INTRODUCTION

There is increasing evidence that small-scale turbulence plays an important role in the plankton community (Marrasé et al., 1997 and references therein). Numerous examples can be found at both physiological and ecological levels. Physiological processes depend on the implications of the shear forces for the transport of molecules in and out of the organisms (e.g. Pahlow et al., 1997) and the structural vulnerability of cells and colonies (e.g. Berdalet and Estrada, 1993). The influence of small-scale turbulence on the behaviour of the organisms (e.g. Karp-Boss et al., 2000), encounter rates (e.g. Yamazaki et...
and formation of microzones (e.g. Squires and Yamazaki, 1995) may also cause indirect effects on ecological interactions, especially predator-prey interactions (Peters et al., 2002).

Any flow of matter or energy through a pelagic ecosystem leaves its imprint on the structure of the plankton community (Rodríguez, 1994). Turbulent kinetic energy (TKE) represents a relevant input of auxiliary energy in the pelagic ecosystem. However, the diversity of processes directly or indirectly related to TKE hampers assessing the overall effect of this factor on the whole community. As there is a strong dependence of TKE effects on the body size of organisms (Lazier and Mann, 1989; Karp-Boss et al., 1996), we suggest the biomass-size spectrum as a tool for undertaking this task. Biomass-size spectra are the result of the combination of physiological (growth, respiration, etc.) and ecological (predation, competence, etc.) scales (Kerr and Dickie, 2001). Using recent approaches, the size spectra and derived parameters also allow the thermodynamic (growth, respiration, etc.) and ecological (predation, etc.) scales (Kerr and Dickie, 2001; Cózar et al., 2003) analysis of the community. Linear size spectra result from a steady state in which predator-prey interactions generate a balanced flow of energy. From this state, fluctuations in energy inflow are accommodated by the size structure in order to accumulate the available free energy (e.g. TKE). The present work aims to characterise the turbulence effect along the plankton size spectrum using a comparative analysis of a natural community exposed to two different TKE levels.

MATERIAL AND METHODS

Artificial phytoplankton blooms were generated in two microcosms (area = 25 x 50 cm², depth = 30 cm) at two well-differentiated TKE levels: a low turbulence microcosm (LTM) and a high turbulence microcosm (HTM). Firstly, each enclosure was filled with 22.5 L of 0.7 µm-filtered seawater. This medium was enriched with nitrate (64 mmols), phosphate (9 mmols), silicate (2 mmols), micronutrients and vitamins (1-70 nmols). The N:P ratio of the addition was 7.3 (N-deficient). Then, each microcosm was completed with 2.5 L of natural seawater from the NW sector of the Alboran Sea, 30 miles offshore from Estepona. This area is characterised by frequent upwelling events.

Microcosms were kept at 18°C and received a constant light intensity of 40 µE m⁻²s⁻¹. Small-scale turbulence was generated through air bubbling. A fraction of the drag force of creeping flow around the bubbles is transformed into TKE. The turbulence dissipation rates were estimated according to Tatterson (1991). The air fluxes were 5 ml min⁻¹ in LTM and 500 ml min⁻¹ in HTM. Therefore, the turbulence dissipation rates were 10⁻³ W m⁻³ in LTM and 10⁻¹ W m⁻³ in HTM. Both values correspond to TKE levels which would be relatively high in the ocean. The turbulence level applied in HTM could be considered an extreme level. It has been measured near the surface and in the zone of breaking waves (Johnson et al., 1994; Terray et al., 1996).

The development of the plankton blooms was monitored for 17 days. Water samples were collected every 2-3 days from an intermediate depth (15 cm from the bottom) and just on the bottom. Subsamples were used to estimate chlorophyll-a concentrations (chl-a) using a Turner Designs-10 fluorometer (calibrated with pure chl a, Sigma Co) following UNESCO (1994). Picoplankton sub-samples were fixed with glutaraldehyde (2% v/v) and nano- and microplankton sub-samples with lugol (1.5% v/v). Mesoplankton was absent during the experiment.

