



## Spatial patterns of large jellyfish *Chrysaora plocamia* blooms in the Northern Humboldt Upwelling System in relation to biological drivers and climate

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In the Northern Humboldt Upwelling System (NHUS), one of the most productive ecosystems in the world, the large jellyfish *Chrysaora plocamia* exhibits high inter-annual variability in population size, often resulting in massive blooms. In this study, we examined the geographic patterns of *C. plocamia* in the NHUS and their spatial overlap with ichthyoplankton, zooplankton, and chlorophyll *a* concentration (Chl *a*) during two El Niño (EN) years (1982–1983 and 1986–1987), and a neutral year (2014). During EN years, the spatial extent of *C. plocamia* medusae was larger than in the neutral year. In 1982–1983, medusae were concentrated mainly in the central-southern and southern regions of Peru, where they were associated with zooplankton, sardine larvae, and Chl *a*. In 1986–1987, medusae occurred in the northern and southern regions and spatially overlapped with sardine larvae and Chl *a*, and with zooplankton and anchoveta larvae, respectively. In 2014, medusae occurred mainly in the northern region, where they were associated with zooplankton, Chl *a*, and anchoveta eggs and larvae. Our results indicate strong EN effects on the distribution and abundance of *C. plocamia*, which can have consequences for zooplankton and ichthyoplankton abundance, as well as fisheries, in the NHUS.

**Keywords:** *Chrysaora plocamia*, El Niño, ichthyoplankton, Perú, scyphomedusae, spatial patterns, zooplankton

### Introduction

Jellyfish (medusae, ctenophores, and siphonophores) are important components of coastal and oceanic marine ecosystems worldwide (Lucas *et al.*, 2014). Large medusae in particular, have

received special attention due to the capacity of a few species to suddenly increase in population size, often resulting in mass occurrences or blooms in marine ecosystems worldwide (Purcell, 2012; Condon *et al.*, 2013). Recent studies have linked mass

occurrences of jellyfish with climatic fluctuations (Purcell, 2005), overfishing (Lynam et al., 2006), pollution, habitat modification, and the translocation of species (Richardson et al., 2009; Purcell, 2012; Duarte et al., 2013). However, the mechanisms behind the formation of these mass occurrences remain poorly understood (Duarte et al., 2013; Gibbons and Richardson, 2013), perhaps due to the scarcity of long-term datasets of jellyfish (Purcell, 2012). Previous long-term studies indicate that jellyfish abundance often co-varies with climate variability at inter-annual and -decadal scales (e.g. Goy, 1989; Lynam et al., 2005a; Purcell, 2005; Brodeur et al., 2008a; Chiaverano et al., 2013; Quiñones et al., 2015). However, our understanding of the environmental processes that influence jellyfish distribution is limited (see Brodeur et al., 2008a, 2014). The potential long term, climate-driven direct and indirect effects on the spatial distribution of jellyfish is almost unknown in most marine ecosystems (see Brodeur et al., 2008a).

Climate-driven distributional shifts of marine taxa can affect species interactions (Kordas et al., 2011). Numerous studies have shown that jellyfish have the potential to consume large amounts of planktonic prey, including fish eggs and larvae (Purcell, 2003; Meredith et al., 2016; Zeman et al., 2016). Hence, efforts have been made towards understanding how environmental (biotic and abiotic) variation is related to the distribution of jellyfish and their overlap with the early life stages of commercially exploited fishes (Purcell, 2003). Spatial overlap between large jellyfish and adult and larval commercially targeted fishes has been reported in several ecosystems, including the Northern California Current (Brodeur et al., 2008a,b, 2014) and in the Barents Sea (Eriksen, 2015). Large jellyfish have also been reported to overlap spatially with sardine and anchovy spawning areas within the North Sea (Lynam et al., 2005b), the Northern Benguela Current System (Flynn et al., 2012), and the North Western Mediterranean Sea (Tilves et al., 2016), suggesting that jellyfish aggregations feed on sardine and anchovy larvae. In addition, other biological factors were correlated with the spatial distribution of scyphozoan jellyfish, including other gelatinous zooplankton taxa (Brodeur et al., 2002; Purcell and Decker, 2005; Costello et al., 2012), Chl *a*, and primary productivity (Schroeder et al., 2014).

The Northern Humboldt Upwelling System (NHUS) is one of the most productive marine ecosystems, supporting the largest single-species fishery in the world (by weight) based on the Peruvian anchoveta (*Engraulis ringens*) (Pennington et al., 2006). Ecosystem function in the NHUS is periodically altered by inter-annual (ENSO cycle) and inter-decadal climate regimes, producing changes from a cool “anchoveta regime” (La Vieja) to a warm “sardine regime” (El Viejo) (Chavez et al., 2003). Such climate variability has also been linked to blooms of the large jellyfish *Chrysaora plocamia* (Quiñones et al., 2015), where biomass has increased during El Niño (EN) years within both a warm “sardine regime” in the 1970 s and 1980 s and a cool “anchoveta regime” in the late 2010s (Quiñones et al., 2015). When abundant, *C. plocamia* become regular by-catch of industrial purse-seine fisheries, which negatively affects the local fishing industry by producing economic losses because processors refuse catches with high jellyfish by-catch (Quiñones et al., 2013).

