Based on phylogenetic marker genes, such as 16S rRNA genes, it is clear that numerous bacterial lineages exist that appear to be quite common in the environment, yet poorly characterized and underrepresented in culture. Two of the most common bacterial phyla in soils that fall into this category are the Acidobacteria and Verrucomicrobiales. Although knowledge of these two groups, and of their roles in global biogeochemical cycles is very limited, their abundance and diversity suggest that they may be ecologically important.

The main objective of this thesis was to gain access to the genomic potential of soil-borne Acidobacteria and Verrucomicrobiales using culture-independent approaches, namely metagenomics. This objective was pursued via the following approaches:

- Studying the diversity and structure of microbial communities in relation to the different experimental plant diversity treatments and across different soil compartments using a combination of 16S rRNA gene-based methods (PCR-DGGE, Q-PCR 16S rRNA gene library analysis) (Chapter 3).
- Examining the diversity of 16S rRNA genes affiliated with the phylum Acidobacteria via three independent approaches: 1) screening of a fosmid metagenome library for inserts containing Acidobacteria-like 16S rRNA genes; 2) PCR-cloning using general bacterial primers; and 3) PCR-cloning with primers specific for acidobacterial 16S rRNA gene sequences (Chapter 4)
- Screening of metagenomic libraries for genomic fragments affiliated with the Acidobacteria and Verrucomicrobia, full-length inserts sequencing of positive clones followed by subsequent gene annotation and evolutionary analyses (Chapter 5 and 6).

Acidobacteria were determined to be relatively more abundant in bulk soil as compared to the rhizosphere, whereas Verrucomicrobia followed an opposite pattern, and plant species composition appeared to have no significant effects on the structure of these two bacteria phyla. Also, distinct differences were observed in the diversity of acidobacterial sequences recovered via the different cloning strategies employed, partly due to observed biases of the primer commonly use to specifically target 16S rRNA genes of the phylum Acidobacteria. PCR-based screening methods were developed and implemented to analyze a fosmid metagenomic library (28,800 clones) for the detection of clones containing Acidobacteria- and Verrucomicrobia-like 16S rRNA genes. The resulting 17 confirmed clones of acidobacterial and 4 of verrucomicrobial origin, representing a broad phylogenetic range, were fully sequenced and annotated. These partial genome analyses provided a glimpse into the functional capabilities within soil-borne members of the bacterial phyla Acidobacteria and Verrucomicrobia, and yielded a novel dataset for comparative genomic analyses.