Two complementary microscopic techniques were employed to analyse the plankton samples (pico-, nano- and microplankton). Picoplankton was counted by epifluorescence microscopy (Leitz Laborloux microscope) with DAPI staining following Porter and Feig (1980). The organisms were measured at 1000x magnification using image analysis software (NIH Image). Biovolumes were calculated from geometric formulae with the best fit to cell shape. A morphological classification of the organisms was performed in this size range. Nano- and microplankton samples were processed with inverted microscopy at magnifications of 250x, 600x and 1000x (Utermöhl, 1958). The organisms were measured with a semiautomatic image analysis system (Analytical Measuring Systems, VIDS V). Biovolumes were also calculated through geometric formulae. Taxonomic classifications were performed in these size ranges. The criterion adopted for scanning with both microscopic techniques was to measure more than 400 cells in each sample in order to keep the counting error within ±10% (Lund, 1945).

To build the biomass-size spectra, the organisms were arranged in size classes with increasing widths following a geometric 2ⁿ series. With this partition, the amplitude of the size-class (∆w) coincides with
its lower limit \((w)\). The normalised biomass in each class \(\beta(w_i)\) can be calculated from biomass \(B\) as:

\[
\beta(w_i) = \frac{B(w_i, w + \Delta w)}{\Delta w}.
\]

When these data are plotted on a log-log axis, it is possible to obtain an overall parameterisation of the normalised biomass-size spectra \(NBSS\) as:

\[
\log \beta(w) = a + s \log w
\]

Comparative analyses of the plankton size structure in different systems are usually based on the parameters derived from the straight line fitted to \(NBSS\) (e.g. Kerr and Dickie, 2001; Rodríguez et al., 2001). The intercept \((a)\) expresses general abundance. The slope \((s)\) gives a synthetic view of the relationship between the abundance of smaller organisms and larger ones. The correlation coefficient \((R^2)\) of the regression can be used as a measurement of the total spectrum irregularity.

RESULTS

Dense blooms of phytoplankton were generated in both microcosms (Fig. 1). HTM showed higher total \(chl-a\) concentrations (mean 19 \(\mu g\) L\(^{-1}\)) than LTM (mean 15 \(\mu g\) L\(^{-1}\)). In the water column, the evolution of the blooms followed a classic pattern. Chlorophyll-\(a\) concentration increased exponentially, reaching 65 \(\mu g\) L\(^{-1}\) on Day 9 in LTM and 106 \(\mu g\) L\(^{-1}\) on Day 8 in HTM. Then, the blooms entered the senescent phase and \(chl-a\) decreased. The evolution of the \(chl-a\) in the bottom of LTM was coupled with the \(chl-a\) in the water column. In the bottom of HTM, the evolution of the \(chl-a\) was less variable.

Diatoms were the dominant planktonic group in both microcosms (Fig. 2). They were more abundant in HTM. Diatoms reached 2.4·10\(^7\) \(\mu m^3 mL^{-1}\) on Day 9 in LTM and 11.0·10\(^7\) \(\mu m^3 mL^{-1}\) on Day 7 in HTM. Motile plankton, however, showed a more favourable growth in LTM. Flagellates and ciliates reached 4.7·10\(^6\) \(\mu m^3 mL^{-1}\) on Day 9 in LTM and 3.0·10\(^6\) \(\mu m^3 mL^{-1}\) on Day 14 in HTM. Bacterial blooms
in both treatments showed a similar evolution. Biomass increased exponentially when the phytoplankton concentrations decreased, reaching a maximum on Day 14 (1.16 \(10^6\) \(\mu m^3\) mL\(^{-1}\) in LTM and 1.10 \(10^6\) \(\mu m^3\) mL\(^{-1}\) in HTM).

A description of the main taxonomic and morphological groups classified in the enclosures is shown in Table 1. Diatoms were mainly represented by *Thalassiosira*, *Skeletonema*, *Chaetoceros* and *Lauderia*. *Thalassiosira* spp. was the dominant genus (> 70% of diatom biovolume in both microcosms). The dominant species were *T. cf. hyalina* and *T. cf. allenii*. A co-dominance of these two species was observed in LTM, while *T. cf. allenii* was practically absent in HTM. These species show well-differentiated body sizes. *T. cf. hyalina* had a mean cellular diameter of 26 \(\mu m\) (varying from 16 to 43 \(\mu m\)) while *T. cf. allenii* had a mean diameter of 11 \(\mu m\) (from 6 to 19 \(\mu m\)). A different species composition linked to different size distributions was also found within *Chaetoceros* and *Lauderia*. Nanoflagellates were classified at the level of taxonomic class. Prymnesiophyceae, Cryptophyceae, Prasinophyceae and Dictyochophyceae were present in the microcosms. The Prymnesiales and Isochrysidales orders (Prymnesiophyceae Class) were also differentiated due to their alternate occurrences and the evident morphological dissimilarities (with and without haptonema respectively). Ciliates were also found in both microcosms, although they only rep-

