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Fish Larvae Ecology on the Western European Shelf: A Multi-Species Perspective

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ABSTRACT

This research investigates the composition and distribution of fish larvae on the Western European Shelf, focusing on their ecological roles and the environmental factors shaping their communities. Data were collected during the Western European Shelf Pelagic Acoustic Survey (WESPAS) using plankton hauls at 77 stations alongside environmental profiling. A total of 1,426 larvae, representing 51 taxa across 25 families, were identified, with *Trachurus trachurus*, *Myctophum punctatum*, and *Scomber scombrus* being the most abundant species. Latitude, temperature, salinity, and depth emerged as key factors influencing distribution patterns, with BIO-ENV analysis showing the highest correlation (r = 0.317) and ANOSIM indicating weak but significant spatial differences (R = 0.263, *P* = 0.001). The highest larval densities were recorded in the Porcupine Bank region. This study highlights how environmental gradients structure larval fish assemblages and provides baseline data for understanding early life stage dynamics. The findings contribute to improved understanding of larval fish ecology and provide a basis for predicting ecosystem responses to environmental variability, supporting fisheries management and marine conservation efforts.

INTRODUCTION

Fish larvae are key components of marine ecosystems, serving as indicators of environmental change and playing an essential role in sustaining fish populations. Understanding their composition, distribution, and environmental drivers is fundamental to fisheries biology and ecosystem management **(Xu *et al*., 2022)**. However, knowledge of fish larvae communities in the inshore waters of the Western European Shelf remains limited, as most studies have focused on offshore areas and commercially important species **(Ibaibarriaga *et al*., 2007; Dransfeld *et al*., 2009)**.

The Western European Shelf Pelagic Acoustic Survey (WESPAS), conducted in 2016, provides a valuable opportunity to address these gaps. By combining acoustic and plankton sampling, the survey captures spatial variability of fish larvae across diverse habitats, from the Irish Continental Shelf to the Porcupine Bank. Environmental factors such as temperature, salinity, and depth are known to influence larval distribution **(Dransfeld *et al.*, 2009; Anderson & Walsh, 2013; Álvarez *et al.*, 2021)**, yet their combined effects in inshore environments remain insufficiently explored.

Although the data for this study were collected in 2016, they remain highly relevant. The findings serve as a critical baseline for understanding how environmental factors shape fish larvae communities, providing a foundation for assessing long-term ecological changes and informing fisheries management. Large scale oceanographic processes influencing fish larvae, such as temperature and salinity gradients, are relatively stable over decadal timescales **(Edwards *et al.*, 2011; Pitois *et al.*, 2015)**. Thus, this study contributes not only to filling historical knowledge gaps but also to addressing emerging challenges in marine ecosystem conservation.

This study provides a distinct contribution by integrating a multi-species fish larvae dataset with multivariate statistical analyses across both offshore and underexplored inshore regions of the Western European Shelf. Unlike previous studies that often focus on single-species or offshore-dominated datasets, this approach enables a more comprehensive evaluation of larval fish assemblages in relation to environmental gradients. By combining community level analysis with environmental drivers, this study offers a broader perspective on larval fish ecology and improves the interpretation of spatial patterns across heterogeneous marine environments.

This research examines fish larvae composition and distribution across the Western European Shelf, with particular emphasis on how environmental gradients structure multi-species assemblages across spatially distinct regions. These findings provide important perspectives on fish larvae community dynamics and their relevance to biodiversity preservation and sustainable fisheries management under changing environmental conditions.

MATERIALS AND METHODS

Survey Area and Coverage

Fish larvae data were collected during the Western European Shelf Pelagic Acoustic Survey (WESPAS) conducted from June 16 to July 30, 2016, aboard the RV Celtic Explorer. The survey encompassed the Irish Continental Shelf, divided into three legs: Leg 1 (Northern Ireland waters, June 17–30), Leg 2 (Western Irish waters, July 4 –

17), and Leg 3 (Southern Irish waters, July 17–30). A total of 77 sampling stations were designated according to acoustic survey intensity and geographical stock demarcations, spanning from 59 °N to 47 °N, encompassing the Porcupine Bank.

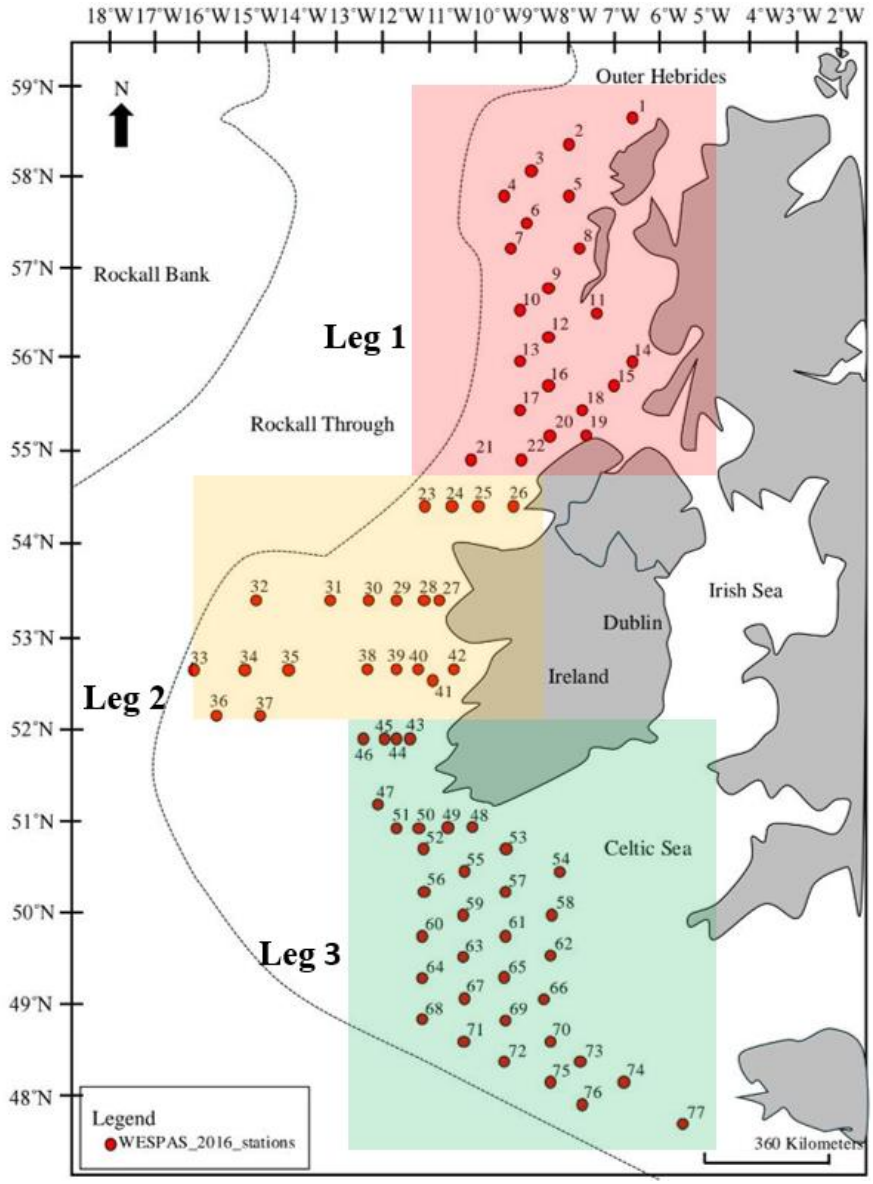

Fig. 1. WESPAS 2016 sampling locations. Division on stations based on Legs were Leg 1: Station 1–22, Leg 2: Station 23–42 and Leg 3: Station 43–77.

