Genetic separation of chum salmon (*Oncorhynchus keta*) collected from the western Bering Sea during summer-autumn 2004

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[1]Pukyong National University
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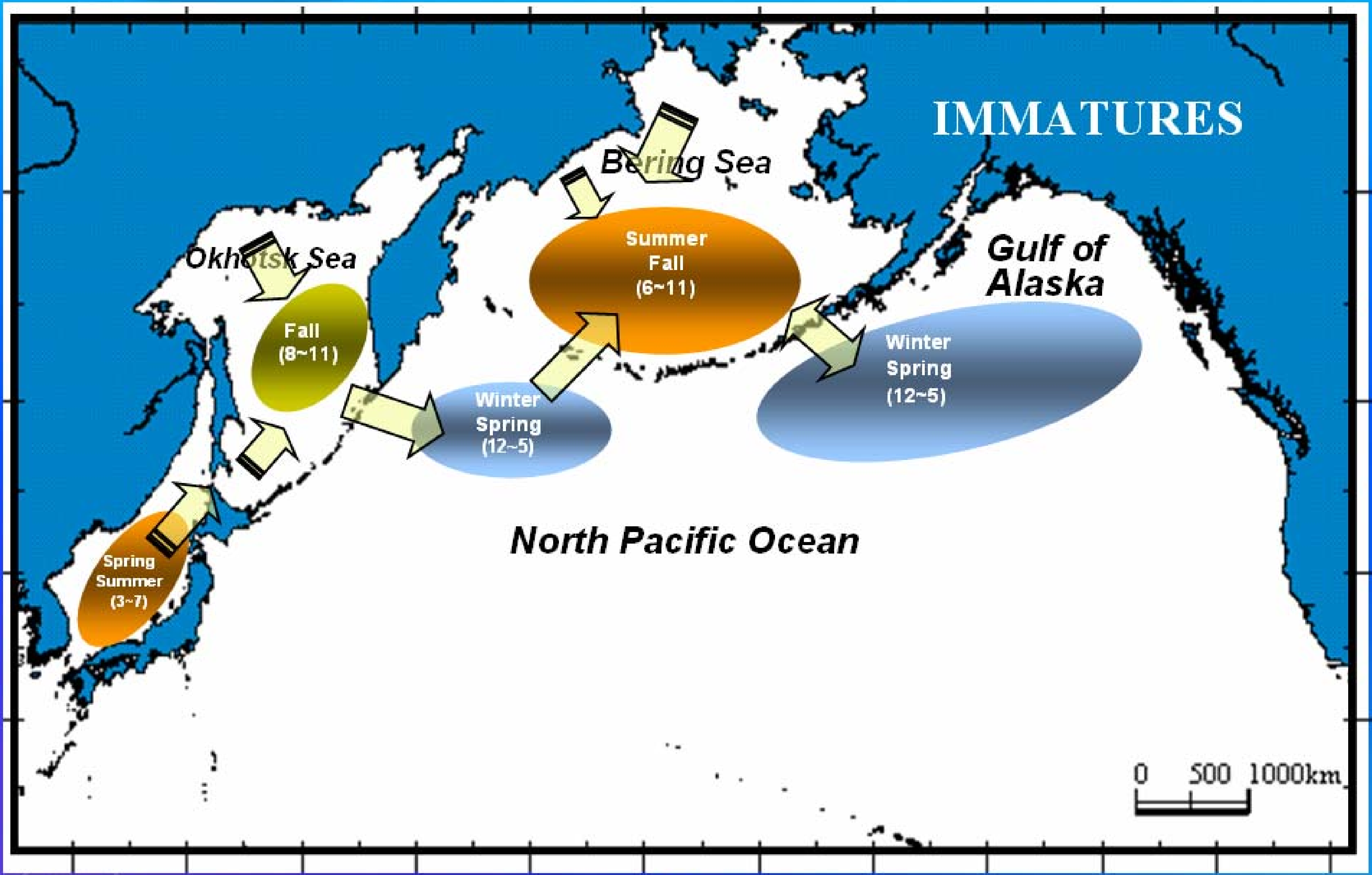
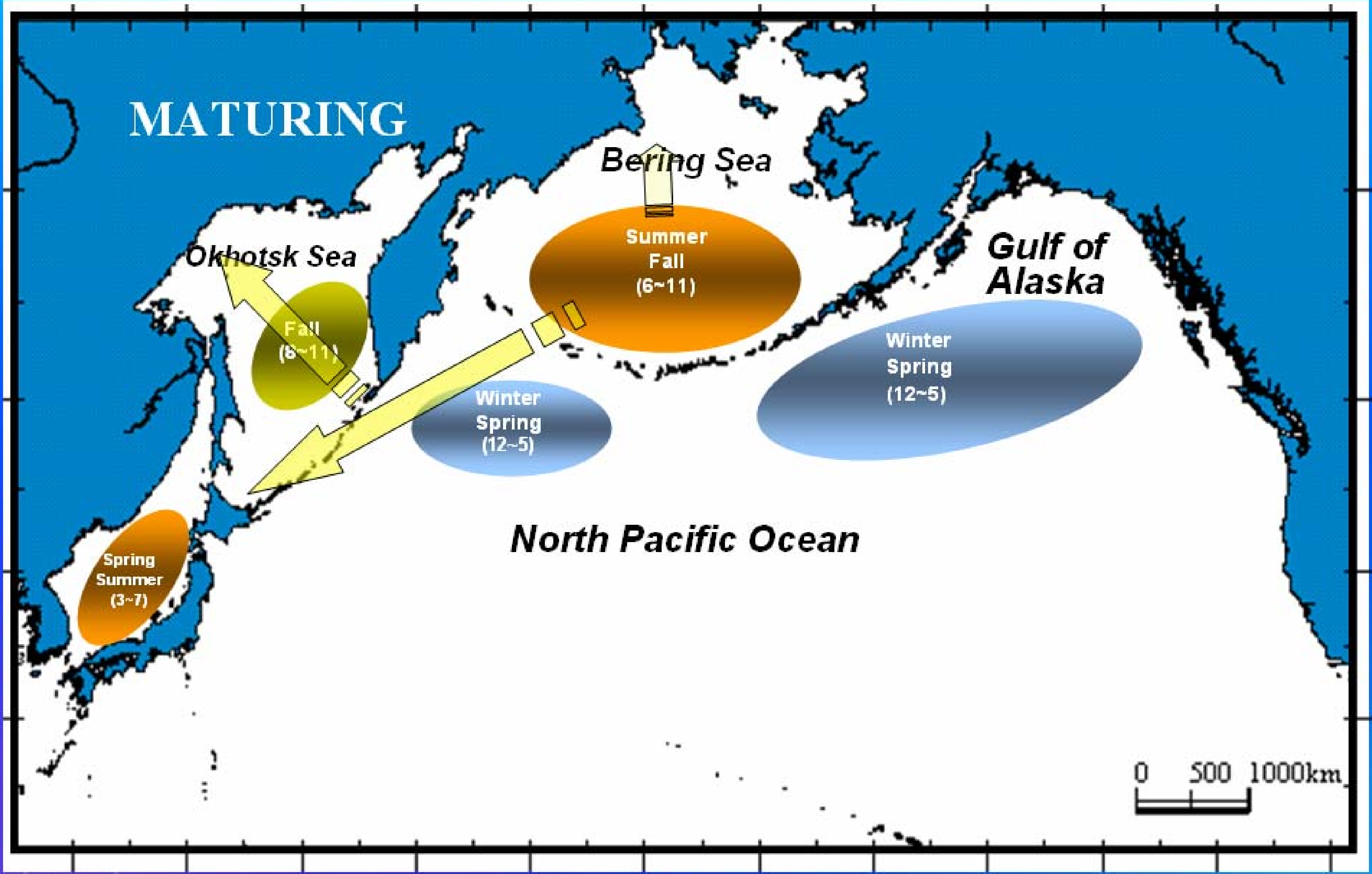
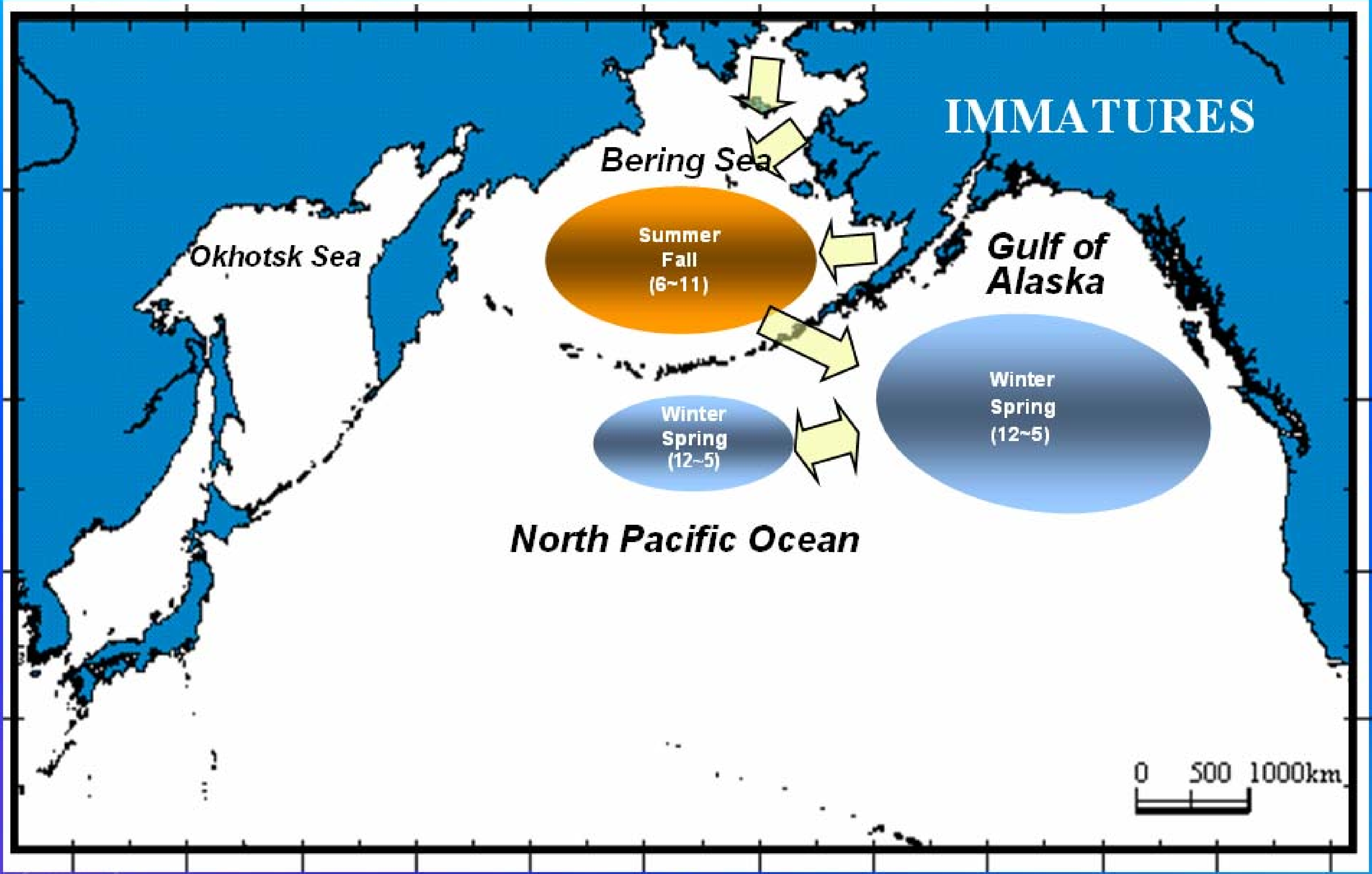
Migration model of Asian chum salmon (Seeb et al. 2004)



