1	Persistence and Decay of Fecal Microbiota in Aquatic Habitats
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40 SUPPLEMENTAL MATERIALS

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- 42 **Table S1.** Effect of sunlight on decay of indicator microorganisms and pathogens in marine and freshwater. + denotes greater decay
- 43 rate in the presence of sunlight; 0 denotes no effect of sunlight on decay rate.

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Organism	Effect of sunlight on decay	Spike Source	Water Type	Method	Comment	Other factors contributing to decay	Reference
FIB							
Fecal coliforms	+ ^b	Raw sewage and effluent from meat-	Seawater	Membrane filtration on mE/esculin-iron agar (enterococci) or mEC agar (fecal	Field study. Fecal coliforms inactivated more rapidly compared to	Temperature	(1)
Enterococci	+ ^b	facility		coliforms)	enterococci		
Fecal coliforms	+ b	Raw sewage	Seawater	Membrane filtration on mFC agar	Field study. Fecal coliforms inactivated more rapidly compared to coliphages	Temperature, seasonality	(2)
Enterococci <i>E. coli</i>	+ b + b	Waste stabilization pond	Freshwater (river)	Membrane filtration on mE/esculin-iron agar (enterococci) or mFC agar/nutrient agar supplemented with MUG (<i>E. coli</i>)	Field study. Enterococci and <i>E.</i> <i>coli</i> inactivated more rapidly compared to coliphages	Seasonality, salinity	(3)

E. coli	+ ^a	Raw sewage, final sewage effluent	Seawater and freshwater (creek)	Colilert (MPN)	Field study. Enterococci decayed significantly faster compared to <i>E. coli</i>	Temperature	(4)
Enterococci	+ ^a			Enterolert (MPN)			
E. coli	+ ^b	Waste stabilization pond	Seawater and freshwater (river)	Membrane filtration on mFC agar/nutrient agar supplemented with MUG (<i>E. coli</i>)	Field study. Faster inactivation in seawater compared to freshwater	Seasonality	(5)
Enterococci	+ ^a	Human, cattle and dog feces	Seawater	Membrane filtration on mEI (enterococci) and by qPCR	Field study. Intact cells (as determined by the PMA	None reported	(6)
Enterococcus qPCR	0 ^a			(Enterola)	persisted longer		
E. coli	+ ^a	Human and cattle feces	Freshwater (river)	Colilert (MPN)	Field study. Exposure to sunlight affected	None reported	(7)
Enterococci	0 b			Enterolert (MPN)	culturable <i>E. coli</i> from cattle feces, but not human.		

E. coli	+ ^a	Raw sewage	Freshwater (river)	Colilert (MPN)	Lab study. Culturable <i>E. coli</i> inactivated more rapidly than any of the qPCR markers tested	Biotic interactions, sediment	(8)
Enterococci	+ ^b	Raw sewage	Raw sewageSeawater and freshwater (creek)	Enterolert (MPN) and by qPCR (Enterola)	Field study. Decay rate of DNA significantly lower compared to	Water type	(9)
Emerococcus qi ex	0				culturable enterococci.		
E. coli	+ ^a	Strains isolated from cattle manure	Freshwater (pond)	Colilert (MPN)	Field study. Effect of sunlight appeared to	Temperature, biotic	(10)
Enterococci	+ ^a			Enterolert (MPN)	observed during the winter months)	interactions	
E. coli	+ ^b	Human, cattle and	Groundwater	Membrane filtration	Field study. Intact	None	(11)
Enterococci	0 ^a	dog feces		and by qPCR (Entero1a), membrane filtration on mTEC (<i>E</i> .	by the PMA treatment) and DNA persisted similarly in	reported	
Enterococcus qPCR	0 ª			coli)	light and dark treatments		
E. coli	0 ^a	Raw sewage	Freshwater	Colilert (MPN)	Field study. Water	Temperature	(12)
Enterococci	0 ^a	feces	(luke)	Membrane filtration on Slanetz& Bartley			

