

Stable isotope patterns in micronekton from the Mozambique Channel

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- 1 Stable isotope patterns in micronekton from the Mozambique Channel
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ABSTRACT

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We measured the stable carbon (δ^{13} C) and nitrogen (δ^{15} N) isotopic composition of tissues of micronektonic organisms (fishes, squids, crustaceans and gelatinous organisms) collected in the Mozambique Channel during two scientific cruises in 2008 and 2009. The oceanic circulation in the Mozambique Channel is dominated by mesoscale cyclonic and anticyclonic eddies which play a key role in biological processes of less-productive deep-sea ecosystems. We investigated the potential impact of mesoscale features on the $\delta^{13}C$ and $\delta^{15}N$ values of 32 taxa of micronekton. Fishes, squids, crustaceans and gelatinous organisms encompassed a wide range of isotopic niches, with large overlaps among species. Our results showed that mesoscale features did not really influence the isotopic signatures of the sampled organisms, although cyclonic eddies can occasionally impact the nitrogen signatures of micronekton. We show that $\delta^{13}\text{C}$ values were intermediate between standard offshore and nearshore signatures, suggesting that pelagic production in the Mozambique Channel could be partly supported by the transport and export of inorganic and organic particles from the Mozambican coast toward the offshore area. Trophic levels calculated from $\delta^{15} N$ values ranged from 2.6 to 4.2, showing that micronekton taxa can be tertiary consumers in the Mozambique Channel. Our findings evidenced clusters of micronektonic organisms according to their $\delta^{15}N$ or $\delta^{13}C$ isotopic signatures, but variations in stable isotope values reflect a complex set of embedded processes linked to physical mesoscale dynamics (rotational dynamics of eddies) and basic biology and ecology of micronektonic organisms (vertical habitat, migration pattern, dietary habits, body length) that are discussed with regard to the stable isotope method based on time-integrated assimilated food.

- **KEYWORDS:** Micronekton, δ^{13} C, δ^{15} N, Mesoscale, Oceanic eddies, Diel vertical migration,
- 39 Trophic level, Mozambique Channel.

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1. INTRODUCTION

The circulation in the Mozambique Channel (south-west Indian Ocean) is ruled by an important mesoscale activity (de Ruijter et al., 2002). Mesoscale rotating eddies propagate southwards along the western edge of the channel (Quartly and Srokosz, 2004; Schouten et al., 2003). These mesoscale features contribute to ocean mixing processes and consequently impact the biological activity at different scales. Cyclonic eddies (clockwise rotating in the southern hemisphere) generate vertical pumping of nutrients in their centres (Bakun, 2006; Chelton et al., 2011; McGillicuddy Jr et al., 1998), enhancing local primary production (Benitez-Nelson et al., 2007; Mizobata et al., 2002; Tew-Kai and Marsac, 2009). On the opposite, anticyclonic eddies (counter-clockwise rotating) are usually associated with low chlorophyll levels (Bakun, 2006; Chelton et al., 2011). However, phytoplankton enrichment has also been associated with the upward movement of nutrient rich waters at the edges of either cyclonic or anticyclonic eddies (Mizobata et al., 2002; Quartly and Srokosz, 2004). In addition, coastal primary production produced on the western side of the channel can be horizontally advected by continuous contra-rotating eddy pairs, referred to as dipoles and propagating southwards (Roberts et al., this issue; Ternon et al., this issue). By influencing the horizontal and vertical distribution at the base of the food web (nutrients, phytoplankton and zooplankton), these features have been suggested to alter the distribution of intermediate trophic links such as micronekton, and thus the distribution of upper-trophic level organisms.

Biological responses to mesoscale eddies have been documented for mesozooplankton and fish larvae (Bakun, 2006; Muhling et al., 2007), for tunas and swordfish (Young et al., 2001); (Seki et al., 2002), for turtles (Lambardi et al., 2008; Polovina et al., 2004), for seabirds (Hyrenbach et al., 2006; Nel et al., 2001; Weimerskirch et al., 2004), or for marine mammals (Bailleul et al., 2010). In spite of their importance, the impact of mesoscale features on micronektonic organisms remains fragmented and is still poorly quantified (see Potier et al., this issue). Recent investigations showed that eddies can shape the distribution and the aggregation patterns of micronekton through bottom-up processes (Drazen et al., 2011; Sabarros et al., 2009). Micronekton refers to small, but actively swimming, organisms (ca. 1 to 20cm), mainly crustaceans, fishes, and squids, that form the link between zooplankton and large fish predators in open-sea ecosystems (Brodeur and Yamamura, 2005; Potier et al., 2007). Most of micronekton performs large diel vertical migrations during the crepuscular periods (dawn and dusk), from depths below 400m during the day to the surface layers at night (Benoit-Bird et al., 2009). In this work, we analyzed the ratios of stable carbon (δ^{13} C) and nitrogen (δ^{15} N) isotopes in the tissues of micronektonic organisms collected in the Mozambique Channel within the framework of the MESOBIO programme (Ternon et al., this issue). Carbon and nitrogen isotopes have often successfully been applied to investigate foraging ecology and trophic relationships in marine ecosystems (Cherel et al., 2010; Fanelli et al., 2011; Ménard et al., 2007; Olson et al., 2010; Revill et al., 2009; Stowasser et al., 2012). Stable isotope ratios of carbon and nitrogen in consumer tissues reflect those of their prey in a predictable manner, and depend on the isotopic signature at the base of the food web (Fry, 2006; Post, 2002). The $\delta^{\rm 15} N$ values mainly estimates the relative trophic position of an animal thanks to predictable enrichment of ¹⁵N with increasing trophic level (Vanderklift and Ponsard, 2003).

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Thus, δ^{15} N has been used for quantifying and comparing trophic levels of consumers (Cherel et al., 2008). By contrast, δ^{13} C variations are used to determine the sources of primary production, inshore versus offshore or pelagic versus benthic contribution to food intake (Rubenstein and Hobson, 2004). Different processes affect isotopic baselines of δ^{13} C and δ^{15} N, including nutrient source, primary productivity, depth and ocean mixing processes (Fry, 2006). The present work aims (1) to investigate the potential impact of mesoscale features on the ratios of stable carbon and nitrogen isotopes of micronektonic organisms, and (2) to interpret the isotopic niches and the trophic levels of micronektonic species in the Mozambique Channel.

