

The influence of nematode diversity on the decomposition of organic matter and on the associated bacterial community: an experimental approach

De Mesel I., T. Moens, and M. Vincx

Ghent University, Biology Department, Marine Biology Section
K.L. Ledeganckstraat 35, B-9000 Gent, Belgium
E-mail : Ilse.DeMesel@rug.ac.be

The last few years, biodiversity is a hot topic in biological research. Most studies concentrate on describing and comparing diversity in different (micro)habitats. Only few studies have examined the role of biodiversity, i.e. the relationship between diversity and process rates.

This project aims to characterise the role of free-living nematodes in the decomposition of plant-derived particulate detritus in a brackish saltmarsh. Nematodes are the dominant metazoan group in saltmarshes and are characterized by a high species diversity. A stimulatory effect of nematodes as a group or of single nematode species on decomposition is known, but this project focuses on the relationship between nematode species diversity and decomposition rate.

Most nematodes associated with cordgrass (*Spartina townsendii*) belong to the same trophic guild ('deposit feeders') and bacteria are representing their main food source. Because of their seemingly low functional diversity, these nematode communities are ideal for the study of species redundancy in ecosystems. The central hypothesis in this project is that nematodes will affect the decomposition process of *Spartina*-detritus, but that this will be independent of species identity or diversity; in other words, nematodes in this decomposition system have a single 'function' that can be maintained by a single species, others thus being redundant.

In order to test this hypothesis, laboratory incubations of *Spartina*-detritus with and without nematodes have been performed. A total of seventeen treatments were kept under controlled abiotic conditions for 100 days: 4 single species additions, 6 two-species combinations, 4 three-species combinations, one four-species combination, one five-species combination and one control treatment without nematodes. Samples were taken every 10 days. In every sample the nematode community, the bacterial community and the decomposition will be analysed.

Nematodes are being counted and biomasses calculated. The decomposition process will be followed by measurements of weight loss, C/N/P-content and protein content of the organic matter. Bacterial activity is represented by respiration rates, enzyme activity and ATP-measurement. The composition and diversity of the bacterial community will be revealed by the molecular technique DGGE (Denaturing Gradient Gel Electrophoresis).

Future experiments will consist of supplementary laboratory experiments and *in situ* incubations using litter bags.