

Heterotrophic prokaryotic production in ultraoligotrophic alpine karst aquifers and ecological implications

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Abstract

Spring waters from alpine karst aquifers are important drinking water resources. To investigate *in situ* heterotrophic prokaryotic production and its controlling factors, two different alpine karst springs were studied over two annual cycles. Heterotrophic production in spring water, as determined by [³H]leucine incorporation, was extremely low ranging from 0.06 to 6.83 pmol CL⁻¹ h⁻¹ (DKAS1, dolomitic-karst-spring) and from 0.50 to 75.6 pmol CL⁻¹ h⁻¹ (LKAS2, limestone-karst-spring). Microautoradiography combined with catalyzed reporter deposition-FISH showed that only about 7% of the picoplankton community took up [³H]leucine, resulting in generation times of 3–684 days. Principal component analysis, applying hydrological, chemical and biological parameters demonstrated that planktonic heterotrophic production in LKAS2 was governed by the respective hydrological conditions, whereas variations in DKAS1 changed seemingly independent from discharge. Measurements in sediments recovered from LKAS2, DKAS1 and similar alpine karst aquifers ($n=12$) revealed a 10⁶-fold higher heterotrophic production (average 19 μmol C dm⁻³ h⁻¹) with significantly lower generation times as compared with the planktonic fraction, highlighting the potential of surface-associated communities to add to self-purification processes. Estimates of the microbially mediated CO₂ in this compartment indicated a possible contribution to karstification.

Introduction

Groundwater resources from alpine or mountainous karstic aquifers are of fundamental importance for public water supply in many regions throughout the world. Hydrogeology is an important factor to consider in such systems, as rainfall events in the catchment area can lead to immediate surface runoff into karst conduits, probably not only altering spring water quality but also influencing biogeochemical cycles and indigenous (micro)organisms within the aquifer (Gibert *et al.*, 1994; Mahler *et al.*, 2000; Farnleitner *et al.*, 2005).

During the past two decades it has become obvious that groundwater resources should not only be viewed as drink-

ing water reservoirs but also as distinct aquatic ecosystems (Gibert, 2001). Diverse microbial communities were found in the deep subsurface, at depths believed to be sterile hitherto (Griebler, 2001; Goldscheider *et al.*, 2006; Griebler & Lueders, 2008; Pronk *et al.*, 2009). These microorganisms are involved in many subterranean geochemical processes, such as diagenesis, weathering, precipitation and in oxidation or reduction reactions of metals, carbon, nitrogen and sulfur (Lauritzen & Bottrell, 1994; Hirsch *et al.*, 1995). However, except for a few reports, mostly dealing with (low-) mountain karstic systems and caves, accessible information on microbial communities in alpine karst aquifers is still sparse (Ghiorse & Wilson, 1988; Gounot, 1994; Rusterholtz & Mallory, 1994; Menne, 1999; Simon *et al.*,

2001; Pronk *et al.*, 2006, 2009). Consequently, studies are needed that lead to a better understanding of the natural structure and function of subterranean systems and thus allow for effective protection of groundwater aquifers and its inhabiting biota (Mösslacher *et al.*, 2001; Danielopol *et al.*, 2003). Knowledge on the prokaryotic communities inhabiting such ecosystems is of interest for both, basic and applied research (water suppliers), because it (1) contributes to the understanding of self-purification processes in the aquifer, regarding allochthonous chemical or microbial contamination, (2) elucidates potential microbially mediated biogeochemical cycles, for example, the possible impact of microorganisms on the karstification process and (3) helps to judge microbial spring-water quality, such as the potential biostability of the abstracted water (i.e. stability during water distribution and storage).

Recently, we could demonstrate the presence of stable autochthonous microbial endokarst communities (AMEC) in alpine spring water (Farnleitner *et al.*, 2005), which form an indigenous part of the endokarst system. Two contrasting springs, having a nearby catchment area but revealing different hydrogeological conditions (i.e. contrasting water storage capacity) were investigated. The LKAS2 (limestone-karst-spring) spring represents a system with well-developed karst conduits (Stadler & Strobl, 1997) allowing for high flow velocities (resulting in detectable microbial surface input during summer) with an average water residence time of 1.5 years, whereas DKAS1 (dolomitic-karst-spring) is dominated by fissured and porous media and an average water residence time of around 22 years (Stadler & Strobl, 1997). However, one should keep in mind that some water will spend much less time in the aquifer than average and some much more, for example, during rainfall events, surface water can pass through the LKAS2 system within hours. Evidence was presented that prokaryotic numbers, biomass and community composition in the spring water was directly related to the respective hydrogeology of the studied aquifers (Farnleitner *et al.*, 2005), as was also shown for other ecosystems (Lindström & Bergström, 2004). Although oligotrophic environments are generally known to have low rates of activity (Church *et al.*, 2000, 2004), measurements of bacterial biomass production are central to infer the role of heterotrophic prokaryotes in food webs and their effect in biogeochemical cycles (Kirchman *et al.*, 1985; Kirschner *et al.*, 1999; Buesing & Gessner, 2003; Cottrell & Kirchman, 2003).

The aim of this study was (1) to determine the variation and control of prokaryotic heterotrophic *in situ* activity in spring water of alpine karst aquifers as important drinking water resources and (2) to elucidate the potential relevance of planktonic vs. sessile endokarst communities on processes within karst groundwater systems (e.g. self-purification, karstification). [³H]Leucine incorporation (Kirchman

et al., 1985; Simon & Azam, 1989) was used to estimate the prokaryotic heterotrophic activity within the plankton community. Furthermore, a combination of catalyzed reporter deposition-FISH (CARD-FISH) (Wilhartz *et al.*, 2007) and microautoradiography (MAR) was applied to examine assimilation of [³H]leucine at the single-cell level, in order to determine the contribution of Bacteria and Archaea to planktonic heterotrophic production (Teira *et al.*, 2004). For porous aquifers it has been concluded that the attached populations reveal higher metabolic activity than planktonic cells (Pedersen, 1993; Alfreider *et al.*, 1997). Sediments in karstic aquifers attracted much attention during the last years (Vesper & White, 2004b; Toran *et al.*, 2006; Herman *et al.*, 2007, 2008). However, they might not only be interesting in terms of transport mechanisms, for example bacteria or certain metallic elements (Mahler *et al.*, 2000; Vesper & White, 2004a), but also because of their huge surface-abetting biofilm formation. There are speculations that CO₂ from aerobic microorganisms could be an important factor when discussing karstification, especially in bare karst areas (Gabrovsek *et al.*, 2000). Therefore, we measured prokaryotic numbers and heterotrophic production ([¹⁴C]leucine) in karst aquifer sediments recovered from LKAS2, DKAS1 and other locations in order to estimate the metabolic potential of attached autochthonous endokarst communities.

