

ORIGINAL ARTICLE

The influence of physical and biological processes on the ichthyoplankton communities in the Gulf of Sirte (Southern Mediterranean Sea)

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Keywords

Gulf of Sirte; ichthyoplankton; larval assemblages; zooplankton.

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Abstract

This paper reports on the first study on the ichthyoplankton community structure in the Gulf of Sirte and its spatial distribution in relation to environmental conditions and zooplankton abundance. The results make an important contribution to the future management of fisheries in this unexplored, but much exploited, area. Biological samples were collected in July 2008 using a Bongo40 net. In total, 1914 larvae were found and 1652 of these were identified. In particular, bathypelagic taxa were the most abundant, followed by demersal, mesopelagic, pelagic and epipelagic taxa. The ichthyoplankton community had a patchwork distribution influenced by oligotrophic conditions, the bottom depth and oceanographical features. The results suggest that environmental forcings were able to transport the ichthyoplankton to productive areas. Indeed, maximum fish egg densities were found in coastal stations in correspondence with the Atlantic Tunisian Current inflow, whereas larvae were mainly concentrated in the east side of the Gulf, probably as a result of advection by the anticyclonic circulation. Additionally, the distribution patterns of the total larvae density and the different assemblages were well matched with the abundance of the zooplankton, probably determining final larval survival, growth and recruitment.

Introduction

The number of studies of ichthyoplankton communities has increased considerably in the last decade, as these studies are known to be a basic tool for understanding trophic dynamics and the fluctuations of commercially important fish stocks. As a consequence, the results of these are valuable for developing stock assessments and fishery management plans (Boeing & Duffy-Anderson 2008).

This is because of the significant influence of habitat conditions on the survival of early life stages of fish, from eggs to juveniles, which strongly affect recruitment

success and consequently the size of the adult population (Bakun 1996; Palomera *et al.* 2007; Tsikliras *et al.* 2010; Basilone *et al.* 2013).

Several factors affect the composition and abundance of larval fish communities (Boehlert & Mundy 1993). The most important factors are the spawning strategies of the adult populations, which are linked to topographical characteristics and hydrographical, chemical and biological conditions (Somarakis *et al.* 2004; Basilone *et al.* 2013; Giannoulaki *et al.* 2013). Moreover, oceanographic structures, such as currents or eddies, govern the formation or disruption of the larval assemblages (Sabatés & Olivar 1996; Lloret *et al.* 2000; Alemany *et al.* 2006;

Bakun 2006; Falcini *et al.* 2015) and are responsible for environmental variations and consequently the survival rate of larvae (McGurk 1986).

Ichthyoplankton surveys make an important contribution to our understanding of marine ecosystems. Such surveys are a way of generating fishery-independent stock assessments. Increases or decreases in stock size can be detected more rapidly and sensitively by monitoring ichthyoplankton rather than the adult population. Moreover, eggs and larvae are easier and more cost effective to sample than in adult fishes (Moser & Smith 1993; Matarrese *et al.* 2003; Doyle *et al.* 2009).

Much information is available about larval communities concerns on western side of the Mediterranean Sea (del Pilar Ruso & Bayle-Sempere 2006; Sabatés *et al.* 2007; Alvarez *et al.* 2012) but there are fewer publications on the eastern part of the area (Isari *et al.* 2008) and the Central Mediterranean Sea (Strait of Sicily: Cuttitta *et al.* 2004). In the study area (Gulf of Sirte, GoS), information on fish populations is based only on fish landings without particular references to species composition and distribution. Accordingly, the present study aimed to analyse the species constituting the ichthyoplankton assemblages in the GoS during the summer with a view to interpreting their spatial

distribution in relation to physical, chemical and biological factors. Moreover, egg and larval abundances were modelled in order to understand the environmental conditions that can support the observed levels of spawning activity and larval concentrations.

Material and Methods

Oceanographic measurements and ichthyoplankton sampling

The GoS is located in the southernmost part of the Mediterranean Sea (30–33°N latitude, 14.5–20.5°E longitude; Fig. 1a). Oceanographic measurements and biological sampling were carried out during the MEDSUDMED08 cruise (from 1 July to 14 July 2008) onboard the R/V *Urania* in stations distributed along transects perpendicular to the coast (Fig. 1b).

Hydrographic profiles covered the region from the very shallow water along the coast to a depth of about 1600 m along the continental slope. In all the hydrological stations, continuous vertical profiles of temperature, salinity, dissolved oxygen and fluorescence were obtained from the surface to the bottom using a CTD SBE 911 plus

