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INVESTIGATION OF HYDROTHERMAL SOURCES IN THE RIO GRANDE RIFT REGION

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Abstract.—Hydrothermal water samples were obtained from 11 locations associated with the Rio Grande Rift and analyzed for chemical and microbial composition. The sampled hydrothermal waters can be categorized into three groups of water: (I) steam-condensing, sulfur-rich acidic water, (II) mixtures of deep thermal water with shallow groundwater and (III) heated meteoric water. Category I water was populated by thermoacidophilic organisms with a high biomass content, while category II water was highly mineralized and indicating a high degree of microbial diversity but low biomass content. Heated meteoric water (category III) was low in biomass content and microbial diversity. We conclude that microbes can be used as tracer for specific types of subsurface environments and aim further studies to reveal which hydrothermal upflow regions are related to each other using microbial, chemical and isotope analyses.

INTRODUCTION

The Rio Grande Rift is one of the dominant structural features of New Mexico (Fig. 1). The Rift zone is characterized a by high thermal gradient and a high heat flux (Laughlin, 1981; Sass and Morgan, 1988). Several hydrothermal springs discharge from the Rift area. However, the hydrothermal waters are believed to have different origins and belong to different thermal fluid types (Goff and Gardner, 1994; Trainer et al., 2000 White, 1986; Vuataz and Goff, 1986). These waters are interesting as a potential energy source as well as for the spa industry and agricultural purposes. In some cases the hydrothermal waters have drinking water quality and could be used as such in the arid areas of New Mexico where water sources are scarce.

Our objective is to characterize the origin and age of the hydrothermal fluids, including the chemical and microbial composition. Variety of different methods – from geochemical (including isotope) analyses to microbial DNA sequencing are used. In this paper we present the results of the on-going project as well as plans for future work.

HYDROTHERMAL FLUIDS AT THE RIO GRANDE RIFT ZONE

The Rio Grande Rift resulted from extensional tectonism, which created this deep structure in the last 35 m.y. (Chapin and Cather, 1994; Cather et al., 1994). The rift structure may thus enhance the percolation of deep fluids to the surface; fluids that are characterized by high temperature and a high degree of mineralization. Many of the springs and wells drilled in the Rio Grande Rift area have those qualities (Trainer et al., 2000; Goff and Gardner, 1994; White, 1986; Vuataz and Goff, 1986; Shevenell et al., 1987; Sass and Morgan, 1988).

A well-known geological feature within the rift is the Valles Caldera, situated on the western bank of the Rio Grande River. It was explored in detail because of its geothermal energy potential (Laughlin, 1981; Sass and Morgan, 1988). The Valles Caldera, formed by volcanic collapse during the late-Cenozoic, is roughly circular in geometry and occurs at the intersection of the Rio Grande Rift and the Jemez Lineament. The Caldera hosts high-temperature (~300 ^{o}C) geothermal systems with several geothermal springs that discharge waters of different chemical composition (Goff and Gardner, 1994).

We define hydrothermal water as any water that is significantly warmer than the average year air temperature of the region, regardless of the water's origin. Hydrothermal fluids occur where heat flow from the Earth's interior is greater than average. The heat flow may be caused by convection and/or conduction. Since increase in water temperature and an increase in flow-path distance generally increases mineral solubility, the convectively circulating waters tend to be highly mineralized (Bowen, 1979). These highly mineralized waters could provide all essential inorganic nutrients for chemolithotrophic microbes (Priest and Goodfellow, 2000). Hydrothermal fluid systems can be considered semi-stable environments for microbes because they persist, with little change, for over several hundreds or even thousands of years. More than

