1   **Dissolved Organic Carbon Influences Microbial Community**

2   **Composition and Diversity in Managed Aquifer Recharge**

3   **Systems**

4   Dong Li[1,2], Jonathan O. Sharp[2], Pascal E. Saikaly[1], Shahjahan Ali[3], Mazahirali

5   Alidina[1], Mohammed S Alarawi[3], Stephanie Keller[1], Christiane Hoppe-Jones[2], and

6   Jörg E. Drewes[1,2*]

7   [1]*Water Reuse and Desalination Center (WDRC), King Abdullah University of Science*

8   *and Technology, Thuwal, Saudi Arabia*

9   [2]*NSF Engineering Research Center ReNUWIt, Civil and Environmental Engineering,*

10   *Colorado School of Mines, Golden, CO, USA*

11   [3]*Biosciences Core Laboratory, King Abdullah University of Science and Technology,*

12   *Thuwal, Saudi Arabia*

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14   Running Title: Microbial Community Structure in MAR Systems

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26   * Corresponding author: JE Drewes, Water Reuse and Desalination Center, King

27   Abdullah University of Science and Technology, Thuwal 23955-6900, Saudi Arabia.

28   E-mail: Jorg.Drewes@kaust.edu.sa

29　　Supplementary Information

30　　**Archaeal community structures in field- and laboratory-scale MAR systems**

31　　As shown in Table S2, few *Crenarchaeota* were detected in the intermediate

32　　infiltration zone samples, averaging 0.004% of total sequences. Compared to

33　　*Crenarchaeota*, significantly higher ratios of total sequences with an average of

34　　0.14% were affiliated with *Euryarchaeota* for intermediate infiltration zone samples

35　　(Wilcoxon matched-pair test, P<0.001). Similar findings were also observed for

36　　samples from the shallow infiltration zone and the unsaturated riverbed. The relative

37　　abundances of *Crenarchaeota* were less than 0.02% for both rivers in shallow

38　　infiltration zones. The ratios of *Euryarchaeota* among the total sequences of each

39　　sample were much higher, with average values of 0.13% for South Platte and Taif

40　　shallow samples, and as high as 2% in the unsaturated riverbed samples.

41　　　*Methanobacteria* and *Methanomicrobia* were the most abundant archaeal classes in

42　　the *Euryarchaeota* phylum for intermediate infiltration zone samples, with the relative

43　　ratios of 0.07% and 0.04% of the total sequences, respectively. These two ratios

44　　decreased to 0.01% and 0.006%, while the average ratio of *Halobacteria* belonging to

45　　*Euryarchaeota* increased to 0.01% for shallow infiltration zone samples. *Halobacteria*

46　　became the most abundant archaea affiliated with *Euryarchaeota* in all unsaturated

47　　riverbed samples, with the average ratio of 1.58% of the total sequences. Meanwhile,

48　　both *Methanobacteria* and *Methanomicrobia* consisted of less than 0.01% of the total

49　　sequences in all unsaturated riverbed samples. No significant difference was observed

50　　for archaeal distribution on phylum level among sediment samples taken from the

51　　same sampling location at different depths (Kendall's W matched-pair test, all

52　　P>0.05).

53　　　For saturated sediment columns, *Archaea* were also detected in both the moderate

54　　and low DOC columns. Less than 0.03% of the total sequences were assigned to

55　　*Crenarchaeota* in each sediment sample, with the ratio of *Euryarchaeota* ranging

56　　from 0.02% to 0.06% and *Halobacteria* as the most abundant class in *Euryarchaeota*

57　　with the average ratio of 0.02%.

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59   TABLE S1. Oligonucleotide primers used in this study

| Primer	Specificity	Sequence (5'–3')	Target genes	Application	Reference
515F	Universal	GTGYCAGCMGCCGCGGTAA	16S rRNA	Pyrosequencing	Caporaso *et al.*, 2011
806R	Universal	GGACTACHVGGGTWTCTAAT	16S rRNA	Pyrosequencing	Caporaso *et al.*, 2011
341F	*Bacteria*	CCTACGGGAGGCAGCAG	16S rRNA	qPCR	Muyzer *et al.*, 1993
518R	*Bacteria*	ATTACCGCGGCTGCTGG	16S rRNA	qPCR	Muyzer *et al.*, 1993
516F	*Archaea*	TGYCAGCCGCCGCGGTAAHACCVGC	16S rRNA	qPCR	Takai and Horikoshi, 2000
806R	*Archaea*	GGACTACVSGGGTATCTAAT	16S rRNA	qPCR	Takai and Horikoshi, 2000
ITS1F	*Fungi*	TCCGTAGGTGAACCTGCGG	-	qPCR	Chow *et al.*, 2009
5.8S	*Fungi*	CGCTGCGTTCTTCATCG	-	qPCR	Chow *et al.*, 2009
27F	*Bacteria*	AGAGTTTGATCCTGGCTCAG	16S rRNA	Cloning	Chivian *et al.*, 2008
1492R	Universal	GGTTACCTTGTTACGACTT	16S rRNA	Cloning	Chivian *et al.*, 2008
A20F	*Archaea*	TCCGGTTGATCCTGCCRG	16S rRNA	Cloning	Chivian *et al.*, 2008

