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-RESEARCH ARTICLE-

Population Structuring and Migration Pathway of Atlantic bonito *Sarda sarda*

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Abstract

Population structure of Atlantic Bonito *Sarda sarda* in the Mediterranean Sea and possible pathway of migration for spawning and feeding was discussed on the bases of genetic and morphological dataset. The effects of topographic and hydrographic factors on the connectivity and migration pattern of Atlantic Bonito in Turkish, Bulgarian and Croatian marine waters and fishery management implications of putative stocks were correspondingly referred.

Keywords:
Atlantic Bonito**,** *Sarda sarda*, genetic structuring, connectivity, migration pattern.

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Introduction

The Atlantic bonito *Sarda sarda* (Bloch 1973) is a commercially valuable small tuna-like species, which occurs along the tropical and temperate coasts of the Atlantic Ocean, the Mediterranean Sea and the Black Sea and inhabit pelagic waters limited by the continental

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shelf (Relini et al., 2005; Collette and Nauen, 1983; Turan et al., 2007). According to ICCAT 2013, the total catch of Atlantic Bonito is 10.019 t in Turkish Seas in 2011 and Turkey takes the first place in Mediterranean with this value (ICCAT, 2013). Atlantic Bonito mainly feed on anchovy, sprat, pilchard, horse mackerel, chup mackerel in Turkish marine waters. The fishery data of these species since 2002 obtained from DIE (2013) was investigated according to years that the catch amount of Atlantic Bonito was increased when anchovy stocks was being crushed in the fishing season 2005-2006 that Atlantic Bonito possibly cause the decline of anchovy stocks due to anchovy based feeding.

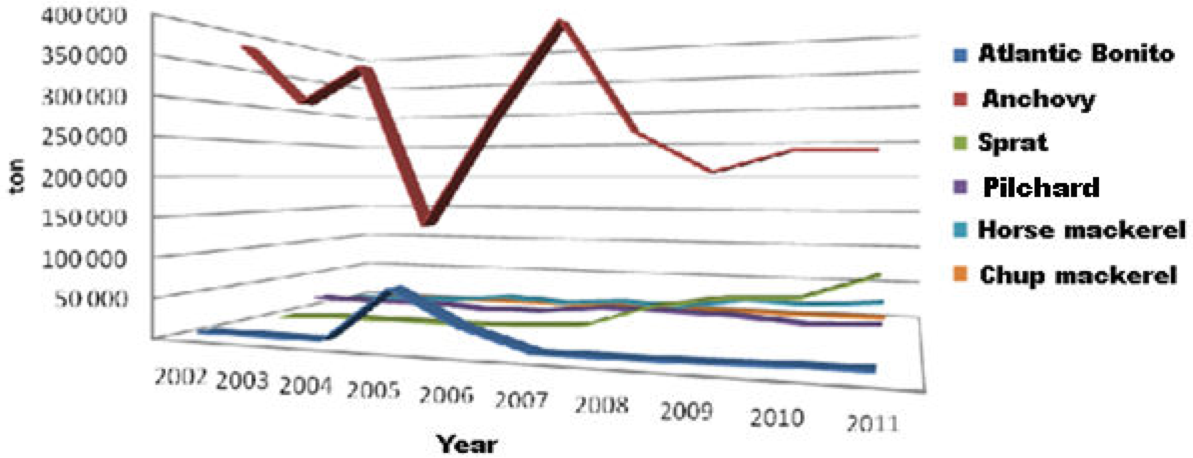

Figure 1. The annual distribution of Atlantic bonito and other feed related species between 2002-2011 years in Turkish Seas.

Little is known about Atlantic bonito migration patterns. Atlantic bonito migrates for feeding and spawning. Three separate spawning grounds are generally accepted to occur for the bonito in the Mediterranean Sea. The first and main spawning ground is the Black and Marmara Seas in the eastern Mediterranean (Yoshida, 1980; Rey et al., 1984). The area between Gibraltar, Balearic Islands and Algeria is the second spawning ground in the western Mediterranean (Rey et al., 1984). The third spawning ground is accepted to be in the northern Balearic Sea (Sabates & Recasens, 2001).

