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Genetic population structure in the Chilean jack mackerel, *Trachurus murphyi* (Nichols) across the South-eastern Pacific Ocean

Leyla Cárdenas[a,*], Andrea X. Silva[a], Antonios Magoulas[b], Josefina Cabezas[c], Elie Poulin[c], F. Patricio Ojeda[d]

[a] *Instituto de Ecología y Evolución, Facultad de Ciencias, Universidad Austral de Chile, Campus Isla Teja, Casilla 567, Valdivia, Chile*
[b] *Institute of Marine Biology and Genetics, Hellenic Centre for Marine Research, P.O. box: 2214, GR 710 013, Iraklio, Greece*
[c] *Instituto de Ecología y Biodiversidad, Departamento de Ciencias Ecológicas, Facultad de Ciencias, Universidad de Chile, Las Palmeras 3425, Casilla 653, Nuñoa, Santiago, Chile*
[d] *Facultad de Ciencias Biológicas, Pontificia Universidad Católica de Chile, Santiago, Chile*

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ABSTRACT

The Chilean jack mackerel *Trachurus murphyi*, is a pelagic fish from the Carangidae family that is distributed in the South Pacific Ocean. Because this species constitutes an important economic resource across the South Pacific and plays an important ecological role in this ecosystem there is a growing interest in determining its population structure. In this study, we used molecular markers (mitochondrial DNA sequences and microsatellites) from Chilean jack mackerel samples to investigate its genetic population structure across the South Pacific Ocean. The mitochondrial DNA did not detect a genetic structure in *T. murphyi* populations in the Pacific Ocean, but revealed very low haplotype diversity and a short genealogy history compared to other small-pelagic species. The same general pattern of a lack of genetic structure was found with microsatellite loci; however, a large genetic diversity was revealed with microsatellite markers. The present results did not support the existence of different stock units for *T. murphyi* across the South Pacific Ocean but a more holistic approach will be necessary to determine an adequate management strategy for this fishery.

1. Introduction

Traditionally, the basic unit for the fisheries management has been the stock unit (Shaklee and Currens, 2003). This concept has many definitions depending on the research being conducted, but the widely accepted general definition refers to an intraspecific group of randomly mating individuals with temporal or spatial integrity (see also Dizon et al., 1992; Waldman, 2005). Although classical fisheries approaches typically focused on factors driving the short-term demographic changes in stock unit, the application of genetic principles to fisheries biology and management has increased the interest in the factors sustaining the dynamics and resilience of exploited species.

The genus *Trachurus* comprises 14 nominal marine fish species occurring in Atlantic, Indian, Mediterranean and Pacific waters. Five of these species have been recorded in the temperate waters of the Pacific Ocean: *Trachurus japonicus* (Temminck and Schlegel), *Trachurus novaezelandiae* (Richardson) and *Trachurus declivis* (Jenyns) in the Western Pacific, and a pair of anti-tropical species, *Trachurus symmetricus* (Ayres) in the North-eastern Pacific, and *Trachurus murphyi* (Nichols) in the South-eastern Pacific (Poulin et al., 2004; Cárdenas et al., 2005).

The Chilean jack mackerel *T. murphyi* (Perciformes: Carangidae) is a highly migratory fish that is widely distributed in the South Pacific Ocean. This pelagic species is found off the Chilean and Peruvian coasts and its distribution extends westward along the "Chilean jack mackerel belt" to the South-west Pacific Ocean around New Zealand and Tasmania. *T. murphyi* has been subjected to heavy exploitation by purse seiners since the beginning of the 1970s. During the last decade, the annual catch of *T. murphyi* has fluctuated between 1 and 5 millions tons, placing it among the 5 major single-species fisheries in the world (FAO, 2009). In the South-eastern Pacific and within the Exclusive Economic Zones (EEZ) of Chile and Peru, three fisheries have traditionally been identified. The first includes southern Peru and northern Chile down to 24°S. A second fishery operates in northern Chile from 24°S to 32°S. Finally, the main fishery is located off central Chile, from 32°S to about 43°S (Grechina, 1998). Beyond the EEZ, the fisheries are comprised of several international fleets mainly from China, the Republic of Korea and Ecuador (FAO, 2009). The Chilean jack mackerel *T. murphyi*, previously unknown in the Western Pacific, was first reported in New Zealand waters in 1985 (Evseenko, 1987; Kawahara