Although the relationship between environmental factors and temporal variability of *C. plocamia* populations has been established (Quiñones et al., 2015), where *C. plocamia* biomass fluctuated with climate drivers at inter-annual and inter-decadal scales, but not with anchovy landings (a proxy of fishing pressure). The potential direct and indirect effects of environmental (biotic and

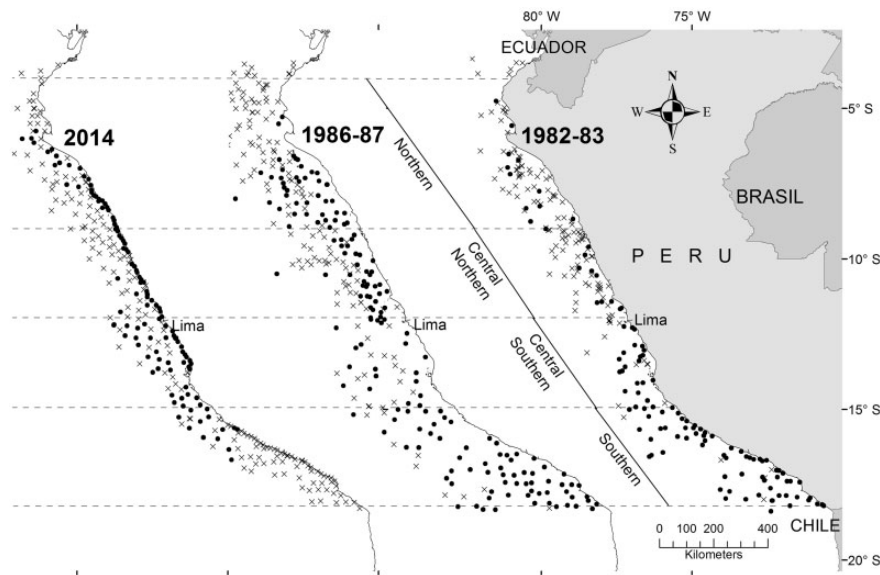
abiotic) variation on the spatial patterns of *C. plocamia* medusae remain unknown. Such information is particularly needed for the NHUS because of the potential impact of jellyfish blooms on the early stages of commercially exploited fish. In this study, we analysed data from three massive bloom years identified from 45 years of pelagic survey data off Peru to establish the distributional patterns of *C. plocamia* medusae, ichthyoplankton, zooplankton, and chlorophyll *a* concentration (Chl *a*) during 2 EN years (1982–1983 and 1986–1987) and a neutral year (2014). To evaluate the potential effect of biotic environmental and climate variability on the distribution of large jellyfish in this highly productive and commercially important system. In the neutral year 2014, abundance of *C. plocamia* medusae was higher than other neutral years; however, the extent of spatial distribution remained unchanged (Quiñones, pers. obs.)

## Methods

### Study area and data

The area of study extended across Peruvian waters from 03°23'S to 18°21'S and 200–280 km km offshore (to a depth about 100 m), covering ~500 000 km<sup>2</sup> (Figure 1). The study area was divided into four regions: Northern (04°S–09°S), Central-Northern (09°S–12°S), Central-Southern (12°S–15°S), and Southern (15°S–18°S) (Figure 1). Three periods of *C. plocamia* blooms were selected for analysis: 1982–1983 (extraordinary EN year), 1986–1987 (strong EN year), and 2014 (neutral year) (Figure 1). In each of these periods, *C. plocamia* abundance was at least 400% higher than the mean abundance of a 45-year data series (see Quiñones et al., 2015).

All data used in this study were collected from fishery-independent surveys conducted by the Instituto del Mar del Peru (IMARPE) at the same locations in space and time (Figure 1) during spring and summer of each selected period. Parallel survey transects were performed every 20–30 km perpendicular to the coast. Medusae of *C. plocamia* (log kg wet weight—WW 1000 m<sup>-3</sup>) were sampled using trawl and purse seine nets that were towed within the upper 100 m of the water column. Both gear types were operated during day and night. Jellyfish biomass (kg—WW) was standardized by the volume filtered (m<sup>3</sup>), which was calculated separately for each sampling gear. The mean net open area (m<sup>2</sup>) and volume filtered (m<sup>3</sup>) was estimated using the net height and width for the trawl nets, and the net height and perimeter for the purse seiners (see Quiñones et al., 2015 for specific details and formulations). Biomass of *C. plocamia* medusae was averaged within digitized sample grid cells used by IMARPE to assess the Peruvian anchoveta fishery, this grid cells were being used since the 1970s and are 18 × 55 km (Gutiérrez and Peraltilla 1999). Each grid cell was categorized into the following upper bounds of abundance: 0, 0.01, 0.1, 1.0, 10, and 100. Chl *a* (µg l<sup>-1</sup>) was obtained from water samples collected at fixed oceanographic stations every 9–18 km using Holm-Hansen et al. (1965). Zooplankton was collected by performing vertical tows (50 m in depth to the surface) using a Hensen net with a 0.33 m<sup>2</sup> mouth area and 300 µm mesh size. Each research cruise lasted between 40 and 50 days; sampling stations were located every 7 km within the first 55 km from the coast and every 9 km from 55 to 280 km offshore. Zooplankton samples were fixed with 2% formaldehyde and zooplankton biovolume (ml per sample) was determined at the time of collection using the displacement method (Kramer et al., 1972). Abundance of eggs and larvae of Peruvian anchoveta



**Figure 1.** Study area of the three selected periods with large jellyfish (*C. plocamia*) blooms in the NHUS. From left to right EN year 1982–1983, EN year 1986–1987, and the neutral year 2014. Presence and absence of *C. plocamia* medusae in hauls are represented by the solid dots and crosses, respectively.

and sardine (*Sardinops sagax sagax*) were obtained by counting eggs and larvae per sampling station and standardizing values to obtain number of eggs and larvae per  $m^2$  (see Santander, 1987).

### Data analysis

All biological explanatory variables were log-transformed and outliers were replaced by the maximum value of the remaining range because kriging estimators are sensitive to the presence of a few unusually large or small values (Armstrong and Boufassa, 1988). Biological variables were then interpolated for each year using ordinary kriging to increase spatial resolution (Lloyd, 2006). Ordinary kriging is a flexible interpolation method that can accommodate changes in the mean value of the surface conducted in ArcGIS 10.1 (ESRI, 2011). However, for the 1982–1983 period, sardine eggs, anchoveta larvae, and anchoveta eggs were excluded from further analyses because values and spatial coverage were low, while in 1986–1987 sardine eggs and anchoveta eggs were excluded for the same reasons. Similarly, sardine egg and larval abundance were not included in further analyses for 2014 because sardine biomass has been severely reduced in Peru since 2000 (FAO FishStats, 2011).