| TABLE 1. – Characteristics of the main groups of plankton organisms identified in LTM (white strip) and HTM (grey strip). The percentage of biovolume in LTM is with respect to HTM. |
|-----------------|-----------------|-----------------|-----------------|-----------------|
|                | Size \((\mu m^3)\) | Biovolume \((10^5\mu m^3/mL)\) | Max | Day | % in LTM |
| Rods & Coci    | 0.09 ± 0.07     | 1.6 ± 14        | 52  |
| Bacteria        | 0.45 ± 0.18     | 0.3 ± 11        | 63  |
| aggregates      | 0.43 ± 0.17     | 0.1 ± 11        |     |
| Filaments       | 1.51 ± 1.13     | 9.6 ± 14        | 52  |
| Isochrysidales  | 8.6 ± 6.1       | 9.0 ± 4         | 46  |
| Cryptophyceae   | 22 ± 17         | 0.7 ± 7         | 36  |
| Prymnesiales    | 52 ± 35         | 3.2 ± 9         | 100 |
| Prasinophyceae  | 60 ± 34         | 10.9 ± 9        | 64  |
| Dictyochophyceae| 118 ± 87        | 28.7 ± 9        | 61  |
| Ciliates        | 146 ± 79        | 1.3 (1.0) ± 7 (14)| 44  |
| Pseudonitzschia | 83 ± 54         | 0.3 ± 9         | 33  |
| sp.             | 77 ± 49         | 0.5 ± 7         |     |
| Th. cf. allenii | 307 ± 222       | 48.9 ± 9        | 96  |
| Chaetoceros     | 537 ± 413       | 0.9 ± 9         | 2   |
| costatum        | 5975 ± 4705     | 68.4 ± 9        |     |
| Skeletonema     | 664 ± 606       | 25.1 ± 9        | 58  |
| costatum        | 860 ± 799       | 24.0 ± 7        |     |
| Guinardia sp.   | 837 ± 736       | 4.7 ± 7         | 67  |
| Lauderia spp.   | 784 ± 708       | 1.8 ± 11        |     |
| Th. cf. hyalina | 2459 ± 496      | 0.8 ± 11        | 1   |
|                | 23048 ± 10806   | 62.0 ± 11       |     |
|                | 6022 ± 3541     | 159 ± 9         | 8   |
|                | 6315 ± 3729     | 1020 ± 7        |     |
resented 5.1% of the total biovolume of motile plankton. The different groups of motile organisms showed a temporal coupling, appearing as a succession of biomass peaks: small phytoflagellates, ciliates, large flagellates and a second peak of ciliates (Table 2). Small phytoflagellates were composed of Isochrysidales. Large flagellates showed higher abundance and trophic diversity. They were mainly composed of Dictyochophyceae and Prasinophyceae. The succession described was observed in

<table>
<thead>
<tr>
<th>ESD (µm)</th>
<th>Swimming speed (µm s⁻¹)</th>
<th>Sedimentation speed (µm s⁻¹)</th>
<th>Sherwood numbers due to Swimming</th>
<th>Sedimentation</th>
<th>TKE in LTM</th>
<th>TKE in HTM</th>
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<td>1</td>
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both microcosms, although it was delayed 2-3 days in HTM. Bacterioplankton was composed of filamentous bacteria, free bacteria (rods and cocci) and bacterial aggregates. Filamentous bacteria were the dominant morphotype (> 85% of bacterial biovolume in both microcosms). Some cyanobacteria were also observed during the last days of the experiment.

A general view of the plankton dynamics is shown in Figure 3. On Day 2, small flagellates (Isochrysidales) began to grow in both treatments (Fig. 3A and 3B). On Day 4, small flagellates reached their maximum biovolume in LTM and large flagellates also began to grow in this microcosm. During the bloom phase (Fig. 3C and 3D), LTM contained a rich community of large flagellates (Dictochophyceae, Prasinophyceae) and small flagellates were practically absent. In HTM, this shift ended during the post-bloom. In both microcosms, Thalassiosira spp. reached their maximum mean cell size during the biomass peak. During the post-bloom (Fig. 3E and 3F), cells rapidly disappeared from the water column in LTM. In HTM, T. hyalina maintained a relatively high biomass until the end of the experiment.

