

## Worldwide genetic structure of albacore *Thunnus alalunga* revealed by microsatellite DNA markers

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**Supplement.** This supplement includes samples (Table S1) and microsatellite loci features (Table S2), PCR conditions (Table S3), summary of genetic variation for each sample and locus (Table S4), genetic differentiation based on allele size (RST - Table S5), pairwise FST values (Table S6), and estimated probability of K (Fig. S1).

Table S1. *Thunnus alalunga*. Sample features. Sample abbreviation, number of individuals per sample (n), sample location, currently defined stock, latitude (Lat) and longitude (Long) decimal coordinates, and year of capture

Sample	n	Location	Stock	Lat	Long	Year
ADR	49	Adriatic Sea	Mediterranean	41.29	17.52	2006
TYR	50	Tyrrhenian Sea	Mediterranean	38.88	11.74	2008
BAL	49	Balearic Sea	Mediterranean	40.00	1.58	2005
BIS	52	Bay of Biscay	North Atlantic	45.10	-4.35	2009
IRE	60	Celtic Sea	North Atlantic	54.17	-12.89	2008
SA	83	South Atlantic	South Atlantic	-24.25	4.42	2009
IN	26	Indian Ocean	Indian	-7.11	54.65	2008–2009
NP	90	North Pacific	North Pacific	43.50	-127.00	2008
SEP	54	South East Pacific	South Pacific	-19.01	-152.84	2004–2005
SWP	38	South West Pacific	South Pacific	-18.53	165.97	2003–2008

Table S2. Microsatellite marker features. Locus name, GenBank accession number, citation, fluorescent dyes labeling the end of forward primers (Dye), multiplex PCR reaction for each locus, and independent automatic runs

Marker	GenBank no.	Source	Dye	Multiplex	Run
<i>Ttho-1</i>	AB043130	Takagi et al. (2001)	VIC	TUNAPLEX1	1
<i>Ttho-4</i>	AB043131	Takagi et al. (2001)	6-FAM	TUNAPLEX1	1
<i>Ttho-6</i>	AB043132	Takagi et al. (2001)	PET	TUNAPLEX1	1
<i>Ttho-7</i>	AB043133	Takagi et al. (2001)	NED	TUNAPLEX1	1
<i>Tth-5</i>	AF441226	McDowell et al. (2002)	NED	TUNAPLEX2	1
<i>Tth-21</i>	AF441229	McDowell et al. (2002)	VIC	TUNAPLEX2	1
<i>tth4</i>	AY396534	Clark et al. (2004)	6-FAM	TUNAPLEX3	1
<i>tth62</i>	AY396527	Clark et al. (2004)	PET	TUNAPLEX3	1
<i>tth1-31</i>	AY396521	Clark et al. (2004)	VIC	TUNAPLEX4	2
<i>tth14</i>	AY396535	Clark et al. (2004)	6-FAM	TUNAPLEX4	2
<i>tth157</i>	AY396540	Clark et al. (2004)	NED	TUNAPLEX4	2
<i>tth178</i>	AY396541	Clark et al. (2004)	NED	TUNAPLEX4	2
<i>tth226</i>	AY396530	Clark et al. (2004)	VIC	TUNAPLEX4	2

Table S3. PCR conditions for TUNAPLEX1, TUNAPLEX2, TUNAPLEX3, and TUNAPLEX4 multiplexes. All multiplexes used 1× buffer

	TUNAPLEX			
	1	2	3	4
DNA (ng)	20	20	10	7.5
MgCl <sub>2</sub> (mM)	1.2	1.5	1	1,5
Primer (μM)	0.4	0.25	0.5	0.6
dNTPs (mM)	0.48	0.2	0.8	0.8
<i>Taq</i> polymerase (U)	0.25	2.5	1	0.5
Final volume (μl)	10	10	10	10

