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

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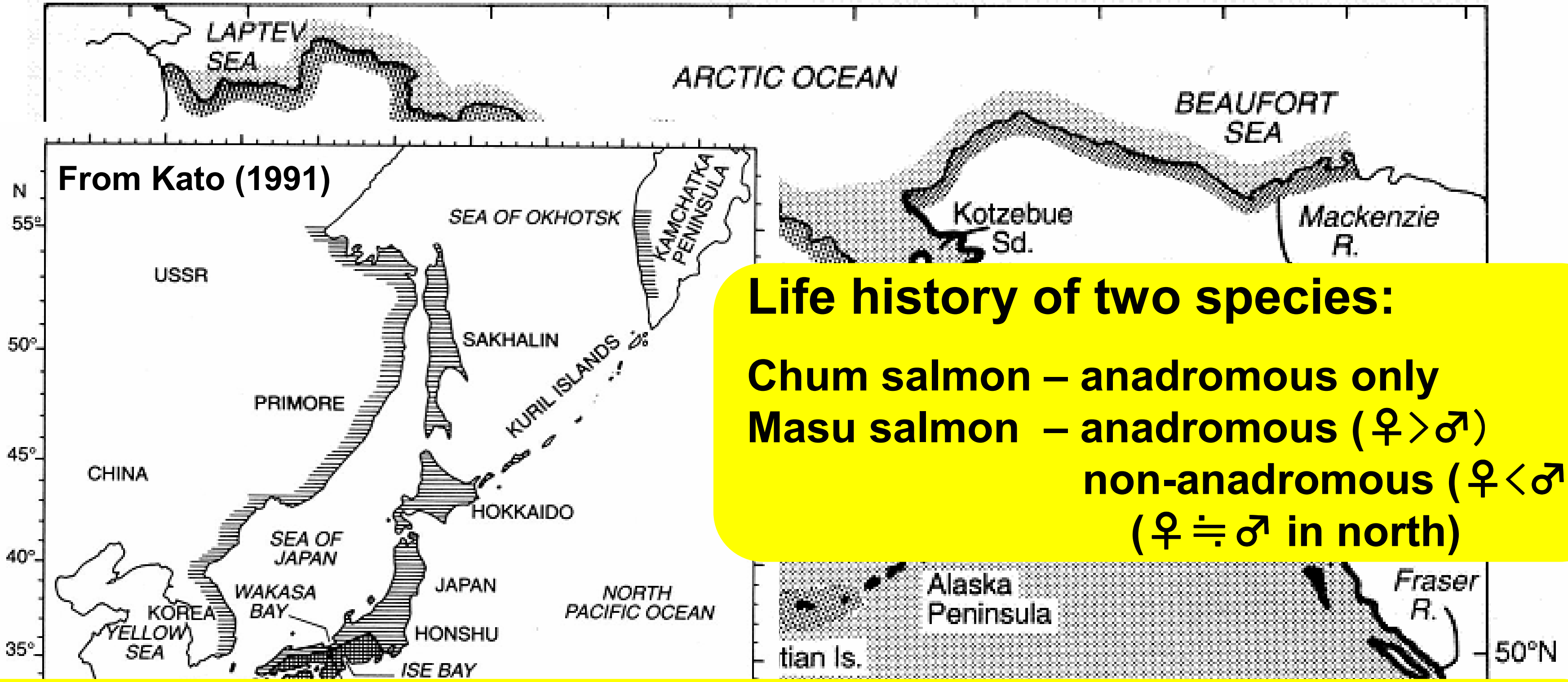
Distribution of chum and masu salmon in the North Paific



From Kato (1991)

Life history of two species:

Chum salmon – anadromous only
Masu salmon – anadromous (♀>♂)
non-anadromous (♀<♂)
(♀≒♂ in north)

OBJECTIVES

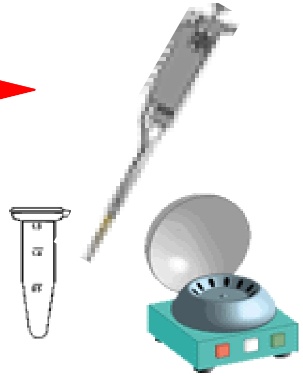
- ♦To analyze the genetic population structure and phylogeography
- ♦To understand evolutionary process of two species using mtDNA and msDNA markers

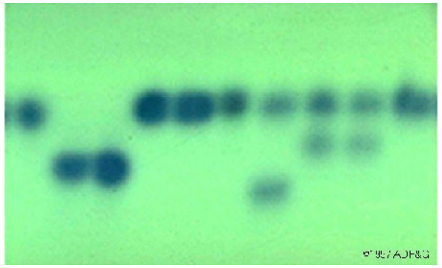
From Salo (1991)

Detection of genetic polymorphisms

liver
blood
adipose fin

DNA extraction

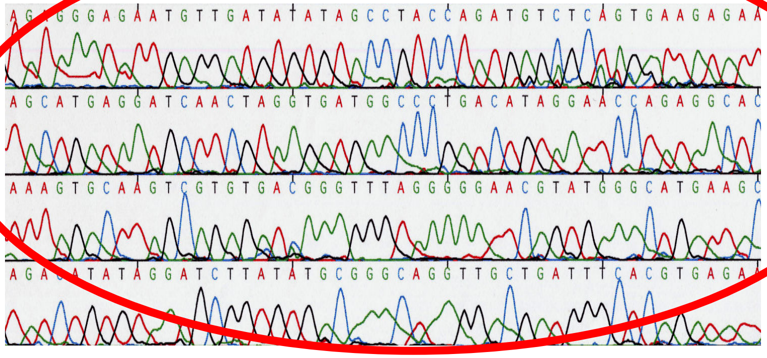


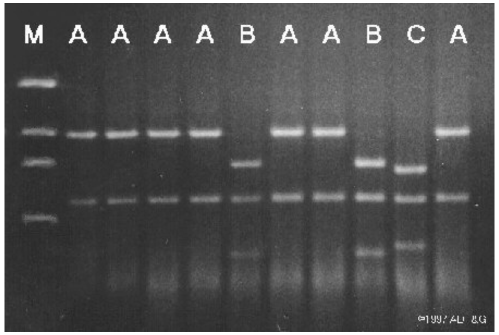


allozyme

Nuclear DNA
Mitochondrial DNA
PCR amplification

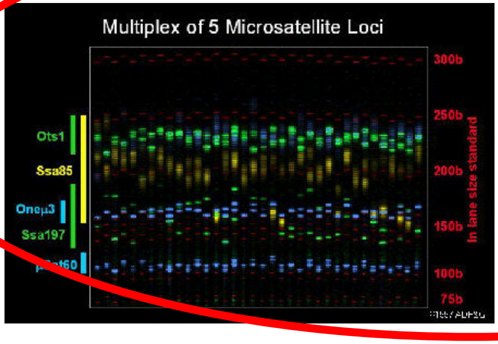
Nucleotide sequencing

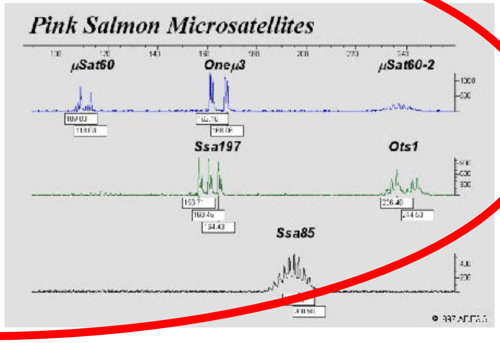




PCR-RFLP

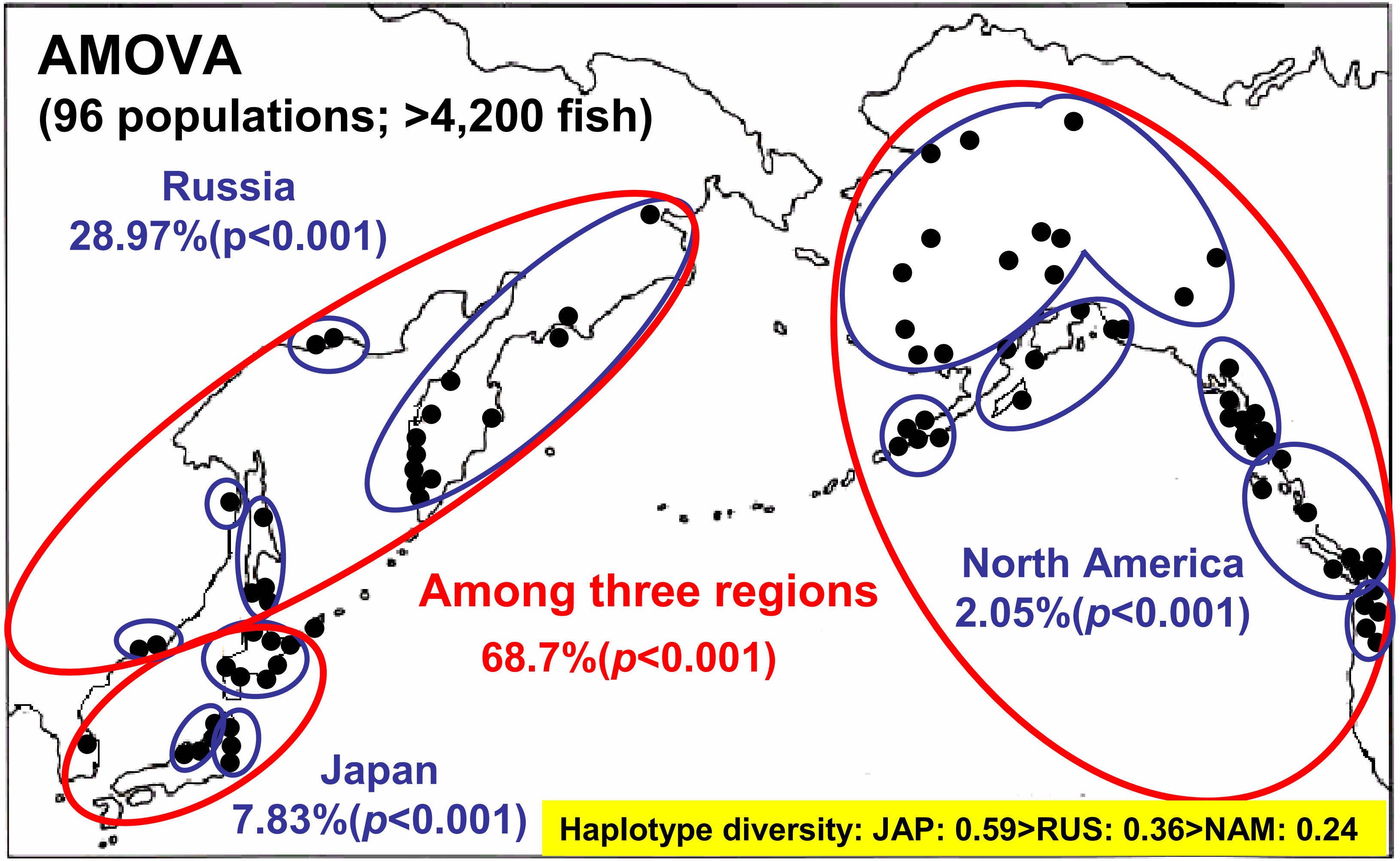
Microsatellite DNA





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%($p<0.001$)