To our knowledge, this is the first study determining prokaryotic heterotrophic *in situ* activity in alpine mountainous karst spring water and its respective aquifer sediments, allowing for leadoff speculations about possible ecological implications of the microbial compartment in such groundwater systems.

Materials and methods

Study site and basic microbiological parameters

The two springs (LKAS2 and DKAS1) are located in the Northern Calcareous Alps in Austria (detailed description in Farnleitner *et al.*, 2005). Samples for microbiological parameters were collected from December 2003 to December 2005 every 3–4 weeks directly at the spring outlet. Additional MAR-CARD-FISH analysis was performed from January to June 2004. Samples for all parallel analysis (unless stated otherwise) were taken aseptically in a sterilized sampling device (20 L), stored at 4 °C (*in situ* temperature) during the transport and processed within 24 h. Sediment samples and the respective overlying water were taken inside the mountain from sediment depositions at 12 different locations within the aquifer area (800 km², Northern Calcareous Alps in Austria) and at one sediment trap installed in LKAS2. The overlying water and the sediment were sampled separately into sterile bottles. All sediment analysis were

performed from homogenized sediment sample and subsamples for production measurements were processed within 2 h.

For determination of prokaryotic numbers in the planktonic fraction, a slightly modified version of the acridine-orange direct count method after Hobbie *et al.* (1977) was applied, as described in Kirschner & Velimirov (1997). Filters were examined under a Leitz Diaplan epifluorescence microscope equipped with a 50 W mercury lamp (OSRAM, Austria) (excitation wavelength 450–490 nm, cut-off filter 515 nm). Prokaryotic cells were sized by an ocular micrometer. Cell volume estimations were based on the assumption that all bacteria are spheres or cylinders with two hemispherical caps. At least 10 microscopic fields per sample were counted and 100–150 cells were measured. Cellular carbon content in fg C per cell (C) was calculated from estimated cell volumes (V , μm^3) assuming the allometric relation $C = 120 \times V^{0.72}$ (Norland, 1993).

Planktonic heterotrophic prokaryotic production

The [^3H]leucine incorporation method (Kirchman *et al.*, 1985; Simon & Azam, 1989) following a modified protocol according to Kirschner & Velimirov (1997) with several additional adaptations to this ultraoligotrophic environment was used. Five samples and three blanks were collected in sterile 50-mL Falcon tubes directly at the spring outlet. Each sample and blank was amended with [^3H]leucine (final concentration 7 nM; 120 Ci mmol^{-1} ; ARC Research Products) before or after the incubation time, respectively, and stopped with trichloroacetic acid [final concentration 5% (v/v); Sigma, Austria]. Sample volume and incubation time varied from 40 mL and 48 h in winter to 10 mL and 24 h during summer months. Incubation was carried out at 4 °C (approximately *in situ* temperature) in the dark. Saturation experiments and time course analysis proved that a 7-nM leucine solution was sufficient to prevent extracellular isotope dilution and that leucine uptake was still in a linear range after 48 h. The radioactivity incorporated into heterotrophic cells was measured with a Canberra Packard scintillation counter (1900 TR). Incorporation rates were converted to carbon production using a conversion factor of 1.55 kg C mol^{-1} leucine (Simon & Azam, 1989) assuming no isotope dilution. The overlying water samples from the corresponding sediment samples were treated in the same way.

MAR

Two replicates of 40 and 20 mL were taken from DKAS1 and LKAS2, respectively, spiked with L-[^3H]leucine (120 Ci mmol^{-1} ; final concentration 20 nM) and incubated at 4 °C in the dark for 8 h. We experimentally estimated that under these conditions the percentage of cells taking up L-[^3H]leucine

reached saturation after 6–8 h. Incubations were terminated by adding paraformaldehyde (final concentration 2%) and samples were fixed at 4 °C in the dark for 14–18 h. Subsequently, the samples were filtered through polycarbonate filters (0.2 μm pore size; Millipore Corp., Bedford, MA), supported by cellulose acetate filters (0.45 μm pore size; Millipore Corp.), washed twice with 5 mL of 0.2- μm filtered Milli-Q water and air dried. Filters were embedded in low-gelling-point agarose [0.1% (w/v) Biozym; in Milli-Q water] dried upside down on a glass Petri dish at 37 °C, dehydrated in 96% (v/v) ethanol (Pernthaler *et al.*, 2002a), air dried and stored at –20 °C. Fixation times of > 3 h and immediate embedding in agarose before the first freezing step minimize the amount of tritium-labelled compounds leaking from the cells (Nielsen *et al.*, 2003a). CARD-FISH was performed as described previously (Wilhartitz *et al.*, 2007) using probes EUB338, EUB338-II, EUB338-III and non-EUB for Bacteria, probe EURY806 for Euryarchaea and probe CREN537 for Crenarchaea. At the last step, dried filter sections were not mounted in 4',6'-diamidino-2-phenylindole (DAPI) mix, but air dried and stored at –20 °C until further processing. The CARD-FISH approach was conscientiously tested and adapted for this specific ultraoligotrophic environment (Wilhartitz *et al.*, 2007). MAR was performed after the protocol of Teira *et al.* (2004). The influence of exposure time on the percentage of cells taking up [^3H]leucine was evaluated by developing slides every 8 h for 3 days, resulting in an optimal exposure time of 36–48 h. Paraformaldehyde-killed samples were used as negative control. Size of silver grain clusters did not further increase after 32 h of exposure and no additional MAR-positive cells could be detected.