Table S4. Summary of genetic variation for 13 microsatellite loci at 10 locations. Number of individuals (n), number of alleles per locus (k), observed heterozygosity ( $H_o$ ), unbiased expected heterozygosity ( $H_e$ ), and inbreeding coefficient ( $F_{IS}$ ). Significance values for  $F_{IS}$  below  $p < 0.01$  are indicated in **bold**. Population (location) abbreviations as in Table S1

Population	<i>Tth-21</i>	<i>Ttho-1</i>	<i>Ttho-4</i>	<i>Ttho-7</i>	<i>tth1-31</i>	<i>tth14</i>	<i>tth157</i>	<i>tth226</i>	<i>tth4</i>	<i>Ttho-6</i>	<i>Tth-5</i>	<i>tth62</i>	<i>tth178</i>	Total
<b>ADR</b>														
n	48	14	20	9	47	47	48	48	42	16	48	29	47	
k	3	3	15	4	11	5	6	16	22	6	17	7	10	
$H_o$	0.646	0.143	0.650	0.889	0.660	0.617	0.583	0.833	0.976	0.500	0.854	0.207	0.723	
$H_e$	0.592	0.262	0.919	0.673	0.742	0.617	0.598	0.909	0.919	0.768	0.890	0.765	0.804	
$F_{IS}$	-0.092	<b>0.464</b>	<b>0.298</b>	-0.347	0.113	0.001	0.024	0.084	-0.063	<b>0.357</b>	0.040	<b>0.733</b>	0.101	
<b>TYR</b>														
n	49	27	28	25	50	48	50	50	31	28	49	22	48	
k	3	6	15	11	10	5	6	16	19	7	17	5	11	
$H_o$	0.612	0.407	0.929	0.800	0.620	0.708	0.560	0.960	0.903	0.643	0.918	0.227	0.688	
$H_e$	0.594	0.461	0.892	0.825	0.794	0.669	0.505	0.905	0.929	0.717	0.921	0.559	0.818	
$F_{IS}$	-0.032	0.117	-0.042	0.031	<b>0.221</b>	-0.059	-0.109	-0.062	0.028	0.105	0.003	<b>0.599</b>	<b>0.161</b>	
<b>BAL</b>														
n	46	44	43	44	48	48	48	48	40	16	47	13	46	
k	5	6	18	11	10	6	7	15	20	4	17	4	10	
$H_o$	0.674	0.614	0.791	0.864	0.667	0.500	0.542	0.917	0.900	0.125	0.681	0.308	0.696	
$H_e$	0.615	0.671	0.883	0.795	0.772	0.614	0.544	0.914	0.918	0.567	0.840	0.689	0.829	
$F_{IS}$	-0.097	0.087	<b>0.105</b>	-0.088	<b>0.138</b>	<b>0.187</b>	0.004	-0.002	0.020	<b>0.785</b>	<b>0.191</b>	<b>0.564</b>	<b>0.162</b>	
<b>BIS</b>														
n	39	38	39	38	48	47	50	46	42	39	49	32	42	
k	3	6	21	11	12	7	7	20	23	9	18	5	13	
$H_o$	0.538	0.658	0.821	0.737	0.771	0.596	0.560	0.913	0.833	0.564	0.592	0.188	0.690	
$H_e$	0.533	0.593	0.901	0.861	0.803	0.644	0.569	0.934	0.947	0.773	0.873	0.629	0.875	
$F_{IS}$	-0.010	-0.111	<b>0.091</b>	<b>0.146</b>	0.041	0.076	0.016	0.023	<b>0.121</b>	<b>0.272</b>	<b>0.324</b>	<b>0.705</b>	<b>0.213</b>	
<b>IRE</b>														
n	58	5	9	5	54	54	59	56	40	5	57	20	56	
k	4	3	11	7	12	6	6	17	24	6	21	6	13	
$H_o$	0.569	0.400	0.778	1.000	0.556	0.685	0.644	0.929	0.925	0.800	0.825	0.200	0.768	
$H_e$	0.519	0.511	0.935	0.911	0.776	0.614	0.572	0.926	0.950	0.889	0.900	0.728	0.865	
$F_{IS}$	-0.098	0.238	0.176	-0.111	<b>0.286</b>	-0.117	-0.128	-0.003	0.027	0.111	<b>0.084</b>	<b>0.730</b>	<b>0.113</b>	

