



Ecohydrodynamic modelling on the cycle of organic carbon

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Abstract

A 2D coupled hydrodynamic-ecosystem model is applied to the simulation of the biological processes on the coastal areas near Tianjin. The biological sub-model describes the carbon cycles through the microbial food web with eight state variables: phytoplankton, zooplankton, bacterioplankton, pelagic detritus, dissolved organic carbon, dissolved organic nitrogen, ammonium and nitrate. In this paper, the results emphasize the relations of the calculating values and the monitoring values of phytoplankton's and bacterioplankton's on the space-time distribution in Bohai Bay. The results of this model also show that the ecohydrodynamic model is adaptive to the water layer of Bohai Bay.

Key words: Bacterioplankton, Ecosystem modelling, Carbon cycle, Bohai bay

1. Introduction

The number of ecological models applied to marine areas is increasing steadily. The scope of their applications is broadening every day. The confidence put on these models by policy makers is also, hopefully, increasing. This is certainly due to the evolution of the ecological models towards a mature stage. The bulk dissolved organic matter (DOM) pool is still largely uncharacterized (Ducklow *et al.*, 1995), despite the importance of DOM dynamics in understanding carbon fluxes in marine systems (Toggweiler, 1988). DOM in surface waters typically exhibits a carbon-rich seasonal increase (Williams, 1995), lagged after chlorophyll peaks (Banoub and Williams, 1973; Ittekkot, 1982; Wafar *et al.*,

1984). A variety of dissolved compounds are produced, ranging from simple sugars and amino acids to complex carbohydrates. The persistence of the DOM pool depends on the rate at which biological and other processes act to break it down. Whereas the smallest molecules may be taken up directly across bacterial membranes, ectoenzymatic hydrolysis (Chróst, 1990), or some other process, must normally occur before larger molecules can be utilized (Anderson, 1998).

One must however recognize that evolution of ecological modeling is characterized by two very slowly converging paths: on one side, the models include a very detailed representation of the biology but miss much of the spatial variability of the system (Billen and Lancelot, 1988; Baretta *et al.*, 1995). On the other side, some models offer a coarser representation of the food web but retain