The diameters of the dominant diatom species (Thalassiosira cf. hyalina, Skeletonema costatum) were significantly (P < 0.001) greater in HTM (Fig. 4). The length of the diatoms may increase greatly due to colony formation. However, colony-forming diatoms appeared mainly as single cells, especially Thalassiosira spp. The 23% (in biovolume) of Thalassiosira spp. was grouped in colonies in LTM and 1% in HTM. Thalassiosira formed few colonies, probably as a result of the relative fragility of the colonies. The longest colonies were formed by S. costatum. These colonies also reached the largest size during the biomass maximum and were significantly (P < 0.001) longer in LTM (Fig. 4). Diatom colonies seemed to be highly vulnerable to the levels of TKE studied. In the picoplankton, we did not found significant differences between the morphological characteristics (length and width) of rods and cocci or bacteria aggregates. Likewise, differences between the averaged lengths of filamentous bacteria or cyanobacteria were not observed.

The parameters derived from the NBSS linearisation were used to compare the community size structures (Fig. 5). The regression coefficient ($R^2$) was generally higher in LTM, indicating higher spectra regularity. Steeper slopes ($s$) were found in LTM, indicating dominance by small organisms. Temporally, slopes decreased during the bloom phase. A compilation of slopes of plankton size

![Figure 4](image1.png)

**Figure 4.** Length and width of Skeletonema costatum colonies during the bloom phase (Days 7, 9 and 11). Stars indicate the day of the biomass peak. Crossed bars show the standard errors.

![Figure 5](image2.png)

**Figure 5.** Temporal evolution of the lineal regression coefficient ($R^2$, B) and the slope ($s$, A) of the normalised biomass-size spectra. LTM (white points) and HTM (black points).
spectra in natural systems shows a range of variation from -1.34 to -0.62 (Choi et al., 1999). During the bloom phase, we observed extremely low slopes, especially in HTM ($s = -0.51$). These values could be related to the unusually high TKE and chl-a concentrations in the enclosures.

**DISCUSSION**

The different timing and magnitude of the phytoplankton response suggested a generally positive effect of the TKE on the growth of the organisms (Fig. 1). The higher spectra irregularity of HTM (lower $R^2$, Fig. 5A) can be interpreted as a stronger disturbance of the steady state resulting from higher inflow of matter in the community (e.g. Cózar et al., 2003). Both microcosms were equally enriched, but TKE seems to affect the matter flux transferred to the plankton community. Small-scale turbulence, such as swimming or sedimentation, diminishes the microzone of laminar shear (diffusive boundary layer) surrounding the cells, facilitating physical-chemical interchange with the fluid by advection. It is known from previous studies that the advection effect is stronger in larger organisms (Lazier and Mann, 1989; Karp-Boss et al., 1996). This study shows the predominance of large-sized organisms in a plankton community exposed to higher levels of TKE (less negative $s$, Fig. 5B). In LTM, small-sized organisms may benefit from the smaller surface to volume ratio (S/V), which favours nutrient uptake (Munk and Riley, 1952).

*Thalassiosira cf. hyaline* was the major species involved in changes in the community structure, composing the highest biomass accumulation along the spectra (Fig. 3). This species had the largest cell size of those in the microcosms. Only some colonies of *Lauderia sp.* in HTM were larger (Table 1). The potential diffusive nutrient supply is greater for solitary cells than for chains of similar volume or similar advective supply (Pahlow et al., 1997). The ability of diatoms to form colonies may result in an overall increase in the size of the organisms. Nevertheless, only chains with large spaces between cells (e.g. *Skeletonema sp.*, *Thalassiosira sp.*) can overcome this disadvantage, and may even obtain a higher nutrient supply than do solitary cells (Pahlow et al., 1997). However, the levels of TKE studied were enough to break this type of colonies (Fig. 4), and the large cells of *T. cf. hyaline* were the dominant morphotype. Schöne (1970) also reported the possibility of colony breaking for species such as *Skeletonema costatum*.