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61 TABLE S2. Relative abundance (%) of major Archaeal phyla and classes in river and
62 sediment column samples

Sample Site	Taif and South Platte Rivers			Moderate DOC Columns	Low DOC Columns
	Infiltration zone 1-2 cm	Infiltration zone 10-50 cm	Unsaturated		
Crenarchaeota	0.004	0.02	0.10	0.02	0
Euryarchaeota	0.14	0.13	2.0	0.06	0.02
Halobacteria	0	0.01	1.58	0.03	0
Methanobacteria	0.07	0.01	0.006	0.006	0
Methanomicrobia	0.04	0.006	0.002	0.004	0.006

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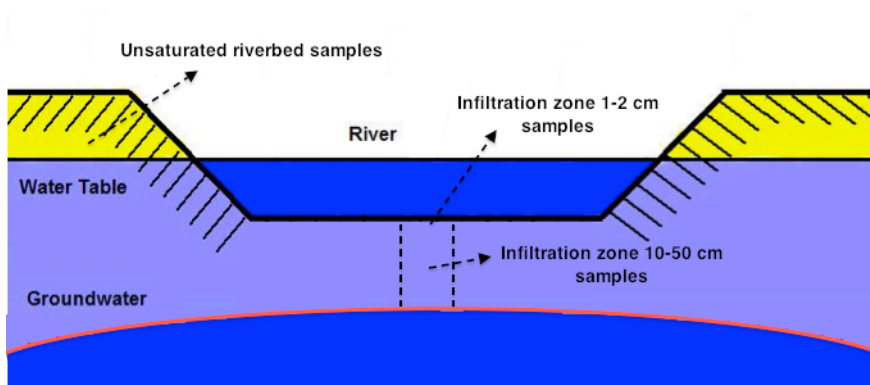
64