* Corresponding author. Tel.: +56 63 221673.
E-mail address: leylacardenas@uach.cl (L. Cárdenas).

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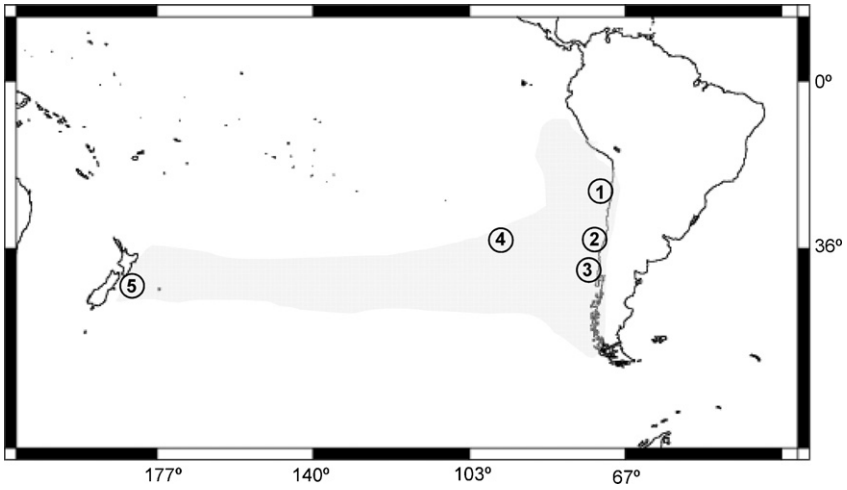

Fig. 1. Map depicting the Chilean jack mackerel distribution and the sampled localities.

et al., 1988; Jones, 1990; Serra, 1991; Elizarov et al., 1993) and it appears to have established itself off the south and east coasts of the South Island by the mid 1980s (Taylor and Julian, 2008). The total range of *T. murphyi* now extends along the entire west coast of South America, across the South Pacific, through much of the New Zealand EEZ, and into the waters off South-eastern Australia (Grechina, 1998). At present, there are several stock structure hypotheses for the Chilean jack mackerel fisheries, and up to four separate stocks have been suggested: a Chilean stock; a Peruvian stock; a central Pacific Ocean stock and a South-west Pacific Ocean stock (Serra, 1991; Cubillos et al., 2008; Taylor and Julian, 2008). Because *T. murphyi* constitutes an important economic resource across the South Pacific Ocean and plays an important ecological role in this ecosystem (Ojeda and Aviles, 1987; Miranda et al., 1998), there is a growing interest in determining its population structure in order to improve management measures across the total area of the jack mackerel fisheries. One of the most important issues that needs to be addressed to ensure adequate management is an understanding of the geographic partition of genetic diversity within a target species (Shaklee and Bentzen, 1998; Nielsen et al., 2006; Delghandi et al., 2008). In this study, we used nucleotide sequences of the mitochondrial control region and microsatellite data from *T. murphyi* samples to describe the geographic distribution of its genetic diversity, to investigate its genetic population structure across the South Pacific Ocean and to provide new information for the stock identification and therefore fisheries management of this species.

2. Material and methods

2.1. Sampling areas

Samples from adult specimens of jack mackerel were collected across the Pacific Ocean as follows: during 2002, samples were taken from the main fishing areas off the Chilean coast, off Iquique, San Antonio and Concepción (20°S, 33°S and 39°S, respectively), and from New Zealand waters (37°15′S, 178°7′E). During 2006 we collected new samples from the open Pacific Ocean (almost 2000 km off Chilean coast; 32°30′S, 91°20′W) (Fig. 1). Sample collection was undertaken on board purse seine vessels. A small piece of muscle tissue from each specimen was immediately preserved in liquid nitrogen or in absolute ethanol.