Marine species usually reveal lower geographical differentiation than terrestrial species, as a result of lack of geographical barriers, large population sizes, high fecundity, wide range of distribution and long pelagic larval phase (Ward, 2000; Nielsen & Kenchington, 2001). Connectivity between populations is generally explained as the degree to which populations are considered to be open or close by gene flow and dispersal patterns (Hellberg et al., 2002; Palsbøll et al., 2007). Therefore, understanding the degree of connectivity and diversity are central issue for conservation, management and recovery of exploited stocks (Carvalho & Hauser, 1994; Schick & Lindley, 2007). There have been several population genetic and tag re-cupture studies for understanding degree of connectivity between populations of Atlantic Bonito in the Mediterranean Sea (Rey et al., 1984; Vinas et al., 2004; Turan et al., 2015). Turan et al. (2015) investigated population genetic structure and connectivity of Atlantic Bonito using mtDNA sequencing analysis in Turkish, Bulgarian and Croatian marine waters in the Adriatic Sea (Figure 2).

Figure 2. Sampling locations of *S. sarda*. The abbreviation of the samples as: BS1, the Black Sea Bulgarian Coast (Varna); BS2, the Black Sea Igneada; the Black Sea Duzce (BS3); the Black Sea Samsun (BS4); the Black Sea Trabzon (BS5); Istanbul Bosporus (BP); MS, Marmara Sea Bandırma; AS, the Aegean Sea Izmir; NMS1, the northeastern Mediterranean Sea Antalya Bay; NMS2, the northeastern Mediterranean Sea Iskenderun Bay; ADS, Adriatic Sea Croatian Coast. Taken from Turan et al. (2015).

MtDNA analysis revealed that populations of Atlantic Bonito in Turkish coastal waters were divided into two genetically different two populations that *Sarda sarda* in the Black Sea and Marmara Sea comprise one genetic unit, and *S. sarda* in the Aegean and Mediterranean coast of Turkey constitute the genetically different second unit. On the other hand, the Adriatic Sea population from the Croatian coast was genetically different from the two genetically different populations in the Turkish coastal waters. This pattern of differentiation was also shown by multi-dimensional scaling analysis of the genetic distance between populations (Figure 3).

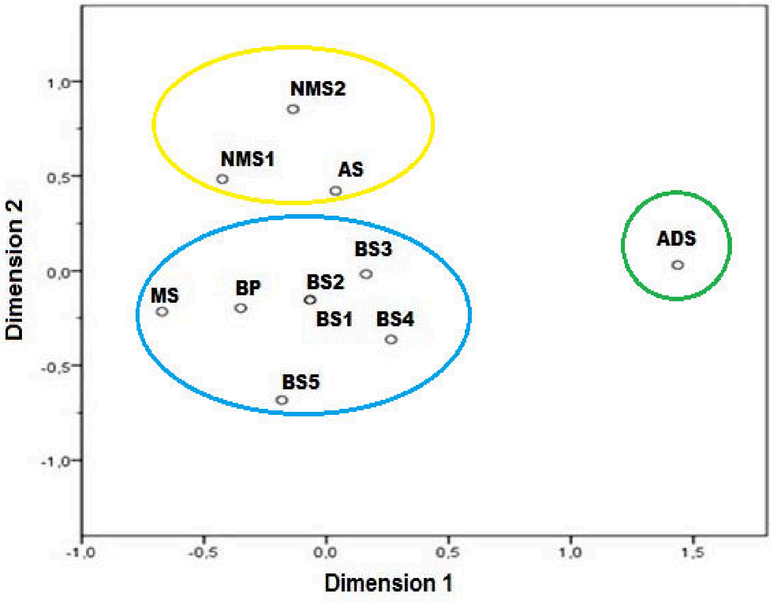

Figure 3. Multi-dimensional scaling plot of pairwise mtDNA D-loop sequencing differences between *S. sarda* populations. Taken from Turan et al. (2015).

Turan (2015) also used microsatellite analysis to investigate population genetic structuring and connectivity between the geographically isolated Atlantic Bonito populations from Turkish, Bulgarian and Croatian marine waters, and found two genetically different population in Turkish coastal waters, first constitute the Black Sea and Marmara Sea population and the second comprise the Aegean and Mediterranean Seas populations. This pattern of differentiation according to microsatellite data was also shown by multidimensional Scaling analysis of the genetic distance between populations (Figure 4).

