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1 **Ultraphytoplankton community structure in subsurface waters along a North-South**
2 **Mediterranean transect**

3
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51 **Abstract**

52 The subsurface ultraphytoplanktonic (< 10 µm) community was assessed along a North-South round-
53 trip Mediterranean transect in the framework of the MERITE-HIPPOCAMPE cruise held on April -
54 May 2019. Along the transect, various additional variables were measured in subsurface waters (2-5
55 m depth): temperature, salinity, and nutrient concentrations. The subsurface ultraphytoplankton
56 community structure was resolved with a few kilometers' spatial resolution and 30-min temporal
57 resolution using an automated pulse shape recording flow cytometer. The subsurface waters were
58 clustered into seven areas based on their temperature and salinity characteristics. *Synechococcus* were
59 by far the most abundant in all prospected zones and nanoeukaryotes were the main biomass
60 contributors representing up to 51% of the ultraphytoplankton carbon biomass. A decreasing gradient
61 in the apparent net primary productivity (NPP) was observed along the transect from north to south,
62 with an NPP mostly sustained by *Synechococcus* in all zones. The results could have several
63 implications in the trophic transfer of contaminants in planktonic food webs as it highlights the
64 potential role of nanoplankton in bioaccumulation processes and that of *Synechococcus* in a likely
65 transfer *via* grazing activities.

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76 **1. Introduction**

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78 Phytoplankton, which represents only 0.2% of the global autotrophic biomass, is responsible for
79 roughly 50% of the net primary production on earth (i.e., 50 Pg C year⁻¹) (Falkowski et al., 1998; Field
80 et al., 1998; Chavez et al., 2011). To understand the exact role of phytoplankton in the biogeochemical
81 cycles, biological carbon pump (Siegenthaler and Sarmiento, 1993), and transfer of energy and matter
82 within the trophic web (Sakka-Hlailli et al., 2014), its characterization in terms of size spectrum,
83 communities/species and their relative production is essential at appropriate spatiotemporal frame.

84

85 Mapping the dynamic distribution of phytoplankton is affected by the sampling and measuring
86 methods used. As an example, the fractional contribution of phytoplankton populations to bulk
87 biomass can be measured from remote sensing using signature of diagnostic pigments (Ciotti and
88 Bricaud, 2006; Brewin et al., 2010; Hirata et al., 2011), but these large-scale observations suffer from
89 small spatio-temporal scale resolution (Levy et al., 2003). Single-cell analyses permitted by flow
90 cytometry combined with in situ and automated sampling can observe fine-scale temporal dynamics of
91 phytoplankton (Dubelaar and Gerritzen, 2000; Thyssen et al., 2008, 2014). Moreover, the most efficient method
92 for quantifying phytoplankton productivity is the estimation of the dividing rate of a population in relation to
93 the cell cycle. The use of several optical properties, based on periodic increase and decrease in light scatter
94 intensity, interpreted as a response of cellular growth and division occurring during the cell cycle (Durand 1995;
95 Binder et al., 1996), linked to cell size gives a good growth rates estimation. Diel variations in the phytoplankton
96 cell dimensions was used as an automated measurement to calculate growth rates of natural phytoplanktonic
97 groups during flow cytometry high frequency surveys (Sosik et al., 2003). This approach has been used to
98 investigate the variability of primary production in different trophic conditions such as in eutrophic
99 bloom areas (Campbell et al., 2010; Brosnahan et al., 2015) to oligotrophic ecosystems (Hunter-
100 Cervera et al., 2014; Ribalet et al., 2015).

101 In the Mediterranean Sea, pigment analysis revealed that more than 80% of the autotrophic
102 biomass originated from the nanoplanktonic and picoplanktonic sized groups (Vidussi et al., 2001; Bel
103 Hassen et al., 2009). These size fractions seem to play a crucial role in the energy transfer to higher
104 trophic levels mainly in oligotrophic marine areas such as the Mediterranean Sea (Pulido-Villena et
105 al., 2014). Moreover, the lower trophic levels of pelagic ecosystems, such as phytoplankton and
106 heterotrophic prokaryotes, are particularly exposed to various metallic and organic contaminants for
107 which the bioconcentration is governed by sorption between the surrounding water and the cells
108 (Wallberg et al., 1997; Sobek and Gustafsson, 2004; Nizzetto et al., 2012). Therefore, characterizing
109 these populations in terms of functional diversity, contribution to bulk fluorescence, carbon biomass
110 and growth rate will provide valuable information on their role in the energy transfer but also in the
111 potential accumulation and transfer of contaminants within planktonic food web, which are strongly
112 influenced by the species/size structure and biomass of plankton community (Alekseenko et al., 2018;
113 Chauvelon et al., 2019).

114 The present study investigates the subsurface ultraphytoplankton distribution along a North-
115 South transect in the Mediterranean Sea using high frequency pulse shape recording flow cytometry
116 in the framework of the MERITE-HIPPOCAMPE cruise. This cruise aimed at studying the
117 accumulation and transfer of metallic and organic contaminants at the atmosphere/water/plankton
118 interfaces and within the plankton food webs (phyto-, zoo- and bacterio-plankton) in areas of scientific
119 and economic interests of the Mediterranean Sea. The main objectives of the present paper are: 1) To
120 characterize the ultraphytoplankton community structure in terms of abundance, biomass, red
121 fluorescence, and apparent growth rate along the North-South Mediterranean transect that crosses areas
122 with different physical structures, hydrological and biogeochemical conditions, and anthropogenic
123 pressures. 2) To assess the productivity of each resolved group in order to provide clues on the
124 phytoplanktonic population turnover and their potential implications in the carbon cycle, and
125 eventually the transfer of contaminants within the plankton food webs.

126 2. Material and Methods

127 2.1. Stations and sampling

128 The MERITE-HIPPOCAMPE cruise was carried out in spring, from 13 April and 14 May 2019,
129 on board the R/V *Antéa*, along a North-South round trip transect from the French coast (La Seyne-sur-
130 mer; North-western Mediterranean Sea) to the Gulf of Gabès in Tunisia (South-eastern Mediterranean
131 Sea) (Tedetti and Tronczynski, 2019) (Fig. 1). The investigation period was divided into two sub-
132 periods Leg 1 and Leg 2. Leg1, from 13 to 28 April, was dedicated to the southward transect, between
133 La Seyne-sur-mer and Tunis, with sampling of five long stations: St2, St4, St3, St10 and St11. Leg2,
134 from 30 April to 14 May, covered the end of the transect to the south (from Tunis to the Gulf of Gabès),
135 then the return trip to the north, from the Gulf of Gabès to La Seyne-sur-mer. Five stations were
136 sampled during leg2: St15, St17, St19, St9 and St1 (Fig. 1). These stations were chosen according to
137 different criteria of physical, biogeochemical, and biological conditions, or anthropogenic influences
138 (see Tedetti et al., this issue). The main characteristics of stations are provided in Table 1. The
139 SOLEMIO station (Site d’Observation Littoral pour l’Environnement du MIO) is part of the French
140 national network of coastal observation SOMLIT (Service d’Observation en Milieu LITtoral –
141 <http://somlit.epoc.u-bordeaux1.fr/fr/>). The JULIO station (JUDicious Location for Intrusions
142 Observations) is dedicated to the study of the intrusions of Liguria current. The PEACETIME cruise
143 (ProcEss studies at the Air-sEa Interface after dust deposition in the MEditerranean sea) took place in
144 May-June 2017 (<http://peacetime-project.org/>). An extra station ‘Zarzis’ has been added to sampling
145 list where biological parameters were sampled but no nutrients were measured.

146 Subsurface temperature and salinity were recorded continuously at high frequency all along the
147 transect from a flow-through pumped seawater at 2-m depth, using a thermosalinograph (TSG, SeaBird
148 SBE 21). A chamber for subsampling the flow-through seawater was plugged for automated flow
149 cytometry measurements. At the ten fixed stations, *in situ* measurements and several operations to
150 collect water, particles and plankton were performed (see details in Tedetti et al., this issue), including

151 the deployment of a trace metal clean carousel equipped with a conductivity-temperature-depth probe
152 (CTD; Seabird SBE 911*plus*) with ten 12-L bottles (1 Niskin, 5 Niskin-X, 4 Go-Flo). The latter allowed
153 for vertical profiles of temperature, salinity, and total chlorophyll *a* (TChl*a*) in the water column, as
154 well as seawater sampling in subsurface (5-m depth) and deep chlorophyll maximum (DCM) for
155 analysis of various parameters including nutrients, Tchl*a*, pigments, dissolved and particulate organic
156 carbon, and metallic trace elements.

157

158 **2.2. Nutrients**

159 Seawater for nutrient analyses was collected at 5-m depth and in the DCM by means of Niskin-
160 X bottles (i.e., Niskin with a completely free, Teflon coated sample chamber; model 101012X). On
161 board, in-line filtration was conducted from the Niskin-X bottles using argon pressure system (as for
162 the Go-Flo). The bottles were pressurized to 0.5 bars with argon (UN1006, compressed, 2.2) while
163 their stoppers were maintained tight by home-made high-density polyethylene (HDPE) clamps. A 10-
164 cm long piece of acid-cleaned silicon tubing was inserted into the drainage tap of the bottles, and
165 perfluoroalkoxy (PFA) filter holders (Savillex[®]) were connected to the tubing. Pre-combusted (450
166 °C, 6 h) glass fiber filters (GF/F, 25-mm diameter, Whatman) were placed in the filter holders. After
167 rinsing filters with several hundred mL of seawater, filtered (~ 0.7 µm) samples for nutrient analyses
168 were collected in cleaned 50-mL polycarbonate bottles and immediately stored on board at – 18 °C.
169 Samples were maintained frozen to the laboratory, where they were analysed for nutrients a few days
170 after the cruise. Nitrate (NO₃⁻), nitrite (NO₂⁻), phosphate (PO₄³⁻) ions were analysed by standard
171 automated colorimetry procedure, using a Seal Analytical continuous flow AutoAnalyser III (AA3)
172 according to the protocol described by [Aminot et K  rouel \(2004, 2007\)](#) (detection limits of 0.05 µM
173 for NO₃⁻ and 0.02 µM for NO₂⁻ and PO₄³⁻). Ammonium (NH₄⁺) ions were analysed by fluorescence
174 according to [Holmes et al. \(1999\)](#) and [Taylor et al. \(2007\)](#).