Sediment samples

For heterotrophic production, six samples and four trichloroacetic acid-killed controls were measured for each sediment. One gram of sediment was incubated with [^{14}C]leucine (306 mCi mmol^{-1} , ARC Research Products; final concentration 2 μM) for 2 h. Measurements were carried out following a protocol used for wetlands (Tietz *et al.*, 2008). Heterotrophic production in the corresponding overlying water was measured as described above.

Sediment for determination of bacterial numbers was split into three aliquots and fixed with formaldehyde (final concentration 2% v/v). The samples were stored at 4 °C and processed within 3 days. Prokaryotic abundance, sediment bulk density, dry mass and pore water were determined as described previously (Farnleitner *et al.*, 2003). Organic content of sediment samples was calculated by subtracting the sample weight after combusting (500 °C, 4 h) from dry mass. Subsamples for grain size distribution and lithological description were taken at every sampling site. The

mineralogical compositions of the samples were analyzed by infrared spectroscopy (Perkin Elmer FTIR Spectrum 100) and in the case of five samples semi-quantitatively by X-ray diffraction (Phillips PW 1800 Co.). The chemical composition of the samples was measured by X-ray fluorescence (Phillips PW 2404). The grain size distribution of one sample (DKAS1 coarse) was determined by dry sieving from 12.5 to 0.63 mm.

About 2 g of the other samples were wet sieved to separate the grain size fractions $< 63 \mu\text{m}$ and $< 40 \mu\text{m}$. The grain size distribution in the fraction $< 40 \mu\text{m}$ down to $0.1 \mu\text{m}$ was measured by a combined gravitative and centrifugal sedimentation analyses using a Shimadzu particle size analyzer (SA-CP2). The specific surface area of the samples was geometrically estimated by the respective grain size distribution data under the assumption that all particles have shapes of rhombic calcite.

Hydrological and chemical parameters

All hydrological and chemophysical data were recovered by in-field on-line sensors. Conductivity, water temperature and discharge-related parameters (water pressure, current meters, inductive discharge measurements) were registered with the data-collecting system GEALOG-S from Logotronnic (Vienna, Austria). The conductivity and pressure probes were Tetracon 96A (WTW, Weilheim, Germany) and PDCR 1830 (Druck, London, UK). Impeller flow sensors were Peek 400 models (Houston), and ELIN Water Technology (Vienna, Austria) current meters were used. Signals from these sensors were converted with algorithms provided by the manufacturers and from discharge stage relations (Stadler & Strobl, 1998). Data were stored every 15 min. Turbidity, spectral absorbance coefficient at 254 nm and pH were measured with a Sigrist and a HL2200 device.

All chemical analyses were performed after Legler (1988). All photometric measurements were performed on a Hitachi U2000+ spectrophotometer in a 5-cm light path (1 cm for higher concentrations) cuvette.

Ion concentrations in the samples were measured by ion chromatography. All columns and chemicals were supplied by Dionex (Sunnyvale, CA). AS-14 columns (DX-120) with AG-14 precolumns were used for anions [SO_4 , NO_3 ; EN ISO 10304-1 (D19)] and CS-12A columns and CG-12A precolumns were used for cations [Ca^{2+} , Mg^{2+} ; EN ISO 14911 (E34)]. Total phosphorus was determined photometrically after dissolution of the unfiltered sample with potassium peroxydisulfate. The fractions were measured as $\text{PO}_4\text{-P}$ using the molybdenium-blue method. Soluble reactive phosphorus was determined as $\text{PO}_4\text{-P}$ in the filtered sample [EN 1189 (D11)]. Total nitrogen was determined photometrically after dissolution of the unfiltered and filtered sample with concentration H_2SO_4 and H_2O_2 . The fractions were

measured using the indophenol-blue method ($\lambda = 655 \text{ nm}$). Total nitrogen can be calculated by addition of nitrite [$\text{NO}_2\text{-N}$ determined photometrically from filtered sample with sulfanilamide and *N*-(1-naphthyl)-ethylene-diamine dihydrochloride solution after the Griess reaction ($\lambda = 543 \text{ nm}$)] and nitrate (NO_3) (EN 26 777/ISO 6777).

Sampling for acid neutralizing capacity, $-p/+p$ -value and free CO_2 was performed in 1-L Winkler glass bottles, wide-mouthed screw-capped bottles [DIN 38409 section 7 (H7)]. The bottles were filled avoiding any headspace. Alkalinity is used interchangeably with acid-neutralizing capacity (Wetzel & Likens, 1991) and refers to the capacity to neutralize strong acids.

Total organic carbon was measured via UV-oxidation after filtration (DIN EN 1484) and dissolved organic carbon (DOC) was measured via UV oxidation of C (DIN EN 1484). For the determination of the biodegradable dissolved organic carbon (BDOC), the protocol of Servais *et al.* (1992) was used.

Statistical analysis

Potential relationships among variables were tested by linear pair-wise correlations (Spearman's correlation analysis). Data were $\log(+1)$ transformed to satisfy the requirements of normality and homogeneity of variance necessary for parametric statistics [(principal component analysis (PCA)]. All statistical analyses were performed with SPSS software for Windows (release 11).

Results

Spring characterization

The dynamics of discharge and conductivity during the sampling period reflected the contrasting hydrological regimes in DKAS1 and LKAS2 (Fig. 1, Supporting Information, Table S1) and were in accordance with previous studies (Stadler & Strobl, 1997, 1998; Farnleitner *et al.*, 2005). The chosen sampling dates covered the full range of discharge variability, as an indicator of hydraulic reactions, and of conductivity, as an indicator of mass transport. Details on chemical parameters are given in Table 1.

Prokaryotic numbers, biomass and prokaryotic heterotrophic production were significantly higher in the dynamic spring-type LKAS2. The determined cellular carbon content of the prokaryotic cells resulted in 15 fg C per cell (1.25 fmol C per cell) in LKAS2 and 12 fg C per cell (0.99 fmol C per cell) in DKAS1. DOC and BDOC were similar in both systems during base-flow conditions. During storm-flow events, DOC concentrations in LKAS2 increased due to enhanced surface runoff (Table 1).