Spatial distributional patterns of *C. plocamia* medusae were examined by using the Getis-Ord Hot Spot analysis (ESRI, 2011), which calculates a GiZScore statistic for gridded and categorized abundance. The resultant  $z$ -scores and  $p$ -values refer to the level of clustering, with low values indicating locations where abundance is relatively low (cold spots) and high values indicating locations where abundance is relatively high (hot spots) (Scott and Warmerdam, 2005). A grid cell hot/cold spot was considered when the  $SD$  was  $\geq 1.96$  of the GiZScore. Spatial relationships were modelled using the “Polygon Contiguity Edges Technique” because grid cells were similar in size and shape (ESRI, 2011). This analysis was performed separately for each of the selected years. Hot Spot size categories were defined as: small ( $>5000$   $km^2$ ), medium (15 000–30 000  $km^2$ ), large (15 000–30 000  $km^2$ ), and very large ( $>30\,000$   $km^2$ ).

To identify biological variables that best explain variation in the distribution of *C. plocamia* abundance across time periods, we fit a series of geographically weighted regressions (GWRs) in ArcGIS 10.1 (ESRI, 2011). GWR provides a method to analyse spatial data by incorporating spatial autocorrelation and non-stationarity in regression coefficients. GWR calculates regression coefficients for each location by incorporating information from the dependent and explanatory variables of features falling within a defined distance of each location and is expressed in the following formula:

$$Y_i = \beta_{0,i} + \sum_{k=1}^p \beta_{k,i} X_{k,i} + \epsilon$$

where  $Y_i$  is the response (jellyfish abundance  $\log$   $kg\ 1000\ m^{-3}$ ) at location  $i$ ,  $\beta_{0,i}$  is the intercept parameter at location  $i$ ,  $\beta_{k,i}$  are the location specific regression coefficients of explanatory variable  $X_{k,i}$  (i.e. Chl  $a$ , zooplankton volume, abundance of sardine larvae and anchoveta eggs and larvae) at location  $i$ , and  $\epsilon$  is the residual error. The distance from each location was selected via Aikake Information Criterion for small sample sizes (AICc), which tries to identify the optimal fixed distance or optimal adaptive number of neighbours. The kernel technique, a tool that calculates the density of features in a neighbourhood around those features, was set as adaptive in order to make the distance bandwidth change according to the spatial density of the jellyfish. Separate GWRs were fit for each biological variable and the biological variables that best explained variation in *C. plocamia* abundance were selected by comparing adjusted  $R^2$  and AICc values. The biological variables that best explain variation in jellyfish abundance were then visualized in a spatial overlap map.

The degree of spatial overlap of *C. plocamia* with biological variables was estimated using the geostatistical methods described in Brodeur *et al.* (2008a, 2014). A Moran’s I test was performed for spatial autocorrelation where the inverse euclidean distance method and a distance threshold of 40 km were employed. Data were determined to be significantly autocorrelated at  $p$ -values

$\leq 0.05$ . Continuous coverage layers (point data) of *C. plocamia* medusa abundance and the selected biological variables were produced using the Geostatistical Analyst technique in ArcMap 10.1 (ESRI, 2011). Given our geographical distance in sample stations, coverage maps are not intended to represent small scale processes but rather to elucidate broad-scale patterns in the spatial distribution of *C. plocamia* and the tested biological variables (Brodeur et al. 2008a). Predicted values were grouped into 3 classes to illustrate areas where *C. plocamia* and each biological variable were absent (abundance = 0), present (biomass > 0), and highly abundant (abundance  $\geq$  75th percentile) for the 1982–1982, 1986–1987, and 2014 time periods. Then polygon maps were produced to estimate where *C. plocamia* and each selected variable overlapped at any level (both values > 0) and where they had the highest overlap (presence and > 75th percentile). The area within each polygon feature was then expressed in square kilometers (km<sup>2</sup>) by means of the “calculate geometry technique” in ArcMap 10.1 and the percent overlap area was calculated by dividing the area of the polygon feature where distributions of jellyfish (present or highly abundant) and each explanatory variable (present or highly abundant) overlapped by the total area surveyed (km<sup>2</sup>)  $\times$  100 (Brodeur et al., 2014). In addition, a latitudinal spatial overlap analysis was performed between *C. plocamia* and each biological variable per each year tested, considering the four regions of the study area.

## Results

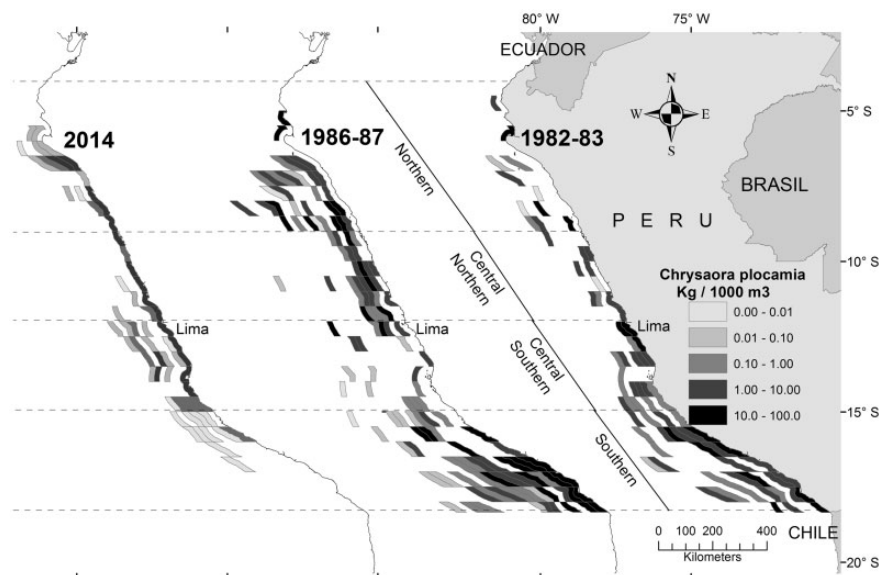
### Distribution of *C. plocamia* medusae