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177

178 **2.3. Automated flow cytometry**

179 The CytoSense, an automated flow cytometer (CytoBuoy b.v. (NL)) designed to study individual
180 or colonial phytoplankton cells between 0.8 and 800 μm , analysed seawater from the continuous flow-
181 through system pumped at 2-m depth, at a rate of 1 L min^{-1} , filling an intermediate 300-mL container
182 isolating the subsample to minimize the spatial extent during the analysing time. A weighted calibrated
183 peristaltic pump was used to sample the seawater and set at $5 \mu\text{L s}^{-1}$. The sample is then surrounded
184 by a sheath loop (NaCl solution 35 ‰ filtered on $0.2 \mu\text{m}$) to separate, align, and drive the particles to
185 the light source (laser OBIS Coherent, 488 nm, 120 mW) and was continuously recycled using a set of
186 two $0.1\text{-}\mu\text{m}$ filters. The light scattered in front of the laser beam (forward scatter, FWS) were collected
187 on two left and right photodiodes and used for laser alignment control. The light scattered orthogonally
188 (sideward scatter, SWS) and fluorescence emissions were separated by a set of optical filters (SWS,
189 488 nm), yellow fluorescence (FLY, 506–601 nm), orange fluorescence (FLO, 601–650 nm) and red
190 fluorescence (FLR, $> 650 \text{ nm}$), and collected on photomultiplier tubes. Fluorescent beads of $3\text{-}\mu\text{m}$
191 (Cyto-Cal™) and $10\text{-}\mu\text{m}$ (Polybead®) diameter were used every 24–72 h to normalize fluorescence
192 and size. Silica beads (Bangs lab®, silica microspheres) of 1.0, 2.02 and $3.13 \mu\text{m}$ were analysed for
193 size estimation of phytoplankton cells.

194 Ultraphytoplankton groups were optically resolved based on their light scatter and fluorescence
195 properties. Two successive samples triggered on 2 FLR signals linked to the emission of chlorophyll
196 (with values of 10 and 20 mV) were acquired, according to the frequency of the events. The
197 phytoplankton groups were classified using the Cytoclus® software. Each cell is thus characterized by
198 a set of optical pulse shapes which constitute the cytometric signature. Microsphere beads ($3 \mu\text{m}$,
199 Polyscience®) were used to discriminate between picoeukaryotes and nanophytoplankton.

200 Cell biovolume was estimated from a calibration relationship between different size
201 predetermined microbeads and their equivalent cytometric forward scatter signature (FWS). The
202 following relationships were established for picophytoplankton (Eq. 1) and nanophytoplankton (Eq.
203 2):

$$204 \quad \text{Log}(\text{Biovolume}) = 0.2132 \times \text{Log}(\text{FWS}) - 1.161 \text{ (Eq. 1)}$$

$$205 \quad \text{Log}(\text{Biovolume}) = 1.1104 \times \text{Log}(\text{FWS}) - 10.426 \text{ (Eq. 2)}$$

206 Eq. 2 was modified and adapted from [Foladori et al. \(2008\)](#) and [Dugenne et al. \(2016\)](#). A carbon
207 biomass conversion was assigned to each population as follow: *Synechococcus* abundances were
208 converted by using the estimation of 200 fg C cell⁻¹ ([Mackey et al., 2002](#)). Picoeukaryotes and
209 nanoeukaryotes carbon biomass were calculated using the equation of [Verity et al. \(1992\)](#):

$$210 \quad Q_{c,\text{cal}} = a V^{0.866} \text{ (Eq. 3)}$$

211 with $Q_{c,\text{cal}}$ the estimated average carbon biomass per cell (in fg C cell⁻¹), V the biovolume (μm^3) and
212 “a” the values of 0.39, 0.32, 0.27 and 0.25 for *Synechococcus*, picoeukaryotes, nanoeukaryotes and
213 Cryptophytes-like, respectively. $Q_{c,\text{cal}}$ for each group is reported in [Table 2](#).

214 The ratio between minimum and maximum mean cell biovolume (Eq. 4) has been used for the
215 estimation of the daily growth rate ([Binder et al., 1996](#); [Vaulot and Marie, 1999](#)). This approach
216 assumes that the population synchronizes between growth and division phases:

$$217 \quad \mu_{\text{ratio}} = \text{Log}(V_{\text{max}}/V_{\text{min}}) \text{ (Eq. 4)}$$

218 with μ_{ratio} the daily growth rate (d⁻¹), and V_{max} and V_{min} , the minimum and maximum mean cell
219 biovolumes ($\mu\text{m}^3 \text{ cell}^{-1}$). The apparent increase in carbon biomass, defined as the net primary
220 production (NPP in mg C m⁻³ d⁻¹) (Eq. 5), was calculated using the carbon conversion factor $Q_{c,\text{cal}}$
221 ([Table 2](#)) as a scalar product with N (abundance) and growth rate exponential:

$$222 \quad \text{NPP} = Q_{c,\text{cal}} \times [e^{\mu_{\text{ratio}}} - 1] \times N \text{ (Eq. 5)}$$

223

224 2.4. Data analysis

225 A hierarchical classification was used to discriminate between the different surface water
226 properties based on their surface temperature and salinity values. A distance matrix describing the
227 dissimilarities of these parameters was constructed. The data were grouped using complete linkage
228 clustering according to Euclidean (root mean squared) distances. The TS plot illustrating the different
229 waters properties was then elaborated using the ODV 5.4.0 software developed by R. Schlitzer at the
230 AWI. The surface water velocity for the sampled days was computed from the Copernicus service
231 infrastructure website (<https://marine.copernicus.eu/>).

232

233 **3. Results**

234 **3.1. Hydrological features**

235 Subsurface temperature distribution showed a rather homogeneity during the two investigated
236 legs (Fig. 2B), with the coldest waters being recorded in the northern stations, and the warmest towards
237 the southern stations. This homogeneity between the two legs was also verified for the subsurface
238 salinity distribution (Fig. 2A) with decreasing values towards the south, except a slight increase in the
239 coastal area of the Gulf of Gabès.

240 The lowest temperatures, around 14 °C, were observed in the Bay of Marseille, while the highest
241 ones were measured in the southern Tunisia coastal waters, with a maximum of 19.5 °C recorded near
242 Djerba and Zarzis (Fig. 2B). The highest salinity values were measured in Ligurian region with a
243 maximum of 38.50. The lowest salinity values (i.e., 37.12) were found in the northern Tunisian coastal
244 waters, particularly in the Gulf of Tunis and in the Sicily Strait (Fig. 2A).

245 A hierarchical classification carried out on these subsurface temperature and salinity values
246 allowed distinguishing 7 geographic zones (Fig. 3A, B). The colors illustrate the result of the
247 hierarchical classification generating 7 zones (Z1 to Z7). Each zone encompassing a different number
248 of stations: Z1, stations 1, 2, 3 and 4, Z2, station 9, Z3, stations 10 and 11, Z4, station 15, Z5, station
249 17, Z6, station 19, and Z7, an additional station called “Zarzis”. The temperature and salinity varied

250 from 13.8–15.5 °C and 38.12–38.21 in the northern basin (i.e., Z1) to 15.8–17.4 °C and 37.13–37.45
251 in the medium basin (i.e., Z4), and 19.2–19.9°C and 37.8–38.0 in the southern basin (i.e., Z7). For the
252 zones in between, temperature and salinity varied for the northern part: 14.5–15.0 °C and 38.2–38.4 in
253 Z2, 14.9–16.9 °C and 37.3–38.1 in Z3, 16.8–17.8 °C and for the southern part 37.2–37.5 in Z5, 17.8–
254 18.7 °C and 37.5–37.7 in Z6.

255 The surface velocity map computed for the 8th of May 2019 (Fig. 4), corresponding to the
256 sampling date of station 9, shows an increased water velocity southwest stations 9 and 10 likely
257 corresponding to the edge of the seasonal northern Balearic front.

258

259 **3.2. Nutrient concentrations**

260 Nutrient concentrations measured at the 10 stations in subsurface waters (5-m depth) showed
261 large differences between the different zones (Fig. 5): NH_4^+ varied from 0.007 to 0.790 μM , $\text{NO}_3^- +$
262 NO_2^- from 0.05 to 0.63 μM , PO_4^{3-} from 0.03 to 0.34 μM , and $\text{Si}(\text{OH})_4$ from 0.7 to 2.2 μM . Nutrient
263 concentrations were relatively high at St4 and St9 (belonging to zones Z1 and Z2), particularly for
264 $\text{NO}_3^- + \text{NO}_2^-$ at St4, and $\text{Si}(\text{OH})_4$ and PO_4^{3-} at St9. High concentration of PO_4^{3-} was also observed in
265 zone Z6. The Redfield N / P ratio (Redfield et al., 1963) varied between 0.24 and 58. In most stations,
266 this ratio was below 16, expressing a potential nitrogen limitation, except in St4 for which the ratio
267 reached 58, highlighting a potential phosphorus limitation. Overall, nutrients showed decreasing
268 concentrations towards the South (Fig. 5), the western basin being relatively mesotrophic and the
269 eastern basin rather oligotrophic.

270

271 **3.3. Distribution and composition of phytoplankton**

272 The functional groups were resolved based on the flow cytometric optical signals from single
273 cell biological features: FWS (i.e., Forward Scatter), SWS (i.e., Sideward Scatter), FLR (i.e., Red
274 Fluorescence) and FLY (i.e., Yellow Fluorescence). Four groups of small plankton < 10 μm sized

275 cells) were determined according to cell optical properties (Fig. 6A, B). The plot of FLR vs. FLY and
276 FLR vs. SWS differentiated two phycoerythrin rich groups. One differentiated by high FLY
277 (phycoerythrin) emission and by small, computed size estimated of $1.05 \pm 0.09 \mu\text{m}$ (Table 2) and was
278 identified as *Synechococcus*. The one presenting high FLY and computed size estimated of 5.69 ± 0.77
279 μm was identified as Cryptophytes-like. Picoeukaryotes and nanoeukaryotes cells presented high FLR,
280 low FLY emission with computed size estimated respectively of $2.45 \pm 0.19 \mu\text{m}$ and $4.16 \pm 0.16 \mu\text{m}$
281 (Table 2).

282 Significant spatial heterogeneity in the distribution of ultraphytoplankton was observed
283 throughout the sampling area (Fig. 7). The total ultraphytoplankton abundance was the highest in the
284 north of the Ligurian basin (Z1 and Z2) and in the Zarzis coasts (Z7) (Fig. 7A). The highest values of
285 FLR per unit of volume, used as a proxy of Chla content, were observed in zones Z1 and Z2 (Fig. 7B),
286 with a maximum of 5.10^{12} a.u. m^{-3} , and moderately high values off Zarzis (10^{12} a.u. m^{-3}). The total
287 ultraphytoplankton carbon biomass (Fig. 7C) fluctuated between 50 and 125 mg C m^{-3} in certain
288 coastal zones, such as in the south of Z7 and in the north of Z1, and up to 150 mg C m^{-3} in Z2.

289 Like the total abundance of the ultraphytoplankton (Fig. 7A), the relative abundance of each
290 group showed similar spatial distribution trends with more contrasted gradients between identified
291 zones (Fig. 8A). In general, abundances varied up to a factor of 10 from the coast of Sardinia (Z4) and
292 the Gulf of Gabès (Z5-Z6), to the northern Balearic front (Z2) and southern Tunisian coasts (Z7), as
293 shown with the *Synechococcus* which abundances varied from $3.4\text{--}9.8 \cdot 10^9$ cells m^{-3} to $30.8\text{--}86.9 \cdot 10^9$
294 cells m^{-3} . In terms of mean cell size (Fig. 8B), the zones from Z1 to Z3 in the north of the transect
295 showed larger *Synechococcus* cells ($> 1 \mu\text{m}$) and smaller picoeukaryotes and Cryptophytes-like cells
296 ($< 2.5 \mu\text{m} / \text{cell}$ and $< 5.5 \mu\text{m} / \text{cell}$, respectively). The mean size distribution of nanoeukaryotes did
297 not exhibit distinguished variations and fluctuated in most waters between 3.8 and 4.6 μm .