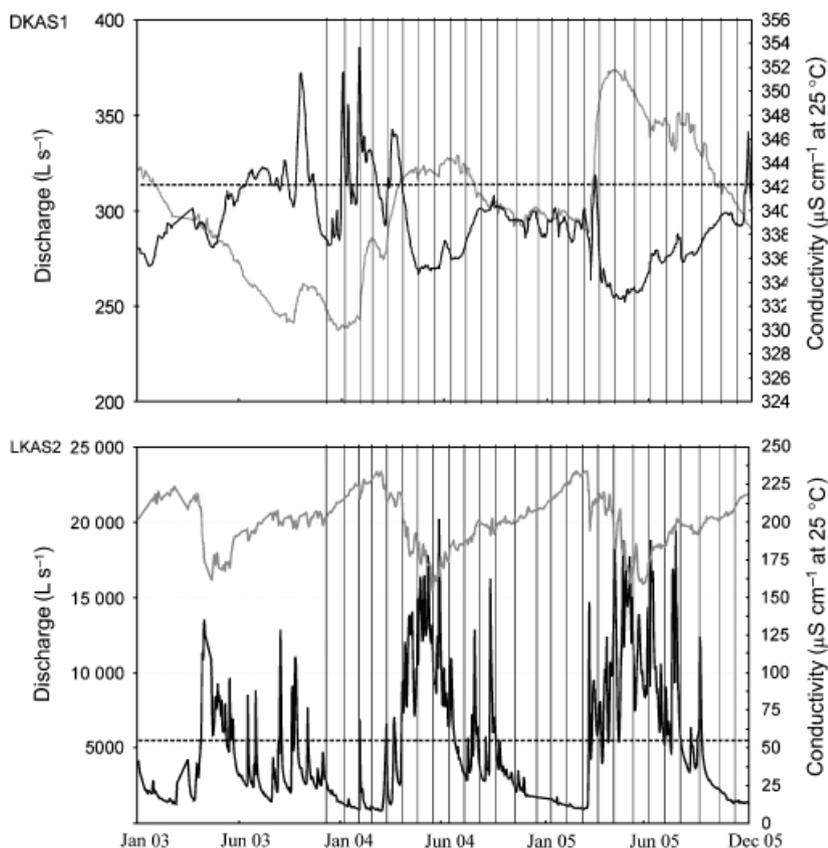


Fig. 1. Hydrological dynamics in the two investigated alpine karst springs. Vertical lines indicate sampling dates during the period from December 2003 to December 2005. The gray lines show the conductivity at 25 °C (right axes); the black lines depict the daily mean discharge (left axes). The mean discharges throughout the investigation period are indicated by broken lines. Note that different scales between aquifers are used.

Heterotrophic prokaryotic production and MAR in the planktonic compartment

Heterotrophic production ranged from 0.1 to 75.6 pmol CL⁻¹ h⁻¹. The lowest production rates in both springs were observed during the winter months (November–February), the highest during storm-flow events in summer and autumn. Seasonal variations were more pronounced in LKAS2 but, in general, congruent with fluctuations in DKAS1 (Fig. 2a). In LKAS2 variations could be explained by a high correlation between discharge and prokaryotic numbers ($r=0.74$; $P < 0.01$) and discharge and heterotrophic production ($r=0.78$; $P < 0.01$) (Table S1). No correlation could be observed between discharge and prokaryotic numbers in DKAS1 ($r=-0.2$; $P > 0.05$) (Table S1). Depending on the hydrogeological situation, [³H]leucine uptake in LKAS2 spring water was 10–100-fold higher than in DKAS1 during the entire investigation period. In contrast, cell-specific uptake rates were similar during base-flow conditions (Fig. 2b), only differing during snow melt or storm-flow events.

The contribution of organisms targeted by probes used for Bacteria and Archaea to the assimilation of [³H]leucine was examined over a period of 6 months (January–June 2004). The recovery efficiency (sum of Bacteria, Crenarchaea

and Euryarchaea) averaged 83% (range, 74–91%) of DAPI-stainable cells. MAR revealed that on average only about 7% (range, 3–14%) of all DAPI-stainable cells visibly assimilated [³H]leucine (Fig. 3). Organisms targeted by the three EUB probes (Bacteria) were the dominating group taking up leucine (76% Bacteria, 24% Archaea; related to the active fraction). Among Archaea, Euryarchaea showed a higher percentage of active cells than Crenarchaea (Fig. 3) with an average of 16% and 8% for LKAS2 and DKAS1, respectively (related to the active fraction). No cells with associated silver grains were observed in the paraformaldehyde-killed controls. Based on the bulk heterotrophic production and the prokaryotic biomass, the average bulk generation time of prokaryotes in LKAS2 and DKAS1 was 202 and 712 days, respectively. Considering, however, only the leucine-assimilating cells, as determined by MAR-FISH the average generation time was 14 days for LKAS2 and 55 days for DKAS1. The average cell-specific uptake rates varied from 1.23 to 195 amol C per cell day⁻¹ in DKAS1 and from 6.18 to 401 amol C per cell day⁻¹ in LKAS2 (Fig. 2, Table 1).

Integrated view of data: PCA

In order to elucidate the main environmental factors describing the spring water quality, the key parameters

Table 1. Biogeochemical and microbial characterization of two different karst spring waters ($n = 19\text{--}25$)*

