Molecular phylogeography of *Nemopilema nomurai* (Class: Scyphozoa) in Korean waters

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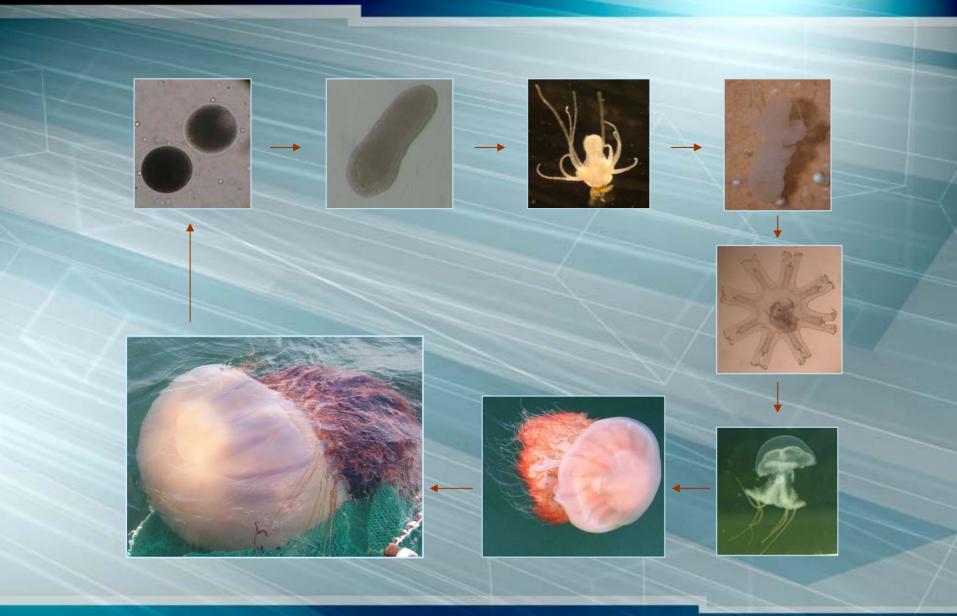
Mass occurrence of Nemopilema nomurai

- Distribution: East China Sea, Korea Peninsula, Japan Sea
- Damage to fishery and human health.
- August, 2003: 44 inds./10,000m², Yellow Sea
- August, 2005: 162 inds./10,000m², Yellow Sea
- August, 2007: 45 inds./10,000m², Yellow Sea

