

The coastal area is of particular interest due to its high productivity, the affluence of freshwater and nutrients from land, and the global carbon flux. In the pelagic marine environment, two contrasting pathways of the flux of biogenic carbon from autotrophic to heterotrophic organisms have been defined: the herbivorous and the microbial food webs (Legendre and Rassoulzadegan, 1995). Physical characteristics of the water column define the food web of a particular area: mixing stimulates the herbivorous food web while stratification favours the microbial food web. We aim at understanding the low trophic level ecosystem structure in a typical estuarine Gulf such as the Gulf of Trieste (Italy). The coupling of the numerical models Princeton Ocean Model (1D) and the Biogeochemical Flux Model (BFM) enables to study how the trophic chain works in a typical estuary such as the Gulf of Trieste (Italy). Statistical analysis was performed on data following the year 2000 in order to force the initial physical data in the model and compare other variables with model results. Two experiments were then performed to investigate the microbial role in the carbon cycling that determines differences between the microbial pathway and the herbivore pathway, and to investigate the competition between plankton and bacteria on nutrients cycling. The experiments tested the model sensitivity with different closure remineralization rates when bacteria were removed from the system and when all the microbial system was isolated. Results demonstrated the high model sensitivity for small changes and therefore the reliability. We show how bacteria play a major role in the definition of the local food web by competing with phytoplankton. Also, we find that when bacteria and the whole microbial system are removed the system shifts from P-limited to N-limited and from "bottom-up" to "top-down" control.