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Biological regulation and control (EcoFINDERS Task 2.3)

A chonosequence on the Veluwe (Netherlands) of former agricultural lands in different stages of land abandonment provides a setting that is ideal to study soil biodiversity and function in a gradient of levels of human impact. These fields are typically managed by low-intensive grazing of natural and introduced vertebrate herbivores, such as roe deer, fallow deer, red deer, horses and Scottish Highland cattle undergoing a transition from an arable system into a species rich grassland. This transition of plant communities associated to agricultural systems to those typical for semi-natural grasslands is a well-accepted model for ecological studies on factors that drive changes in plant communities.

Currently, three studies are being performed:

1. Nutrient cycling (For background see 1.2.3 page 13 project proposal EcoFINDERS)

^{13}C-CO_2 pulse labeling and ^{15}N labeling has been employed to assess the short term fate, turnover and retention of recent plant assimilated carbon and nitrogen in living soil cores. This has been followed by sequential sampling of aboveground and belowground plant tissues, soil bacterial and fungal PLFA biomarkers, nematodes enchytraeds, mites, collembolan, earthworms and other soil fauna. Question: How is the carbon and nitrogen sequestered in the different components of the soil food web in the different land abandonment types?

2. Resistance and resilience (For background see 1.2.2 page 12 project proposal EcoFINDERS)

We have manipulated soil biodiversity to be able to couple biodiversity loss to loss of soil functions. A greenhouse mesocosm experiment has been performed in which sterilized soils from the Veluwe LTO chronosequence have been re-inoculated with a dilution series of soil suspensions (from only bacteria, fungi and protozoa) to manipulate soil diversity. These mesocosms have been planted with a plant community of plants that occur in all of the grasslands along the land abandonment chronosequence. We have measured microbial community development, plant biomass, nitrogen and phosphorous, and used ^{15}N and ^{13}C-CO_2 pulse labeling to assess the short term fate, turnover and retention of recent plant assimilated carbon and nitrogen in soil. This has been followed by sequential sampling of aboveground and belowground plant tissues, soil bacterial and fungal PLFA biomarkers. Microbial end communities will be pyro-sequenced and the activity of functional genes within the carbon and nitrogen cycle will be assessed using Q-PCR. Question: Does loss of soil biodiversity leads to loss of soil functions (nitrification, denitrification, ammonification) involved in C and N cycling?