Parameters	Unit	LKAS2		DKAS1	
		Median	Range min.–max.	Median	Range min.–max.
Hydrographical parameters					
Q	L s ⁻¹	5340	902–15 479	319	290–373
EC	μS cm ⁻¹	195	156–222	338	333–345
Temp	°C	5.3	4.9–5.8	6.7	6.7–6.7
pH [†]	–	8.1	7.8–8.3	8.0	7.4–8.7
SAC	m ⁻¹	1.7	0.44–4.10	Nd	Nd
TUR	NTU	0.16	0.03–0.96	Nd	Nd
Geochemical parameters					
Total hardness	mval L ⁻¹	2.08	1.68–2.43	3.63	3.50–3.73
Ca ²⁺	μM	875.8	722.6–976.4	1200.2	1162.4–1252.1
Mg ²⁺	μM	160.3	117.3–240.5	612	584–638
Cl ⁻	μM	ND	ND	64.6	42.0–120.7
SO ₄ -S	μM	11.1	5.9–19.9	29.0	21.7–41.6
NO ₃ -N	μM	9.0	6.5–17.6	16.5	15.4–17.1
TN	μM	42.3	32.0–81.4	74.4	69.0–77.3
SRP	μM	0.15	0.13–0.17	ND	ND
TP	μM	0.18	0.13–0.48	ND	ND
Biological parameters					
PN	10 ⁶ cells L ⁻¹	44.4	27.0–69.7	13.1	11.2–19.0
PB	nmol C L ⁻¹	58.28	28.31–94.08	13.32	9.16–19.15
HP	pmol C L ⁻¹ h ⁻¹	12.9	0.5–75.6	0.7	0.1–6.8
HP per cell [‡]	amol C per cell h ⁻¹	0.29	0.06–0.96	0.06	0.01–0.61
Carbon-associated parameters					
DOC	μM C	46.6	16.7–99.1	25.0	18.3–45.0
BDOC	μM C	4.16 [§]	0.83–11.66	4.16 [§]	0.83–18.32
CO ₂ [‡]	μM	32.5	15.7–55.5	254	97–637
P-value	mmol L ⁻¹	0.04	0.01–0.21	0.14	0.01–0.59
ANC	mval L ⁻¹	2.04	1.63–2.43	3.4	3.32–3.51

*Samples were taken monthly over a 2-year period.

[†]Measured in laboratory.

[‡]Calculated parameter.

[§]Both medians resulted in identically low values.

Q, discharge; EC, electrical conductivity; SAC, spectral absorbance coefficient at 254 nm; TUR, turbidity; NTU, nephelometric turbidity unit; TN, total nitrogen; SRP, soluble reactive phosphorus; TP, total phosphorus; PN, prokaryotic number; PB, prokaryotic biomass; HP, heterotrophic prokaryotic production; CO₂, free CO₂; P-value, amount of OH⁻ to reach pH 8.3; ANC, acid neutralization capacity (≡ alkalinity); Temp, temperature; ND, not detectable; Nd, not determined.

for both systems were used for PCA (Table 2). The component matrix revealed fundamental differences for LKAS2 and DKAS1. Three significant components with an eigenvalue > 1 were extracted for LKAS2 explaining 93.5% of the total variation. The main variations in spring water from the limestone spring type (LKAS2) were characterized by the first component (comprising discharge, heterotrophic production, DOC and prokaryotic numbers) responsible for 60.8% of the total variation. In combination with the second component (comprising discharge, conductivity and SO₄) they revealed that the main forces determining LKAS2 were the dynamic hydrological components, explaining 78.9% of the system's variation (discharge was represented in both components). Only one parameter (BDOC) showed a correlation higher than $r = 0.5$ to the third component, describing 13.1% of total variation.

The three significant components extracted for DKAS1 explained 87.2% of the total variation, but revealed completely different coherences compared with LKAS2. The first, the hydrographical component comprising SO₄, discharge and conductivity, explained 42.8% of the system's variation but showed no direct relationship with the microbiological and biological parameters included in the second and third components. The second component included prokaryotic numbers and BDOC, and the third component, including DOC and heterotrophic production, together were responsible for 44.4% of the total variation.

Prokaryotic numbers and prokaryotic heterotrophic production in the sediment

Average prokaryotic numbers (42×10^7 cells L⁻¹) and heterotrophic production (41 pmol C L⁻¹ h⁻¹) in the overlaying

water from the 12 sediment locations were comparable to the values obtained in the spring water of LKAS2 and DKAS1. In contrast, values in the sediment were dramatically higher than that in the planktonic fraction. Prokaryotic numbers averaged 4.03×10^{11} cells dm^{-3} (range, 1.25×10^{11} – 7.91×10^{11} cells dm^{-3} , $n = 12 \times 6$) and heterotrophic production averaged $19 \mu\text{mol C dm}^{-3} \text{h}^{-1}$ (range, 3–71 $\mu\text{mol C dm}^{-3} \text{h}^{-1}$, $n = 12 \times 6$). On a volumetric basis this depicts a 10^6 -fold increase when comparing heterotrophic production in the planktonic and the attached autochthonous endokarst community. Heterotrophic production in LKAS2 averaged $25 \mu\text{mol C dm}^{-3} \text{h}^{-1}$ ($n = 18$) resulting in generation times of 24 h (Table 3). Unlike uptake rates in the planktonic fraction, [^{14}C]leucine incorporation in DKAS1 was higher than in LKAS2, revealing lower generation times in the range of some hours (Table 3). Averaged cell-specific

uptake rates calculated for the sediment bulk community were $75.9 \text{ pmol C per cell h}^{-1}$ for LKAS2 and $218.2 \text{ pmol C per cell h}^{-1}$ for DKAS1. In comparison, the average cell-specific uptake rates for the planktonic community were $0.29 \times 10^{-6} \text{ pmol C per cell h}^{-1}$ for LKAS2 and $0.06 \times 10^{-6} \text{ pmol C per cell h}^{-1}$ for DKAS1 (Table 1).

Sediment analysis

Lithological analysis of the recovered aquifer sediments showed almost the same composition for all samples. Sediments were composed of dolomite, calcite and quartz with dolomite being the quantitatively prevalent component. The dominant grain size distributions varied between 2 and 60 μm in diameter except for one coarse sediment sample, from DKAS1, ranging from 0.3 to 100 mm. The averaged specific surface area for the sediment fraction $< 63 \mu\text{m}$ (the dominant size fraction) was $188 \text{ m}^2 \text{ dm}^{-3}$. The pore volume, as determined from water content, was $288 \text{ cm}^3 \text{ dm}^{-3}$. The correlation between heterotrophic production and surface area (fraction $< 63 \mu\text{m}$) was high ($r = 0.81$) but not significant.