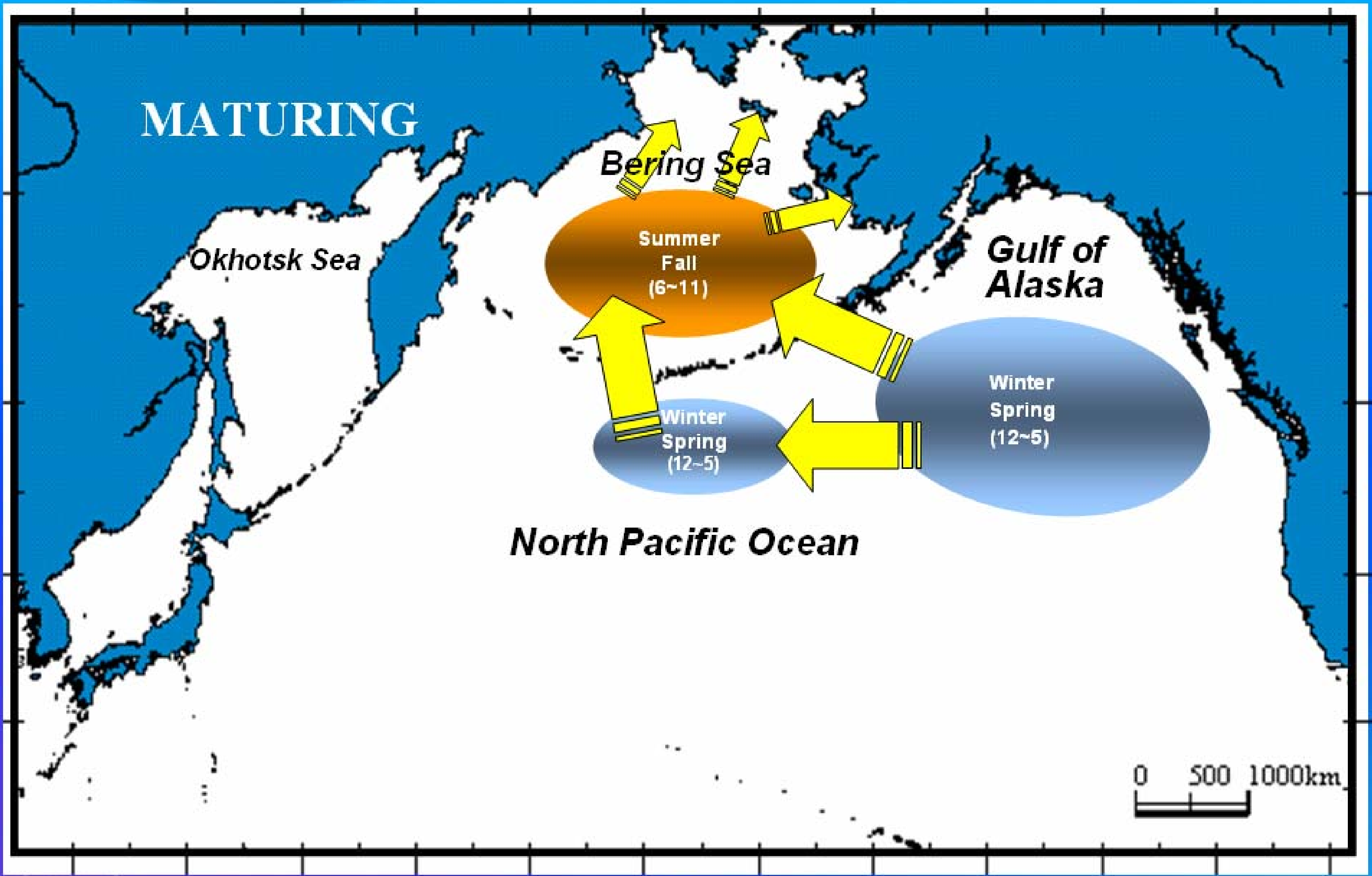
Migration model of Asian chum salmon (Seeb et al. 2004)



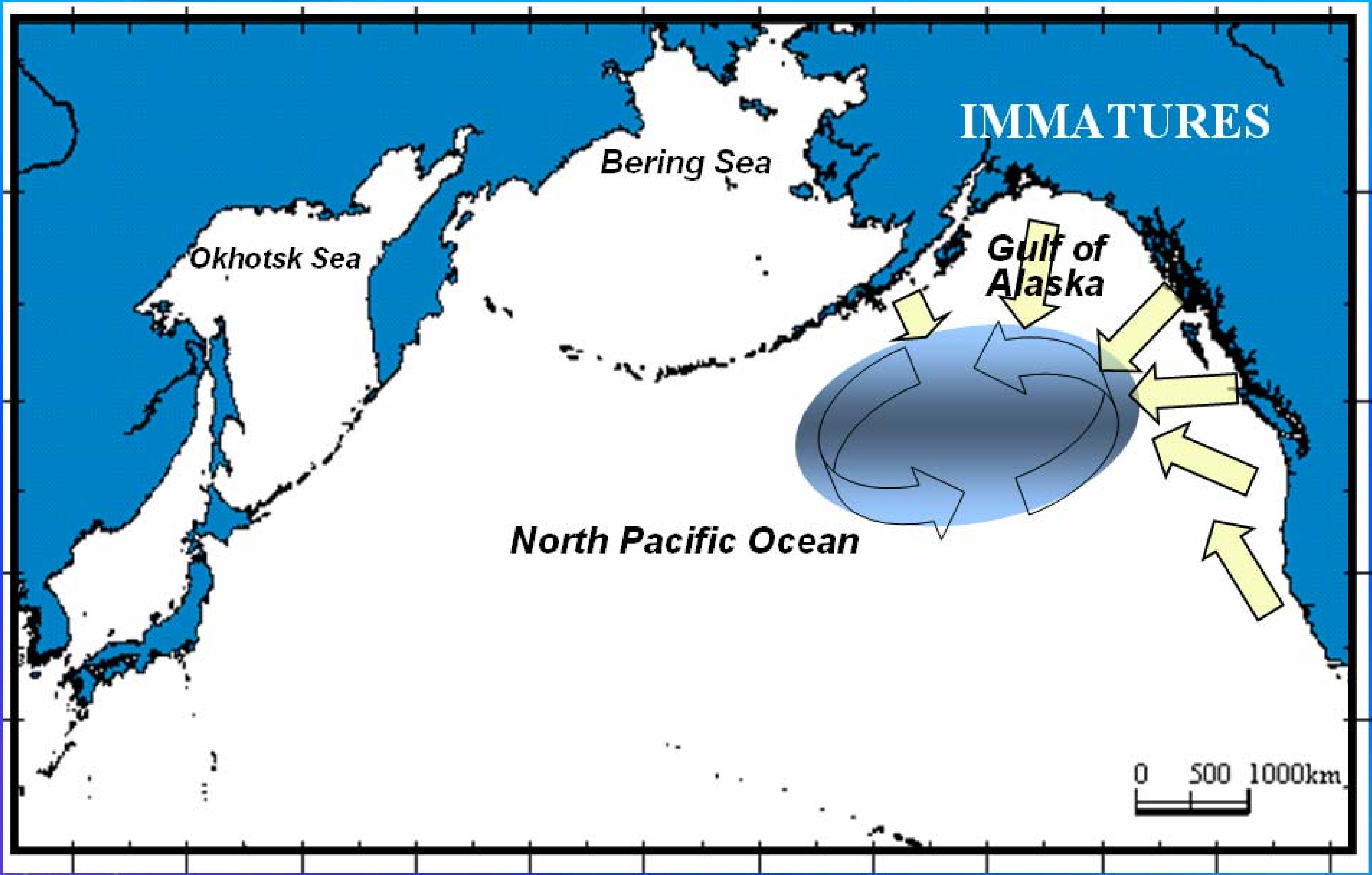
Migration model of western Alaskan chum salmon (Seeb et al. 2004)



