CORE
Metadata, citation and similar papers at core.ac.uk
Provided by Elsevier - Publisher Connector

Available online at www.sciencedirect.com
SciVerse ScienceDirect
Procedia Earth and Planetary Science 7 (2013) 842 – 845
Procedia
Earth and Planetary Science

Water Rock Interaction [WRI 14]

Using water chemistry, isotopes and microbiology to evaluate groundwater sources, flow paths and geochemical reactions in the Death Valley flow system, USA

James M. Thomas[a]*, Duane P. Moser[b], Jenny C. Fisher[b], Jessica Reihle[b], Alexandra Wheatley[b], Ronald L. Hershey[a], Cristi Baldino[c], Darrick Weissenfluh[c]

[a]*Desert Research Institute, 2215 Raggio Pwky, Reno, NV, USA 89512;* [b]*Desert Research Institute, 755 E. Flamingo Rd, Las Vegas, NV, USA 89130;*
[c]*US Fish and Wildlife Service, Ash Meadows NWR, Amargosa Valley, NV, USA 89020*

Abstract

Springs of Ash Meadows and Furnace Creek (near or in Death Valley, CA) have nearly constant flow, temperature, chemistry, and similar δ^2H and $\delta^{18}O$ signatures. These factors indicate shared water sources and/or analogous geochemical reactions along similar flow paths. DNA-based (16S rRNA gene) microbial diversity assessments further illuminate these relationships. Whereas, all Ash Meadows springs share related archaeal populations, variations in carbon-14 (Crystal Spring) and strontium isotopes, Na^+, SO_4^{2-}, and methane concentrations (Big Spring), correspond with microbial differences within and between the two discharge areas. Similar geochemical signatures linking Ash Meadows and Furnace Creek springs appear to support a distinct end member at Big Spring in Ash Meadows, which is also supported by coincident enrichment in microbial methanogens and methanotrophs. Conversely, DNA libraries from a deep carbonate well (878 m) located between Ash Meadows and Furnace Creek (BLM-1), indicate no shared microbial diversity between Ash Meadows or Furnace Creek springs.

© 2013 The Authors. Published by Elsevier B.V. Open access under CC BY-NC-ND license.
Selection and/or peer-review under responsibility of the Organizing and Scientific Committee of WRI 14 – 2013

Keywords: geochemistry, isotopes, microbiology, regional flow systems

1. Introduction

The Death Valley Flow System (DVFS) consists of highly fractured mostly carbonate-rock aquifers that form a regional groundwater flow system covering hundreds of square km and extending from inferred recharge areas associated with Central Nevada Uplands and the Spring Mountains to large discharge springs in Amargosa Valley and the Furnace Creek area of Death Valley. Groundwater flows north and west from the Spring Mountains recharge area and southwest from Central Nevada Uplands to discharge at Ash Meadows in central Amargosa Valley (Fig. 1). Some groundwater is thought to continue to flow beneath Ash Meadows into southern Amargosa Valley and then through the Funeral Mountains to the Furnace Creek area of Death Valley (Fig. 1). As groundwater flows from Ash Meadows to Death Valley, it also likely combines with other groundwater in Amargosa Valley. For a detailed description of the hydrogeology, water

* Corresponding author. Tel.: +1-775-673-7305 fax: +1-775-673-7363.
E-mail address: jthomas@dri.edu.

1878-5220 © 2013 The Authors. Published by Elsevier B.V. Open access under CC BY-NC-ND license.
Selection and/or peer-review under responsibility of the Organizing and Scientific Committee of WRI 14 – 2013
doi:10.1016/j.proeps.2013.03.033

chemistry and isotopic data the reader is referred to the following references [1-12]. To date, published microbiological characterizations of these systems have been limited to cultivation-based studies performed in the 1980s on the springs at Ash Meadows and volcanic tuffs from the Nevada National Security Site.

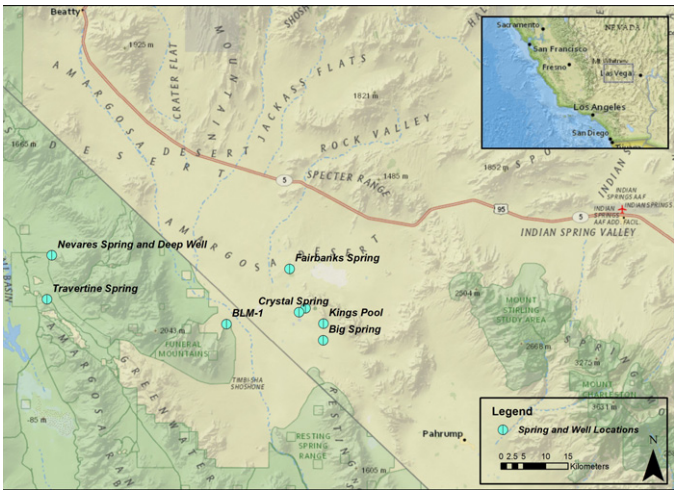

Fig. 1. Location of study area with spring and well locations.