Discussion

Heterotrophic prokaryotic production in alpine spring water

In situ measurements of heterotrophic production in different aquatic habitats ranges from $738 \mu\text{g CL}^{-1} \text{ h}^{-1}$ ($61.5 \mu\text{mol CL}^{-1} \text{ h}^{-1}$) in hypertrophic shallow soda lakes (Eiler *et al.*, 2003) to 0.01 – $0.05 \mu\text{g CL}^{-1} \text{ h}^{-1}$ (0.83 – $4.12 \text{ nmol CL}^{-1} \text{ h}^{-1}$) in an ultratrophic Antarctic lake (Laybourn-Parry *et al.*, 2001). To our knowledge, this is the first study directly measuring *in situ* prokaryotic heterotrophic production in groundwater from an alpine karst aquifer. Considering the values ranging from 0.1 to $75.6 \text{ pmol CL}^{-1} \text{ h}^{-1}$, heterotrophic production is extremely low, pointing toward a high biostability of the abstracted water, used for water supply (low *in situ* cell activity),

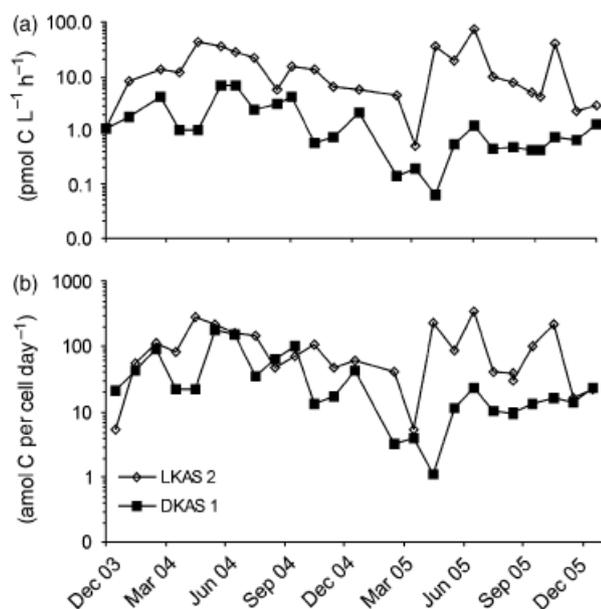


Fig. 2. Dynamics of bulk prokaryotic heterotrophic production rates (a) and cell-specific production (b) of the planktonic microbial communities of two alpine karst springs; y-axes in log scale.

Fig. 3. CARD-FISH and MAR results for the two alpine karst springs revealed that Bacteria (Eub; probe-mix of EUB338, EUB338II and EUB338III) comprise the largest fraction of the microbial community in both springs. About 10% of the community were identified as Euryarchaea (probe EURY806) and Crenarchaea (probe CREN537). MAR-active cells were found in both prokaryotic fractions. The picture depicts CARD-FISH positive cells showing green fluorescence, and two cells that are additionally surrounded by black silver grains indicating [^3H]leucine uptake. All counts were made in relation to DAPI counts.

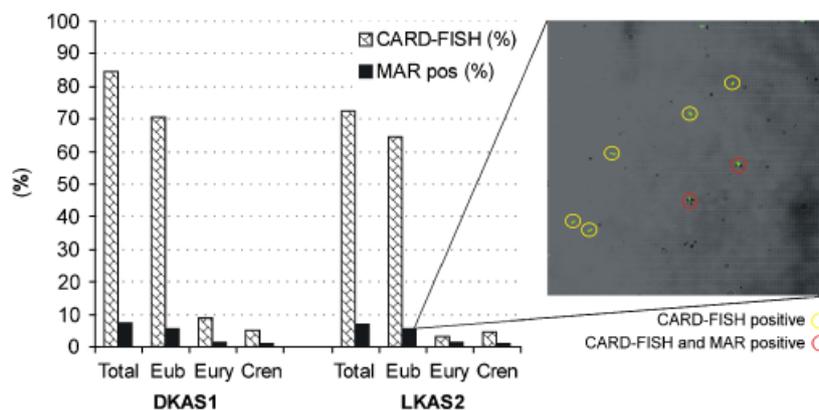


Table 2. Component matrix for two different spring types

LKAS2*				DKAS1*			
Parameters	1	2	3	Parameters	1	2	3
HP	0.92	-0.32	-0.01	SO ₄	0.97	0.14	0.06
DOC	0.87	0.07	0.37	Q	-0.96	-0.13	-0.10
Q	0.83	-0.51	-0.11	EC	0.90	-0.12	0.16
PN	0.77	-0.29	0.37	PN	-0.18	-0.91	0.10
EC	-0.17	0.98	-0.05	BDOC	-0.07	0.88	0.21
SO ₄	-0.27	0.90	-0.27	DOC	0.12	-0.14	0.90
BDOC	0.15	-0.17	0.97	HP	0.12	0.29	0.85
% of variance	60.8	18.0	14.7		42.8	24.4	20.0
Cumulative		93.5%				87.2%	

Correlations > 0.5 are in bold. Extraction method: PCA – varimax rotated with Kaiser normalization. Abbreviations are as given in Table 1.

Data set for PCA was reduced to the key parameters that were available for both springs ($n = 19-21$).

*Three components extracted.

Table 3. PN and HP measured in sediments and the respective overlaying water in LKAS2 and DKAS1 ($n = 18$)

	Overlaying water		Sediment				
	PN (cells L ⁻¹)	HP (pmol C L ⁻¹ h ⁻¹)	PN (cells dm ⁻³)	PB* (μmol C dm ⁻³)	HP (min.–max.) (μmol C dm ⁻³ h ⁻¹)	HP per cell (pmol C per cell h ⁻¹)	g [†] (h)
LKAS2	4.7×10^7	61	3.5×10^{11}	590	25 (15–36)	75.9	24
DKAS1	1.7×10^7	32	1.8×10^{11}	302	41 (10–61)	218.2	8

*PB was calculated with 20 fg C per cell.

†g, generation time.