				agar, followed by Bile Esculin Azide Agar	significant impact on decay		
Enterococci Enterococcus qPCR	+ ^a 0 ^a	Laboratory grown strain	Seawater	Enterolert (MPN), membrane filtration on mEI, spread plating on TSA and by qPCR (Entero1a) with and without PMA	Field study. Under anoxic conditions, sunlight did not affect decay of culturable enterococci when enumerated by Enterolert and TSA, but it was a significant factor when enterococci when enumerated using mEI	Oxidative stress	(13)
Enterococci <i>E. coli</i>	+ ^a 0 ^a	Cattle manure, primary treated sewage	Seawater and freshwater (river)	Membrane filtration on mEI (enterococci) and mTEC (<i>E. coli</i>)	Field study. Sunlight significantly affected only decay of sewage-borne enterococci.	Biotic interactions, fecal source	(14)
Enterococci	+ ^a	Primary treated sewage	Freshwater (river)	Membrane filtration on mEI (enterococci) and by qPCR (Entero1a)	Field study. Sunlight exposure was more important for culturable <i>E. coli</i>	Biotic interactions	(15)
Enerococcus qPCR	+ " + a			Membrane filtration on mTEC	compared to enterococci. There was no statistically significant correlation in decay of culturable enterococci compared		

					to the corresponding qPCR signal.		
Enterococci	+ *	Raw sewage, human feces	Seawater	Membrane filtration on mEI (enterococci) and by qPCR	Field study. Culturable enterococci and <i>E</i> .	Biotic interactions, fecal source	(16)
Enterococcus qPCR	+ ^a			(Enterola)	than their molecular		
E. coli	+ ^a		Membrane filtration on mTEC and by qPCR (EC23S857)	affected by sunlight more.			
E. coli qPCR	+ ^a						
Enterococci	+ ^b	Raw sewage	Seawater, brackish	Enterolert (MPN)	Field study. Generally faster	None reported	(17)
E. coli	+ ^b		water, freshwater (lagoon)	Colilert (MPN)	decay in clear (seawater) and shallow waters.		
Enterococci	+ ^a	Raw sewage	Seawater	Enterolert (MPN) and by qPCR (Entero1a)	Field study. Enterococci (culture and qPCR) decayed	Seasonality	(18)
Enterococcus qPCR	+ ^a				in the winter under		
E. coli	+ ^a			Colilert (MPN)	the same sunlight intensity, while the opposite was the case for <i>E. coli</i> .		

E. coli qPCR Enterococcus qPCR	O ^a	Cattle feces	Freshwater (river) and seawater	qPCR	Field study. <i>Enterococcus</i> qPCR signal decayed significantly faster than <i>E. coli</i> . Culturable enterococci and <i>E.</i> <i>coli</i> decayed faster than their molecular counterparts.	Water type	(19)
Bacterial Pathogens							
Salmonella enterica Campylobacter jejuni	+ b	Laboratory grown strains	Seawater and freshwater (river)	Preston broth/ Exeter agar (MPN, <i>Campylobacter</i>), membrane filtration on XLD agar (<i>Salmonella</i>)	Field study. <i>Campylobacter</i> and <i>Salmonella</i> inactivated more rapidly compared to <i>E. coli</i>	Seasonality	(5)
<i>E. coli</i> O157:H7	+ ^b	Laboratory grown strain	Freshwater (pond)	Lauryl tryptose broth (LTB) enrichment combined with qPCR for confirmation (MPN)	Field study. Decayed significantly slower compared to FIB	None reported	(10)
Salmonella enterica Campylobacter jejuni	0 ^a 0 ^a	Laboratory grown strains	Groundwater	qPCR	Field study. Intact cells (as determined by the PMA treatment) but not DNA (no PMA) of <i>C</i> . <i>jejuni</i> decayed faster when exposed to	None reported	(11)