2. Results and Discussion

The δ^2H and $\delta^{18}O$ values of groundwater discharging from springs in the Furnace Creek and Ash Meadows discharge areas of the DVFS vary little over time and are similar (Table 1), indicating that both spring discharge areas likely receive most of their water from the same recharge areas. Additionally, numerous springs in both discharge areas have nearly constant spring flow, water temperature, and major ion chemistries over time, indicating the presence of a stable and deep groundwater flow system. Most of the major ion concentrations are similar among the different springs (Table 1), indicating that the water chemistry is derived from the same geochemical reactions along geologically similar flow paths in the aquifer. However, there are water chemistry, $\delta^{87}Sr$, and microbial community differences among springs in Ash Meadows and between the Ash Meadows springs and Death Valley springs and especially a well (BLM-1) located between these two spring discharge areas (Fig. 1). These differences indicate that flow paths are not the same for all springs in a common spring discharge area and between spring discharge areas. In the Ash Meadows spring complex, significant variations in Na^+, SO_4^{2-}, and dissolved methane concentrations are observed in Big Spring (Fig. 1; Table 1) [3,5,8,10]. These differences likely result from slightly different flow paths that encounter non-carbonate and/or carbonate rock enriched in Na^+ and SO_4^{2-} as compared to most aquifer rock, or the entrainment of an end member containing higher Na^+, SO_4^{2-}, and methane. Previous studies have also shown that the largest discharging spring in Ash Meadows, Crystal Spring (also referred to as Crystal Pool Spring), has a significantly higher carbon-14 value than any other spring [3] and that the three southernmost springs in the discharge area (Big Spring being the largest) have anomalous strontium isotopic values (Table 1) [8, 14].

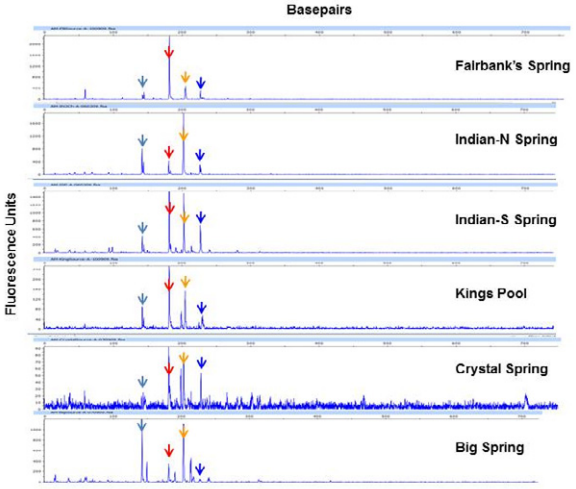

Fig. 2. Archaeal T-RFLP profiles from a subset of Ash Meadows springs. Colored arrows are included to help the eye follow specific ribotypes (e.g. distinct at ca. genus level) between stacked profiles. This profile suggests: 1) relatively simple communities across the springs sampled and 2) shared community structure across the sample set.

Prior to this study, almost nothing was known about the indigenous microbial populations of any subsurface or spring habitat in the Southern US Great Basin. DNA-based (16S rRNA gene) assessments of microbial diversity developed for this study show that Ash Meadows spring waters contain exceptional bacterial diversity at both shallow (species-level) and deep (phylum-level) measures of genetic relatedness. Among our bacterial gene libraries, with the exception of one highly dominant betaproteobacterial lineage in Big Spring (an inferred methanotroph, 46 of 72 library clones), very few multiple occurrences were noted within or between

springs (375 distinct predicted species from 407 total sequences).

Unlike for the bacteria, however, as evidenced by complementary DNA-based approaches (gene libraries, T-RFLP fingerprinting), all Ash Meadows springs share relatively simple (134 predicted species from 376 total sequences) and closely affiliated (Fig. 2) archaeal populations. In our gene libraries, this shared signal is dominated by the subdomains, Crenarcheota (57/376), Euryarcheota (23/376), and especially Thaumarchaeota (292/376). The crenarchaeotes and thaumarchaeaotes are uniformly distributed across the entire sample dataset, with multiple examples of nearly identical sequences appearing in most or all of the samples. The striking degree of similarity in archaeal diversity profiles (Fig. 2) is consistent with a shared water source, flowing along similar flow paths, providing the majority of flow to Ash Meadows springs. Although the ecological role of the Thaumarchaeota remains unknown, the confluence of archaeal methanogens, inferred bacterial methanotrophs and relatively high concentrations of methane in Big Spring (Table 1) suggests methane cycling in the chemically and isotopically inferred Death Valley end member. Unfortunately, no archaeal DNA has been detected by our methods in the Nevares Spring Deep Well water and Travertine Spring has yet to be analyzed. This comparison would have afforded an opportunity to track the most relevant domain of microorganisms that may link the Death Valley end member with south Ash Meadows springs (Big Spring being the main southern spring).