2. MATERIAL AND METHODS

2.1. Sample collection

Micronekton samples were collected from two scientific cruises during December 2008 on board R/V Fridtjof Nansen (2008 ASCLME survey n°4, called hereafter MC08A) and during November 2009 on board R/V ANTEA (referred to as MC09B). A Young Gadoid Pelagic Trawl (YGPT) was used during MC09B with a cod-end lined with 5mm knotless nylon delta mesh netting, while an Akrahamn pelagic trawl with cod-end 10mm was used during MC08A. Trawls were conducted during the day on aggregations detected by acoustics, and during the night at the surface on sound scattering layers (0-200m). Night trawl depth was selected according to highest acoustic detections. Each trawl was towed for 30 min at a speed of 3 to 4 knots. A total of 16 and 18 trawls were performed during MC08A and MC09B, respectively (from which 2/3 were carried out at nighttime). The whole catch was sorted and soft tissues of selected micronekton species were removed for further isotopic analyses: dorsal muscle for fishes, mantle for squids, abdomen for crustaceans and body wall for pelagic gastropods

molluscs, siphonophorans, leptocephali larvae and salps. Body length of each individual was measured except for salps: standard length (SL) for fishes, dorsal mantle length (DML) for squids, cephalothorax length (CT) for crustaceans, and total length for the other taxa.

2.2. Stable isotope analysis

Samples were freeze-dried and ground to a fine homogeneous powder. Since lipids are depleted in 13 C, lipids were removed using dichloromethane on an accelerated solvent extraction system (ASE®, Dionex;(Bodin et al., 2009). This method does not alter δ^{15} N signatures. The extent of lipid extraction was checked through the C/N mass ratio of the samples (Post et al., 2007). Lipid-free samples were dried at 50°C before processing, and then 300 to 400 μ g of homogenized powder were packed into 8 \times 5mm tin containers. Isotopic ratios were determined by a continuous flow mass spectrometer coupled on line to an elemental analyzer. Replicate measurements of internal laboratory standards indicated measurement errors less than 0.15‰ and 0.20‰ for δ^{13} C and δ^{15} N, respectively. Triplicate measurements performed on some samples confirmed that analytical reproducibility was very good (0.2‰ maximum variation). Isotopic ratios are expressed in the conventional δ notation as parts per thousand (‰) deviations from the international standards: atmospheric nitrogen (N₂) for δ^{15} N and VPDB Belemnite for δ^{13} C.

$$\delta X = (R_{\text{sample}}/R_{\text{standard}} - 1) \times 1000 \tag{1}$$

where X is ¹⁵N or ¹³C, R is the corresponding ratio ¹⁵N/¹⁴N or ¹³C/¹²C.

2.3. Data analysis

Satellite altimetry allows identification of mesoscale features (Chelton et al., 2007). One mesoscale feature among five classes (anticyclone, A; cyclone, C; divergence, D; front, F; and

shelf station, S) was assigned to each of the 34 trawling stations. The classification of each individual station was processed using three explanatory variables (sea level anomaly, geostrophic speed and bathymetry) and a discriminant function estimated from an extra training dataset (Lamont et al., this issue). Ocean bathymetry was extracted from ETOPO1 Global Topography (data access: http://www.ngdc.noaa.gov/mgg/global/global.html). Sea level anomaly and the corresponding geostrophic speed were extracted from AVISO products "DT-MSLA Ref" (Delayed Time, DT; Reference, "Ref") with 0.33 × 0.33° spatial resolution on a Mercator grid. The predictions from the linear discriminant analysis were estimated for each station using the values taken by the three explanatory variables at the corresponding temporal and spatial positions. Links between isotope values ($\delta^{15}N$ and/or $\delta^{13}C$), and broad categories and mesoscale features were investigated using multivariate analysis of variance (MANOVA), Kruskal-Wallis (KW) non-parametric tests and univariate regression tree (URT). URT is a powerful statistical tool that explains the variation of a single response variable ($\delta^{15}N$ or $\delta^{13}C$) using several explanatory variables by growing a tree that partitions the data set into mutually exclusive groups (Venables and Ripley, 2002). The objective is to partition the response into homogeneous groups. All the data are represented by a single node at the top of the tree. Then the tree is built by repeatedly splitting the data. Each split is defined by a simple rule based on a single explanatory variable. Splits are chosen to maximize the homogeneity of the resulting two nodes. However, the splitting procedure grows an overlarge tree. To keep the tree reasonably small, a prune back procedure is applied. Each final group is characterized by mean values of $\delta^{15}N$ or $\delta^{13}C$.

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As the content of ¹⁵N in animal tissues is biomagnified along the length of a food chain (Post, 2002), trophic levels (*TL*) of micronekton taxa were calculated on the basis of isotopic measurements using the following equation:

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$$TL = 2.0 + \frac{\delta^{15} N_i - \delta^{15} N_{primary\ consumer}}{3.2}$$
 (2)

where $\delta^{15}N_i$ is the nitrogen isotopic composition of any given micronekton taxon i, $\delta^{15}N_{primary}$ consumer is the $\delta^{15}N$ reference baseline value at trophic level 2, and 3.2% is an estimate of the average increase of $\Delta^{15}N$ per trophic level (Cherel et al., 2010; Sweeting et al., 2007). Using primary consumers as a baseline might reduce error in the estimation of TL (Martínez del Rio et al., 2009). Salps are known to be filter-feeders grazing on phytoplankton and other small food items. They were often chosen as the primary consumer species for estimating trophic levels using equation (2) (Cherel et al., 2010, 2008; Stowasser et al., 2012). Therefore, we chose average $\delta^{15}N$ value of Salpa maxima as the reference value for the food base. The mean was computed using three $\delta^{15}N$ values (5.0, 5.2, 5.2%) from MC08A and one (5.2%) from MC09B.