					sunlight compared to dark treatments.		
Campylobacter jejuni	+ ^b	Laboratory grown strains	Freshwater (river)	Preston broth enrichment, followed by sub-culturing on Karmali agar (MPN)	Lab and field study. No correlation between decay and pH, oxygen concentrations or conductivity	Temperature	(20)
Coliphage							
Somatic coliphage	+ ^b	Raw sewage	Seawater	Double agar layer	Field study. F-RNA	Temperature, seasonality	(2)
F-RNA coliphage	+ b			filtration-swirling elution method	susceptible to longer solar wavelengths than somatic coliphage	seasonanty	
Somatic coliphage	+ ^b	Waste stabilization	Freshwater (river)	Double agar layer	Field study. Somatic	Seasonality,	(3)
F-RNA coliphage	+ ^b	pond		filtration-swirling elution method	longer than F-RNA coliphage	salinity	
F-specific coliphage	+ ^a	Raw sewage, final sewage effluent	Seawater and freshwater (creek)	Double agar layer	Field study. Coliphage decayed significantly slower than FIB	Temperature	(4)
Somatic coliphage F-specific coliphage	+ ^b + ^b	Laboratory grown strains	Seawater	Double agar layer	Lab study. Somatic coliphage more sensitive to light	None reported	(21)

Viral Pathogens Adenovirus 2	+ ^a		Seawater				(21)
F-specific coliphage	+ ^a	Raw sewage	Seawater	Double agar layer	Field study. Somatic coliphage more sensitive to light compared to F- specific coliphage	Biotic interactions	(16)
F-specific coliphage	+ b	Laboratory grown strain	Freshwater (wetland)	Double agar layer	Lab and field study. No significant difference in decay at two different depths (5 cm and 20 cm)	None reported	(23)
F-specific coliphage	+ ^b	Laboratory grown strain	Seawater, brackish, freshwater (lagoon, wetland)	Double agar layer	Lab study. Exogenous sunlight damage caused by external reactive species was more important than the direct (endogenous) damage	Water composition	(22)
Somatic coliphage	0 ª	Raw sewage and cattle feces	Freshwater (lake)	Double agar layer	Field study. Persistence significantly lower in August compared to March and November	Temperature	(12)
					compared to F-RNA coliphage		

Poliovirus 3	+ ^a	Laboratory grown strains		Mammalian cell culture	Lab study. MS2 coliphage and Adenovirus2 more resistant to sunlight compared to other coliphages and Poliovirus	None reported	
Adenovirus 2	0 ª	Laboratory grown strain	Ground water	qPCR	Field study. No significant difference in decay compared to <i>C. jejuni</i> and <i>S.</i> <i>enterica</i> with respect to dark and sunlight exposed treatments	None reported	(11)
Poliovirus 3 Adenovirus 2	+ ^b + ^b	Laboratory grown strain	Seawater, brackish, freshwater (lagoon, wetland)	Mammalian cell culture	Lab study. Generally, Poliovirus decayed faster than Adenovirus or F- specific (MS2) coliphage	Water composition	(22)
Poliovirus 3	+ ^b	Laboratory grown strain	Freshwater (wetland)	Mammalian cell culture	Lab and field study. Inactivated slower compared to the F- specific (MS2) coliphage	None reported	(23)
Protozoan Pathogens	5						

C. parvum	+ ^a	Cattle feces	Freshwater (lake, reservoir)	Mammalian cell culture combined with qPCR	Field study. Increased dissolved organic carbon reduced inactivation	Water type	(24)
MST Markers							
Human-associated (HF183, HF134)	0 ^a	Human and cattle feces	Freshwater (river)	qPCR	Field study. Persistence of cells (as determined by	None reported	(7)
Ruminant-associated (CF193)	O ^a				RNA quantification) was significantly		
Ruminant-associated (CF128)	+ *				only for the human- associated MST markers.		
General marker of fecal pollution (BacUni-UCD)	0 ^a	Human, cattle and dog feces	Seawater	qPCR	Field study. Detection of intact cells (as determined by the PMA	None reported	(6)
Human-associated (BacHum-UCD)	0 ^a				treatment) and DNA differed significantly		
Dog-associated (BacCan-UCD)	0 ^a				and dark treatments		
Cow-associated (BacCow-UCD)	+ ^a						
General marker of fecal pollution (AllBac)	+ *	Raw sewage	Freshwater (river)	qPCR	Lab study. Decay of human-associated	Biotic interactions, sediment	(8)

