**ABSTRACT**

Among coral reef systems, Tuamotu atolls are of great interest because they are very productive compared to the surrounding ocean and they host numerous pearl oyster farms in their lagoons, with a high economic value. To improve the understanding of the nutritional behavior of larvae, juveniles and adults of the pearl oyster *Pinctada margaritifera*, an European program has begun in 2008 for 3 years (1) to study the planktonic productivity of Ahe atoll and (2) to evaluate experimentally the contribution of the various nature and size of organisms and particles (Transparent Exopolymeric Particle, bacteria, pico-nanophytoplancton, microphytoplankton, protists, metazooplankton) to the diet of pearl oysters.

The first survey conducted in May 2008 revealed a spatial and temporal distribution of plankton in the lagoon which was different of planktonic structure observed in surrounding ocean (e.g. lower concentrations of bacteria but higher bacterial diversity, lower abundances of picoautotrophs and ciliates). Specific biological characteristics were noted at the station located in the west part of the lagoon (noted L1) such as lower concentrations of *Prochlorococcus* (picocyanobacteria) and photosynthetic capacity values of picophytoplankton and higher concentrations of nanoflagellates and ciliates. The metazooplankton dominated by small organisms (bivalve larvae, copepod nauplii, *Oithona* spp, Clausocalanidae) displayed a clear spatial pattern with higher abundance at two stations (P1 and P11).

At the atoll scale (4 stations and 3 depths at three dates), the principal preys for larvae and juveniles of oysters can be represented in term of carbon biomass as follow: nanoflagellates (35% of heterotrophs) followed by bacteria, autotrophic picophytoplankton dominated by picocyanobacteria (*Synechococcus*: 61%; *Prochlorococcus*: 4.8% and picoeukaryotes: 4.1%). The microplankton (ciliates and diatoms) was low represented in the lagoon system. Grazing pressure by larvae and juveniles on these preys was estimated by experiments in batches.

**Keywords**

Atoll lagoons; larvae, juveniles and adult of pearl oyster; plankton, distribution.

**INTRODUCTION**

The planktonic food webs of coralline atolls have become the focus of interest in recent years because of the development of pearl oyster farming. These oysters interact directly with the planktonic food web. Additionally, they have attracted attention because of the seemingly increasing frequency of mass faunal mortality events abetted by algal blooms. Thus, the lack of knowledge concerning the global functioning of the planktonic community has become apparent. So far, the planktonic system has remained poorly described in coral reef ecosystems [1, 2] as most studies have focused on open shallow reefs dominated by benthic metabolism [3].

In this paper, we report preliminary results about (1) the spatial and temporal abundance and biomass of potential food for pearl oyster, especially the phytoplankton by size classes (< 2 µm-pico, between 2 and 20 µm-nano, > 20 µm-micro), bacteria, zooplankton (2) the diet (potential retention rate) of different class size of oysters during the first survey, in May 2008 in the Ahe lagoon.

**1. MATERIAL AND METHODS**

**1.1 Sites and sampling**

We sampled the lagoon of Ahe in May 2008 along transects of 4 stations at 3 depths. In addition, we also prospected an oceanic station (OCE) located at 500 m outside of the reef (Figure 1). Water samples were collected at each station with a Niskin bottle (5 L) at 0.5 m, 10 m, and 20 m depths.
1.2 Methods

Bacteria and picophytoplankton were fixed with 0.2 µm filtered formaldehyde (final concentration 2%), frozen in liquid N₂ and enumerated using a MoFlo cytometer (DAKO) [4]. Diversity of free bacteria was analyzed by PCR-DGGE method from DNA extracted from cells collected on 0.22 µm pore size filter [5]. Nanoflagellates were fixed with buffered paraformaldehyde (final concentration 1%) then stained with DAPI and counted on 0.8 µm pore-size black polycarbonate filters by epifluorescence microscopy [6]. Heterotrophic nanoflagellates (HNF) were distinguished from autotrophic nanoflagellates (ANF) by the absence of chlorophyll fluorescence. Ciliates were stained with alkaline lugol (1% final concentration), counted and measured by inverse microscopy [7]. Mesozooplankton was collected from vertical tows using a 60 µm mesh WP2 net, preserved in buffered formaldehyde (final concentration 4%) and counted under a binocular microscope.

To convert the abundance of the various planktonic compartments (pico-nano and microplankton) into carbon biomass, conversion factors from the literature were applied to the abundances obtained in this study (Table 1).

