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Comparative diversity and composition of bacterial communities inhabiting natural forest soils

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We compared the diversity and composition of the soil bacterial communities in six natural forest reserves in Austria by using terminal restriction fragment length polymorphism (T-RFLP or TRF) analysis and sequence analysis of 16S rRNA genes. The study revealed that the bacterial communities in soils under Austrian pine forests, representing azonal forest types, were distinct from those in soils under zonal oakhornbeam and spruce-fir-beech forests, which were more similar in community composition. The pine forest soils appeared to be dominated by high G+C gram positive bacteria, while bacteria from oak-hornbeam and spruce-fir-beech forest soils seemed to be mainly affiliated with the *Holophaga/Acidobacterium* group. Bacterial community data were related to soil chemical properties and other microbiological characteristics of the soils such as microbial phospholipid fatty acids (PLFAs) patterns, microbial activity and nitrogen turnover.