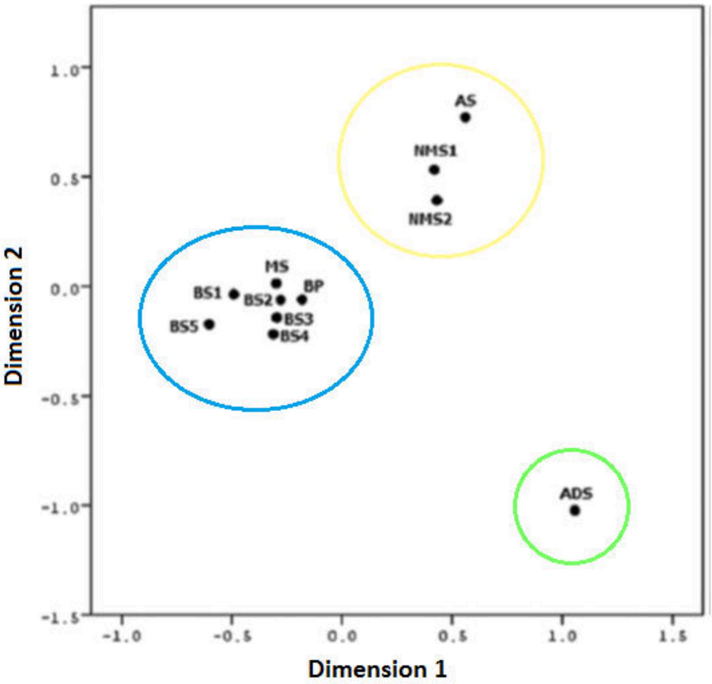

Figure 4. Multi-dimensional scaling plot of pairwise microsatellite differences between *S. sarda* populations. Taken from Turan (2015).

We analysed also morphological characters such as morphometric and meristic o the same sample set. The Truss network system was used for morphometric analysis (Figure 5). Numbers of unbranched and branched rays in the first and second dorsal, first and second anal, pectoral, ventral fins and gill rakers on the upper limb and lower limb of the first gill arch, vertebrate numbers were obtained under a binocular microscope for the meristic characters.

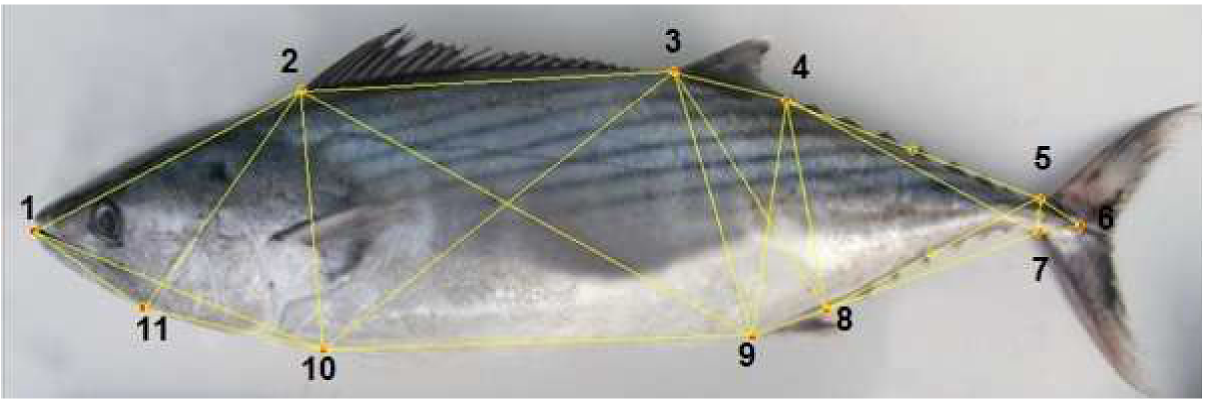

Figure 5. The Truss network system and eleven landmarks on Atlantic bonito for morphometric analysis.

Only the Adriatic Sea sample from Croatian coast revealed morphological differences based on morphometric characters (Figure 6). Meristic analysis of the Atlantic bonito populations did not show any morphological differences between the geographically separated populations which were overlapped together in the discriminant space (Figure 7).

