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Genetic and Some Bio-Ecological Characteristics of Lessepsian Lizardfish *Saurida lessepsianus* from the Northeastern Mediterranean Sea

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Research Article

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Abstract

Genetic structure and some bio-ecological characteristics of lessepsian lizardfish *Saurida lessepsianus* populations collected from the Iskenderun, Mersin, and Antalya Bays were revealed by mtDNA sequencing of Cyt b dataset and length-weight relationships and the parameters of von Bertalanffy growth function. The highest genetic divergence was detected between the Mersin and Antalya populations (0.0026), whereas the lowest was between the Iskenderun and Antalya populations (0.0014). The length-weight relationships for all individuals of Iskenderun, Mersin, and Antalya populations were calculated as $W = 0.0042 \times L^{3.2207}$, $W = 0.0039 \times L^{3.1627}$ and $W = 0.0196 \times L^{2.6515}$, respectively. The von Bertalanffy growth parameters (L_∞, k, and t_o) were estimated for all individuals as $L_\infty = 47.33$ cm, $k = 0.024$, and $t_o = -1.28$ for Iskenderun; $L_\infty = 41.74$ cm, $k = 0.085$ and $t_o = -1.72$ for Mersin and $L_\infty = 50.99$ cm, $k = 0.154$ and $t_o = -2.41$ for Antalya. This study examines the genetic structure and bio-ecological characteristics of the *S. lessepsianus* populations on the Mediterranean coast of Türkiye together for the first time. Genetic findings and bio-ecological parameters of populations generally support each other and can provide support for future studies.

Keywords: *Saurida lessepsianus, population genetics, mtDNA sequencing, growth parameters, Northeastern Mediterranean Sea*

Introduction

The lessepsian lizardfish *Saurida lessepsianus* Russell, Golani and Tikochinski, 2015, was previously erroneously identified as *S. undosquamis* (Richardson, 1848) and *S. macrolepis* Tanaka, 1917 due to

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their morphological similarities (Inoue and Nakabo, 2006) is a recently described species belonging to the Synodontidae family, which is widely distributed in the Red Sea and established by entering the Mediterranean via the Suez Canal (Russell et al., 2015; Tikochinski et al., 2016; Silpa et al., 2021). Nowadays, the species, whose first specimens in the Mediterranean were reported as *S. grandisquamis*, the junior synonym of *S. undosquamis*, off the coast of Israel in December 1952 by Ben-Tuvia (1953), has reached a wide range expansion in the Eastern Mediterranean, from Libya to the south of the Aegean Sea, making it one of the most successful colonists in the Levant basin (Russell et al., 2015; Turan et al., 2018).

The species, which is mainly found on sandy or muddy surfaces up to about 100 m but has a widespread distribution on islands or shores at a depth of 20-30 m, is important for trawling in the Gulf of Suez and the Mediterranean coast of Egypt, where fisheries pressure is quite intense (El-Halfawy et al., 2007; Mahmoud et al., 2014). Until 1955, catch yields were relatively low; nevertheless, with the intensive use of bottom trawling (Ben-Yami and Glaser, 1974), although occasional fluctuations occurred thereafter, catches have significantly increased (Golani, 1993). In Türkiye, it is considered a commercially important species that is frequently caught in Iskenderun, Mersin, and Antalya Bays (Ismen, 2003; Yaglioglu and Turan, 2012), constituting approximately one-third of the commercial trawl catch in the Northeastern Mediterranean (Russell et al., 2015). The spawning season lasts over a wide period, March-December on the coasts of Israel (Golani, 1993), between spring and autumn in the Gulf of Suez (Egypt) (Amin et al., 2007; El-Etreby et al., 2013), December-April in the Northern Gulf of Suez (Suez), June-March and August-February in the Southeastern Mediterranean (Port Said) along the Egyptian coasts (Roshdy et al., 2021), August-January in Parangipettai coasts (Southern India) (Kadharsha et al., 2013), while in Türkiye, spawning occurs in two periods: May-July and September-November in Iskenderun Bay (Ismen, 2003). The *S. lessepsianus* is a piscivorous species, preying on smaller fish (such as anchovies and mullets) in its habitat for its main source of sustenance, as well as feeding on crustaceans and other invertebrates (Fischer et al., 1990).