Abbreviations are as given in Table 1.

especially during base-flow conditions. However, high variations were observed during two seasonal cycles (Fig. 2). Peaks in heterotrophic production in LKAS2 coincide with peaks in discharge ($r = 0.78$, $P < 0.01$), prokaryotic numbers ($r = 0.53$, $P > 0.05$), DOC ($r = 0.64$, $P < 0.01$) and total phosphorus ($r = 0.74$, $P < 0.01$). As phosphorus concentrations were below the detection limit in DKAS1, these results indicate a phosphorus limitation in alpine karst aquifers as was also described for other freshwater ecosystems (Wilhelm & Suttle, 1999). Higher cell abundance and biomass in LKAS2 during the summer months can be explained by (1) detachment of cells from biofilms like it has been shown for streams and rivers (Blenkinsopp & Lock, 1994) and (2) an increased input of allochthonous cells by surface runoff into the aquifer also providing (3) enhanced substrate supply (DOC, total phosphorus), stimulating the growth of the indigenous prokaryotes. These factors were probably also responsible for the higher heterotrophic production in LKAS2 during periods of increased discharge. In contrast to LKAS2, heterotrophic production in DKAS1 was only correlated with the P-value ($r = 0.74$, $P < 0.01$), indicating a minor, maybe indirect, role of the input of transient microorganisms and allochthonous nutrients, and pointing toward seasonal variations within the indigenous microbial community [e.g. interplay with viruses and protozoan as

known from other habitats (Weinbauer & Höfle, 1998)]. The higher NO₃ concentrations in DKAS1 probably arise from differences in the vegetation of the two catchment areas (Dirnböck & Greimler, 1999b) and are not necessarily related to biogeochemical cycles within the aquifer. Isotopic analyses would be required to decipher the origin of both nitrate and sulfate in this study (Einsiedl & Mayer, 2005, 2006).

A small fraction of active cells in alpine karstic spring water

The combined technique of CARD-FISH (or FISH) and MAR allows to link key physiological features to the identity of microorganisms and has been applied in various systems (Ouverney & Fuhrman, 1999, 2000; Ito *et al.*, 2002; Nielsen *et al.*, 2003b; Teira *et al.*, 2004, 2006). In highly productive shallow soda lakes in Austria, the percentage of active cells ranged from 40% to 90% (Eiler *et al.*, 2003). In contrast, a recent study showed that in the North Atlantic deep water the fraction of active cells can be lower than 5% (Teira *et al.*, 2006). This is in accordance with our results revealing an average cell fraction of about 7% of the total cells taking up leucine. One could speculate that the planktonic fraction mainly constitutes of swarming cells released from the biofilm to colonize new surfaces.

Although new findings suggest that the fraction of active Archaea can be larger than that of Bacteria in some oligotrophic marine environments (Teira *et al.*, 2004), the average fraction of Euryarchaea and Crenarchaea taking up leucine in alpine spring water comprised less than one-fourth of the total active community.

As prokaryotic activities in nutrient-poor environments are low, doubling times for the microbial community of decades and centuries have been calculated (Phelps *et al.*, 1994). However, bulk calculations of doubling times, including all microorganisms are overestimates. Taking into account that only 7% of the cells took up [³H]leucine, growth rates averaged 0.07 day⁻¹ in LKAS2 and 0.02 day⁻¹ (ranging from 0.13 to 0.001 day⁻¹) in DKAS1. These values are comparable with results obtained in the deep ocean (0.01–0.008 day⁻¹) (Bendtsen *et al.*, 2002; Reinthaler *et al.*, 2006). The average cell-specific uptake rates, except for measurements during storm-flow events, were in the range of uptake rates determined for sea water (0.53–47.4 amol C per cell day⁻¹) (Sintes & Herndl, 2006).

PCA

PCA can be used for dimensionality reduction in a data set by retaining those characteristics of the data set that contribute most to its variance. In this study it was used to elaborate differences between the two spring systems, especially with respect to key parameters influencing heterotrophic production. Therewith, we tried to shed light on the ecological drivers in such systems.

To a certain degree, the nature of the sediment matrix in porous aquifers determines the heterogeneity in the distribution and activity of microorganisms in the subsurface (Griebler, 2001). In agreement with these observations from porous aquifers, the component matrix for DKAS1 and LKAS2 revealed fundamental differences when evaluating the factors dominating the microbial fraction within these karstic systems. All parameters in LKAS2, except BDOC, were directly related to variations in discharge (Table 2). The first component constituted the 'input factor,' describing an enhanced surface influence within the spring water during increased discharge, represented by positive correlations with prokaryotic numbers, DOC and heterotrophic production. The second component constituted the 'dilution factor' and comprised parameters that typically decrease as surface water enters the system, like conductivity and SO₄ concentration. This obvious dependence on discharge corresponds with the morphology of this spring type, showing well-developed karst conduits (Stadler & Strobl, 1997) that allow for a very quick discharge response after precipitation and, hence, for a pronounced surface influence. A different situation is given in DKAS1 where the component matrix revealed microbiological characteristics within the system

that are not directly related to hydrographical parameters. Biotic factors are more important in describing the variance of the system, whereas the influence of discharge-related components halved compared with LKAS2 (Table 2). Porous and fissured rock (such as in DKAS1) does not allow for high-velocity fluxes and is characterized by high water residence times. These conditions possibly allow for the development of a microbiologically dominated compartment within the aquifer and boost the potential impact of biofilms.

Heterotrophic prokaryotic production of surface-associated endokarst communities

For porous aquifers it has already been concluded that well-water prokaryotes do not accurately reflect attached microbial communities and planktonic cells might be subsets of biofilms (Hazen *et al.*, 1991; Pedersen, 1993; Alfreider *et al.*, 1997). In many cases, the attached microbial communities showed distinctive morphological and physiological patterns compared with the planktonic cells in the interstitial groundwater (e.g. higher portion of gram-positive cells, higher morphologic diversity, sessile forms, higher activity rates, higher degradation potential for complex compounds) (Kölbl-Boelke & Hirsch, 1989; Griebler *et al.*, 1999, 2002). Heterotrophic production in alpine karst aquifer sediments as determined in this study, exceeded measurements in the respective planktonic fraction by orders of magnitudes, revealing generation times that were surprisingly low (hours).

As it was impossible to recover samples from the matrix surface within the aquifer, the sediments in this study constituted of material that was flushed out of the system and was either deposited at the spring outlet or collected in a sediment trap. Nevertheless, sediment analysis confirmed that the sediment composition was comparable at all sampling sites (dolomite) and in accordance with the lithological composition described for this area (Bryda, 2001). Therefore, heterotrophic production data obtained in this study are likely to reflect the general situation for clastic sediments within the aquifer matrix.