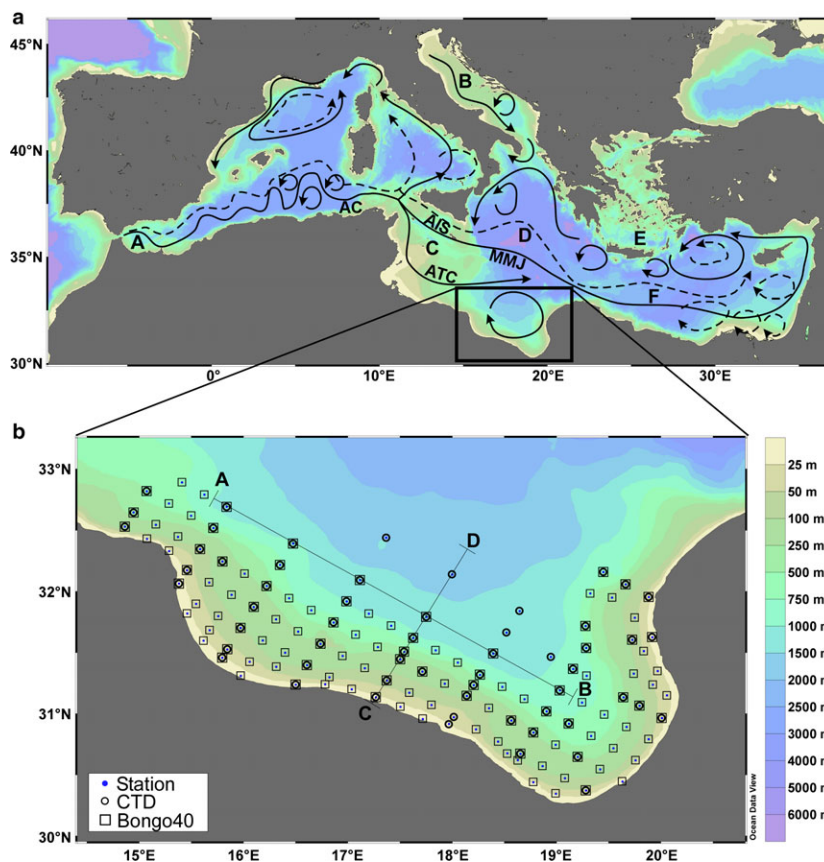


Fig. 1. (a) Bathymetric map of the Mediterranean Sea. Black and dashed lines follow the path of surface water circulation respectively in winter and summer. Major currents and semi-permanent features are illustrated. Arrows indicate: AC, Algerian Current; AIS, Atlantic Ionian Stream; ATC, Atlantic Tunisian Current; MMJ, Mid Mediterranean Jet. Bold letters represent: A, the Strait of Gibraltar; B, the Adriatic Sea; C, the Sicily Channel; D, the Ionian Sea; E, the Aegean Sea; F, the Levantine Sea. (b) Map of the Gulf of Sirte with the location of stations where CTD profiles and Bongo40 samples were collected. The sections A–B and C–D represented in Fig. 2 are indicated.

mounted on a General Oceanics rosette equipped with 24 Niskin bottles. The probes were calibrated before and after the cruise at the NATO Undersea Research Centre in La Spezia, Italy.

Each CTD parameter was calculated as the average of values measured from the surface to 20 m depth. Within the thermocline depth was about 50 m. In order to estimate the values in the areas without direct CTD measurements, these environmental parameters were interpolated using generalized additive models (GAM; Hastie & Tibshirani 1986) applied to the geographic coordinates.

Biological samples were collected using a Bongo40 net with a 200 μm mesh size on both sides of the frame. Flow meters were used in each net (General Oceanics, model 2030R). A depressor was used during net hauling to enhance the stability of the instrument. The lowering speed of the net was $0.75 \text{ m}\cdot\text{s}^{-1}$ and the ascending speed $0.33 \text{ m}\cdot\text{s}^{-1}$. The Bongo40 net hauls described an oblique trajectory from the surface to 100 m depth or close to the bottom in areas where the depth was $<100 \text{ m}$, at a constant vessel speed of 2 knots with a cable inclination of about 45° . A total of 124 samples was collected using a regular sampling grid of 12 n.m. (Fig. 1b). The samples were fixed immediately after collection and preserved in a 4% buffered formaldehyde seawater solution. Ichthyoplankton composition was estimated on samples from one of the 2 mouths of the Bongo40 net using a stereomicroscope.

Sixty-six taxonomic units were recognized following the taxonomic concepts described in Cuttitta *et al.* (2011). In order to provide an immediate and synthetic framework for ecological assessments, the taxa were grouped on the basis of their known autoecology in the following classes: demersal, mesopelagic, bathypelagic, small pelagic and pelagic [fishes of the NE Atlantic and the mediterranean (Whitehead *et al.* 1986) and check-list of the fishes of the eastern tropical Atlantic (Carpenter 1992) keys]. The number of fish larvae and eggs from each sample was standardized to $\text{n}\cdot 10^{-3}\cdot\text{m}^{-3}$ according to Perez-Ruzafa *et al.* (2004).

Zooplankton weight measurements were acquired in the laboratory following the procedures indicated in Goswami (2004).

Data analysis

Generalized Additive Models (GAMs) (Hastie & Tibshirani 1986) with quasi-Poisson error distributions and log link functions were applied to define the set of environmental factors that affect egg and larva abundance in the study area. The zooplankton weights were transformed into natural logarithms in order to achieve uniform distributions necessary for the GAM application (Hastie & Tibshirani 1986). The highest abundance value for the

eggs (359 eggs) was truncated to 102, which was the second highest value. The best model was chosen based on a stepwise forward selection method. Specifically, the selection of the variable to be included was made following three criteria. Including the variable, the generalized cross-validation should decrease and the level of explained variation (0–100%) should increase and the plotted confidence band for the smooth should not include zero everywhere. All the first-order interactions of the main effects were tested. To simplify the interpretation of the results, the maximum degrees of freedom of each smoothing function was limited to 4 for the main effect and 20 for the first-order interaction effects. Finally, the validation graphs (e.g. residuals *versus* fitted values, quantile-quantile-plots and residuals *versus* the original explanatory variables) of the final model were analysed to prevent possible model misspecification.

To identify the distribution of different families in relation to the environmental parameters, the stations were grouped through cluster analysis based on family density data. The Bray–Curtis index as the distance measure (Bray & Curtis 1957) and the Ward linkage (Ward 1963) as the grouping method were chosen. An analysis of similarities (ANOSIM) was performed to test the differences in assemblage structure defined by a cluster analysis (Clarke 1993). A similarity percentages analysis (SIMPER) was applied to determine the families that were most responsible for the discrimination amongst the clusters. In particular, a comparison between each pair of clusters was performed to identify the contribution percentage of each family to the total Bray–Curtis dissimilarity (Clarke 1993).

Station groups were then plotted on a map of the sampled region to see if they were geographically distinct. Levels of occurrence and abundance of species and geographical distinctness amongst station groups were then used as subjective criteria to fine-tune the identification of the groups.

The relationships between the environmental parameters and the station clusters were explored by means of a one-way analysis of variance (Heiberger & Neuwirth 2009) if the variables met the underlying conditions of normality (Shapiro–Wilk's test; Shapiro *et al.* 1968) and by a Kruskal–Wallis (KW) test (Kruskal & Wallis 1952) if they did not. *Post-hoc* pairwise multiple comparisons of the environmental parameters amongst the station groups were also performed using Mann–Whitney (MW) tests (Wilcoxon 1945).