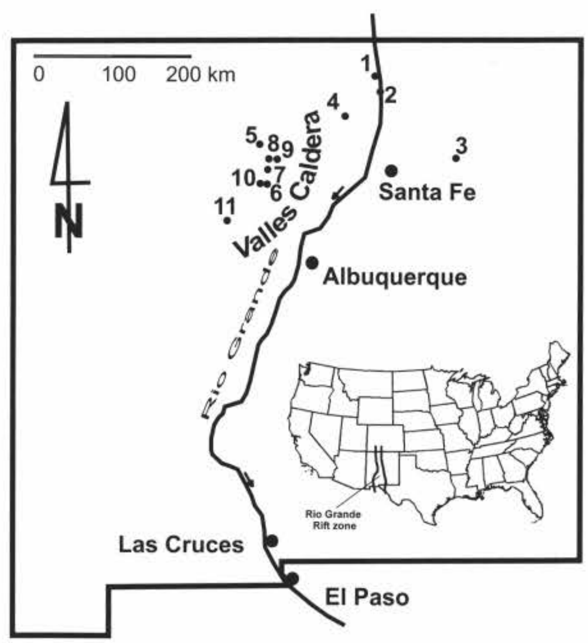

FIGURE 1. Location of study area (Rio Grande Rift) and schematic map of sampling points. 1 – Blackrock Spring, 2 – Manby Spring, 3 – Montezuma Springs, 4 – Ojo Caliente, 5 – San Antonio Spring, 6 – Soda Dam Spring, 7 – Spence Spring, 8 – Sulfur Spring I, 9 – Sulfur Spring II, 10 – Travertine Mound, 11 – San Ysidro Spring.

twenty different genera of microorganisms are currently known that can grow at the temperatures characterizing hydrothermal fluids systems (Priest and Goodfellow, 2000). Thus, it can assumed that hydrothermal water associated with the Rio Grande Rift is also colonized with thermophilic (heat-loving) microbes.

DESCRIPTION OF SAMPLING LOCATIONS

In the first phase of the project, water samples were collected from 11 locations shown on Figure 1. The sampled hydrothermal springs are grouped in two areas: Valles Caldera (7 samples) and Upper Rio Grande Basin (Taos Area, 3 samples), plus one sample from Montezuma Hot Springs, which is located outside the Rift area (near Las Vegas, New Mexico). Another phase of the project will lead to sampling and describing geochemical and microbial compositions of thermal fluids along the southern Rio Grande Rift in southern New Mexico and western Texas. The description of the host rocks for each spring is given in Table 1.

The four springs sampled in the Taos Area were Blackrock Spring, Manby Spring, Montezuma Spring and Ojo Caliente Spring (Fig. 1). Blackrock Spring and Manby Spring discharge on the banks of the Rio Grande and are natural springs that are occasionally flooded by the river. During sampling the river stage was relatively high, but was not flooding the springs. Although the spring were sampled as close to the source as possible, it can not be excluded that some of the river water may have mixed in with the geothermal water during sampling. Ojo Caliente Spring (also called Arsenic Spring) is developed as a spa and was sampled directly from its source. Montezuma Spring is developed as a shallow well. Water was collected as close to the inflow as possible but some water from the surface area of the well was probably mixed in during sampling (Table 1).

In the Valles Caldera area, three sampled springs are located within the Santa Fe National Forest in the Jemez Mountains: Soda Dam Spring, San Antonio Spring, and Spence Spring (Fig. 1). Soda Dam Spring is a natural spring in a spectacular deposit of travertine. Spence Spring and San Antonio Spring are both situated in pine forest of the outer rim of the caldera separated several kilometers from each other (Fig. 1). Travertine Mound Spring is located within the town limits of Jemez Springs on the bank of the Jemez River. Hydrothermal water is gurgling up from the center of the mound creating a travertine deposit around it (Table 1).

Two samples were taken from the Sulfur Springs area (Fig. 1). The Sulfur Spring area contains several natural springs, two of which were sampled. One sampling site, located near the former bathhouse (N 35° 54.466', W 106° 36.949') was named Sulfur Spring I. The other sampling site, near the southern end of the area (N 35° 54.449', W 106° 37.017') was named Sulfur Spring II (Table 1).

One hydrothermal water sample was taken from the San Ysidro Spring (named also San Ysidro Hot Spring), which is located on the Nacimiento Fault south of the Valles Caldera (Table 1).

METHODS

At the beginning of each sampling event, the field parameters temperature, dissolved oxygen, electrical conductivity, pH and

TABLE 1. Short description of the host rocks of sampled springs.

