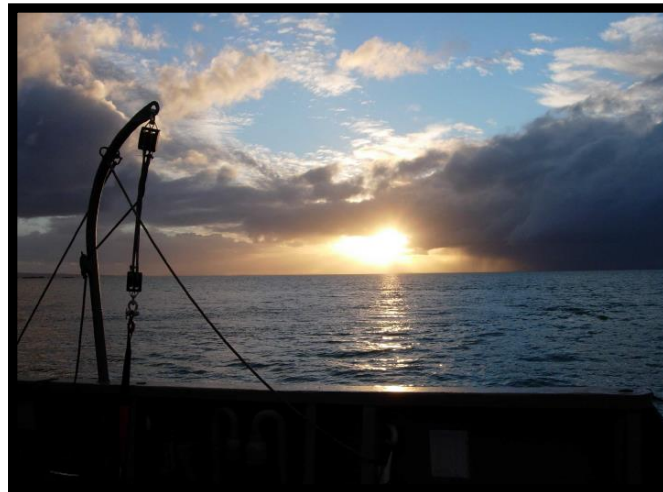


CARBON FLUXES OF TWO PELAGIC COMMUNITIES IN THE NORTH CHILEAN PATAGONIAN COASTAL SYSTEM



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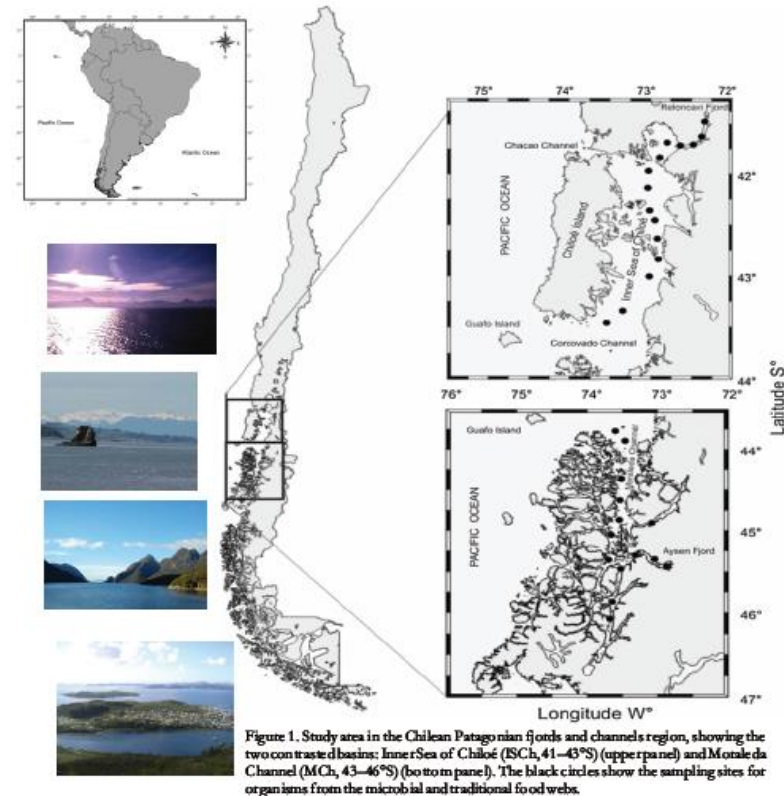
ABSTRACT

We built two Ecopath models for the Chilean marine patagonian ecosystems, Inner Sea of Chiloe – ISCh and, Moraleda Channel – MCh (Fig. 1)

Our objective was to study the role of different marine functional groups in the trophic carbon fluxes through the pelagic food webs. The models included 4 small-scale fisheries and 36 functional groups.

Biomass

The ISCh total biomass was ~1.5 times higher than in the MCh (13.5 g C m⁻² vs. 8.9 g C m⁻²). *MCh*: higher biomass in top predators, Gadiformes, Hydromedusae and Nauplii. *ISCh*: Mphyto, Bacteria, Copepoda.



Carbon fluxes to the detritus

In ISCh and MCh was produced ~ 699 and 376 g C m⁻² y⁻¹ m year of detritus, respectively, of which 63% and 59% were in the form of DOM and the rest was POC (Fig. 2).

Mphyto produced 49% and 56% of the DOM in ISCh and MCh, and the pico- and nanoplankton were responsible for 46% and 38% of this total DOM (Fig. 3).