Among three regions
68.7%($p<0.001$)

North America
2.05%($p<0.001$)

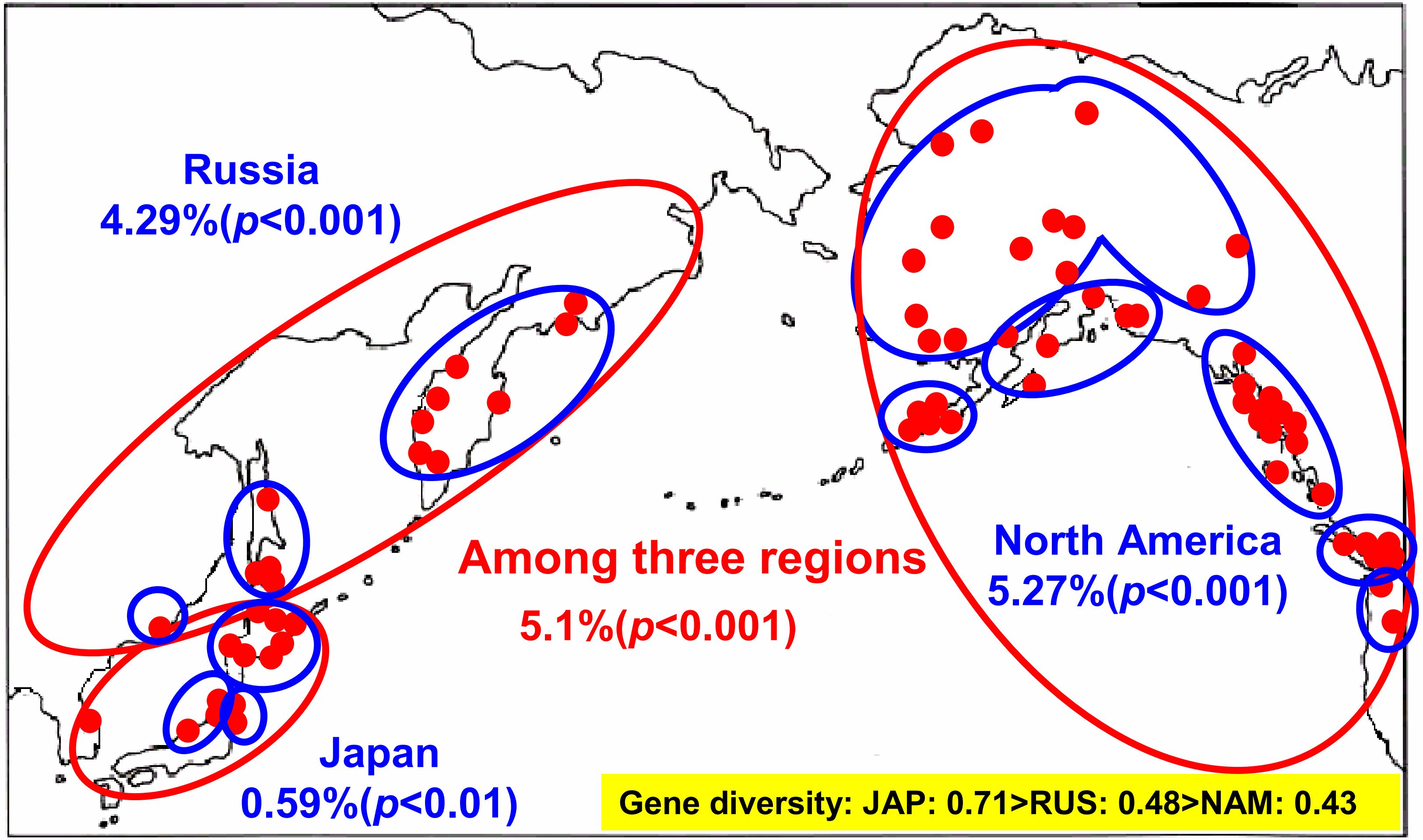
Japan
7.83%($p<0.001$)

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

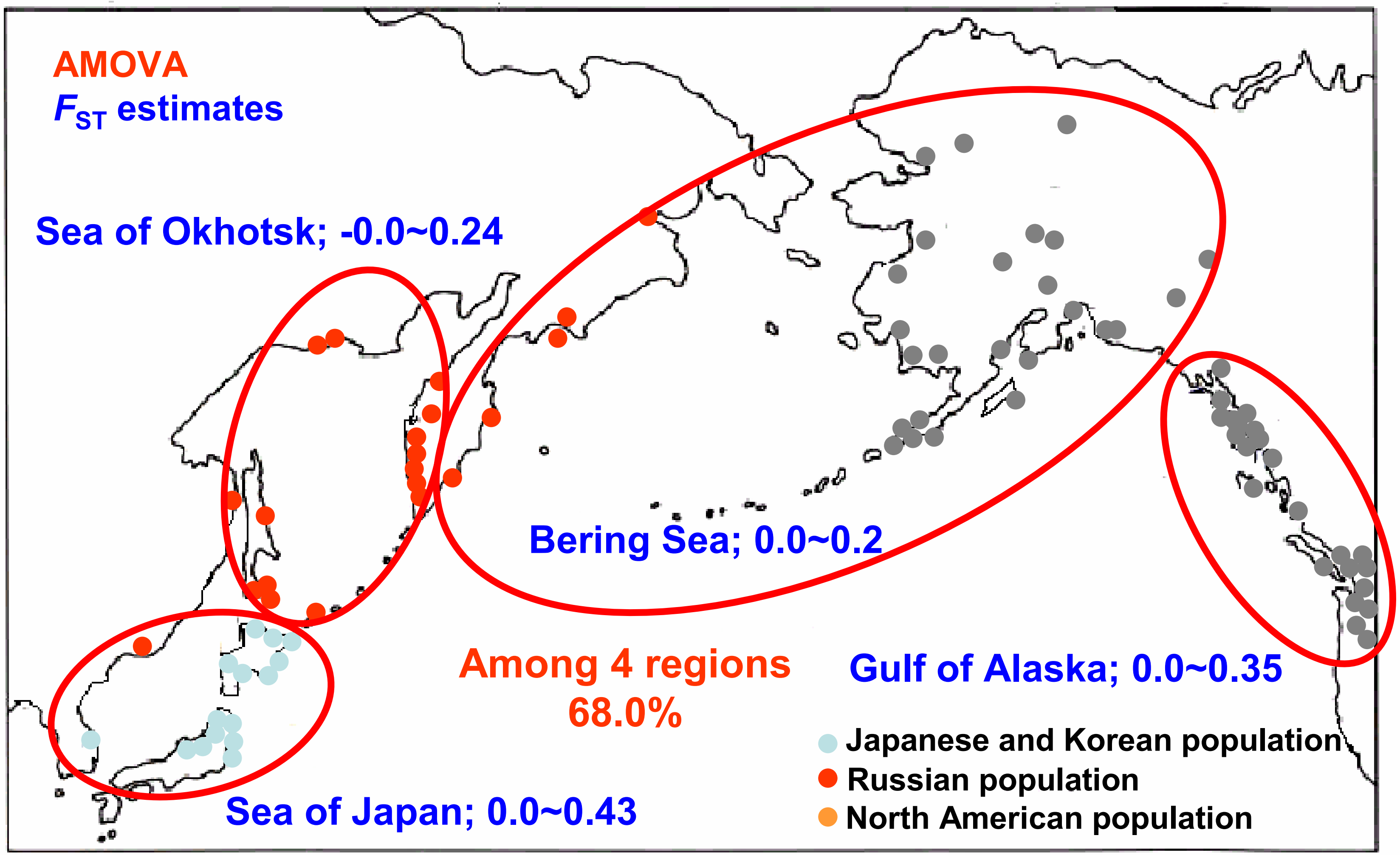
AMOVA (75 populations)



Gene diversity: JAP: 0.71>RUS: 0.48>NAM: 0.43

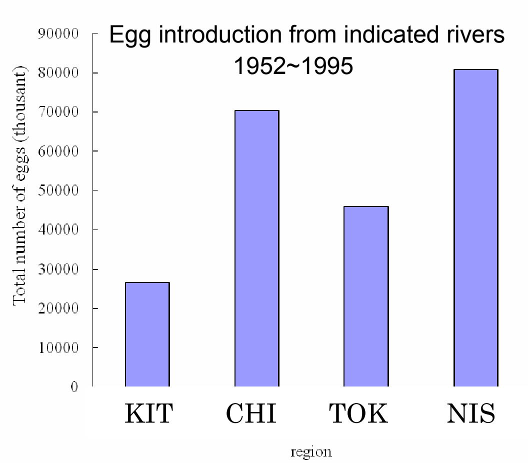
(Yoon et al. 2009)

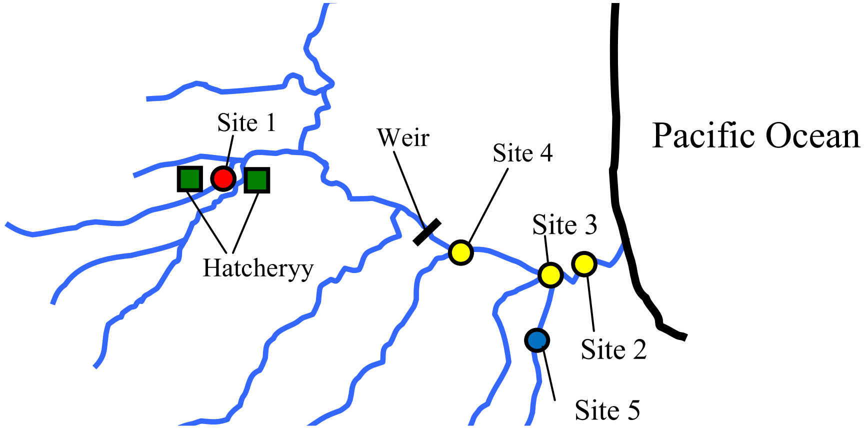
AMOVA and pairwise F_{ST} estimates for genetic differentiation of chum salmon populations



