype distribution in the Pacific Rim chum salmon populations



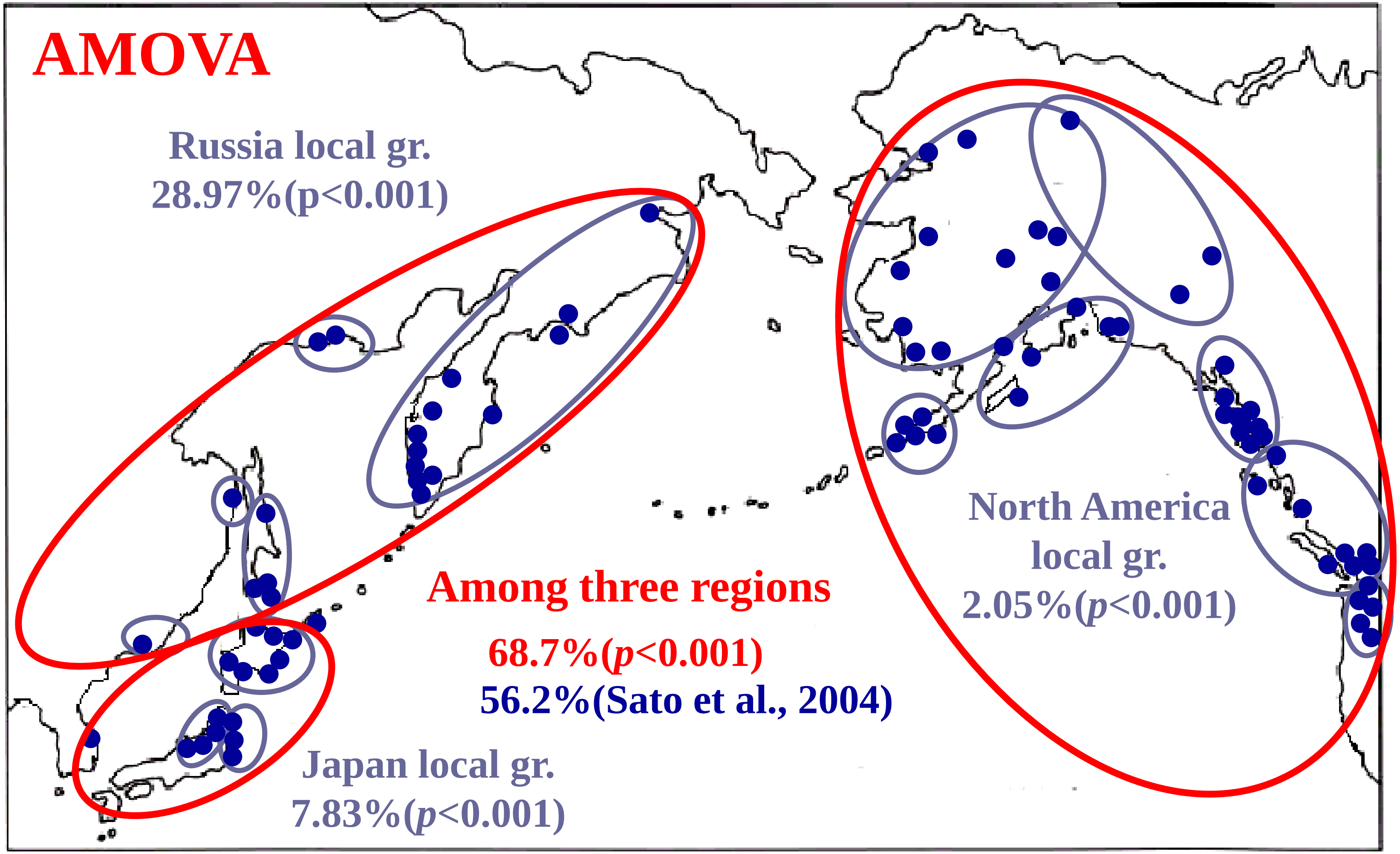
Haplotype diversity

Korea/Japan (0.63±0.01)

Russia (0.39±0.02)

North America (0.26±0.01)

Geographical structure of Pacific Rim chum salmon populations based on mtDNA data



AMOVA

Russia local gr.
28.97%($p<0.001$)

North America local gr.
2.05%($p<0.001$)

Among three regions

68.7%($p<0.001$)

56.2%(Sato et al., 2004)

Japan local gr.
7.83%($p<0.001$)