<b>SA</b>													
n	18	4	20	5	81	81	81	83	4	16	35	5	75
k	4	4	13	7	16	5	6	21	6	9	14	3	13
$H_o$	0.444	0.750	0.750	0.800	0.802	0.630	0.494	0.880	0.750	0.250	0.400	0.000	0.613
$H_e$	0.560	0.643	0.777	0.911	0.808	0.590	0.495	0.937	0.893	0.839	0.793	0.711	0.838
$F_{IS}$	0.212	-0.200	0.036	0.135	0.007	-0.068	0.002	0.061	<b>0.182</b>	<b>1.000</b>	<b>0.499</b>	<b>0.709</b>	<b>0.269</b>
<b>IN</b>													
n	25	24	25	25	22	23	25	23	23	24	25	20	23
k	2	6	15	15	9	3	5	19	21	9	13	8	7
$H_o$	0.440	0.500	0.760	0.680	0.727	0.652	0.680	1.000	1.000	0.625	0.360	0.250	0.696
$H_e$	0.458	0.536	0.810	0.860	0.759	0.569	0.598	0.947	0.945	0.801	0.863	0.803	0.821
$F_{IS}$	0.040	0.069	0.063	<b>0.212</b>	0.043	-0.150	-0.141	-0.057	-0.060	<b>0.223</b>	<b>0.588</b>	<b>0.694</b>	0.156
<b>NP</b>													
n	86	68	65	61	89	89	89	83	73	56	82	64	80
k	4	7	22	18	12	8	6	19	24	11	19	10	13
$H_o$	0.523	0.627	0.862	0.885	0.809	0.517	0.629	0.904	0.945	0.607	0.512	0.328	0.713
$H_e$	0.479	0.687	0.838	0.871	0.772	0.569	0.603	0.920	0.943	0.734	0.871	0.760	0.858
$F_{IS}$	-0.094	0.088	-0.029	-0.017	-0.048	0.092	-0.044	0.018	-0.003	<b>0.175</b>	<b>0.413</b>	<b>0.570</b>	<b>0.170</b>
<b>SEP</b>													
n	47	42	47	44	50	50	50	54	47	38	46	35	51
k	3	7	19	16	11	4	5	18	21	9	19	9	11
$H_o$	0.532	0.667	0.766	0.818	0.860	0.580	0.660	0.833	0.894	0.553	0.696	0.343	0.863
$H_e$	0.525	0.707	0.845	0.868	0.789	0.554	0.606	0.894	0.941	0.639	0.890	0.782	0.867
$F_{IS}$	0.016	0.057	0.094	0.058	-0.091	-0.047	-0.090	0.069	0.051	0.137	<b>0.221</b>	<b>0.565</b>	0.005
<b>SWP</b>													
n	32	24	25	27	34	33	34	37	25	23	31	21	37
k	3	8	15	10	11	5	6	17	19	8	14	10	10
$H_o$	0.688	0.583	0.840	0.704	0.735	0.697	0.676	0.892	0.760	0.826	0.677	0.619	0.730
$H_e$	0.546	0.645	0.872	0.855	0.773	0.614	0.583	0.901	0.923	0.744	0.887	0.765	0.827
$F_{IS}$	-0.264	0.098	0.037	<b>0.180</b>	0.050	-0.137	-0.163	0.010	<b>0.180</b>	-0.113	<b>0.240</b>	<b>0.195</b>	0.119