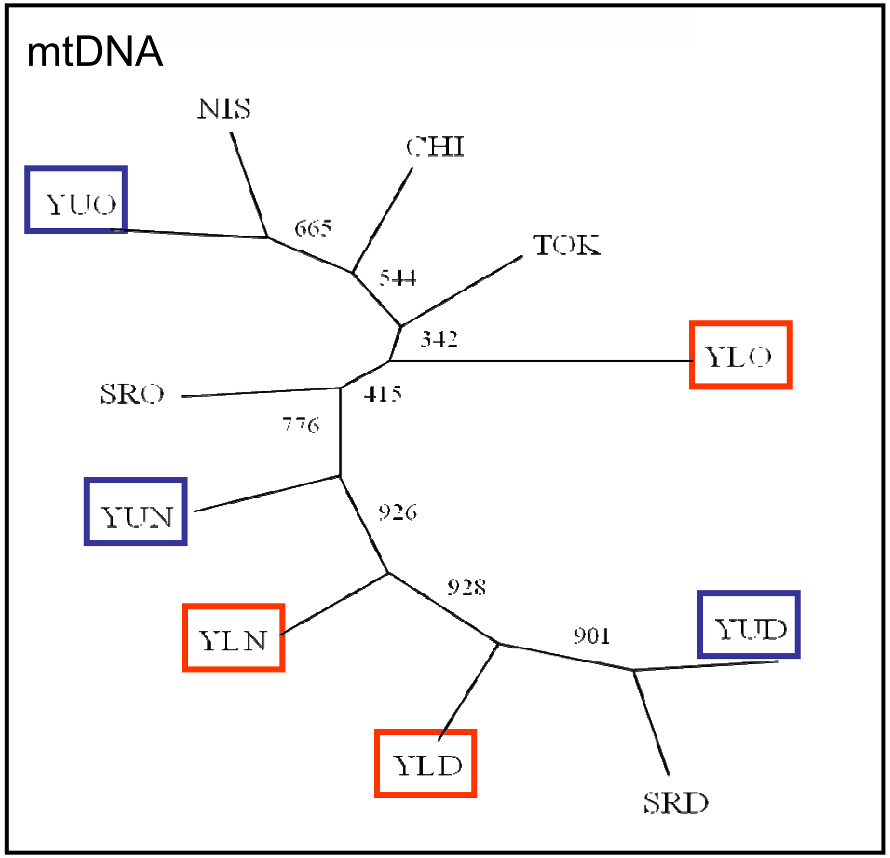
(Yoon et al. 2008)

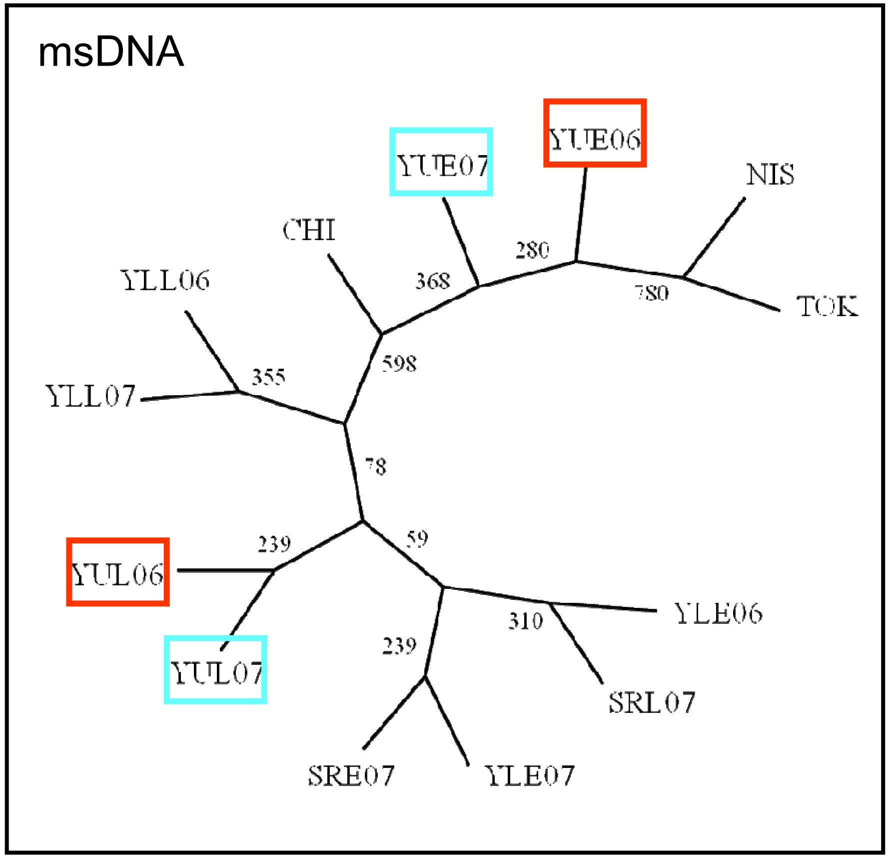
Genetic differentiation of chum salmon within the Yurappu River



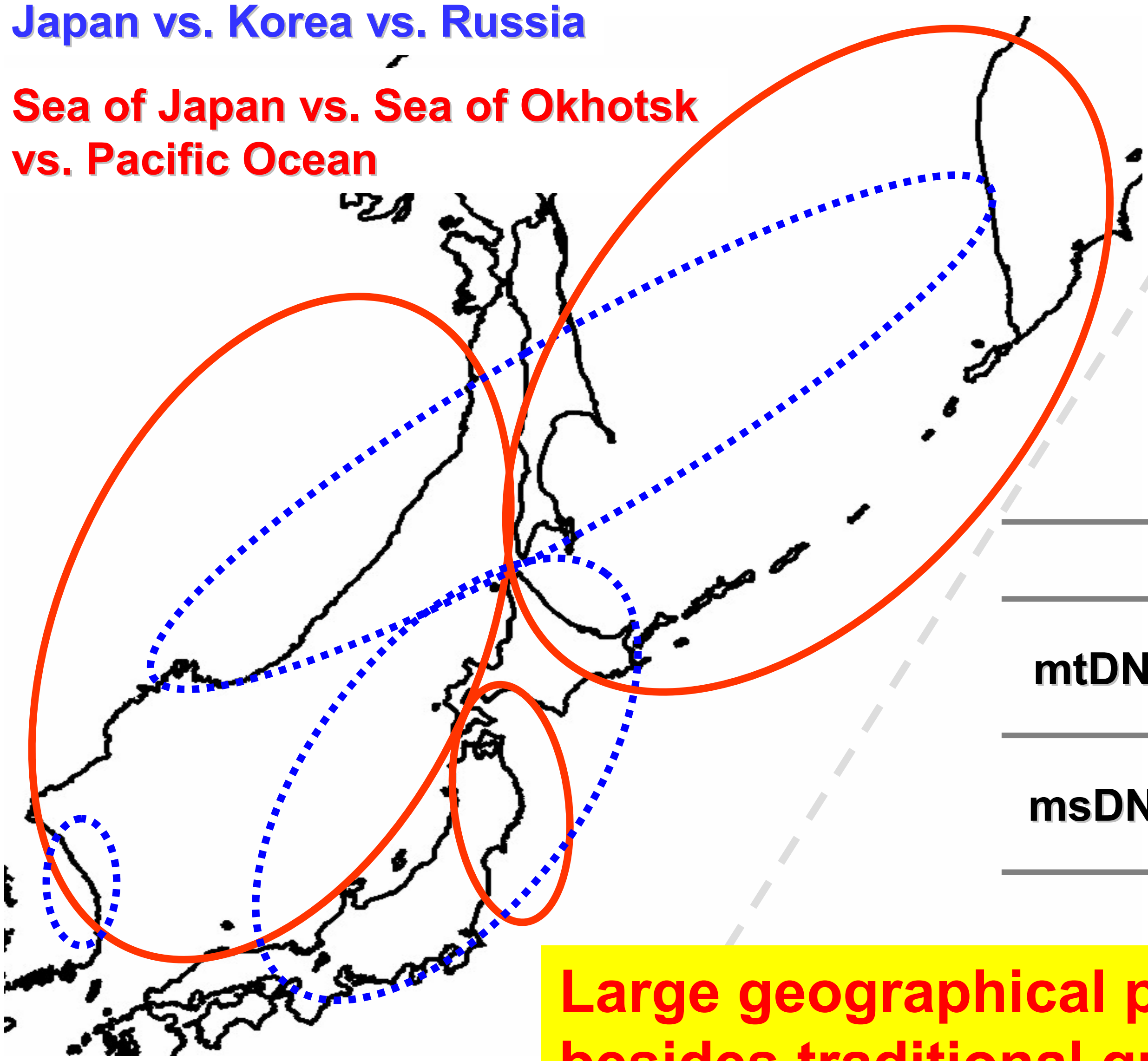


(Yokotani et al. 2009)





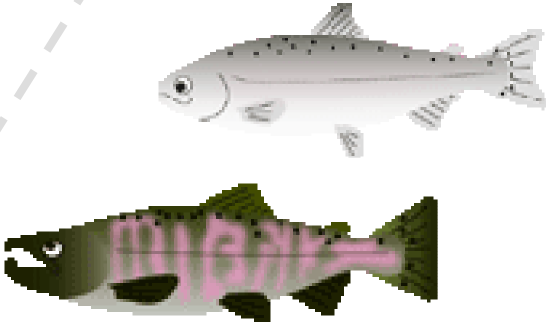
AMOVA with 21 mtDNA haplotypes (ca. 560bp of *ND5*) and 6 msDNA loci in masu salmon (24 populations)



Japan vs. Korea vs. Russia

Sea of Japan vs. Sea of Okhotsk vs. Pacific Ocean

*>1,100 fish



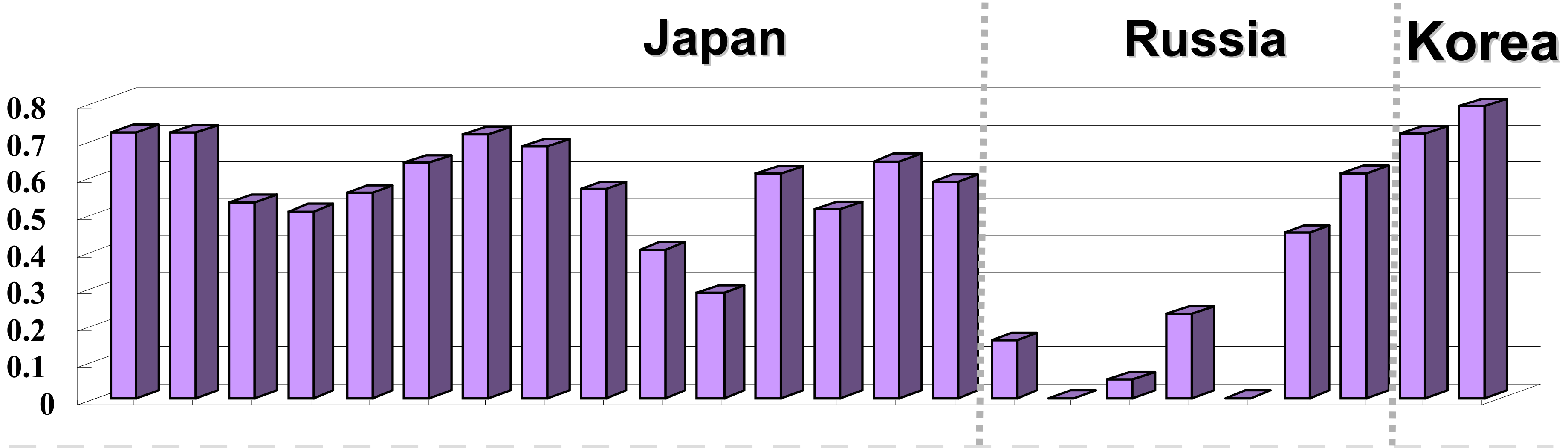
(Yu et al. 2010a)

	countries	<	waters
mtDNA	3.83% (P<0.05)		5.19% (*P*<0.01)
msDNA	1.65% (P<0.001)		1.88% (*P*<0.001)