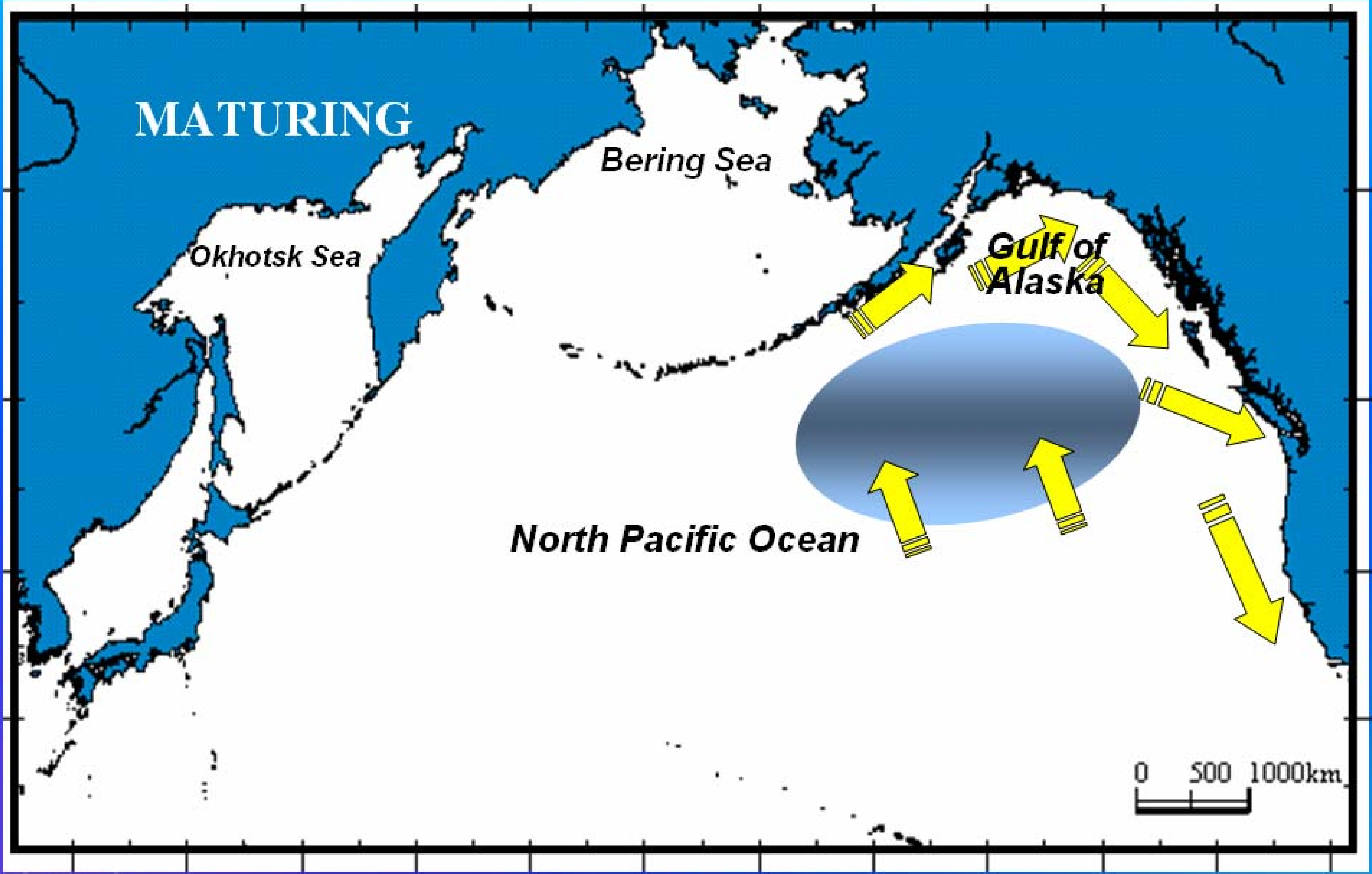
Migration model of western Alaskan chum salmon (Seeb et al. 2004)



Migration model of other North American chum salmon (Seeb et al. 2004)



Migration model of other North American chum salmon (Seeb et al. 2004)



Objectives

The aims of this presentation are to

- provide the basic information on baseline data of chum salmon along the North Pacific coast
- clarify their genetic relationships and phylogeny
- calculate the Genetic Stock Identification (GSI) of mixing stocks in the western Bering Sea

Contents

PART 1. Genetic population structure of chum salmon in the Pacific-rim

- 1-1 Materials and methods for baseline data
- 1-2 Results
  - 1-2-1 Haplotype composition in the baseline data
  - 1-2-2 Haplotype distribution in the baseline data
  - 1-2-3 Geographic differentiation in the Pacific-rim populations

Re-analysis mtDNA baseline data collected from hatcheries along the Pacific-rim.

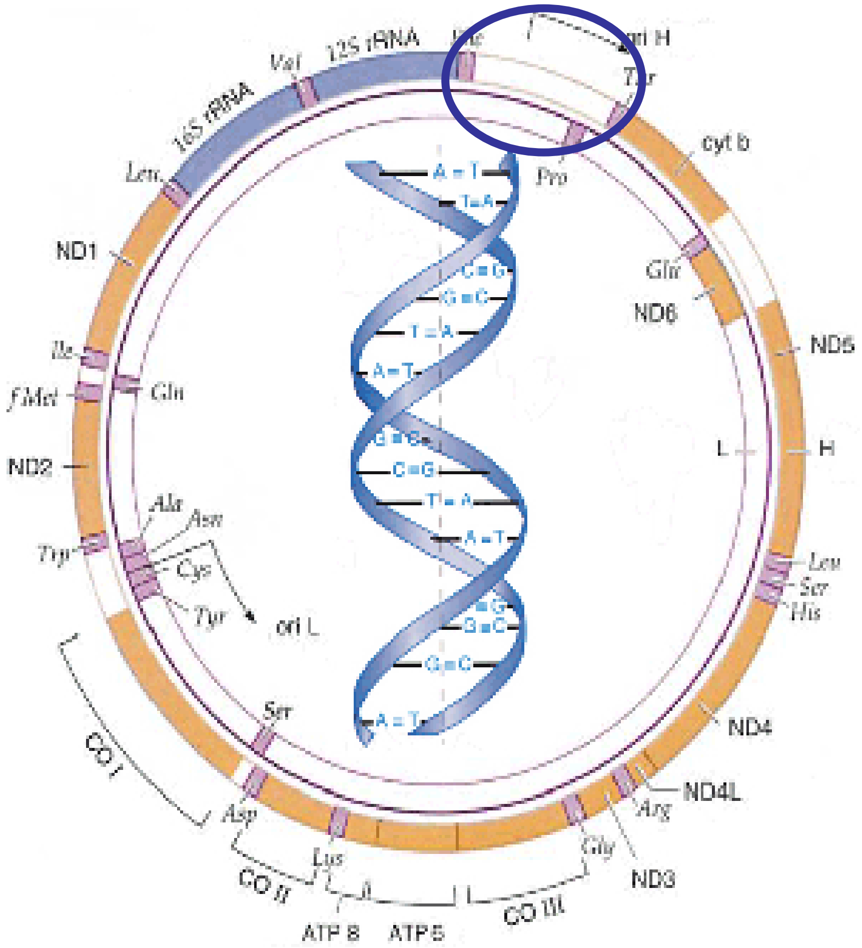
Contents

Mixing status of ocean catch was investigated with BASIS samples collected from the western Bering Sea (2004).

PART 2. Genetic stock identification of chum salmon in the western Bering Sea during fall 2004

- 2-1 Materials and methods for mixing stock
- 2-2 Results
  - 2-2-1 Haplotype compositions and distribution of mixtures in the western Bering Sea
  - 2-2-2 Genetic stock identification (GSI)

Methods



- Control region
- PCR Purification
- Direct sequencing PCR method
- Seqencing analysis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Methods

- The haplotype (H) and nucleotide diversity (π) in the mtDNA control regions

- Phylogenetic tree: Phylip software

- Geographic structuring: AMOVA test (Arlequin software)

Materials for Baseline data

Previously analyzed

- 48 populations (Sato et al., 2004)
- 48 + 28 populations (Yoon et al., 2004)