3. RESULTS

Fig. 1 displays the location of the 34 trawls categorized in four mesoscale feature classes (cyclones C, anticyclones A, fronts F, divergences D and shelf station S). A total of 545 organisms amongst 32 taxa were analyzed (Table 1). Not all micronekton taxa were caught at all mesoscale features, in particular few individuals were collected in anticyclones and cyclones (68 and 77, respectively) compared with those collected in divergences and fronts (187 and 121, respectively).

3.1. Micronekton assemblage

Taxa were divided in four broad categories: gelatinous organisms (Salpa maxima, siphonophorans, the pelagic gastropod molluscs Carinaria lamarckii and leptocephali larvae), crustaceans (Funchalia spp., Oplophorus sp. and O. typus), squids (Cranchia scabra, Ornithoteuthis volatilis, Sthenoteuthis oualaniensis), and fishes. Fishes represented 16 species, 5 genera and 1 family. The family Bramidae grouped juveniles of Pterycombus petersii and of other undetermined species: they were not segregated by both $\delta^{15}N$ (Kruskall-Wallis, H = 1.19, P > 0.27) and δ^{13} C values (H = 0.43, P > 0.50). The Thunnus spp. category comprised very small juvenile scombrids that were not identified. Psenes spp. comprised 2 species (*P. cyanophrys*, *P. whiteleggii*) that were not segregated by their $\delta^{15}N$ signatures (Kruskall-Wallis, H = 1.78, P > 0.18), but slightly segregated by δ^{13} C (Kruskall-Wallis, H = 4.0, P = 0.045). The genus *Diaphus* is taxonomically one of the most difficult in the family Myctophidae. We accurately identified three species (D. garmani, D. metopoclampus, D. richardsoni). The Diaphus spp. category groups other species that were not identified. Juveniles were collected for Bramidae, Decapterus sp., Pterycombus petersii, Psenes spp. and Thunnus spp only. Means of C/N mass ratio encompassed a narrow range (between 3.0 and 3.4 for 30 taxa; only Salpa maxima and leptocephali larvae had ratios greater than 4; Table 1). Such small values indicated low lipid content after lipid removal, thus allowing accurate comparisons of δ^{13} C values among sample types. Isotopic analyses revealed a considerable range of δ^{13} C and δ^{15} N mean values, 3.3 and 6.9%, respectively. The δ^{13} C mean values ranged from –20.6 \pm 0.57‰ (letocephal larvae) to –17.3 \pm 0.24‰ (<code>Oplophorus</code> sp.) (Table 1). The $\delta^{15} N$ ranged from 5.2 \pm 0.11% (Salpa maxima) to 12.1 \pm 0.44% (Diaphus metopoclampus). The four broad categories (fishes, squids, crustaceans and gelatinous organisms) were segregated by their isotope signatures of both nitrogen and carbon treated as a multivariate

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response (MANOVA, Wilk's lambda, $F_{3,540}$ = 58.37, P < 0.0001). They were also segregated in 203 their isotopic signatures in both $\delta^{13}C$ (univariate analysis, KW test, H = 115.0, P < 0.0001; 204 pairwise comparisons indicated that crustaceans and squids were not significantly different) 205 and $\delta^{15}N$ values (KW test, H = 56.0, P < 0.0001; fishes and squids did not differ significantly). 206 Fig. 2 displays a summary of δ^{13} C and δ^{15} N values (mean \pm standard deviation) of all the taxa 207 grouped by broad categories. To give a better picture of the trophic structure of the 208 209 assemblages, taxa of the four broad categories were placed in sequence according to their nitrogen and carbon mean values (Fig. 3a and 3b, respectively). Tests were then conducted 210 211 by categories: 212 - The 22 taxa of fish were segregated by their overall isotopic signatures (MANOVA, Wilk's lambda, $F_{21.354} = 14.99$, P < 0.0001), and both δ^{13} C (KW test, H = 151.1, P < 0.0001) and δ^{15} N 213 values (KW test, H = 249.6, P < 0.0001). The most enriched values were found for known 214 deep migrating mesopelagic fishes such as several Myctophidae (all of the genus Diaphus, 215 Lobianchia gemellarii), the bregmacerotid Bregmaceros macclellandii, the notosudid 216 217 Scopelosaurus hoedti, and the sternoptychid Argyropelecus aculeatus. Cubiceps pauciradiatus (Nomeidae) and Decapterus sp. (Carangidae) exhibited large standard 218 deviations of $\delta^{15} N$ thanks to a subset of specimens caught in one cyclone of MC09B with very 219 high δ^{15} N values (see below). 220 - Overall isotopic signatures differed between the three squid species (MANOVA, Wilk's 221 222

lambda, $F_{2,101}$ = 4.90, P < 0.001), but only the KW test based on δ^{13} C signatures was significant (H = 10.62, P < 0.005 for δ^{13} C; H = 0.85, P = 0.66 for δ^{15} N). 223

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- For crustaceans (three taxa) and gelatinous organisms (four taxa), multi- and univariate tests were all significant. Standard deviations of both $\delta^{13}C$ and $\delta^{15}N$ for leptocephali larvae were very high, while the nitrogen signatures of Salpa maxima varied very little (5.2 \pm 0.11‰). Oplophorus typus (crustacean) was the only non-fish taxa having a δ^{15} N average greater than 10.0‰ (Fig. 3a), and Oplophorus sp. had the most 13 C enrichment.

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3.2. Impact of mesoscale features