When estimating the carbon demand needed to sustain the measured production rates, the data suggest that 1 dm³ of sediment would hypothetically consume the DOC content in 1 L of spring water within hours (0.5 h for DKAS1 and 1.4 h for LKAS2). This result implicates that attached AMEC are probably effective in degrading allochthonous DOC entering the spring system and thus significantly enhance the resulting spring-water quality. The depletion in degradable carbon is likely to be stronger in the matrix-flow component, in areas where water percolates slowly through pores and fractures in the bedrock. The rock matrix in natural karst aquifers provides surface areas that range from 30 m² m⁻³ (limestone) to 300 m² m⁻³ (dolomitic limestone) (Decker *et al.*, 1998) and thus the bedrock itself can act as a

'trickling filter.' Clearly, these surface areas are low when compared with the loose sediments collected in this study. Nevertheless, the estimated time span needed for degrading the measured DOC ranges from 10 days in a bare dolomitic bedrock [assuming $300 \text{ m}^2 \text{ m}^{-3}$, low DOC ($17 \mu\text{M C}$)] to 369 days in a bare limestone bedrock [assuming $30 \text{ m}^2 \text{ m}^{-3}$, high DOC ($99 \mu\text{M C}$)], and is therefore even shorter than the estimated average transit time for the dynamic spring-type LKAS2 (1.5 years). The degree of DOC consumption will therefore depend on the bedrock and the amount of clastic sediment on the passage floor and walls. It should be mentioned that for the given scenarios only DOC concentration in the spring outlets were considered. Real-input DOC concentrations may be higher but are currently not available for calculations. However, DOC concentrations as determined during the seasonal cycles, including summer events probably showing the maximum DOC input possible in this catchment, should be a first good approximation. Furthermore, DOC concentrations measured in the spring water during base flow might also contain fractions that are not degradable by prokaryotes, suggesting the need for other sources to meet the carbon demand of the autochthonous endokarst communities (e.g. internal turnover).

It is a long-known fact that in some karst systems the CO_2 introduced from external sources, namely soil or atmosphere, is not sufficient to explain for the extent of karstification observed. There are some studies suggesting that there has to be a CO_2 source, other than the soil compartment or the atmosphere, especially in the deeper regions of the vadose and phreatic zone (Atkinson, 1977; Wood, 1985; Gabrovsek *et al.*, 2000). Based on our heterotrophic production measurements in alpine karst groundwater aquifers a possible influence on geological processes (e.g. karstification) by the microbial community was evaluated by estimating their CO_2 production. The theoretical time needed to reach CO_2 levels measured in the respective spring water was calculated. CO_2 input from the surface and CO_2 consumption within the aquifer were not included in the calculation, as equilibrium chemistry and kinetics of dissolution reactions are very complex and vary over space and time (White, 1988; Vesper & White, 2004b; Groves & Meiman, 2005). The estimated time needed for the planktonic fraction to produce the prevailing CO_2 level was 2 years for LKAS2 and 81 years for DKAS1, assuming a bacterial growth efficiency of 1% (calculations showed that bacterial growth efficiency was, in any case, smaller than 3%, but due to the extremely low values it could not be determined accurately). Estimates with higher bacterial growth efficiencies lead to results of up to 1174 years for DKAS1. When considering the estimated average water residence times of 1.5 years for the LKAS2 and 22 years for the DKAS1 system (Stadler & Strobl, 1998), these findings show that plankton microbial communities are very unlikely to influence geomorphological processes in

the aquifer. Considering the high heterotrophic production in aquifer sediments, microbially mediated CO_2 would reach CO_2 -levels measured in DKAS1 and LKAS2 within hours in the case of an equivalent available surface per volume ratio of respective aquifer locations. Considering the prevailing natural rock matrix, CO_2 levels would approximately be reached within < 1 year in a bare limestone bedrock ($30 \text{ m}^2 \text{ m}^{-3}$) and within about 1 month in a bare dolomitic bedrock ($300 \text{ m}^2 \text{ m}^{-3}$). Given the fact that there are areas where water moves only slowly through fractures and pores and has a longer transit time, these results indicate a considerable potential for microorganisms to contribute to the prevalent CO_2 level and with that to geomorphological processes. Gabrovsek *et al.* (2000) already speculated that this influence would increase in a bare catchment and in deeper aquifers where external CO_2 supply decreases. DOC supply is crucial in this context, because little CO_2 input in a bare area normally also denotes a reduced DOC input due to the absence of a soil layer. One effect that could enhance microbially mediated CO_2 level, in this case, is that viral lysis products including phages turn over relatively rapidly, especially in oligotrophic, P-limited environments (Noble & Fuhrman, 1999). This 'viral loop' could help to replenish the nutrient pool in deeper aquifers and provide DOC for prokaryotic growth. Lysis products are available to bacteria at the expense of a reduced growth efficiency, which should enhance prokaryote-mediated CO_2 production (Weinbauer, 2004). In a recent study 10^5 – 10^7 virus-like particles per milliliter were found in granitic groundwater (Kyle *et al.*, 2008). First measurements in the investigated springs were in a similar range (unpublished data), giving room for speculations.

However, it is likely that the microbially mediated CO_2 fraction is not linked to the CO_2 measured at the spring outlet, as it is produced in microzones very close to the rock surface (boundary layer) and is hence immediately involved in redox reactions to re-establish an equilibrium state.

Conclusion

In situ activity of planktonic prokaryotic spring communities were extremely low, indicating a high potential biostability of the abstracted water, especially during base-flow conditions. Most of the planktonic fraction is apparently in an inactive or dormant state. These findings are relevant for public water supply as biostability is an important factor considering the regrowth potential of water in a distribution network. The crucial compartment regarding prokaryotic heterotrophic production is the surface-associated autochthonous microbial endokarst community (AMEC). These attached communities could contribute to important biogeochemical processes taking place in alpine groundwater aquifers (e.g. energy or matter fluxes, karstification).

Microbial-mediated processes are probably mainly restricted to the matrix-flow component of karstic systems where large surface areas and long water residence times prevail. In contrast, storm-flow runoff – partly through large, temporarily activated conduits – bypasses these areas of ‘metabolic transformation’ and decreases water quality at the spring outlet. With respect to the given hydrogeological situation, spring water management is of fundamental importance to guarantee raw water of high quality.

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Supporting Information

Additional Supporting Information may be found in the online version of this article:

Table S1. Spearman's correlation (a) (LKAS2) and (b) (DKAS1).

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