Spring	Host rock	Reference	Other information
Blackrock Spring	Santa Fe group sediments (late Tertiary) underlying the Pliocene Servilleta Basalt, and recent alluvial sediments	Garrabrant, 1993	Rio Grande River bank
Manby Spring	Santa Fe group sediments (late Tertiary) underlying the Pliocene Servilleta Basalt, and recent alluvial sediments	Garrabrant, 1993	Rio Grande River bank
Ojo Caliente Spring	Precambrian metarhyolite	Summers, 1976	
Montezuma Spring	Fractured Precambrian granite	Summers, 1976	
Soda Dam Spring	Faults separating Precambrian granite, the Permian Abo Formation, and the Madera limestone (Pennsylvanian)	Summers, 1976	Spectacular travertine deposit near the spring
Spence Spring	Banco Monito vitrophyre (member of Valles rhyolite), which overlies rocks of the Permian Abo Formation	Hawley, 1978	
San Antonio Spring	Valles rhyolite	Summers, 1976	
Travertine Mound Spring	Quaternary alluvium, Bolson deposits	Abeyta and Delaney, 1990	Travertine deposit
Sulfur Springs (locations I and II)	Ash-flow tuff and volcaniclastic sandstone	Goff and Gardner, 1994	
San Ysidro Spring	Triassic fluvial, mud-rich Chinle formation in contact with the Poleo sandstone	Summers, 1976	Located on the Nacimiento Fault

turbidity (based on visual categorization) were recorded. After measuring the field parameters the water samples were taken in pre-prepared sampling bottles using sterile gloves. Samples collected for PLFA analysis had formaldehyde as preservative (20 ml of 37 % formaldehyde solution in a 2-L bottle); samples collected in a 2-L bottle for DNA analysis had no preservative. Water samples collected for anion analysis were collected in sampling bottles that contained a chemical-specific preservative. Samples collected for cation analysis were collected in sterile sampling bottles and acidified within 12 hours after sampling. Samples collected for anion and microbial analysis were shipped (on ice) to commercial laboratories. Cation analyses were done at the geochemical laboratory of University of Texas at El Paso using an ICP mass spectrometer.

The microbial analysis included the determination of viable biomass and characterization of the 16S rDNA nucleic acid sequences. Phospholipid fatty acids (PLFA) analysis was used to measure viable microbial biomass. Denaturing Gradient Gel Electrophoresis (DGGE) allowed the identification of primary species of the sampled hydrothermal water. The DGGE nucleic-acid analysis technique approximates the species composition of complex microbial populations based on the characterization of 16S rDNA sequences. Schulze-Makuch and Kennedy (2000) give the detailed description of the microbial analysis methods.

RESULTS

Field parameters as well as the ionic compositions of the sampled waters are provided in Table 2. The chemical composition of the studied hydrothermal fluids is consistent with previous reports (Shevenell et al., 1987; Goff and Gardner, 1994; Trainer et al., 2000). The pH of the water samples was mostly around neutral, only two samples were strongly acidic (Sulfur Spring I and II, pH-values of 1.40 and 1.98, respectively), and three springs (Montezuma Spring, San Antonio Spring and Spence Spring) were slightly alkalic (pH-values of 8.87, 8.35 and 8.10, respectively). Measured temperatures were between 21.7 °C (San Ysidro Spring) and 69.1 °C (Travertine Mound Spring). The measured discharge temperatures for Sulfur Spring I and II were 33 °C and 40 °C, respectively. The microbial analyses results showed that the water from both sampling locations had a significantly higher biomass content (as a total amount of PLFA) then any other spring. As shown in Figure 2, the total values were 461 pmol PLFA/g dry wt. for Sulfur Spring I and 654 pmol/g for Sulfur Springs II, respectively. Sulfur Spring I contained only bacterial biomass, while Sulfur Spring II contained bacterial (547 pmol/g) and eukaryotic (107 pmol/g) biomass. Results of DGGE (Denaturing Gradient Gel Electrophoresis) analyses revealed one DNA band for Sulfur Spring I identified as being related to

TABLE 2. Field parameters and ionic composition of hydrothermal water samples.