Several molecular studies have been performed to reveal the genetic characterization of some synodontid species' populations e.g., Bombay-duck *Harpadon nehereus* (Guo et al., 2019; Yang et al., 2022), brushtooth lizardfish *Saurida undosquamis* (Li et al., 2019; 2020; Tan et al., 2022), and greater lizardfish *Saurida tumbil* (SriHari et al., 2021), while very limited studies have been conducted on *S. undosquamis* (misidentification of *S. lessepsianus*) populations (Yaglioglu and Turan, 2012; Tikochinski et al., 2016). On the other hand, growth parameters (Tureli and Erdem, 1997; Cicek, 2006; Amin et al., 2007; El-Halfawy et al., 2007; Gokce et al., 2007; Cicek and Avsar, 2011; Manasirli et al., 2011; El-Etreby et al., 2013; Mahmoud et al., 2014; Gundogdu and Baylan, 2015, 2016), length-weight relationships (Abdallah, 2002; Can et al., 2002; Cicek et al., 2006; Sangun et al., 2007; Ceyhan et al., 2009; Erguden et al., 2009; Manasirli et al., 2011; Mahmoud et al., 2014; Ozvarol, 2014; Akel, 2016; Turker et al., 2020; Yedier et al., 2020; Mehanna and Farouk, 2021), and reproductive biology (Ismen, 2003; Amin et al., 2007; El-Etreby et al., 2013; Roshdy et al., 2021) of the lessepsian lizardfish have been examined in numerous studies conducted in the Red Sea and the Mediterranean.

To manage marine stocks, it is crucial to evaluate gene flow levels among populations and bio-ecological parameters (Uyan et al., 2020; Turan et al., 2021; Doğdu et al., 2022). Having advantageous features such as haploid structure, maternal inheritance, non-recombining feature, high evolution rate, etc., mitochondrial DNA (mtDNA) allows it to be easily amplified and sequenced under optimal conditions, because of its several markers used to analyze the degree of differences between populations (Harrison, 1989; Turan et al., 2015; Doğdu and Turan, 2021). Cytochrome b (Cyt b), one of the relatively well-understood protein-coding genes of mtDNA, is an ideal molecular marker that allows specific identification of the status of germplasm resources and population genetic structure (Parson et al., 2000; Doğdu and Turan, 2016; Karan et al., 2019).

To our knowledge, nucleotide variations based on mtDNA sequencing among *S. lessepsianus* populations in Turkish marine waters are still not known in detail. Thus, in this study, the genetic structures based on mitochondrial Cyt b sequence data and some bio-ecological parameters of *S. lessepsianus* from the Northeastern Mediterranean (Iskenderun, Mersin, and Antalya Bays) populations were investigated in point of the ecosystem-based fisheries management.

Material and Methods

S. lessepsianus specimens were collected by commercial trawlers from the fishing areas of Iskenderun Bay (ISK), Mersin Bay (MER), and Antalya Bay (ANT) between 2017 and 2019 (Figure 1). Twenty-five specimens from each location were studied for population genetic analysis. The collected samples were transported to the laboratory by keeping the cold chain in a cooler box and stored in a deep freezer at -21°C until DNA extraction. A total of 1037 specimens, of which 336 ISK, 390 MER, and 311 ANT populations, were sampled to estimate the length-weight relationships and growth parameters. The total length of the samples was measured to the nearest 0.1 cm and the weight to the nearest 0.01 g.