During the 1982–1983 period, the bulk (>70%) of *C. plocamia* medusae were distributed within 75 km from the coast, with individuals occurring up to 185 km offshore in lower abundances (Figure 2). Mean abundance per grid cell was 3.5 (SD: 1.5) kg 1000 m<sup>-3</sup> in 1982–1983, ranging from 1.7 to 7.8 ( $n = 467$ ). During the 1986–1987 period, medusae were distributed further offshore, reaching up to 280 km from the coast. Approximately 50% of medusae were distributed within 75 km, with 32% and 12% of medusae in waters between 75 to 185 and 185 to 280 km, respectively (Figures 2 and 3a). In 1986–1987, mean abundance

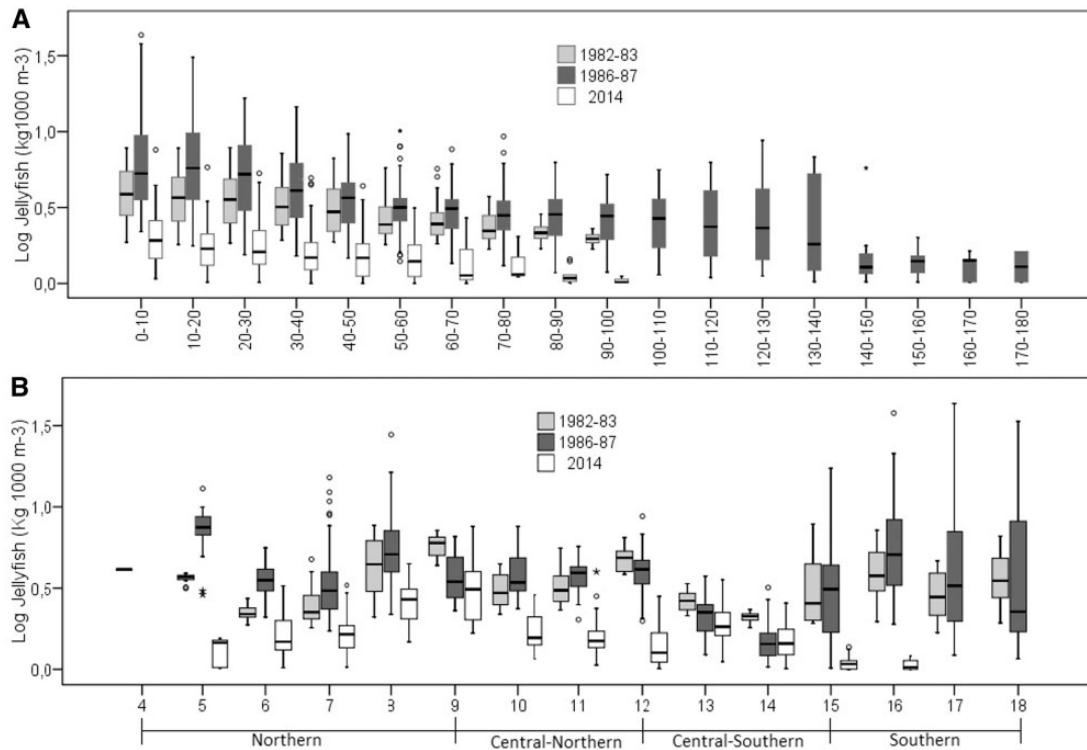
per grid cell was 4.4 (SD: 4) kg 1000 m<sup>-3</sup>, ranging from 1 to 43.2 ( $n = 835$ ). In 2014, the distribution of medusae was relatively constrained to the coast, with the majority (~68%) distributed within 35 km, 23% was recorded between 75 and 110 km, and ~9% were recorded between 110 and 185 km offshore (Figures 2 and 3a). In 2014, mean abundance per grid cell was 1.8 (SD: 0.8) kg/1000 m<sup>3</sup>, ranging from 1 to 7.6 ( $n = 366$ ).

During the 1982–1983 period, 6% of the *C. plocamia* medusae were distributed in the Northern region of the study area, 28% in the Central-Northern region, ~21% in the Central-Southern region, and 44% in the Southern region (Figure 3b). In 1986–1987, 6% of the medusae were registered in the Northern region, ~31% in the Central-Northern region, ~19% in the Central-Southern region, and 44% in the Southern region (Figure 3b). In 2014, ~10% of the medusae were distributed in the Northern region, ~41% in the Central-Northern region, 38% in the Central-Southern and ~11% in the Southern region (Figure 3b). In both 1982–1983 and 1986–1987 periods, *C. plocamia* abundance was greatest in the Southern region, while in 2014 the peak of abundance was recorded in the Central-Northern region (Figure 3b). Spatial coverage maps of *C. plocamia* medusae and biological variables are presented in the Supplementary Figures S1–S3.