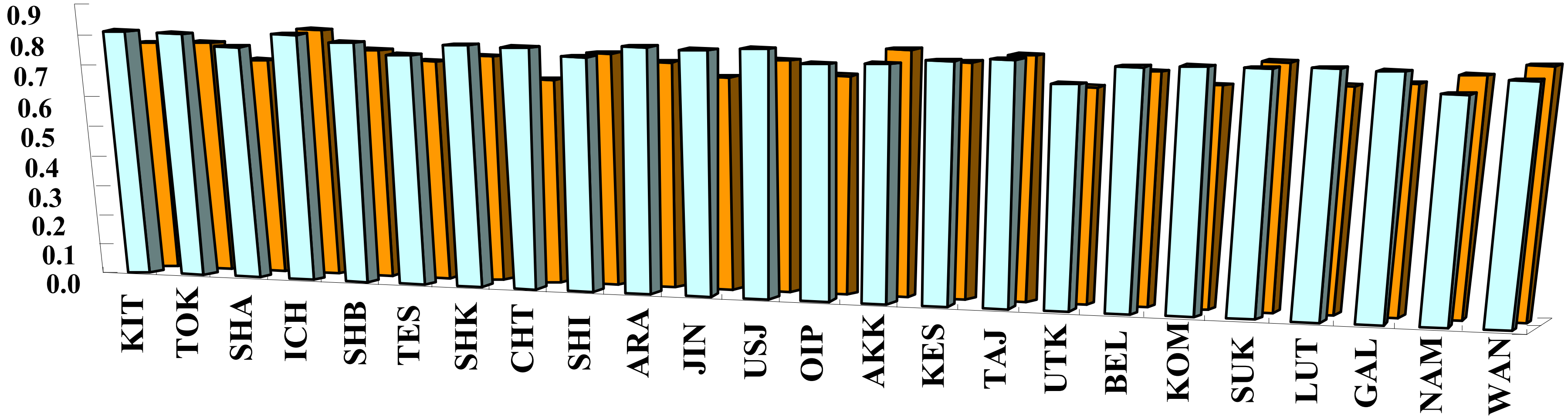
Large geographical population groups besides traditional grouping by country

Genetic diversity of masu salmon in the Far East

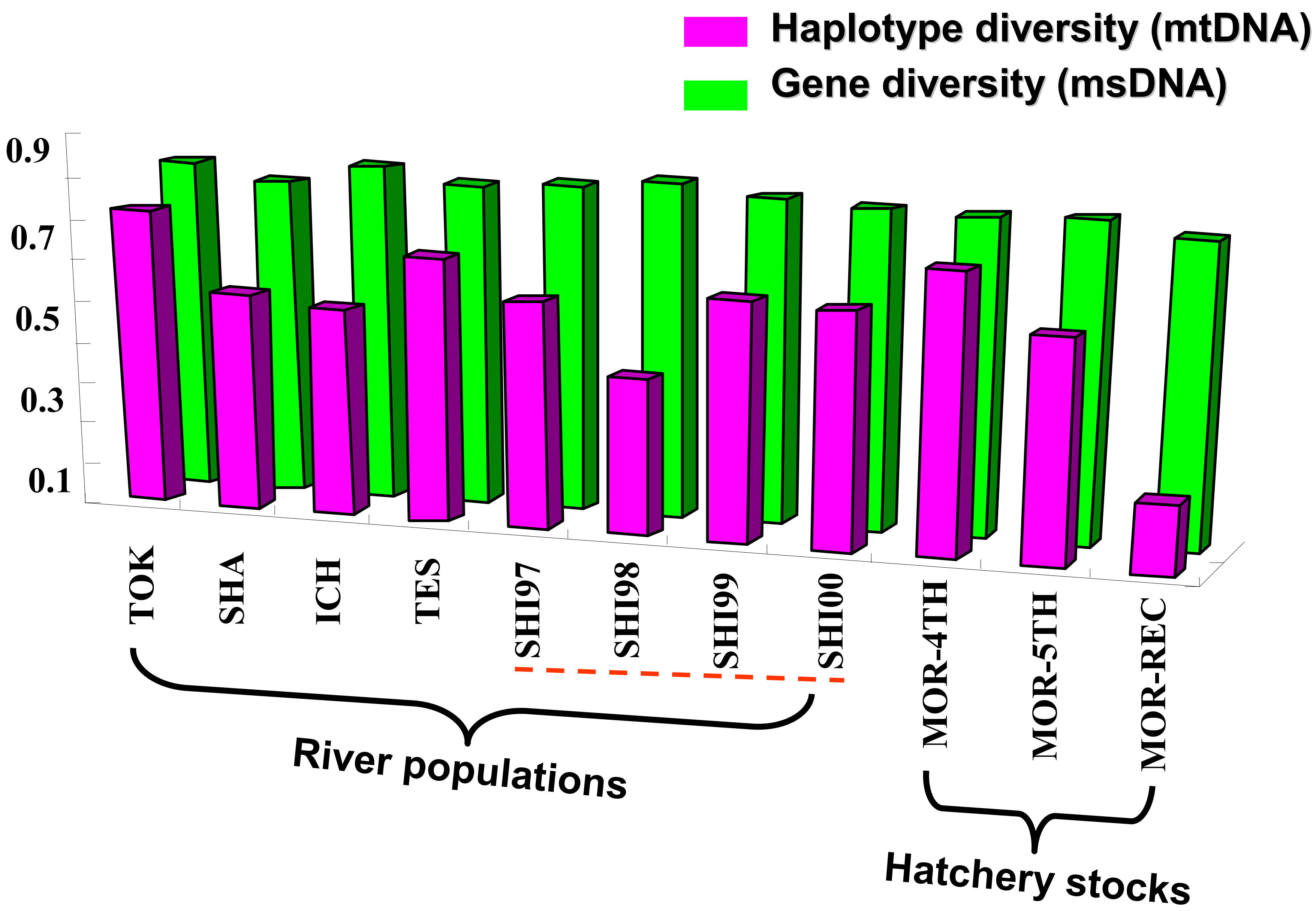
A) Haplotype diversity - mtDNA *ND5*



B) Expected (*he* 🟦) and observed heteroygosity (*ho* 🟧) – msDNA



Genetic diversity in hatchery stocks and mother populations of masu salmon



Genetic differentiation among hatchery stocks and spawning populations（F_{ST}）

⇨ $0 \leqq F_{ST} \leqq 1$

← differentiation →

below diagonal : msDNA 、above diagonal : mtDNA

*$P<0.05$、**$P<0.001$ (Bonferroni correction)

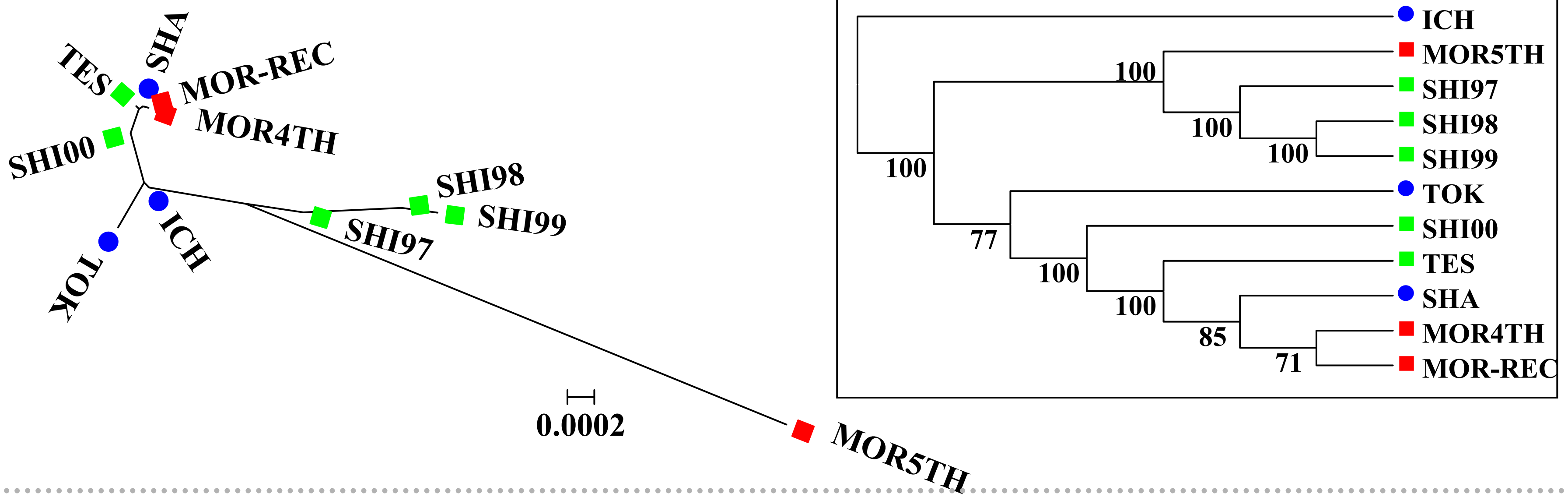
	TOK	SHA	ICH	TES	SHI97	SHI98	SHI99	SHI00	MOR REC	MOR 4TH	MOR 5TH
TOK		-0.007	0.079**	0.221**	0.217**	0.224**	0.161**	0.188**	**0.226****	**0.173****	**0.213****
SHA	0.023**		0.072*	0.236**	0.230**	0.235**	0.167**	0.198**	**0.241****	**0.192****	**0.232****
ICH	0.016**	0.026**		0.093**	0.073**	0.064**	0.033	0.051**	**0.080****	**0.067****	**0.097****
TES	0.044**	0.074**	0.052		[illegible]	[illegible]	0.021	0.008	**0.080****	**0.015**	**0.003**
SHI97	0.027**	0.052**	0.032	[illegible]		[illegible]	0.004	-0.008	**0.055***	**0.003**	**0.000**
SHI98	0.029**	0.052**	0.029**	0.015**	0.004		0.012	0.001	**0.040***	**0.027***	**0.015**
SHI99	0.030**	0.058**	0.033**	0.014	0.004	0.004		-0.007	**0.038***	**0.003**	**0.034***
SHI00	0.035**	0.064**	0.041**	0.006**	0.001	0.005	0.003		**0.046****	**-0.007**	**0.014**
MORREC	**0.043****	**0.062****	**0.054****	**0.045****	**0.041****	**0.034****	**0.031****	**0.039****		**0.085****	**0.132****
MOR4TH	**0.026****	**0.051****	**0.039****	**0.032****	**0.019****	**0.025****	**0.019****	**0.021****	**0.042****		**0.024***
MOR5TH	**0.029****	**0.049****	**0.038****	**0.058****	**0.037****	**0.043****	**0.039****	**0.048****	**0.030****	**0.044****	