<b>All pops</b>														
Mean n	44.800	29.000	32.100	28.300	52.300	52.000	53.400	52.800	36.700	26.100	46.900	26.100	50.500	40.846
SE n	18.896	19.653	16.381	18.673	19.726	19.726	19.254	18.480	18.037	14.798	15.702	15.961	16.834	20.249
Mean k	3.000	6.000	15.000	11.000	11.000	5.000	6.000	17.500	21.000	8.500	17.000	6.500	11.000	10.654
SE k	0.843	1.713	3.502	4.372	1.897	1.430	0.667	1.932	5.216	2.044	2.558	2.497	1.969	5.868
Mean $H_o$	0.547	0.595	0.775	0.813	0.728	0.618	0.606	0.906	0.899	0.589	0.682	0.237	0.703	0.664
SE $H_o$	0.088	0.178	0.074	0.097	0.093	0.072	0.064	0.052	0.084	0.218	0.188	0.157	0.064	0.203
Mean $H_e$	0.542	0.621	0.877	0.855	0.774	0.605	0.576	0.919	0.935	0.757	0.876	0.739	0.830	0.754
SE $H_e$	0.050	0.136	0.050	0.069	0.020	0.036	0.040	0.017	0.018	0.093	0.036	0.076	0.024	0.148
Mean $F_{IS}$	-0.063	0.067	0.062	0.042	0.064	-0.007	-0.055	0.022	0.030	<b>0.230</b>	<b>0.245</b>	<b>0.603</b>	<b>0.156</b>	<b>0.114</b>
SE $F_{IS}$	0.024	0.028	0.030	0.039	0.042	0.034	0.020	0.014	0.022	0.060	0.061	0.045	0.027	0.047

Table S5. Genetic differentiation based on allele size for the 8 neutral microsatellite loci.  $R_{ST}$ , mean permuted  $R_{ST}$  ( $pR_{ST}$ ), 95% confidence interval (CI) and p value. \*Significant p values of allele size permutation test ( $p < 0.05$ )

Marker	$R_{ST}$	$pR_{ST}$	(95% CI)		p
<i>Tth-21</i>	0.009	0.007	-0.002	0.027	0.846
<i>Ttho-1</i>	-0.002	0.009	-0.013	0.033	0.535
<i>Ttho-4</i>	0.037	0.008	-0.010	0.035	0.038*
<i>tth1-31</i>	0.008	0.002	-0.007	0.015	0.304
<i>tth14</i>	0.041	0.008	-0.001	0.028	0.001*
<i>tth157</i>	0.023	0.009	-0.005	0.031	0.213
<i>tth226</i>	-0.004	0.008	-0.006	0.034	0.125
<i>tth4</i>	0.030	0.012	-0.008	0.046	0.214
Multilocus	0.023	0.009	-0.001	0.024	0.060

Table S6. Pairwise  $F_{ST}$  values (below the diagonal) and p values (above the diagonal) among samples using only *Tth-21*, *tth1-31*, *tth14*, *tth157*, and *tth226*. Sample (location) codes as in Table S1. \* $p < 0.05$

	ADR	TYR	BAL	BIS	IRE	SA	IN	NP	SEP	SWP
ADR	–	0.182	0.306	0.038*	0.026*	0.236	0.090	0.000*	0.023*	0.092
TYR	0.003	–	0.793	0.039*	0.013*	0.200	0.048*	0.000*	0.002*	0.028*
BAL	0.002	-0.003	–	0.015*	0.017*	0.276	0.029*	0.001*	0.049*	0.067
BIS	0.008*	0.008*	0.011*	–	0.916	0.618	0.812	0.021*	0.039*	0.555
IRE	0.008*	0.010*	0.009*	-0.004	–	0.580	0.895	0.144	0.045*	0.478
SA	0.008	0.003	0.002	-0.002	-0.002	–	0.642	0.073	0.100	0.267
IN	0.008	0.010*	0.012*	-0.005	0.006	0.003	–	0.366	0.129	0.395
NP	0.017*	0.017*	0.013*	0.007*	0.003	0.005	0.001	–	0.326	0.264
SEP	0.009*	0.014*	0.007*	0.008*	0.007*	0.006	0.006	0.001	–	0.738
SWP	0.006	0.010*	0.008	-0.001	0.000	0.002	0.001	0.002	-0.003	–

Fig. S1. Estimated posterior probabilities of the data,  $\ln \Pr(X|K)$ , and the posterior probability of  $K$ ,  $\Pr(K)$