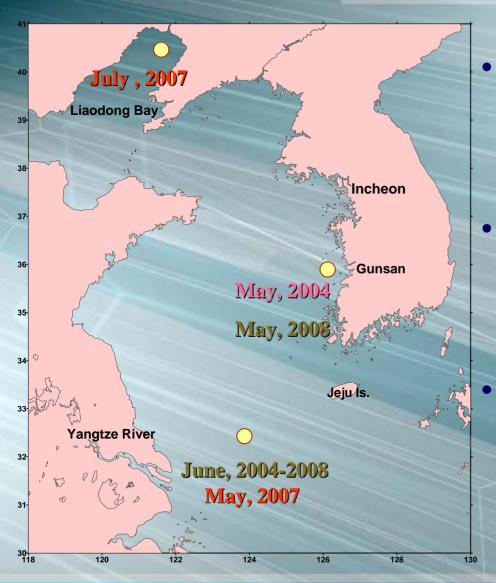




Life history of N. nomurai

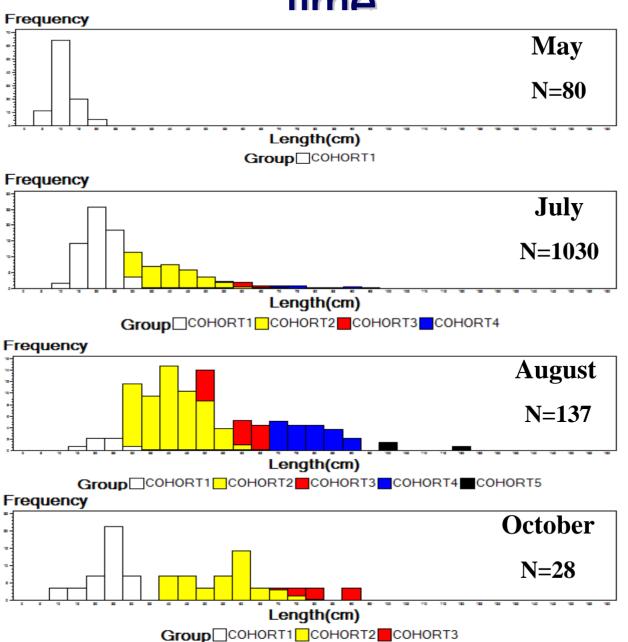


Early appearance of N. nomurai

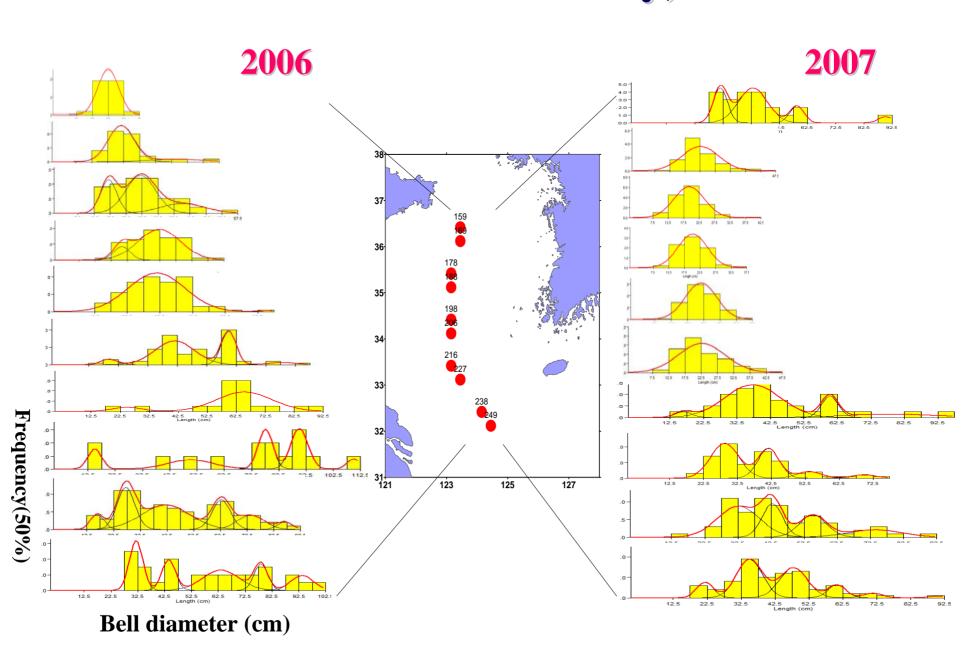


- East China Sea
 - Mid June, 2004-2008
 - Late May, 2007 (2.5-20 cm)
- Korean waters
 - May, 2004 off Gunsan (2-9 cm)
 - June, 2008 off Gunsan (9-55 cm)
- **Chinese waters**
 - Late June early July, 2007
 (2-6 cm) at Liaodong Bay
 (Jing Dong, IJW4, 2007)

Cohorts analysis of *N. nomurai* with



Cohorts of N. nomurai in July, Yellow Sea



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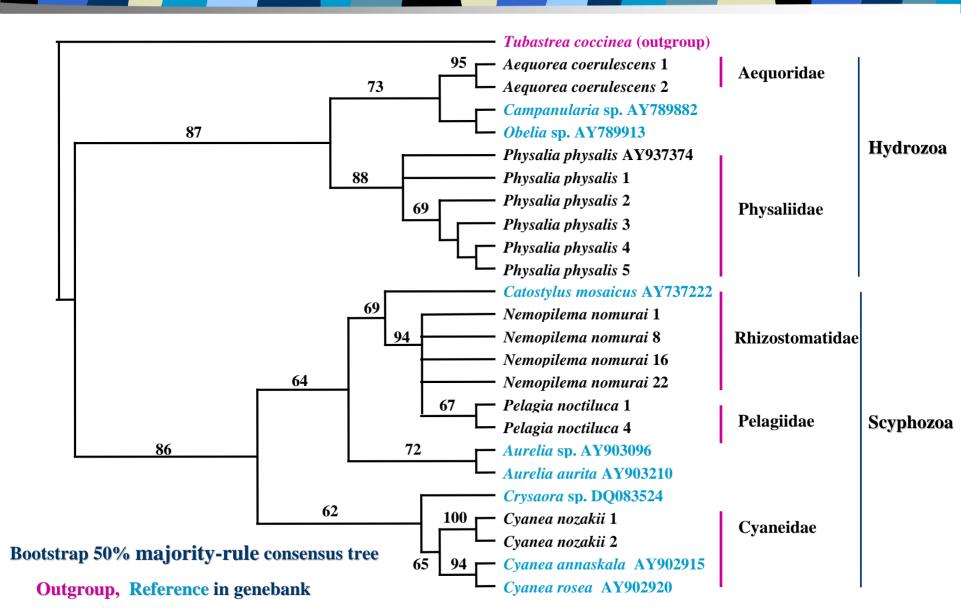
Materials & Methods