comparison with mother populations

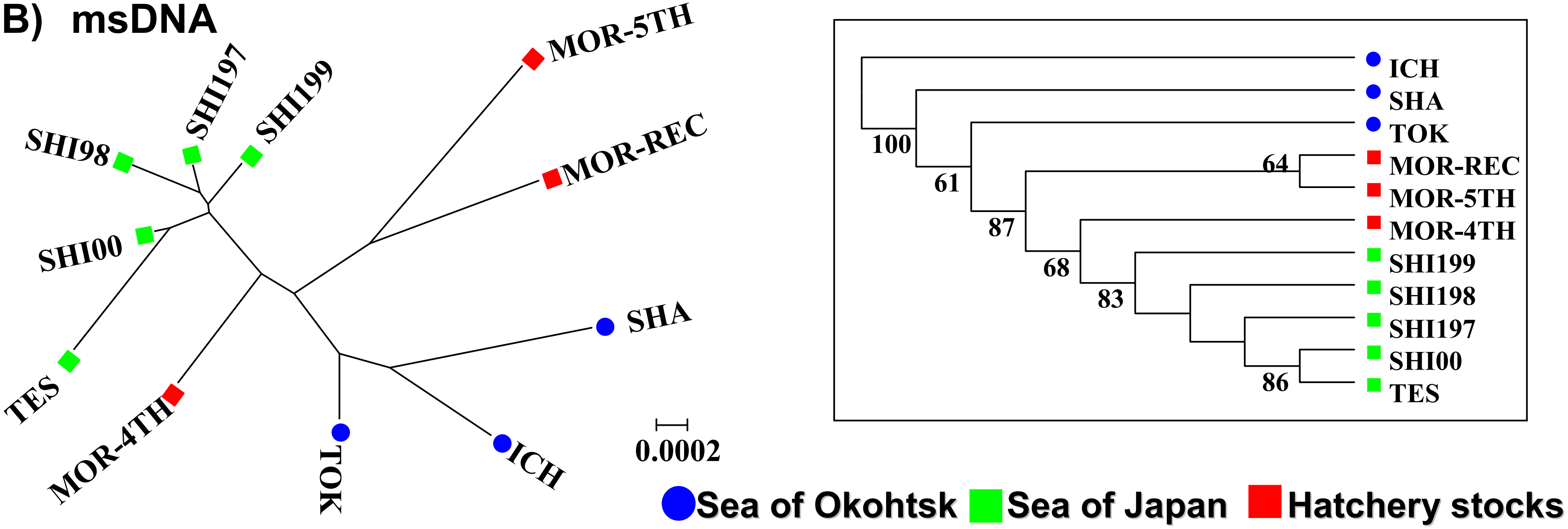
between hatchery stocks

Neighbor-joining population tree by mtDNA and msDNA

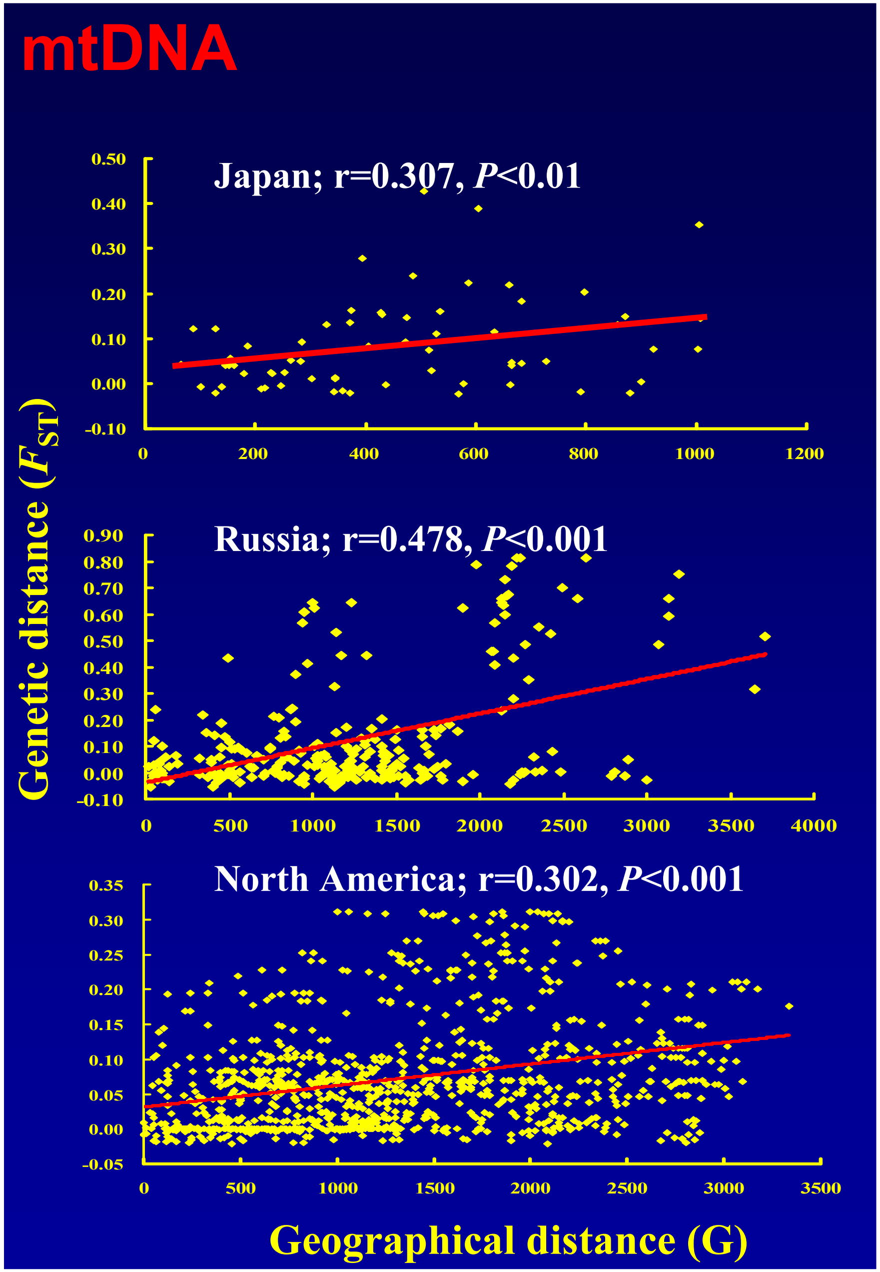
A) mtDNA

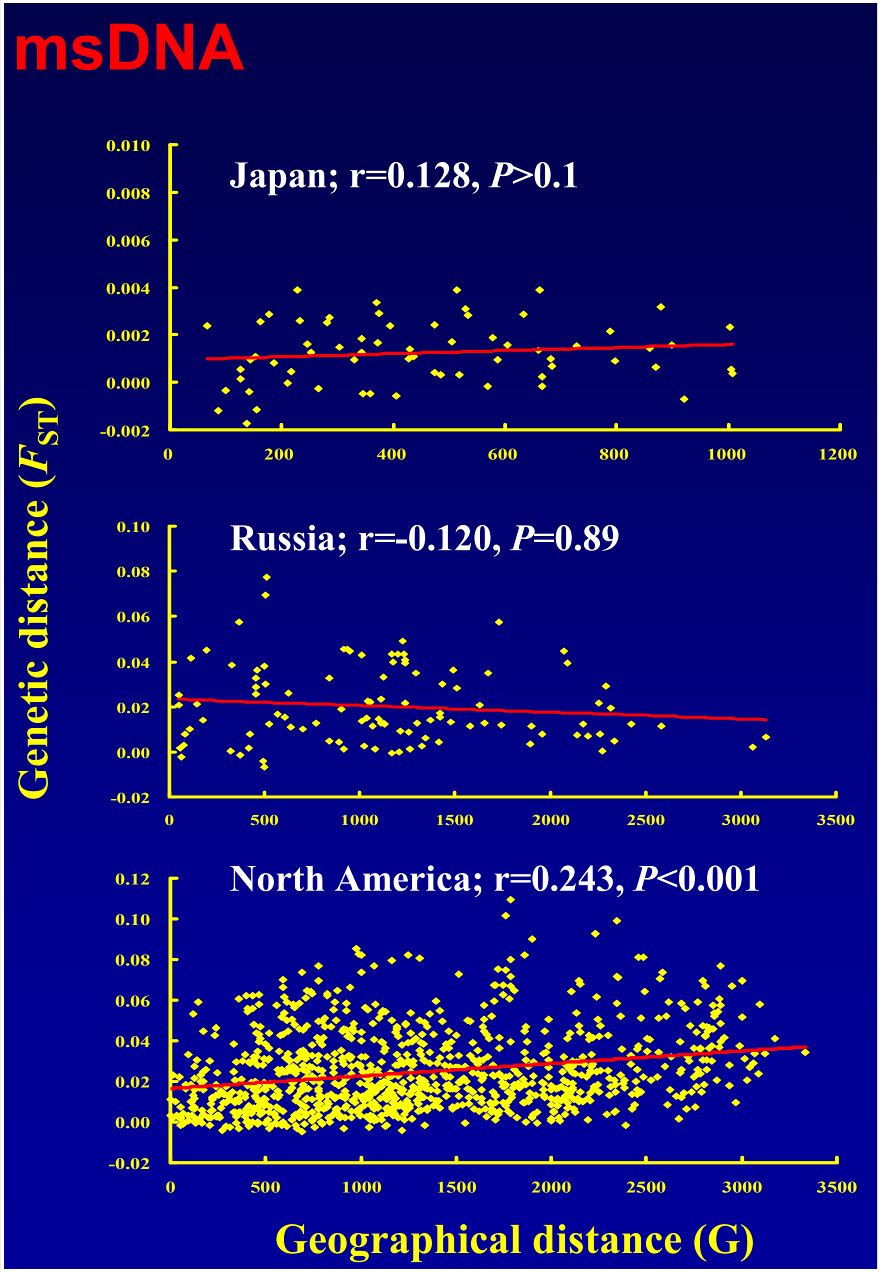


B) msDNA



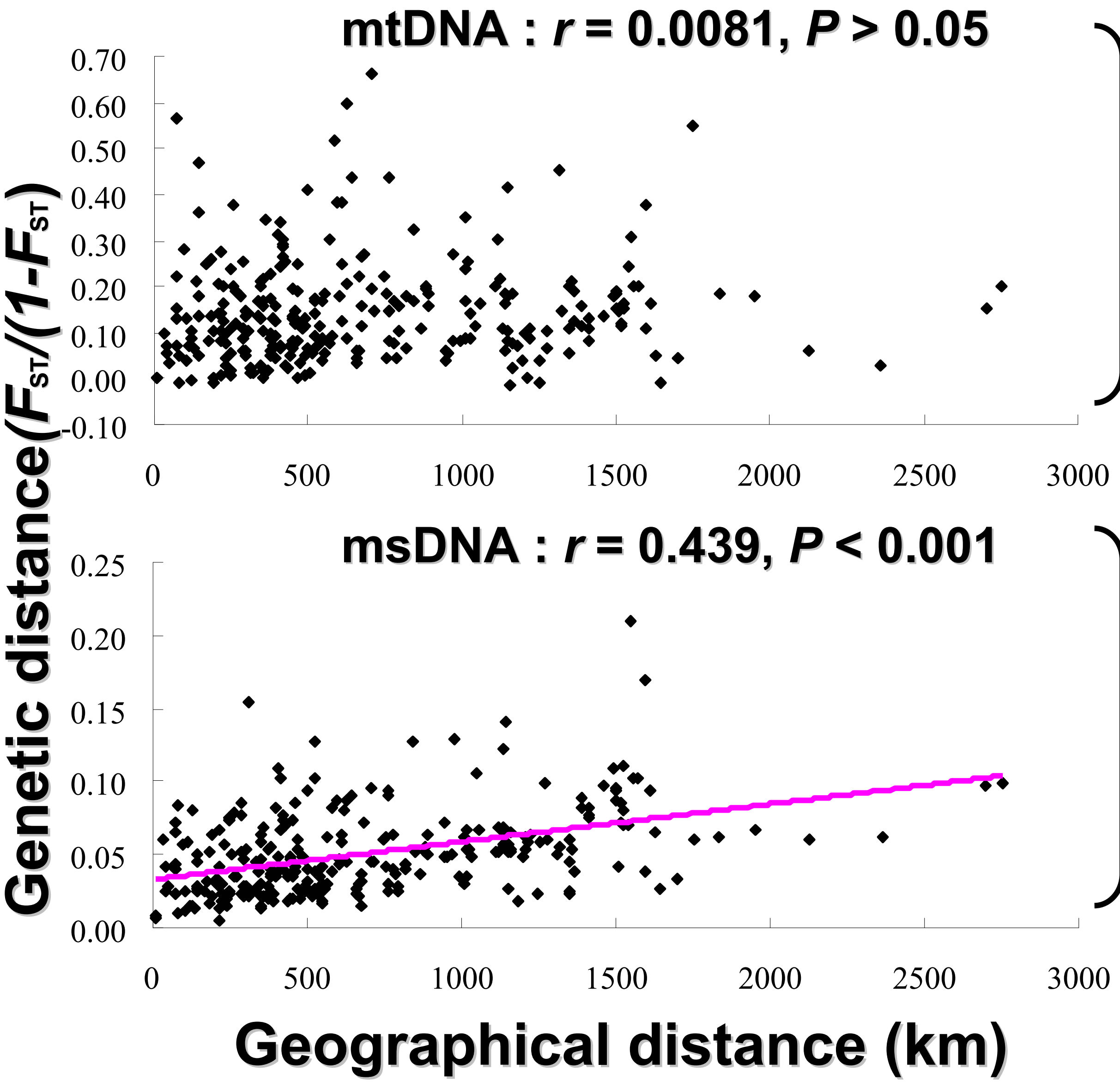
Pairwise genetic and geographical distance measures in chum salmon





(Yoon et al. 2008)

Pairwise genetic and geographical distance measures In anadromous masu salmon