No clear pattern emerged from δ^{13} C vs. δ^{15} N bi-plots of the 545 individuals categorized by broad category and by mesoscale feature (figures not shown). To investigate the structure of the data and assess the influence of eddies, we conducted univariate regression tree analyses (URT) on $\delta^{15} N$ and $\delta^{13} C$ values using cruise, broad category, mesoscale feature, taxon and body length as covariates. Five groups were identified by the URT based on $\delta^{15}N$ values (Fig. 4a). Groups were sorted in order of increasing $\delta^{15}N$ predicted values (Fig. 4b). The first splits of the pruned tree separated taxa: one group of low $\delta^{15}N$ values clustered gelatinous organisms (except siphonophorans), small fishes and one crustacean (Funchalia spp.); the other group put together deep migrating mesopelagic organisms (11 fish taxa and the crustacean *Oplophorus typus*) with rather high $\delta^{15}N$ values. A further split separated cyclonic eddies from the four other classes (anticyclones, divergences, fronts and shelf stations). The non cyclonic group mixed taxa from the four broad categories. The "cyclonic" branch of the pruned tree separated two groups (Fig. 4a and 4b): Cyclonic 1 grouped 22 individuals (14 fishes, three specimens of the crustacean Oplophorus sp. and five specimens of the squid *Cranchia scabra*) with intermediate $\delta^{15}N$ values (predicted value of 9.4%); Cyclonic 2 clustered six specimens of Cubiceps pauciradiatus (fish) and one Ornithoteuthis volatilis (squid) collected in the same cyclone sampled in November 2009 (cruise MC09B), with the highest δ^{15} N values (predicted value of 14.1%). Four groups were identified by the URT based on δ^{13} C values. Taxon was the only significant covariate used to develop the pruned tree (Fig. 5a and 5b). Group 2 clustered most of the micronekton taxa (Fig. 5a and 5b) with a predicted average of -18.7%. Group 3 classified taxa with the highest 13 C enrichment (predicted δ^{13} C value of -18.2%). Leptocephali larvae were segregated owing to their low δ^{13} C values.

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3.3 Trophic levels and size

Since size is an important factor structuring trophic links, we looked at the potential relationships between body length and $\delta^{15}N$ values. However we were limited by sample sizes and body length ranges, and size effect was tested for ten taxa only (Table 1). The fishes Bramidae, Cubiceps pauciradiatus, Thunnus spp. and the squid Sthenoteuthis oualaniensis showed a significant body length effect (Fig. 6 and Table 2). One outlier for S. oualaniensis was removed from the linear regression (Fig. 6b). Fig. 6c reveals that a simple model was not appropriate for C. pauciradiatus: the six individuals sampled in the cyclone of November 2009 were cut off from the other individuals. The final model did not select two separate linear regressions. The most parsimonious model retained parallel regressions (same estimated slope) and different intercepts (Table 2). Estimated TLs within the micronekton consumers of Mozambique Channel ranged from 2.2 (leptocephali larvae) to 4.2 (the fish D. metopoclampus), encompassing theoretically two trophic levels (Table 1). Of course, estimated TLs exhibited the same patterns as $\delta^{\rm 15} N$ values because the only unknown in equation (2) was the nitrogen isotopic composition of micronekton taxa. The three squid species shared the same TL (3.3 to 3.4), and the deep migrating mesopelagic fishes and the crustacean O. typus had the highest TLs.

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4. DISCUSSION

To our knowledge this study is the first that investigates the potential impact of mesoscale eddies on the isotopic signatures of a large assemblage of micronekton from gelatinous organisms to fish. An extensive investigation conducted on two counter-rotating eddies off Western Australia analyzed mainly the impact of eddies on the isotopic composition of dissolved inorganic nitrogen, particulate organic matter and mesozooplankton (Waite et al., 2007). Fish larvae identified at the family level were also collected with small nets, allowing the analysis of eel leptocephals and of small-sized specimens of Myctophidae, Sternoptychidae, Paralepididae, Phosichthyidae and Scorpaenidae only. The results of Waite et al. (2007) showed no significant difference in the $\delta^{15}N$ signature between the fish larvae from the two eddies, but myctophid larvae from the warm-core eddy (i.e., counter-clockwise rotational sense) are significantly enriched in ¹³C relative to those from the cold-core eddy (i.e., cyclonic rotation). In our study, the fish taxa sampled covered several main open-ocean micronekton fish families (juveniles and/or adults) found in the Mozambique Channel: Myctophidae, Nomeidae, Bramidae, Phosichthyidae, Sternoptychidae, Notosudidae, Gonostomatidae, Paralepididae, Bregmacerotidae and Carangidae. Our findings showed that mesoscale features did not have any clear impact on the carbon and nitrogen signatures of micronekton in the Mozambique Channel. The 32 taxa of crustaceans, squids and fishes encompassed a wide range of isotopic niches, with large overlaps among species. Regression trees evidenced patterns with clusters of organisms according to their $\delta^{15}N$ or $\delta^{13}C$ isotopic signatures. We attempt henceforward to examine some hypotheses supported by our results, taking into account the nature of our data and the stable isotope method.

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4.1 Isotopic patterns amongst mesoscale features

Eddies play a key role in biological processes of less-productive deep-sea ecosystems by converting physical energy into trophic energy (Bakun, 2006; Godø et al., 2012). They have been suggested to impact the distribution of marine organisms through bottom-up effects (Domokos, 2009; Domokos et al., 2007; Drazen et al., 2011; Muhling et al., 2007; Sabarros et al., 2009; Seki et al., 2002; Tew Kai and Marsac, 2010). On the one hand few individuals in our study had their $\delta^{15} N$ values directly impacted by mesoscale features which on the other hand did not influence the carbon signatures of the sampled organisms. Six specimens of the nomeid C. pauciradiatus and one O. volatilis (Ommastrephidae) were grouped by the regression tree based on their $\delta^{15}N$ values (*Cyclonic 2*, Fig. 4). These specimens were collected in the same cyclone sampled in November 2009 during the MC09B cruise, and had distinctly higher $\delta^{15} N$ signatures than their congeners sampled in other mesoscale features. Surprisingly, specimens from other species or taxa (leptocephali larvae, the squid Cranchia scabra, the crustacean Funchalia spp., and the fishes Argyropelecus aculeatus, Hygophum hygomii and Vinciguerria nimbaria) collected in the same cyclone did not show a similar pattern. Their $\delta^{15}N$ signatures did not differ significantly from specimens collected in other features (all KW test had a p-value much greater than 10%). This singular pattern could suggest possible residency for the nomeid *C. pauciradiatus* into the eddy, while other species or taxa could move among the water masses. Lamkin (1997) showed indeed that adult spawning grounds and larval habitat of C. pauciradiatus can be tied to frontal systems along eddy rings in the Gulf of Mexico. Mesoscale features impacted the nitrogen signatures of Thunnus spp. only, with higher $\delta^{15}N$ signatures within anticyclones (KW test, H=15.0, P<0.001). Two extra individuals sampled in the same cyclone could have been added to the Cyclonic 2 group: one Decapterus sp. which had the highest $\delta^{15}N$ value (16.6%) and one Lobianchia gemellarii ($\delta^{15}N = 12.4\%$). In cyclonic eddies, vertical fluxes of nitrate can

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dominate production leading to higher δ^{15} N signatures of the phytoplankton compared with an anticyclonic eddy, where nitrate supply to the surface could be physically limited (Bakun, 2006; McGillicuddy Jr and Robinson, 1997; Muhling et al., 2007; Waite et al., 2007). To impact the isotopic signature of pelagic consumers such as micronekton organisms, one should assume that this isotopic baseline is incorporated and conserved through several trophic levels trapped in the water mass of the cyclonic eddy. However this hypothesis is challenged by the ecology and behaviour of micronekton organisms.