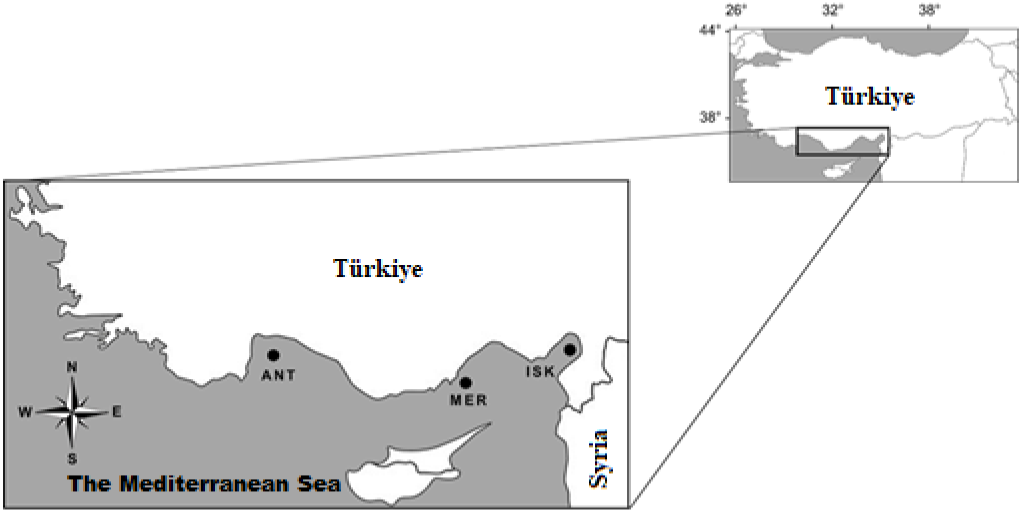

Figure 1. Sampling locations of *Saurida lessepsianus*: ISK, Iskenderun Bay; MER, Mersin Bay; ANT, Antalya Bay.

Genetic Analysis

The standard phenol: chloroform: isoamyl alcohol process was implemented with minor modifications for DNA isolation from the muscles of all fish samples (Sambrook et al., 1989). To analyze genetic variation, a partial mitochondrial Cyt b gene was amplified by Polymerase Chain Reaction (PCR) with universal primers L14724 (5’-CGAAGCTTGATATGAAAAACCATCGTTG-3’) and H15149 (5’-AAACTGCAGCCCCTCAGAATGATATTTGTCCTCA-3’) (Kocher et al., 1989). The PCR was run for a 25 µl total volume including 5 units of Taq polymerase, 2 mM of each primer, 10 mM of dNTPs, 25 mM MgCl2, 10 mM Tris-HCl (pH 8.8), 50 mM KCl and 1 µL template DNA (~10-25 ng). The thermal cycling conditions were adjusted as follows: initial denaturation at 95°C for 1 min, followed by 35 cycles of strand denaturation at 94°C for 30 s, annealing at 50°C for 30 s, and primer extensions at 72°C for 45 s, and final elongation for 7 min at 72°C. To visualize the amplicons, 4 µL samples of each PCR product were loaded onto 1.5% agarose gels. Ultimately, sequencing analysis of PCR products was executed in the forward direction with an automated sequencer.

Sequence Alignment and Statistical Analysis

The initial and final alignments of the partial Cyt b sequences were manually carried out with BioEdit (Hall, 1999). MEGA X (Kumar et al., 2018) was used to perform an evolutionary investigation and construct a phylogenetic tree of aligned Cyt b sequences. The most suitable model of DNA evolution was revealed with ModelTest (Posada and Crandall, 1998). The Neighbour-Joining (NJ) tree (Saitou and Nei, 1987) was used to depict genetic differentiation between populations. The statistical robustness and reliability of the branching order within the NJ tree were approved by bootstrap analysis using 1000 replicates. Tajima’s D test (Tajima, 1989) was performed to analyse the relationship of DNA sequence evolution to neutrality. A minimum-spanning haplotype network of Cyt b sequences was built using the software PopART (Bandelt et al., 1999).

Bio-Ecological Analysis

The length-weight relationships (LWRs) were independently estimated for each lessepsian lizardfish population of all individuals with the formula $W = a \ x \ L^b$ (Ricker, 1975). This equation can be expressed logarithmically as log $W = log \ a + b \ log \ L$, where W is total body weight (g), L is total length (cm), and a is a coefficient relative to body form and exponent b is the allometry coefficient of the linear regression equation expressing isometric (= 3), positive allometric (> 3) and negative allometric (< 3) growth in length. To verify whether the b values obtained in the linear regressions were significantly different from the null hypothesis of isometric growth ($H0$: b = 3), a student t-test with a ±95% confidence interval was applied, expressed by the formula: $t_s = (b - 3) / S_b$, where t_s is the t-test value, b the exponent and S_b the standard error of b (Morey et al., 2003).

Age readings were taken by counting growth annuli from all sagittal otoliths as suggested by Holden and Raitt (1974). All otoliths were cleared in ethanol and then immersed in glycerine for examination. A reflected light binocular microscope was used to determine age.

The theoretical growth patterns for all individuals were calculated using the von Bertalanffy growth function (VBGF) (Beverton and Holt, 1957) $L_t = L_\infty \ [1 - e^{-k(t-to)}]$, where L_t is the fish length (cm) at the time t (year), L_∞ is the mean asymptotic length (cm), k is the growth coefficient (year^{-1}), and t_o (year) is the theoretical time at which the length is equal t_o zero.