Sampling Protocols

In this survey, RV Celtic Explorer conducted plankton hauls from 77 sampling stations hauls using 200-micron mesh size Hydrobios Ring Trawl (CalCOFI) net of 100 cm ring diameter. Vertical plankton tows were carried out to within 5 m of the seabed for stations where total depth was less than 100 m and to a 100-m maximum for all other

stations depths. The volume of water filtered was obtained using internal flowmeters mounted in the mouth of the net. Once back aboard, the cod-end was removed, a second cod-end was attached and the plankton net was washed down. The cod-ends were then brought to the lab, and the plankton sample was washed out. The sample was preserved in 4% buffered formalin and then were brought back to the laboratory for further analysis.

The 100 m sampling depth limit was selected to ensure consistent coverage of the upper water column, where most fish larvae are typically concentrated due to feeding and developmental requirements. In shallower stations (<100 m), sampling was conducted close to the seabed to capture the full vertical distribution of larvae.

The survey period (June - July 2016) corresponds to peak seasonal productivity and spawning activity in the region, providing representative conditions for assessing larval fish distribution across the Western European Shelf.

Environmental Data Collection

A calibrated SeaBird 911 CTD supplied with fluorometer was used to provide measurements of temperature, conductivity salinity and fluorescence. The SeaBird 911 electronics system is a sensor package for plankton samplers which enables sensor data to be either transmitted in real time via a coaxial cable to a PC display on board the sampling vessel or logged internally for subsequent download. The standard set of sensors consists of depth, temperature and salinity internal flow (i.e. volume of water filtered) and external flow (for an index of sampler efficiency).

In situ data of sampling depth (m), temperature (°C) and salinity collected from each station were presented using the Ocean Data View V4.7.10 **(Schlitzer, 2025)** software to obtain vertical profiles. Prior to analyzing environmental parameters, average values for different parameters at each water column layer (temperature and salinity) were calculated.

Laboratory Analysis

In the laboratory, fish larvae were separated from zooplankton and classified to their lowest taxonomic level based on morphological traits and reference identification guides **(Russell, 1976; Fahay, 1983; Oliver & Fortuno, 1991)**. Developmental stages were assigned based on **Kendall Jr *et al*. (1984)**. Zooplankton biomass was estimated using the displacement volume method **(Postel *et al*., 2000)**, with adjustments for large gelatinous organisms In the laboratory, all fish larvae were sorted from other zooplankton and transferred into 85% ethanol. These larvae were identified to the lowest possible taxon through their morphological characteristics, namely vertebrae/myomere counts, pigmentation, shapes, supination, fin development patterns, fin placement and eye shape

guided with appropriate identification keys **(Russell, 1976; Fahay, 1983; Oliver & Fortuno, 1991; Re & Meneses, 2009)**.

Zooplankton biomass was estimated using the displacement volume method following **Postel *et al*. (2000)**. Samples were transferred into graduated cylinders (500 or 1000 ml depending on sample volume), and the total volume of plankton and water was recorded. The sample was then filtered through a 150 µm sieve, allowed to drain, and the remaining water volume was measured. The difference between the two measurements represented the displacement volume. This value was standardized via dividing by the volume of water filtered during sampling. Large gelatinous organisms such as jellyfish and salps were removed prior to measurement to avoid bias, following established protocols **(Napp *et al*., 2002; Coyle *et al*., 2011)**.

For visualization and statistical analysis, stations were grouped into three groups namely Leg 1 (L1), Leg 2 (L2) and Leg 3(L3).

Data Standardization

In every haul, there were variations between stations in depth, distance of tow and volume of water filtered through the net. Therefore, it was essential to standardize the data prior to analysis. According to **Smith and Richardson (1977)**, data standardization was carried out in terms of the volume of water filtered and the quantity of fish larvae gathered in each sample:

$$\textbf{Volume filtered } (m^3) = \frac{\text{Flowmeter revs} * \text{Nose cone aperture} * \text{Efficiency factor}}{\text{Flowmeter calibration}}$$

Where,
Flowmeter revs = Revolutions number made by the flowmeter propeller during plankton net tow
Nose Cone Aperture = The area of the nose-cone aperture of the sampler in m^2 (πr^2)
Flowmeter-calibration = Flowmeter revolutions number per meter towed, gained from the flume or sea calibration in free flow

$$\textbf{Larvae } m^{-2} = \frac{\text{Larvae counted} * \text{Depth} * \text{Factor}}{\text{Volume filtered}}$$

Where,
Larvae counted = Number of larvae in the sample
Depth = the sampling depth, in metres
Factor = Raising factor from sub-sample to whole sample

The relative frequency (f) of each species in the sampling stations was estimated according to the formula described by **Goettsch and Hernandez (2006)**

$$f = ss / ts$$

Where,
ss = number of stations/sites in which the species occurs
ts = total number of stations/sites

The species frequency of occurrence (in percentage) was estimated as the ratio between the samples in which a species was found and the total number of samples collected.

Statistical Analysis

Statistical analyses were performed to determine fish larvae community composition and abundance, their spatial distribution, potential relationships with oceanographic features of the study area and species contribution to station ordination for both years. Analyses were carried out using PRIMER 7 (V7.0.12). Larval fish abundance was square-root transformed before further analysis to down-weight the contribution of highly abundant taxa. Hierarchical clustering methods were also used to determine a cohesive group of stations that had similar taxonomic composition. A Similarity Profile (SIMPROF), which is a permutation test to cluster stations *a priori* into statistically significant groups, was calculated using ranked Bray-Curtis similarities (observed) and those ranks were compared with permutations of the family density data (expected). The π statistic was used to determine the difference between the observed and expected profile and was calculated using the sum of absolute differences, which was repeated 999 times. SIMPROF was calculated for each branch of the cluster analysis to determine if the cluster was significantly different using the π value; if the π value was greater than the expected, then the grouping was considered significant ($p < 0.01$) **(Clarke & Gorley, 2015)**.