A random forest (RF) analysis (Breiman 2001) was subsequently used to rank the importance of the parameters in the cluster classifications. Each tree was constructed using a different bootstrap sample from the original data. About one-third of the cases [out-of-bag (OOB) data] were not used in tree construction, but pro-

duced a running unbiased estimate of the classification error and were used to estimate the importance of the variables. The most important variables were chosen according to the higher values of the mean decrease in accuracy. It is the normalized difference of the classification accuracy for the OOB data when the data for that variable are included as observed and the classification accuracy for the OOB data when the values of the variable in the OOB data are randomly permuted (Liaw & Wiener 2002). The selection of the most important variables was made by a procedure that carried out variable elimination using the OOB error as the minimization criterion (Diaz-Uriarte & Alvarez de Andres 2006). The selected variables were used to develop a final RF model

(Liaw & Wiener 2002) and to estimate a classification of the net hauls. This classification was then compared to the groups defined by the cluster analysis by means of a confusion matrix.

All the statistical analyses were carried out using the statistical software R (R 3.0.1, R Development Core Team 2013).

Results

Oceanographic data

The main physical and chemical oceanographic data are shown in Fig. 2, which illustrates the upper water column

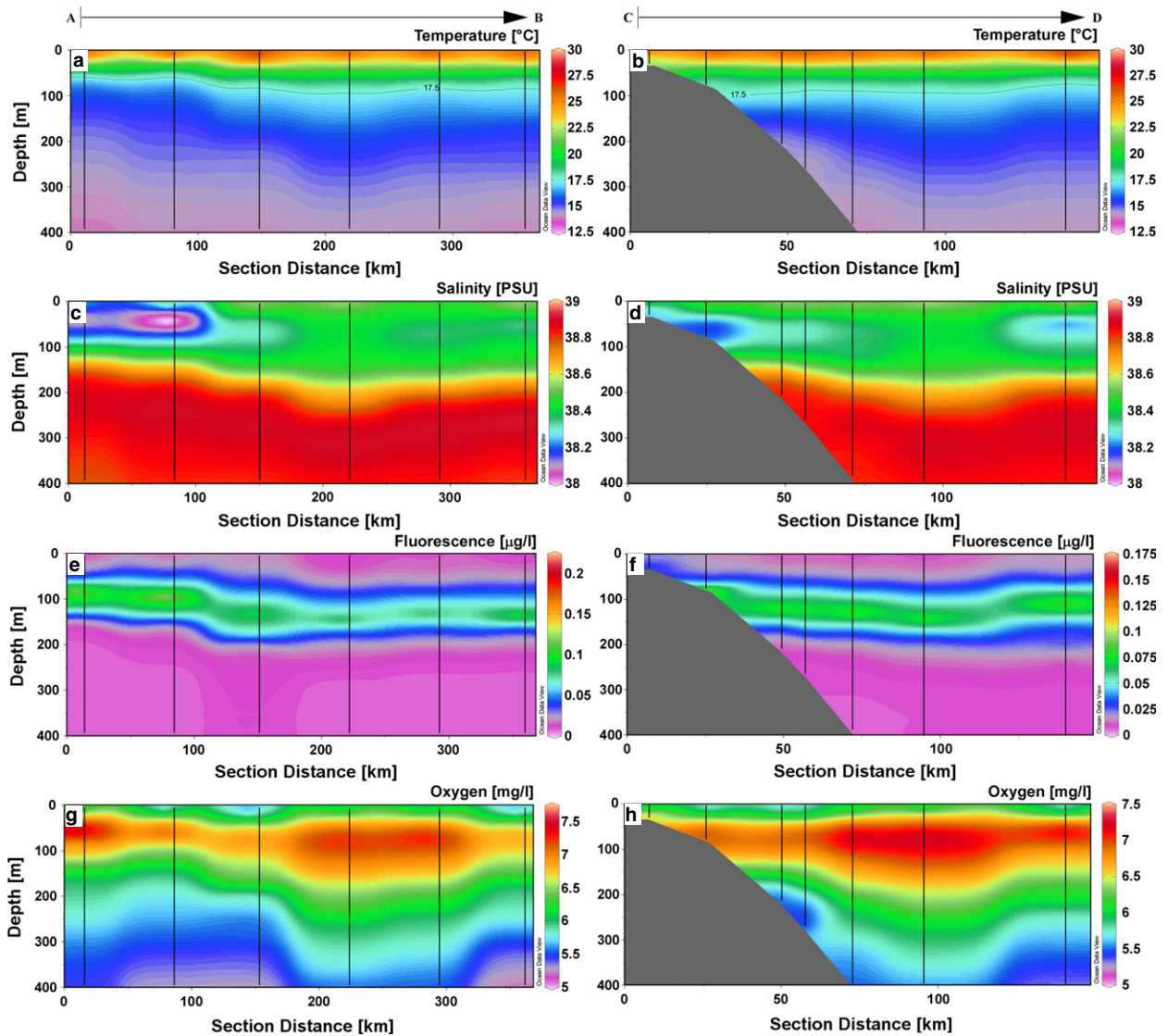


Fig. 2. Sections of data collected from CTD profiles along the transects A–B and C–D (Fig. 1b) in the upper 400 m. (a–b) temperature; (c–d) salinity; (e–f) fluorescence; (g–h) Oxygen.

profile data (0–400 m) in two selected transects (transects A–B and C–D in Fig. 1b). Surface temperatures ranged from 25 to 27.5 °C. A steep thermocline was evident, the base of which (about 17.5 °C) was located at a water depth of 50–75 m. Salinity values ranged between 37.5 and 38.9. A large anticyclonic circulation was present in the central part of the GoS and cyclonic vortexes in the eastern and western sectors (Fig. 2).

The core of the low-salinity water, associated with the eastwards transport of the Atlantic Tunisian Current (ATC) and mostly evident in the westernmost stations (Fig. 2), was located at a depth of around 50 m. High salinity values below 100–150 m depth were related to the inflow of the Levantine Intermediate Water.

A more detailed oceanographic characteristics of the study area may be found in Placenti *et al.* (2013).