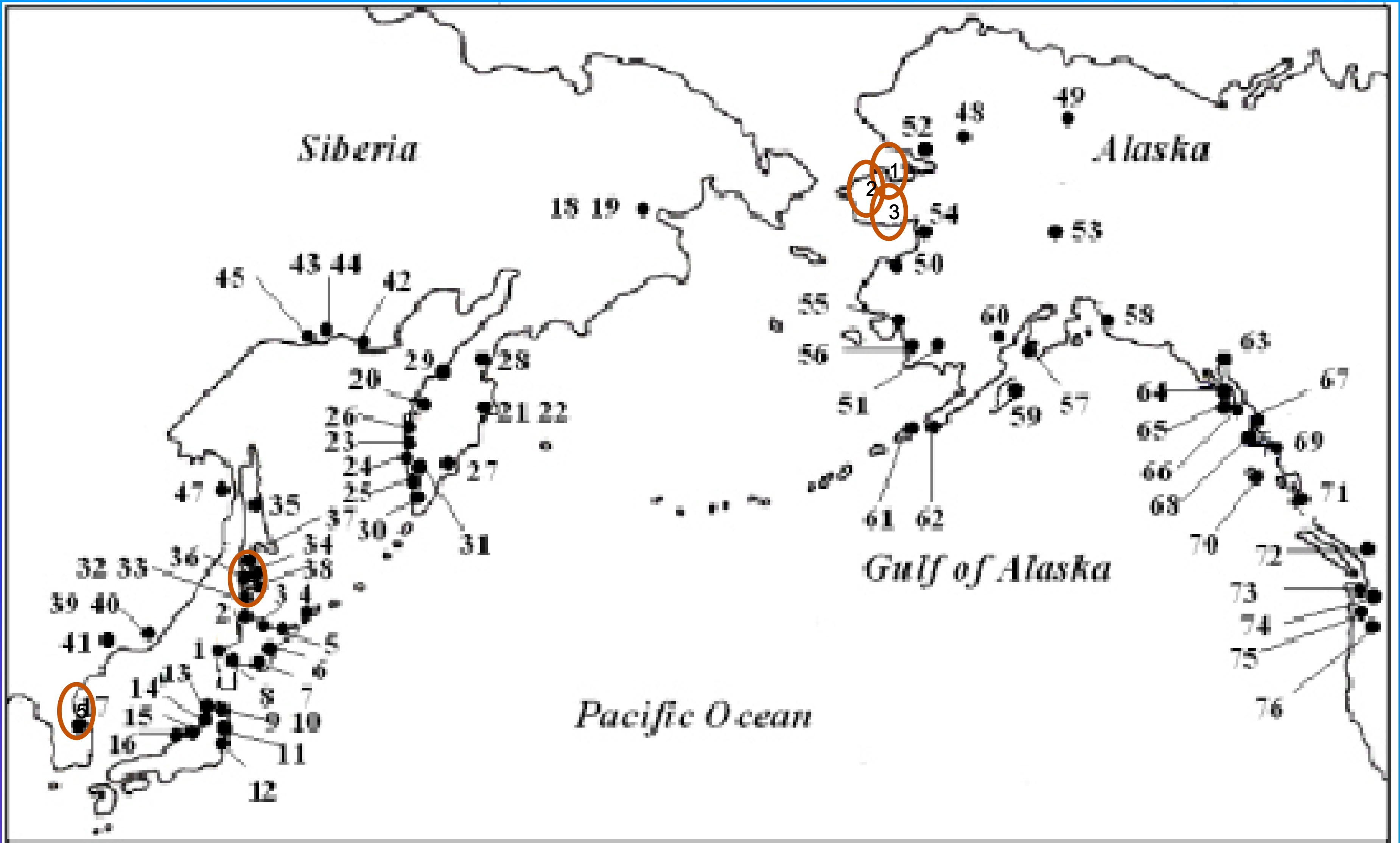
We added five more populations

- Namdae river (Korea, 2004)
- Taranai river (Russia, 2004)
- Niukluk, Kwiniuk, Fish river (Alaska, 2004)

So, totals of 81 populations were analysed in this study.

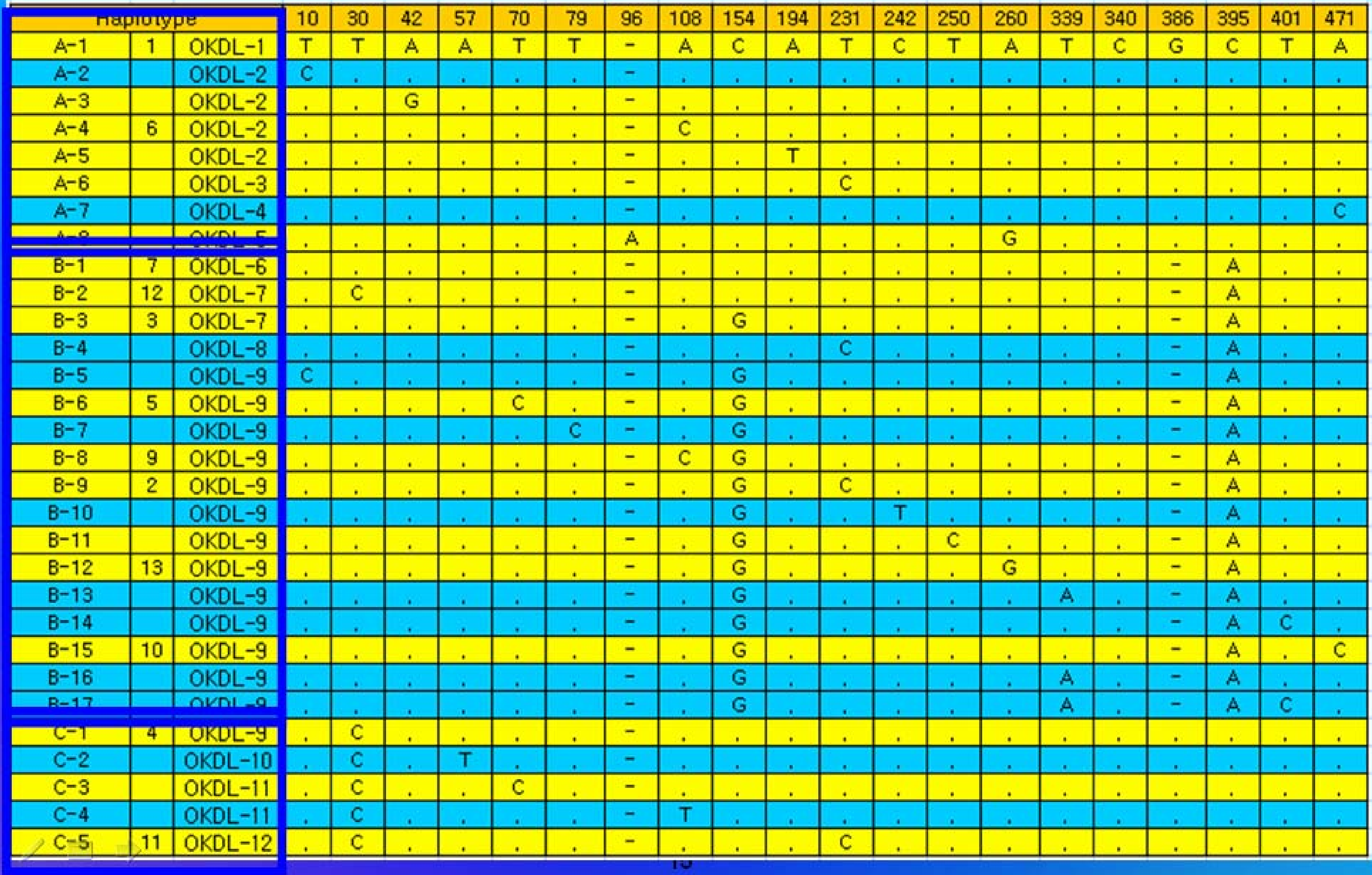
Materials

Geographical locations of Baseline data (Yoon et al., 2004)



Haplotype composition in the Baseline data

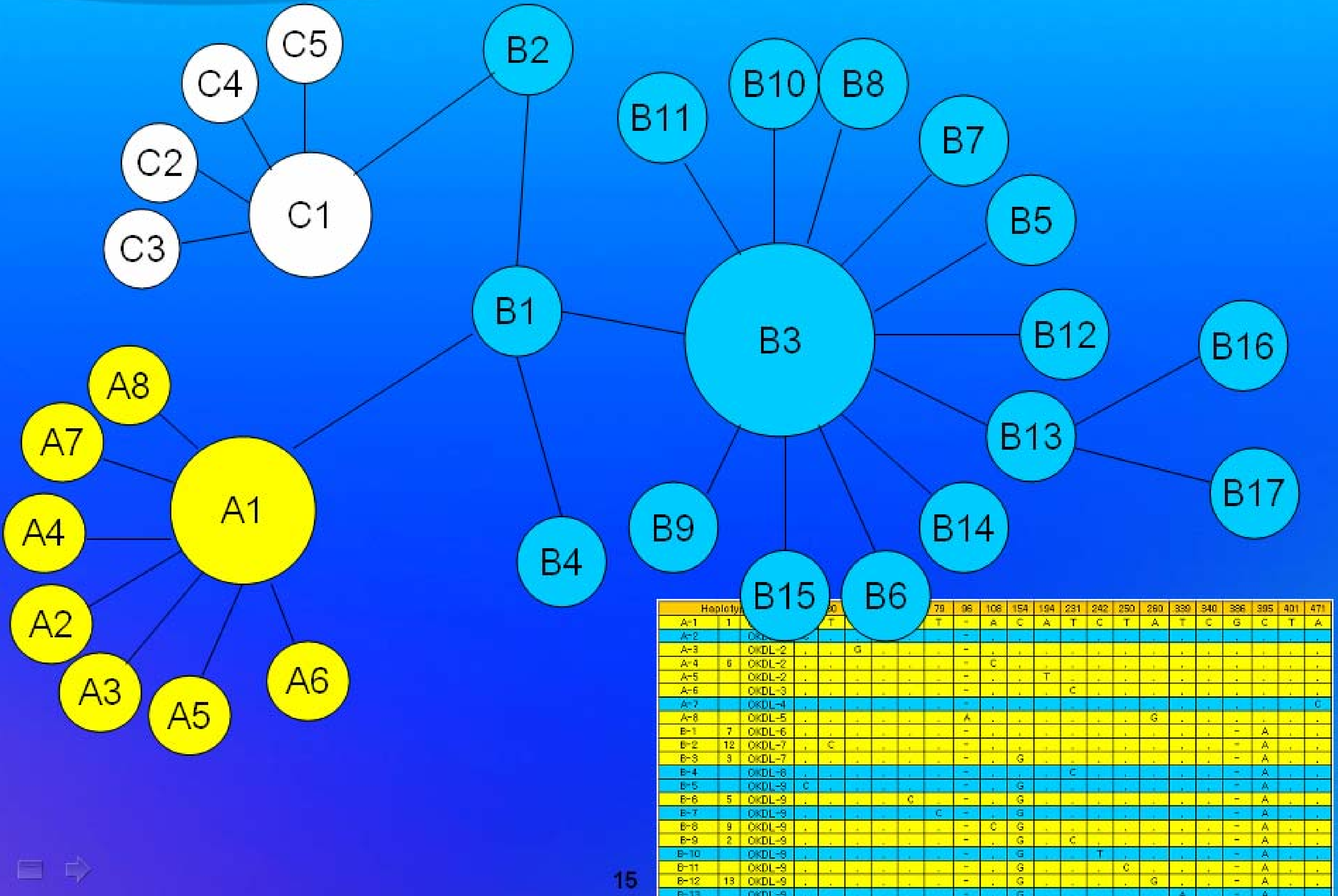
(Sato et al., 2004)