The influence of algal biomass on the observed changes in the plankton structure was considerable. Chlorophyll-$a$ explained 94% of the variability of spectrum slope (Fig. 6). The use of the slope represents a consistent parameterisation of the size structure of the whole community. Classical studies have conceptually related body size and biomass (Margalef, 1978). Small plankton characterises stagnant and oligotrophic waters, while larger cells dominate eutrophic and turbulent waters. The succession between large diatoms and nanoflagellates often occurs during the seasonal cycle (Kiørboe, 1993). Figure 6 shows the linkage between biomass and size structure over a shorter timescale. This linkage was common for both treatments. Thus, TKE had a combined effect on both biomass and size structure following a common pattern. This pattern was exponential and showed higher abundance of large-sized organisms with increasing biomass in the community. The rapid change in the size structure when $s$ values are in the interval (-1.2, -0.7) may be a result of the adaptability of the community to using the free energy (nutrients and TKE) available in the enclosures. Thermodynamically, the principle of least specific dissipation indicates that any system will tend towards a local minimum in the rate of energy dissipation per unit biomass so as to accumulate the maximum energy (Prigogine, 1955). Choi *et al.* (1999) showed that the possibility of modifying the energy dissipation rate in nature is restricted to the interval (-1.2, -0.7). Less negative slopes (abundant large-sized organisms) are related to communities with a lower energy dissipation rate, which reaches the min-
imum value when \( s = -0.7 \). In this study, we observed a positive correlation between biomass and size but high increases in biomass did not significantly modify the size structure beyond \( s = -0.7 \). On the other hand, rapid changes in community structure associated with fluctuations in energy influxes are thermodynamically unsteady and the energy excesses (located in biomass accumulations along the spectra) are rapidly relaxed (Kerr and Dickie, 2001; Cózar et al., 2003). Slopes of both microcosms suddenly decreased when the availability of free energy diminished in the post-bloom (Fig. 5B).

Intra-specific variability in the body size of the main species contributed to maintaining the biomass-size linkage in the community (Fig. 4). At short time scales, the ontogenic adjustments of the population are particularly significant (Jiménez et al., 1987). Nevertheless, differences in taxonomic composition are also necessary to increase the variability of the size structure. The most relevant example was the absence of *T. cf. allenii* in HTM. The average cellular diameter of this species was 58% smaller than *T. cf. hyalina*. The development of swimming capacity was also different and cellular motility was a more common strategy in LTM. Likewise, flagellates and ciliates grew rapidly in this enclosure.

Evidence of the influence of TKE on bacterial uptake remains less clear (Logan and Kirchman, 1991). Differences between the averaged lengths of filamentous bacteria were not found with the TKE levels compared. Nevertheless, the maximum size of filamentous bacteria was different in the two enclosures. Indirect effects of turbulence on bacterial abundance have been related to the influence of TKE on the coupled food web (Peters et al., 2002). In each microcosm, the maximum bacterial size coincided with the respective biomass peaks of proto-zooplankton (flagellates and ciliates). Concepts such as size thresholds for predation are essential for explaining these results (Jürgens et al., 1999; Prieto et al., 2002). There is a size range affected by predation, the smaller and larger cell sizes appearing to be a refuge. Alterations of the prey size distribution may be expected as result of trophic relations (Benoit and Rochet, 2004). We found a significant correlation between the average size of potential prey and the biomass of the potential predators (Fig. 7). A common pattern of predator-prey interaction was observed for both microcosms. However, the different temporal evolution of the predators resulted in small temporary differences in the bacteria size distribution.

Assessing the influence of turbulence along the planktonic size spectra

By comparing the size spectra of both microcosms, an assessment of the TKE effects along the plankton size spectrum can be made. The similarity or divergence of the spectra would indicate a lower or higher influence of TKE on the different size classes. Due to the wide range of biomass values along the spectrum, we quantified the differences of biomass in each size class through a logarithmic subtraction: \( \log \left( \frac{B_{\text{HTM}}}{B_{\text{LTM}}} \right) \). Three planktonic size intervals were identified: picoplankton, small nanoplankton and diatoms (Fig. 8).

Picoplankton was mainly represented by the bacterioplankton. In the ocean, picoplankton abundance tends to be constant regardless of the temperature, salinity or nutrient concentrations (Fogg, 1986). Figure 8 also seems to support constancy in relation to TKE. This interval showed the smallest differences between the spectra of LTM and HTM.