298 The distribution of FLR per cell followed approximately that of the abundances (Fig. 8C). The
299 highest values were mainly recorded in the areas that represented the highest abundances. Its variability

300 within each group fluctuated in Z2 with factors of 3 for small size fractions (*Synechococcus* and
301 picoeukaryotes), 4 for Cryptophytes-like and 5 for nanoeukaryotes.

302 Conversely, the maxima of abundance were synchronized with the minima in mean cell size.
303 This pattern was particularly highlighted in Z2 (Fig. 8 and Fig. 10), especially for *Synechococcus* and
304 picoeukaryotes with abundances varying from 30.8 to 86.9 10^9 cells m^{-3} and 1.7 to 3.8 10^9 cells m^{-3}
305 and the mean cell size from 0.9 to 1.4 μm and 2.1 to 2.6 μm , respectively.

306 The nanoeukaryotes and the *Synechococcus* cells contributed the most to the FLR per unit of
307 volume in the 7 identified zones (Fig. 9B). Their carbon biomasses (Fig. 9A) could respectively reach
308 up to 70 and 30 mg C m^{-3} , with nanoeukaryotes as main contributors (Table 3). The coastal areas
309 showed the highest relative contributions of nanoeukaryotes and *Synechococcus*. In the Gulf of Gabès
310 (Z7), they were up to 51 and 22%, respectively, whereas they were about 62.1 and 19.3% in the
311 Ligurian Basin (Z2), respectively (Table 3). The Cryptophytes-like were small contributors to total
312 biomass, and their carbon content varied considerably among zones, being in Z2 and Z7 up to 3 times
313 much higher than in the other areas (Table 3). The transition from coastal zone to offshore areas was
314 followed by a reverse trend in the contribution of *Synechococcus* and picoeukaryotes to carbon
315 biomass, where *Synechococcus* contributed more in coastal areas contrary to picoeukaryotes,
316 contributing more offshore (Fig. 9A).

317 The spatial distribution of the median-normalized abundance, mean size and mean FLR_{cell}
318 according to the identified water physical characteristics showed that three zones stand out from the
319 others in terms of abundance, mean cell size and red FLR_{cell} (Fig. 10), namely Z1 and Z2 zones in the
320 north of the Ligurian basin and the zone Z7 in the borders of Zarzis. These areas are characterized by
321 relatively high abundances that may vary by a factor 10 for *Synechococcus* and Cryptophytes-like
322 compared to the other areas (Fig. 10A). In terms of mean cell size (Fig. 10B), these same areas showed
323 relatively smaller cells with values below the median of normalized sizes for all groups probably
324 reflecting diurnal cell cycles that differ from one area to another. The examination of the growth rates

325 (Fig. 11) of the identified groups were variable among groups, the lowest growths were recorded for
326 nanoeukaryotes, whereas the highest were for Cryptophytes-like and *Synechococcus*, with
327 Cryptophytes-like reaching more than 2 divisions per day in Z3, Z4 and Z6. This yielded net primary
328 production of about 36.6 mg C m⁻³ d⁻¹ and 15.8 in north Mediterranean in Z2 and Z1, respectively,
329 mostly contributed by *Synechococcus* and nanoeukaryotes, 5.8 mg C m⁻³ d⁻¹ in Z4 in the central
330 Mediterranean, and about 11 mg C m⁻³ d⁻¹ in southern Mediterranean in Z6 and Z7 (Table 4).

331

332 4. Discussion

333 The general circulation pattern in the Mediterranean Sea western basin is characterized by the
334 Atlantic Water (AW) transport from the Algerian Basin and spread off to the Liguro-Provencal limit
335 thus forming the North Balearic front (Milot et al., 1991; Milot and Taupier-Letage, 2005). During
336 this study, this hydrological structure (Fig. 4) was highlighted and corresponded to Z2 characterized
337 by high salinity over 38.5 and low temperature between 14 and 15 °C. Like all frontal zones, high
338 nutrient concentrations were recorded in this area particularly in terms of nitrate, silicate, and
339 phosphate (Estrada et al., 1996). The dependence of ultraphytoplankton spatial distribution on meso
340 or sub-meso scale hydrodynamic features like fronts that generate distinct water masses has been
341 particularly documented in the Mediterranean Sea (Denis et al., 2010).

342 The part of the AW that progresses through the channel of Sardinia in its southern part (North-
343 Tunisia vein) continues along the embankment, enters the Strait of Sicily and then in the eastern basin,
344 going to feed the Atlantic Tunisian Current (ATC). The ATC flows eastward mainly along the 200-m
345 isobath (Beranger et al., 2005). It splits into two branches South of Lampedusa. The first branch
346 directly flows toward the southern part of the Levantine basin, while the second flowing over the
347 Tunisian shelf. The later divides into two branches, the first one invades the Tunisian shelf in the Gulf
348 of Gabès and recirculates anticyclonically on the shelf, while the second continues flowing south-
349 eastward as an important coastal current and comes close to the Libyan coast (Jaber et al., 2014). The

350 salinity barrier of 37.5 characterizing the AW in the Gulf of Gabès (Bel Hassen et al., 2009) was
351 detected at the entrance of the Gulf corresponding to Z5 (Fig. 3A), the mixing with the high salinity
352 of the coastal waters of the Gulf makes the detection of the AW less evidenced mainly in zones Z6 and
353 Z7.

354 The progressing towards the south was accompanied with a decreasing nutrient gradient mainly
355 nitrogen and a slow increase of phosphate at station St19. The meteorological conditions during this
356 period were characterized by a dust storm accompanied with weak rain (< 1 mm). High concentration
357 of PO_4^{3-} observed in zone Z6, potentially due to atmospheric inputs of nutrients from a Saharan dust
358 episode that occurred on 03/05/2019 and for which concentration of 1.06 μM was measured for PO_4^{3-}
359 in the rainfall water collected on board. Thus, atmospheric input was a main source of phosphorus in
360 the coastal water during dust storm (Guieu et al., 2014) and the annual input in area like the Gulf of
361 Gabès was demonstrated to be the highest in south Mediterranean (Markaki et al., 2010; Khammeri et
362 al., 2018). Overall, there was not an evident gradient in the abundance of the ultraphytoplankton
363 fraction between the northern mesotrophic Mediterranean part and the southern oligotrophic part (Fig.
364 6). The maximum of abundance, FLR_{cell} and biomass were recorded in the Balearic frontal area (Z2),
365 confirming that the large-scale phytoplankton distribution in the Mediterranean was specifically
366 affected by hydrodynamics (Casotti et al., 2003; Denis et al., 2010). This area was particularly rich in
367 silicate and phosphate and exhibited the highest abundance of larger size fractions (nanoeukaryotes
368 and Cryptophytes-like) ($P < 0.05$ and $R^2 > 0.7$) (Fig. 7), confirming that low nutrient regions are
369 dominated by small phytoplankton, mostly *Synechococcus*, *Prochlorococcus* and picoeukaryotes,
370 whereas more productive regions support not only these small cells but also abundances of larger
371 species (Raimbault et al., 1998; Hirata et al., 2011).

372 *Synechococcus* were by far the most abundant group in all prospected zones, its highest relative
373 biomass was reached in the Gulf of Gabès (Table 3). *Prochlorococcus* were not resolved in our study.
374 The nonresolution of *Prochlorococcus* in subsurface water using a CytoSense could be related to their

375 dim fluorescence signature due to high light intensity affecting surface waters in April-May, combined
376 to a high background noise in the sheath fluid as no coal filter was used to lower the trigger level as it
377 has been shown to greatly improve the resolution of this group (Marrec et al., 2018). Nevertheless, the
378 analysis of samples from the DCM using the same instrument showed the presence of *Prochlorococcus*
379 at depth below 50 m (data not shown). This is consistent with previous patterns observed along the
380 Tunisian coasts with the presence of *Prochlorococcus* at warm and stratified water more than 60 m in
381 depth (Khemmari et al., 2020; Quéméneur et al., 2020). Nonetheless, this dominance of *Synechococcus*
382 over *Prochlorococcus* already reported in the Mediterranean confirms the statement that
383 *Synechococcus* is more adapted to the general hydrodynamic and nutrient conditions in the
384 Mediterranean Sea (Denis et al., 2010).

385 *Synechococcus* mean estimated size and associated biovolume of $1.05 \pm 0.09 \mu\text{m}$ and 0.6 ± 0.17
386 μm^3 , respectively (Table 2), were in the same range of 0.8 to 1.2 μm and 0.25 to 1.00 μm^3 , respectively
387 reported in previous studies (Morel et al., 1993; Shalapyonok et al., 2001; Sosik et al., 2003; Hunter-
388 Cevera et al., 2014; Marrec et al., 2018). Relatively smaller *Synechococcus* cells with values below
389 the median of normalized sizes were observed in the low latitude and warm southern Tunisian waters
390 (Fig. 9B), confirming that their distribution appears to be principally controlled by water temperature
391 and latitude (Pittera et al., 2014). A likely genomic differentiation within this group could also be
392 suggested, although a dominance of the clade III has been reported in the Mediterranean Sea, but this
393 did not exclude an ecologically meaningful fine-scale diversity within currently
394 defined *Synechococcus* clades (Farrant et al., 2016).

395 The mean size of the main nanoeukaryotes functional group observed was $4.15 \pm 0.16 \mu\text{m}$ (Table
396 2). This is consistent with the value of $4.1 \pm 0.5 \mu\text{m}$ reported by Marrec et al. (2018) in the north-
397 western Mediterranean Sea. No significant variations in the mean size of nanoeukaryotes along the
398 transect was observed (Fig. 9B) suggesting that this community might be dominated by similar genera.
399 Indeed, the major feature of the Mediterranean basin in various regions and season is a biomass

400 dominated by Prymnesiophytes (Latasa et al., 1992; Claustre et al., 1994; Bustillos-Guzman et al.,
401 1995; Vidussi et al., 2000) with the genus *Chrysochromulina* (3.2–4.0 μm) largely represented in the
402 north-western Mediterranean (Percopo et al., 2011). Conversely, the contribution of Prymnesiophytes
403 to chlorophyll biomass considered as prominent feature in the Mediterranean was rather low in the
404 Gulf of Gabès (Bel Hassen et al., 2008; 2009a) and mainly explained by the dominance of smaller
405 chlorophyll b containing nanoplankton like prasinophytes. Nanoeukaryotes were the main contributors
406 (> 60 %) in terms of pigment content (defined by FLR) and carbon biomass. The contribution of nano
407 and picoeukaryotes in terms of pigment fluctuated between 80 and 84% in central Mediterranean, and
408 between 69 and 77% in both northern and southern Mediterranean (Table 3), where the prokaryotes
409 (*Synechococcus*) exhibited their highest contribution (between 15 to 18.9% of FLR). This is less than
410 the prokaryotes contribution (32 to 47%) to total Chl_a reported using chemotaxonomic approach by
411 Barlow et al. (1997) in the southern Mediterranean region and the ranges of 26 and 28% found by Bel
412 Hassen et al. (2009a) in the Gulf of Gabès during spring and summer, respectively. These deviations
413 could be in part explained by the presumed contribution of *Prochlorococcus*, not resolved in our case
414 in surface water. Indeed, when comparing the only contribution of *Synechococcus* in the Gulf of Gabès
415 (15-17%) (Table 3) we found consistent values (15% in mean) with what reported using
416 chemotaxonomic approach in the same area for the same period (Bel Hassen et al., 2009a).

