SOIL MICROBIAL COMMUNITIES AND ITS RELATED FUNCTIONS-

 Introduction

Soil [microbial communities](https://www.sciencedirect.com/topics/agricultural-and-biological-sciences/microbial-communities) play an important role in [agroecosystem](https://www.sciencedirect.com/topics/agricultural-and-biological-sciences/agroecosystem%22%20%5Co%20%22Learn%20more%20about%20Agroecosystem%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages) functioning and are on the field scale essential for [plant nutrition](https://www.sciencedirect.com/topics/agricultural-and-biological-sciences/plant-nutrition) and health. On a larger scale, they contribute to global element cycling. Furthermore, they are involved in turnover processes of organic matter, breakdown of xenobiotics and formation of soil aggregates. In contrast to plant diversity, and the macro and meso fauna, the aspect of soil microbial diversity is a rather new approach. A major problem in soil microbial analysis has been that most soil microorganisms cannot be characterised by classical microbiological cultivation techniques. It is estimated that approximately 80–90% of soil microorganisms are not yet cultured by means of classical methods.

At the beginning of the last decades, cultivation-independent techniques became more frequent, leading to a broader view of microbial life in soil. It is now widely accepted that a given soil consists of members belonging to all three domains of the [biosphere](https://www.sciencedirect.com/topics/agricultural-and-biological-sciences/biosphere), the *Bacteria*, the *Eucarya* and the *[Archaea](https://www.sciencedirect.com/topics/agricultural-and-biological-sciences/archaea%22%20%5Co%20%22Learn%20more%20about%20Archaea%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages)*. Cultivation-independent molecular approaches are based on the direct extraction of DNA from soil and a subsequent analysis molecular marker genes (e.g. genes coding for ribosomal RNA). These genes are functionally conserved in all organisms and contain conserved, variable and highly variable regions and can therefore be used as marker genes to describe structural microbial diversity. At present, more than 15000 sequences of rRNA genes are available in databases. Apart from structural genetic analyses, soil microbial communities can also be studied in terms of their in situ functions by means of molecular techniques. There are several PCR-based assays available for the detection of functional genes with respect to key processes during C and N cycling .

Another cultivation-independent technique for the analysis of the structural diversity of soil microorganisms is the [phospholipid](https://www.sciencedirect.com/topics/agricultural-and-biological-sciences/phospholipid%22%20%5Co%20%22Learn%20more%20about%20Phospholipid%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages) approach. Phospholipids are essential components of membranes of all living cells, and their fatty acid (PLFA: phospholipid fatty acids) or ether-linked isoprenoid side chains (PLEL: phospholipid etherlipid) allow a taxonomic differentiation within complex microbial communities. This approach is now well established in [soil ecology](https://www.sciencedirect.com/topics/agricultural-and-biological-sciences/soil-ecology) and serves as a phenotypic and thus complementary tool to genotypic (molecular genetic) approaches.

Soil microbial communities and related functions were studied under the constraints of agricultural land use in general and the specific aspects of Research Station Scheyern in particular. Hence, the impact of copper from previous hop cultivation in Scheyern was also investigated as well as the more general aspects of [herbicide degradation](https://www.sciencedirect.com/topics/agricultural-and-biological-sciences/pesticide-degradation) and soil [tillage](https://www.sciencedirect.com/topics/agricultural-and-biological-sciences/tillage) practices.

# Effects of Agricultural Practices on the Physical, Chemical and Biological Properties of Soils:Effect of some Agricultural Practices on the Biological Soil Fertility

The microbiological aspects of the positive effects of some agricultural practices on soil fertility and crop production has been recently revised.

Tillages, crop rotation and fertilization improve the physical condition of soil; they provide a more favourable reaction for the activities of the numerous soil bacteria and admit large quantities of oxygen which are necessary for the growth of the aerobic organisms. These treatments are of great importance in soil fertility, not only because they produce in the soil favourable physical and chemical conditions for plant growth, but also create more favourable conditions for the activity of the microbes which effect more rapid liberation of the soil nutrients.

However, recent researches showed that soil tillages affect in a favourable way mainly the important groups of micro-organisms involved in the soil organic matter transformation, mineralization and nitrification; but affect unfavourably the most important process bound to the biological soil fertility as the nitrogen fixation by free micro-organisms.

The biological soil fertility is also more stimulated in soils submitted to crop rotation than in soils with monocultures, since the succession of different rhizospheric microbial populations exert a positive effect not only on the organic matter transformation and on biological nitrogen fixation but also against the pathogenic plant microbes.