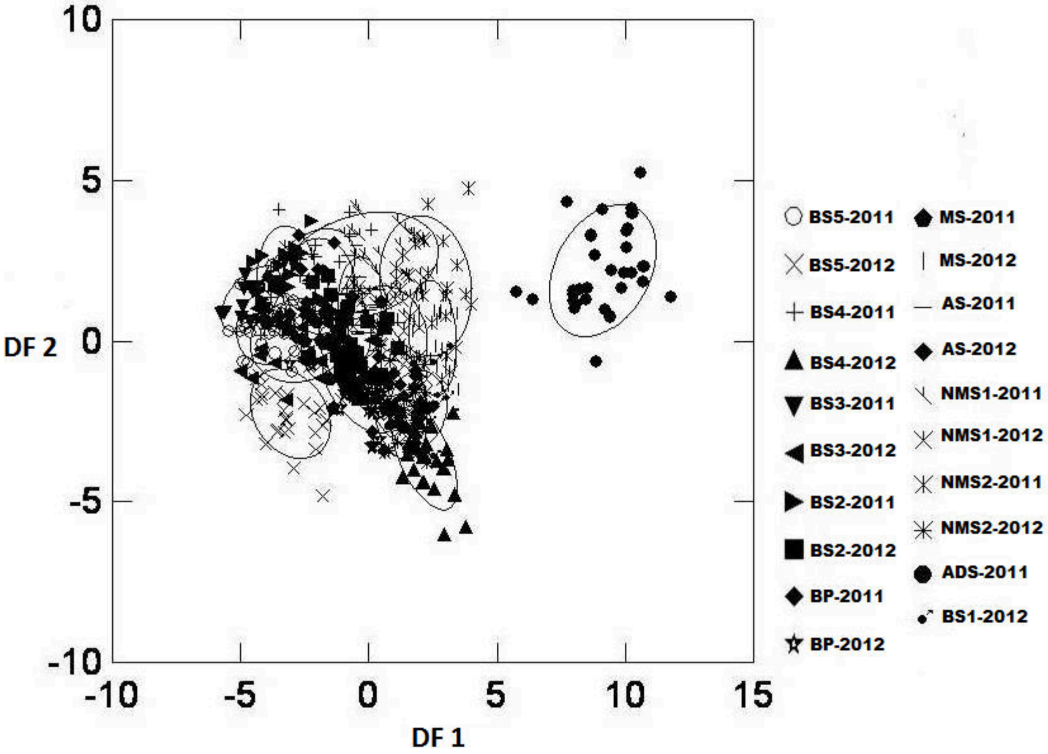

Figure 6. Discriminant function analysis of morphometric characters of Atlantic Bonito. Sample abbreviations are given in Figure 1.

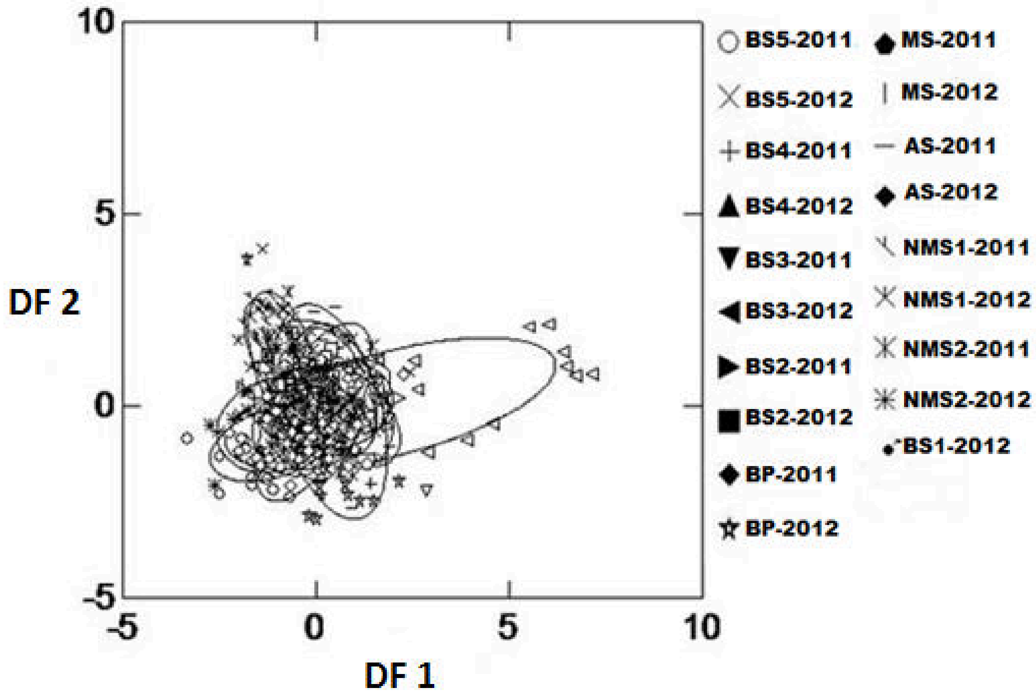

Figure 7. Discriminant function analysis of meristic characters of the Atlantic bonito. Sample abbreviations are given in Figure 1.