	FIELD PARAMETERS			ANIONS [mg/L]					CATIONS [mg/L]				
	Temp [°C]	pH	Conduct. [μS/cm]	**Cl**	**S**	**N**	**P**	**HCO_3**	**Na**	**Mg**	**K**	**Ca**	**Fe**
Blackrock Spring	38.2	7.73	775	55.2	151.6	BDL	6	151	131	4.7	10.9	23	0.64
Manby Spring	33.8	7.4	460	23.8	62.1	0.9	4.5	159.3	67	5.5	6.8	30	<0.01
Montezuma Spring	44	8.87	850	133.3	35.6	BDL	43	44.1	163	<0.1	5.5	3.4	<0.01
Ojo Caliente Spring	41.9	6.8	3620	235	158	BDL	34	2187	958	8.4	22	28	0.47
San Antonio Spring	40	8.35	199	1.9	6.4	BDL	2.6	45.9	21	0.3	1.3	2.9	<0.01
Soda Dam Spring	44.6	6.55	5100	1493	28	BDL	BDL	1108	1030	24	185	370	0.14
Spence Spring	39.9	8.1	268	6.6	14.6	BDL	BDL	119.6	50	1.7	0.9	6.3	<0.01
Sulfur Spring I	33.2	1.4	29500	46	8390	BDL	BDL	BDL	2.6	3.5	22	3.8	26.2
Sulfur Spring II	39.6	1.98	8030	BDL	3011	BDL	BDL	BDL	14	19	43	89	54.4
Travertine Mound Spring	69.1	6.7	3520	833.2	38.4	BDL	12.8	609.1	672	4.3	69	138	0.11
San Ysidro Spring	21.7	6.6	7470	1849	1237	BDL	BDL	1584	1900	65	75	300	2.85

Note: BDL = below detection limit.

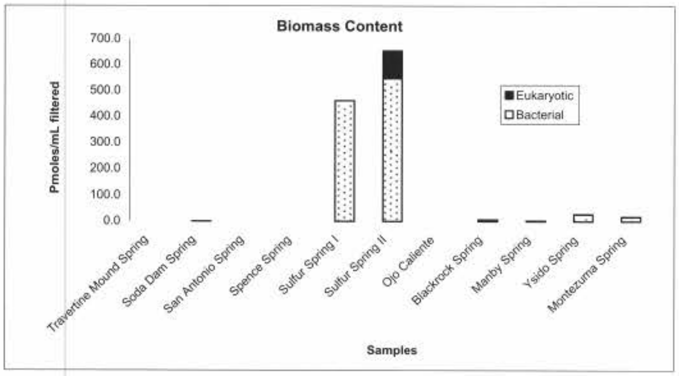

FIGURE 2. Biomass content is presented as the total amount of phospholipid fatty acids (PLFA) present in a given sample. PLFA comprise a large proportion of the membranes of all living cells, but decompose quickly upon cell death. Bacterial biomass is calculated based upon PLFA attributed specifically to bacteria whereas eukaryotic biomass is based on PLFA associated with higher organisms.

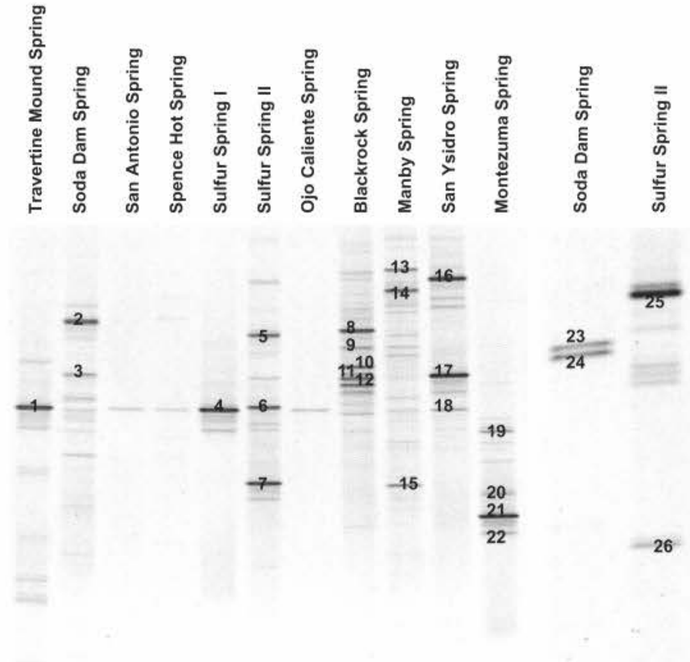

FIGURE 3. DGGE gel image of the bacterial domain. Banding patterns and relative intensities of the recovered bands provide a measure of change in the community. Dominant species must constitute at least 1-2% of the total bacterial community to form a visible band. Labeled bands were excised and sequenced. Results from sequencing can be found in Table 3. The second part of the image (bands 23-26) shows DGGE gel image of the archael domain for fluids of Soda Dam spring and Sulfur Spring II.