mtDNA : $r = 0.0081$, $P > 0.05$

msDNA : $r = 0.439$, $P < 0.001$

No significant correlation between genetic and geographical distance

Significant correlation between genetic and geographical distance

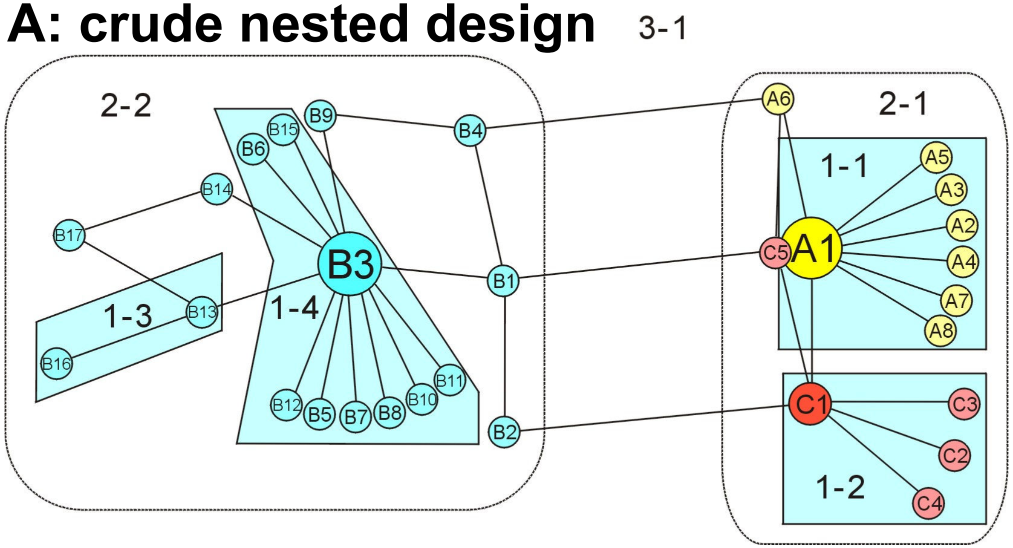
↓

Resticted gene flow with isolation by distance

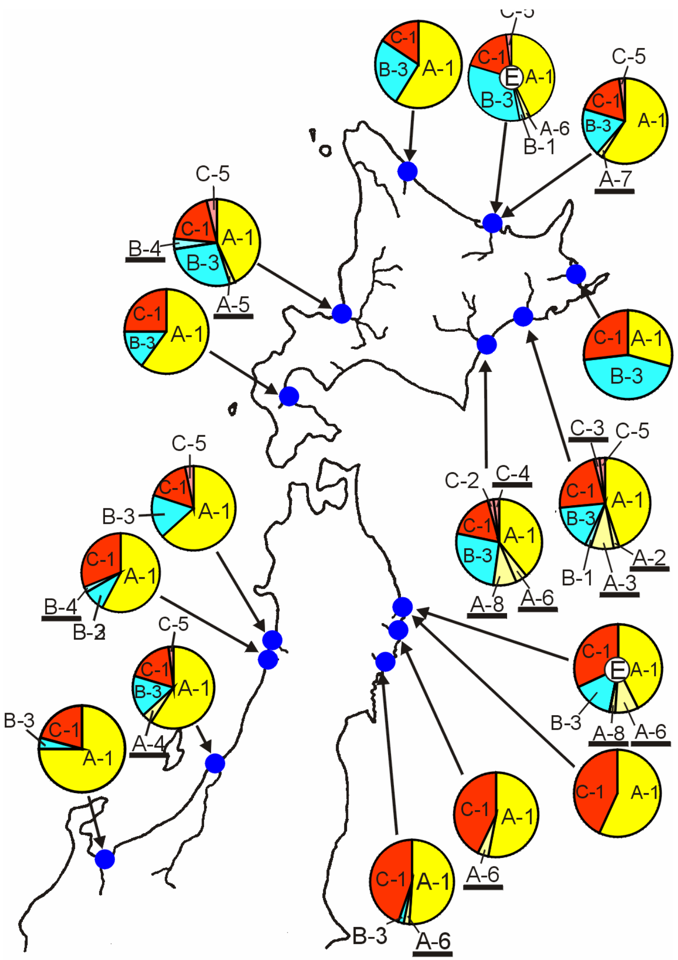
(Yu et al. 2010a)

Nested clade phylogeographical analysis (NCPA)