Results

398 bp partial Cyt b gene sequences were obtained after alignment. Overall nucleotide composition of Cyt b sequences was A: 23.1; T: 31.0; G: 17.4 and C: 28.5%. The Cyt b dataset comprised 11 variable sites, 6 of which were parsimony informative. A total of 12 haplotypes were generated from Cyt b sequences, of which a single haplotype (Hap_1) was shared between populations (Table 1). The mean haplotype diversity was 0.4411. Three representative sequences from each population were deposited in GenBank under accession numbers OR345562-OR345570.

Table 1. Distribution and frequency of Cyt b haplotypes of *S. lessepsianus* populations.

Haplotype	ISK	MER	ANT
Hap_1	20	19	17
Hap_2	2	-	-
Hap_3	1	-	-
Hap_4	1	-	-
Hap_5	1	-	2
Hap_6	-	3	-
Hap_7	-	1	-
Hap_8	-	2	-
Hap_9	-	-	3
Hap_10	-	-	1
Hap_11	-	-	1
Hap_12	-	-	1
Total	**25**	**25**	**25**

The Minimum Spanning Tree was obtained to elucidate phylogenetic relationships depending on sequence variations between haplotypes from *S. lessepsianus* populations (Figure 2).

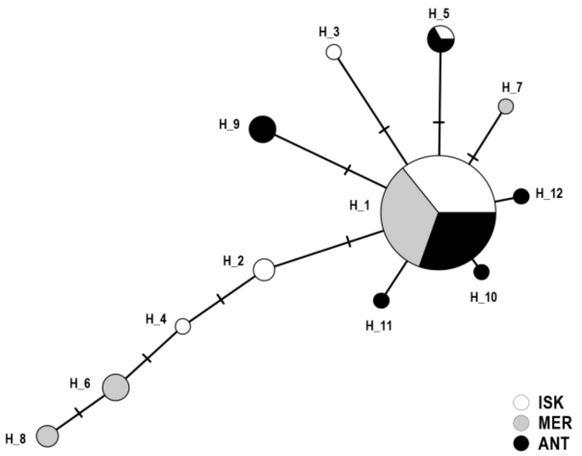

Figure 2. Minimum spanning tree of the Cyt b haplotypes obtained from *S. lessepsianus* populations.

The pairwise differentiation between populations and mean nucleotide diversity within populations inferred from Cyt b sequences are given in Table 2. The highest nucleotide diversity was observed in the MER population, while the lowest was in ISK. The mean nucleotide diversity between populations was found to be 0.0019. The mean genetic divergence between populations was 0.0021. The highest genetic differentiation was found between the MER and ANT populations, while the lowest was between ISK and ANT populations.

Table 2. Pairwise genetic distance between populations (below the diagonal). Bold numbers represent mean genetic diversity within populations, * $p < 0.05$.

Populations	ISK	MER	ANT
ISK	**0.0012**		
MER	0.0023	**0.0031**	
ANT	0.0014	0.0026*	**0.0015**

Statistically, pairwise comparisons revealed significant differentiation ($p < 0.05$) between the MER and ANT populations (Table 2). In the NJ tree, the MER differed from the ISK and ANT populations grouped together (Figure 3).

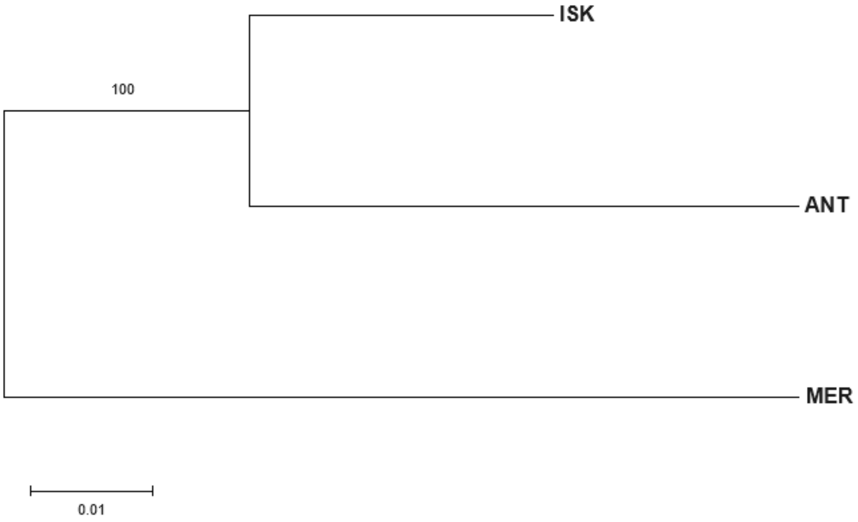

Figure 3. The NJ tree reflecting the genetic relationship of *S. lessepsianus* populations.