Archaea were detected in the BLM-1 well, but our analysis of 21,794 partial rRNA gene sequences generated by pyrotag analysis showed that groundwater from this deep source (878 m) revealed absolutely no overlap at the species level with archaeal sequences from any of the Ash Meadows springs. Thus, patterns of archaeal diversity indicate that deep groundwater in BLM-1 well is not groundwater flowing along flow paths that supply Ash Meadows springs, even though δ^2H and $\delta^{18}O$ data indicate that they have the same recharge area sources. Likewise, bacterial libraries for the BLM-1 well and the well at Nevares Spring, while being dominated by functionally similar populations (e.g. Firmicute predicted sulfate reducers and Nitrospirae), do not share a single overlapping lineage at the species level. Thus, microbial data fail to support a hydrologic connection across the Funeral Mountains between the BLM-1 well and the Furnace Creek springs (the waters are not along the same flow path), even though a large fault system connects BLM-1 with the springs. Rather, consistent with BLM-1 well's high temperature (58°C) and anaerobic condition, this water is more likely derived from a heretofore unrecognized, isolated deep flow path. Thus, although the δ^2H and $\delta^{18}O$ data show that the Ash Meadows and Furnace Creek springs have the same recharge sources, our microbial data indicate that they do not follow the same flow paths in the deep carbonate aquifer system. To the best of our knowledge, this study represents the first systematic application of a combined microbial/biogeochemical/isotopic approach for inferring subsurface fluid flow at the regional scale.

Table 1. Water chemistry and isotopic data for springs and wells in the Death Valley flow system. Water chemistry and isotopic data include data collected for this report and historical data [3, 5, 8, 10, 13, and 14].

Site Name	Temp	Cond	Ca	Mg	Na	K	HCO3	SO4	Cl	CH_4	δ^2H	$\delta^{18}O$	$\delta^{87}Sr$
	°C	µS/s	mg/L	mg/L	mg/L	mg/L	mg/L	mg/L	mg/L	µM	permil	permil	permil
Ash Meadows Discharge area													
Fairbanks Spring	27	690	48	21	69	8.0	310	82	21	8.8	-103	-13.8	4.99
Indian South Spring	30	NA	50	20	70	8.9	NA	80	22	<1	NA	NA	NA
Devils Hole	33	690	49	21	67	7.9	290	80	21	NA	-103	-13.4	4..46
Kings Spring	32	NA	49	21	68	7.8	310	80	21	17.4	-102	-13.6	4.57
Crystal Spring	31	700	47	21	73	9.4	310	85	23	18.3	-102	-13.7	4.60
Big Spring	27	770	44	19	96	9.2	310	108	24	65.3	-102	-13.4	11.05
Death Valley Furnace Creek Discharge area													
Nevares Deep Well	42	NA	44	21	160	11	NA	170	36	<1	-103	-13.4	NA
Nevares Spring	42	1030	44	21	160	11	340	170	36	NA	-102	-13.5	10.70
Travertine Spring	35	1000	36	19	140	10	340	160	40	NA	-102	-13.5	11.48
Amargosa Valley-Funeral Mountain area well													
BLM-1 Well	58	NA	36	16	250	19	NA	160	43	NA	-103	-13.5	NA

Acknowledgements

Thanks to Michael King, Walter Slack, and others at Hydrodynamics Group; Levi Kryder, Jamie Walker, Roger McRae and others from the Nye County Nuclear Waste Repository Program Office (NWRPO); and Richard Friese, Linda Manning and others at the National Park Service for material support including access to BLM-1 and Nevares DW2. This work was funded by grants from the NWRPO, USFWS, DOE SBR Program, and the Desert Research Institute. Thanks also to the Deep Carbon Observatory and the Census of Deep Life Program for DNA sequencing support.

References

[1] Hunt CB, Robinson TW, Bowles WA, Washburn AL. Hydrologic Basin Death Valley California. US Geological Survey Professional Paper 494-B, pp. B1-B147; 1966.

[2] Winograd IJ, ThordarsonW. Hydrogeologic and Hydrochemical Framework, South-Central Great Basin, Nevada-California, with Special Reference to the Nevada Test Site. US Geological Survey Professional Paper 712-C, 3 plates, 126p; 1975.