2.2. Mitochondrial DNA sequences

Total genomic DNA was extracted from the muscle tissue using a standard phenol/chloroform protocol and subjected to the polymerase chain reaction (PCR). The control region (CR) was amplified and sequenced with 2 primers designed from tRNA-Pro and tRNA-Phe sequences of carangids (GenBank AF271658, AP004445, AP003092, AF055590). Primer sequences were: JUR1 5′-CAGAAAAAGGAGACTCTAACTCCTG-3′ and JUR2 5′-TGCTTGCGGGGCTTTCTA-3′.

DNA was amplified in 25 μL reactions containing 1 μL of 1 ng genomic DNA, 1.6 μL of $MgCl_2$ (50 mM), 2.5 μL 10× buffer (0.1 M Tris–HCl, pH 8.5), 2 μL dNTP mix (2.5 mM), 0.5 μL of each primer (10 pM), 5 U in 1 μL Taq DNA polymerase, and 15.9 μL deionized water. Amplifications were carried out on a PCR 9600 thermocycler (Applied Biosystems, Foster City, CA, USA) with an initial denaturation at 94 °C for 3 min, followed by 30 cycles of amplification (denaturation at 94 °C for 0.5 min, annealing at 55 °C for 1.5 min and extension at 72 °C for 1.5 min) with a final extension at 72 °C for 10 min.

Amplification products were cleaned using the purification kit QIAquick PCR (Quiagen) and then were run on an ABI 3100 automated sequencer (Applied Biosystems, Foster City, CA, USA). The forward strand was sequenced with primer JUR1 and the reverse strand with the JUR2 primer. Contiguous DNA fragments were assembled using ProSeq v 2.9 beta (Filatov, 2002) and sequence alignment sequences were aligned using ClustalX (Thompson et al., 1997; Larkin et al., 2007). Sequences contained no insertion or deletion and alignments were unambiguously checked by eye. For all genetic analyses, 772 base pairs of the mitochondrial CR were used.

Table 1
Description of the 4 microsatellite loci in *Trachurus murphyi*.

Locus name	Repeat motif	Primer sequence (5′–3′)	Range of alleles (bp)	Ta (°C)	$MgCl_2$ (mM)	Accesión Number
Tt29	$(AC)_{13}$	F: ACTGACGCAAGGAAACATGC R: GTGCAGGTCAAGCCAGCTAC	164–196	56	3.0	FJ936108
Tt62	$(TG)_{14}$	F: GTCAGGTGCTCTGGGTGC R: CTCTGGCGTGTCAGGAATG	141–185	56	3.0	FJ936109
Tt74	$(AC)_{19}$	F: TGAGCATCAAATGGCAGC R: GACGCAGAAATAGACTGACGG	103–215	56	3.0	FJ936110
Tt133	$(AC)_{24}$	F: GATCTCAGACTCTCCACCGTA R: AGCACATCCACACACTTCCA	96–264	56	3.0	FJ936111

2.3. Microsatellites and genotyping

To study the genetic structure of *T. murphyi* we tested a cross-amplification of microsatellite loci previously developed for *T. trachurus* below the framework of the EU project HOMSIR (Horse Mackerel Stock Identification Research, QLK5-Ct1999-01438). The loci used are those described by Kasapidis and Magoulas (2008) plus the locus TT74. Repeat motif of each loci, size range for alleles and PCR conditions (annealing temperature and $MgCl_2$ concentration) in *T. murphyi* are shown in Table 1.