Multi-dimensional scaling (MDS) was used to visualize the similarity matrix of species community composition at different stations in a 2-dimensional MDS plot. Cluster analysis was carried out to identify groups of stations that aggregated at the same level of similarity. The major similarity levels were later used to visualize these station groups in the MDS plot. The stress level of the MDS plots indicates how well the set of biological data fit into two-dimensional space. Values close to 0.2 give a useful representation of their distribution, while values above 0.2 indicate that the ordination are close to being arbitrary **(Clarke *et al*., 2014)**.

Analysis of similarity (ANOSIM) was used to test for differences in species composition between station clusters generated by SIMPROF within and between years. ANOSIM generates a measure of the degree of separation of sites, R, which is close to 0 when similarities between and within sites are, on average, the same. An R-value of 1

indicates that all replicates within sites are more similar to each other than any replicate from different sites. In addition, ANOSIM gives a *p*-value like an ANOVA, with values of $p < 0.05$ indicating significance **(Anderson & Walsh, 2013)**. If differences were found using ANOSIM, then Similarity Percentage Analysis (SIMPER) was used to identify which species accounted for observed differences in assemblages between clusters and between years. SIMPER generates a ranking of the percent contribution of the species that are most important to the significant differences between factors. These analyses used a matrix composed of the Bray–Curtis similarity coefficient that generated transformed species abundance data **(Clarke *et al*., 2014)**.

To categorize environmental variables by station, SIMPROF analysis and a correlation-based Principal Components Analysis (PCA) based on Euclidean distance were performed using environmental variables for every station. SIMPER was then applied to identify which variables significantly contributed to the observed similarities or dissimilarities within each water mass category **(Clarke *et al*., 2014)**.

To link the distribution patterns of the biological data to the set of environmental variables, BIO-ENV analysis was carried out. BIO-ENV calculates the Spearman rank correlations between the similarity matrix of biological data (created using the Bray-Curtis coefficient) and the similarity matrices (created using Euclidean distance) derived from all the possible sequential combinations of the measured environmental variables. The highest value obtained (best value) indicates which combination of variables best explains the biological ordination. The statistical significance of the best value was tested by a global permutation test (499 permutations). Vectors were also used in the MDS plots to represent environmental variables to illustrate their directional increase through the biological ordination **(Clarke *et al*., 2014)**.

RESULTS and DISCUSSION

Environmental Conditions

The hydrographic conditions were represented by temperature, salinity, and chlorophyll a (based on fluorescence), as shown in Figs. (2–4). The temperature ranged from 11.6–18.5 °C at the near surface (5 m depth) (Fig. 2–5 m), 10.1–17.8 °C at 20m depth (Fig. 2–20 m), 9.2–15.4 °C at 50 m depth (Fig. 2–50 m), and 9.1–13.8 °C at the maximum sampling depth (Fig. 2–Max). The salinity ranged from 34.1–35.6 PSU at the near surface (5 m depth) (Fig. 3–5 m), 34.2–35.6 PSU at 20 m depth (Fig. 3–20 m), 34.5–35.6 PSU at 50 m depth (Fig. 3–50 m), and 34.6–35.6 PSU at the maximum sampling depth (Fig. 3–Max). The fluorescence ranged from 0.67–3.0 mg·m-3 at the near surface (5 m depth) (Fig. 4–5 m), 0.7–3.6 mg·m-3 at 20 m depth (Fig. 4–20 m), 0.7–2.0 mg·m-3

at 50 m depth (Fig. 4–50 m), and 0.6–1.3 mg·m-3 at the maximum sampling depth (Fig. 4–Max).

Survey results indicated a clear temperature gradient, with warmer surface waters observed in southern areas and cooler conditions dominating in northern locations, consistent with summer seasonal patterns (Fig. 2). Exceptions were observed along coastal margins, where the influence of riverine inputs was evident in terms of lower temperature and reduced salinity (Fig. 3). At depths below the thermocline (35–55 m) and near the seabed, the impact of warmer southern waters was confined to areas south of 53 °N, where it was disrupted by an intrusion of cooler water extending toward the mid-Celtic Sea (Fig. 2).

Recent studies emphasize that such thermal and salinity gradients are critical for structuring fish larvae habitats, influencing species-specific growth rates and larval retention **(Chivers *et al.*, 2017; Mason *et al.*, 2023)**. Coastal margins, enriched by riverine nutrients, are often linked to higher productivity zones, creating feeding hotspots for larvae **(Álvarez-Fernández *et al.*, 2015)**.

