

Summary

The objective of this project is to assess a „baseline“ of microbiological properties in 18 different long-term grassland sites in Baden-Württemberg. Additionally, methods should be established, in order to ensure a practicable and economical procedure of the environmental monitoring in the future, particularly with regard to genetically modified organisms (GMOs). The studies focus on the functional characteristics (soil enzyme activities) of soil microbial communities. The activities of α - and β -D-glucosidase, N-acetyl-glucosaminidase, xylosidase, cellobiosidase, acid phosphatase, L-leucin and L-tyrosinaminopeptidase were measured using the fluorescence-method. This method yields reproducible data, comparable to the colorimetric analyses of invertase-, xylanase- and protease activities. Both approaches result in coefficients of variation in the common range of variance in soil analyses.

The functional characterisation of the microbial communities according to the vegetation unit was evaluated by discriminant function analysis. The units 1 („Halbtrockenrasen“) and 2 („versaumte Halbtrockenrasen“) were very similar. The unit 3 („beweidete Magerrasen“) matches well with type 1 and 2, but showed tendencies to a transitional position between the first 2 units and the types 4 and 5 („Magerrasen mit dominierend *Molinia cearulea*“ and „Borstgrasrasen“). The latter 2 groups were clearly separated from the other vegetation units. The separation of the different vegetation types is mainly based on the soil pH and the activity of the enzyme xylosidase.

The phospholipid fatty acid (PLFA) and DNA pattern was analysed to characterize the structure diversity of the soil microbial community. It is recommended to continue these analyses to account for spatial as well as temporal variation of microbial properties. In addition, the application of fuzzy logic will allow to classify different sites.