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The vast majority of micronekton organisms typically occurs in the surface layer during the night and migrates below 400m depth during the day (Behagle et al., this issue). Micronekton ascents and descents during the crepuscular periods (dawn and dusk) characterize this process of diel vertical migration (Benoit-Bird et al., 2009). In the Humboldt Current system, the vertical extent of the water mass trapped in eddies has been recently estimated to 240m and 530m in cyclonic and anticyclonic eddies respectively, with a global decrease of the physical gradients with depth (Chaigneau et al., 2011). These estimates are most likely variable from eddy to eddy and from one area to another. In eddies of the Mozambique Channel, swirl velocities are weaker in deeper layers than they are at the surface (Ternon et al., this issue). In addition, Kolasinski et al. (2012) showed that physicochemical characteristics of deep waters (including carbon and nitrogen isotopic values of POM) from cyclonic and anti-cyclonic eddy of the Mozambique Channel were alike. Consequently, the diel vertical migration causes micronekton to stay half of the time in water masses weakly impacted by eddies. Contrary to the study of Godø et al. (2012) in the Norwegian Sea, we believe that horizontal structure is not preserved during diel vertical migration in the Mozambique Channel: migration did not take place in accordance with the

water mass trapped in eddies. In addition, eddies are translated rather slowly in the Mozambique Channel (5.2cm.s⁻¹; (de Ruijter et al., 2002) while the average speed of a mesopelagic fish was measured acoustically to be about 30cm.s⁻¹ (Torgersen and Kaartvedt, 2001). Therefore, fish and most likely squids would still have the ability to swim across eddies at any depth. However very few studies investigated how crustaceans swim. Morris et al. (1985) analyzed the swimming in a small calanoid copepod (*Pleuromamma xiphias*, 6mm): they estimated maximal velocities to be 0.3m.s⁻¹ during the power strokes of an entire swimming cycle, and less than 0.1m.s⁻¹ during the recovery strokes. The total lengths of the three crustacean taxa in our study are at least five times the size of *P. xiphias* and maximal swimming velocity scales with body length. We thus believe that micronekton is rarely trapped in the water mass of a particular eddy and thus does not necessarily feed on concentrations of zooplankton prey found in the eddy only.

Isotopic incorporation in animal tissues is linked to turnover rates that vary according to tissue, body size, growth or taxon (Martínez del Rio et al., 2009). The dynamics of isotopic incorporation can then blur the interpretation of our field isotopic measurements. Indeed, a sampled micronekton specimen that had recently moved into an eddy from surrounding waters may have had a previous δ^{15} N or δ^{13} C signature that would have been gradually modified as they fed on new food sources trapped in the eddy. Depending on tissue-specific isotopic turnover, stable isotope measurements reflect average dietary records over days (e.g., whole fish larvae; Herzka and Holt, 2000) to years (e.g., elasmobranch muscle; MacNeil et al., 2006; Logan and Lutcavage, 2010). No clear studies estimated isotopic turnovers for micronekton but several weeks seem a reasonable order of magnitude. Consequently, the

particular isotope baseline of an eddy is likely not conserved through these pelagic consumers.

However, migration can be a multifaceted and plastic response of micronekton. Partial diel vertical migration has been reported in the literature, showing that resident and migrant strategies can co-exist in some populations (Mehner and Kasprzak, 2011; Olsson et al., 2006). In addition several taxa in our data were clearly epipelagic (leptocephali larvae, *Salpa maxima*, *Thunnus* sp., *Decapterus* sp.). Notwithstanding their swimming abilities and assuming a passive transport, all these species would then be more sensitive to eddy structure. If trapped in the water mass of the eddy, they can prey on local concentrations of zooplankton propagating the baseline of the "eddy" isotopic signature. This scenario might be true for the specimens of the grouping *Cyclonic 2*.

4.2 Carbon isotope patterns

There was no significant difference in δ^{13} C signatures of micronekton between mesoscale features. The δ^{13} C values ranged from -20.6 to -17.3% suggesting that micronekton organisms sampled exploit different sources of primary production, giving rise to different trophic pathways. However, most of δ^{13} C mean values encompassed a narrow range between -19 and -18% (all squids, 19 fish taxa, two crustacean genera, Fig. 4b). Only gelatinous organisms and three fishes (*Psenes* spp., *Diaphus metopoclampus* and *Pterycombus petersii*) were depleted in 13 C compared with the other taxa. Leptocephali larvae which could feed on detritical materials and fecal pellets (Lecomte-Finiger et al., 2004) had the most 13 C-depleted carbon signature with a large variance of δ^{13} C values too. Surprisingly, our δ^{13} C values were intermediate between standard offshore pelagic

signatures and nearshore signatures measured in this region (Hill et al., 2006; Kolasinski et al., 2012), suggesting that pelagic production in the Mozambique Channel could be partly supported by the transport and export of inorganic and organic particles from the Mozambican coast toward offshore area, through the "vacuum-cleaner effect" due to rotational dynamics of eddies (Tew-Kai and Marsac, 2009).

