

Abstract

Forest ecosystems represent a huge reservoir of carbon. The volume of deadwood in managed forests is in the tens of $\text{m}^3 \text{ha}^{-1}$, while unmanaged forests have the volume of deadwood in hundreds of $\text{m}^3 \text{ha}^{-1}$. Deadwood is a substrate with a high potential for decomposition. However, deadwood is a specific habitat that has a high C/N ratio and changes due to ongoing decomposition. The C/N ratio decreases with increasing decay time. In addition to the C/N ratio, the pH also changes during the wood pulping process, due to the decomposition of plant biomass by fungi. Moreover, deadwood has a high impermeability. The main decomposers of dead wood are fungi. In addition to them, bacteria, which are numerous in deadwood, also contribute to decomposition. Bacterial communities that decompose woody biomass are affected by these factors, and their distribution is also affected by dead tree species. The aim of this study was to describe how bacterial communities associated with deadwood change during decay. The most significant factor in the decomposition by bacterial communities is the time of decay. Bacteria found in short-decaying wood (less than 16 years old) are more diverse than those found in long-decaying wood. Methylophilic bacteria and N-fixing bacteria are common in short-decaying wood as well. N-fixing bacteria were present in this study throughout the decay of deadwood. The N-fixation was represented by the genus *Bradyrhizobium*. In long-decaying wood, are mainly representatives of the strain *Acidobacteria*, which prefer the more acidic conditions that long-decaying wood offers. The genera *Burkholderia*, *Conexibacter*, *Bradyrhizobium* and *Pseudomonas* were present across all age groups. However, dead wood is primarily decomposed by fungi, which can be colonized by bacteria as another potential substrate for decomposition. Fungal biomass has a lower C/N ratio than dead wood and is a more easily degradable substrate. Bacteria therefore colonize the mycelium and fruiting bodies of fungi and decompose them. The second aim of this study was to describe the bacterial communities associated with the fruiting bodies of the wood-decomposing fungi *Fomes fomentarius* and *Ganoderma applanatum*, which were divided into two age categories - young and old fruiting bodies. The distribution of the community of bacteria occurring in the fruiting bodies of the wood-decomposing fungi *Fomes fomentarius* and *Ganoderma applanatum* of different age classes is not significantly influenced by any factor, neither the age of the fruiting body nor the species specificity. Frequent representatives included *Fronidhabitans*, *Pedobacter*, *Sphingomonas* and *Mucilaginibacter*. Those bacteria were associated with fungal biomass in the past. *Microbacterium*, *Fronidhabitans*, *Pseudomonas* and *Pedobacter* displayed a high potential for chitin degradation, due to the high number of chitin degrading genes.

Key words: bacteria; ecology of microorganisms; decomposition; forest soils; deadwood; cellulose; chitin; N fixation