The analysis of fragments was performed using a 310 ABI Perkin-Elmer Automatic Sequencer ABIPRISM 310. Forward primer of each locus was ordered NED-labeled (PE Applied Biosystems, USA). Rox-500 size standard (PE, Applied Biosystems, USA) was added to the PCR products and mix was automatically injected in a capillary filled with the POP4™ polymer. The polymer was automatically changed at each new run. Electrophoresis was carried out at 15 kV, 50 °C for 36 min in 1× ABI310-Automatic Analyzer buffer™. Allele sizes were scored using Genemarker software (SoftGenetics, PA, USA).

In order to study the genetic structure pattern between New Zealand and Chilean populations of *T. murphyi,* we did genotyping analysis for samples collected from the eastern and Western Pacific coast during the year 2002.

2.4. Statistical analyses

2.4.1. MtDNA data analysis

For mtDNA data, the standard diversity indices, such as the number of haplotypes (k) and segregating sites (S), mean number of pairwise differences (Π) as well as haplotype and nucleotide diversity (He and π, respectively) were estimated for each sample based on the aligned CR sequences. Estimates of these parameters and their standard errors were obtained with the program DnaSP version 4.90.1 (Rozas et al., 2003).

Population structure analysis was conducted among *T. murphyi* samples with the Arlequin 3.11 program package (Excoffier et al., 2005) by calculating pairwise F_{st} values and testing their significance with 10,000 permutations. To further examine the population history of the *T. murphyi* populations, neutrality tests of Tajima's *D* (Tajima, 1989) and Fu's *F* statistics (Fu, 1997) were carried out. These statistics were originally developed to test the neutral hypothesis but are now widely used to detect changes in population size (Mousset et al., 2004). They estimate the deviation from neutrality, which is based on the expectation of a constant population size at mutation-drift equilibrium. To further assess demographic change indicated by the mtDNA data, we constructed the mismatch distribution and compared it to the Poisson expectation for both constant and varying population sizes (Slatkin and Hudson, 1991).

The genealogical relationships between haplotypes were assessed using a haplotype network constructed using a median-joining algorithm (Bandelt et al., 1999) as implemented in Network 4.5 software (available from fluxus-engineering.com). We applied a maximum parsimony algorithm to simplify the complex branching pattern and to represent all the most parsimonious intraspecific phylogenies (Polzin and Daneschmand, 2003).

2.4.2. Microsatellite data analysis

Although amplification patterns at the four loci used were unambiguous, we checked the microsatellite data for evidence of null alleles and technical artefacts like stuttering and large allele drop-out using MICRO-CHEKER 2.2.3 software (Van Oosterhout et al., 2004). The statistical independence between loci was assessed using GENEPOP version 3.4 (Raymond and Rousset, 1995). Genotypic linkage disequilibria between each pair of loci and populations and between each pair of loci over the whole dataset were tested by Fisher exact tests using a Markov chain. Tests for deviation from genotypic proportions expected under Hardy–Weinberg equilibrium were carried out using GENEPOP. To adjust for multiple comparisons, Bonferroni-adjusted *P* values were examined (Rice, 1989).

The amount of genetic diversity within populations is a critical parameter in evolutionary studies and species management. For each locality, allele frequencies, number of alleles (N_{all}), gene diversity (He) per locus and population were estimated using FSTAT 2.9.3.2 (Goudet, 2001). To take into account variation in sample size, allelic richness (R_{all}) was calculated for each of the localities using a rarefaction procedure as implemented in HP-RARE v1.4 (Kalinowski, 2005). Genetic differentiation was studied using the software GENEPOP version 3.4. Differentiation among localities was investigated by calculating θ (Weir and Cockerham, 1984); an estimator of F_{st} (Wright, 1951). Exact tests of allelic differentiation were carried out between populations.