Ichthyoplankton data

In the 50 offshore stations (bottom depth ≥ 250 m), the total fish larval concentrations ranged between ~ 1000 and $\sim 12 \cdot 10^{-3} \cdot \text{m}^{-3}$ (mean $233.44 \cdot 10^{-3} \cdot \text{m}^{-3}$, median $183.9 \cdot 10^{-3} \cdot \text{m}^{-3}$; Fig. 3a), whereas the total egg concentrations varied between ~ 4700 and $\sim 9 \cdot 10^{-3} \cdot \text{m}^{-3}$ (mean $167.4 \cdot 10^{-3} \cdot \text{m}^{-3}$, median $45.26 \cdot 10^{-3} \cdot \text{m}^{-3}$), with only seven stations having no eggs (Fig. 3b). In the 73 coastal stations (bottom depth < 250 m), the total fish larval concentrations ranged between ~ 1700 and $\sim 22 \cdot 10^{-3} \cdot \text{m}^{-3}$ (mean $253 \cdot 10^{-3} \cdot \text{m}^{-3}$, median $204.89 \cdot 10^{-3} \cdot \text{m}^{-3}$), with only four stations without larvae (Fig. 3a). The total egg concentrations varied between $\sim 66,600$ and $\sim 15 \cdot 10^{-3} \cdot \text{m}^{-3}$ (mean $1481.40 \cdot 10^{-3} \cdot \text{m}^{-3}$, median $297.71 \cdot 10^{-3} \cdot \text{m}^{-3}$), with 10 stations having no eggs (Fig. 3b).

In general, the larvae showed a patchwork distribution in the offshore and coastal areas, with higher concentrations of larvae in the eastern coastal sector (19–20.5°N longitude; Fig. 3a). Meanwhile, the highest concentrations of eggs were found mainly in the coastal stations and

mainly in the west side between Misratah and Sirte town, reaching $66,600 \text{ larvae}/10^3 \text{ m}^3$ (Fig. 3b).

A total of 1914 larvae was found in the ichthyoplankton community and 1652 of these were identified (11 orders, 34 families, 38 genera and 37 species; Table 1). Bathypelagic fish larvae were 605 in number and grouped into four families with four genera. There were also 562 demersal fish larvae grouped into 22 demersal families with 20 genera; 263 mesopelagic fish larvae grouped into two families with nine genera; 118 small pelagic fish larvae grouped into two families with two genera and 104 pelagic/epipelagic fish larvae grouped into five families with four genera (Table 1).

The larval fish community in the GoS was found to be composed of both neritic and oceanic taxa. In particular, the bathypelagic taxa were the most abundant (32%), followed by demersal (29%), mesopelagic (14%), small pelagic (6%) and pelagic/epipelagic taxa (5%) (unidentified taxa: 14%). Only seven families dominated the assemblages: Phosichthyidae ($\sim 16\%$) and Gonostomatidae ($\sim 14\%$) for the bathypelagic group, Myctophidae ($\sim 13\%$) for the mesopelagic group, Gobiidae ($\sim 9\%$) and Labridae ($\sim 8\%$) for the demersal group, and Clupeidae and Engraulidae (both 3%) for the pelagic group.

The dendrogram obtained by the cluster analysis was cut at a level of Bray–Curtis distance equal to two, choosing four main groups of stations, that were significantly different in terms of family composition and abundance (ANOSIM: Global R = 0.5841; $P < 0.001$).

Table 2 shows the families most responsible (with a percentage contribution $> 6\%$) for the differences between each pair of clusters from the SIMPER analysis. These results are informative with regard to the composition of the assemblages because they show a ranking of the families responsible for the separation between each pair of defined clusters. The families Gonostomatidae, Phosichthyidae and Myctophidae contributed the most to explaining the dissimilarities between cluster 1 and all the other clusters, with mean densities greater than all the

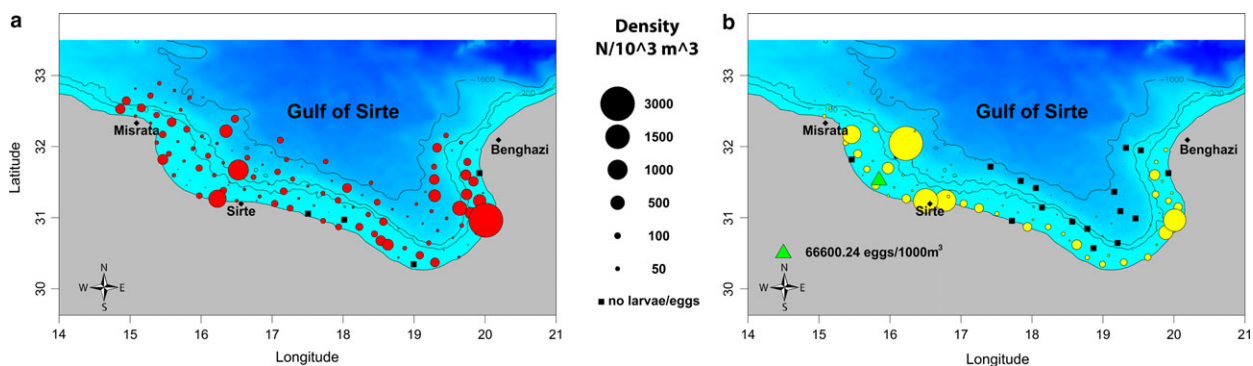


Fig. 3. Larval (a) and egg (b) distribution in the study area. The circle dimension is proportional to the density. The cross indicates the absence.