Tajima’s D (Tajima, 1989) for the populations of *S. lessepsianus* from the Northeastern Mediterranean was found to be -1.742520 which points out that the observed heterozygosity is lower than that expected (Table 3).

Table 3. Neutrality tests and estimated discordance distribution parameters.

m	*S*	*Ps*	*Θ*	*π*	*D*
75	11	0.027638	0.005654	0.002035	-1.742520

m, number of sequences; *S*, number of segregating sites; *Ps*, polymorphic site rate; *Θ*, population mutation rate; *π*, average pairwise distance; *D*, Tajima’s D.

Length-Weight Relationships and Growth Parameters

The LWRs were independently calculated for each population of all *S. lessepsianus* individuals and were presented in Figure 4. The exponent b proved positive allometric growth for ISK and MER samples, while negative allometric growth for ANT samples. The length-weight relationships for ISK, MER, and ANT populations of all individuals were determined as $W = 0.0042$ x <$L^{3.2207}$ ($n = 336$, $R^2 = 0.9840$), $W = 0.0039$ x $L^{3.1627}$ ($n = 390$, $R^2 = 0.9868$) and $W = 0.0196$ x $L^{2.6515}$ ($n = 311$, $R^2 = 0.9815$), respectively. The regression coefficient (R^2) showed that fish length had a highly significant correlation with weight.

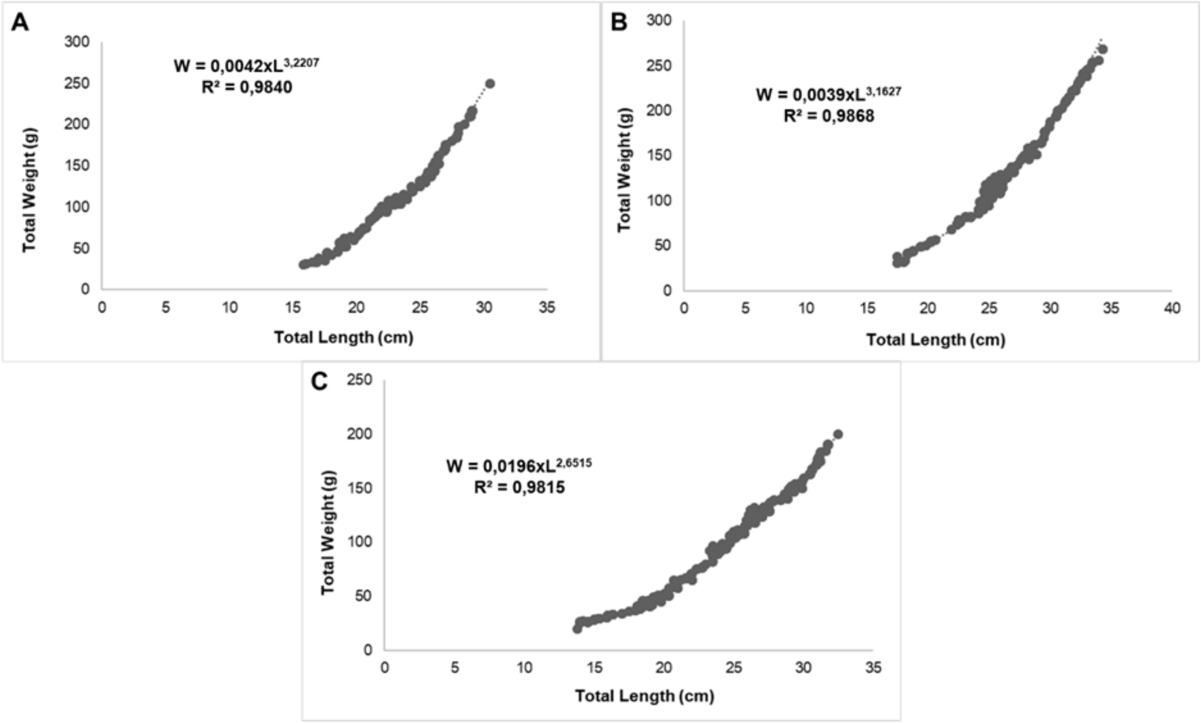

Figure 4. The LWRs for all individuals of ISK (A), MER (B), and ANT (C) populations.