3. Results

3.1. MtDNA analysis

Over the whole data set (a total of 173 CR sequences) we identified 17 polymorphic sites leading to the definition of 20 haplotypes (Table 2). Only two haplotypes (H1 and H8) were found in every population and were shared by 84% of the total number of individuals. H1 was the most widely distributed with a total frequency of 80%. Two other haplotypes were found in two localities, H13 was shared by San Antonio and Iquique while H10 was shared by Talcahuano and New Zealand. However, the frequency of both haplotypes was low, 2.3% and 1.2%, respectively. Finally the other haplotypes were found in only one locality, most of them being singleton haplotypes. The genetic diversity was low with He ranging from 0.15 ± 0.09 for New Zealand to 0.51 ± 0.11 for San Antonio. This was also the case for the nucleotide diversity (π), which was extremely low with values from 0.0002 ± 0.0003 in New Zealand to 0.0008 ± 0.0007 in San Antonio.

Table 2
Molecular genetic diversity of *Trachurus murphyi* based on a 772 bp region of the mitochondrial control region (*P* values of Tajima and Fu tests.

Localities	Latitude–longitude	*N* samples	*N* haplotypes (k)	Polimorphic site (S)	Gene diversity (He)	Nucleotide diversity (π)	Mean pairwise differences (Π)	Tajima *D* test	Fu's *Fs*
(1) Iquique	20°58′S–70°18′W	30	6	5	0.36	0.0007	0.51	−1.62*	−3.83***
(2) San Antonio	33°35′S–71°37′W	30	7	6	0.51	0.0008	0.58	−1.76*	−4.89***
(3) Talcahuano	39°38′S–75°17′W	35	5	4	0.22	0.0004	0.33	−1.62*	−3.54**
(4) Open ocean	32°30′S–91°20′W	52	9	8	0.41	0.0007	0.55	−1.86**	−7.29***
(5) New Zealand	37°15′S–178°7′E	26	3	2	0.15	0.0002	0.15	−1.51*	−2.18***
Total		173	20	17	0.34	0.0006	0.45	−1.67*	−4.34***

* $p < 0.05$.
** $p < 0.01$.
*** $p < 0.001$.

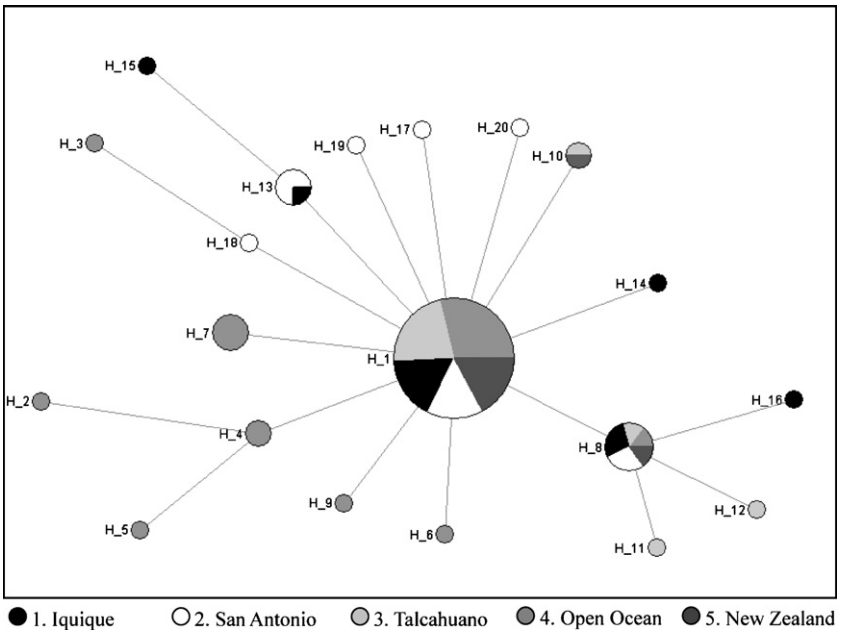

Fig. 2. Haplotype network for 173 control region sequences of Chilean jack mackerel. The numbers of population are in accordance with Fig. 1.