Haplotype			10	30	42	57	70	79	96	108	154	194	231	242	250	260	339	340	386	395	401	471
A-1	1	OKDL-1	T	T	A	A	T	T	-	A	C	A	T	C	T	A	T	C	G	C	T	A
A-2		OKDL-2	C	.	.	.	.	.	-	.	.	.	.	.	.	.	.	.	.	.	.	.
A-3		OKDL-2	.	.	G	.	.	.	-	.	.	.	.	.	.	.	.	.	.	.	.	.
A-4	6	OKDL-2	.	.	.	.	.	.	-	C	.	.	.	.	.	.	.	.	.	.	.	.
A-5		OKDL-2	.	.	.	.	.	.	-	.	.	T	.	.	.	.	.	.	.	.	.	.
A-6		OKDL-3	.	.	.	.	.	.	-	.	.	.	C	.	.	.	.	.	.	.	.	.
A-7		OKDL-4	.	.	.	.	.	.	-	.	.	.	.	.	.	.	.	.	.	.	.	C
A-8		OKDL-5	.	.	.	.	.	.	A	.	.	.	.	.	.	G	.	.	.	.	.	.
B-1	7	OKDL-6	.	.	.	.	.	.	-	.	.	.	.	.	.	.	.	.	-	A	.	.
B-2	12	OKDL-7	.	C	.	.	.	.	-	.	.	.	.	.	.	.	.	.	-	A	.	.
B-3	3	OKDL-7	.	.	.	.	.	.	-	.	G	.	.	.	.	.	.	.	-	A	.	.
B-4		OKDL-8	.	.	.	.	.	.	-	.	.	.	C	.	.	.	.	.	-	A	.	.
B-5		OKDL-9	C	.	.	.	.	.	-	.	G	.	.	.	.	.	.	.	-	A	.	.
B-6	5	OKDL-9	.	.	.	.	C	.	-	.	G	.	.	.	.	.	.	.	-	A	.	.
B-7		OKDL-9	.	.	.	.	.	C	-	.	G	.	.	.	.	.	.	.	-	A	.	.
B-8	9	OKDL-9	.	.	.	.	.	.	-	C	G	.	.	.	.	.	.	.	-	A	.	.
B-9	2	OKDL-9	.	.	.	.	.	.	-	.	G	.	C	.	.	.	.	.	-	A	.	.
B-10		OKDL-9	.	.	.	.	.	.	-	.	G	.	.	T	.	.	.	.	-	A	.	.
B-11		OKDL-9	.	.	.	.	.	.	-	.	G	.	.	.	C	.	.	.	-	A	.	.
B-12	13	OKDL-9	.	.	.	.	.	.	-	.	G	.	.	.	.	G	.	.	-	A	.	.
B-13		OKDL-9	.	.	.	.	.	.	-	.	G	.	.	.	.	.	A	.	-	A	.	.
B-14		OKDL-9	.	.	.	.	.	.	-	.	G	.	.	.	.	.	.	.	-	A	C	.
B-15	10	OKDL-9	.	.	.	.	.	.	-	.	G	.	.	.	.	.	.	.	-	A	.	C
B-16		OKDL-9	.	.	.	.	.	.	-	.	G	.	.	.	.	.	A	.	-	A	.	.
B-17		OKDL-9	.	.	.	.	.	.	-	.	G	.	.	.	.	.	A	.	-	A	C	.
C-1	4	OKDL-9	.	C	.	.	.	.	-	.	.	.	.	.	.	.	.	.	.	.	.	.
C-2		OKDL-10	.	C	.	T	.	.	-	.	.	.	.	.	.	.	.	.	.	.	.	.
C-3		OKDL-11	.	C	.	.	C	.	-	.	.	.	.	.	.	.	.	.	.	.	.	.
C-4		OKDL-11	.	C	.	.	.	.	-	T	.	.	.	.	.	.	.	.	.	.	.	.
C-5	11	OKDL-12	.	C	.	.	.	.	-	.	.	.	C	.	.	.	.	.	.	.	.	.

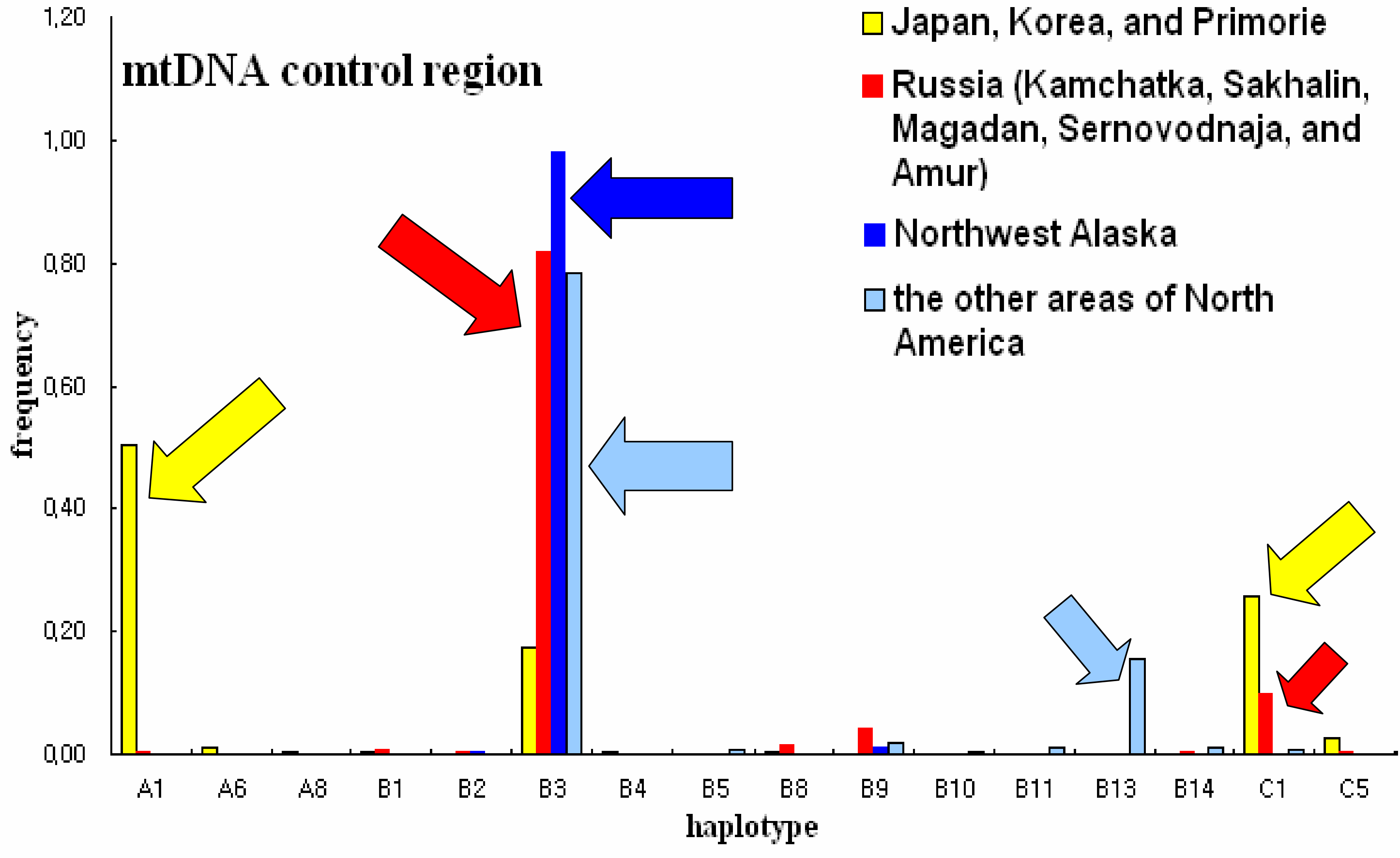
Haplotype composition in the Baseline data

(Sato et al., 2004)