417 The growth rate, estimated from the difference in minimal and maximal values of biovolume,
418 showed that the highest rates were observed for the orange fluorescing phycoerythrin containing cells,
419 i.e., Cryptophytes-like and *Synechococcus*. The *Synechococcus* growth rate estimates fluctuated
420 between 0.38 and 1.1 d^{-1} . This was consistent with values of 0.48–0.96 d^{-1} reported by Ferrier-Pages
421 and Rassoulzadegan (1994) and with the value of 0.49 d^{-1} reported in the north-western Mediterranean
422 Sea (Marrec et al., 2018). Cryptophytes-like growth rates showed their highest variability (0.3-1.7 d^{-1})
423 in Z1 but is still consistent with the rate of 0.75 d^{-1} determined in spring 2004 in the center of the
424 Liguro-Provencal basin (Gutierrez-Rodriguez et al., 2010). The yielded *Synechococcus* apparent NPP

425 rates showed their highest values in Z1 (1.3-12 mg C m⁻³ d⁻¹) and Z2 (13.9-23 mg C m⁻³ d⁻¹), combined
426 with high abundances recorded in these areas. These NPP were higher than the range of 0.01-1 mg C
427 m⁻³ d⁻¹ reported by the study of [Agawin et al. \(1998\)](#) by means of a biovolume to C conversion over
428 the course of 1997-1998 (February to May), and also the value of 2.68 mg C m⁻³ d⁻¹ reported by
429 [Marrec et al. \(2018\)](#) in north-western Mediterranean Sea during fall season. These studies used
430 different approximations to calculate the biovolume to cellular carbon content. However, it has been
431 demonstrated by [Marrec et al. \(2018\)](#) that cyanobacteria NPP rates obtained from different calculations
432 provides similar specific C uptake rates suggesting that these populations follow a daily dynamic at
433 equilibrium. Nanoplankton was expected to be the main contributor to the NPP because of its high
434 abundance and high cellular carbon content ([Table 3](#)), but its relative low growth rates generally under
435 0.3 d⁻¹, even lower than the range (0.48-2.4 d⁻¹) reported in north-western Mediterranean ([Ferrier-
436 Pages and Rassoulzadegan, 1994](#)), could explain this low NPP particularly in central Mediterranean
437 and in the northern Tunisian coasts. It is worth noting that NPP estimation does not accommodate any
438 cells removal processes that could be caused by grazing or physical transport. Even if this estimation
439 is valuable for all the resolved groups, nevertheless the grazing pressure on nanoplankton and its motile
440 capabilities are largely underestimated. Indeed, an active top-down control of ultraphytoplankton was
441 largely suspected in the southern Tunisian coasts ([Hamdi et al., 2015](#); [Khammari et al., 2020](#))
442 preventing from nanoeukaryotes accumulations. Moreover, the approach used for the calculation of
443 the growth rate based on the ratio between max and minimum cell biovolume ([Binder et al., 1996](#);
444 [Vaulot and Marie, 1999](#)) assumes that cell growth and division are separated in time (synchronous
445 population), whereas these processes occur simultaneously in a population. The growth rates
446 calculation based on cell size distribution allowed for superior estimation than using the ratio
447 $\text{Log}(V_{\text{max}}/V_{\text{min}})$, especially for asynchronized populations like nanoeukaryotes and Cryptophytes-
448 like. The picoeukaryotes NPP varied between 0.48 to 19 mg C m⁻³ d⁻¹, which is consistent with range

449 of picoplankton production rates of 2.2–19.6 mg C m⁻³ d⁻¹ compiled by [Magazzu and Decembrini](#)
450 [\(1995\)](#) in the Mediterranean Sea.

451 Except the Gulf of Gabès (Z6 and Z7), which is submitted to atmospheric forcing events, a
452 decreasing gradient in the NPP was observed along the North-South transect, confirming this general
453 trend in the Mediterranean, based on the whole phytoplankton size population ([Colella et al., 2003](#)).
454 The size fractioned NPP assessment conducted in the present study focused on the size under < 10 µm,
455 demonstrated to represent 20% of NPP measured by ¹⁴C particulate organic carbon production rates in
456 a NW coastal Spanish station ([Cermeno et al., 2006](#)). The focus on this size fraction is justified by
457 their high accumulation capabilities of contaminants (see this issue). The determination of the groups
458 that present the high carbon assimilation could provide an important insight into the characterization
459 of the phytoplankton mostly involved in the contaminant transfer in the trophic chain.

460

461 **5. Conclusions**

462 The monitoring of the subsurface ultraphytoplankton at high frequency along a North-South
463 Mediterranean round-trip transect highlighted the following conclusions:

- 464 - The Balearic frontal region showed the highest abundances and biomasses mostly attributed to
465 *Synechococcus* and nanoplankton. The productivity was mostly sustained by *Synechococcus*.
466 This pattern confirms the general statement that hydrodynamics is an important factor shaping
467 the structure of this ultraphytoplanktonic community.
- 468 - *Synechococcus* was by far the most abundant group in subsurface water with high biomass
469 concentration in the coastal zones, reaching up to 22% in the Gulf of Gabès.
- 470 - Nanoplankton represented up to 51% of the total ultraphytoplankton biomass in all zones. If
471 we consider that the transfer of contaminants to phytoplankton species is mainly biomass
472 related, nanoplankton will be the relevant group to monitor. The straight conclusion coming
473 out from this result is that the southern Tunisian coasts, with the lowest nanoplanktonic

474 biomasses, were probably the ecosystem that accumulates the least contaminants in its trophic
475 chain

476 - In almost all zones, the highest carbon turnover was ensured by *Synechococcus*. Its contribution
477 to the contaminant transfer to higher trophic levels is largely dependent on the potential grazing
478 activities.

479

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Table 1. Main characteristics of the ten stations sampled along a North-South Mediterranean transect during the MERITE-HIPPOCAMPE cruise (13 April-14 May 2019). (a) The SOLEMIO station (Site d'Observation Littoral pour l'Environnement du MIO) is part of the French national network of coastal observation SOMLIT (Service d'Observation en Milieu Littoral – <http://somalit.epoc.u-bordeaux1.fr/fr/>). (b) The JULIO station (JUDicious Location for Intrusions Observations) is dedicated to the study of the intrusions of Liguria current. (c) The PEACETIME cruise (ProcEss studies at the Air-sEa Interface after dust deposition in the MEditerranean sea) took place in May-June 2017 (<http://peacetime-project.org/>) (d) Consensus ecoregions of the Mediterranean Sea as defined by Ayata et al. (2018).

Station	Latitude (N)	Longitude (E)	Location	Characteristics	Depth (m)	Period
St2	42° 56.020'	5° 58.041'	Toulon – offshore (Maures Escarpement)	Limit of the continental shelf; Boundary of the Ligurian ecoregion ^d	1770	14-16/04
St4	43° 14.500'	5° 17.500'	Bay of Marseille (SOLEMIO ^a station)	Urbanized bay	58	16-18/04
St3	43° 08.150'	5° 15.280'	Marseille – offshore (JULIO ^b station)	Southeast entrance to the Gulf of Lion; Liguria current intrusions	95	18-20/04
St10	40° 18.632'	7° 14.753'	Offshore (PEACETIME ^c 2 station)	Near the North thermal front of the Balearic Islands	2791	22-24/04
St11	39° 07.998'	7° 41.010'	Offshore (PEACETIME ^c 3 station)	Algerian ecoregion ^d ; Gyres, intermediate primary production	1378	25-26/04
St15	36° 12.883'	11° 07.641'	Gulf of Hammamet	Phytoplankton area and high density of small pelagic fishes	100	29-30/04
St17	34° 30.113'	11° 43.573'	Boundary Gulf of Gabes	Gabès ecoregion ^d boundary; High density of small pelagic fishes	48	01-02/05
St19	33° 51.659'	11° 18.509'	Gulf of Gabes – South	Gabès ecoregion ^d ; High density of small pelagic fishes and phytoplankton area	50	02-05/05
St9	41° 53.508'	6° 19.998'	Offshore (PEACETIME ^c 1 station)	Ligurian ecoregion ^d boundary	2575	08-09/05
St1	43° 03.819'	5° 59.080'	Bay of Toulon	Urbanized bay	91	10-11/05
Zarzis	33° 37.952'	11° 17.73'	Zarzis	Saharan dust deposit	30	03-04/05

Table 2. Mean and SD of FWS, estimated size and biovolume of the *Synechococcus*, picoeukaryotes, nanoeukaryotes and Cryptophytes-like
 (1) Verity et al. (1992), (2) Campbell et al. (1994) and Shalapyonok et al. (2001), (3) Marrec et al. (2018)

Parameters	<i>Synechococcus</i>	Picoeukaryotes	Nanoeukaryotes	Cryptophytes-like
FWS (a.u. cell ⁻¹)	292.4 ± 110	6078 ± 1480	34200 ± 4395	91200 ± 47049
Estimated size (µm)	1.05 ± 0.09	2.46 ± 0.19	4.15 ± 0.16	5.59 ± 0.77
Biovolume (µm ³ cell ⁻¹)	0.60 ± 0.17	7.76 ± 1.72	37.43 ± 4.36	91.47 ± 42.12
Conversion coefficients (a,b)	(0.39,0.86) ¹	(0.32,0.8666) ¹	(0.27,0.8666) ¹	(0.25,0.8666) ¹
Calculated Qc,cal (fg C cell ⁻¹)	253	1871	6258	12273
Literature Qc (fg C cell ⁻¹)	100 ⁽³⁾ -250 ⁽²⁾	2108 ⁽²⁾	9000 ⁽³⁾	-

Table 3. Community contribution by zone in terms of abundance (cells cm⁻³), biomass (µg C m⁻³) and total FLR (a.u. cm³) (Syn=*Synechococcus*, Pico= picoeukaryotes, Nano=nano-eukaryotes, Cry=Cryptophytes-like)