(a)
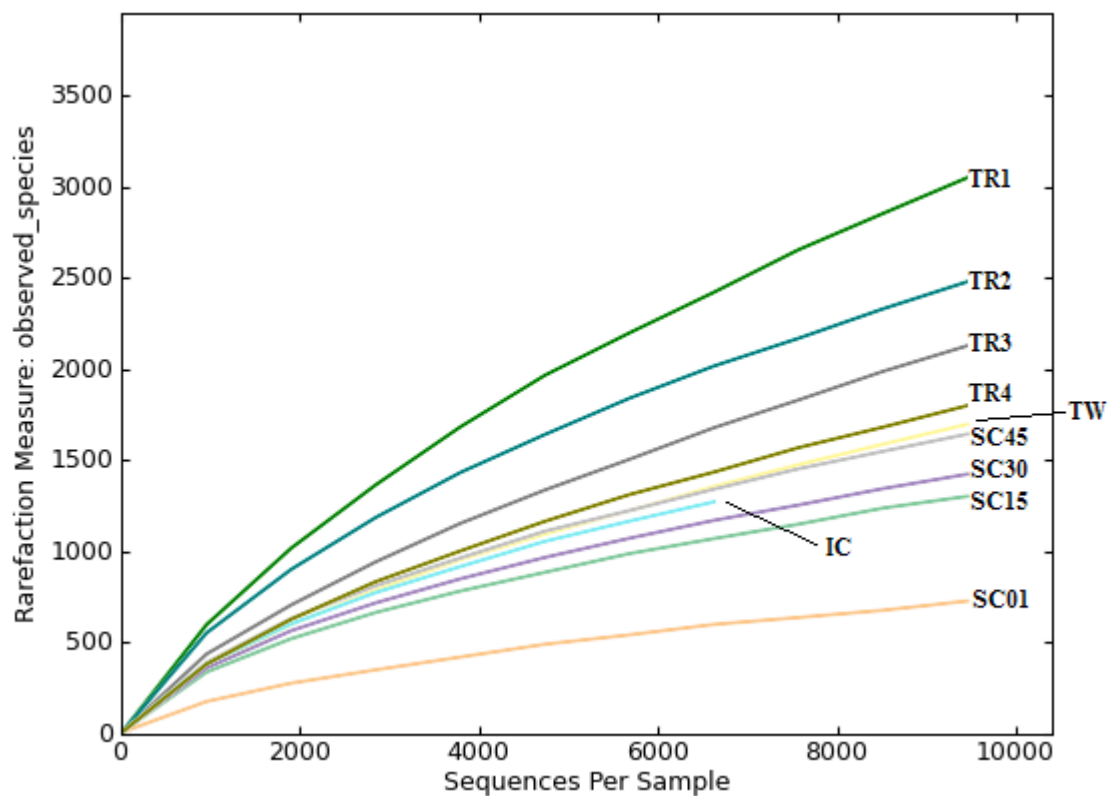

(b)
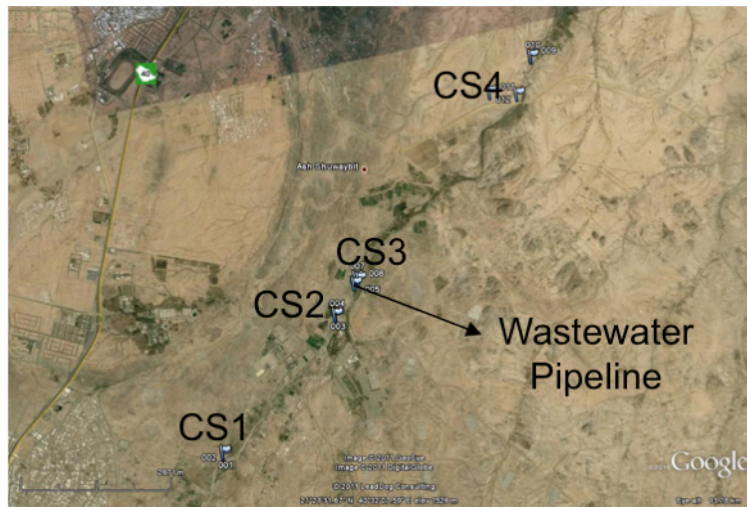
FIG. S1. (a) Sampling map of the Taif River in Saudi Arabia; (b) Sketch map of
sampling locations of shallow infiltration zone (1-2 cm), intermediate infiltration zone
(10-50 cm), and unsaturated riverbed samples.

FIG. S2. Rarefaction curves of bacterial and archaeal 16S rRNA pyrosequencing reads for representative samples fully spanning the range found this study. TR1-4: Taif River cross section 1-4; TW: Taif wastewater effluent; SC01, 15, 30 and 45: moderate DOC laboratory column 1 cm, 15 cm, 30 cm and 45 cm; IC: low DOC laboratory column.

Legend:
- Archaea;Euryarchaeota
- Archaea;Other
- Bacteria;Acidobacteria
- Bacteria;Actinobacteria
- Bacteria;Bacteroidetes
- Bacteria;Chlamydiae
- Bacteria;Chlorobi
- Bacteria;Cyanobacteria
- Bacteria;Firmicutes
- Bacteria;Fusobacteria
- Bacteria;Gemmatimonadetes
- Bacteria;Nitrospira
- Bacteria;OD1
- Bacteria;OP10
- Bacteria;Other
- Bacteria;Planctomycetes
- Bacteria;Proteobacteria
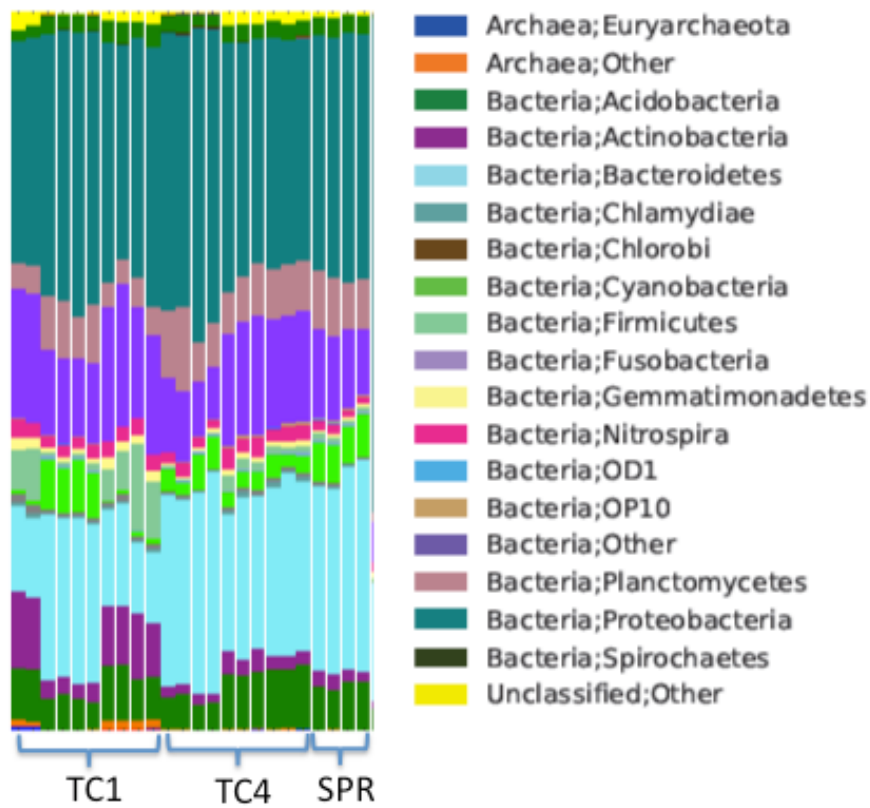- Bacteria;Spirochaetes
- Unclassified;Other

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FIG. S3. The microbial phyla distribution of representative sediment samples derived
from shallow and intermediate infiltration zones of Taif River cross sections 1 (TC1)
and 4 (TC4), as well as South Platte River (SPR) collected in different seasons.

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