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The interface of preserved wood and soil microbial communities

The wood protection industry has refined their products from chrome, copper, and arsenate-based wood preservatives towards solely copper-based preservatives in combination with organic biocides. Environmental use of copper-based preservatives leads to an enrichment of copper tolerant microbial communities in respective soil environments. Such soil communities are, overall, able to decompose copper-based preserved wood over a long time period and thus leading to major damages in wooden stakes. To investigate the effect of wood preservatives on fungal and bacterial community structure and composition, five different vineyard and fruit-growing soil environments were evaluated over time. In total, 440 soil samples (5 soil environments, 4 incubation times, 5 preservative treatments, 4 replicates, >40 virulence controls) were collected across Germany and southern Europe and incubated in accelerated soil incubation studies. To test the efficacy of wood preservatives, wooden specimens were impregnated with water (A as reference) or different biocide-based preservation treatments (B=containing copper, triazoles and benzalkonium chloride; C=containing triazoles and benzalkonium chloride, encapsulated; D=containing triazoles and benzalkonium chloride, non-encapsulated; and E=containing copper). Samples were selected for next-generation sequencing and quantitative PCR by 16S rRNA and ITS gene region, respectively, based on mass loss and bending elasticity results. For all dominant taxa, the composition and diversity of fungal and bacterial communities were significantly environment specific and remained less affected by the wood preservative treatment and incubation time. Surprisingly, about 80% and 30% of the genera of the bacterial and fungal community, respectively, were phylogenetically similar but unevenly distributed within the samples. The Shannon diversity index (H') over time was evenly distributed in the bacterial community and was not influenced by preservative treatments. In contrast, the corresponding H' of the fungal community shifted towards high abundance of Ascomycota and Talaromyces in the treatment E of northern and central Germany as well as in southern France. Members of the genus Talaromyces are known cellulose-degrading organisms with potentially high tolerance towards copper. In conclusion, a decreasing fungal community composition over time indicates that few fungi were functionally superior in the main wood decay process.

Biography

Matthias Noll received his Diploma from University of Kassel, Germany, 2001 and PhD degree from Philipps-University of Marburg, Germany 2004. Since 2001, he has been working at the Department of Biogeochemistry at the Max Planck Institute for Terrestrial Microbiology, Marburg as a PhD student and, thereafter, as PostDoc candidate. From 2005 to 2006, he was PostDoc at the Department of Environmental Microbiology of the Institute of Biogeochemistry and Pollutant Dynamics at the Swiss Federal Institute of Technology

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