Zone	Abundance (%)				Biomass (%)				Red fluorescence (%)			
	Syn	Pico	Nano	Cry	Syn	Pico	Nano	Cry	Syn	Pico	Nano	Cry
Z1	79.2 ±15.5	7.5 ±10.1	11.6 ±6.4	0.7 ±0.3	19.3 ±17.6	11.1 ±5.5	62.1 ±13.5	7.0 ±2.0	18.9 ±15.0	8.3 ±3.2	60.9 ±9.7	8.4 ±6.4
Z2	80.6 ±14.2	5.3 ±4.8	12.9 ±9.4	1.7 ±0.4	17.1 ±10.3	6.4 ±2.9	63.9 ±10.5	12.6 ±3.4	9.9 ±7.8	3.8 ±2.4	73.2 ±8.1	12.9 ±3.5
Z3	59.1 ±18.8	18.5 ±6.7	19.7 ±13.1	0.6 ±0.3	7.7 ±5.4	19.2 ±4.3	68.5 ±8.3	3.6 ±1.0	8.9 ±7.8	13.9 ±2.9	70.8 ±8.5	5.1 ±1.9
Z4	70.1 ±18.4	11.5 ±6.8	16.6 ±12.1	0.2 ±0.1	11.8 ±8.9	16.6 ±3.1	69.2 ±9.9	2.4 ±1.0	11.8 ±9.3	12.7 ±2.3	71.5 ±8.9	3.6 ±1.8
Z5	74.6 ±12.3	12.3 ±6.2	12.4 ±6.3	0.3 ±0.1	13.7 ±7.9	16.0 ±2.3	65.3 ±6.9	4.0 ±0.8	12.4 ±8.4	15.7 ±3.9	64.8 ±6.4	6.9 ±2.5
Z6	80.1 ±11.2	9.4 ±4.9	10.5 ±6.8	0.3 ±0.2	16.1 ±6.8	17.7 ±3.7	61.9 ±7.2	3.7 ±1.0	17.0 ±7.7	13.8 ±3.3	64.8 ±7.3	5.2 ±1.8
Z7	81.0 ±2.1	8.4 ±1.8	9.0 ±1.5	1.3 ±0.3	22.6 ±3.4	12.2 ±2.4	51.5 ±2.5	13.2 ±2.6	15.1 ±2.2	10.1 ±2.0	63.6 ±2.4	10.9 ±1.4

Table 4. NPP production per ultraphytoplankton group ($\text{mg C m}^{-3} \text{d}^{-1}$) (min, max and mean under brackets) values calculated using Equation (3) by zone.

Group	Z1	Z2	Z3	Z4	Z5	Z6	Z7
<i>Synechococcus</i>	1.3-12.0 (4.8)	13.9-23.1 (18.5)	0.8-4.8 (2.2)	0.3-4.1 (1.6)	0.4-2.6 (1.2)	0.7-4.2 (5.2)	0.9-9.4 (3.0)
<i>Picoeukaryotes</i>	0.6-5.2 (2.4)	2.6-3.1 (2.8)	1.1-2.4 (1.6)	0.4-3.3 (1.7)	0.4-1.2 (0.8)	0.6-7.9 (1.3)	0.5-2.1 (2.7)
<i>Nanoeukaryotes</i>	0.7-14.6 (5.3)	8.1-14.9 (11.5)	1.9-6.2 (3.4)	0.7-3.3 (1.7)	0.5-0.7 (0.7)	1.6-5.0 (4.0)	0.9-7.1 (2.6)
<i>Cryptophytes-like</i>	1.0-12.5 (3.3)	3.1-4.4 (3.8)	0.7-4.1 (1.7)	0.3-1.8 (0.8)	0.2-0.9 (0.6)	0.3-4.6 (1.2)	0.6-1.7 (1.9)

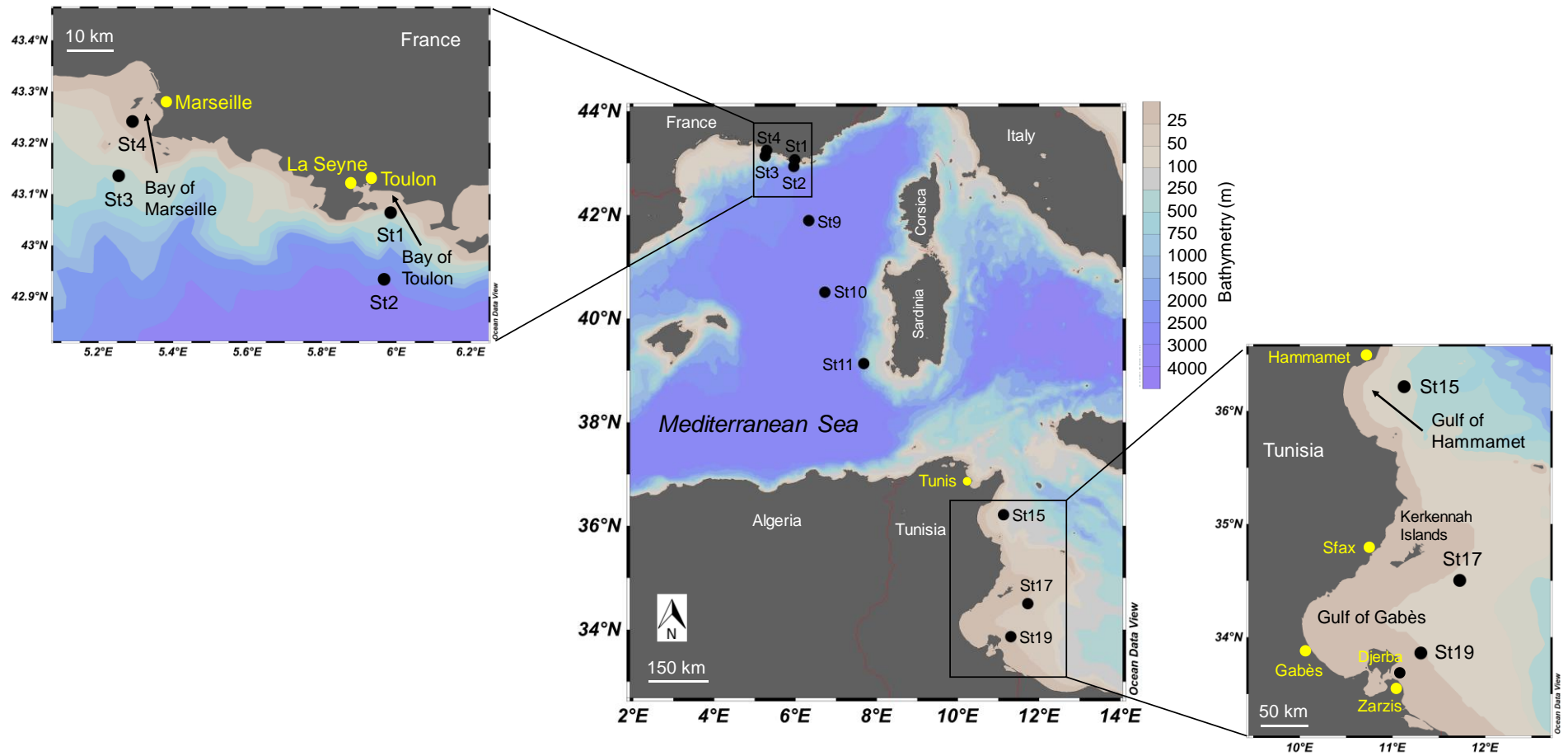


Figure 1 Map of the MERITE-HIPPOCAMPE cruise track in the Mediterranean Sea with the positions of the ten stations sampled.

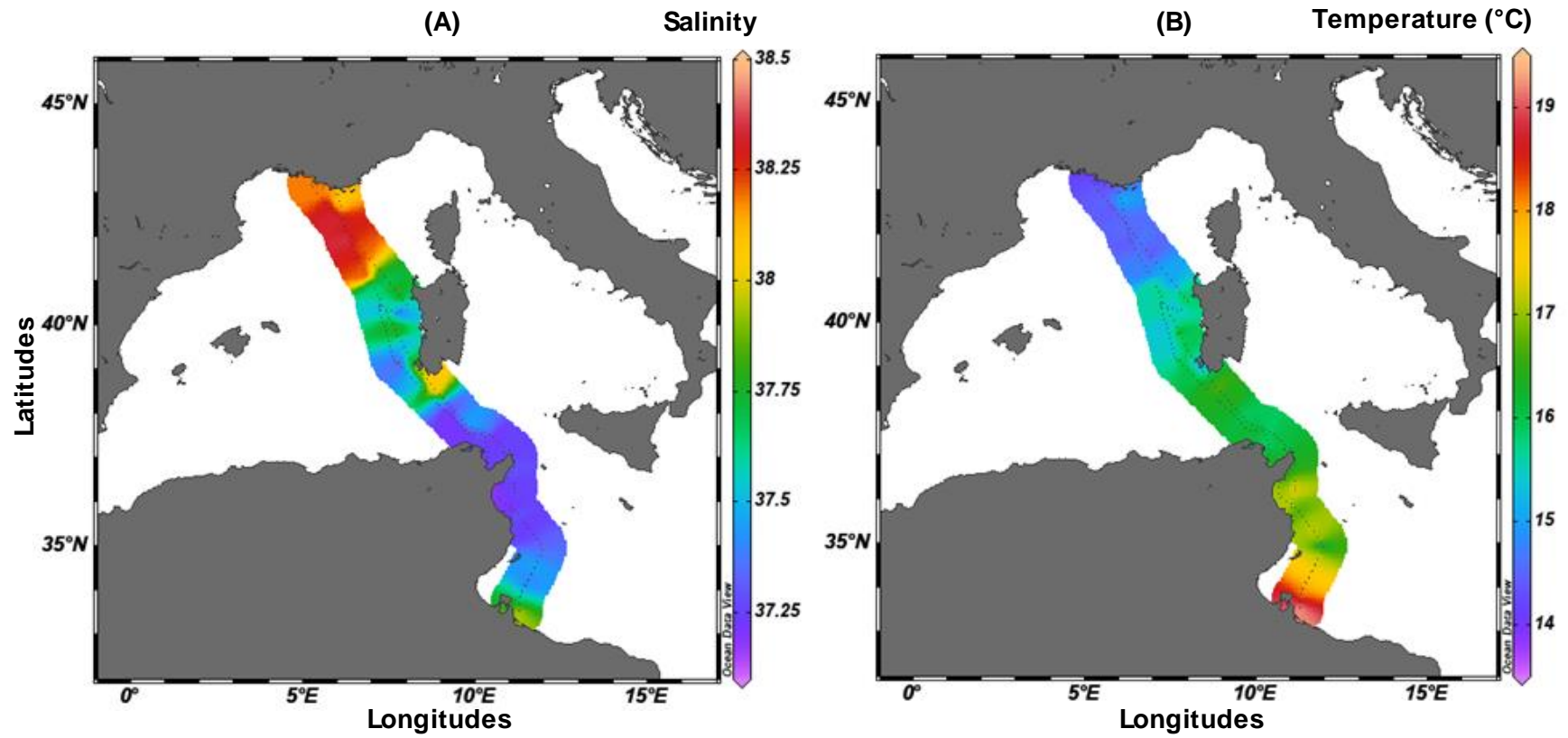


Figure 2 Subsurface temperature (A) and salinity (B) distributions along the Mediterranean transect during the MERITE-HIPPOCAMPE cruise