Table 1. List of larval fish taxa, family and order, and ecological group membership, with abundance and percentage of total (total abundance = 1914).

order	family	ecological group	larval taxon	abundance	% of total
Anguilliformes	Muraenidae	D	<i>Muraena helena</i>	1	0.05
			unknown	2	0.1
	Ophichthidae	D	<i>Echelus myrus</i>	1	0.05
	Congridae	D	<i>Ariosoma balearicum</i>	2	0.1
unknown			3	0.16	
Clupeiformes	Clupeidae	SP	<i>Sardinella aurita</i>	31	1.62
			unknown	30	1.57
Stomiiformes	Engraulidae	SP	<i>Engraulis encrasicolus</i>	57	2.98
	Gonostomatidae	B	<i>Cyclothone (unknown)</i>	271	14.16
Stomiiformes	Sternoptychidae	B	<i>Maurolicus muelleri</i>	30	1.57
			<i>Vinciguerria attenuata</i>	81	4.23
			<i>Vinciguerria nimbaria</i>	51	2.66
	Phosichthyidae	B	<i>Vinciguerria poweriae</i>	47	2.46
			<i>Vinciguerria (unknown)</i>	126	6.58
	Stomiidae	B	<i>Stomias boa</i>	1	0.05
			<i>Synodus saurus</i>	14	0.73
Aulopiformes	Synodontidae	D	<i>Lestidiops jayakari</i>	5	0.26
			<i>Lestidiops affinis</i>	8	0.42
	Paralepididae	M	<i>Paralepis coregonoides</i>	4	0.21
			unknown	6	0.31
Myctophiformes	Myctophidae	M	<i>Ceratoscopelus maderensis</i>	17	0.89
			<i>Lobianchia dofleini</i>	2	0.1
			<i>Diaphus holti</i>	5	0.26
			<i>Electrona risso</i>	44	2.3
			<i>Hygophum benoiti</i>	22	1.15
			<i>Hygophum (unknown)</i>	53	2.77
			<i>Lampanyctus crocodilus</i>	21	1.1
			<i>Lampanyctus pusillus</i>	47	2.46
			<i>Myctophum punctatum</i>	14	0.73
			unknown	15	0.78
Gadiformes	Phycidae	D	<i>Phycis (unknown)</i>	1	0.05
	Gadidae	D	unknown	24	1.25
Ophidiiformes	Ophidiidae	D	<i>Ophidion (unknown)</i>	1	0.05
			<i>Ophidion barbatum</i>	5	0.26
			<i>Parophidion vassali</i>	1	0.05
Syngnathiformes	Centriscidae	D	<i>Macroramphosus scolopax</i>	2	0.1
Scorpaeniformes	Scorpaenidae	D	<i>Scorpaena porcus</i>	1	0.05
			<i>Scorpaena (unknown)</i>	4	0.21
			unknown	3	0.16
Perciformes	Triglidae	D	unknown	5	0.26
	Serranidae	D	<i>Epinephelus costae</i>	2	0.1
			unknown	16	0.84
	Carangidae	P/EP	<i>Trachurus (unknown)</i>	2	0.1
			unknown	18	0.94
	Bramidae	P/EP	unknown	4	0.21
	Sparidae	D	<i>Pagrus pagrus</i>	1	0.05
			<i>Lithognathus mormyrus</i>	4	0.21
	unknown		68	3.55	
	Cepolidae	D	<i>Cepola macrophthalma</i>	5	0.26
	Pomacentridae	P/EP	<i>Chromis chromis</i>	5	0.26
	Labridae	D	<i>Coris julis</i>	24	1.25
unknown			132	6.9	
Ammoditydae	D	<i>Gymnammodytes cicereus</i>	6	0.31	
Blenniidae	D	unknown	11	0.57	

Table 1. Continued

order	family	ecological group	larval taxon	abundance	% of total
Pleuronectiformes	Callionymidae	D	<i>Callionymus maculatus</i>	7	0.37
			<i>unknown</i>	2	0.1
	Gobiidae	D	<i>unknown</i>	179	9.35
	Scombridae	P/EP	<i>Thunnus (unknown)</i>	28	1.46
			<i>Auxis rochei</i>	21	1.1
			<i>unknown</i>	21	1.1
	Centracanthidae	P/EP	<i>unknown</i>	5	0.26
	Scophthalmidae	D	<i>Lepidorhombus boscii</i>	1	0.05
	Bothidae	D	<i>Arnoglossus (unknown)</i>	22	1.15
			<i>Bothus podas</i>	1	0.05
<i>unknown</i>			10	0.52	
Soleidae	D	<i>unknown</i>	1	0.05	
unidentified larvae				261	13.64

B = bathypelagic fish; P/EP = pelagic/epipelagic fish; SP = small pelagic fish; M = mesopelagic fish; D = demersal fish.

other families (~ 0.06 , ~ 0.04 and $\sim 0.06 \text{ n}\cdot\text{m}^{-3}$, respectively). Accordingly, they may be considered to be the distinguishing elements of cluster 1. Only one family (Gobiidae) contributed the most to explaining the dissimilarities between cluster 2 and all the others, with a mean density of $\sim 0.04 \text{ n}\cdot\text{m}^{-3}$, whereas Gobiidae and Labridae contributed the most to explaining the highest

dissimilarities between cluster 3 and all the others (mean density ~ 0.12 and $\sim 0.06 \text{ n}\cdot\text{m}^{-3}$, respectively) and Myctophidae, Scombridae and Engraulidae characterized cluster 4 (mean density ~ 0.03 , ~ 0.015 and $\sim 0.015 \text{ n}\cdot\text{m}^{-3}$, respectively; Table 3).