Human-associated (HF183 and BacHum)	+ *				MST markers was similar		
General marker of fecal pollution (GenBac3)	0 ^a	Raw sewage	Seawater and freshwater (creek)	qPCR	Field study. Persistence longer in seawater compared to freshwater	Water type	(9)
Human-associated (BsteriF1, BuniF2, HF183, HF124, HumM2)	0 a				lieshwater		
General marker of fecal pollution (BacUni-UCD)	0 ª	Human, cattle and dog feces	Groundwater	qPCR	Field study. Intact (PMA) treated cells persisted significantly longer than the (non-	None reported	(11)
Human-associated (BacHum-UCD)	0 ^a				PMA treated) DNA. Cow associated MST		
Dog-associated (BacCan-UCD)	0 ^a				rapidly than others.		
Cow-associated (BacCow-UCD)	0 ^a						
Human-associated (BacH)	0 ^a	Raw sewage and cattle feces	Freshwater (lake)	qPCR	Field study. Persistence of MST markers not	Temperature	(12)
Ruminant associated (BacR)	0 ª				significantly different from FIB and coliphage		

General marker of fecal pollution (GenBac3) Human-associated (HF183 and HumM2)	+ ^a + ^a	Primary treated sewage	Freshwater (river)	qPCR	Field study. More pronounced effect of sunlight in the early stages of decay (< 72 hours) compared to subsequent time points	Biotic interactions	(15)
General marker of fecal pollution (GenBac3) Cattle/ruminant associated (CowM2, CowM3, Rum2Bac)	0 ^a +/0 ^a	Cattle feces	Freshwater (river) and seawater	qPCR	Field study. Sunlight affected the decay of CowM2 and Rum2Bac, but not CowM3	Water type	(19)
Human-associated (HF183 and HumM2) General marker of fecal pollution (GenBac3)	+ ^a + ^a	Raw sewage, human feces	Seawater	qPCR	Field study. The magnitude of the effect varied across different time points and pollution sources	Biotic interactions, fecal source	(16)
General marker of fecal pollution (GenBac3) Human-associated (HF183, HumM2 and BacHum)	0 ^a	Raw sewage	Seawater	qPCR	Field study. When exposed to sunlight, culturable FIB decayed significantly faster than the MST markers	None reported	(18)

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46 ^aStatistical significance reported