The parameters of VBGF (L_∞, k, and t_o) were also separately estimated for all individuals of lessepsian lizardfish as $L_\infty = 47.33$ cm, $k = 0.024$, and $t_o = -1.28$ for ISK; $L_\infty = 41.74$ cm, $k = 0.085$ and $t_o = -1.72$ for MER and $L_\infty = 50.99$ cm, $k = 0.154$ and $t_o = -2.41$ for ANT specimens.

Discussion

The present study evaluated the genetic and bio-ecological characteristics of *S. lessepsianus* populations together for the first time. The MER population demonstrated the highest nucleotide diversity. The MER and ANT populations were statistically different from each other ($p < 0.05$). Additionally, the lowest *b* value was estimated in the ANT population, whereas the highest was in the ISK population. The highest L_∞ and *k* were determined in the ANT population.

The mean haplotype and nucleotide diversity of lessepsian lizardfish populations were found to be 0.4411 and 0.0019, respectively. Compared with other studies on *Cyt b* data for related synodontids, our results are higher than Guo et al. (2019) but lower than Li et al. (2019). Guo et al. (2019) examined the genetic structure of *Harpadon nehereus* along the Chinese coasts and observed haplotype and nucleotide diversity as 0.3026 and 0.0003, respectively. Conversely, Li et al. (2019) carried out the genetic analysis of *Saurida undosquamis* populations from the Chinese continental shelf and found higher haplotype (0.9650) and nucleotide diversity (0.0034) than the present study. Based on a comparison of *Cyt b* data sets of species that share similar habitats with lessepsian lizardfish along the Northeastern Mediterranean, Salcioglu et al. (2021) examined the phylogeography of *Spicara flexuosa* from Levantine coasts and found lower haplotype (0.1910) and nucleotide diversity (0.0005) than the present study. On the other hand, the haplotype and nucleotide diversity of lessepsian lizardfish populations were lower than those found in the former studies using various mtDNA markers on *Saurida* spp., conducted by Tikochinski et al. (2016), Li et al. (2020), and SriHari et al. (2021). However, compared to Tan et al. (2022), haplotype diversity in this study is similarly low but nucleotide diversity is high. Tikochinski et al. (2016) revealed genetic variations in the Red Sea and Mediterranean populations of *S. lessepsianus* inferred from control region sequences and found haplotype and nucleotide diversity to be 0.6333 and 0.0065 for Red Sea samples, 0.9935 and 0.0062 for Mediterranean samples, respectively. Li et al. (2020) investigated the control region-based genetic structure of the *S. undosquamis* populations from the Chinese coasts and detected, in that order, the haplotype and nucleotide diversity as 0.9873 and 0.0132. SriHari et al. (2021) elucidated the stock structure of *S. tumbil* populations from the Arabian Sea based on the control region data set and detected, respectively, haplotype and nucleotide diversity as 0.8840 and 0.0030. Tan et al. (2022) studied the phylogenetic relationships of *S. undosquamis* populations depending on *16S rRNA* from the east coast of Peninsular Malaysia and determined haplotype and nucleotide diversity to be 0.6820 and 0.0012, in that order. Therefore, the low haplotype and nucleotide diversity of lessepsian lizardfish, despite reaching a wide distribution area and becoming one of the most successful colonizers, may be linked with ecological factors and specific characteristics of the marine species, as well as possible bottleneck effects caused by intense overfishing pressures (Turan et al., 2009; 2019).

The mean nucleotide diversity within populations of lessepsian lizardfish was detected as the lowest (0.0012) in the ISK population. In Iskenderun Bay, compared to this study, the nucleotide diversity of *Diplodus annularis* based on *Cyt b* sequences was found to be higher (0.0027) by Bektas et al. (2016), while that of *Spicara smaris* (0.0002) and *S. flexuosa* (0.0001) was found to be low by Bektas et al. (2018). The low genetic diversity observed in the population of Iskenderun Bay can be mainly due to the discharges resulting from intense industrial activities such as iron-steel, ferrochrome, paint, plastic, food, fertilizer and oil industry, maritime activities, and potential municipal wastes (Kocak et al., 2010), the exposure of regional fish stocks to intensive fishing activities by an increasing number of trawlers every year and the Increasing water temperature due to climate change in the last 40 years affecting the biodiversity in this region (Yemisken et al., 2014; Turan et al., 2016; 2018; Doğdu et al., 2019; Langeneck et al., 2023).