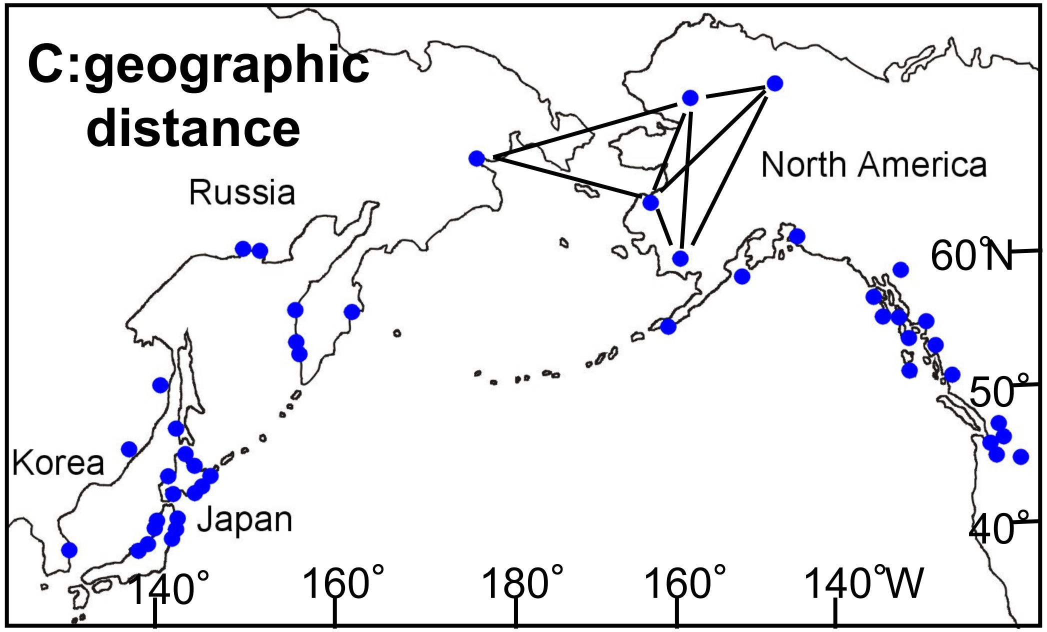
A: crude nested design



B: haplotype distribution



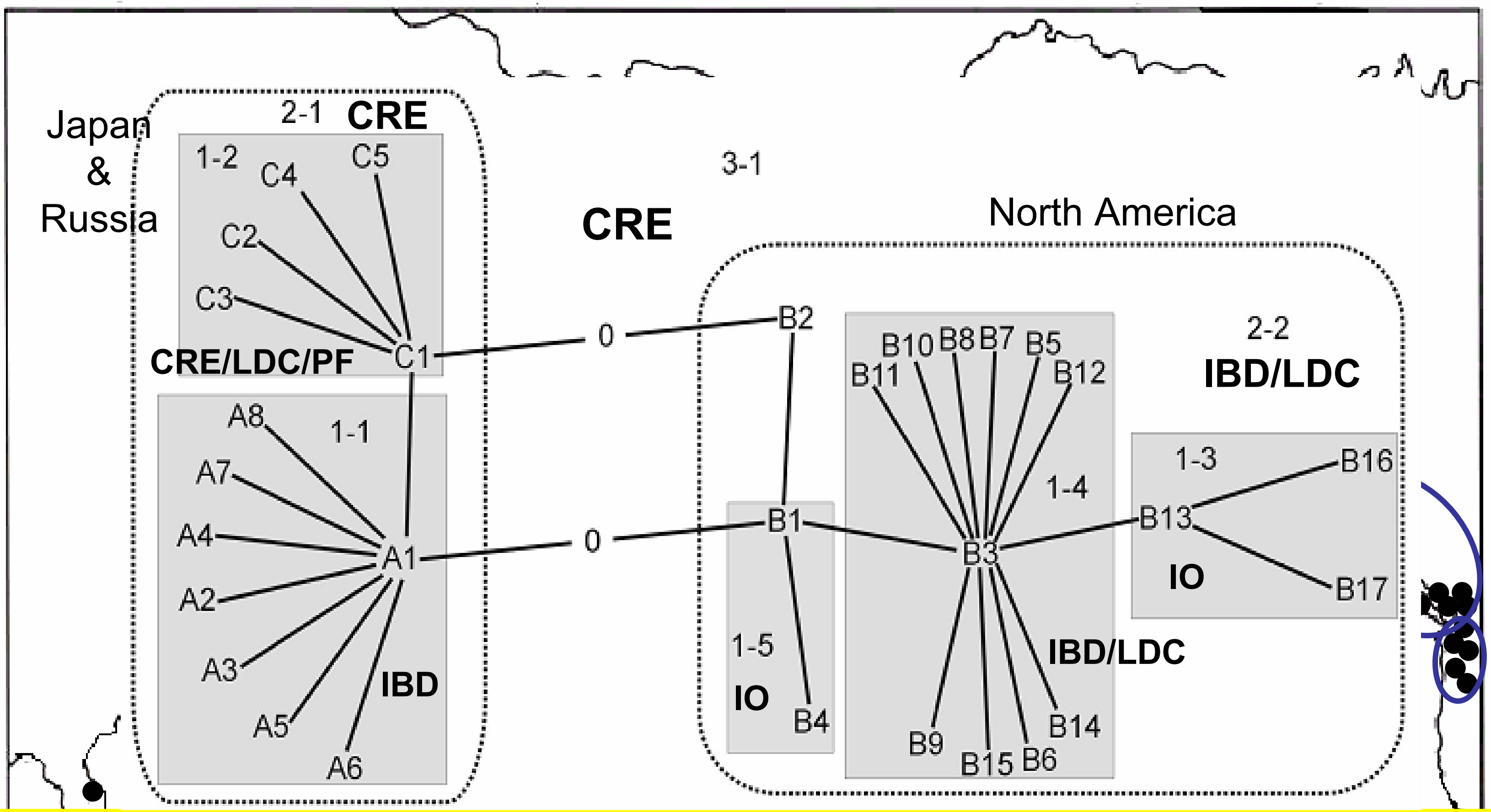
C:geographic distance



Speculation of historical event in population structure

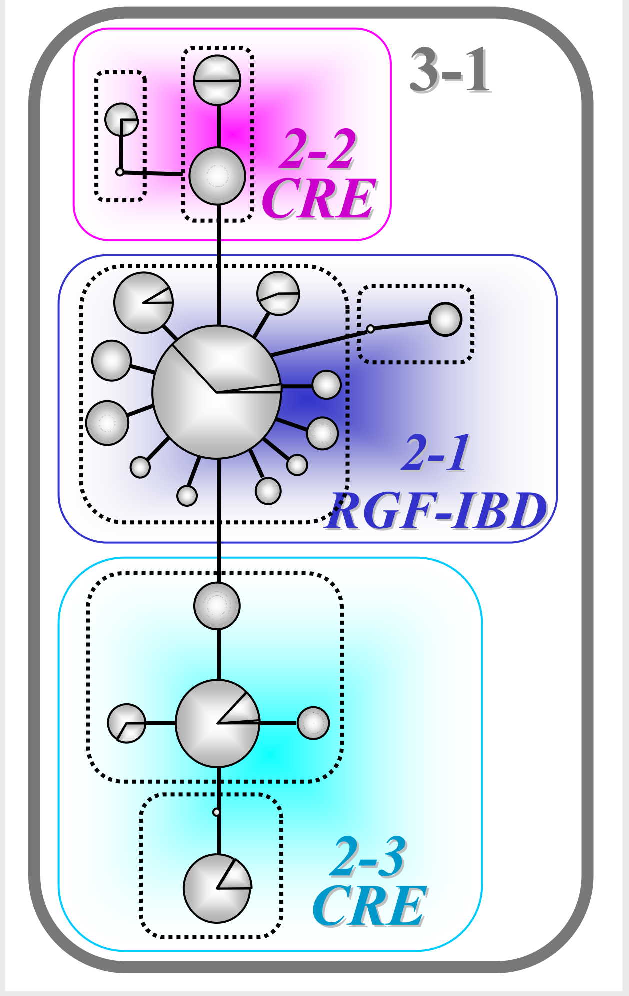
Nested clade phylogeographical analysis on geographical association of 32 mtDNA haplotypes in chum salmon

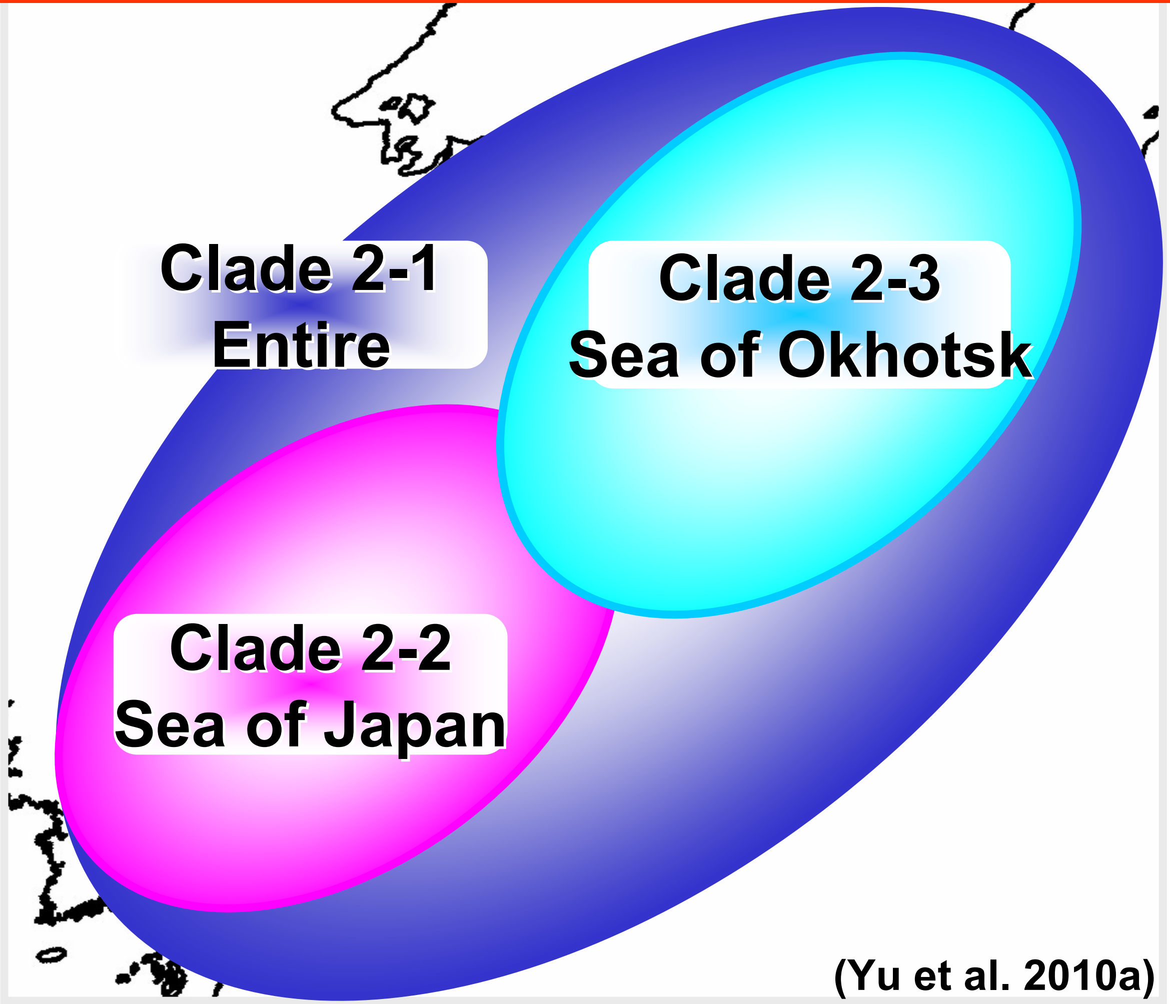
(Sato et al., in preparation)



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

Nested clade phylogeographical analysis on geographical association of 21 mtDNA haplotypes in masu salmon