Class	Order	Family	Speicies	Location & Date	No. of samples
Scyphozoa	Rhizostomeae	Rhizostomidae	Nemopilema	Ieo-do: May, 2007	29
			nomurai	Ieo-do: July, 2007	20
				Incheon: August, 2007	19
				Center of the Yellow Sea: July, 2007	18
				Gunsan: August, 2007	15
				Busan: July, 2007	20
				Kangnung: August, 2007	19
	Semaeostomeae	Pelagiidae	Pelagia noctiluca	Kijang : May, 2008	2
		Cyaneidae	Cyanea nozakii	Center of Yellow Sea: July, 2007	2
Hydrozoa	Siphonophora	Physaliidae	Physalia physalis	Sungsan-po: July, 2007	5
	Leptomedusae	Aequoridae	Aequorea coerulescens	Kijang: May, 2008	2

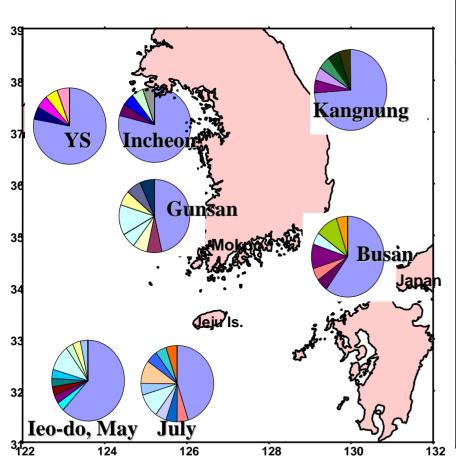
Materials & Methods

- Extraction: CTAB extraction method (Asahida et al., 1996)
- Amplifying : COI mtDNA
- Sequencing: 3730 xl DNA analyzer
- Phylogeny
 - Maximum Likelihood (ML) analysis (PAUP 4.0b 10)
 - Modeltest 3.7
- Population genetics
 - Genetic diversity, differentiation and AMOVA test (Arlequin 3.1)
 - Gene genealogy (TCS program)

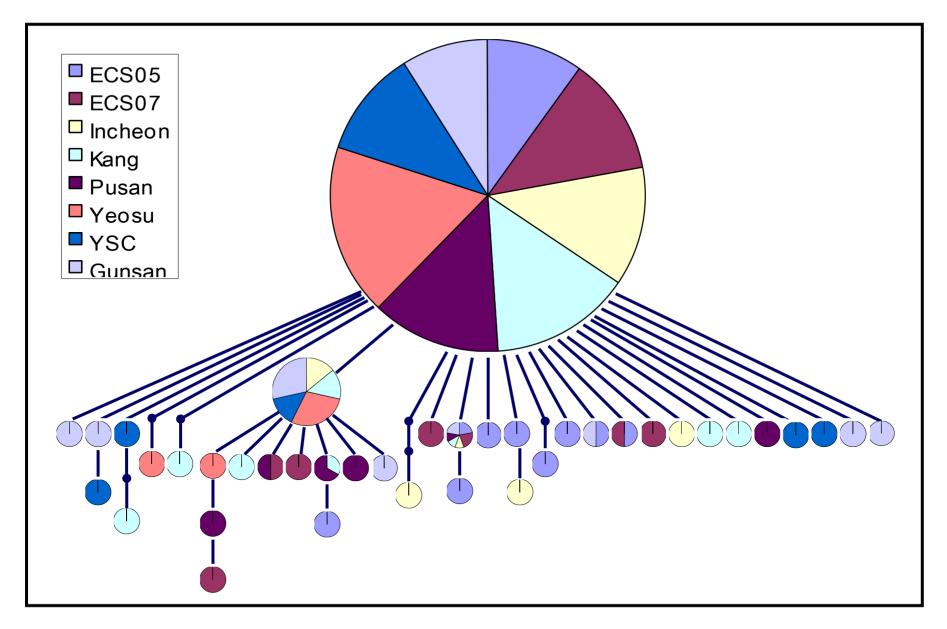
Result: COI mtDNA genetic trees of medusozoan