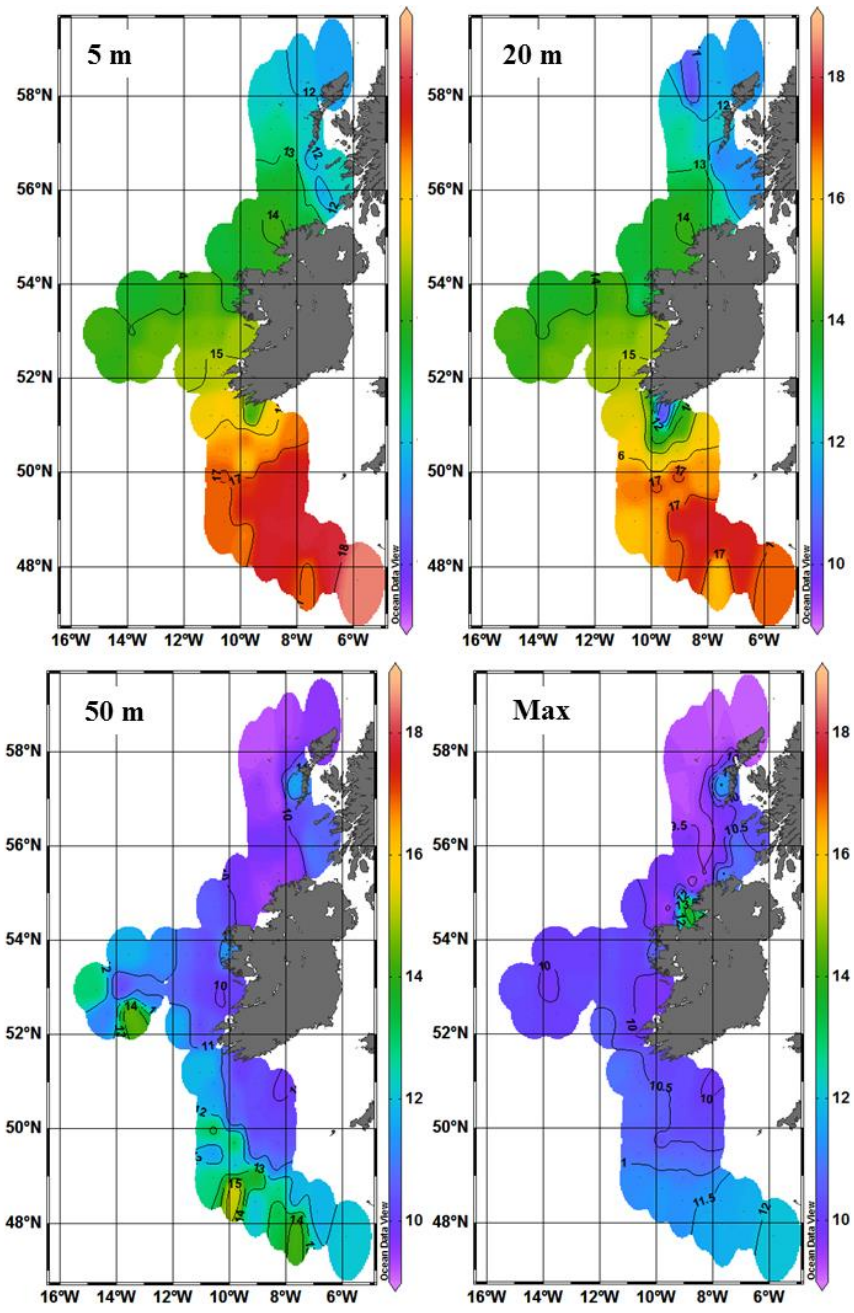

Fig. 2. Spatial distribution of temperature (°C) across all sampling stations at four depth layers (5 m, 20 m, 50 m, and maximum depth). A clear latitudinal gradient is observed, with warmer conditions in southern regions and cooler waters in the north, reflecting seasonal stratification patterns.

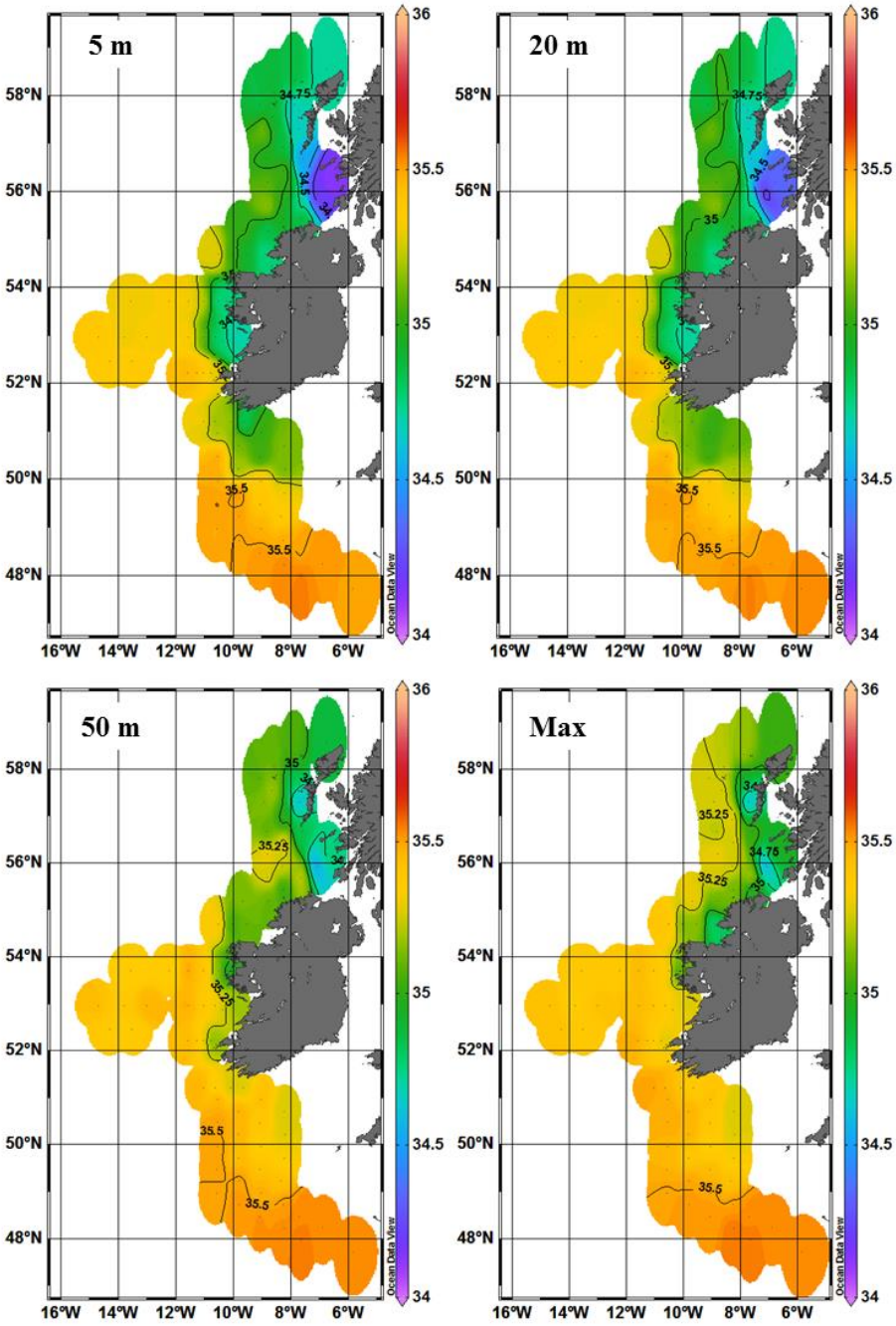

Fig. 3. Salinity (Unit in PSU) recorded from all stations at four depths (5 m, 20 m, 50 m and maximum depth).