The pairwise F_{st} analysis revealed a lack of genetic structure among the sampled areas. The pairwise F_{st} values were low and in the main not significant, except for the comparison between San Antonio and the open ocean site (pairwise $F_{st} = 0.022$ and P value = 0.03). The Tajima's D and Fu's neutrality tests were both significantly negative for each population and for the whole data set (Table 2) indicating that, under a neutral model, this species may have experienced a demographic expansion event. These results agree with the network analysis (Fig. 2). The haplotype network of *T. murphyi* was characterized by a highly dominant central haplotype (H1) and a very short genealogy. Most haplotypes were separated by only one or two mutational steps from H1 showing a strong "star-like" phylogeny pattern. The distribution of pairwise differences among sequences was L-shaped, as a consequence of the large majority of individuals sharing the same haplotype. The mismatch distributions did not differ from the expected stepwise expansion model (data not shown).

3.2. Microsatellite analysis

All loci were polymorphic over the whole dataset with a total allele number ranging from 14 to 58 per locus (Table 3). Data analyses carried out for each locus with the software MICRO-CHECKER did not provide evidence of null alleles, scoring-errors, stuttering or drop-out. Two out of the 24 tests for linkage disequilibrium were significant at $P < 0.05$ (Tt62 and Tt133 from Talcahuano and Tt29 and Tt62 from New Zealand). However, after Bonferroni correction all tests became non-significant. The f values across loci were low in all localities (ranging from 0.002 to 0.04). We found deviations from HWE in two of the four localities after global tests across loci and Bonferroni corrections (Iquique and New Zealand, Table 3). These deviations were due to only one locus (locus Tt74).

High genetic diversity indices (Nall, He, Ar) were found in every studied sample (Table 3). Values of He within localities ranged from 0.71 to 0.94. The highest He value corresponded to the Iquique site (0.87 ± 0.5) while the lowest value was for New Zealand (0.80 ± 0.5). For the allelic richness (R_{all}, Table 3), we conducted a rarefaction procedure where the minimum sampled size was setup as 26. The highest mean value for total allelic richness was 17.8 for Iquique and the lowest was 16 for San Antonio (Table 3). The global test for genetic differentiation among all populations revealed a lack of significant differences ($\theta = -0.0013$, $P = 0.07$). Of the six pairwise tests performed between localities, two were significant at the 5% nominal level but no significant vales remained after Bonferroni corrections.

4. Discussion

In marine species, high dispersal ability is frequently accompanied by decreased population structure (e.g. Waples, 1987; Avise, 1992; Doherty et al., 1995) such that this relationship has achieved the status of a paradigm (Palumbi, 1995). The present results support this paradigm indicating little or no genetic differentiation in the Chilean jack mackerel *T. murphyi* across its entire distribution range. Both mtDNA and microsatellite markers failed to detect any significant differences among localities. This result supports the hypothesis that a single population of *T. murphyi* inhabits the entire South Pacific.

The observed genetic homogeneity in *T. murphyi* has also been documented in other *Trachurus* species. For example, Karaiskou et al. (2004) developed a restriction analysis of the whole control region (D-loop) of mitochondrial DNA for three horse mackerel species from the Atlantic and Mediterranean populations. No differentiation was revealed among populations within the 3 studied species. They attributed this to species-specific life history characteristics as well as the absence of hydrographic barriers, which would act to contain fish populations within defined areas (Karaiskou et al., 2004). The same approach was used to study genetic differentiation among population of *T. trachurus*, *T. mediterraneus* and *T. picturatus*, in the North-eastern Mediterranean, Aegean Sea, Sea of Marmara and Black Sea (Bektas and Belduz, 2008). Again, no genetic structure within species was founded in the three *Trachurus* species studied. More recently, in the context of the interdisciplinary HOMSIR project, results of multilocus allozyme electrophoresis (Cimmaruta et al., 2008), mitochondrial DNA sequencing of the control regions (Comesaña et al., 2008), and microsatellite DNA (Kasapidis and Magoulas, 2008), showed that there was little genetic differentiation in *T. trachurus* across the Northeast Atlantic and Mediterranean Sea. Again, these authors

Table 3
Genetic diversity in *Trachurus murphyi*. Data for each studied population and locus. For each locus the estimator of the fixation index Fis (*f*) is indicated with the exact probability of the test for deviations from HW expectations.