Clusters 1 and 4 comprised sampling sites mainly located offshore at a bathymetry of over 250 m, whereas

Table 2. Pairwise comparisons of groups defined by cluster analysis based on the percentage of contribution to total Bray–Curtis dissimilarity of the most important families from SIMPER analysis (percentage contribution >6%).

	cluster 1	cluster 2	cluster 3	cluster 4
cluster 1		Gonostomatidae	Gonostomatidae	Gonostomatidae
		22.89%	17.72%	21.16%
		Phosichthyidae	Phosichthyidae	Phosichthyidae
		19.25%	15.78%	12.52%
		Myctophidae	Myctophidae	Myctophidae
		15.34%	12.57%	14.36%
cluster 2		Gobiidae	Gobiidae	Scombridae
		12.05%	30.92%	9.28%
			Labridae	Engraulidae
			8.73%	6.70%
			Gobiidae	Gobiidae
			13.76%	25.74%
cluster 3			Labridae	Myctophidae
			14.26%	17.50%
				Scombridae
				13.38%
				Engraulidae
				13.01%
				Gobiidae
				22.31%
			Labridae	
			11.79%	
			Myctophidae	
			11.07%	
			Scombridae	
			9.98%	
			Engraulidae	
			8.37%	

Table 3. List of all families with mean density ($n \cdot m^{-3}$) within each identified cluster.

family	cluster 1	cluster 2	cluster 3	cluster 4
Gonostomatidae	0.0588	0.0026	0.0069	0.0040
Phosichthyidae	0.0629	0.0066	0.0007	0.0048
Sternoptychidae	0.0050	0.0000	0.0017	0.0022
Myctophidae	0.0453	0.0078	0.0101	0.0149
Paralepididae	0.0038	0.0000	0.0026	0.0007
Carangidae	0.0021	0.0021	0.0042	0.0021
Centranchidae	0.0011	0.0000	0.0000	0.0007
Pomacentridae	0.0014	0.0000	0.0000	0.0000
Scombridae	0.0067	0.0000	0.0023	0.0260
Clupeidae	0.0079	0.0000	0.0247	0.0014
Engraulidae	0.0064	0.0036	0.0036	0.0145
Ammodytidae	0.0000	0.0000	0.0000	0.0035
Blenniidae	0.0019	0.0000	0.0051	0.0000
Bothidae	0.0042	0.0012	0.0082	0.0020
Callionymidae	0.0010	0.0000	0.0042	0.0000
Cepolidae	0.0000	0.0000	0.0037	0.0000
Congridae	0.0011	0.0000	0.0000	0.0000
Gadidae	0.0024	0.0000	0.0128	0.0000
Gobiidae	0.0093	0.0394	0.1235	0.0000
Labridae	0.0113	0.0000	0.0616	0.0063
Ophidiidae	0.0011	0.0000	0.0015	0.0006
Scorpaenidae	0.0014	0.0000	0.0007	0.0007
Serranidae	0.0004	0.0012	0.0112	0.0000
Sparidae	0.0091	0.0012	0.0213	0.0007
Synodontidae	0.0017	0.0000	0.0049	0.0006
Triglidae	0.0006	0.0012	0.0015	0.0000

clusters 2 and 3 were located along the Libyan coast, within 250 m of the bottom depth (Fig. 4).

Relationships between biological and environmental variables

The model for the eggs included fluorescence and salinity as main effects (Table 4). The final model explained 24.3% of the total deviance. The results of this model indicated it is more likely to find greater abundance of eggs in water with a salinity <38.4 and higher values of fluorescence ($>0.02 \mu g \cdot l^{-1}$; Fig. 5a). The model for the larvae explained 41.5% of the total deviance and included the natural logarithm of the zooplankton weight and the water density (Table 4). The positive effect on larval abundance was in water with high values of zooplankton weight ($>2.7 g$) and water density ($>1025.7 kg \cdot m^{-3}$; Fig. 5b).

The four clusters differed significantly in terms of environmental conditions. The parameters that were significantly different amongst the four clusters were temperature (KW = 8.036; P-value = 0.0453), fluorescence (KW = 40.446; P-value <0.0001) and zooplankton weight (KW = 23.435; P-value <0.0001). In particular,

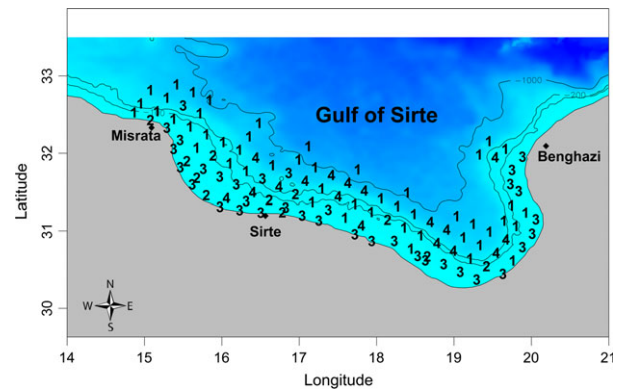


Fig. 4. Map of the Gulf of Sirte with the location of groups defined by cluster analysis.

the temperature values of the net hauls in cluster 4 were significantly higher than those in cluster 3 (MW test P-value = 0.036; Fig. 6a). Lower values of fluorescence characterized the net hauls of clusters 1 and 4 compared with clusters 2 and 3 [MW test P-value = 0.0223 (clusters 1 versus 2); MW test P-value <0.0001 (clusters 1 versus 3); MW test P-value = 0.0022 (clusters 2 versus 4); MW test P-value <0.0001 (clusters 3 versus 4); Fig. 6b]. Meanwhile, cluster 1 differed from the other clusters in terms of zooplankton weight [MW test P-value = 0.0462 (clusters 1 versus 2); MW test P-value = 0.00011 (clusters 1 versus 3); MW test P-value = 0.0214 (clusters 1 versus 4); Fig. 6c]. No remarkable differences emerged amongst the clusters in relation to salinity, density or oxygen.

The selected variables for discriminating the four clusters were fluorescence, zooplankton weight and temperature (RF analysis). The confusion matrix (Table 5) showed that the RF model and data agreed on 57.76% of classified cases. The stations of clusters 1 and 3 were the most correctly classified, with error rates of 24.52% and 35.29%, respectively. Clusters 2 and 4 were very confused (90.9% and 77.8% classification error, respectively).

Discussion

The present study makes an important contribution to our knowledge of the ichthyoplankton communities in the GoS because little is generally known about this area from an ecological point of view. The GoS is characterized by two main hydrographical features: the ATC and the GoS anticyclone. The former is responsible for the transport of low-salinity Modified Atlantic Water (MAW) along the African coast, following the 200 m isobath (Onken *et al.* 2003; Béranger *et al.* 2004; Gasparini *et al.* 2008; Bonanno *et al.* 2014). Meanwhile, the GoS anticyclone is a permanent mesoscale structure

Table 4. Analysis of deviance for generalized additive model co-variables of the final model fitted for egg and larvae abundance.

	parameter	deviance explained (%)	GCV	P-value
egg	null model		22.344	
	fluorescence	15.1	19.866	0.0022
	fluorescence + salinity	24.3	18.625	0.0001; 0.0034
larvae	null model		11.853	
	zooplankton weight	28.5	9.008	~0
	zooplankton weight + density	41.5	7.697	~0; ~0

GCV = generalized cross-validation.