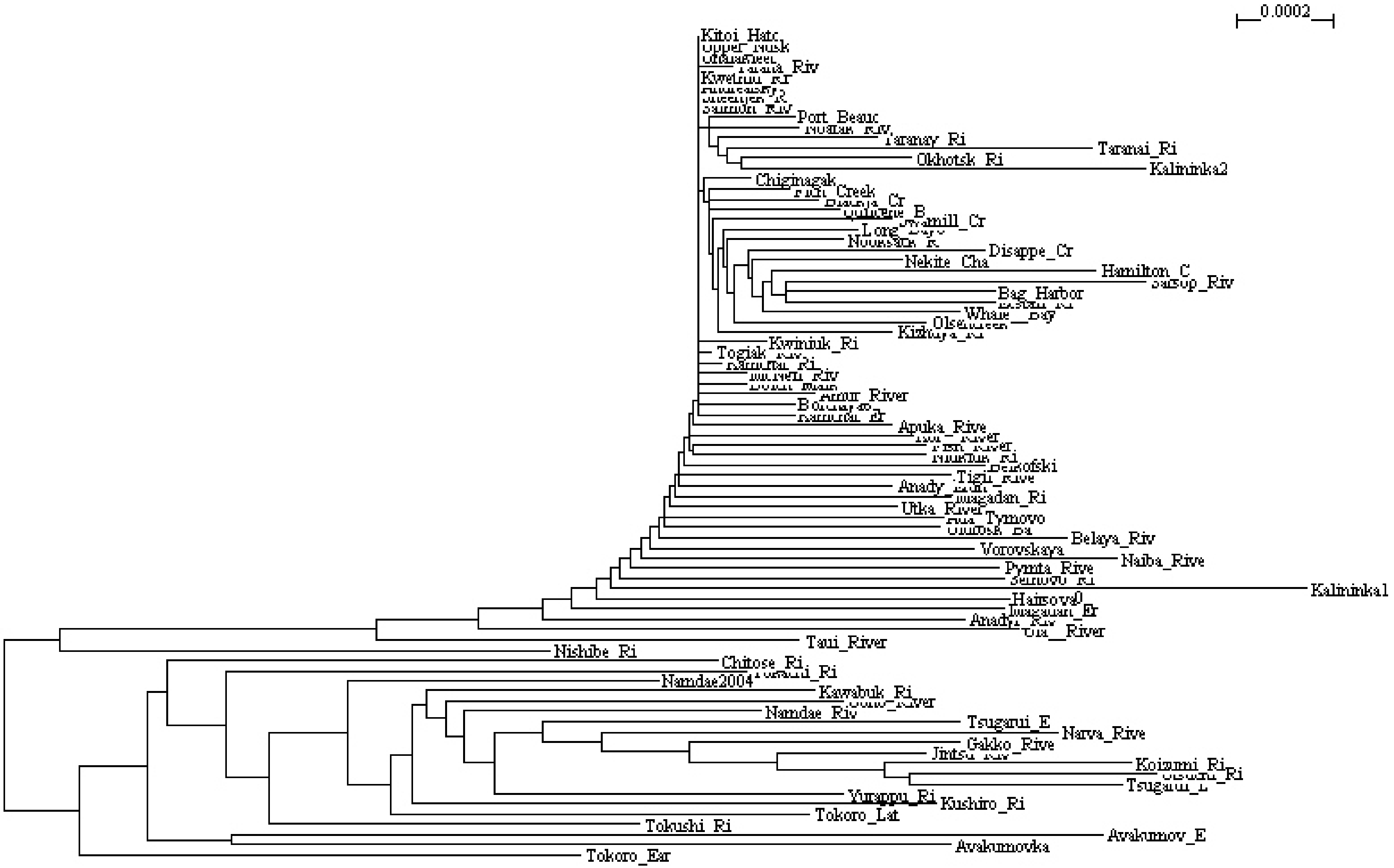


Haplotype			[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	79	96	106	154	194	231	242	250	260	339	340	386	395	401	471
A-1	1	[illegible]	[illegible]	T	[illegible]	[illegible]	[illegible]	T	-	A	C	A	T	C	T	A	T	C	G	C	T	A
A-2		[illegible]	[illegible]	.	[illegible]	[illegible]	[illegible]	.	-	.	.	.	.	.	.	.	.	.	.	.	.	.
A-3		OKDL-2	.	.	G	.	.	.	-	.	.	.	.	.	.	.	.	.	.	.	.	.
A-4	6	OKDL-2	.	.	.	.	.	.	-	C	.	.	.	.	.	.	.	.	.	.	.	.
A-5		OKDL-2	.	.	.	.	.	.	-	.	.	T	.	.	.	.	.	.	.	.	.	.
A-6		OKDL-3	.	.	.	.	.	.	-	.	.	.	C	.	.	.	.	.	.	.	.	.
A-7		OKDL-4	.	.	.	.	.	.	-	.	.	.	.	.	.	.	.	.	.	.	.	C
A-8		OKDL-5	.	.	.	.	.	.	A	.	.	.	.	.	.	G	.	.	.	.	.	.
B-1	7	OKDL-6	.	.	.	.	.	.	-	.	.	.	.	.	.	.	.	.	-	A	.	.
B-2	12	OKDL-7	.	C	.	.	.	.	-	.	.	.	.	.	.	.	.	.	-	A	.	.
B-3	3	OKDL-7	.	.	.	.	.	.	-	.	G	.	.	.	.	.	.	.	-	A	.	.
B-4		OKDL-8	.	.	.	.	.	.	-	.	.	.	C	.	.	.	.	.	-	A	.	.
B-5		OKDL-9	C	.	.	.	.	.	-	.	G	.	.	.	.	.	.	.	-	A	.	.
B-6	5	OKDL-9	.	.	.	.	C	.	-	.	G	.	.	.	.	.	.	.	-	A	.	.
B-7		OKDL-9	.	.	.	.	.	C	-	.	G	.	.	.	.	.	.	.	-	A	.	.
B-8	9	OKDL-9	.	.	.	.	.	.	-	C	G	.	.	.	.	.	.	.	-	A	.	.
B-9	2	OKDL-9	.	.	.	.	.	.	-	.	G	.	C	.	.	.	.	.	-	A	.	.
B-10		OKDL-9	.	.	.	.	.	.	-	.	G	.	.	T	.	.	.	.	-	A	.	.
B-11		OKDL-9	.	.	.	.	.	.	-	.	G	.	.	.	C	.	.	.	-	A	.	.
B-12	13	OKDL-9	.	.	.	.	.	.	-	.	G	.	.	.	.	G	.	.	-	A	.	.
B-13		OKDL-9	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	-	[illegible]	G	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	A	[illegible]	-	A	[illegible]	[illegible]

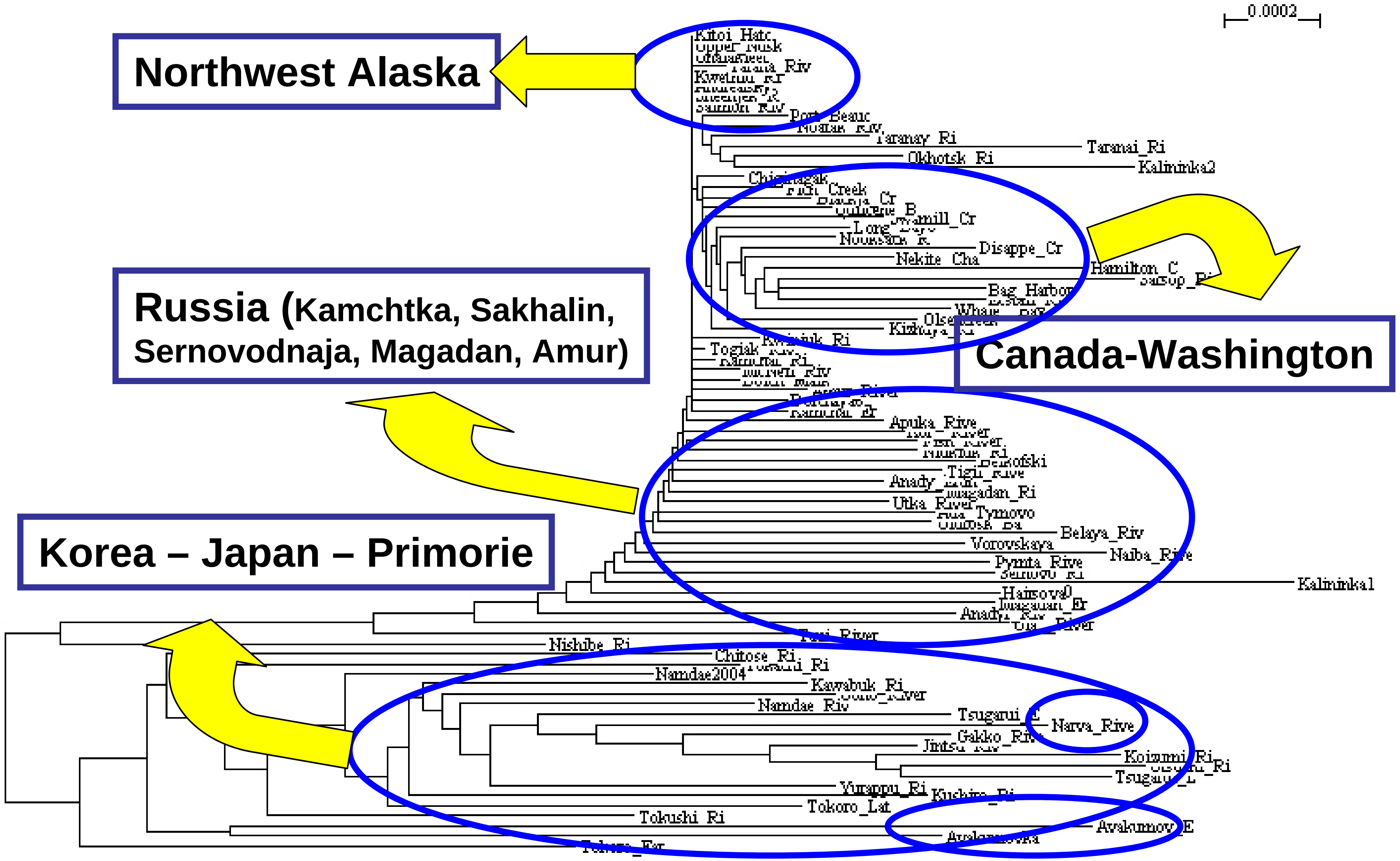
Haplotype distribution in the Baseline data



