



Modelling soil properties and organisms' diversity and interactions by food webs

Ch. Mulder and A.M. Breure

Numerical Ecology, National Institute for Public Health and the Environment (RIVM-LER),
P.O. Box 1, NL-3720 BA Bilthoven, the Netherlands (christian.mulder@rivm.nl)

In the Netherlands, we developed a biological indicator for the sustainability of soil use and ecosystem resilience, based on belowground food web interactions, traits and ecological processes of microorganisms, microfauna and mesofauna. We wish to introduce a new school of thought in the diversity-stability debate to achieve a method for complete comparison of structure and functioning of allometrically-scaled food webs, properties of soil systems (incorporating non-living components and soil texture in the analyses of multiple equilibria) and environmental impact (such as excessive herbivory, intensity of land use, or climate change) at different locations.

We evaluated the multi-trophic dynamics, composition, biodiversity, and numerical abundance of the belowground arthropod and nematode community using non-metric multidimensional scaling and cluster analysis, and investigated the influence of management regime (and as far as possible, recent land use history) on the nematode and arthropod communities with multiple regression analysis and Mantel tests. Lower taxonomic levels showed weaker patterns, with the functional diversity of most investigated families not discriminating between site histories. Soil characteristics did not differ significantly between the 110 grasslands on Pleistocene sand (disturbed or even polluted sites included), or between mature, high-productive, and undisturbed sites. In contrast, nematode communities at all sites were, as a group (taxocene), significantly different from both conventional/organic and intensively managed sites (*Functional Ecology* 17: 516-525, 2003).

Our terrestrial food webs, plotted according to this new methodology, show that bacteria, soil organic matter and terrestrial fauna fall near a diagonal where the mean slope of the body mass of the organisms as function of their numerical abundance equals

–1. In such models, this regression slope implies that a consumer's total biomass equals its resource's total biomass. As the scaling of metabolic rate with body mass is nearly universal, we can easily predict by metabolic scaling theory the cumulative temperature-dependent respiratory rate for multiple soil organisms within the two independent energy pathways: the fungal channel and the bacterial channel (*Ecology Letters* **8**: 80-90, 2005).

To our knowledge, it is the first time that the coupling of biodiversity with metabolic scaling and food web structure provides governmental panels with simple, accurate and unbiased summary of the ecosystem functioning it seeks. With this method, the decrease in the biodiversity of microbivores under specific environmental conditions (opener landscapes, higher temperatures, dampish habitats) can be easily pointed out by a simple comparison of regression slopes. These slopes measure the relative occurrence of small (microfauna) to large species (macrofauna) in relation to their resources, and tend to be more steeply negative in highly productive intensive farming systems with a low bacterial population (unsustainable soil biota). Even the existence of different patterns among and between soil food webs appears to be in clear agreement with functional differences at higher trophic level between species-poor and species-rich ecosystems.