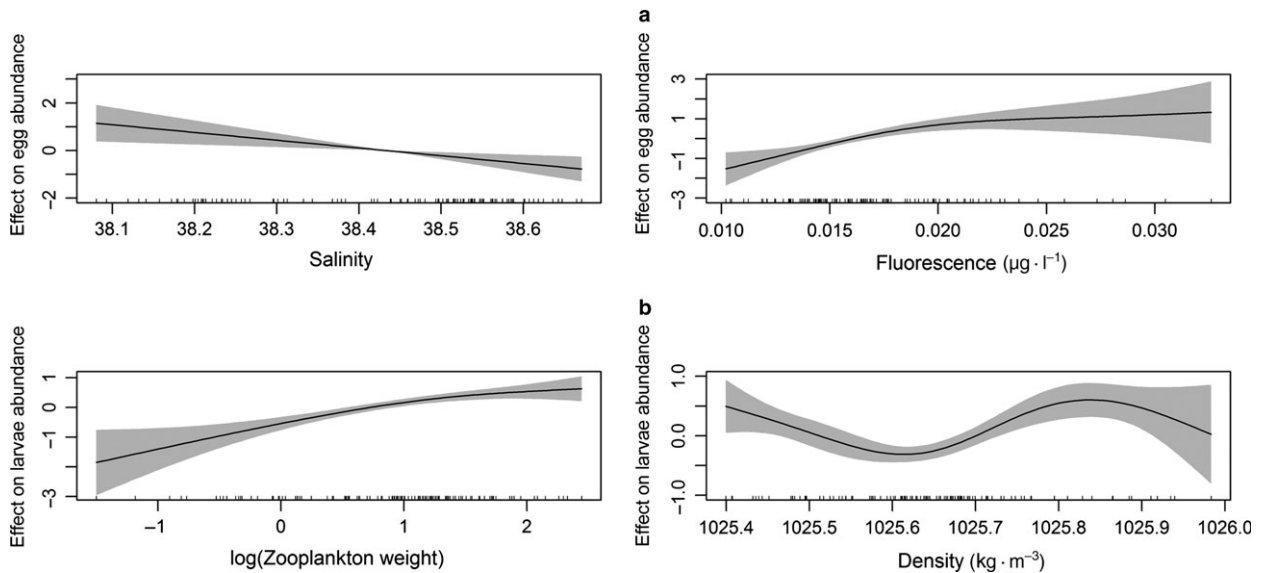


Fig. 5. Plots of the smoothing response of the Generalized Additive Model for egg abundance (a) and larvae abundance (b). Black thick line indicates the value of the GAM smoothing response and grey area represents the 95% confidence intervals.

induced by wind stress (Molcard *et al.* 2002): it can be evidenced by a positive sea surface height (Pinaridi & Masetti 2000; Beauvier *et al.* 2010) and drifter trajectories (Gerin *et al.* 2009). The overall mesoscale circulation determines an oligotrophic regime for this area, which is slightly influenced by coastal processes of nutrient enrichment (Strobl *et al.* 2009). Following the classification of D’Ortenzio & Ribera d’Alcalà (2009) based on the satellite-detected sea surface chlorophyll *a* concentration, the study area falls into a ‘non-blooming’ cluster, i.e. it is characterized by a seasonal cycle with low biomass during late spring–summer and higher biomass in late autumn–winter.

Knowledge of the early life-history patterns of fish (the egg and larval stages) and their specific links to the marine ecosystem is significant for the development of valid models to explain the success of recruitment. Recruitment depends on multiple deterministic and stochastic factors,

operating on several life stages and determining the abundance and variability of the adult population. For these reasons, specific links between the marine ecosystem and the early life history of fish is essential (Doyle *et al.* 2009).

The present study provides for the first time a model for describing the potential adult reproduction habitat in the GoS, using an analysis of the distribution of eggs and larvae during the summer, which corresponds to the late phase of the reproductive period of some species in the Mediterranean Sea, such as anchovy and round sardinella (Pawson & Giama 1985; Somarakis *et al.* 2004; Gaamour *et al.* 2005; Basilone *et al.* 2006; Tsikliras & Antonopoulou 2006; Palomera *et al.* 2007). The models presented here support the idea of significant variations in the abundance of eggs and larval fishes that are related to specific physical variables. Fluorescence and salinity were the most important variables for the estimation of egg

