

# Modeling microbial food webs in the East China Sea before the construction of the Three Gorges Dam

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## ABSTRACT

Using Ecopath with Ecosim, mass-balanced trophic models were constructed at sites along transects from the Changjiang Estuary and the coast of mainland China across the East China Sea to the west edge of Kuroshio to characterize the microbial carbon flows in the euphotic zone. Each model comprises 7 compartments, including large phytoplankton (>3 $\mu\text{m}$ ), small phytoplankton (<3 $\mu\text{m}$ ), heterotrophic bacteria, flagellates, ciliates, particulate organic carbon (POC) and dissolved organic carbon (DOC). Total biomass increased from the coast waters to Kuroshio. Phytoplankton was normally the most dominant compartment in the East China Sea, however, bacteria dominated near the estuary, but shifted to phytoplankton in summer. Total system throughput (TST) was highest in summer and lowest in autumn. Bacteria respired 12-158 % of the primary production, flagellates respired 3-6 %, and ciliates respired 1-2 %. The most important pathways of microbial carbon flow were DOC being absorbed by bacteria, reaching 15~23% of TST. Exports of POC and DOC from microbial food web to upper trophic level or to the deeper ocean were respectively estimated to be  $0.020\sim 0.479 \text{ g C m}^{-2} \text{ d}^{-1}$  and  $-0.104\sim 1.009 \text{ g C m}^{-2} \text{ d}^{-1}$  or  $9058 \times 10^9 \text{ g C yr}^{-1}$  and  $8915 \times 10^9 \text{ g C yr}^{-1}$ .

KEY WORDS: Ecopath, Continental shelf, Microbial food web, Trophic model, POC, DOC