4.3 Trophic levels of micronekton

Micronekton form a key trophic link between top predators and zooplankton (Brodeur and Yamamura, 2005), and are theoretically assumed to constitute the tertiary level of pelagic food webs. The lowest trophic level except salps was occupied by leptocephali larvae (TL = 2.2), and TLs less than 3.0 were estimated for the carnivorous heteropod *Carinaria lamarckii*, the penaeids *Funchalia* spp. and juveniles of three fish taxa (*Thunnus* spp., *Pterycombus petersii* and *Psenes* spp.). The remaining estimated TLs encompassed a continuum of values between 3.1 and 4.2, very close to those obtained by Cherel et al. (2010) and Stowasser et al. (2012) for myctophids in the Southern Ocean. Our results show that micronekton sampled can occupy relatively high trophic positions: the high TL of the myctophid *Diaphus metopoclampus* probably fits with a diet based on euphausiids or small fish larvae, and the high TL of the crustacean *Oplophorus typus* is explained by a diet strongly dominated by detritus (Karuppasamy and Menon, 2004), which are known to be ¹⁵N-enriched. However our organisms were preying upon a similar range of herbivorous and omnivorous consumers, mainly meso- or macrozooplankton.

Body size is known to play a crucial role in predator–prey interactions (Sheldon et al., 1977). Body length can influence δ^{15} N values (then TL) of one species because larger specimens can

catch larger prey as they grow (e.g. Parry, 2008). However intraspecific variation in δ^{15} N with body length was identified in three fish taxa and one squid species only (Fig. 6 and Table 2). For these taxa, the positive significant relationships may be indicative of larger specimens feeding at higher trophic levels. We probably cannot conclude for the other taxa as pelagic trawls used for sampling micronekton selected limited size ranges for each species (Table 1). Interestingly, a model with two intercepts and one slope was fitted to the data of the fish *Cubiceps pauciradiatus*. The common slope may be indicative of consistent ontogenetic variability (i.e. a similar intraspecific variation), while different intercepts can result from a shift in habitat use (i.e., δ^{15} N values impacted by a baseline change in a cyclonic eddy). Furthermore the linear relationship between TL and body length means of taxa was not significant ($F_{1,28} = 1.95$, P = 0.17 for 30 taxa), showing that the structuring effect of size was not depicted in our data with regard to the range of the body length averages (Table 1). Leptocephali larvae were indeed an outlier in the dataset (very low TL associated with high body length) and salps were unfortunately not measured onboard.

But the interpretation of trophic level estimated from $\delta^{15}N$ values presents caveats. Isotopic baseline can vary from year to year and can be conserved through several trophic levels. Three salp samples were collected in December 2008 (MC08A) and one in November 2009 (MC09B) only, preventing statistical comparison. However $\delta^{15}N$ values were very close and year effect (a confounding variable with the cruise factor which was one covariate in the regression tree) was never significant. In addition sources of variation of the discrimination factor are numerous (Martinez del Rio et al., 2009). These biases in isotopic TL calculation can alter our estimates. In addition, the basic biology and ecology of micronekton

(ontogenetic migration, feeding habits) remain poorly known, making interpretation difficult.

4.4. Limitations of the data

The spatial and temporal resolutions of our isotope data are limited by the sampling coverage of the pelagic trawls that were carried out during two cruises. The two surveys did not sample the same patterns of mesoscale eddies. In 2009 (MC09B), mesoscale features were very stable and well established compared to 2008 (MC08A), where eddies were in their early phases (Ternon et al., this issue). Contrary to Waite et al. (2007) who investigated extensively the same dipole in one area, we sampled mesoscale features at different maturation phases. Eddies are characterized by their dimension, intensity (e.g., sea surface height, geostrophic and rotational velocities), lifetime, origin, trajectory, and propagation distance (Bakun, 2006; Chelton et al., 2011). In addition eddies develop over time scales of weeks to months while biological responses such as diel vertical migration can occur within a day. All these eddy properties and development phases shape biological responses and then impact the stable isotope signatures of the organisms.

In summary, biogeochemical and biological responses to mesoscale dynamics along the food chain up to mid-trophic levels such as micronekton are variable and the underlying mechanisms are complex to disentangle. The stable isotope method, based on time-integrated assimilated food, allowed us to better depict the trophic relationships in this micronekton assemblage. Some species had distinct isotopic niches, but others showed strong overlap. In addition isotopic differences attributed to mesoscale dynamics were evidenced for individuals of the same species. Thus the variations in stable isotope values in

our data reflect a complex set of embedded processes linked to physical mesoscale dynamics and basic biology and ecology of micronektonic organisms (e.g. vertical habitat, migration pattern, dietary habits and body length).

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Table 1. Body lengths and ranges (standard length for fishes, dorsal mantle length for squids, cephalothorax length for crustaceans, total length for gelatinous organisms; in mm), δ^{13} C and δ^{15} N values (per mil), C/N ratios, and estimated trophic levels of micronekton from the Mozambique Channel. Species or taxa are placed in broad class. Total number n and numbers per Anticyclone, Cyclone, Divergence, Front, and Shelf are indicated. Values are mean \pm standard deviation. * indicates taxon for which body length effect was tested.

Table 2. Linear regression models fitted to $\delta^{15}N$ values (per mil) and body length (SL: standard length in mm; DML: dorsal mantle length in mm) of four taxa of micronekton from the Mozambique Channel. Models fitted to the squid *Ornithoteuthis volatilis*, and for the fish taxa *Decapterus* sp., *Lestrolepis intermedia*, *Myctophum spinosum*, *Psenes* spp. and *Symbolophorus evermanni* were not significant. Sample sizes and body length ranges precluded model fitting for the remaining taxa.