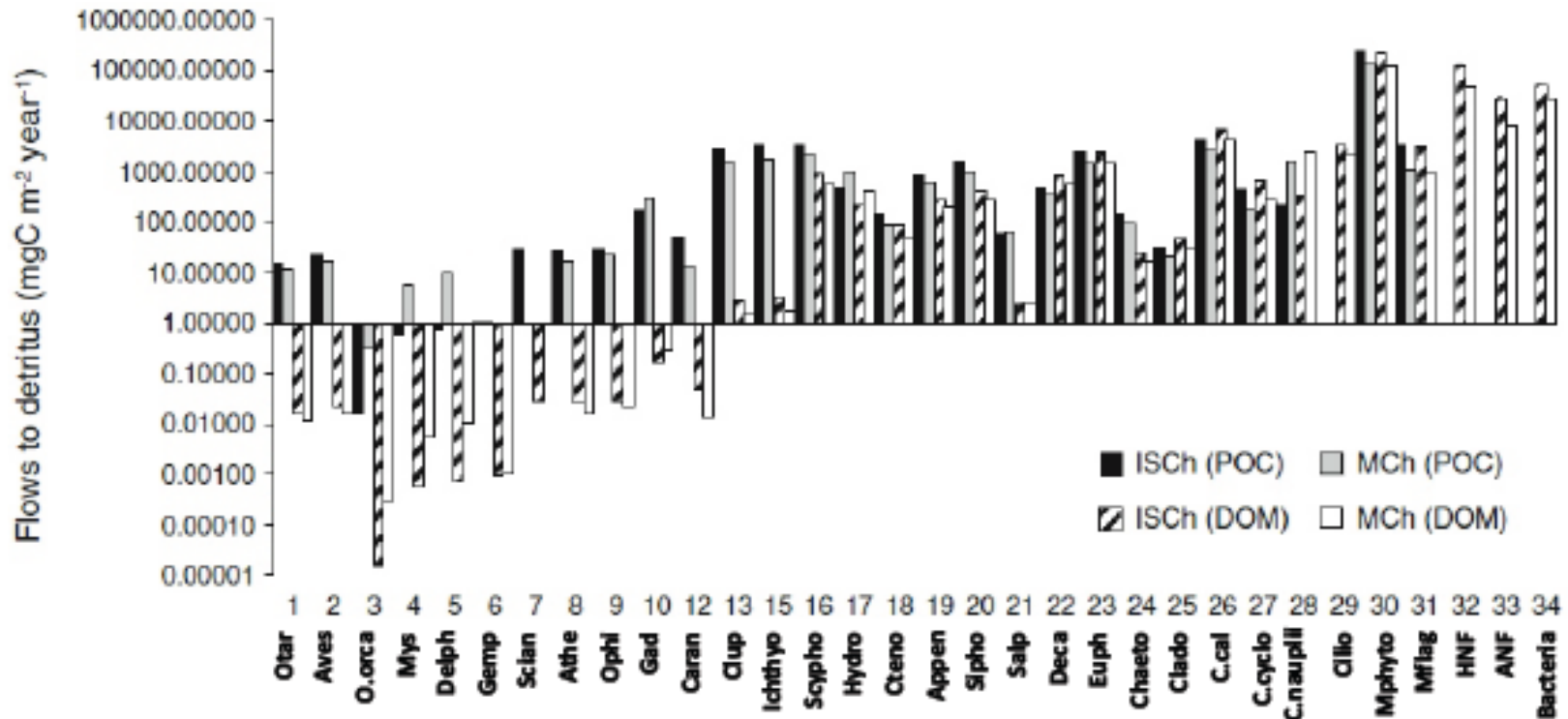


Figure 2. Carbon flow (mgC m⁻² y⁻¹) to detritus from the different functional groups of the Northern Patagonia pelagic system: Moraleda Channel (MCh) and Inner Sea of Chiloé (ISCh). The functional groups are numbered as in Table 1. Note log scale in the abscise.

Carbon fluxes to the detritus

The Mphyto contributed with 90% of the total POC, macro-, mesoplankton groups added 7%, and the nekton contributed 3%.

Keys groups in the detritus flow:

Top predator: Aves

Fishes: Clupeiformes

Gelatinous plankton: Scyphomedusae

Chitinous plankton: Cop. Calanoida

Microplankton: Mphyto

Nanoplankton: HNF

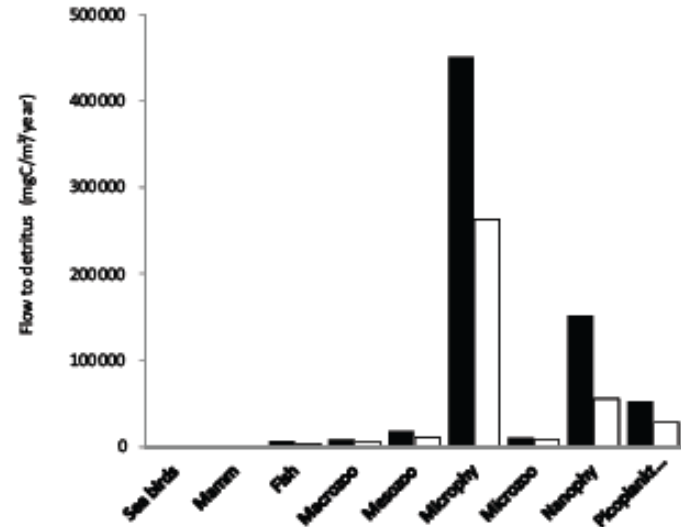


Figure 3. Carbon flow (mgC m⁻² y⁻¹) to detritus from the different marine groups of the Northern Patagonia pelagic system: Moraleda Channel (MCh) and Inner Sea of Chiloe (ISCh).

Final ideas:

In this research it was possible to highlight the key role of the microbial loop over traditional food web in the functioning of the carbon biological pump in Patagonia ecosystems.

It was also possible to determine the more important functional group in terms of carbon flux along the food web analyzed.

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