

Supplementary material

Persistence, loss and appearance of bacteria upstream and downstream of a river system

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Table S1. Abundance of heterotrophic bacteria determined by flow cytometry

R1, R2 and R3 are sample numbers. HDNA, high-DNA subpopulation; LDNA, low-DNA subpopulation

Sample	Subpopulation abundance ($\times 10^7$ cells mL ⁻¹ (95% CI, <i>n</i>))		
	LDNA	HDNA	Total
Up R1	2.91	1.57	4.48
Up R2	4.54	1.67	6.22
Up R3	2.54	1.66	4.20
Upstream average	3.33 (1.2×10^7 , 3)	1.64 (6.2×10^5 , 3)	4.97 (1.2×10^7 , 3)
Down R1	2.06	0.79	2.85
Down R2	2.85	1.58	4.43
Down R3	1.89	0.97	2.86
Downstream average	2.27 (5.8×10^6 , 3)	1.11 (4.7×10^6 , 3)	3.38 (2.9×10^7 , 3)

Table S2. Resulting power-law values for maximum-likelihood testing of upstream (Up) and downstream (Down) sites and their corresponding samples (R1, R2 and R3)

KS, Kolmogorov–Smirnov; n , number of species

Site and sample	n	Minimum abundance (x_{min})	Alpha (α)	KS statistic (D_n)	KS critical value (95% confidence)
Down R1	34	1.97×10^{-3}	1.803	0.0904	0.2372
Down R2	33	1.18×10^{-3}	1.609	0.0612	0.2399
Down R3	35	1.06×10^{-3}	1.629	0.0747	0.2331
Up R1	29	1.62×10^{-3}	1.707	0.1094	0.2555
Up R2	24	2.47×10^{-3}	1.748	0.0846	0.2803
Up R3	23	2.69×10^{-3}	1.773	0.1402	0.2862
Down combined	83	1.84×10^{-3}	1.695	0.0774	0.1542
Up combined	68	2.45×10^{-3}	1.744	0.0615	0.1607

Table S3. Exclusive upstream bacterial taxa

Upstream taxon	
<i>Candidatus solibacter</i>	<i>OP3 PBS-25</i>
<i>Rhodococcus</i>	<i>Gemmata</i>
Micrococcaceae	<i>DH61</i>
Chloroplast – Stramenopiles	Kiloniellales
Oscillatoriophycideae	Beijerinckiaceae
<i>Phormidium</i>	Erythrobacteraceae
<i>GN02 3BR-5F</i>	<i>NB1-j MND4</i>
Alcaligenaceae	Aeromonadaceae
<i>Ellin6067</i>	Shewanella
<i>Dechloromonas</i>	<i>Crenothrix</i>
<i>Pedosphaerales auto67_4W</i>	Chthoniobacteraceae

Table S4. Exclusive downstream bacterial taxa

Asterisks indicate that the taxon was found only in downstream outlier sample

Downstream taxon		
<i>Chloracidobacteria RB41</i> *	Moraxellaceae*	<i>Finegoldia</i> *
Acidimicrobiales*	<i>Acinetobacter</i> *	<i>Gallicola</i> *
Varibaculum*	<i>Acinetobacter rhizosphaerae</i> *	<i>Peptoniphilus</i> *
<i>Corynebacterium</i> *	<i>Staphylococcus</i> *	Tissierellaceae WAL_1855D*
<i>Microbacterium maritypicum</i> *	<i>Enhydrobacter</i> *	<i>Anaerostipes</i> *
Nocardioideaceae*	<i>Moraxella</i> *	<i>Blautia</i> *
<i>Propionibacterium acnes</i> *	Pseudomonadaceae*	<i>Bacillus</i> *
<i>Propionibacterium granulosum</i> *	<i>Pseudomonas</i> *	<i>Veillonella dispar</i> *
<i>Pseudonocardia</i> *	<i>Pseudomonas nitroreducens</i> *	Erysipelotrichaceae*
Coriobacteriaceae*	<i>Thermomonas fusca</i> *	<i>Fusobacterium</i> *
Coriobacteriaceae atopobium*	<i>Herbaspirillum</i>	<i>Leptotrichia</i> *
<i>Collinsella aerofaciens</i> *	Nitrosomonadaceae	Clostridiaceae*
<i>Rubrobacter</i> *	Tremblayales	Lachnospiraceae*
Gaiellaceae*	Bacteriovoracaceae	<i>Lactococcus</i> *
<i>Niabella</i> *	<i>Bdellovibrio</i>	<i>Streptococcus</i> *
Prevotella*	Haliangiaceae	<i>Streptococcus infantis</i> *
Paraprevotella*	Coxiellaceae	Clostridiales*
Bacteroides*	<i>Hydrocarboniphaga effusa</i>	Tissierellaceae*
<i>Bacteroides uniformis</i> *	<i>Treponema</i>	<i>Anaerococcus</i> *
Porphyromonas*	<i>Gemm-3</i>	<i>Faecalibacterium prausnitzii</i> *
<i>Porphyromonas endodontalis</i> *	OD1 SM2F11	Oscillospira*
Prevotella;*	OP3 koll11GIF10kpj58rc	Ruminococcus*
<i>Prevotella copri</i> *	Ochrobactrum*	<i>Staphylococcus aureus</i> *
Rikenellaceae*	<i>Agrobacterium</i> *	<i>Facklamia</i> *
<i>Adhaeribacter</i> *	Rhodospirillales	<i>Granulicatella</i> *
Weeksellaceae*	<i>Phaeospirillum fulvum</i>	Planococcaceae*
<i>Chryseobacterium</i> *	<i>Sphingobium</i> *	<i>Jeotgalicoccus</i> *
<i>Cloacibacterium</i> *	<i>Comamonas</i> *	<i>Haemophilus parainfluenzae</i> *
<i>Capnocytophaga ochracea</i> *	<i>Herbaspirillum</i> *	<i>Coprococcus</i> *
Gitt-GS-136*	<i>Ralstonia</i> *	Ruminococcaceae*
Chloroplast – Streptophyta*	Neisseriaceae*	Enterobacteriaceae*
<i>Elusimicrobia MVP-88</i>	<i>Campylobacter</i> *	