Broad class	Species	Phase	n	Body length mean (mm)	Body length range (mm)	$\delta^{13}\text{C}$	$\delta^{15} \text{N}$	C/N	TL	Anticyclone	Cyclone	Divergence	Front	Shelf
	Carinaria lamarckii	adults	5	33.0	30-40	-19.7 ± 0.28	7.4 ± 0.61	3.4 ± 0.19	2.7 ± 0.2		5			
	Leptocephali larvae	larvae	10	217.6	170-260	-20.6 ± 0.57	5.8 ± 1.55	4.2 ± 0.37	2.2 ± 0.5		5			5
	Salpa maxima	solitary zooid	5	-	-	-19.4 ± 0.38	5.2 ± 0.11	4.1 ± 0.21	2				1	4
	Siphonophora		5	42.3	40-45	-19.3 ± 0.47	8.5 ± 0.63	3.2 ± 0.11	3.1 ± 0.2	3				2
Squids	Cranchia scabra	juveniles	9	40.1	35-47.1	-18.6 ± 0.49	9.4 ± 0.44	3.1 ± 0.21	3.3 ± 0.1	4	5			
	Ornithoteuthis volatilis*	juveniles & adults	18	102.3	63.8-179	-18.5 ± 0.4	9.5 ± 0.8	3.1 ± 0.07	3.4 ± 0.2		1	7	5	5
	Sthenoteuthis oualaniensis*	juveniles & adults	77	92.8	21.7-360	-18.2 ± 0.35	9.4 ± 0.77	3.1 ± 0.08	3.3 ± 0.2	19		38	14	6
Crustaceans	Funchalia spp.	adults	22	16.4	13.8-18.4	-18.6 ± 0.27	7.8 ± 0.8	3 ± 0.07	2.8 ± 0.3		8	3	7	4
	Oplophorus sp.	adults	8	13.0	12.7-13.5	-17.3 ± 0.24	9.3 ± 0.94	3 ± 0.04	3.3 ± 0.3		3		5	
	Oplophorus typus	adults	10	13.0	11.6-14.4	-18.1 ± 0.38	10.2 ± 0.32	3.3 ± 0.15	3.6 ± 0.1	5		5		
Fishes	Argyropelecus aculeatus	adults	23	56.8	42-77	-18.5 ± 0.46	10.5 ± 0.88	3.1 ± 0.08	3.7 ± 0.3		3	10	10	
	Bramidae*	juveniles	6	82.2	43-152	-18.9 ± 0.61	9.2 ± 0.86	3.1 ± 0.03	3.3 ± 0.3		2	3	1	
	Bregmaceros macclellandii	adults	5	77.6	71-82	-18.6 ± 0.15	10.9 ± 0.44	3.1 ± 0.02	3.8 ± 0.1				5	
	Ceratoscopelus warmingii	adults	5	59.6	53-65	-18.9 ± 0.26	9.4 ± 0.57	3.1 ± 0.02	3.3 ± 0.2	5				
	Cubiceps pauciradiatus*	juveniles & adults	55	98.1	23-140	-18.2 ± 0.4	9 ± 2.23	3.1 ± 0.06	3.2 ± 0.7		6	37	7	5
	Decapterus sp.*	juveniles	13	83.1	35-116	-18.5 ± 0.23	9.2 ± 2.23	3.1 ± 0.07	3.3 ± 0.7		10		3	
	Diaphus garmani	adults	5	56.2	40-75	-18.4 ± 0.35	10.4 ± 0.94	3.3 ± 0.03	3.7 ± 0.3				5	
	Diaphus metopoclampus	adults	6	57.7	54-62	-19.3 ± 0.19	12.1 ± 0.44	3.3 ± 0.04	4.2 ± 0.1			5	1	
	Diaphus richardsoni	adults	39	47.0	36-59	-18.9 ± 0.23	10.8 ± 0.52	3.2 ± 0.1	3.8 ± 0.2	5			14	20
	Diaphus spp.	adults	16	62.7	50-80	-18.5 ± 0.29	10.5 ± 0.62	3.1 ± 0.04	3.7 ± 0.2	5			5	6
	Gonostoma elongatum	juveniles & adults	5	108.8	96-120	-18.9 ± 0.12	9.7 ± 0.39	3 ± 0.02	3.4 ± 0.1			5		
	Gymnoscopelus sp.	adults	5	68.6	60-76	-18.6 ± 0.19	10.2 ± 0.38	3.1 ± 0.02	3.6 ± 0.1				5	
	Hygophum hygomii	adults	15	52.1	37.3-62	-18.8 ± 0.2	9.9 ± 0.66	3.1 ± 0.02	3.5 ± 0.2	5	5	1	4	
	Lestrolepis intermedia*	juveniles & adults	17	127.1	75-171	-18.8 ± 0.48	9.7 ± 0.83	3.2 ± 0.09	3.4 ± 0.3		2	4	3	8
	Lobianchia gemellarii	adults	5	50.0	45-70	-18.4 ± 0.18	11.1 ± 0.73	3.1 ± 0.01	3.9 ± 0.2		1			4
	Myctophum spinosum*	juveniles & adults	33	65.7	40-86	-18.8 ± 0.24	8.9 ± 0.38	3.2 ± 0.05	3.2 ± 0.1	2		16	10	5
	Psenes spp.*	juveniles	8	47.4	36-76	-19.2 ± 0.65	7.6 ± 0.34	3.2 ± 0.24	2.8 ± 0.1	2	6			
	Pterycombus petersii	juveniles	5	58.2	35-77	-19.6 ± 0.2	8.2 ± 0.66	3 ± 0.03	2.9 ± 0.2		3	2		
	Scopelosaurus hoedti	adults	6	123.7	112-126	-18.9 ± 0.04	11.4 ± 0.33	3.1 ± 0.01	3.9 ± 0.1		1			5
	Symbolophorus evermanni*	adults	57	77.4	42-108	-18.6 ± 0.24	9.3 ± 0.69	3.2 ± 0.07	3.3 ± 0.2	5		30	12	10
	Thunnus spp.*	juveniles	33	43.0	23-84	-18.3 ± 0.51	7 ± 0.8	3.1 ± 0.06	2.6 ± 0.2	8	6	16		3
	Vinciquerria nimbaria	adults	14	39.9	32-46	-18.8 ± 0.29	10 ± 0.43	3.1 ± 0.03	3.5 ± 0.1		5	5	4	

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Taxon	Regression equation	r² (%)	р	n
Bramidae	δ^{15} N = 7.77 + 0.0179 x SL	87.4	0.006	6
Thunnus spp.	δ^{15} N = 6.05 + 0.0226 x SL	19.9	0.01	33
Sthenoteuthis oualaniensis	δ^{15} N = 8.27 + 0.0122 x DML	46.4	< 0.0001	76
Cubiceps pauciradiatus (not Cyclone)	δ^{15} N = 6.04 + 0.0242 x SL	90.24	< 0.0001	6
Cubiceps pauciradiatus (Cyclone)	δ^{15} N = 11.80 + 0.0242 x SL	90.24	< 0.0001	49

Fig. 1. Map showing the 34 sampling stations carried out in 2008 (cruise MC08) and 2009 (cruise MC09B) in the Mozambique Channel. Stations are categorized according to mesoscale features (no cyclone was sampled in MC08A).