Clavibacter michiganese. Five bands identified for Sulfur Spring II (Fig. 3, Table 3) included three unidentified DNA sequences and 2 DNA sequences related to *Desulfurella kamchatkensis* and *Thiobacillus sp.*, respectively. Both microbial species are sulfur-oxidizing acidophiles (Priest and Goodfellow, 2000). Recordable biomass was also detected at San Ysidro Spring and Montezuma Spring (28 pmol/g and 18 pmol/g, respectively), and traces of biomass in the other springs. The results of DGGE analysis provided also other identified bacterial species in the sampled hydrothermal waters: *Chromobacterium, Leptothrix discophora, Aquabacterium sp., Pseudomonas sp., Planktothrix rubescens, Comamonas sp., Arthrobacter sp.,* and strains of DhA-73, LCK-08, BrG2 and clones of BPC028, CRE-FL50, CRE-FL68 (Fig. 3, Table 3). One band (band 6) is described as "novel sequence" since it is only loosely affiliated with *Nitrospina*, and four bands (band 23 – 26) had no similarity to the database collections of bacterial DNA (available databases: RDP and GenBank), and thus were named "unique sequences" (Table 3).

DISCUSSION

The results of the chemical analyses show that the fluids sampled from two springs (Sulfur Spring I and II) represent compositions typical for acid sulfate waters. They have a strong acidity (pH 1.40 and 1.98, respectively), and very high concentration of sulfate ions, especially Sulfur Spring I (8390 mg/L). These kinds of fluid derive from the condensation of steam (boiling of shallow groundwater), and the oxidation of H_2S to form natural sulfuric acid (Goff and Gardner, 1994). These fluids are referred to as Group I waters.

The bacterial analyses revealed large biomass contents in the Sulfur Springs samples (Fig. 2). The larger biomass and the identified microbial species (*Desulfurella kamchatkensis* and *Thiobacillus sp.*) in the water indicate that thermoacidophilic sulfur-metabolizing microbes adapt very well to that type of environment given a rich nutrient source. In addition, since only a few microbial species can thrive in such an environment, it can be expected that no protozoans or other predators are present that would reduce bacterial numbers. In all other sampled hydrothermal waters biomass was much lower (Fig. 2).

One of the objectives of the sampling events was to obtain deep reservoir water for analysis, since hydrothermal springs can be understood as natural windows to the deep subsurface. However, in reality, sampled waters almost always represent mixtures from deep thermal fluids diluted by more shallow groundwaters (Goff and Gardner, 1994). Typical examples for these kind of waters, in the following also referred to as Group II waters, are the chemical composition of Travertine Mound Spring, Montezuma Spring and Soda Dam Spring. The chlorine concentrations are much higher (1493 mg/L in case of Soda Dam Spring) than the sum of the sulfate (SO_4) and bicarbonate ion (HCO_3) concentrations. Significantly high is also the concentration of sodium – 1030 mg/L in Soda Dam Spring water (Table 2). The source of alkalinity in water from Montezuma Spring (pH 8.9) is currently unknown. The water is discharging from igneous rocks and low in total dissolved solids. Thus, even a slight pickup of alkaline ions anywhere in the hydrothermal upflow region may result in alkaline discharge water at Montezuma Spring. San Ysidro Spring water should also be considered belonging to this group, as it is a highly concentrated brine, but it also has high concentrations of sulfate (SO_4) and bicarbonate ions (HCO_3). In the water of the four springs 12 DGGE (Denaturing Gradient Gel Electrophoresis) bands (which

TABLE 3. Sequence results from bands excised from Figure 3. Identifications are based upon the Ribosomal Database Project (RDP). Similarity indicates above .800 are considered excellent, .600-.700 are good and below .500 are considered to be unique sequences.