The overall genetic differentiation between lesssepsian lizardfish populations was found to be 0.0021. Compared to our study, Guo et al. (2019) found lower (0.0003) genetic diversity in *H. nehereus* populations in the China Sea, while Li et al. (2019) found the genetic diversity of *S. undosquamis* populations in the China Sea to be equal (0.0021) to that in our study. Generally, marine species commonly demonstrate limited genetic differentiation owing to the absence of substantial geographical obstacles to dispersion and gene flow (Avise et al., 1987; Turan et al., 2009).

Calculation of Tajima's *D* for *S. lessepsianus* populations at -1.742520 indicates that the observed heterozygosity is higher than expected. In the event of selective sweep or population expansion where new mutations occur in high amounts, the *D* value is negative (Innan and Stephan, 2000). This situation is consistent with the fact that the haplotype and genetic diversity values generally decrease in direct proportion and that the species has a wide distribution area in the Eastern Mediterranean.

LWR and VBGF, which contain basic parameters in fisheries biology and stock assessments, help predict the metamorphosis, gonad maturity, and feeding rate of fish (Le Cren, 1951). These parameters of *S. lessepsianus* estimated from previous studies in the Mediterranean and Red Seas were tabulated in Table 4. In the LWRs, the *b* value showed positive allometric growth in ISK (3.2207) and MER (3.1627) individuals while negative allometric in ANT (2.6515) individuals. In terms of the positive allometric *b* values presented in Table 4, the MER population is generally consistent with previous studies conducted both in Mersin Bay (Cicek et al., 2006; Manasirli et al., 2011) and in various geographical regions. The *b* value of the ISK population was also found to be close to those obtained from studies in other locations and Yedier et al. (2020) (positive allometry), whereas Can et al. (2002), Cicek (2006), Erguden et al. (2009), and Cicek and Avsar (2011) found different *b* values (negative allometry). The *b* value of the ANT population is compatible with Turker et al. (2020) (negative allometry) but is incompatible with Ozvarol (2014) (positive allometry). These differences in *b* value may be related to a combination of one or more factors such as sampling site, habitat, season, maturity, sex, age, and diet (Ricker, 1975; Bagenal and Tesch, 1978; Ergüden and Doğdu, 2021; Turan et al., 2023; Doğdu and Turan, 2024).

The asymptotic length (L_∞) of *S. lessepsianus* derived from all three populations in this study is generally around the previous studies, except for Tureli and Erdem (1997), Amin et al. (2007), El-Halfawy et al. (2007) and Cicek and Avsar (2011), however, L_∞ was found to be 50.99 cm for ANT individuals, which stands out as the highest in the Mediterranean (Table 4). Tureli and Erdem (1997) and Cicek and Avsar (2011) found L_∞ to be 22.43 and 38.05 cm for the Iskenderun Bay, and Amin et al. (2007) and El-Halfawy et al. (2007) estimated L_∞ as 31.03 and 35.56 cm for the Gulf of Suez, respectively. Similar to L_∞ of ISK individuals (47.33 cm), Gundogdu and Baylan (2015, 2016) obtained 47.51 and 48.86 cm, while Cicek (2006) and Gokce et al. (2007) found L_∞ to be 41.27 and 42.00 cm, lower than our study, in that order, from Iskenderun Bay. Closely to MER individuals' L_∞ (41.74 cm), Manasirli et al. (2011) estimated L_∞ as 41.57 cm from Mersin Bay. Wotton (1990) suggested that fish populations of the same species in different geographical regions may exhibit highly variable individual growth rates. Moreover, some differences in growth traits may be related to possible food quality and water temperature (Santic et al., 2002). On the other hand, variations in estimated asymptotic length can be attributed to the phylogeographic diversity of each population, such as fisheries, climate, and pollutants (Ergüden et al., 2010; Uyan et al., 2020; Turan et al., 2021; Doğdu et al., 2022).

