

## COULD $^{234}\text{Th}$ PARTITIONING IN SEAWATER BE KRILL-DRIVEN?

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### Abstract

$^{234}\text{Th}$  is considered a useful tracer of oceanic biogeochemical processes occurring over timescales of days to weeks. Traditionally,  $^{234}\text{Th}$ -based particle export mathematical models have not taken into consideration the biological compartment, as typical zooplankton biomass values are not likely to result in significant biologically-mediated interactions with such models. However, recent experimental results for the Mediterranean krill *Meganyctiphanes norvegica* suggest that, if rapid  $^{234}\text{Th}$  uptake by krill is not considered in the modeling, the occurrence of a synchronized molting event within a high-biomass krill school may result in an overestimation of  $^{234}\text{Th}$  based particle flux by as much as one order of magnitude.

**Keywords :** Crustacea, Models, Particle Flux, Radionuclides.

### Introduction

$^{234}\text{Th}$  is a naturally-occurring radionuclide constantly produced in seawater by its soluble parent  $^{238}\text{U}$ . Due to its high particle reactivity and relatively short half-life ( $t_{1/2} = 24.1$  days),  $^{234}\text{Th}$  is commonly used as a proxy to estimate POC export from the upper oceanic water column [1]. This export is usually assessed by quantifying total  $^{234}\text{Th}$  deficits with respect to its conservative parent nuclide  $^{238}\text{U}$  in seawater (*ibid.*). Recent findings for three species of Antarctic crustaceans have suggested that under certain conditions krill-associated  $^{234}\text{Th}$  would generate a several-fold positive export bias in depth-integrated  $^{234}\text{Th}$  profiles [2]. Thus, we have tested this hypothesis by conducting analogous experiments using specimens of *Meganyctiphanes norvegica* krill collected in the NW Mediterranean.

### Material and Methods

Live *Meganyctiphanes norvegica* from the NW Mediterranean were transported to the IAEA-MEL premises (Monaco), where they were acclimated for two weeks to laboratory conditions simulating their original temperature and light conditions (14°C; 37 p.s.u; darkness).

Specimens were individually placed in a 500 ml container containing 400 ml of natural filtered seawater spiked with  $^{234}\text{Th}$ . The seawater was changed and the radionuclide spike was renewed daily. During seawater renewal operations, animals were fed shortly on a mixture of uncontaminated phytoplankton and freshly hatched brine shrimp larvae.

At different times, each individual was  $\gamma$ -counted (high-resolution  $\gamma$ -spectrometry system) alive to determine the radionuclide uptake kinetics. At the end of the 7.5-d exposure period, the individuals were placed for 10 d in new containers with clean filtered seawater that was renewed daily. Individuals were then  $\gamma$ -counted daily to determine radionuclide loss kinetics.

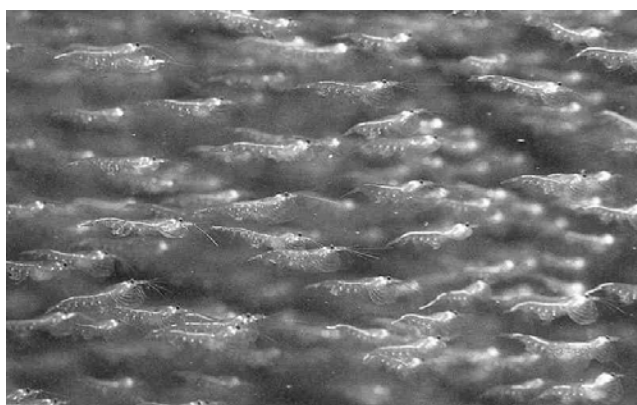


Fig. 1. *Euphausia superba* - Krill [3]

### Results and Discussion

Krill rapidly took up  $^{234}\text{Th}$ , reaching a steady-state concentration factor of about 200 in less than one week, and strongly retained the accumulated radionuclide until molting occurred. At 14 °C krill molt on average every 8 days [4], and during the experiment 9 molting events were observed which indicated that ca. 50% of whole-body  $^{234}\text{Th}$  activity was associated with the exoskeleton.

Immediately following molting a corresponding amount of  $^{234}\text{Th}$  was rapidly adsorbed on the newly formed cuticle. These results, coupled with published values of krill densities as high as  $100 \text{ g l}^{-1}$  [5] (Fig. 1) which commonly occur in the Southern Ocean suggest that  $^{234}\text{Th}$  bioaccumulation could result in up to >90 % of total water-column  $^{234}\text{Th}$  being associated with krill (Fig. 2). Hence, the occurrence of a synchronized molting event [4] within a high-biomass krill school could cause the  $^{234}\text{Th}$  distribution in the water column to be almost entirely a result of radionuclide uptake by these organisms and consequently bias the results of traditional  $^{234}\text{Th}$  based models by more than one order of magnitude.

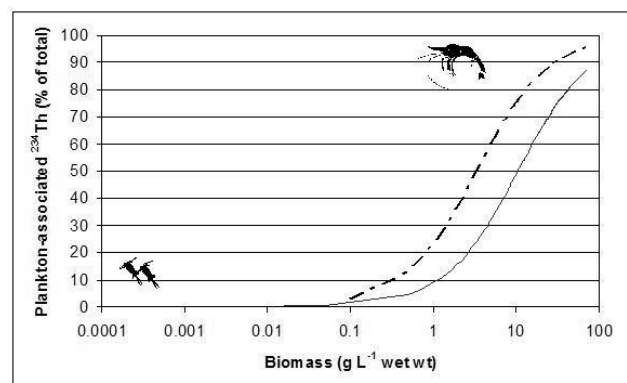


Fig. 2. CF-based computation representing the fraction (%) of total  $^{234}\text{Th}$  in the water column associated with different biomasses of crustacean zooplankton ( $\text{g l}^{-1}$  wet wt), based on mean CF derived from experiments on Antarctic isopods and amphipods (fine dashed line [2]) or on Mediterranean krill (heavy solid line; present study).

### References

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