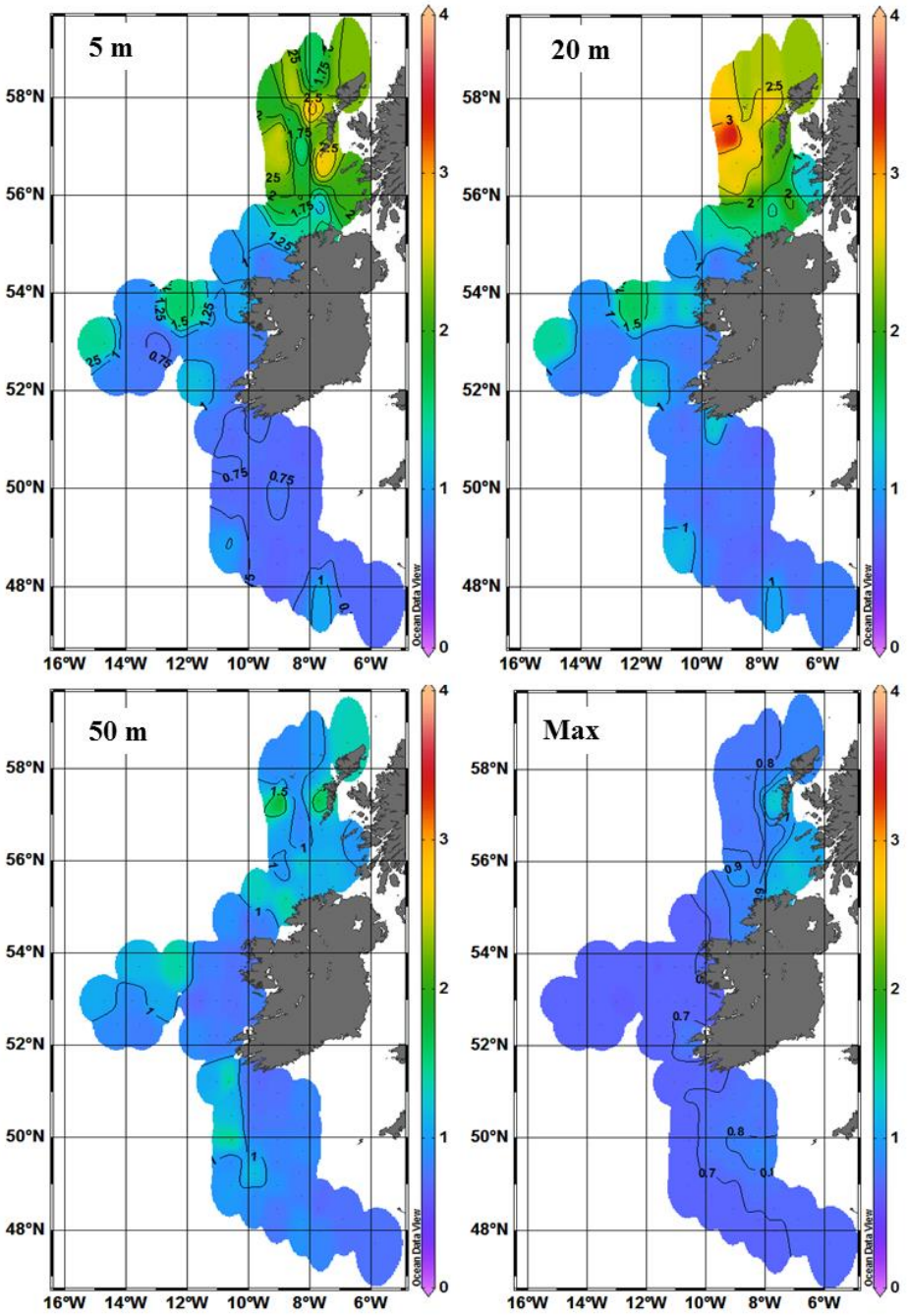

Fig. 4. Spatial distribution of chlorophyll-a concentration (mg·m^{-3}) across all sampling stations at four depth layers (5 m, 20 m, 50 m, and maximum depth). Higher concentrations near surface layers indicate areas of increased primary productivity, particularly in coastal and shelf regions.

Fish Composition and Abundance

A total of 1,426 larval specimens, spanning 51 taxa and 25 families, were identified (Table 1). The most abundant species included *Trachurus trachurus* (Atlantic horse mackerel) (17.6% of the total fish larvae abundance/relative abundance), *Myctophum punctatum* (spotted lanternfish) (15.9% of the total fish larvae abundance/relative abundance) and *Scomber scombrus* (Atlantic mackerel) (8.35% of the total fish larvae abundance/relative abundance). Within the family Gadidae, 8 species were identified, followed by 7 species of gobies (family Gobiidae). In terms of abundance, the most common species were *Pomatoschistus minutus* (7.15% of the total fish larvae abundance) and *Lebetus guilleti* (6.1% of the total fish larvae abundance), both belonging to the family Gobiidae. While, the lowest relative abundance (0.07%) was recorded for two species: *Pollachius pollachius* (pollack) and *Mullus surmuletus* (surmullet). Detailed species composition and relative abundance are presented in Table (1).

Recent studies have highlighted the ecological roles of dominant mesopelagic species like *Myctophum punctatum*, which plays critical roles in trophic energy transfer, serving as both prey and predators in pelagic food webs **(Hidalgo *et al.*, 2019; Médieu *et al.*, 2024)**. Similarly, the high abundance of *Trachurus trachurus* in shelf areas emphasizes its ability to exploit diverse habitats, consistent with findings on its ecological plasticity in the Northeast Atlantic **(Walsh *et al.*, 2015)**.

The fish larval density from all stations is shown in Fig. (5). The highest density was recorded from Station 34 (106 fish larvae per m^2), followed by Station 33 (91 fish larvae per m^2) and Station 36 (67 fish larvae per m^2). All these stations were located at the Porcupine Bank, west coast of Ireland. The lowest density (one fish larva per m^2) was recorded from stations 11, 15, 42, and 59.

Porcupine Bank's productivity aligns with global studies identifying oceanic banks and shelf breaks as hotspots for larval fish due to enhanced upwelling and nutrient availability **(Hidalgo *et al.*, 2019)**. The high densities observed may reflect localized spawning activity and favorable hydrographic conditions.

Across the three sampling legs, L2 recorded the highest larval abundance (578 individuals), followed by L1 (454 individuals) and L3 (394 individuals). L1 exhibited relatively higher species diversity, with notable contributions from gobiid species such as *Lebetus guilleti* and *Pomatoschistus minutus*. In contrast, L2 was dominated by *Myctophum punctatum*, reflecting its preference for deeper and mesopelagic conditions characteristic of the west coast of Ireland **(Edwards *et al.*, 2011)**. L3 showed strong dominance of *Trachurus trachurus*, consistent with known spawning activity in southern

Ireland. Overall, these patterns indicate clear spatial variation in species composition and dominance across the study area.

Table 1. Fish larvae species composition recorded across 77 stations. The table includes the total number of specimens collected, their relative abundance in total catches, and the frequency index of positive hauls (fi = n1/NT).

Family	Taxa	N	Relative abundance (%)	Relative frequency (%)
Ammodytidae	*Ammodytes marinus*	41	2.88	10.39
Argentinidae	*Argentina sphyraena*	14	0.98	10.39
Belonidae	*Belone belone*	2	0.14	1.30
Bothidae	*Arnoglossus laterna*	56	3.93	12.99
	Arnoglossus imperialis	3	0.21	2.60
Callionymidae	*Callionymus lyra*	26	1.82	11.69
	Callionymus reticulatus	4	0.28	1.30
Caproidae	*Capros aper*	50	3.51	15.58
Carangidae	*Trachurus trachurus*	251	17.60	29.87
Carapidae	*Echiodon drummondii*	4	0.28	3.90
Clupeidae	*Sardina pilchardus*	24	1.68	7.79
Gadidae	*Gadiculus argenteus*	2	0.14	1.30
	Melanogrammus aeglefinus	2	0.14	1.30
	Merlangius merlangus	13	0.91	5.19
	Micromesistius poutassou	3	0.21	2.60
	Pollachius pollachius	1	0.07	1.30
	Phycis blennoides	2	0.14	1.30
	Trisopterus esmarkii	5	0.35	2.60
	Trisopterus minutus	6	0.42	2.60
Gobiidae	*Gobius flavescens*	4	0.28	2.60
	Gobiusculus flavescens	4	0.28	2.60
	Lebetus guilleti	87	6.10	24.68
	Lebetus scorpioides	22	1.54	10.39
	Pomatoschistus microps	28	1.96	11.69
	Pomatoschistus minutus	102	7.15	25.97
	Gobius spp.	8	0.56	1.30
Labridae	*Labrus mixtus*	4	0.28	3.90
	Labrus bergylta	8	0.56	5.19
Lotidae	*Ciliata Mustela*	12	0.84	3.90
	Molva molva	40	2.81	11.69
	Molva dypterygia	2	0.14	1.30
Merlucciidae	*Merluccius merluccius*	37	2.59	9.09
Moronidae	*Dicentrarchus labrax*	24	1.68	2.60
Mullidae	*Mullus surmuletus*	1	0.07	1.30
Myctophidae	*Ceratoscopelus maderensis*	35	2.45	6.49

