

mixture. The QS of  $\text{NH}_4^+$  obtained by the SSD curve computed for the single compound highly underestimated the fraction of the potentially affected species, that were more sensitive to  $\text{NH}_4^+$  when it was considered in the mixture with Imazamox in the SSDs. According to the QS of  $\text{NH}_4^+$  derived from our studies, the actual environmental policy fails to protect groundwater copepods from acute exposure to  $\text{NH}_4^+$  in at least 4 EU Member States.

**31-O Interactions between geochemical and ecological status of the groundwater ecosystem: what do the resident biological communities tell us?** *Annamaria Zoppini*<sup>1</sup> - *Stefano Amalfitano*<sup>1</sup> - *Tiziana Di Lorenzo*<sup>2</sup> - *Daniele Parrone*<sup>1</sup> - *David Rossi*<sup>1</sup> - *Stefano Ghergo*<sup>1</sup> - *Elisabetta Preziosi*<sup>1</sup>

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The groundwater ecosystems are threatened by the increasing water demand and anthropic activities. Groundwater hosts numerous organisms belonging to a wide range of faunal groups that generally are neglected by the monitoring plans, commonly based on the hydrogeochemical parameters. Basic research is needed to establish the effects of the environmental stress on the whole system.

The groundwater ecosystems are populated by highly adapted biota, dominated by microorganisms and invertebrates. Microbial communities are at the base of the heterotrophic food chain, playing a key role in the organic matter processing, including organic pollutants. Important ecosystem services are attributed to groundwater metazoa, especially invertebrates, such as the maintenance of hydraulic conductivity in porous sediments, through their feeding on microbial biofilms, and bioturbation. The analyses of the microbial and crustaceans communities in the groundwater along with changes in hydrogeochemical parameters may contribute to shed more light upon the state and dynamics of such ecosystems. A comprehensive study of a water table aquifer flowing through a quaternary volcanic district (Latium Region, central Italy) was performed. Field data (GPS localization, well depth, water table level, temperature, pH, alkalinity, dissolved oxygen, conductivity) were measured together with the analysis of major cations (Optical Emission Spectroscopy), major anions (Ionic Chromatography), trace elements (Coupled Plasma Mass Spectrometry),  $\text{NO}_2$ ,  $\text{PO}_4$ ,  $\text{NH}_4$  (Spectrophotometry) and dissolved organic carbon (Shimadzu TOC-5000 analyzer). The Colilert-18 test was used to verify the occurrence of fecal contamination (total coliforms and *Escherichia coli*). Flow cytometry and epifluorescence microscopy was utilised to determine the prokaryotic abundance and cells with high and low nucleic acid content (HNA, LNA). BIOLOG EcoPlates™ were utilised to describe changes in the metabolic profiles of the microbial communities. Pore water ( $1\text{m}^3$ ) was filtered through a  $63\text{-}\mu\text{m}$  mesh net to sample crustaceans specimens, successively sorted under a stereomicroscope for taxonomic identification.

The sampled sites were differently affected by natural and anthropogenic factors (arsenic, fluoride and fecal pollution). The analysis of the results showed as differences in the aquifer typologies affect the structure and functional properties of the bacterial communities (range  $10^3\text{-}10^4$  cells/ml). The microbial communities metabolic profiles (BIOLOG) were surprisingly different among the sites for all the classes of substrata analyzed (amines/amides, amino acids, carboxylic acids, carbohydrates, polymers), implying a high metabolic diversity. The crustacean community was constituted by 12 taxa, nine of which were stygobionts. Interestingly four sampling sites, belonging to the same sector of the aquifer, with a lower salinity and sulfate content, harbored no crustacean specimens.