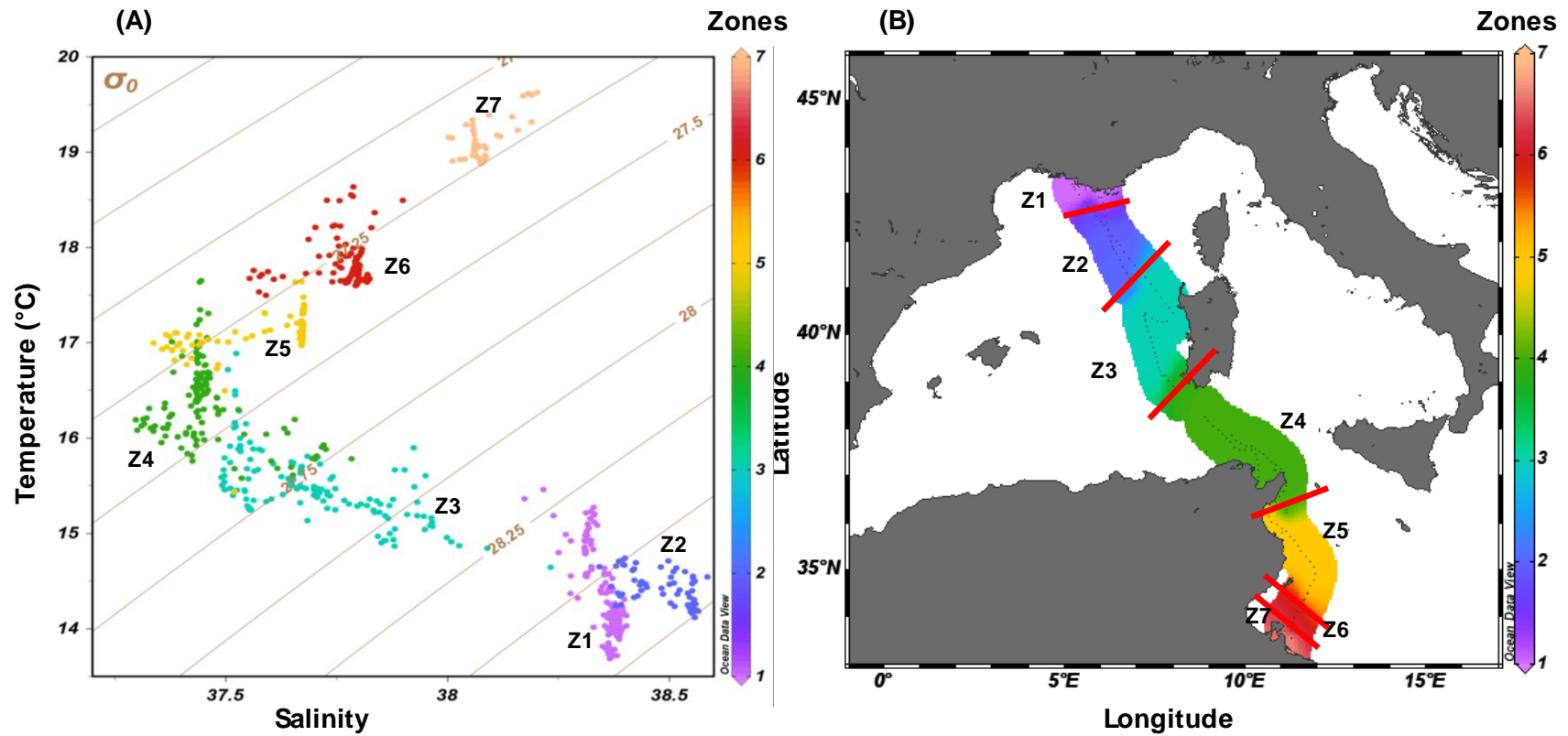


Figure 3 Temperature vs salinity of subsurface waters (A) sampled at 2-m depth. Surface distribution of the 7 zones along the round trip transect (B).

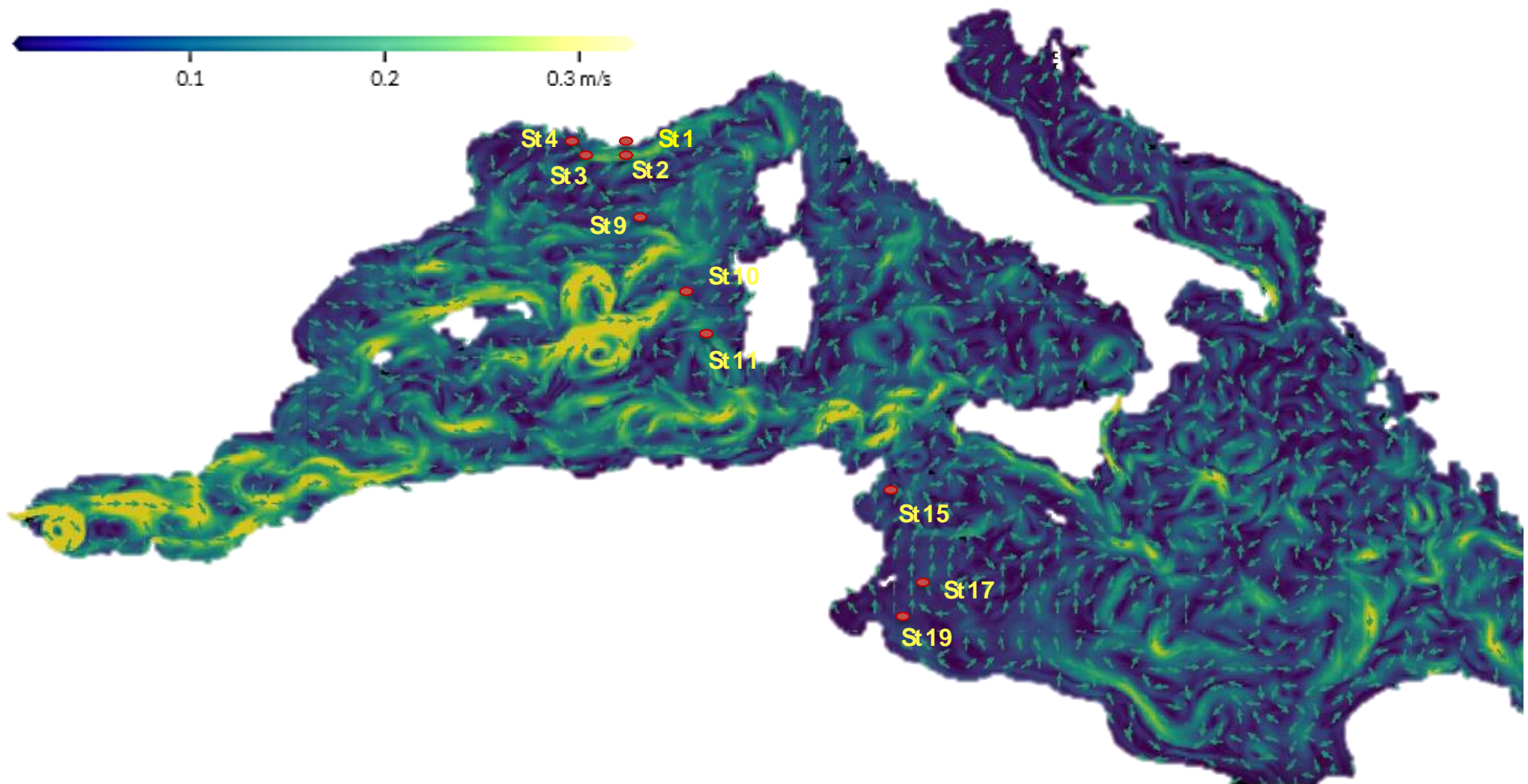


Figure 4 Surface water velocity map of the Mediterranean Sea on May 8th, 2019 (from MyOcean Pro COPERNICUS online interface)

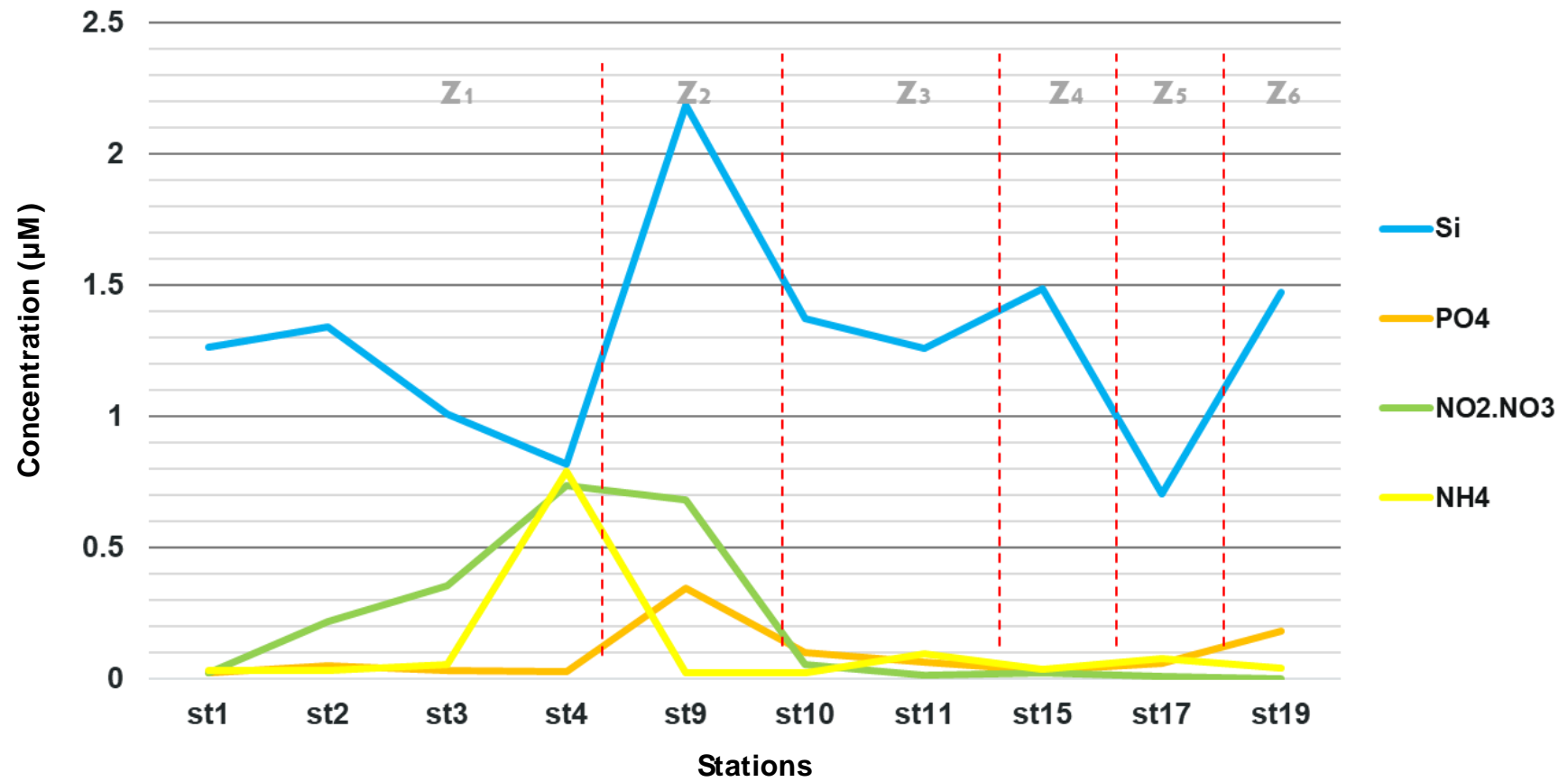


Figure 5 Concentrations (μM) of $\text{Si}(\text{OH})_4$ (blue line), PO_4^{3-} (orange line), $\text{NO}_3^- + \text{NO}_2^-$ (green line) and NH_4^+ (yellow line) in subsurface waters (5-m depth) at the ten stations. Zone 7, which does not contain any of the ten stations (and thus no nutrient data), is not displayed here.