[3] Winograd IJ, Pearson FJ. Major carbon 14 anomaly in a regional carbonate aquifer: possible evidence for megascale channeling, south central Great Basin. *Water Resour. Res.* 1976; **12**:1125-1143.

[4] Miller GA. Appraisal of Water Resources of Death Valley, California. US Geological Survey Open-File Report 77-728, 68p; 1977.

[5] Thomas JM, Welch AH, Dettinger MD. Geochemistry and Isotope Hydrology of Representative Aquifers in the Great Basin Region of Nevada, Utah, and Adjacent States. US Geological Survey Professional Paper 1409-c; 1996.

[6] D'Agnese FA, Faunt CC, Turner AK, Hill MC. Hydrogeologic Evaluation and Numerical Simulation of the Death Valley Regional Ground-Water Flow System, Nevada and California. US Geological Survey Water-Resources Investigations Report 96-4300, 124p; 1997.

[7] Faunt CC. Effect of Faulting on Ground-Water Movement in the Death Valley Region, Nevada and California. US Geological Survey Water-Resources Investigations Report 95-4132, 42p; 1997.

[8] Steinkampf WC, Werrell WL. Ground-Water Flow to Death Valley as Inferred from the Chemistry and Geohydrology of Selected Springs in Death Valley National Park, California and Nevada. US Geological Survey Water-Resources Investigations Report 98-4114, 37p; 2001.

[9] Belcher, W.R., and Sweetkind, D.S., eds., Death Valley regional groundwater flow system, Nevada and California—Hydrogeologic framework and transient groundwater flow model: U.S. Geological Survey Professional Paper 1711, 398p; 2010..

[10] Anderson K, Nelson S, Mayo A, Tingey D. Interbasin flow revisited: the contribution of local recharge to high-discharge springs, Death Valley, California. *Journal of Hydrology* 2006; **323**: 276-302.

[11] Bedinger MS, Harrill, JR. Hydrogeology of Death Valley [California and Nevada]. *Hydrological Science and Technology, American Institute of Hydrology* 2007; **23**(1-4): 27-38.

[12] Belcher WR, Bedinger, MS, Back, JT, Sweetkind, DS. Interbasin Flow in the Great Basin with Special Reference to the southern Funeral Mountains and the source of Furnace Creek Springs, Death Valley, California, U.S. *Journal of Hydrology* 2009; **369**: 30-43.

[13] Hershey, RL, Mizell, SA, Earman, S. Chemical and Physical Characteristics of Springs Discharging from Regional Flow Systems of the Carbonate-Rock Province of the Great Basin, Western United States. *Hydrogeology Journal* 2010; **18**:1007-1026.

[14] Peterman ZE, Stuckless JS, Mahan SA, Marshall BD, Gutentag ED, Downey JS. Strontium isotope characterization of the Ash Medows ground-water system, southern Nevada, USA. In: Kharaka YK, Maest S, editors. *Water-Rock Interatctions:* A.A. Balkema, Rotterdam 1992; **1** :825-829.

[15] DeSantis, T. Z., P. Hugenholtz, N. Larsen, M. Rojas, E. L. Brodie, K. Keller, T. Huber, D. Dalevi, P. Hu, and G. L. Andersen. 2006. Greengenes, a chimera-checked 16S rRNA gene database and workbench compatible with ARB. *Appl Environ Microbiol* **72**: 5069-5072.

[16]. Hammer, Ø., Harper, D.A.T., Ryan, P.D. . 2001 PAST: Paleontological Statistics Software Package for Education and Data Analysis. . Palaeontologia Electronica **4**(1): 9p.

[17]. Lozupone, C., M. Hamady, and R. Knight. 2006. UniFrac--an online tool for comparing microbial community diversity in a phylogenetic context. *BMC Bioinformatics* **7**: 371.

[18]. Moser, D. P., T. C. Onstott, J. K. Fredrickson, F. J. Brockman, D. L. Balkwill, G. R. Drake, S. M. Pfiffner, D. C. White, K. Takai, L. M. Pratt, J. Fong, B. S. Lollar, G. Slater, T. J. Phelps, N. Spoelstra, M. Deflaun, G. Southam, A. T. Welty, B. J. Baker, and J. Hoek. 2003. Temporal shifts in the geochemistry and microbial community structure of an ultradeep mine borehole following isolation. *Geomicrobiology Journal* **20**: 517-548.

[19]. Tamura, K., Dudley, J., Nei, M., and Kumar, S. 2007. MEGA4: Molecular Evolutionary Genetics Analysis (MEGA) software version 4.0. *Molecular Biology and Evolution* **24**: 1596 -1599.