SIMULATIONS OF THE PHYSICAL AND BIOLOGICAL VARIABILITY AT A NORTHERN ADRIATIC SEA STATION: THE IMPACT OF TURBULENCE CLOSURE SCHEMES AND BOUNDARY FORCING

Marcello Vichi [1], Sandro Carniel [2]*, Lakshmi Kantha [3], Mauro Sclavo [2]
[1] Istituto Nazionale di Geofisica e Vulcanologia, Via D. Creti, 12, Bologna I-40100, Italy - vichi@bo.ingv.it
[2] National Research Council, Istituto per le Scienze del Mare San Polo 1364, Venice I-30125, Italy
* Sandro.Carniel@ve.ismar.cnr.it - Mauro.Sclavo@ve.ismar.cnr.it
[3] Department of Aerospace Engineering Sciences, CB 431, University of Colorado, Boulder, CO 80309, United States
kantha@colorado.edu

Abstract

A 1-D model, coupling the physical model GOTM and the ecosystem model ERSEM, has been used to hindcast physical and biological variability in the northern Adriatic Sea. We studied the impact of the turbulence closure model (TCM) on the thermal structure and biological productivity. Results compare favorably with physical observations (Fig. 1). The hindcast of biological variables is however less satisfactory. The results are not sensitive to the second moment TCM used. Changes are however, striking when different boundary conditions are applied on nutrients (Fig. 2). This suggests that sources of uncertainties other than the TCM, need to be explored to hindcast the biological state better.

There is a generalized, widely-held view that an accurate simulation of the physical state is a pre-requisite to the proper simulation of the biological state. Biology is expected to directly respond to physical variability, and ecosystem models should be able to encompass this dynamical behavior. The aim of this work was to investigate how relevant the description of physical processes is in the dynamics of shallow ecosystems with respect to other potential sources of uncertainties.

Therefore, a 1-D coupled physical-biological model has been used to hindcast the observed seasonal variability for the year 2001 at a shallow water station in the northern Adriatic Sea of approximately 29m depth (Lat 45.25° N, Long 12.76° E).

The model couples two existing state-of-the-art submodels: the General Ocean Turbulence Model (GOTM, [1]) and the most recent version of the European Regional Sea Ecosystem Model (ERSEM III, [2]).

A relatively high abundance of biological observations are available at this site for comparison with the model results.

We tested a variety of turbulence closure models (TCMs) and boundary forcings, and assessed their impact on the simulation of the thermal structure (Fig.1) and primary producers (e.g. flagellates, Fig. 2) at the station. The chosen schemes were: 1) k-epsilon; 2) generic length scale; 2) k-omega and 3) a simple 1-equation model.

Significant differences in the thermal cycle between the model and the observations become evident only when low-order TCMs are adopted (see differences between k-epsilon and 1-equation in Fig. 1) or when the surface forcing is incomplete (e.g., salinity prescribed only at surface) or when the frequency of surface forcing is changed (e.g., wind stress from hourly to 6-hourly). Significant differences also show up in the biochemical variables under these conditions (Fig. 2).

The use of high-frequency physical forcing lets the model achieve a satisfactory agreement between modeled and measured temperatures in the water column The results differ only slightly when different state-of-the-art second order TCMs are used, which suggets that these TCMs have converged in recent years. Biological variables in these cases are mostly unaffected by the changes in TCM.

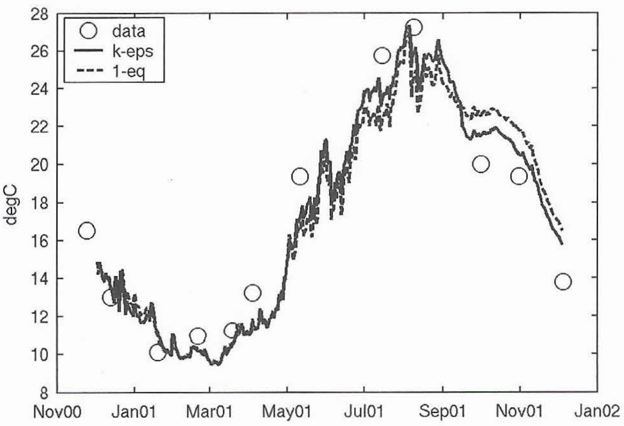

Fig. 1. Model-data comparison for temperature. Model results obtained with the k-epsilon and the 1-equation TCMs.

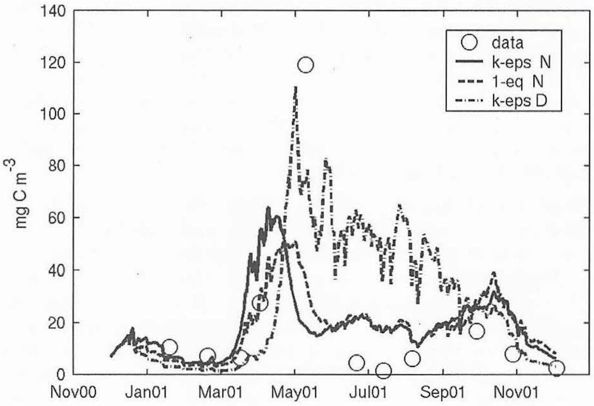

Fig. 2. Model-data comparison for phytoplankton (e.g. flagellates). k-eps N = k-epsilon TCM with Neumann BC; 1-eq N = 1-equation TCM with Neumann BC; k-eps D = k-epsilon TCM with Dirichlet BC

Our conclusions are that, at least in this case, the current status of physical model is such that it is able to provide a sufficiently accurate description of the physical state of the water column.

However, the description of the observed biochemical variability is still far from satisfactory. Therefore, we investigated the importance of other potential sources of unertainty, as for example the ways of including the nutrient data as boundary conditions (BC), which are extremely important in this area due to the presence of the Po river. Fig. 2 shows how phytoplankton results are strongly sensitive to the change of BC from von Neumann to Dirichlet methods. Similar results are obtained if other important model parameters are varied, such as the ones involved in the C:Chl ratio dynamics.

It appears thus necessary to focus on the refinement of the parameterization of biochemical processes, and explore the interactions with other unknown factors such as the proper assimilation of external inputs.

References

1 - Burchard, H., Bolding, K., Villarreal, M.R., 1999. GOTM, a general ocean turbulence model. Theory, implementation and test cases, European Commission, Report EUR 18745, 103 p.

2 - Vichi, M. Baretta, J.W., Baretta-Bekker, J.G., Ebenhöh, W., Kohlmeier, C., Ruardij, P. European Regional Seas Ecosystem Model III. Review of the biogeochemical equations. http://www.bo.ingv.it/ersem3