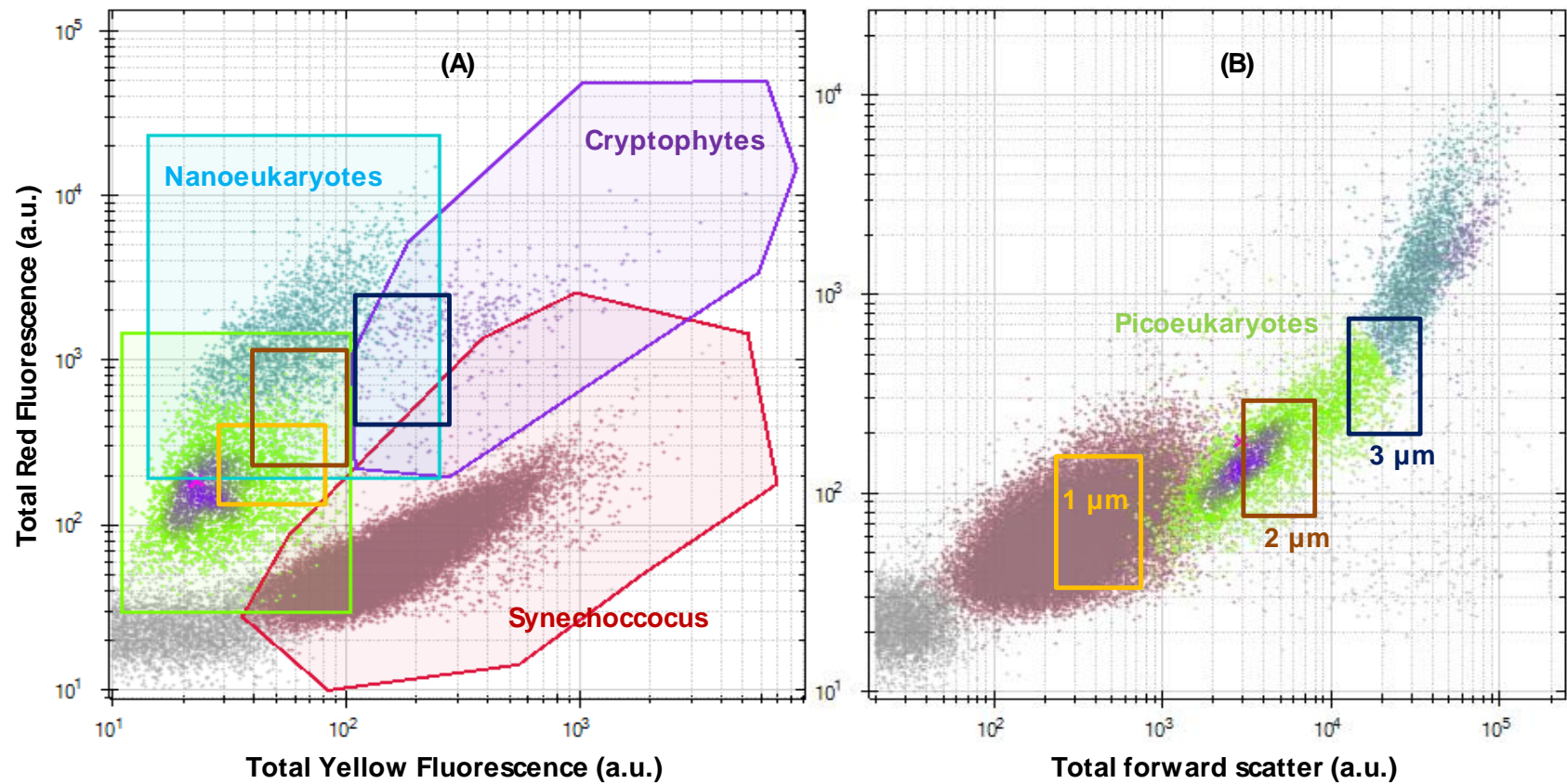


Figure 6. Cytograms representing the Total Red Fluorescence (Total stands for area under the pulse shape curve, a.u.) vs Total Yellow Fluorescence (a.u.) signatures used to classify *Synechococcus* and *Cryptophytes*-like (A) and the Total Red fluorescence (a.u.) vs the Total Forward scatter (a.u.) for the classification of picoeukaryotes and nanoeukaryotes (B). Scares represent the areas where silica beads are observed as a memory footprint for size classification.

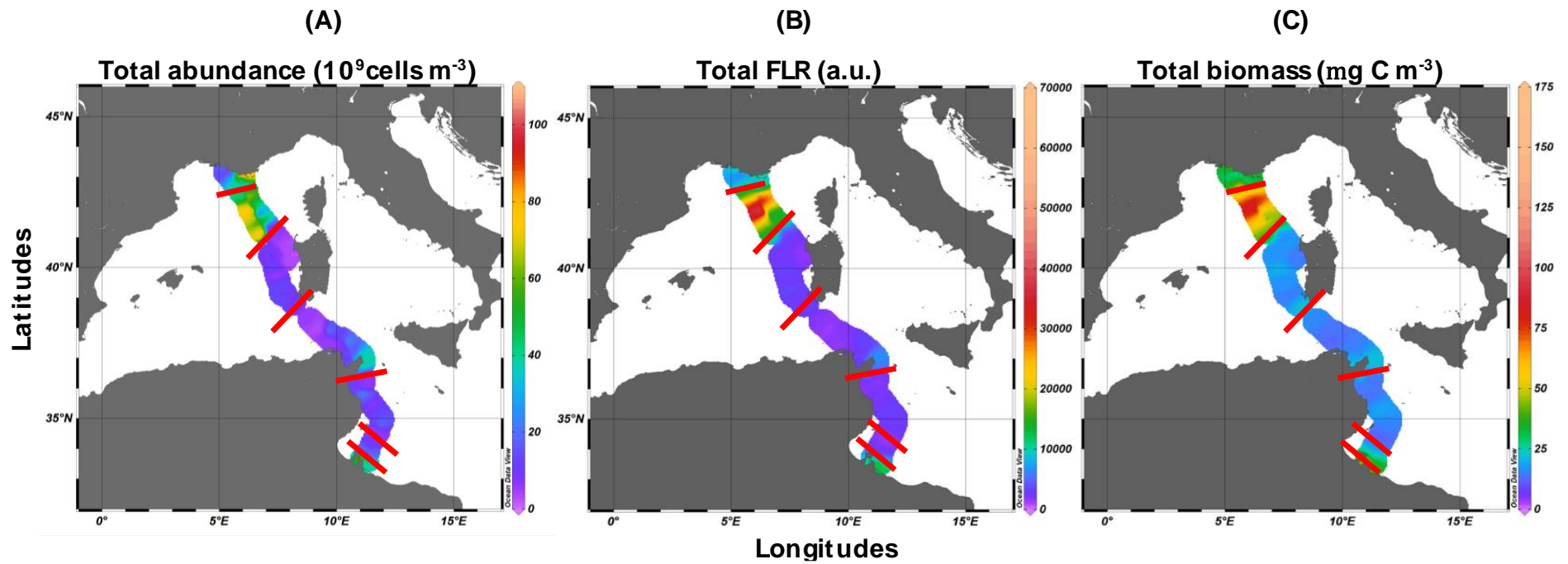


Figure 7. Distribution of total (sum of each ultraphytoplankton group) abundance ($10^3 \text{ cells m}^{-3}$) (A), FLR per unit of volume (a.u. m^{-3}) (B), and biomass (mg C m^{-3}) (C) in the subsurface waters of the round trip transect.

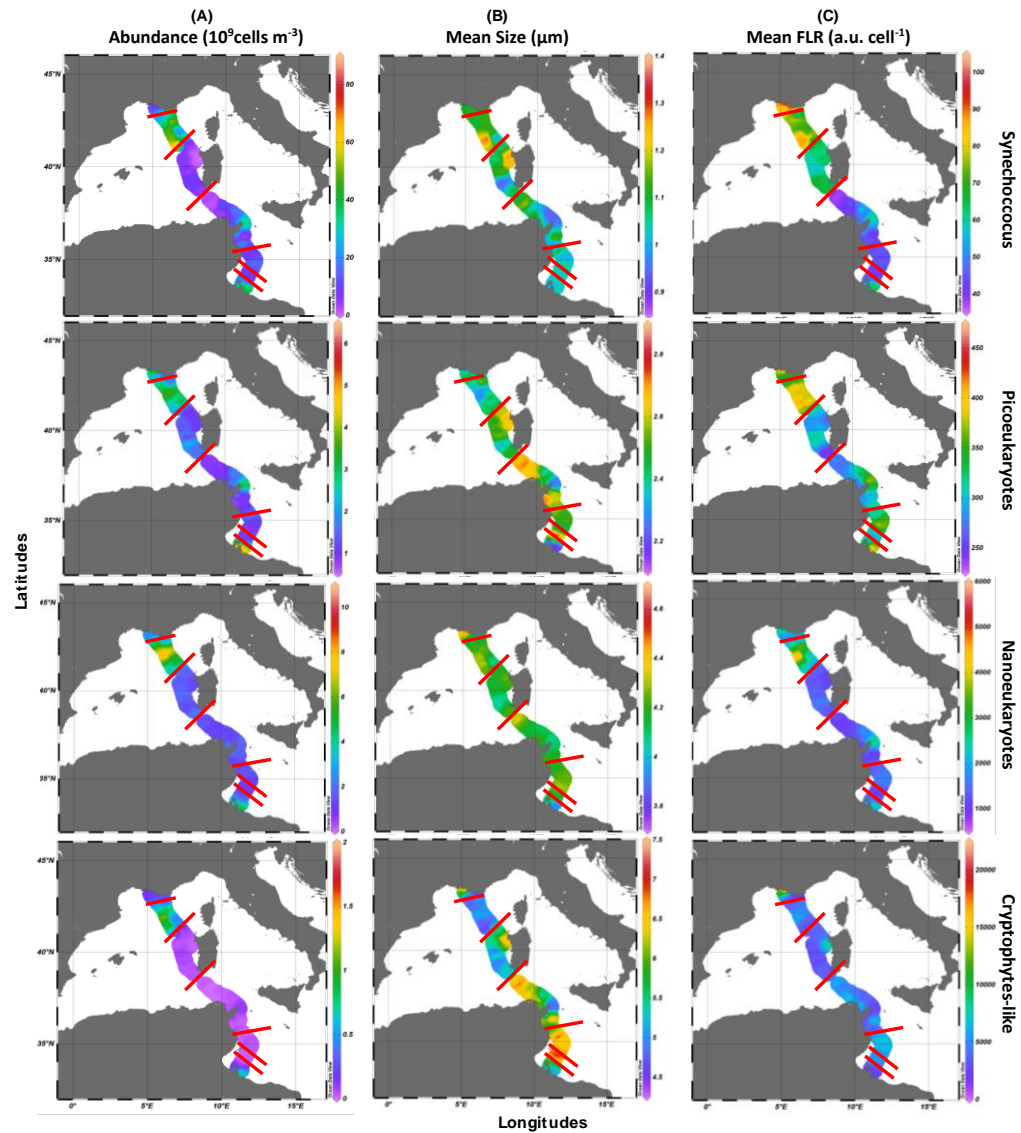


Figure 8 Spatial distribution of the abundances ($10^9 \text{ cells m}^{-3}$) (A), mean cell size (μm) (B) and mean FLR (a.u. cell^{-1}) for the four resolved groups. Red lines represents the 7 zones (Z1 to Z7) generated by hierarchical classification.