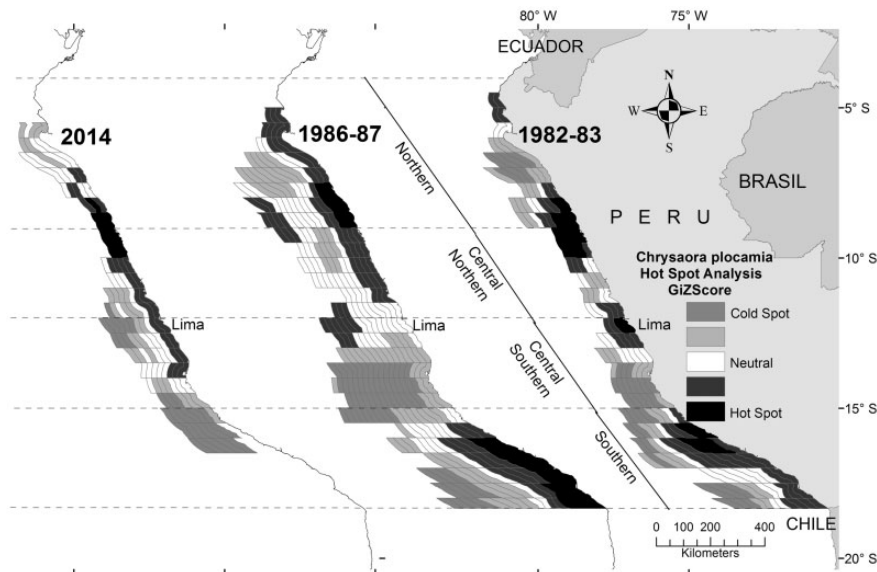
Three hot spots *C. plocamia* were identified in the NHUS during 1982–1983 (Figure 4). The largest hot spot (18 414 km<sup>2</sup>) was located in the northern/central-northern of the study area at 08°–10°S within 90 km from the coast. A medium size hot spot (10 938 km<sup>2</sup>) was located off the southern coast between 15° and 16°S within 75 km from the coast and a small hot spot (2981 km<sup>2</sup>) was located off the central coast of Peru at 12°S within 35 km of the coast (Figure 4). In 1986–1987, two hot spots were identified, a very large hot spot (32 542 km<sup>2</sup>) located along the southern coast between 16° and 18°S and up to 55–75 km from the coast and a medium size hot spot (11 601 km<sup>2</sup>) located along the northern coast (07°–08°S) within 55 km from the coast (Figure 4). In 2014, only a medium hot spot of *C. plocamia* (12 260 km<sup>2</sup>) was identified along the northern coast between 08° and 09°S within 35 km from the coast (Figure 4). In 2014,



**Figure 2.** Grid-cells distribution of *C. plocamia* medusae in the NHUS (off Peru) during warm EN years (1982–1983 and 1986–1987) and a neutral year (2014). Abundance is expressed in log kg jellyfish 1000 m<sup>-3</sup>.



**Figure 3.** Jellyfish (*C. plocamia*) abundance (log kg jellyfish 1000 m<sup>-3</sup>) in relation to distance to the coast (x-axes) (a) and latitudinal degree (x-axes) (b) for EN year 1982–1983, EN year 1986–1987, and the neutral year 2014.



**Figure 4.** Distribution of “hot spots” (GIZ Score > 2.9; black polygons) of *C. plocamia* medusae abundance in the NHU (off Peru) during warm EN years (1982–1983 and 1986–1987) and a neutral year (2014). Abundance is expressed in log kg jellyfish 1000 m<sup>-3</sup>.

*C. plocamia* did not exhibit high abundances in the south of the study area, contrary to the medium sized hot spots identified in 1982–83 and 1986–1987 (Figure 4).

**Spatial overlap with biological variables**

The GWR analyses indicated that in 1982–1983 and 1986–1987, the variable that best correlated abundance of *C. plocamia* was

Chl *a*, followed by zooplankton biovolume, and abundance of sardine and anchoveta larvae (Table 1). In contrast, in 2014, *C. plocamia* abundance was best explained by abundance of anchoveta eggs, followed by zooplankton volume, Chl *a* and anchoveta larvae (Table 1). The geostatistical analysis indicated that in 1982–1983, *C. plocamia* displayed the highest spatial overlap with sardine larvae (55.2%), followed by zooplankton volume

**Table 1.** Summary of the results from the GWR between the dependent variable (*C. plocamia*) and the explanatory variables.

Year	1982–1983		1986–1987		2014	
	$r^2$ -adjusted	AICc	$r^2$ -adjusted	AICc	$r^2$ -adjusted	AICc
Chl <i>a</i>	0.942*	–563	0.905*	–668	0.743*	–334
Zooplankton	0.876*	–465	0.689*	–300	0.802*	–356
Sardine larvae	0.719*	–325	0.623*	–253		
Sardine eggs	0.251	–169	0.352	–670		
Anchoveta larvae	0.152	–147	0.649*	–263	0.716*	–317
Anchoveta eggs	0.530	–250	0.431	–108	0.819*	–356.2

The asterisks (\*) indicate selected variables (higher  $r^2$ -adjusted and lower AICc).

(31.5%), and Chl *a* (31.5%). For 1986–1987 the highest overlap was with zooplankton volume (39.2%), followed by sardine larvae (37.2%), anchoveta larvae (37%), and Chl *a* (33.8%). For 2014 the highest overlap was with zooplankton volume (37.3%), followed by anchoveta eggs (33.2%), Chl *a* (29.4%), and anchoveta larvae (28%) (Figure 5).

Within years and areas of high medusa and biological variable values ( $\geq 75$ th percentile), spatial overlap between *C. plocamia* and biological variables varied with latitude (Table 2). In 1982–1983, *C. plocamia* and sardine larvae exhibited the highest spatial overlap in the northern areas (17.6%), while medusae displayed high spatial overlap with Chl *a* (9.5%) and zooplankton (10.1%) in the southern areas. In 1986–1987, medusae displayed the highest spatial overlap with Chl *a* (20.2%) and sardine larvae (17.2%) in the northern areas, and with zooplankton (12.7%) and anchoveta larvae (10.6%) in the southern areas. In 2014, *C. plocamia* showed the highest overlap with Chl *a* (25.9%) in the northern area and with anchoveta eggs and larvae (21.4%) in the central and northern areas (Figure 5; Table 2).