On the bases of genetic results described by Nümann (1954), Turan et al. (2015) and Turan (2015), the first genetically different unit or stock of *Sarda sarda* has spawning grounds in the Black Sea that migrate to the Marmara Sea for feeding and some parts of which also migrate to the Aegean Sea. This adult Atlantic bonito group may also go back to the Marmara and Black Sea for spawning during the spring. The second stock of Atlantic bonito is located in the Aegean and Mediterranean part of Turkey (Figure 8). The possible spawning ground of this stock may be Antalya Bay (based on personal communication with fishermen), and this stock possibly has different spawning pathways and migrate between Aegean and Mediterranean Seas for feeding. The Adriatic Sea population from the Croatian coast was also genetically different from the two genetically different populations in the Turkish coastal waters (Figure 8).

The differentiation of the Adriatic Sea population from Turkish populations was also indicated by Roberti et al. (1993), Pujolar et al. (2001) and Vinas et al. (2004). Roberti et al. (1993) also indicated the high degree of differentiation between Italian and Turkish *Sarda sarda* stocks based on mtDNA Cytochrome b sequencing analysis. Pujolar et al. (2001) found a small but significant differentiation between the Aegean Sea and two western samples, namely the Ionian Sea and the Ligurian Sea using allozyme electrophoresis and argued that the barrier to gene flow between east and west is located in the region that separates the Ionian and the Aegean seas.

Figure 8. Possible genetically different populations and their extension. Putatively different populations are indicated with different colour according to their possible extension.

Vinas et al. (2004) investigated mtDNA control region sequences of *S. sarda* on the Balearic, Ligurian, Ionian and Aegean Seas and reported the lack of genetic differentiation between the Balearic Sea and the Ionian Sea and found significant differentiation between the Aegean Sea population and both Balearic and the Ligurian Sea populations. Vinas et al. (2004) also found two mitochondrial control region clades, Clade I (Atlantic) and Clade II (Mediterranean) (Figure 9).

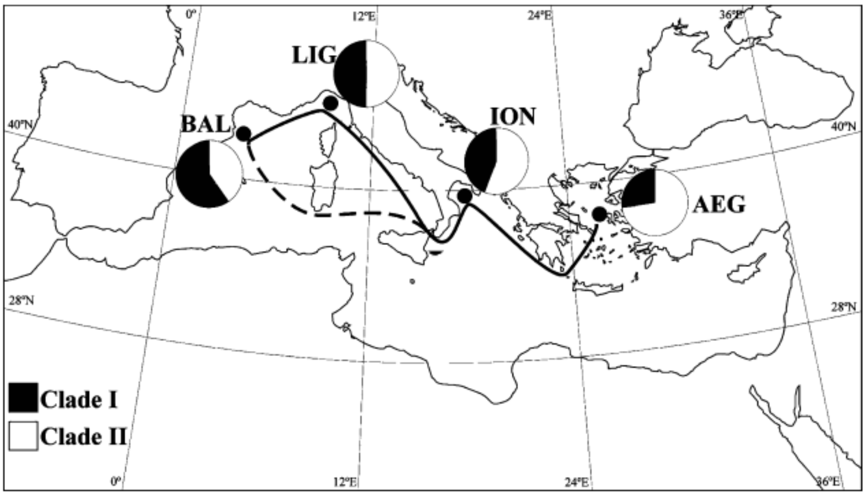

Figure 9. Pie diagrams of distribution of the two mitochondrial control region clades. Clade I (Atlantic) and Clade II (Mediterranean). Lines represent the putative gene flow corridor among localities with no significant genetic distance. Dotted line represents the putative gene flow between the Balearic Sea and Ionian Sea. Taken from Vinas et al. (2004).