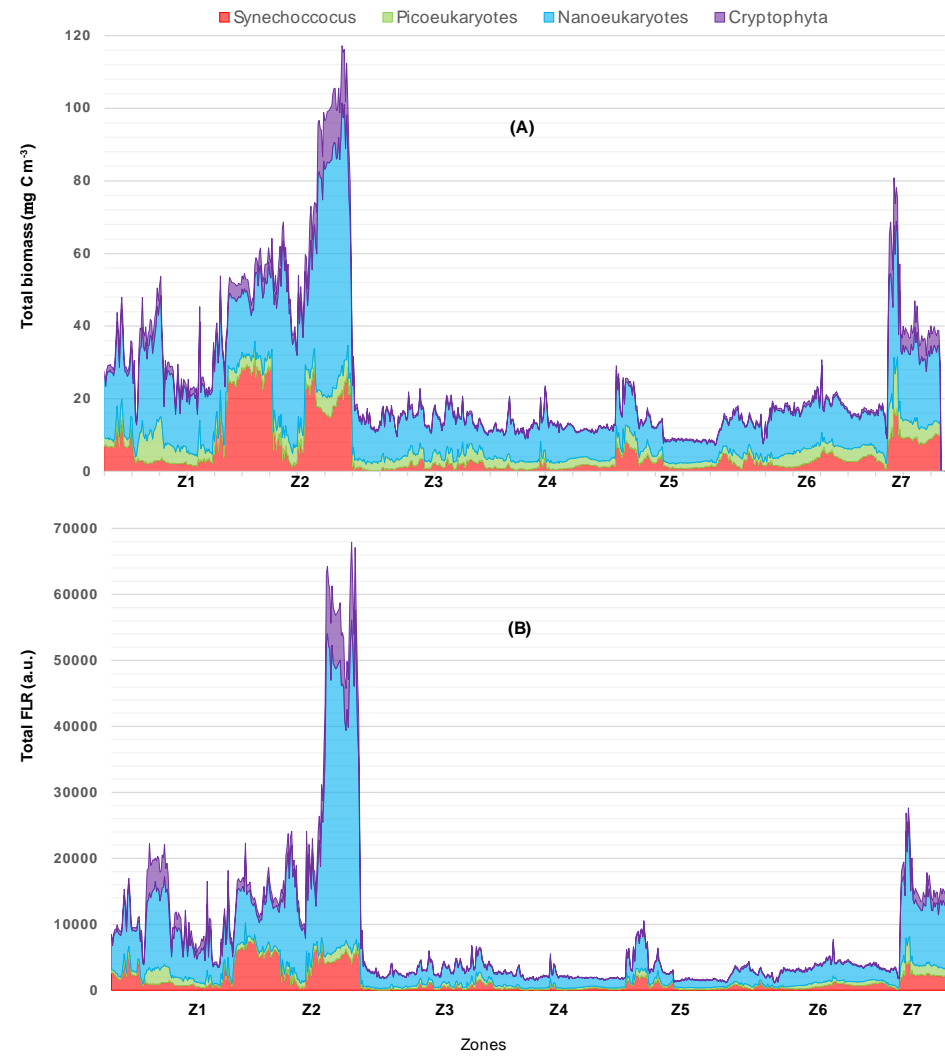


Figure 9 Total biomass contribution of *Synechococcus*, *picoeukaryotes*, *nanoeukaryotes* and *Cryptophytes-like* along the 7 zones in terms of biomass (mg C m^{-3}) (A) and FLR_{cell} (B)

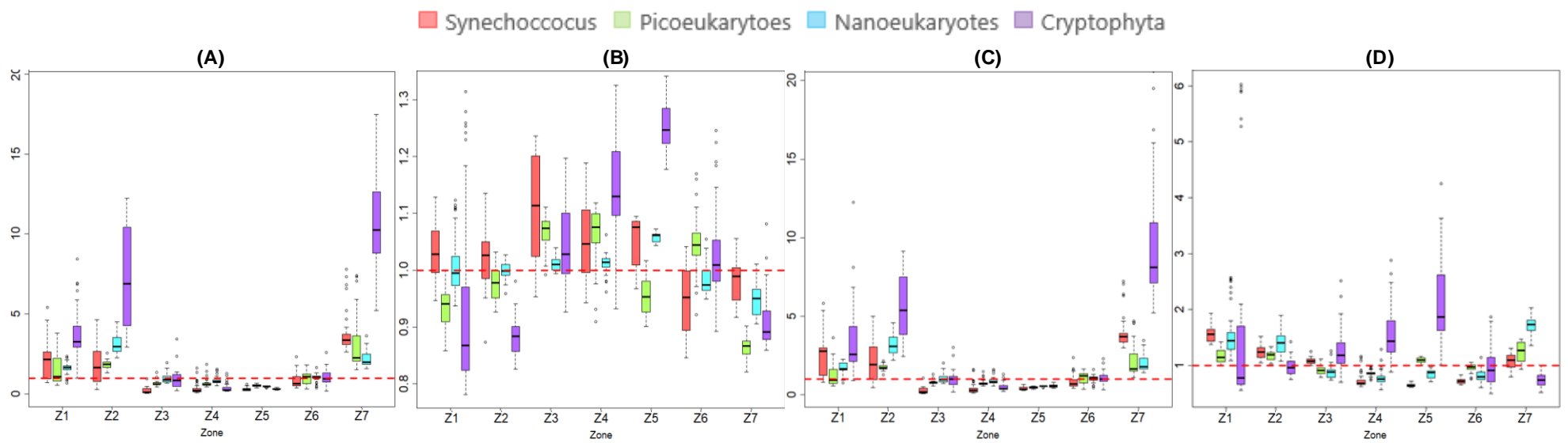


Figure 10 Spatial variability of median-normalized abundance (A), mean size (B), FLR_{cell} (C) and biomass (D) for each ultraphytoplankton group; with red line representing the normalized median =1

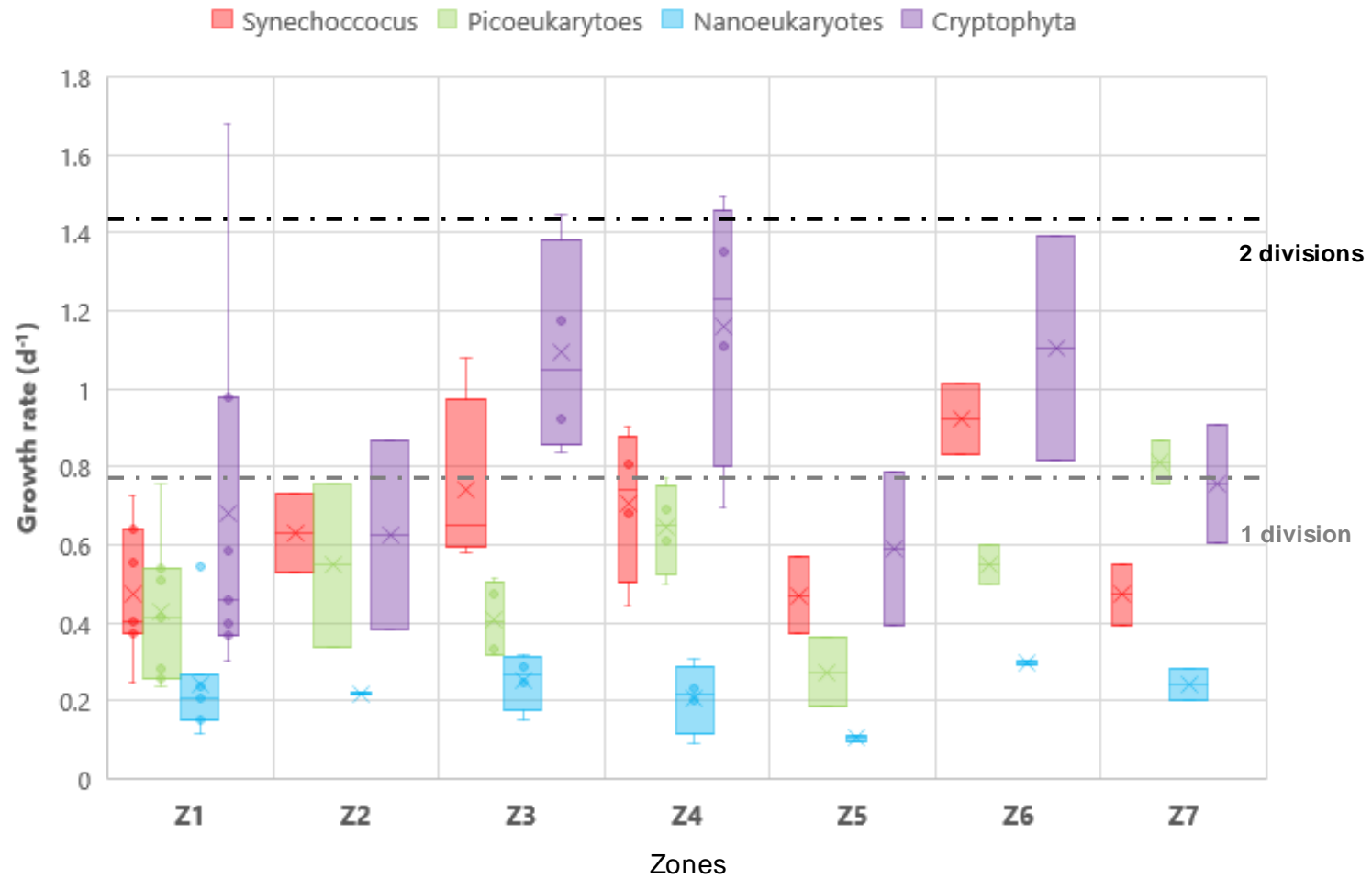


Figure 11 Growth rate variation by zones for the Synechococcus, picoeukaryotes, nanoeukaryotes and Cryptophytes-like with 0.69 (grey dotted line) and 1.38 (black dotted line) respectively corresponding to 1 and 2 divisions per day