Impact of water on microbial nitrogen transformation in soil causing atmospheric nitrous acid (HONO) and nitric oxide (NO) emissions

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Biological soil crusts (referred to as biocrusts hereafter) represent communities comprising a fraction of photoautotrophs (photoautotrophic bacteria, algae, lichens, and bryophytes) growing together with heterotrophic organisms like bacteria, archaea, and fungi. The organisms are all poikilohydric, which means they are only active if water is present. They occur frequently in dryland ecosystems, where vascular vegetation is sparse or even absent, or wherever dry microclimatic conditions occur. Biocrusts fulfill a wide range of important ecosystem services, as they are relevant in regional water cycling, soil stabilization, plant germination and growth, and also global carbon (C) and nitrogen (N) cycling. According to initial estimates, they are supposed to globally emit ~1.7 Tg of reactive nitrogen (Nr) per year, corresponding to ~20% of the global nitrogen oxide emissions from soils under natural vegetation. The underlying mechanisms of Nr emissions in biocrusts, however, are not well understood and are still a focus of ongoing research.

This study aimed to explore the functional roles of microbial organisms in Nr emissions along a full wetting and drying cycle. Therefore, Nr fluxes were analyzed at three key hydration stages, i.e., immediately after wetting (T1), prior to (T2), and after maximum Nr fluxes (T3). At all three stages, the transcriptome (microarray analysis) and proteome (metaproteomics) were profiled to highlight changes in biological processes linked to nitrogen transformation. Additionally, at T1 and T2, the bacterial, archaeal, and nitrite-oxidizing bacterial communities were quantified utilizing catalyzed reporter deposition fluorescence in situ hybridization (CARD-FISH). Soil nitrite and nitrate contents of both intact and sterilized biocrust samples were analyzed before and after a measurement cycle.

Our results showed a fast recovery of microbial activity minutes after wetting of the biocrusts (T1)
by means of mRNA expression of nitrogen transformative genes. Transcripts of genes encoding all major N-cycling processes that are already known from soil were detected. The number of N-transforming species and processes detected by the microarray analysis significantly increased from T1 to T2 to T3. The most prominent nitrogen transforming microorganisms belonged to Alpha- and Gammaproteobacteria. The CARD-FISH data showed a significant increase in archaeal numbers from T1 to T2, which is in line with an observed increase in N\(_\text{r}\) emissions. The majority of identified proteins were related to ATP synthesis, photosynthesis, protein biosynthesis and stress response, whereas proteins assigned to N transformation could not be observed. Soil N-content analysis showed a significant increase of nitrite in living biocrusts after a wetting and drying cycle, which was likely promoted by nitrifying Archaea and Proteobacteria, but also by various denitrifying bacteria, as suggested by microarray analysis and CARD-FISH. This indicates that N\(_\text{r}\) fluxes largely originated from nitrite formed by various aerobic and anaerobic biotic processes, likely occurring simultaneously in different microhabitats within the biocrust.