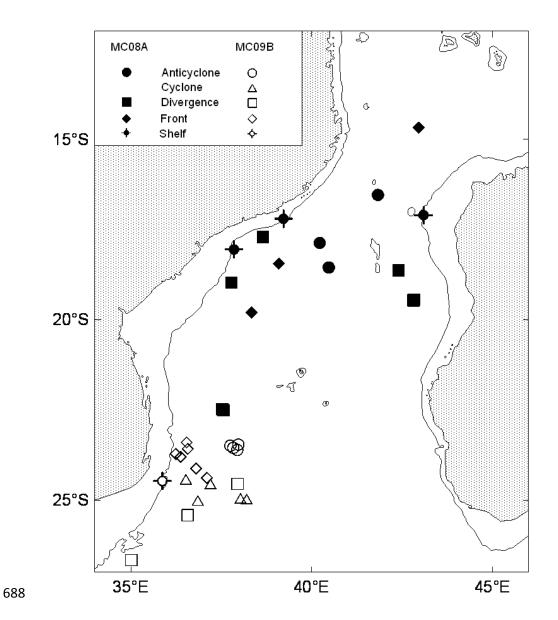
Fig. 2. Summary of δ^{13} C and δ^{15} N isotope signatures (mean \pm standard deviation in per mil) of micronekton taxa sampled in the Mozambique Channel. Set diagrams group the four broad categories (fishes, squids, crustaceans and gelatinous organisms).

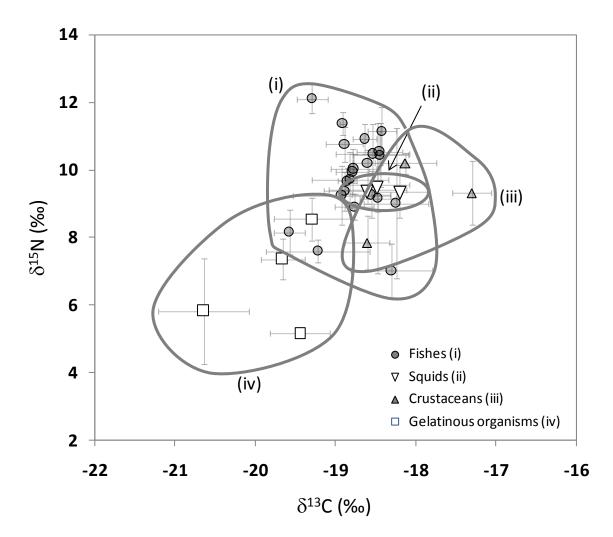
Fig. 3. $\delta^{15}N$ (a) and $\delta^{13}C$ (b) isotope signatures (mean \pm standard deviation in per mil) of micronekton taxa sampled in the Mozambique Channel. Taxa are placed in broad class and then isotope signatures of both nitrogen and carbon are sorted in order of decreasing depletion.

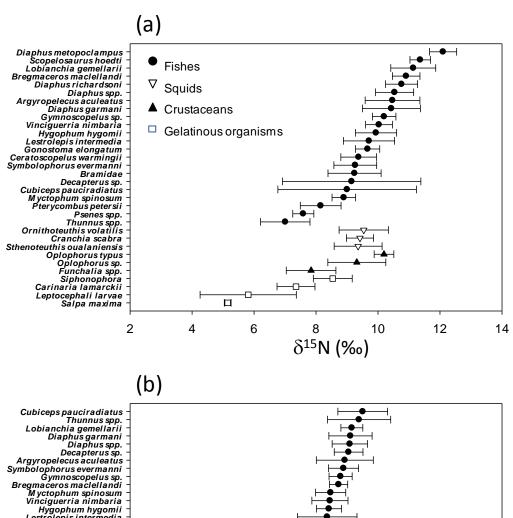
Fig. 4. Pruned regression tree that predicts the $\delta^{15}N$ signatures of five groups of micronekton organisms. Each terminal node is characterized by $\delta^{15}N$ value (per mil), number of individuals, corresponding taxa and mesoscale feature (A – Anticyclonic, C – Cyclonic, D – Divergence, F – Frontal, S – Shelf). Covariates used to develop the tree are taxon and mesoscale features.

Fig. 5. Pruned regression tree that predicts the $\delta^{13}C$ signatures of four groups of micronekton organisms. Each terminal node is characterized by $\delta^{13}C$ value (per mil), number of individuals, corresponding taxa and mesoscale feature (A – Anticyclonic, C – Cyclonic, D – Divergence, F – Frontal, S – Shelf). Covariate used to develop the tree is taxon.

Fig. 6. δ^{15} N values (per mil) from (a) Bramidae (b) *Sthenoteuthis oualaniensis* (c) *Cubiceps pauciradiatus* (d) *Thunnus* spp. plotted versus body length (standard length in mm for (a), (c) and (d); dorsal mantle length in mm for (b)). Simple linear regressions for δ^{15} N values versus body length are plotted (see text and Table 2).







Cubiceps pauciradiatus
Thunnus spp.
Lobianchia gemellarii
Diaphus garmani
Diaphus spp.
Decapterus sp.
Argyropelecus aculeatus
Symbolophorus evermanni
Gymoscopelus sp.
Bregmaceros maciellandi
Myctophum spinosum
Vinciguerria nimbaria
Hygophum hygomii
Lestrolepis intermedia
Gonostoma elongatum
Ceratoscopelus warmingii
Diaphus richardsoni
Scopelosarus hoedti
Bramidae
Psenes spp.
Diaphus netopoclampus
Pterycombus petersii
Sthenoteuthis oulainiensis
Ornithoteuthis volatilis
Cranchia sabra
Oplophorus typus
Funchalia spp.
Siphonophora
Salpa maxima
Carinaria lamarckii
Leptocephali larvae

-22 -21 -20 -19 -18 -17 -16