Table 4. Comparison of the LWRs including growth type (GT) and VBGF parameters of *Saurida lessepsianus* from various geographic localities.

Locations	N	LWR constants			GT*	von Bertalanffy growth constants			Author(s)
		a	***b***	***R^2***		***L_∞***	***k***	***t_o***	
Iskenderun Bay	333	-	-	-	-	22.43	0.597	-1.365	Tureli and Erdem (1997)
Mediterranean coast of Egypt	465	0.003	3.30	0.953	PAG	-	-	-	Abdallah (2002)
Iskenderun Bay	100	0.0117	2.7971	0.90	NAG	-	-	-	Can et al. (2002)
Iskenderun Bay	275	0.0083	2.8791	0.9627	NAG	41.27	0.118	-1.895	Cicek (2006)
Mersin Bay	1801	0.0039	3.165	0.968	PAG	-	-	-	Cicek et al. (2006)
Gulf of Suez, Egypt	390	0.0042	3.1315	0.985	PAG	31.03	0.44	-1.05	Amin et al. (2007)
Gulf of Suez, Egypt	434	0.0038	3.1666	0.987	PAG	35.56	0.26	-1.059	El-Halfawy et al. (2007)
Iskenderun Bay	4711	-	-	-	-	42.00	0.51	-0.29	Gokce et al. (2007)
Northeastern Mediterranean	416	0.0039	3.159	0.96	PAG	-	-	-	Sangun et al. (2007)
Gokova Bay	80	0.0046	3.109	0.951	PAG	-	-	-	Ceyhan et al. (2009)
Iskenderun Bay	304	0.0063	2.968	0.988	NAG	-	-	-	Erguden et al. (2009)
Iskenderun Bay	275	0.0083	2.789	0.96	NAG	38.05	0.124	-1.680	Cicek and Avsar (2011)
Mersin Bay	2757	0.0047	3.095	0.988	PAG	41.57	0.118	-1.895	Manasirli et al. (2011)
Gulf of Suez, Egypt	965	0.004	3.107	0.965	PAG	51.252	0.131	-1.45	El-Etreby et al. (2013)
Mediterranean coast of Egypt	3444	0.0094	2.899	0.9506	NAG	41.77	0.232	-	Mahmoud et al. (2014)
Antalya Bay	211	0.0037	3.190	0.968	PAG	-	-	-	Ozvarol (2014)
Iskenderun Bay	467	-	-	-	-	47.51	0.009	-2.05	Gundogdu and Baylan (2015)
Mediterranean coast of Egypt	75	0.0432	3.1263	0.9868	PAG	-	-	-	Akel (2016)
Iskenderun Bay	400	-	-	-	-	48.86	0.107	-1.733	Gundogdu and Baylan (2016)
Antalya Bay	54	0.0107	2.846	0.9035	NAG	-	-	-	Turker et al. (2020)
Iskenderun Bay	110	0.002	3.366	0.9766	PAG	-	-	-	Yedier et al. (2020)
Mediterranean coast of Egypt	361	0.0060	3.0656	0.95	IG	-	-	-	Mehanna and Farouk (2021)
Iskenderun Bay	336	0.0042	3.2207	0.9840	PAG	47.33	0.024	-1.28	Present study
Mersin Bay	390	0.0039	3.1627	0.9868	PAG	41.74	0.085	-1.72	
Antalya Bay	311	0.0196	2.6515	0.9815	NAG	50.99	0.154	-2.41	

*PAG, positive allometric growth; NAG, negative allometric growth; IG, isometric growth. N, sample number.

In conclusion, this study provided the first contribution in which the genetic structure and bio-ecological characteristics of *S. lessepsianus* populations were discussed together in terms of ecosystem-based fisheries management in the Northeastern Mediterranean. It is obvious that the results obtained from genetic analysis and bioecological parameters generally support each other and will be useful to fisheries biologists and managers in knowing the population structure of this species and will shed light on future studies.

Conflict of Interest

The authors declare that they have no competing interests.

Author Contributions

A.U. abd C.T. performed all the experiments and drafted the main manuscript text. A.U., C.T., S.A.D., M.G., D.Y., and B.S., performed genetic and morphological analysis. All authors reviewed and approved the final version of the manuscript.

Ethical Approval Statements

Local Ethics Committee Approval was not obtained because experimental animals were not used in this study.

Data Availability Statement

The data used in the present study are available upon request from the corresponding author.

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