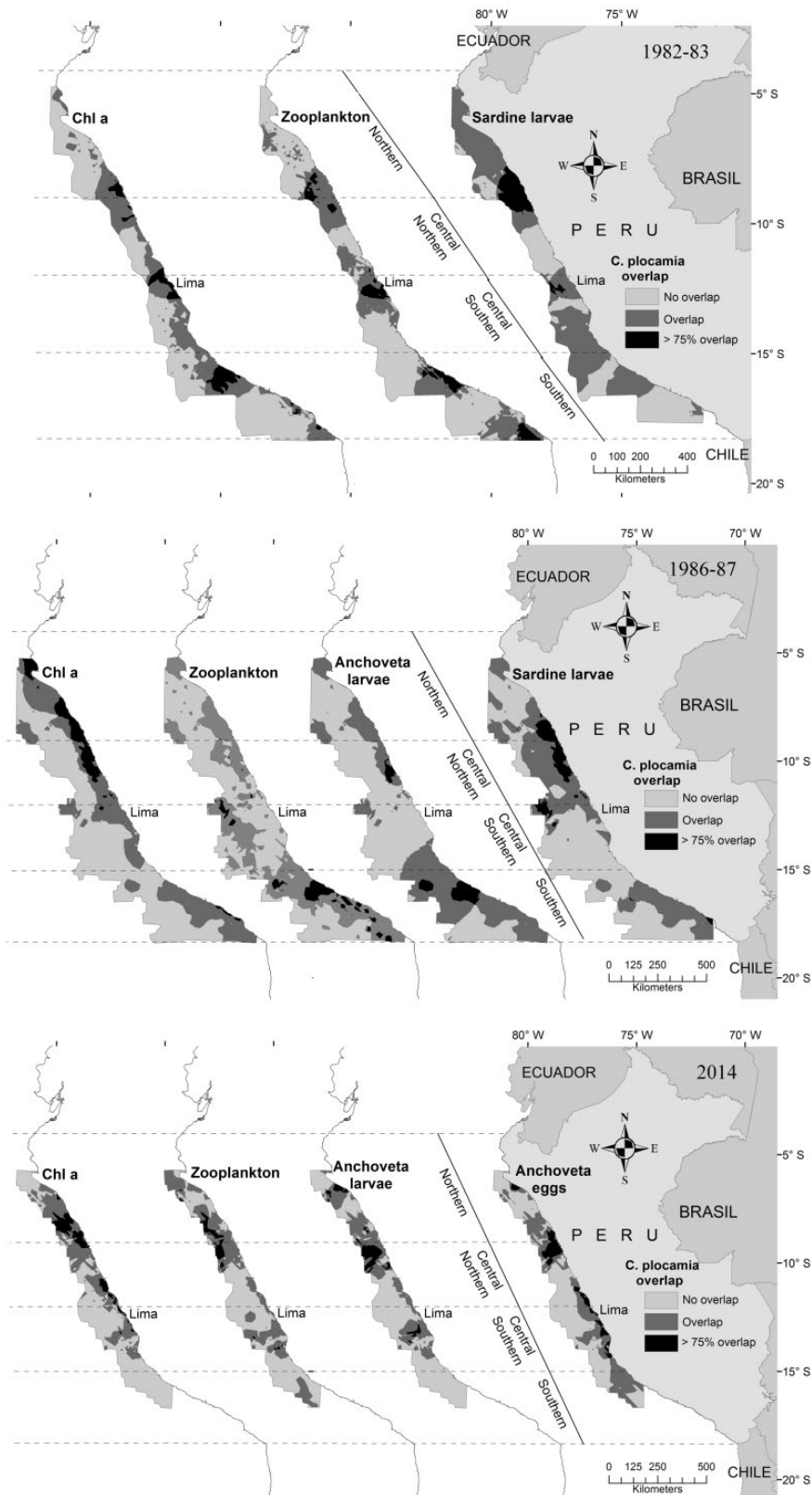
## Discussion

The spatial distribution of *C. plocamia* medusae varied considerably between climatic periods, suggesting that environmental conditions play a critical role in determining the spatial pattern of abundances of these large jellyfish in the NHUS. At the same time, the environmental conditions that normally benefit jellyfish occurrence and abundance in certain areas may be detrimental to other biological variables. If this happens, some spatial segregation could be occurring (Brodeur et al., 2014). The massive blooms of *C. plocamia* reported in EN years 1982–1983 and 1986–1987 were mainly distributed within the first 75 km from the coast and were even present up to 280 km offshore. Conversely, blooms during a neutral year (2014) were primary restricted to the coastal areas within 35 km from the coast. During both EN periods, oceanographic conditions were similar and consisted of highly stratified waters and a strong thermal gradient (IMARPE, 1988; Gutiérrez et al., 2011), elevated sea surface temperature (SST), SST anomalies, and a pronounced deepening of the thermocline (Arntz and Tarazona, 1990; IMARPE, 1988). A prolonged deepening of the thermocline can prevent the upwelling of cold, nutrient-rich waters, which results in a reduction of diatoms and an increase in flagellate species (Ochoa et al., 2010) because diatoms sink in highly stratified waters (Smetacek, 1985). Flagellates are common prey for mesozooplankton, which

represents the main prey for most jellyfish; consequently increased in flagellate abundance can lead to increased jellyfish abundance (Parsons and Lalli, 2002; Richardson et al., 2009). Previous research in the NHUS suggests that high prey availability, mainly ichthyoplankton and gelatinous zooplankton, can trigger jellyfish population growth (Quiñones et al., 2015). Therefore, such shifts in plankton community composition likely have a role in the extended distribution of *C. plocamia* during both EN years 1982–1983 and 1986–1987. How environmental factors affect the distribution of *C. plocamia* medusae under cold La Niña (LN) conditions (1975, 2007, and 2013) is less clear. However, during LN years 2007 and 2013, *C. plocamia* was almost absent from open waters, and were mainly restricted below the thermocline in enclosed areas. (Quiñones, pers. obs.).