Small nanoplankton was mainly composed of flagellates. The slight difference in the spectra of the two treatments does not show a clear relation of the biomass to the TKE level or body size. The influence of TKE on the transport of substances in and out of the motile organisms seems to be highly variable. Flagellates and ciliates often use swimming or self-generated currents to increase the encounter rate with prey. The prey perception may be harmed in most flagellates, especially among predators perceiving the prey in a chemical or mechanical way (Kistørboe, 1997). However, helioflagellates such as...
Dyctochophyceae (the dominant motile group) are stationary when feeding. These organisms depend on the prey motility and small-scale turbulence to find prey (Shimeta and Jumars, 1991). The prey are caught when they touch a sticky pseudopod. Other examples even show a reduction in the assimilation of inorganic nutrients as a result of TKE effects (Karp-Boss et al., 1996). This complexity, together with the diversity of flagellates composing the nanoplankton range, could explain the variable influence of TKE on this size interval.

The diatom interval showed the clearest differences between the two microcosms. Arin et al. (2002) showed that the relative contribution of diatoms to phytoplankton biomass increases in turbulent environments. We found a divergence of the spectra as size increased in the diatom interval. The highest difference between the two spectra (or the highest influence of TKE) was observed during the post-bloom. This result is probably related to the importance of nutrient availability on the magnitude of the TKE effects (Arin et al., 2002). Advective or diffusive transport supplies nutrients in the vicinity of the cell. However, when the environmental nutrient concentrations are high, phytoplankton cannot completely absorb all the nutrients that diffusion and advection are able to supply. During the post-bloom, when nutrients are exhausted, the possible advantages of turbulent advection would be more significant.

The combined effects of small-scale turbulence and sedimentation would explain the divergence of the spectra of the two microcosms along the diatom size interval. The influence of small-scale turbulence in reducing the diffusive boundary layer around the organisms increases with body size (Lazier and Mann, 1989; Karp-Boss et al., 1996). On the other hand, a different plankton vertical distribution occurred in the two enclosures as a result of the large-scale turbulence. The mean proportion of chl-a in the bottom to total chl-a was 0.13 in HTM and 0.50 in LTM. The higher resuspension of large organisms in HTM involved large organisms in a rapid resuspension-sedimentation cycle. In the open ocean, similar mechanisms re-introduce large organisms into the euphotic zone (Rodríguez et al., 2001). The effect of sedimentation on the diffusive boundary layer is also positively related with size through Stokes’s law.

The Sherwood number ($Sh$) is the dimensionless relation between the rate of mass transport by advection and by diffusion in the cell (see Kisyboe, 1993). If the advective transport is zero, $Sh$ is 1. This parameter allows the theoretical size-based assessment of the different effects of sedimentation, swimming and TKE on the uptake kinetics (Table 2). Sedimentation and TKE have significant effects on the organisms larger than 10 µm because of the dramatic decrease in the diffusive transport with body size. The uptake by diffusion is inversely related to the square of size. Thus, an increase from 1 to 10 µm would cause a 100-fold decrease in the diffusive transport. The effect of the swimming...
capacity on nutrient uptake was, however, significant in small-sized organisms. The advantages of the swimmer capacity increase considerably with body size. The advantages offered by both sedimentation and TKE ($Sh = 1.11$ and $Sh = 1.21$ respectively) would not explain the absence of motile organisms larger than 10 $\mu$m. The effect of swimming would be more favourable ($Sh = 5.26$).

However, the survival strategy of the motile organisms shows a higher dependence on their motility and structural integrity. The behavioural changes or cellular damage caused by TKE (e.g. Berdalet and Estrada, 1993; Karp-Boss et al., 2000) could hamper the occurrence of large-sized swimmers. In the microcosms, the effect of the shear forces on the larger organisms has been demonstrated with the colonies breaking. Indeed, only small nanoplankton was able to use a strategy of “swimming” instead of “sedimentation and turbulence”.

The present study shows a progressive increase in TKE effects towards large non-motile organisms. Biomass-size spectra started diverging above 10 $\mu$m of ESD. This result agrees with the estimations of Lazier and Mann (1989). Using a one-order lower shear rate, these authors established 100 $\mu$m as the threshold at which TKE starts having significant effects. The physical dependence of the diffusive and advective transport on body size and the detrimental effects of TKE on large motile organisms suggest the existence of a typical pattern of TKE influence along the plankton size spectra. Nevertheless, future studies are necessary to test how repeatable these findings are.

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