	Iquique ($n=60$)				San Antonio ($n=30$)				Talcahuano ($n=79$)				New Zealand ($n=50$)				Total ($n=219$)		
	N_{all}	He	R_{all}	f	N_{all}	He	R_{all}	f	N_{all}	He	R_{all}	f	N_{all}	He	R_{all}	f	N_{all}	*He*	R_{all}
Tt29	11	0.80	10.02	−0.00	9	0.71	9.00	0.08	12	0.77	9.78	−0.04	9	0.76	8.74	0.04	14	0.76	9.55
Tt62	13	0.82	11.15	−0.09	9	0.84	8.93	−0.11	14	0.84	10.29	−0.04	11	0.83	9.82	−0.14	17	0.83	10.40
Tt74	32	0.95	23.93	0.09**	24	0.94	23.60	0.04	34	0.95	24.56	0.06	27	0.96	27.57	0.04***	56	0.95	25.76
Tt133	42	0.91	26.08	0.06	23	0.84	22.40	−0.15	37	0.88	22.40	−0.02	37	0.86	20.42	0.1	58	0.87	22.70
Mean	24.5	0.87 ± 0.5	17.8	0.02	16.3	0.82 ± 0.5	16	−0.04	24.3	0.84 ± 0.5	16.8	−0.01	21	0.80 ± 0.5	16.6	0.01***	36.3	0.85 ± 0.1	17.1

** $P<0.01$.
*** $P<0.001$.

suggested that the absence of population genetic structure could be a consequence of the life history of the species and its recent demographic history (Abaunza et al., 2008). All these results suggest that genetic homogeneity among populations is an intrinsic characteristic of *Trachurus* species reflecting a high degree of migratory behaviour in these species.

The absence of genetic structure could also be a consequence of the reproductive characteristics of *T. murphyi*. The spawning area of the Chilean jack mackerel is widespread and located in oceanic waters (Cubillos et al., 2008). It includes the Subtropical Convergence Zone (SCZ), extending from the Chilean coast out to between 150°W and 160°W (Evseenko, 1987; Bailey, 1989). Off central Chile, in the main spawning area, the reproductive strategy of Chilean jack mackerel is to disperse over a large area of oceanic waters, without forming schools or aggregations (Konchina et al., 1996; Barbieri et al., 1999). This reproductive behaviour might promote the long distance dispersal of the early development stages of the Chilean jack mackerel and, consequently, prevent the development of a genetic structure across its distribution range.

Mitochondrial DNA markers have been shown to be useful to describe the historical demography of species (Avise, 2000). A pattern of high values of genetic and nucleotide diversity, typical of species with large stable populations and a long evolutionary history has been reported in several migratory fish (e.g. bigeye tuna, Alvarado-Bremer et al., 1998; Atlantic mackerel, Nesbø et al., 2000; and three *Trachurus* species, Karaiskou et al., 2004; Comesaña et al., 2008). However for *T. murphyi* low haplotype and nucleotide diversity was found in all sampled locations. These low values of genetic diversity, related to low population effective sizes, may reflect important demographic variation of *T. murphyi*. The Southeastern Pacific is characterized by strong coastal upwelling and supports highly productive ecosystems, linked to atmospheric and oceanic forcing (Cury et al., 2000). Population size variation and biological regime shift of small-pelagic fish species have been well documented in this area and are associated with different timescale events affecting ocean productivity such as El Niño-La Niña cycles (ENSO), Pacific-Decadal Oscillation (PDO) and beyond at millennial scales (Chavez et al., 2003).