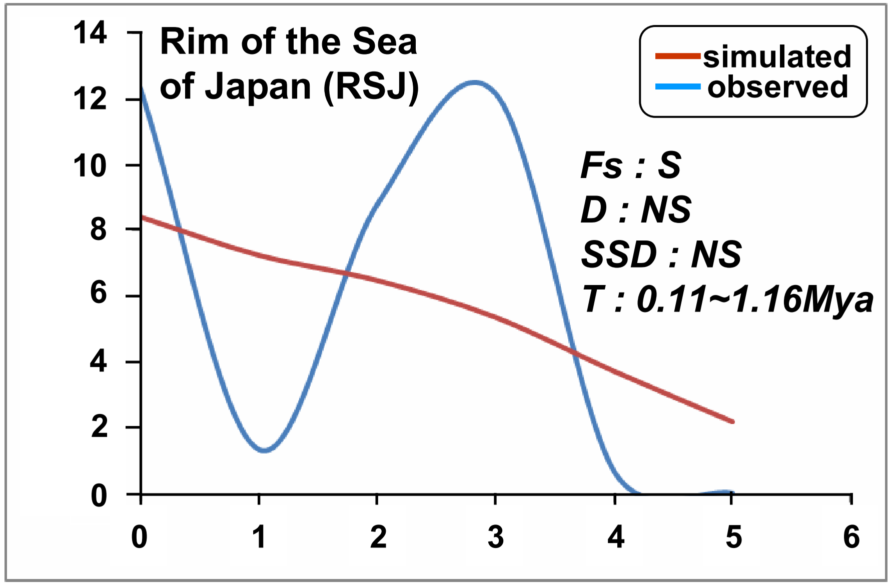




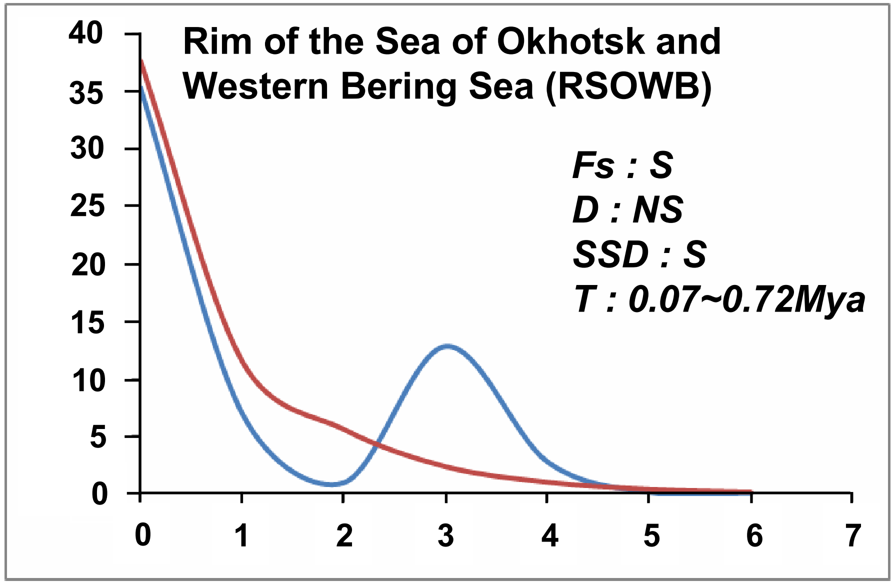
(Yu et al. 2010a)

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

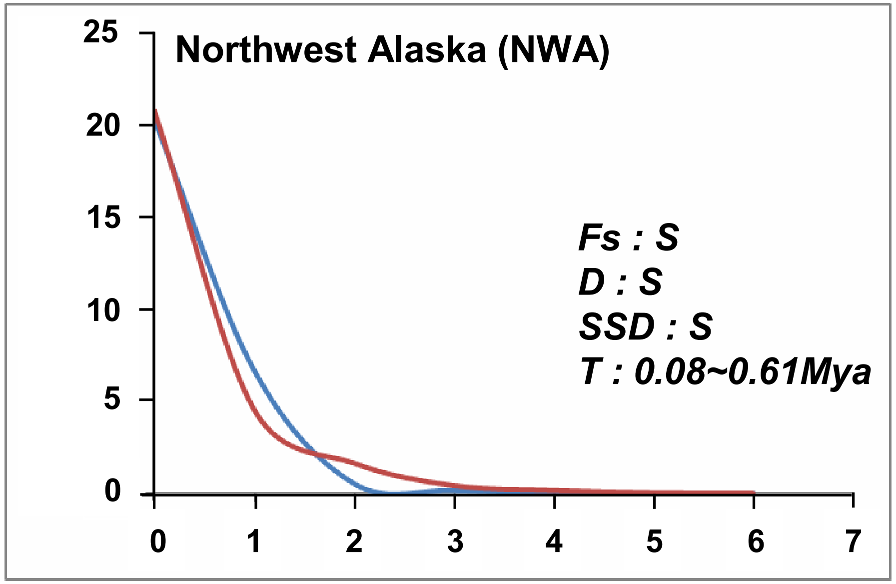
Mismatch distribution analysis and Neutrality tests for demographic history in chum salmon (mtDNA)



Fs : S
D : NS
SSD : NS
T : 0.11~1.16Mya



Fs : S
D : NS
SSD : S
T : 0.07~0.72Mya



Fs : S
D : S
SSD : S
T : 0.08~0.61Mya

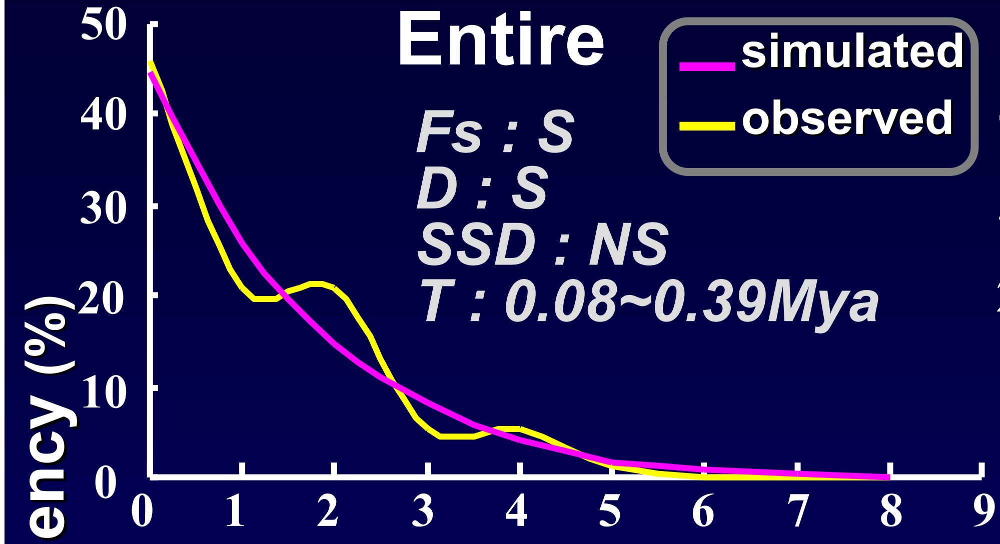
RSJ: multiple population expansion in the middle to late Pleistocene

RSOWB: multiple population expansion in the late Pleistocene

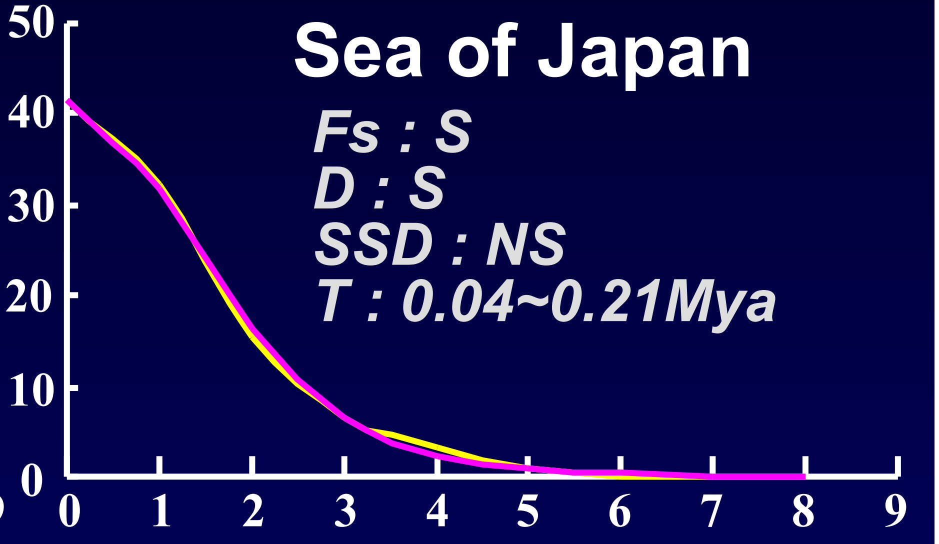
NWA: most recent sudden population expansion in the late Pleistocene
***similar to the Gulf of Alaska**

(Sato et al., in preparation)

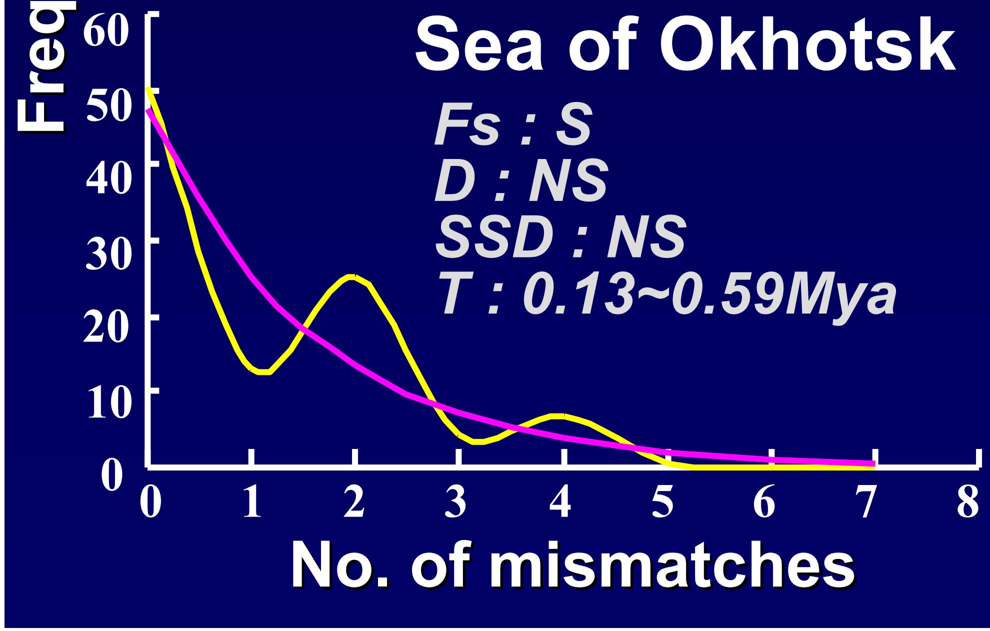
Mismatch distribution analysis and Neutrality tests for demographic history in masu salmon (mtDNA)


Entire

Fs : S
D : S
SSD : NS
T : 0.08~0.39Mya


Sea of Japan

Fs : S
D : S
SSD : NS
T : 0.04~0.21Mya


Sea of Okhotsk

Fs : S
D : NS
SSD : NS
T : 0.13~0.59Mya

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

(Yu et al. 2010a)

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

Graduate School of Science, Hokkaido University, Sapporo, Japan
National Salmon Resources Center, Sapporo, Japan
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!