Band	Closest Match	Similarity Index	Phylogenetic Affiliation
1	*Clavibacter michiganense*	.875	Gram Positive bacteria
2	Strain LCK-08	.856	Epsilon Proteobacteria
3	Clone BPC028	.759	Dichelobacter subgroup in Gamma Proteobacteria
4	*Clavibacter michiganense*	.885	Gram Positive bacteria
5	*Desulfurella kamchatkensis*	.807	Delta Proteobacteria
6	Novel Sequence	-	Loosely affiliated with Nitrospina
7	*Thiobacillus* sp.	.937	Gamma Proteobacteria
8	Chromobacterium	.781	Beta Proteobacteria
9	Failed	-	-
10	Strain BrG2	.924	Beta Proteobacteria
11	*Leptothrix discophora*	.779	Beta Proteobacteria
12	*Aquabacterium* sp.	.970	Beta Proteobacteria
13	*Pseudomonas* sp.	1.000	Gamma Proteobacteria
14	*Pseudomonas* sp.	1.000	Gamma Proteobacteria
15	Clone CRE-FL50	.865	Beta Proteobacteria
16	Clone CRE-FL68	.853	Beta Proteobacteria
17	*Planktothrix rubescens*	.905	Cyanobacteria
18	*Comamonas* sp.	.825	Beta Proteobacteria
19	Strain DhA-73	.794	Beta Proteobacteria
20	*Arthrobacter* sp.	1.000	Gram Positive bacteria
21	Strain DhA-73	.829	Beta Proteobacteria
22	Strain DhA-73	.815	Beta Proteobacteria
23	Unique Sequence	-	-
24	Unique Sequence	-	-
25	Unique Sequence	-	-
26	Unique Sequence	-	-

represent recognizable DNA sequences) were identified (48% of all 25), which is nearly half of all identified DNA sequences (Fig. 3). These results indicate that this group of waters has a large microbial diversity, while the Sulfur Springs fluids have a much lower diversity (but significantly higher biomass). Microbes belonging to the Beta Proteobacteria (Table 3) dominated fluids from the deep reservoir springs (four springs).

The third group of fluids is heated meteoric waters. They are characterized by having bicarbonate ion (HCO_3) as the dominant ion with a higher concentration than the sum of sulfate and chlorine ions. They usually also exhibit a neutral pH and a low degree of mineralization. Water samples of Manby Spring, San Antonio Spring, Spence Spring, and Blackrock Spring belong to this group of fluids. Ojo Caliente Spring water is also strongly dominated by bicarbonate ions (HCO_3), but exhibits a high degree of mineralization and high concentrations of sodium. Thus, Ojo Caliente Spring water shares some chemical similarities to Group II waters. The biomass contents detected in fluids of this group were very low. In San Antonio Spring, Spence Spring and Ojo Caliente Spring no bands were visible and identifiable with DGGE analyzes – the survey gave faint banding patterns only, which is likely due to the very low content of bacterial biomass in this type of fluids. Some bands were identified in water from Blackrock Spring (those microbes belonged to the Beta Proteobacteria) and Manby Spring (Beta and Gamma Proteobacteria). Those microbes, however, may have derived from mixing of spring water with Rio Grande river water (Fig. 3, Table 3).

There appears to be a definite correlation of microbial activity to water type and origin. Based on our results deeper fluids with a higher degree of mineralization provide in general better conditions for microbes. However in case of the Sulfur Springs area, the low pH, high temperature environment appears to provide an ideal environment for specially adapted microbes (sulfur-metabolizing thermoacidophiles), which thrive in a type of environment that can support large population numbers of organisms (Fig. 2).

The investigation is still continuing. In the next phase of this project we will sample additional thermal springs, conduct the analyses described previously, and in addition will also do isotope analysis to gain further insight into the origin of the water and the microbial fractionation of the water (microbial activity results in a preferred use of lighter isotopes). The additional sampling will allow us to better correlate between microbial composition of the hydrothermal water and geochemical indicators as well as to shed more light on the origin of the hydrothermal water. Possibly we may also be able to reveal some subsurface structures of the rift system.

CONCLUSIONS

The chemical composition of the studied hydrothermal fluids is consistent with previous reports by Shevenell et al. (1987), Goff and Gardner (1994) and Trainer et al. (2000). A microbial analysis revealed that the sampled hydrothermal waters were low in biomass except for the Sulfur Springs Area. Water derived from a deep hydrothermal source had a higher microbial diversity than heated meteoric water. Several novel DNA sequences were detected from microbes previously unknown. Further sampling events should improve correlation between microbial composition of the hydrothermal water and geochemical indicators as well as to shed more light on the origin of hydrothermal waters of the region.

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