	Myctophum punctatum	226	15.85	16.88
	Hygophum reinhardtii	2	0.14	1.30
	Diaphus spp.	2	0.14	1.30
Paralepididae	*Paralepis coregonoides*	2	0.14	1.30
Pleuronectidae	*Glyptocephalus cynoglossus*	2	0.14	1.30
	Lepidorhombus whiffiagonis	7	0.49	3.90
	Microstomus kitt	15	1.05	9.09
Scombridae	*Scomber scombrus*	119	8.35	19.48
Scophthalmidae	*Lepidorhombus boscii*	2	0.14	1.30
	Zeugopterus punctatus	2	0.14	1.30
	Scophthalmus spp.	2	0.14	1.30
Sebastidae	*Helicolenus dactylopterus*	2	0.14	1.30
Soleidae	*Microchirus variegatus*	15	1.05	7.79
	Pegusa lascaris	12	0.84	3.90
Syngnathidae	*Nerophis ophidion*	2	0.14	1.30
Triglidae	*Eutrigla gurnardus*	24	1.68	14.29
Unidentified		63	4.42	11.69

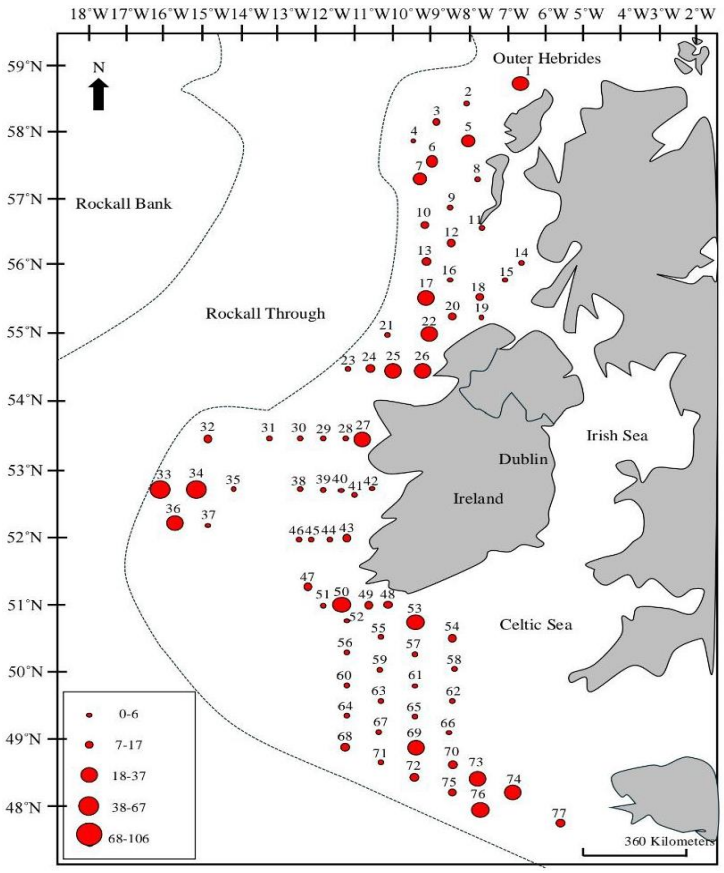

Fig. 5. Distribution of fish larval density (number of larvae per m²) across all sampling stations.

The high contribution of *Trachurus trachurus* in L3 reflects its known spawning grounds in southern Ireland, consistent with historical records of its production values during peak spawning periods **(Dransfeld *et al.*, 2014)**.

Fish Larvae Spatial Distribution

Fig. (6) illustrates the spatial distribution of larval fish abundance in the study area. The MDS analysis generally indicated no distinct separation between stations and fish larval assemblages, likely influenced by the sampling location within the continental shelf. Leg 3 stations seemed separated from the other legs (Leg 1 and Leg 2), which were amalgamated. The stations from Leg 3 and Leg 1 are grouped together as these areas are different from each other. The MDS stress value of 0.08 indicates a well-structured ordination, minimizing the likelihood of misinterpretation **(Clarke *et al.*, 2014)**.

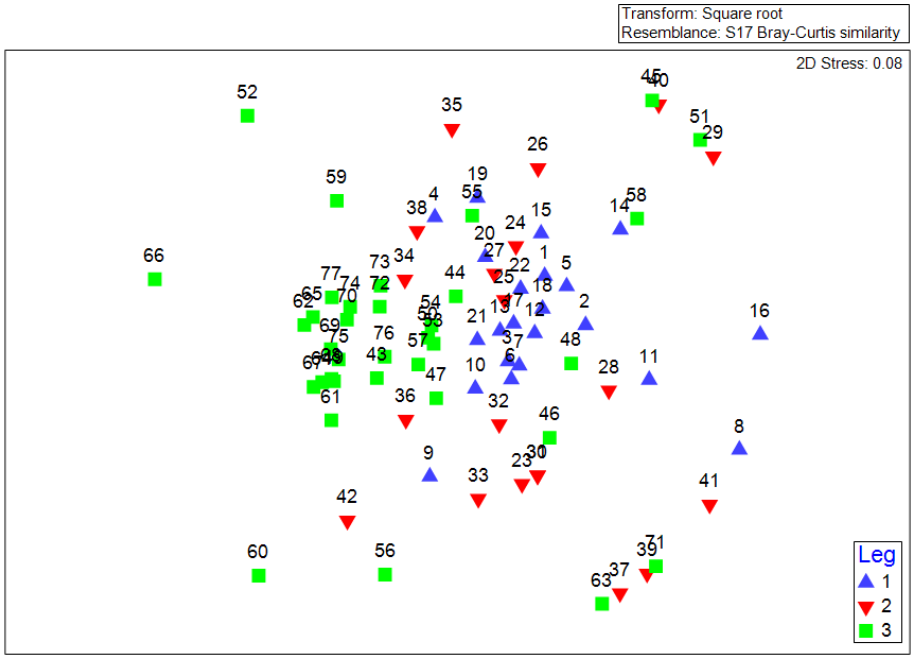

Fig. 6. Multi-dimensional scaling (MDS) ordination illustrating fish larvae assemblages across three designated sampling legs of the WESPAS cruise.