Phylogenetic Tree; Neighbor-joining method



Phylogenetic Tree; Neighbor-joining method



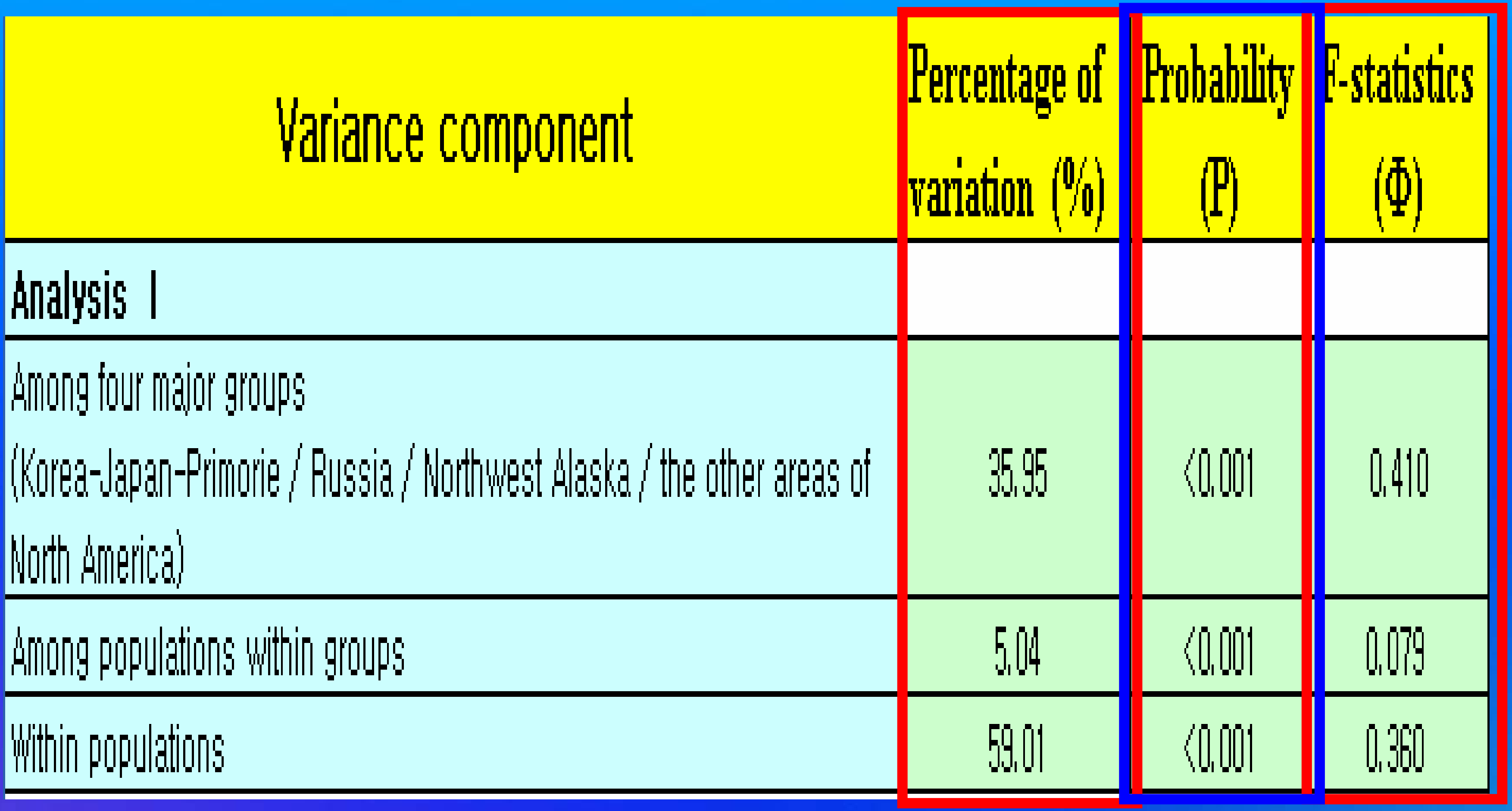
Northwest Alaska

Canada-Washington

Russia (Kamchtka, Sakhalin, Sernovodnaja, Magadan, Amur)

Korea – Japan – Primorie

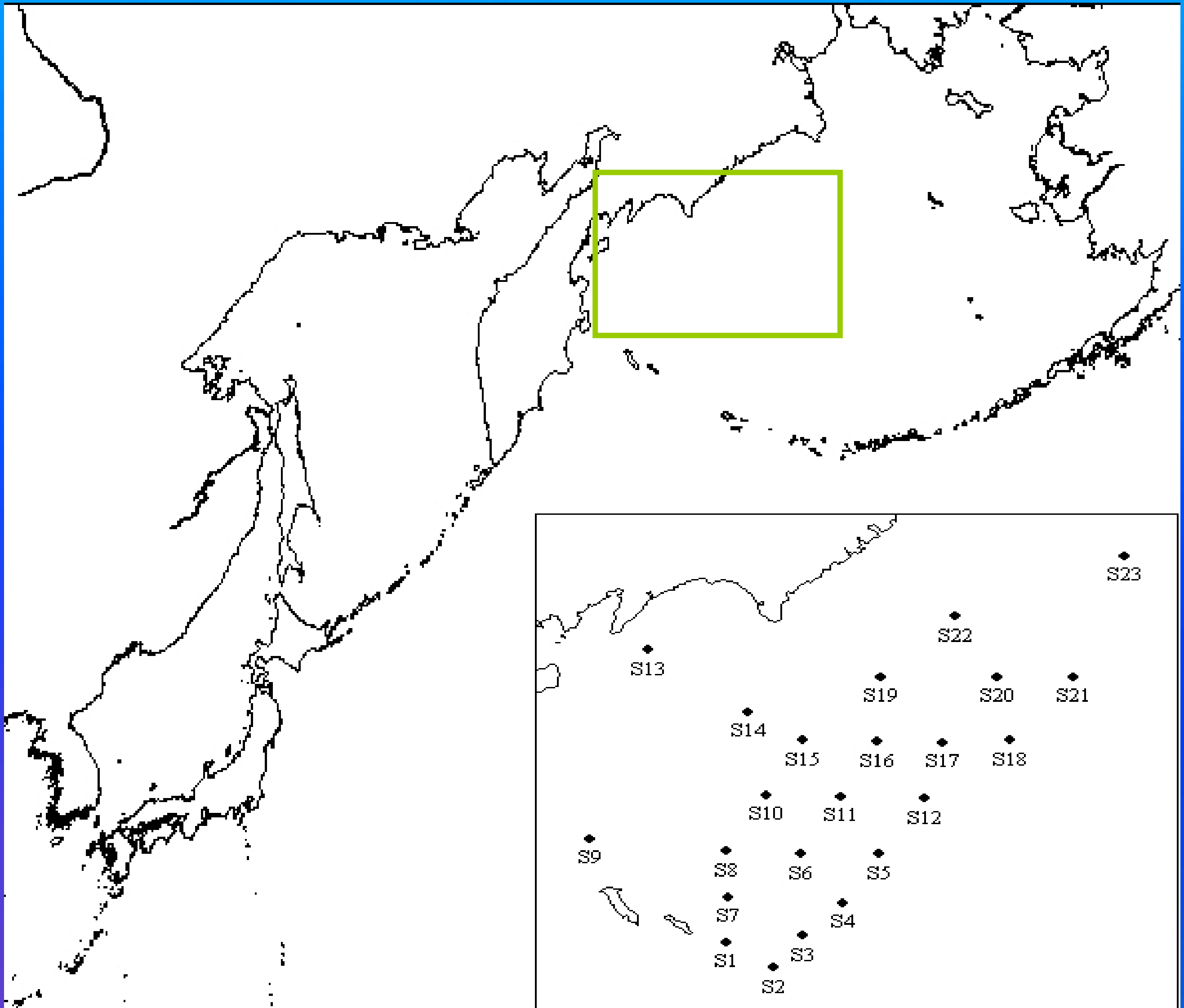
Analysis of molecular variance (AMOVA) Test in the Baseline data



Variance component	Percentage of variation (%)	Probability (P)	F-statistics (Φ)
Analysis I			
Among four major groups (Korea-Japan-Primorie / Russia / Northwest Alaska / the other areas of North America)	35.95	<0.001	0.410
Among populations within groups	5.04	<0.001	0.079
Within populations	59.01	<0.001	0.360

Materials for mixing stock

Geographical locations of Mixing stocks



- **Sampling date:**

  Sept. 26 ~ Oct. 23, 2004

- **Sampling gear:**

  TINRO research cruise

- **Speed of trawl:**

  ~ 4.4 knots

- **A total of 826 specimens from 48 stations**

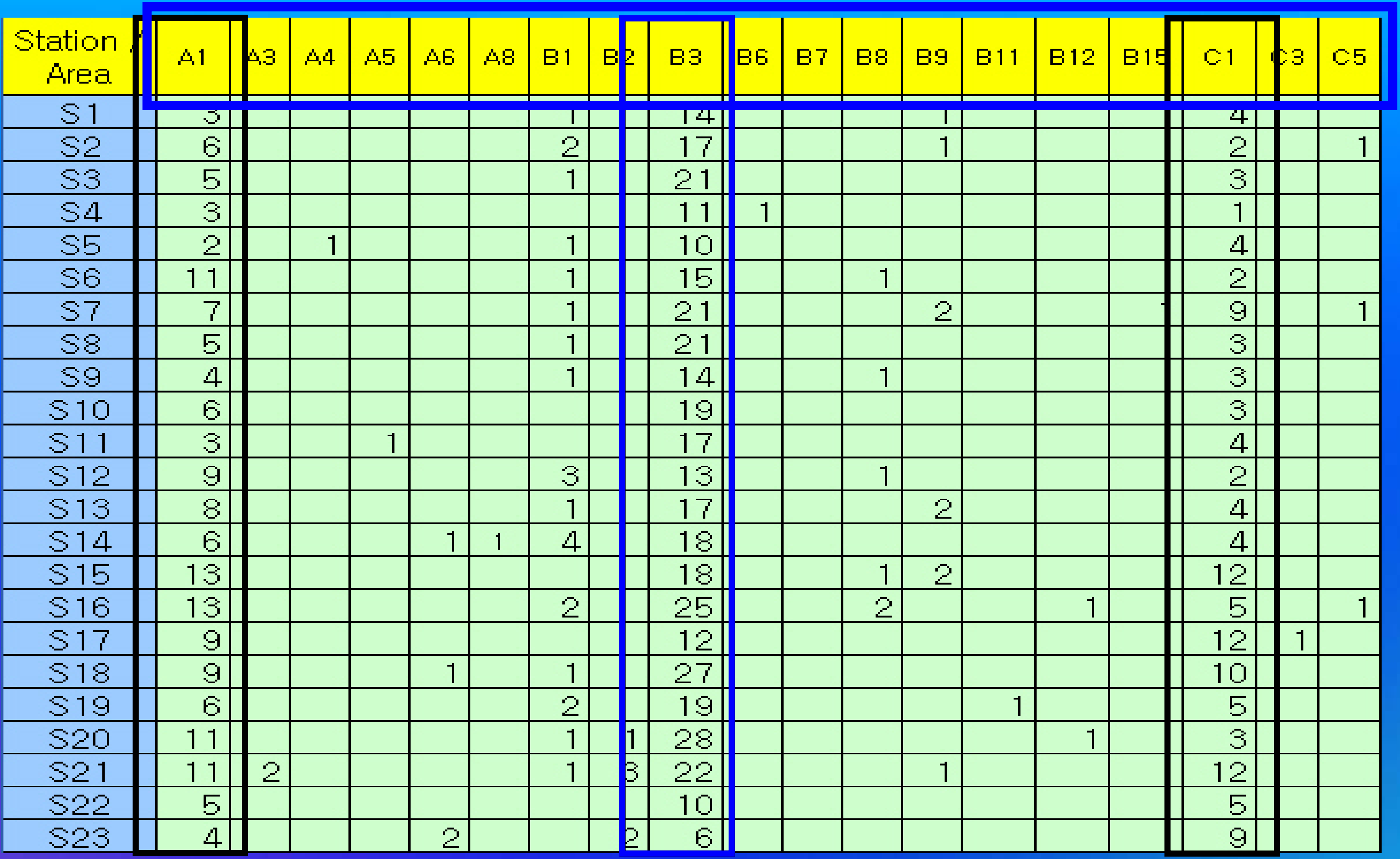
Methods

- The haplotype (H) analysis for stock composition
- Estimation of regional proportion:

Statistic Programs for Analyzing Mixtures (SPAM version 3.7, ADGF 2003)