Variability in pelagic planktonic assemblages may partially explain the restriction of *C. plocamia* blooms to coastal waters in 2014. During this year, zooplankton was less abundant in offshore waters, with a lower percentage of gelatinous organisms (IMARPE, unpublished data). Jellyfish of the genus *Chrysaora* feed on a wide array of prey, including gelatinous zooplankton (Brodeur et al., 2002; Purcell and Decker, 2005; Costello et al., 2012) and reduced offshore prey availability likely limited the offshore expansion of *C. plocamia* in 2014. The hot spots of *C. plocamia* medusae during EN years 1982–1983 and 1986–1987 are also likely a reflection of patches of potential prey items in high abundance (e.g. sardine and anchoveta larvae, meso zooplankton), while the only one hot spot detected in 2014 is perhaps a consequence of low food availability in offshore waters. For example, hot spot analyses indicated that *C. plocamia* medusae was most abundant in areas of the NHUS where biological variables (sardine larvae, anchoveta eggs and larvae, zooplankton volume, Chl *a*) were most abundant. Medusae displayed the greatest spatial overlap with sardine larvae during both EN years 1982–1983 and 1986–1987, while in 2014 the highest spatial overlap was with anchoveta eggs. Variation in the spatial overlap between *C. plocamia* medusae and anchoveta eggs and sardine larvae suggests a possible diet change resulting from climate-driven regime shifts, from anchoveta to sardine in the NHUS (Chavez et al., 2003). For example, anchovy eggs are the most common prey item of *C. plocamia* in northern Chile during cool anchoveta years (Riascos et al., 2014). However, their diet preferences during neutral (warm) years remain unclear. There are several reports on overlap and predation of some medusa on ichthyoplankton. *Pelagia noctiluca* in the Northwest Mediterranean overlaps with larval European anchovy (*Engraulis encrasicolus*), its most frequently ingested prey item (Tilves et al., 2016). In addition, medusae of *C. quinquecirrha* in Barnegat Bay, New Jersey disproportionately consume fish eggs and larvae (Meredith et al., 2016), overlapping in space and time (P. Bologna, pers. comm.). In the Northern California Current, anchovy eggs (*Engraulis mordax*) are the most consumed prey item by medusae of *C. fuscescens* (Zeman et al., 2016), and there is a high spatial overlap between these medusae and adult anchovies (Brodeur et al., 2008b, 2014). Furthermore, a strong positive selection for ichthyoplankton (fish eggs and larvae) has been observed in *C. fuscescens* off the coast of Oregon, USA (Zeman et al., 2016) and by *C. quinquecirrha* in the Chesapeake Bay, USA (Purcell et al., 1994).

Zooplankton volume had an important degree of spatial overlap with *C. plocamia* medusae in the NHUS. During the 1982–1983 EN year, zooplankton assemblages were dominated by gelatinous zooplankton, mainly consisting of chaetognaths,



**Figure 5.** Study area showing the spatial overlap between *C. plocamia* medusae and the biological (explanatory) variables during warm EN years (1982–1983 and 1986–1987) and a neutral year (2014). The distribution of the explanatory variable tested is depicted in light grey. Total overlap between *C. plocamia* and a given explanatory variable is represented in dark grey, while the area of maximum overlap (>75th percentile of biomass of both combined jellyfish and explanatory variable) is shown in black.

**Table 2.** Overlap circumscribed by the high *C. plocamia* concentration areas ( $\geq 75\%$ ) (black areas in Figure 5) and the biological variables per geographic latitudinal area.

Year/variables	Chl <i>a</i>		Zooplankton		Sardine larvae		Anchoveta larvae		Anchoveta eggs	
	Overlap (km <sup>2</sup> )	%	Overlap (km <sup>2</sup> )	%	Overlap (km <sup>2</sup> )	%	Overlap (km <sup>2</sup> )	%	Overlap (km <sup>2</sup> )	%
<b>1982–1983</b>										
Northern	2735	4.7	3697	6.4	10213*	17.6*				
Central-Northern	2250	6.1	2141	5.8	6608	18.0				
Central-Southern	4676	9.6	5818	12.0	2096	4.3				
Southern	10547*	9.5*	11182*	10.1*	0	0.0				
<b>Total</b>	<b>20 208.1</b>	<b>8.0</b>	<b>22 837.9</b>	<b>9.0</b>	<b>18 917.8</b>	<b>8.4</b>				
<b>1986–1987</b>										
Northern	18417*	20.4*	64	0.1	8797*	9.7*	0.0	0.0		
Central-Northern	13219*	16.4*	1067	1.3	13905*	17.2*	4203	5.2		
Central-Southern	502	0.4	2757	2.4	4367	3.9	0	0.0		
Southern	1755	1.1	19537*	12.7*	1363	0.9	16270*	10.6*		
<b>Total</b>	<b>33 893.0</b>	<b>7.7</b>	<b>23 425.1</b>	<b>5.3</b>	<b>28 431.8</b>	<b>6.5</b>	<b>20 472.6</b>	<b>4.7</b>		
<b>2014</b>										
Northern	11 662*	25.9*	5534	12.3			1779	3.9	3365	7.5
Central-Northern	5853	12.3	4303	9.1			10173*	21.4*	10017*	21.4*
Central-Southern	1500	2.4	940	1.5			2317	3.7	4985	8.1
Southern	0	0.0	0.0	0.0				0.0	0.0	0.0
<b>Total</b>	<b>19 015.3</b>	<b>10.3</b>	<b>10 776.0</b>	<b>5.9</b>			<b>14 268.8</b>	<b>7.8</b>	<b>18 367.6</b>	<b>10.0</b>

Areas of high overlap ( $> 10,000 \text{ km}^2$ ) are marked with an asterisk (\*), as well as high percentages of overlap.

