CARBON STEADY STATE MODEL OF THE PLANKTONIC FOOD WEB IN THE BIZERTE LAGOON

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Abstract

A steady state model of the planktonic food web of the Bizerte Lagoon (Tunisia, western Mediterranean) was developed to characterize the structure and the functioning of its planktonic system. Carbon stocks of eight chosen compartments were determined and flows were assigned for each one from field data. Missing flows were, however, calculated by inverse analysis. The model showed a high phytoplankton and bacterial productions, which were actively channelled to mesozooplankton *via* severe grazing by microzooplankton. Moreover, results indicated that detritus played key role in the carbon cycling of the lagoon. Indeed, detritus were actively consumed by mesozooplankton and/or transformed to dissolved organic carbon (DOC) which was mostly consumed by bacteria. *Keywords : Plankton, Food Webs, Inverse Methods, Lagoons.*

Introduction

Since inverse method constitutes a powerful tool to estimate ecosystem flows, it has been used to build complete models of carbon flows in a wide range of aquatic environments [1-2]. These models provide an internally consistent description of trophic interactions among various functional groups of the ecosystem. The Bizerte Lagoon is under a high anthropogenic pressure, but until now the global functioning of the planktonic community wasn't investigated. The aim of the study was to build up a model of the planktonic food web in the lagoon.

Material and methods

Study was carried out on July 2004 at one station of the lagoon, which is under urban pollution. Water sampling was performed at three depths. Samples were used for determination of dissolved organic carbon (doc) and particular organic carbon (poc) concentrations [3], and carbon stocks of bacteria (bac), phytoplankton (ph1, ph2, ph3) and microzooplankton (mic). Vertical tow was performed to determinate carbon biomass of mesozooplankton (mes). Production rates of phytoplankton and bacteria and microzooplankton consumption rates on them were estimated from dilution method [4]. Vertical fluxes of carbon particles were measured with sediment traps [5]. Missing flows were calculated by inverse approach [1], which was also used to construct the complete steady state carbon flows. To characterize efficiently the food web structure, network analysis were applied to the resulting flows.

Results and discussion

Inverse solution for the planktonic food web flows is represented in the figure 1.



Fig. 1. Inverse solution for planktonic food web flows in the Bizerte Lagoon during summer 2004.

Each carbon flow is represented by an arrow that width is proportional to the calculated value. The main carbon input was supported by the primary production (1495 mg C m⁻² d⁻¹). >10 μ m phytoplankton (ph3) con-

tributed largely (93%) to this carbon input. Allochthonous carbon input accounted for 106 mg C m^{-2} $d^{-1}.$

Total respiration represented 60% (947 mg C m⁻² d⁻¹) of the total carbon input. Algal respiration did not exceed 5% of their primary production, which corresponded to the minimum given by the constraint on the respiration. Heterotrophic bacteria and zooplankton were the major contributors to the respired carbon loss (485 and 381 mg C m⁻² d⁻¹, respectively). The remaining carbon outputs from the system were driven by the sinking fluxes (561 mg C m⁻² d⁻¹, 35% of carbon outputs) and the consumption of mesozooplankton by the highest trophic levels (93 mg $C m^{-2} d^{-1}$, 5% of carbon outputs). Grazing by microzooplankton (705 mg C m $^{-2}$ d $^{-1})$ removed 21% and 49% of the production of 2 $\cdot 10~\mu m$ phytoplankton (ph2) and ph3, respectively. Mesozooplankton grazed only on ph3 and contributed of 5% of their production loss. doc exudation by algae (329 mg C m⁻² d⁻¹) accounted of 22% of primary production. The most important flows were those where bacteria was implicated. Indeed. >80% of the DOC uptake by bacteria originated from the exudation of the living compartments. The bacterial path was important in Bizerte Lagoon, with major pathways going from living compartments to detritus (det), then to doc and finally to bacteria. These latter were in turn consumed by microzooplankton. Microzooplankton grazing on bacteria (485 mg C m⁻² d⁻¹) represented 50% of bacterial production. Bacterivory and herbivory accounted for 40 and 60% of microzooplankton diet, respectively. However, herbivory contributed of only 20% of the mesozooplankton diet. Microzooplankton provided the remainder carbon demand of mesoconsumers. The carbon flow that has a cyclic pathway through the system is determined by Finn Cycling Index which value was 26. The main emergent property of the system is a good recycling activity with a balance between herbivory against bacterivory.

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