



Tree species metrics and canopy microbial communities affect aboveground hydrology and biogeochemistry

Beate Michalzik (1,3), Tim Richter (1), Alexander Tischer (1), Kirsten Küsel (2,3), Patricia Geesink (2), Martina Herrmann (2,3)

(1) Soil Science, Institute of Geography, Friedrich Schiller University Jena, Germany, (2) Aquatic Geomicrobiology, Institute of Biodiversity, Friedrich Schiller University Jena, Germany, (3) German Center for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, Germany

In forested ecosystems, throughfall and stemflow function as key components in the cycling of water and associated biogeochemistry because of their substantial contribution to soil inputs. However, the impact of tree species related tree metrics as well as phyllosphere-associated microorganisms on fluxes of canopy-derived water and matter to the ground is insufficiently understood.

Throughfall (TF) and stemflow (SF) fluxes of three tree species (5-6 yr-old beech, pine, spruce trees) were analyzed for water fluxes, dissolved and particulate C (DOC, POC) and N species (DN, PN, NH₄-N, NO₃-N, DON) and tree metrics (e.g. trunk basal area, leaf numbers, primary branch count and branch angle). To further elucidate N and C processes in tree canopies, phyllosphere-associated microorganisms were characterized using a NGS (Next Generation Sequencing) Illumina MiSeq approach targeting bacterial 16S rRNA genes. ¹⁵NH₄¹⁵NO₃ was applied to track the fate of inorganic N in the phyllosphere using Nanoscale Secondary ion mass spectrometry (NanoSims) of leaf and needle surfaces in combination with Scanning electron microscopy (SEM) imaging.

Tree species reveal significant differences in tree metrics encompassing: tree height, primary branch count and mean primary branch angle, total leaf count and foliar biomass. Across all trees, primary branch count and total leaf count appear to promote SF and lower TF volumes. The canopy functions as a source for most C and N compounds except for NH₄-N in TF under beech and pine. Tree species significantly differ in TF POC (beech > pine > spruce) and TF NH₄-N and SF NH₄-N fluxes (spruce > pine > beech). SF matter fluxes per unit basal area were 30-420 times higher than in TF. Across all trees, TF fluxes of most N species were positively related to total leaf count, leaf area and foliar biomass and negatively affected by the trunk lean. However, on a tree species level, only few correlations were significant but were heterogeneously distributed between tree species and C and N species. We assume that phyllosphere-associated microbial communities attached to leaf and needle surfaces might affect especially N processes and speciation in tree canopies. We found distinct bacterial communities on each tree species, with a dominance of Alphaproteobacteria, Bacteroidetes, and Gammaproteobacteria. Differences in the community-dependent extent of N assimilation or also N₂-fixation by the phyllosphere microbiota might underlie tree species related differences in canopy N dynamics. As successfully verified by NanoSims leaf surface imaging, applied ¹⁵N was enriched in fungal hyphae and bacteria biomass forming part of the phyllosphere microflora. In essence, this pilot study exhibited that both tree species metrics and canopy microbial communities affect tree species hydrology and associated biogeochemistry.