Table 1: Conversion factors from the literature used to convert abundance to carbon biomass. C: carbon

<table>
<thead>
<tr>
<th>Compartment</th>
<th>Conversion factor</th>
<th>References</th>
</tr>
</thead>
<tbody>
<tr>
<td>Prochlorococcus</td>
<td>60 fg C/cell</td>
<td>Charpy and Blanchot (1998) [10]</td>
</tr>
<tr>
<td>Synechococcus</td>
<td>178 fg C/cell</td>
<td>Charpy and Blanchot (1998) [10]</td>
</tr>
<tr>
<td>Nanoflagellates</td>
<td>3140 fg C/cell</td>
<td>Flegri et al (1999) [12] modified by this study</td>
</tr>
<tr>
<td>Ciliates</td>
<td>2318 pg C/cell</td>
<td>Putt and Stoecker (1989) [13]</td>
</tr>
</tbody>
</table>

2. PRELIMINARY RESULTS AND DISCUSSION

2.1 Spatial distribution of planktonic organisms in May 2008

In the lagoon, total plankton abundance (without diatoms and dinoflagellates, not enumerated yet) was not different between the stations (average of 8x10⁷ cells/mL). In the ocean, abundance was twice lower than in the lagoon (4x10⁵ cells/mL, Figure 2).

In term of carbon biomass, the ocean station had the lowest carbon biomass (100 µg C/L) (Figure 2). There was a gradient of carbon biomass between L1 (> 200 µg C/L) to L9 and the station L11 was an intermediate station (< 150 µg C/L).

2.2 Composition, abundance and carbon biomass of planktonic organisms

2.2.1 Picoplankton

The picoplankton was composed by bacteria, Prochlorococcus, Synechococcus and picoeukaryotes (Figure 3). In term of abundance, bacteria dominated in and outside of the lagoon, followed by Synechococcus, Prochlorococcus and picoeukaryotes. In term of biomass, Synechococcus and bacteria dominated the plankton. Prochlorococcus and picoeukaryotes have a very low contribution of carbon biomass.
Diversity of bacterial communities was analyzed by PCR-DGGE and showed a relative low diversity with well defined bands corresponding to the most abundant bacterial species (Figure 4). After image analysis, we can note, that certain bands were found whatever the sampling station whereas others were specific of one station or one level (Figure 5). Re-amplification and sequencing of DNA fragments excised from the bands is under going analyses in order to identify the main strains.

2.2.2 Nanoflagellates

Nanoflagellate abundance showed the same pattern than those of the carbon biomass. Nanoflagellates were dominated by ANF with a minimum at station L9 and ocean (Figure 6).
2.2.3 Ciliates

Ciliate abundances also showed the same pattern than the carbon biomass. The abundance and biomass of ciliates in the ocean was very low (< 100 cells/L) (Figure 7). There was a gradient between L1 and L9 with a maximum value at stations L1 and L11, far of the lagoon mouth.

![Figure 7: Mean of ciliates abundance (cells/mL) and biomass (µg C/L) for the three depths according to the station.](image)

2.2.4 Mesozooplankton

The metazooplankton was composed by a majority of copepod nauplii, *Oithona* spp, Clausocalanidae and bivalve larvae in meroplankton (Figure 8).

![Figure 8: Mean abundance of the main metazooplankton groups (organisms/m³) according to the station.](image)

The metazooplankton was more abundant in the lagoon than in the ocean particularly at stations L1 and L11. There was more meroplankton at station L1. The abundance presented the same pattern than the carbon biomass. Finally, the herbivorous biomass was similar to the carnivorous part in the lagoon, but represented 80% of total biomass in the ocean.

2.2.5 Autotrophy/heterotrophy ratio

The ratio of heterotrophy/autotrophy was near 1 in the ocean corresponding to an equilibrium between the two metabolic processes (Figure 9). In the lagoon, the heterotrophy/autotrophy ratio was more lower (mean of 0.6) suggesting that the primary production was higher and preponderant in lagoon versus ocean.

![Figure 9: Heterotrophy/autotrophy ratio according to the station](image)

To summarize, in lagoonal and oceanic waters, 95 % of abundance of planktonic organisms was composed by cells with a size less than 2 µm (picoplankton) with a dominance of bacteria. In term of biomass, nanoflagellates dominated largely with 73 % of carbon biomass in the lagoon (Figure 10).

![Figure 10: Example of % of each planktonic group at station L1 of total abundance (left) and carbon biomass (right).](image)

2.3. Potential retention of planktonic organisms by the pearl oyster: focus on different sizes of oysters

The percentage of contribution of each taxon to the total retained resource (without diatoms, dinoflagellates and mesozooplankton) by different size of oysters (3, 6 and 10 cm) was calculated to multiply the clearance rate of oyster (known by ecophysiology experiments) by carbon biomass of each potential taxon (Figure 11: example for an oysters of 3 cm). The calculation of the potential retention of one oyster was conducted in each station of the lagoonal water.
In conclusion, diet of juveniles and adult oysters are composed whatever the station by around 90 % of nanoflagellates (Figure 10). The other carbon sources are secondary in the diet with very few percentages whatever the class size of oysters. In Ahe lagoon, the oysters *Pinctada margaritifera* seem to have the same composition of diet in May 2008. The picoplankton organisms are dominant in term of abundance (95 %) but they participate indirectly in the diet of pearl oysters from juveniles to the adults (average of 10 %). Thus, microbial food web appears very active and appears essential to the accessibility of the carbon source for juveniles to adult’s pearl oysters.

3. ACKNOWLEDGMENTS

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4. REFERENCES


