

# **Albacore (*Thunnus alalunga*) in the Northwestern Pacific are composed of two distinct clades**

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## **Abstract**

Population structure of Albacore (*Thunnus alalunga*) in the Northwestern Pacific Ocean was investigated using mitochondrial (mt) DNA sequence data specifically of the first hypervariable region (HVR-1). A total of 175 individuals were caught and sampled from three regions in the North-western Pacific Ocean (Taiwan, Japan, and Hawaii). Reconstructed neighbor-joining phylogeny tree based on the data analyzed suggested that haplotypes in these regions can be grouped into three clades (Clade I, Clade II and Clade III). Hierarchical AMOVA tests and pairwise  $\Phi_{ST}$  analysis showed that albacore tuna in the NW pacific constitutes a single stock with no significant differences in geographic distributions.

## **Introduction**

Albacore (*Thunnus alalunga*) is a highly migratory pelagic species distributed throughout all areas of tropical, subtropical and temperate oceans from about 45N to 50S including the Mediterranean Sea (Collette and Nauen, 1983). At present, without a detailed and thorough understanding of its genetic structure, the global albacore population is mainly divided by geographic separation and managed as different stocks and recent analyses using both mitochondrial DNA (mtDNA) and nuclear DNA markers have been supporting this policy. By the use of restriction fragment length polymorphism (RFLP) analysis of the mitochondrial ATPase gene amplified by PCR, significant heterogeneity between the Atlantic and Pacific albacore samples was found (Chow & Ushiyama, 1995). Later studies working with highly polymorphic nuclear microsatellites (Takagi *et al.*, 2001) further demonstrated genetic subdivision between the northern and southern samples within the Atlantic and Pacific Oceans. Furthermore, genetic isolation between the Atlantic and Mediterranean albacore populations was also reported (Nakadate *et al.*, 2005). However, although genetic differentiation has been reported on Pacific albacore, the small sample size and

collection date may not represent its present population structure and therefore further studies needs to be performed. In this study, we employed PCR-based mitochondrial (mt) DNA sequencing using the first hypervariable region (HVR-1) to study the genetic structure of the northwestern Pacific albacore population to infer the global stock structure and contribute to decision making on future management of the species.

## Reference

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Population	Location	Date	<i>n</i>	H	S	<i>Hd</i>	<i>k</i>	$\pi$	$\theta$
Taiwan 2002	123°~129°E; 18°~22°N	Jun 2002	30	29	87	0.998±0.009	23.5±10.7	0.069±0.035	23.5±11.9
Taiwan 2003	124°~130°E; 14°~23°N	Apr 2003	38	38	84	1.000±0.006	20.8±9.4	0.061±0.031	20.7±6.4
Taiwan 2004	119°~140°E; 14°~21°N	Jul 2004	27	26	76	0.997±0.011	22.1±10.1	0.065±0.033	20.5±6.8
Japan	153°~175°E; 27°~41°N	Jan 2002	50	47	92	0.997±0.005	23.6±10.5	0.069±0.034	21.0±6.1
Hawaii	161°~171°W; 34°~43°N	Oct 2002	30	28	68	0.991±0.012	20.5±9.3	0.060±0.030	17.2±5.6

Table 1. Descriptive statistics for the studied *T. alalunga* samples.

*N*, sample size; H, number of haplotypes ; *S*, number of polymorphic sites; *Hd*, gene diversity (Nei, 1987) ; *k*, mean pairwise nucleotide differences (Tajima, 1983) ;  $\pi$ , nucleotide diversity (Nei, 1987) ;  $\theta$ , expected heterozygosity per site (Watterson, 1975)

Structure tested	Observed partition			
	Variance	% total	$\Phi$ statistics	<i>p</i>
<i>1. One gene pool (Taiwan, Japan and Hawaii)</i>				
Among populations	-0.01	-0.07	$\Phi_{ST} = -0.001$	0.40
Within populations	11.22	100.07		
<i>2. One gene pool Clade I (Taiwan, Japan and Hawaii)</i>				
Among populations	0.04	0.63	$\Phi_{ST} = 0.006$	0.22
Within populations	6.43	99.37		
<i>3. One gene pool Clade II (Taiwan, Japan and Hawaii)</i>				
Among populations	-0.13	-1.90	$\Phi_{ST} = -0.019$	0.98
Within populations	7.16	101.90		

Table 2. Genetic structuring of *T. alalunga* populations based on mitochondrial control region sequence data

Sampling area	Taiwan	Japan	Hawaii
Taiwan		0.34	0.25
Japan	0.0002		0.83
Hawaii	0.0040	-0.0125	

● Significant values at  $p < 0.01$

Table 3. Matrix of pairwise  $F_{ST}$  (below diagonal) values and associated *p* value (above diagonal) among *T. alalunga* phylogroups based on mitochondrial control region sequence data