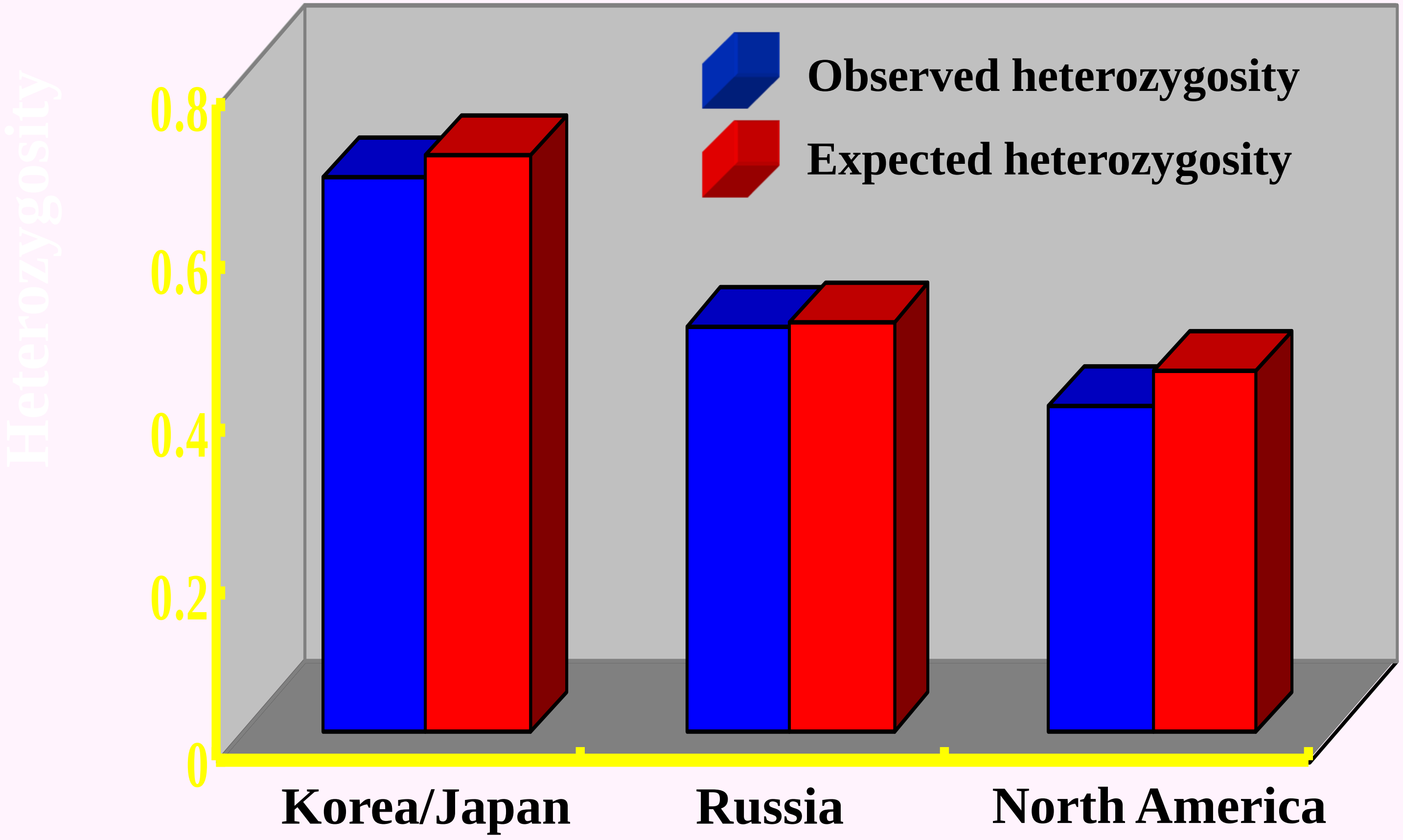
Variation among four microsatellite DNA loci

From 8 msDNA loci isolated previously (Abe et al., 2002)

Locus	Number of alleles	H_{O}	H_{E}	F_{IS}	F_{ST}
OKM4	**20**	**0.516**	**0.541**	**0.048**	**0.085**
OKM5	**20**	**0.556**	**0.608**	**0.087**	**0.089**
OKM7	**19**	**0.171**	**0.206**	**0.164**	**0.092**
OKM8	**31**	**0.673**	**0.689**	**0.029**	**0.088**
Mean	**22.5**	**0.479**	**0.511**	**0.064**	**0.088**

- Observed heterozygosity (H_{O}), expected heterozygosity (H_{E}), and F-statistic at four msDNA loci among 76 chum salmon populations.
- 14(OKM4), 7(OKM5), 8(OKM7), 24(OKM8) of 76 populations were significant departures from the Hardy-Weinberg equilibrium.

Genetic variation is highest in **the population of Korea/Japan!**



Geographical structure of Pacific Rim chum salmon populations based on mtDNA and msDNA data

Source of variation	**mtDNA**	**msDNA**
Among regional groups (Japan, Russia and North America)	**68.7% (*P*<0.001)**	**5.1% (*P*<0.001)**
Among local groups in Japan	**7.8% (*P*<0.001)**	**0.6% (*P*<0.01)**
Among local groups in Russia	**29.0% (*P*<0.001)**	**4.3 (*P*<0.001)**
Among local groups in North America	**2.1% (*P*<0.001)**	**5.3 (*P*<0.001)**

Conclusions

- Three regional groups of Pacific Rim chum salmon revealed by mtDNA and msDNA analysis
  - Highest genetic variation in Japanese populations
  - Geographic structuring

- Besides the above geographic structuring, another structure (four regional groups) suggested by mtDNA analysis

- Congruence of both markers useful for construction of a better baseline for genetic stock identification of chum salmon in high-seas

Thank you very much!