The distribution patterns of larval fish assemblages are frequently shaped by hydrographic features like thermoclines and salinity fronts, affecting larval drift and retention **(Hidalgo *et al.*, 2019)**. Additionally, the observed clustering may stem from larval behavioral adaptations to specific regional environmental factors, including temperature variations and prey availability **(Olivar *et al.*, 2018)**.

ANOSIM results indicated significant variation among survey legs; however, the global R value remained low (R = 0.263, p = 0.001), suggesting that differences in fish larvae assemblage structure across legs were relatively weak **(Clarke *et al.*, 2014)**.

Pairwise comparisons between legs yielded low R values (L1 versus L2: Pairwise R = 0.128, $p = 0.001$; L1 versus L3: Pairwise R = 0.296, $p = 0.001$; L2 versus L3: Pairwise R = 0.217, $p = 0.001$). According to **Beldade *et al*. (2006)**, the small differences in structure observed between sampling stations or legs are likely the result of two factors, namely (i) the smaller number of taxa shared between the stations (or legs) and (ii) the substantial variation in the average densities of the most dominant species across different stations. Hydrodynamic processes such as coastal upwelling and mesoscale eddies could play a role in maintaining localized assemblages, contributing to the subtle differences observed across sampling legs **(Hidalgo *et al*., 2019)**.

SIMPER analysis identified the key larval species driving similarity in the L1 (Northern Ireland) group as *Lebetus guilleti*, *Pomatoschistus minutus*, *Scomber scombrus*, *Molva molva*, and *Ammodytes marinus*. For the L2 (West Ireland) group, *Myctophum punctatum*, *Lebetus guilleti*, and *Trachurus trachurus* were the primary contributors to similarity. Only one species contributed to the Southern Ireland group (L3), namely *Trachurus trachurus*, as this species was the highest caught in Leg 3.

The dominance of *Myctophum punctatum* and *Trachurus trachurus* in respective regions is consistent with their spawning preferences and ecological niches. *Myctophum punctatum* often thrives in mesopelagic conditions, while *Trachurus trachurus* is strongly associated with shelf and coastal waters during spawning seasons **(Edwards *et al*., 2011; Médieu *et al*., 2024)**.

Lebetus guilleti (Guillet's goby) contributed the most to the L1 fish larvae assemblages (27.87%), owing to its broad distribution across the northeastern Atlantic, including Madeira, the Canary Islands, and the Mediterranean Sea **(Herler *et al*., 2016)**. This species also showed the second-highest contribution to the species similarity in L2 (7.75%), which includes stations located west of Ireland. This situation is in accordance with the record by Miller (1986), where *Lebetus guilleti* is found on the west coast of Ireland. Additional records indicate the presence of *Lebetus guilleti* in the Kattegat Sea, including the Great Belt (Denmark), as well as in Britain, ranging from the Shetland Isles through the Irish Sea to the Channel **(Hope & Shucksmith, 2010)**. Its distribution also extends to Brittany (France), the coastal regions of Portugal and Spain **(Miller, 1986)**, and further to Madeira and the Canary Islands **(Carneiro *et al*., 2014)**. The widespread distribution of *Lebetus guilleti* underscores its adaptability to varying habitat conditions, likely due to its preference for sheltered benthic environments and tolerance to different salinity levels **(Rochard & Elie, 1994)**.

Pomatoschistus minutus (Sand goby) showed the second-highest similarity contribution (17.95%) in the L1 assemblages. This species is present in coastal areas of the eastern Atlantic from Norway to Spain **(Rochard and Elie, 1994)** and has also been

recorded on the west coast of Ireland **(O'Brien & Fives, 1995)**. The other three species that also contributed to the similarity value in L1 assemblages were *Scomber scombrus* (Atlantic mackerel) (9% contribution), *Molva molva* (Ling) (8.06% contribution), and *Ammodytes marinus* (Lesser sand-eel) (7.82% contribution). These species also contributed to the similarities in L1, even though their percentage contributions were smaller.

In the west of Ireland (L2), the highest contributor to the species similarity in the group was *Myctophum punctatum* (spotted lanternfish) (59.06% - Table 2). This mesopelagic species inhabits both the Northern Atlantic and the Mediterranean **(Re & Meneses, 2009)** and is among the dominant taxa in midwater assemblages around the Mid-Atlantic Ridge **(Médieu *et al.*, 2024)**. **Edwards *et al.* (2011)** reported that this species is becoming more common in the southern part of the Northeast Atlantic. The other two species, namely *Lebetus guilleti* and *Trachurus trachurus*, also contributed to the species similarities in L2, even though their percentages were smaller (7.75% and 6.77%, respectively).

Table 2. SIMPER analysis presenting the key species contributing to similarity within the northern, western, and southern Ireland water groups.

Species	Av.Abund	Av.Sim	Sim/SD	Contrib%	Cum.%
L1 (Northern Ireland)					
Lebetus guilleti	0.89	4.31	0.49	27.87	27.87
Pomatoschistus minutus	0.84	2.78	0.5	17.95	45.82
Scomber scombrus	0.82	1.39	0.34	9	54.82
Molva molva	0.6	1.25	0.35	8.06	62.88
Ammodytes marinus	0.5	1.21	0.3	7.82	70.7
L2 (West Ireland)					
Myctophum punctatum	1.01	3.89	0.28	59.06	59.06
Lebetus guilleti	0.39	0.51	0.17	7.75	66.81
Trachurus trachurus	0.63	0.45	0.12	6.77	73.58
L3 (Southern Ireland)					
Trachurus trachurus	1.42	12.92	0.69	74.21	74.21

Trachurus trachurus was the only species that contributed to species similarities from L3 (located in Southern Ireland). The percentage of contribution was 74.21% – reflecting that this species showed the highest catch in L3 (43.91% relative abundance). This is because the coverage area in L3 is the spawning area of *Trachurus trachurus*, based on the production values between 2001 and 2010 **(Dransfeld *et al.*, 2014)**.

Linkage Between Fish Larvae Community and Oceanographic Variables

BIO-ENV analysis was used to further investigate the relationship between fish larvae assemblages and environmental factors. The findings indicate that latitude, temperature, salinity, and depth play a role in shaping species composition, aligning with **Dransfeld *et al*. (2009)**, who reported that larval communities in various Northeast Atlantic habitats are strongly linked to dominant oceanographic conditions (Table 3 - 'Overall', marked with an asterisk). When the BIO–ENV analysis was carried out between samples in the same factor (in this study: sampling Leg), latitude was not the best combination of variables (Table 3 - 'Within Sampling Leg Factor', marked with an asterisk *). This shows that within the sampling Leg, only temperature, salinity, and depth regulate fish larvae composition.