doliolids, siphonophores, hydromedusae, and larvaceans (Carrasco and Santander, 1987; S. Carrasco, pers. comm.). During the 1986–1987 EN year, zooplankton was primarily composed of small copepods and gelatinous taxa, such as doliolids, pteropods, and larvaceans (IMARPE, 1988). During 2014 on the other hand, small hydromedusae (Trachymedusae and Narcomedusae) were more abundant than in previous years (P. Ayón, pers. obs.). Previous research indicates that species of the genus *Chrysaora* feed on gelatinous zooplankton, among other taxa. For instance, medusae of *Chrysaora quinquecirrha* in the Chesapeake Bay, USA feed on the ctenophore *Mnemiopsis leydyi* (Purcell and Decker, 2005; Costello et al., 2012), and medusae *C. melanaster* in the Bering Sea feed on gelatinous macrozooplankton when available (Brodeur et al., 2002). Although the diet of *C. plocamia* off Peru has not been examined extensively, decapod zoeae, fish eggs, and hydromedusae can be found in their guts during warm years like 2017 (Aller, 2017). Therefore, the high abundance of gelatinous zooplankton prey in the NHUS may play as well an important role in the distribution of *C. plocamia* observed in this system. Similarly, there was high overlap between *C. plocamia* and Chl *a* in the NHUS. Previous studies have shown scyphomedusae and ctenophore concentrations can be correlated with concentrations of Chl *a* (Kideys et al., 2008). The apparent influence of Chl *a* on the distribution of *C. plocamia* however, likely represents an indirect effect, since jellyfish feed on mesozooplankton taxa that in turn feed directly on diatoms and flagellates (Parsons and Lalli, 2002; Chiaverano et al., 2013).

The spatial overlap between *C. plocamia* medusae and biological drivers exhibited a clear latitudinal component. Overlap between jellyfish and fish eggs and larvae was consistently greatest within the northern part of the study area (7–10°S) in all study periods. Such trends are likely due to the consistent location of spawning for fish in upwelling ecosystems (Bakun, 2006a; Acha et al., 2015) given the selection for areas with particular water dynamics that promote egg and larval retention (Bakun, 2006b). Although highly productive, areas of upwelling can also be highly advective, transporting eggs and larvae offshore (Acha et al., 2015). Minimal overlap between *C.*

*plocamia* and ichthyoplankton in the Central-Southern area is likely a result of high advection and poor larval habitat for pelagic fish given high wind anomalies from 1979 to 2010 and the presence of an intense upwelling-core at ~13°S–16°S (Rahn and Garreaud, 2014). Hot spots in the Southern area (15°–18°20'S) in 1982–1983 and 1986–1987 however, were highly associated with high zooplankton volume. This area also has a relatively strong annual cycle of heat content (Takahashi, 2005). Temperature is positively correlated with jellyfish production in the NHUS (Quiñones et al., 2015) and likely explains local productivity in this area.

Most scyphozoan medusae, such as *C. plocamia*, are produced and released from benthic polyps. Hence, there appears to be a direct relationship between polyp abundance and medusa population size (Schiariti et al., 2014). To date, *C. plocamia* polyps have not been observed in the wild, but obtained through artificial fertilization under laboratory conditions. Riascos et al., (2013) showed that under simulated EN conditions from northern Chile, *C. plocamia* exhibited a rapid polyp recovery after an initial decrease in somatic growth. However, polyp survival was considerably lower under EN-like (22.3°C) thermal conditions compared with neutral-like (14.3°C) to La Niña-like (12.5°C) thermal conditions. Their results appear to not support our findings, most likely due to differences in environmental conditions between both areas of study. In our study, off of the coast of Peru, sea surface temperatures during the tested EN can easily reach 28–30°C, and primary productivity and food availability are considerably higher than in northern Chile (Bakun and Broad, 2003; Pennington et al. 2006). Thus, it is likely that *C. plocamia* polyp populations in Peru experience different environmental conditions than those in Chile, leading to different responses in terms of polyp productivity, medusa distribution and abundance. Future studies will help to elucidate these potential discrepancies.

## Conclusions

These results and those by Quiñones et al., (2015), allow us to propose two environmentally driven scenarios that can lead to jellyfish blooms in the NHUS. First, both *C. plocamia* abundance



and spatial distribution are expected to increase during warm EN years most likely as a consequence of increased food availability during the warm El Viejo regime (high concentration of sardine larvae in the north and anchovy larvae in south together with zooplankton abundance) and suitable oceanographic conditions (high SST, strong thermal gradient and deeper thermocline) that can potentially promote medusae growth and increase production. This scenario is represented by the 1982–1983 and 1986–1987 EN years, during which the spatial overlap of *C. plocamia* was greatest with potential prey items like sardine and anchoveta larvae and zooplankton in areas associated with sardine and anchoveta spawning and zooplankton production (Bakun and Broad, 2003; Alheit and Niquen, 2004). Second, during neutral (or slightly warm) years, high abundance of *C. plocamia* medusae will likely be restricted to coastal waters. This scenario is represented by 2014, where *C. plocamia* was higher than other neutral years, however the same spatial pattern was observed. In this year, *C. plocamia* distribution was limited most likely as a consequence of relatively less favourable environmental conditions, such as reduced prey availability in offshore areas and changes in the trophic structure of the NHUS leading to maximal shelf (coastal) retention of ichthyoplankton and prey concentration (Brochier *et al.*, 2011). For both scenarios, blooms of *C. plocamia* are expected to be distributed along oceanographic features associated with the retention of ichthyoplankton and thermal gradients that promote jellyfish production.

Understanding the spatial distribution of *C. plocamia* medusae, and the environmental effects on it in the NHUS can be highly beneficial for fisheries in this commercially important area. The spatial patterns presented and the scenarios proposed here may be used to assist the anchoveta fishery fleet in avoiding areas of high concentration of *C. plocamia* medusae and minimize jellyfish bycatch, which can lead to important economic losses (Quiñones *et al.*, 2013). Alternatively, the identification of large jellyfish hot spots can also assist the establishment of a jellyfish fishery to support the demand from Asian markets (Brotz *et al.*, 2017). Last, spatial patterns of jellyfish abundance, as well as their spatial overlap with commercial fish eggs and larvae, could be used to assist in ecosystem-based fishery management approaches for the NHUS, and other highly productive, commercially important marine systems worldwide.

## Supplementary data

Supplementary material is available at the ICESJMS online version of the article.

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