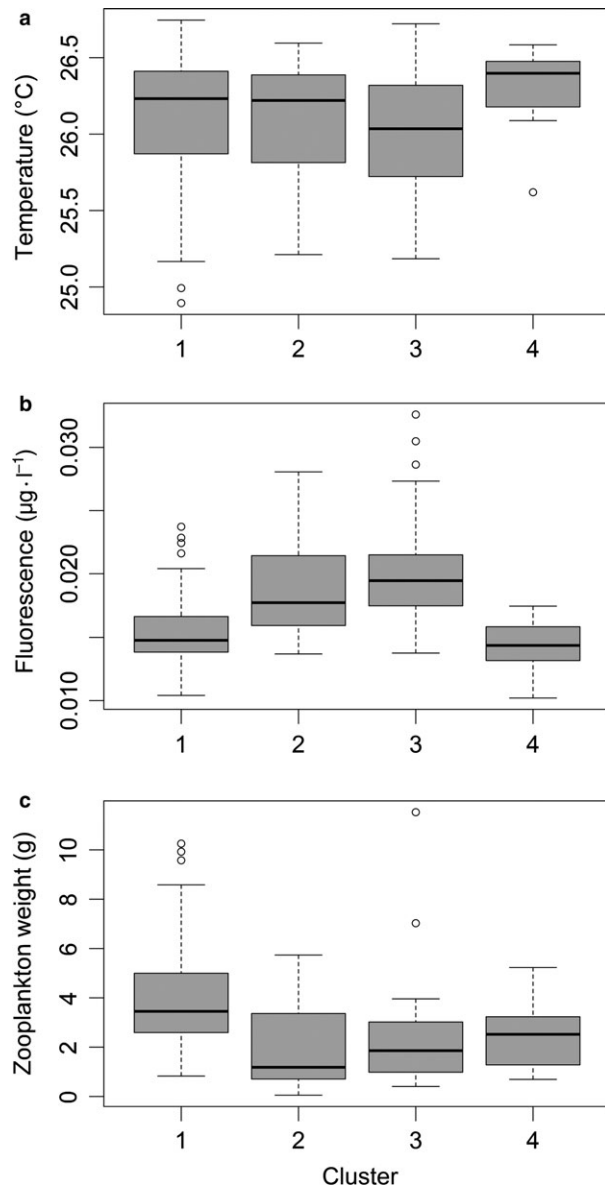


Fig. 6. Box-and-Whisker plots of temperature (a), fluorescence (b) and zooplankton weight (c) values grouped by clusters. The bottom and top of the boxes are the first and third quartiles. The band inside the box is the median. The bottom and top of the whiskers are minimum and maximum.

abundance in the study area, implying that they were the primary factors controlling the spawning habitat, in practice operating as proxies for the presence of favourable conditions related to food availability. Zooplankton weight and density were the variables that mainly affect the larval concentrations. These results suggest that ichthyoplankton distribution is probably correlated with both oceanographical patterns and the availability of food. In fact, the maximum fish egg density in the western part of the GoS corresponded to the ATC inflow,

Table 5. Confusion matrix of the prediction measured by the random forest analysis and estimated error of predictive ability based on the out-of-bag data (estimate of error rate: 42.24%).

	cluster 1	cluster 2	cluster 3	cluster 4	classification error (%)
cluster 1	40	0	6	7	24.5
cluster 2	4	1	5	1	90.9
cluster 3	10	1	22	1	35.3
cluster 4	12	0	2	4	77.8

which was also confirmed by the negative relationship with salinity, whereas the larval retention in the eastern-most side of the GoS corresponded to the anticyclonic circulation, probably as a result of advection by surface currents (Placenti *et al.* 2013). It is also worth noting that the maximum larval concentration was found in association with maximum values of zooplankton weight, suggesting a possible trophic relationship. Therefore, it is evident that the larval distribution was associated with environmental forcings that appear to be the direct cause of enhanced production, contributing to final survival. Several authors have highlighted the importance of frontal structures in creating concentration areas favourable to the early life stages of fish (Palomera 1992; Sabatés *et al.* 2001; Bakun 2006; Muhling *et al.* 2007; Basilone *et al.* 2013).

Another important aspect to study is the formation of larval fish assemblages, which is the outcome of species-specific evolutionary adaptations (reproductive strategies, selection of spawning habitats, larval behaviour and interactions with dominant currents) that increase the survival and sustenance of the populations (Cushing 1990).

The results of our study essentially confirm the summer ichthyoplankton species composition reported by Bonomo *et al.* (2012) for the marine area off the Western Libyan coasts, which is contiguous to the GoS investigated herein but quite different in terms of the main oceanographical features. For example, the GoS, compared to Western Libyan waters, is characterized by a different bottom depth range and lower dynamics in the surface waters (Pinardi *et al.* 2013).

Relationships between habitat conditions and larval assemblage structures were also identified. Higher temperature values characterized the pelagic group, whereas the zooplankton weight was positively related to the distribution of the meso- and bathypelagic groups. Fluorescence and dissolved oxygen were linked to the demersal group. Although these relationships suggest adaptive spawning strategies in response to environmental conditions, the primary factor determining the assemblage

structure seems to have been the bathymetry. Two main groups were identified: neritic and offshore. Pelagic, mesopelagic and bathypelagic fish larvae were located in areas with a bottom depth of over 250 m, whereas demersal fish larvae were found at a bottom depth shallower than 100 m. These groups were discriminated by fluorescence and zooplankton data, with higher fluorescence values inshore and higher zooplankton densities offshore. Numerous studies have subdivided these two basic groups, using an array of terms for the identified assemblages. From shallow to deep areas, the terms lagoonal/near-reef, nearshore/coastal, mid-shelf/neritic, outer-shelf/transitional, slope and oceanic assemblages have been used (Boehlert & Mundy 1993; Leis 1993; Richards *et al.* 1993; Sanvincente-Añorve *et al.* 2000; Granata *et al.* 2011; Giordano *et al.* 2014). In the temperate waters of the Mediterranean, demersal larvae likewise dominate shallow nearshore catches (Sabatés *et al.* 2003; Beldade *et al.* 2006). Similarly, in the tropical nearshore waters of Australia, New Zealand and Hawaii, larval gobiids, labrids, sparids, clinids and tripterygiids dominate catches (Leis & Miller 1976; Kingsford & Choat 1989; Gray 1993). Myctophidae and Gonostomatidae are characteristic members of the oceanic group (Boehlert & Mundy 1993). Generally, inshore species are pelagic (Tsikliras & Koutrakis 2011), in contrast to our results for the present study area. This bathymetric gradient seems to be the result of adult preferences for specific habitat characteristics of the spawning areas, but could also be influenced by the movement of water masses. In particular, the hydrographical processes that characterize the study area (ATC inflow and anticyclonic circulation) may play an important role in ichthyoplankton distribution, probably transporting larvae from spawning areas to areas with suitable food available, which is one of the most important factors influencing larval survival, growth and recruitment.

Conclusions

The results of the present study make a great contribution to our understanding of population dynamics in the GoS, which is an unexplored area, but is heavily exploited because of the lack of proper monitoring. In this context, the investigation of early life stage dynamics could help with the future management of fisheries, providing an important way to help to avoid the depletion of the spawning components of populations and minimize the associated ecological consequences of such depletion.

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