Table 3. BIO-ENV analysis showing environmental combination that characterized the fish larvae assemblages. The best variable combinations are marked with an asterisk (*) ($p < 0.001$). Lat: Latitude, Temp: Temperature, Sal: Salinity, Depth: Depth, ZooBio: Zooplankton Biomass.

Overall		**Within Sampling Leg factor**	
Combination variables	**Correlation value**	**Combination variables**	**Correlation value**
*Latitude, Temp, Sal, Depth	0.317	*Temp, Sal, Depth	0.254
Latitude, Salinity, Depth	0.314	Latitude, Temp, Sal, Depth	0.253
Latitude, Temp, Sal, ZooBio, Depth	0.311	Temp, Sal	0.250

The interplay of temperature, salinity, and depth as key regulators of fish larvae assemblages have been confirmed in recent studies, which emphasize the physiological responses of larvae to temperature gradients and salinity thresholds **(Schickele *et al*., 2020)**. Depth also plays a vital role in structuring larval communities by influencing access to prey and exposure to predators **(Bashevkin *et al*., 2020)**.

For the entire survey area, the combination of latitude, temperature, salinity, and depth yielded the highest correlation value of 0.317. These results suggest that the combined influence of these four variables plays a crucial role in defining the spatial distribution and species composition of fish larvae throughout the Western European Shelf. The high correlation suggests that the interplay between geographic position (latitude) and

oceanographic conditions (temperature, salinity, and depth) is crucial in determining fish larvae assemblages. The significant role of latitude implies that geographic location significantly influences larval distribution, likely due to varying climatic and oceanographic conditions across different latitudes. Latitude as a proxy for broader climatic conditions reflects large-scale oceanographic processes, such as stratification and current systems, which directly affect larval dispersal and recruitment success **(Hidalgo *et al*., 2019)**.

Other notable combinations of variables include latitude, salinity, and depth, which had a correlation value of 0.314, and latitude, temperature, salinity, zooplankton biomass, and depth, with a correlation value of 0.311. These results highlight the importance of salinity in conjunction with other environmental factors. The inclusion of zooplankton biomass in one of the significant combinations underscores its role as a potential food source, affecting larval survival and distribution. Zooplankton biomass has been identified as a critical determinant of larval fish success, linking trophic interactions to larval growth and recruitment **(Moriarty & O'Brien, 2013; Bashevkin *et al*., 2020)**. High zooplankton concentrations often correlate with productive areas such as upwelling zones and nutrient-rich coastal waters **(Hidalgo *et al*., 2019)**.

When the analysis is confined to individual survey legs, the combination of temperature, salinity, and depth showed the highest correlation value of 0.254. This suggests that within specific regions, local oceanographic conditions are more critical than latitude in explaining the distribution of fish larvae. The slightly lower correlation values within individual legs compared to the overall analysis indicate that regional factors like temperature, salinity, and depth are vital in these contexts. However, the broader geographic context provided by latitude offers additional explanatory power when considering the entire survey area. Localized studies focusing on individual legs reveal fine-scale dynamics that may be masked in broader analyses. Such approaches are crucial for identifying site-specific habitat preferences and species interactions **(Olivar *et al*., 2018)**.

Other significant combinations within the sampling legs include latitude, temperature, salinity, and depth, with a correlation value of 0.253, and temperature and salinity, with a correlation value of 0.250. These results underscore the critical influence of temperature and salinity in determining fish larvae distributions within specific regions. The importance of these variables is consistent with previous studies that have demonstrated the role of oceanographic conditions in shaping marine communities **(Anderson & Walsh, 2013)**. Temperature and salinity directly influence larval buoyancy, vertical positioning, and metabolic rates, which are critical for survival and dispersal **(Schickele *et al*., 2020)**.

The findings from the BIO–ENV analysis highlight several important implications for understanding fish larvae assemblages. The combined effect of geographic location (latitude) and oceanographic conditions, including temperature, salinity, and depth, is critical in determining larval fish distributions. This underscores the necessity of integrated monitoring programs that address both regional and broader-scale environmental factors. Such frameworks have been shown to enhance predictions of larval distributions and ecosystem responses to environmental variability **(Walsh *et al.*, 2015)**.

The variability of significant environmental variables across different regions emphasizes the importance of localized studies in capturing the unique dynamics of fish larvae communities. These findings suggest that conservation and management strategies must be tailored to the specific environmental conditions of each region to be effective. Adaptive strategies are essential in addressing the effects of climate fluctuations on fish stocks, supporting biodiversity conservation and the sustainability of fisheries **(Hidalgo *et al.*, 2019)**.

Additionally, the inclusion of zooplankton biomass as a significant variable highlights the critical role of food availability in shaping fish larvae distributions **(Abrantes *et al.*, 2015)**. Changes in zooplankton dynamics, often driven by ocean warming, could disrupt food web stability, leading to cascading effects on larval survival and recruitment **(Bashevkin *et al.*, 2020)**. These findings underscore the importance of considering trophic interactions in marine ecosystem studies and fisheries management **(Moriarty & O'Brien, 2013)**.

The observed relationships between larval fish assemblages and environmental gradients suggest that hydrographic conditions play a critical role in structuring early life stages. These patterns are likely to influence larval survival, dispersal, and ultimately recruitment success, which are key processes determining adult population dynamics and fisheries productivity.

These findings are particularly relevant in the context of ongoing environmental change, where shifts in temperature and salinity regimes may alter larval habitat suitability and distribution patterns. Such changes could have cascading effects on marine food webs and ecosystem stability, especially in shelf systems that are sensitive to hydrographic variability.

This study is subject to several limitations. The data were derived from a single survey period, which may not fully capture temporal variability in larval fish assemblages. Additionally, sampling constraints and the reliance on morphological identification may have limited taxonomic resolution, particularly for early developmental stages where diagnostic features are not fully developed. Future studies

incorporating temporal replication and molecular identification approaches would further enhance understanding of larval fish ecology.

CONCLUSION

This study provides a detailed analysis of fish larvae composition and distribution around the Western European Shelf, focusing on Ireland's waters. The WESPAS survey identified 1,426 larvae from 51 taxa and 25 families, with *Trachurus trachurus*, *Myctophum punctatum*, and *Scomber scombrus* being the most abundant species. Variations in spatial and environmental conditions, driven by temperature, salinity, and depth, played a crucial role in shaping larval distribution patterns. The findings underscore the importance of environmental drivers in predicting the impacts of ecosystem changes on fish populations. This extensive dataset provides a crucial foundation for future studies and fisheries management, aiding in marine biodiversity conservation and the sustainable utilization of resources. Future research integrating long-term monitoring and predictive modeling approaches will be essential to better understand larval fish responses to environmental variability. Such efforts will support more effective fisheries management and marine conservation strategies under changing oceanographic conditions.

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DECLARATION

Competing interests

The authors declare no competing interests.

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