Topographic and hydrographic factors may contribute the connectivity and migration pattern of Atlantic Bonito in Turkish marine waters. The Turkish straits form an “acclimatization zone” for transiting species, allowing those from the Mediterranean to adjust to the different environmental conditions in the Black Sea, and vice versa (Turan, 2014). Therefore, the Turkish Straits System may be a sieve to select or eliminate some genetic traits for the migratory species, or prevent migration between the two Seas. The Dardanelle strait system seems to be a geographic barrier to limit gen flow between the Black Sea and Aegean Sea populations, and cause genetic differentiation of *S. sarda* populations (Figure 10). Moreover, the wide geographic interval between the Adriatic and the other S. *sarda* populations seems to be limiting intermingling and rising the detected genetic differentiation.

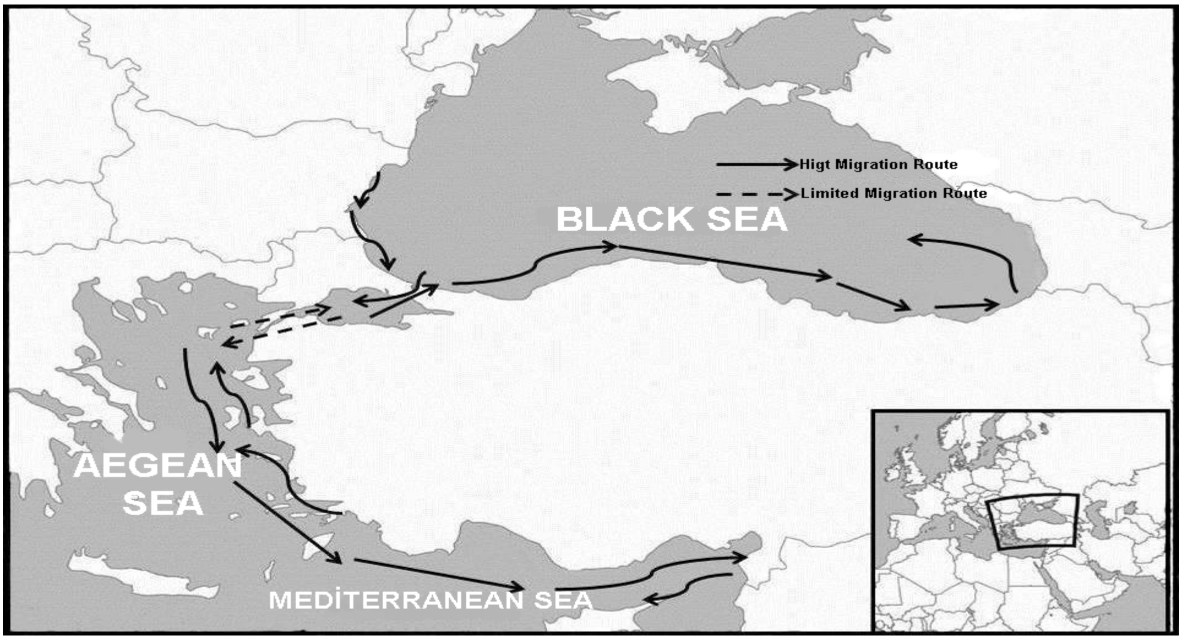

Figure 10. Possible migration pathway of Atlantic bonito in Turkish and Bulgarian marine waters, based on Turan et al. (2015) and Turan (2015).

In conclusion, a degree of reproductive isolation detected by genetic markers, Atlantic bonito in the Black and Marmara Sea populations comprise one genetically discontinuous unit, and the Aegean and Mediterranean coast of Turkey populations constitute the genetically different second unit. Atlantic bonito fishery stocks are reportedly declining with the existing heightened fishing pressure (Oray and Karakulak, 1997; Prodanov et al., 1997; Zengin et al., 1998). Thus, managing the two units separately may be worth considering. Identification of management units is very important for the effective management of marine resources. Significant genetic differentiations among the stocks were found with different genetic markers. The findings indicate that there is a localized population subdivision of Atlantic bonito. Management units should be established for populations that exhibit a level of genetic divergence that is consistent with demographic independence (Palsbøll et al., 2007). Atlantic bonito is currently managed as a single population in Turkish, Bulgarian and Croatian marine waters. The studies indicates the formation of a meta population of different stocks with limited genetic exchange. Applying the same management approach to these two unconnected stocks that is differing their resilience to exploitation may result in overfishing and likely collapse of the fishery.

Acknowledgements

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