Result - Genetic diversity of N. nomurai among sites



Group	Sample size	No. of haplotypes	Genetic diversity	
leodo - May	29	10	0.6158 +/- 0.1035	
leodo – July	20	10	0.8000 +/- 0.0886	
Gunsan	15	8	0.7905 +/- 0.1049	
Busan	20	7	0.6421 +/- 0.1176	
Incheon	19	5	0.3860 +/- 0.1398	
Yellow Sea (37°E, 123°N)	18	5	0.4052 +/- 0.1489	
Kangnung	19	6	0.4678 +/- 0.1396	



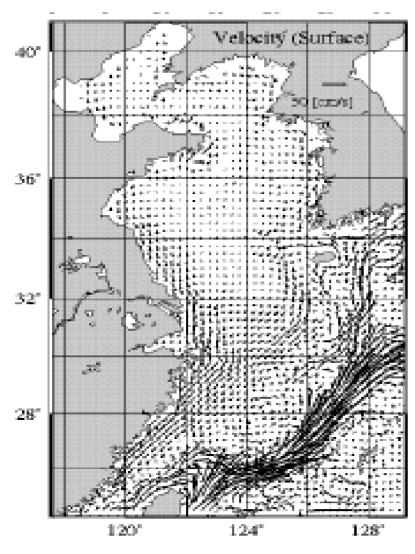
Haplotype network based on COI mtDNA (TCS)

Genetic differentiation & distance between groups

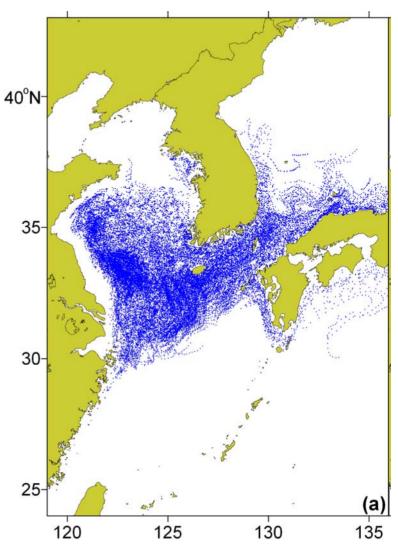
	Ieo-do, May	Ieo-do, July	Incheon	Yellow Sea	Gunsan	Busan	Kangnung
Ieo-do, May	0						
Ieo-do, July	0.318	0					
Incheon	0.974	7.879	0				
Yellow Sea	0.828	7.011	-2.490	0			
Gunsan	-0.896	-2.400	7.597	6.670	0		
Busan	-1.583	0.200	1.766	1.667	-0.239	0	
Kangnung	-0.421	5.064	-2.060	-2.274	4.593	-0.464	0

F-statistics from haplotype frequencies (%)

Significant Fst P values (level=5.00)



The current system in the East China Sea and the Yellow Sea



Simulated positions of tracers deployed off the north East China Sea

Conclusion

- Genetic diversity of the *N. nomurai* in the north East China Sea was the highest but the lowest in the center of Yellow Sea in accordance with the increasing number of cohorts in the north East China Sea.
- Genetic differentiation and distance between *N. nomurai* groups in Incheon-Yellow Sea and the groups in the East China Sea were significantly different.
- Genetic discontinuity of the jellyfish in the Yellow Sea and in the north East China Sea seem to occur based on the genetic diversity and differentiation of *N. nomurai*.

Conclusion

- However, the jellyfish groups in Gunsan and Busan and the groups in the East China Sea were significantly related.
- Tsushima warm current and Changjian Dilute Water to affect water movement in East China Sea, Yellow Sea and Korean Strait might affect to the genetic structure of the medusae in Korean waters.
- Genetic dispersal might occurs from the East China Sea to the Yellow Sea and founder effect might be existed with considering the connectivity of genetic haplotypes.