Results

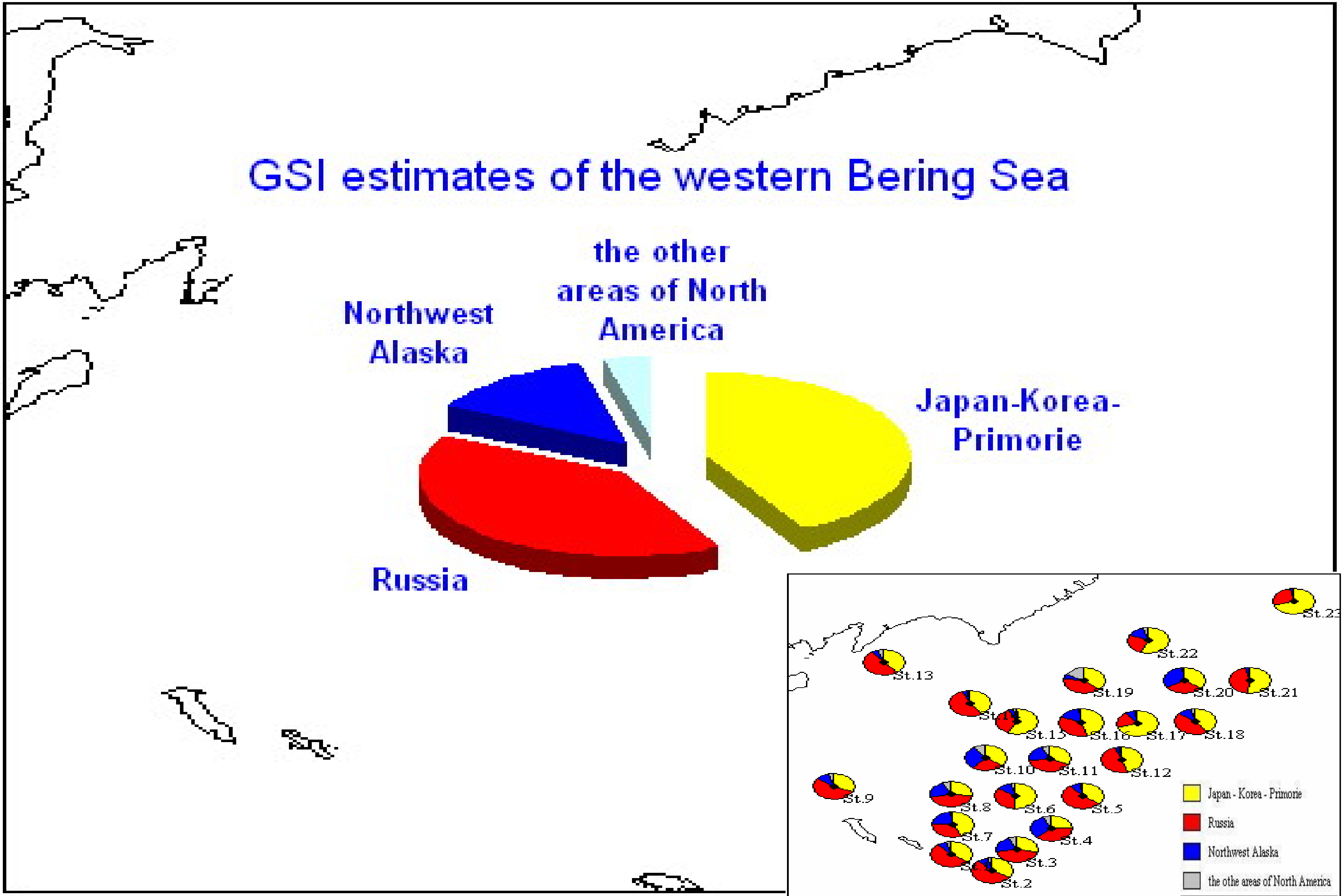
< Haplotype composition and distribution of mixtures in the western Bering Sea >



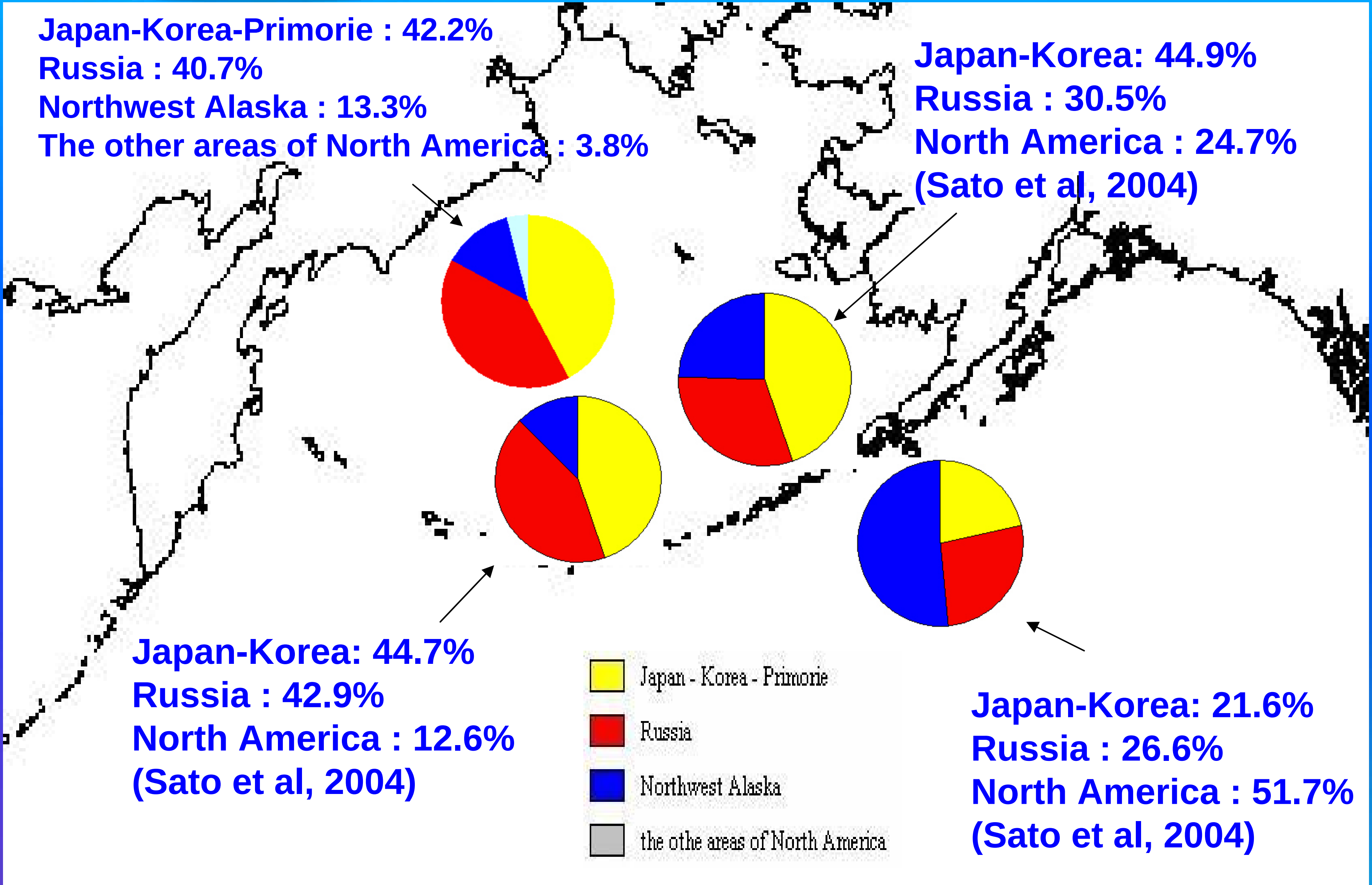
Station Area	A1	A3	A4	A5	A6	A8	B1	B2	B3	B6	B7	B8	B9	B11	B12	B15	C1	C3	C5
S1	3						1		14				1				4		
S2	6						2		17				1				2		1
S3	5						1		21								3		
S4	3								11	1							1		
S5	2		1				1		10								4		
S6	11						1		15			1					2		
S7	7						1		21				2			1	9		1
S8	5						1		21								3		
S9	4						1		14			1					3		
S10	6								19								3		
S11	3			1					17								4		
S12	9						3		13			1					2		
S13	8						1		17				2				4		
S14	6				1	1	4		18								4		
S15	13								18			1	2				12		
S16	13						2		25			2			1		5		1
S17	9								12								12	1	
S18	9				1		1		27								10		
S19	6						2		19					1			5		
S20	11						1	1	28						1		3		
S21	11	2					1	3	22				1				12		
S22	5								10								5		
S23	4				2			2	6								9		

GSI (Genetic Stock Identification):

Maximum likelihood algorithm (Pella-Masuda model)



Results



Japan-Korea-Primorie : 42.2%
Russia : 40.7%
Northwest Alaska : 13.3%
The other areas of North America : 3.8%

Japan-Korea: 44.9%
Russia : 30.5%
North America : 24.7%
(Sato et al, 2004)

Japan-Korea: 44.7%
Russia : 42.9%
North America : 12.6%
(Sato et al, 2004)

Japan-Korea: 21.6%
Russia : 26.6%
North America : 51.7%
(Sato et al, 2004)

Conclusion

1. In the phylogenetic relationship,
   Primorie population was closer to Japan/Korea group

2. The population structure indicates four groups of chum salmon populations in the North Pacific

   Japan-Korea-Primorie group
   Russian group (around the Okhotsk Sea)
   Northwest Alaskan group (Bering Sea)
   The other areas of North American group
   (Gulf of Alaska, Canada, Washington, etc.)

Conclusion

3. Genetic stock identification in the western Bering Sea;

Japan-Korea-Primorie: 42.2%
Russia: 40.7%
Northwest Alaska: 13.3%
The other areas of North America: 3.8%

Some portions of Chum salmon released from the mainland North America migrate to the Bering Sea during marine life!!!

Future works

Approach for determining the distribution of chum salmon at sea by using

⇨ patterns of variation in polymorphic DNA marker

⇨ relative abundance of immature and maturing salmon in time and space

Thank you