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The variation in genetic material of a high Alpine catchment reveals (sub)surface exchange

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In the past years, it has been proposed that stream networks can accumulate genetic material over a given area. Accordingly, a sample of environmental DNA (eDNA) from streamflow at the outlet of a catchment can be used as an indicator of the upstream biodiversity. eDNA's use in ecological studies is becoming more and more common and it seems reasonable to assume that eDNA might also offer a powerful tool as a hydrologic tracer. However, the original ecological proposition largely simplifies the complexity of any seasonal, diurnal, or spatial variation according to hydrologic flow paths and processes. From a hydrological perspective, this shortcoming is particularly problematic in Alpine headwater catchments, where the combination of snowmelt-dominated summer flow and particularly high climatic and geomorphologic heterogeneity results in hydrologic flow paths that are especially dynamic in space and time.

We were interested to see if on one hand, eDNA could teach us something new about hydrologic (subsurface) flow paths, and on the other hand, if biodiversity assessment should consider hydrologic variation in detail. To do so, we sampled natural occurring eDNA at 11 points distributed over the 13.4 km², intensively monitored Vallon de Nant (1189-3051 m. a.s.l., Switzerland) between March and September 2017. We chose points corresponding to three different potential microhabitats and flow regimes (main channel, tributary, and spring) likely both inhabited by characteristic organismal communities and of interest for identifying hydrologic flow paths. We found that at moments when streamflow was increasing rapidly, biological richness in upstream points in the main channel and in tributaries was highest contrary to springs, where richness was higher when electrical conductivity was highest. Thus, the main conclusion from our work is that elevated richness corresponds to moments in time when multiple mechanisms transport additional, probably terrestrial, DNA into water storage or flow compartments. These mechanisms could include overbank flow, stream network expansion, and hyporheic exchange. Our data demonstrates that biodiversity assessments using eDNA do need to consider hydrologic

processes and shows that there is a potential future for eDNA among hydrologic tracers. We will give recommendations in this talk about how to sample eDNA to answer hydrologic questions.