Another important piece of information has arisen from fishery registers. Long-term temporal records of catch, available since 1950, indicate that specimens of *T. murphyi* were caught for the first time in New Zealand waters in the early 1980s (Kawahara et al., 1988). Since then, this species has spread all around New Zealand and Tasmania, supporting a western range expansion of the Chilean jack mackerel (Taylor and Julian, 2008). Moreover, an important increase in the total catch in this area was correlated with the general observation of a decline in *T. murphyi* in other areas (Taylor and Julian, 2008). Evidence of this western expansion is still detectable in the present genetic data. Genetic diversity measured from the mtDNA marker was clearly lower in New Zealand compared to the eastern and oceanic areas (Table 2). Moreover, and contrary to all other areas, the New Zealand sample did not exhibit any private haplotypes (Fig. 2). Under the hypothesis of neutrality, our mtDNA results also detected the signal of a recent sudden demographic expansion of the Chilean jack mackerel in the South Pacific. The star like network (Fig. 2), the significant and negative values of Tajima and Fu's test (Table 2) and the L-shaped mismatch distribution supported this hypothesis. Therefore, the absence of a genetic structure in the Chilean jack mackerel between the eastern and western sides of the South Pacific may be a direct consequence of its recent westward invasion. The relationship between genetic structure and gene flow intensity is only established in a migration-drift equilibrium model that implies stability in time of the population structure as well as the connectivity pattern. In this context, important changes in population size and/or distribution range may cause a decoupling between genetic structure and the

current migration pattern. For example, no genetic differences will be found among local populations after a recent expansion of the distribution range although they represent true reproductive units. Such equilibrium will be reached only after numerous generations, depending on the mutation time unit of chosen molecular marker.

Finally, based on mtDNA sequencing and 4 microsatellite loci, we have provided new evidence that supports the hypothesis of a single genetic population across the distribution range of *T. murphyi*. In this context, and in the absence of further data that support the existence of different stock units in this species, Chilean jack mackerel exploitation should follow a single stock fishery model, particularly unifying the heavily exploited EEZs of Chile/Peru and their adjacent open ocean regions. However, it is worth keeping in mind the limitations of the genetic stock identification (GIS) approach, and more generally, of all single tool methods. First of all, like other tests to detect stock structure, failure to reject the panmixia hypothesis by genetic data does not prove the existence of a single stock (i.e. null hypothesis acceptance), although it is consistent with this conclusion (Shaklee and Currens, 2003). Additionally, low migration rates among local populations may allow genetic homogeneity across the entire distribution range while the stock fishery concept is primarily based on a time stable relationship between recruitment and spawning population (Ward, 2000; Abaunza et al., 2008). Therefore, for a global decision about this fishery, a holistic approximation to stocks identification is needed (Cadrin et al., 2005) and the experience gained from the study of several other highly migratory species has demonstrated the benefits of a multidisciplinary approach. This was the case with the HOMSIR project that studied the stock structure of horse mackerel, *Trachurus trachurus*, incorporating different molecular genetic markers, parasitological surveys, body and otolith shape analysis, tagging, life history traits analysis, and an interdisciplinary analysis (Abaunza et al., 2008; www.homsir.com); Other examples are the REDFISH project focused in the golden redfish (*Sebates marinus*), which included morphometric analyses, elemental analysis of otoliths and various genetic methods (Rätz, 2004; www.redfish.de); and the WESTHER project on the identification of herring (*Clupea harengus* L.) stock components, which combined morphometrics, meristics, parasites, genetics, otolith microstructure, and otolith microchemistry (Hatfield et al., 2005; www.clupea.net/westher). These projects are international in scope and involve a collaborative effort among many research institutes from the involved countries. Finally, we strongly recommended that such holistic and international approach be initiated to characterize stock unit in *T. murphyi* across the South Pacific Ocean in order to provide the basis for a sound assessment for the effective management of this species.

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