47 ^bStatistical significance not reported

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49 **REFERENCES**

- Sinton LW, Davies-Colley RJ, Bell RG. 1994. Inactivation of enterococci and fecal coliforms from sewage and meatworks effluents in seawater chambers. Appl Environ Microbiol 60:2040-2048.
 Sinton LW, Finley PK, Lynch PA, 1000. Sunlight inactivation of fecal heaterionhages and heaterin is
- Sinton LW, Finlay RK, Lynch PA. 1999. Sunlight inactivation of fecal bacteriophages and bacteria in sewage-polluted seawater. Appl Environ Microbiol 65:3605-3613.
- Sinton LW, Hall CH, Lynch PA, Davies-Colley RJ. 2002. Sunlight inactivation of fecal indicator
 bacteria and bacteriophages from waste stabilization pond effluent in fresh and saline waters. Appl Environ
 Microbiol 68:1122-1131.
- Noble RT, Lee IM, Schiff KC. 2004. Inactivation of indicator micro-organisms from various sources of
 faecal contamination in seawater and freshwater. J Appl Microbiol 96:464-472.
- 5. **Sinton L, Hall C, Braithwaite R.** 2007. Sunlight inactivation of *Campylobacter jejuni* and *Salmonella enterica*, compared with *Escherichia coli*, in seawater and river water. J Water Health **5:**357-365.
- 6. Bae S, Wuertz S. 2009. Rapid decay of host-specific fecal *Bacteroidales* cells in seawater as measured by
 quantitative PCR with propidium monoazide. Water Res 43:4850-4859.
- Walters SP, Field KG. 2009. Survival and persistence of human and ruminant-specific faecal
 Bacteroidales in freshwater microcosms. Environ Microbiol 11:1410-1421.
- Bick LK, Stelzer EA, Bertke EE, Fong DL, Stoeckel DM. 2010. Relative decay of *Bacteroidales* microbial source tracking markers and cultivated *Escherichia coli* in freshwater microcosms. Appl Environ
 Microbiol 76:3255-3262.
- 69 9. Green HC, Shanks OC, Sivaganesan M, Haugland RA, Field KG. 2011. Differential decay of human faecal *Bacteroides* in marine and freshwater. Environ Microbiol 13:3235-3249.
- Jenkins MB, Fisher DS, Endale DM, Adams P. 2011. Comparative die-off of *Escherichia coli* O157:H7
 and fecal indicator bacteria in pond water. Environ Sci Technol 45:1853-1858.
- Bae S, Wuertz S. 2012. Survival of host-associated bacteroidales cells and their relationship with
 Enterococcus spp., *Campylobacter jejuni*, *Salmonella enterica* serovar Typhimurium, and adenovirus in
 freshwater microcosms as measured by propidium monoazide-quantitative PCR. Appl Environ Microbiol
 78:922-932.
- Sokolova E, Astrom J, Pettersson TJ, Bergstedt O, Hermansson M. 2012. Decay of *Bacteroidales* genetic markers in relation to traditional fecal indicators for water quality modeling of drinking water
 sources. Environ Sci Technol 46:892-900.
- Sassoubre LM, Nelson KL, Boehm AB. 2012. Mechanisms for photoinactivation of *Enterococcus faecalis* in seawater. Appl Environ Microbiol **78**:7776-7785.
- Korajkic A, McMinn BR, Harwood VJ, Shanks OC, Fout GS, Ashbolt NJ. 2013. Differential decay of
 enterococci and *Escherichia coli* originating from two fecal pollution sources. Appl Environ Microbiol
 79:2488-2492.
- Korajkic A, McMinn BR, Shanks OC, Sivaganesan M, Fout GS, Ashbolt NJ. 2014. Biotic interactions
 and sunlight affect persistence of fecal indicator bacteria and microbial source tracking genetic markers in
 the upper Mississippi river. Appl Environ Microbiol 80:3952-3961.
- Wanjugi P, Sivaganesan M, Korajkic A, Kelty CA, McMinn B, Ulrich R, Harwood VJ, Shanks OC.
 2016. Differential decomposition of bacterial and viral fecal indicators in common human pollution types.
 Water Res 105:591-601.
- Maraccini PA, Mattioli MC, Sassoubre LM, Cao Y, Griffith JF, Ervin JS, Van De Werfhorst LC,
 Boehm AB. 2016. Solar Inactivation of Enterococci and *Escherichia coli* in Natural Waters: Effects of
 Water Absorbance and Depth. Environ Sci Technol 50:5068-5076.
- Mattioli MC, Sassoubre LM, Russell TL, Boehm AB. 2017. Decay of sewage-sourced microbial source
 tracking markers and fecal indicator bacteria in marine waters. Water Res 108:106-114.
- 19. Korajkic A, McMinn BR, Ashbolt NJ, Sivaganesan M, Harwood VJ, Shanks OC. 2019. Extended
 persistence of general and cattle-associated fecal indicators in marine and freshwater environment. Sci
 Total Environ 650:1292-1302.
- 99 20. Rodriguez S, Araujo R. 2012. Effect of environmental parameters on the inactivation of the waterborne pathogen *Campylobacter* in a Mediterranean river. J Water Health 10:100-107.
- Love DC, Silverman A, Nelson KL. 2010. Human virus and bacteriophage inactivation in clear water by
 simulated sunlight compared to bacteriophage inactivation at a southern California beach. Environ Sci
 Technol 44:6965-6970.

50

- Silverman AI, Peterson BM, Boehm AB, McNeill K, Nelson KL. 2013. Sunlight inactivation of human viruses and bacteriophages in coastal waters containing natural photosensitizers. Environ Sci Technol
 47:1870-1878.
- Silverman AI, Nguyen MT, Schilling IE, Wenk J, Nelson KL. 2015. Sunlight inactivation of viruses in open-water unit process treatment wetlands: modeling endogenous and exogenous inactivation rates.
 Environ Sci Technol 49:2757-2566.
- King BJ, Hoefel D, Daminato DP, Fanok S, Monis PT. 2008. Solar UV reduces *Cryptosporidium parvum* oocyst infectivity in environmental waters. J Appl Microbiol 104:1311-1323.
- 112