

# Decipher groundwater food web interactions by means of stable isotope and gut microbiome analyses

Christian Griebler<sup>‡</sup>, Clemens Karwautz<sup>‡</sup>, Moritz Grabner<sup>‡</sup>, Ayac Jimenez Salvador<sup>‡</sup>, Felix Puff<sup>‡</sup>, Rajiv-Raphael Kumar<sup>‡</sup>, Mona Lauritz<sup>‡</sup>, Lina Vinkovic<sup>§</sup>, Julian Kiralyhidi<sup>‡</sup>, Gertraud Steniczka<sup>|</sup>, Andreas Fuchs<sup>‡</sup>

<sup>‡</sup> University of Vienna, Vienna, Austria

<sup>§</sup> University of Zagreb, Zagreb, Croatia

<sup>|</sup> WasserCluster, Lunz am See, Austria

Corresponding author: Christian Griebler ([christian.griebler@univie.ac.at](mailto:christian.griebler@univie.ac.at))

## Abstract

The traditional perception of groundwater food webs is that of short and poorly structured food chains extending to only few trophic levels. This is mainly attributed to the lack of light and the shortfall of substantial primary production as well as the shortage of dissolved organic carbon and nutrients. It is frequently argued that microbes form the basis of groundwater food webs. In reality, the obvious lack of comprehensive biofilms may point to detritus as the main common food source and an opportunistic and omnivorous feeding strategy with most groups and species. Also, the relative stability of groundwater environments may have led to low trait variability. However, recent research also contrasts the paradigm of poorly structured food chains against emerging convoluted mechanisms sustaining a great range of biotic diversity and functional complexity. In summary, understanding of the ecological and functional linkages among stygofaunal groups, and their interaction with the microbial community, is still in its infancy. Stygofauna sampled from three spots of a shallow alluvial aquifer in the vicinity of the Danube River in the city of Vienna, Austria, has been analyzed by means of bulk stable carbon and nitrogen isotope and gut microbiome analysis to disentangle food web interactions. Our preliminary data revealed the following pattern:

1. plant material, terrestrial insects, and detritus show a narrow range in carbon ( $-32$  to  $-25\delta^{13}C$ ) and a wide range in nitrogen ( $-1.5$  to  $6.5\delta^{15}N$ ) isotope signatures. In terms of nitrogen isotope values, the next trophic level is represented by isopods and gastropods, followed by ostracods, oligochaetes and amphipods. The broader range of stygofauna in carbon isotope signatures indicate an additional food source; most probably microbes;

2. gut microbiome analyses indicate differences with oligochaetes, gastropods, ostracodes, isopods and amphipodes, however, with a few individuals from the later three groups sharing a very similar gut microbiome;
3. within the amphipods, there is obviously a difference in gut microbiome composition with species and sampling sites;
4. carbon and nitrogen isotope signatures underline amphipod-species differences;
5. microbiome diversity in all cases was less diverse in the animal guts when compared to environmental water, sediment and detritus samples.

Finally, we first collected evidence for anaerobic processes taking place in animal guts living in an oxic groundwater environment. In light of our data, putative groundwater food web interactions in the shallow alluvial aquifer are discussed.

## **Keywords**

groundwater, food web, stygofauna, stable isotope analysis, gut microbiome

## **Presenting author**

Christian Griebler

## **Presented at**

25th International Conference on Subterranean Biology in Cluj-Napoca, July 2022

## **Conflicts of interest**