**31-O Groundwater biodiversity in the challenging sulfidic karst: copepod assemblages of the Frasassi cave system (Italy).** *Diana M.P. Galassi*<sup>1</sup> - *Barbara Fiasca*<sup>1</sup> - *Alessandro Montanari*<sup>2</sup> - *Alessia Di Cioccio*<sup>1</sup> - *Tiziana Di Lorenzo*<sup>3</sup> - *Simone Fattorini*<sup>1</sup>

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The Frasassi cave system hosts one of the few worldwide examples of groundwater metazoan communities depending on chemoautotrophic microbes. Despite the challenging conditions represented by high levels of hydrogen sulphide and low concentration of oxygen, this cave system is home to many species of ostracods, amphipods, and copepods. We analysed here the copepods inhabiting three sulfidic lakes and two dripping pools fed by non-sulfidic water to investigate how the extreme environmental conditions of sulfidic habitats influence community structure. To this end, we have sampled copepod assemblages in both low- and high-water periods characterised by different physico-chemical conditions. Overall similarity in species composition among species assemblages was investigated by cluster analysis

(Sørensen coefficient + UPGMA) whereas relationships between species composition and environmental parameters were analysed by canonical correspondence analysis (CCA). To investigate if copepod community structure was influenced by sulfidic conditions, we compared diversity, dominance and equitability values of sulfidic lakes during low- and high-water periods. Cluster analysis and CCA separated the dripping pools (whose species assemblages were associated to higher pH and oxygen concentrations) from sulfidic lakes (whose species composition was strongly affected by ionic concentration). These results indicate that the distribution of stygobiotic copepods within the cave system is ecologically and spatially structured. For example, the planktonic *Eudiaptomus intermedius* and *Diacyclops cosanus*, and the inbenthic/interstitial *Eucyclops intermedius* and *Nitocrella stammeri*, are able to cope with the high ionic content and hypoxia of the sulfidic lakes, even if they avoid sulfidic microbial mats below the chemocline. Contrary to expectation, sulfidic lakes showed lower dominance, higher diversity and higher evenness in the higher sulfidic state. This paradoxical situation was due to the fact that extreme conditions reduced the abundance of dominant planktonic species, thus making the community structure more balanced. Species assemblages of dripping pools were very different from those found in the sulfidic lakes and included both stygobiotic and non-stygobiotic species. Differences in relative species abundances between pools suggest that the epikarst fracture network has interconnected but different drainage pathways. The relatively high biodiversity and complex community structure of the copepods inhabiting the Frasassi cave system indicate that a chemosynthetically produced food source allowed ancestral populations of surface-water crustaceans to settle permanently in sulfidic groundwater, probably due to their preadaptation to tolerate harsh environmental conditions.

### 31-O StygoTracing-EZG - applying population genetical methods on hydrogeological catchment assessment. *Susanne van den Berg-Stein, Hans Juergen Hahn*

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A central challenge both for quality assurance of water supply and for wetland management is the description of hydrological connectivity and water fluxes in the catchment area.

For that purpose a molecular biological method was developed – StygoTracing. StygoTracing is based on population genetics and identifies hydrological fluxes using animals as biological tracers. The technique has yet been applied for water lice both in drinking water supply systems and in the outdoors catchment.

The application for the hydrogeological investigation in the field using different tracer species is in its very beginning. It shall be optimized for practise by StygoTracing-EZG. EZG stands for the „Einzugsgebiet“ (German for catchment). StygoTracing-EZG is an applied research project focussed on the stygophilous and stygobitic fauna in the catchment. The project aims to use these animals as biotracers for hydrogeological connectivities.

In this presentation the conception of the project and the perspectives of the new technique are presented.

### 31-O Groundwater flooding: responses of groundwater ecosystems to an extreme recharge event.

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The winter of 2013-2014 was the wettest in the UK since records began resulting in extremely high groundwater levels and very extensive groundwater recharge, particularly in chalk aquifers. Understanding of the impact of such conditions on the unique ecosystems that exist in groundwaters is very limited yet such extreme events are predicted to become more frequent under climate change.

We hypothesised 1 that the composition of the groundwater community will change following flooding cessation and the onset of community recovery. 2 Dissolved Organic Carbon (DOC) will be highest immediately after flooding, the microbial compartment will respond rapidly to high DOC levels and groundwater macrofauna will recover more slowly. We collected environmental data (e.g. DOC, nutrients, oxygen profiles) and measured microbial functional diversity, fungal activity, and the abundance and biomass of bacteria, protozoa, meiofauna and macrofauna. We did this at multiple boreholes in each of two chalk aquifers across a 7 month period following the recharge event.

We found that DOC and bacterial abundance were higher shortly after the recharge event and then declined whereas protist biomass and macrofaunal abundance increased with increasing distance from the recharge event. However,