	All samples	Clade I	Clade II	Clade III
<i>Goodness of fit tests</i>				
Tajima $D$	-0.25	-1.12	-0.95	-0.33
Fu's $F_S$	-23.75*	-24.28*	-24.27*	0.12
<i>Demographic parameters</i>				
$H_{ri}$	0.0007	0.0015	0.0024	0.4444
$SSD$	0.0042	0.0012	0.0016	0.1975
$S$	122	93	87	15
$\theta_0$	0.016	3.221	4.203	0.002
$\theta_1$	45.818	62.305	196.172	4682.5
$\tau$	29.674	11.773	9.554	10.438

● Significant values at  $p < 0.05$

Table 4. Statistical tests of neutrality, and demographic parameters estimates for *T. alalunga* entire mitochondrial control region data set, and phylogroups (Clade I and II)

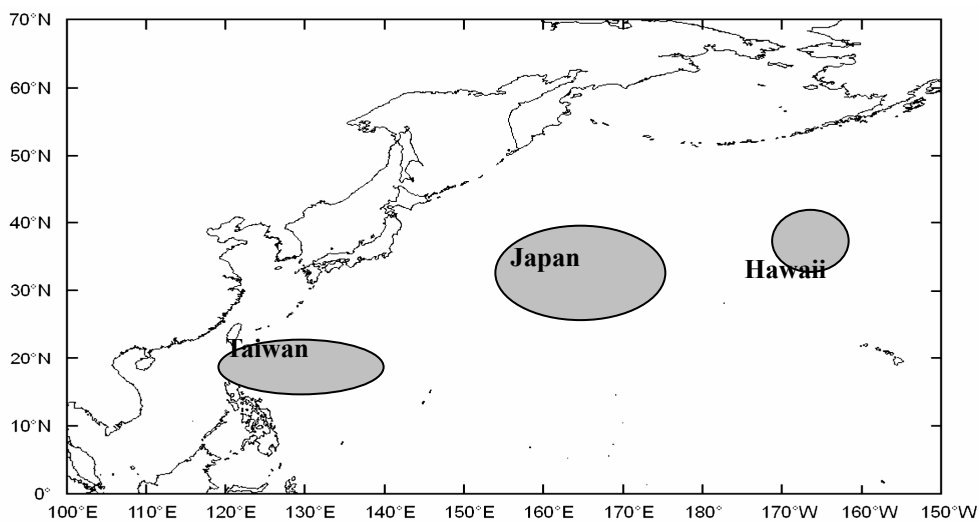


Fig.1 Map showing the albacore sampling areas under study.



Fig 2. Neighbor-joining tree estimated with the Tamura and Nei model among mtDNA lineages of albacore tuna. Haplotypes collected from the Northwest Pacific Ocean. Numbers at nodes indicate the bootstrap values. Only values >50% are shown.

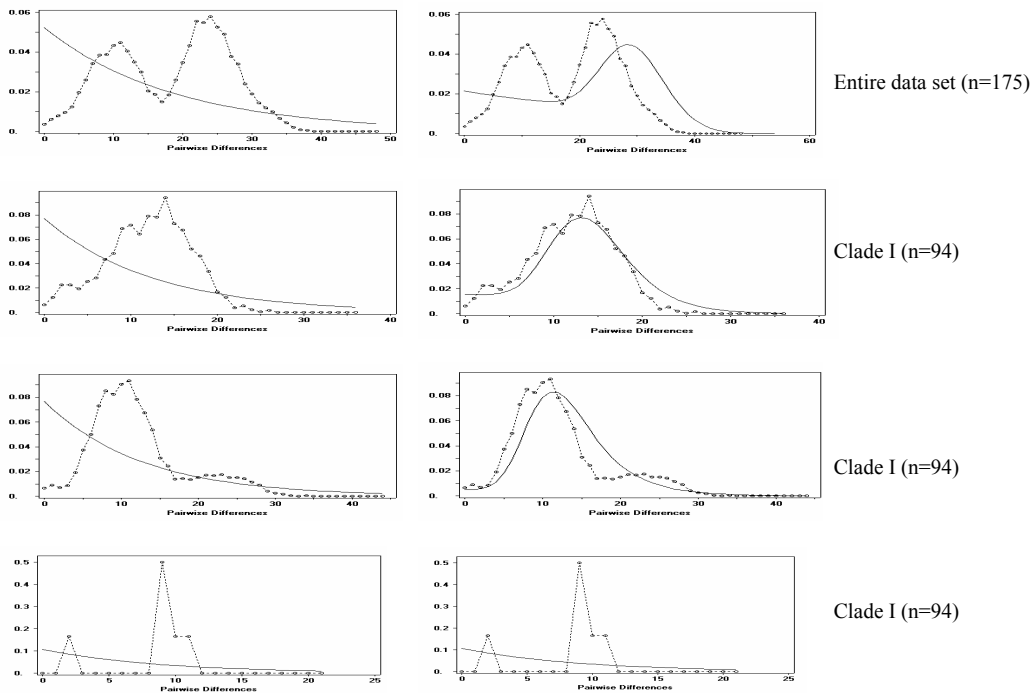


Fig.3. Observed, growth-decline model, and constant population model mismatch distributions for all pairwise combinations of: the entire mitochondrial control region data set, 175 individuals; Clade I, 94 individuals; Clade II, 77 individuals; Clade III, 4 individuals.