

Supplementary Materials

1. Supplementary Tables

Table S1. List of samples collected in this study. DNA samples were collected in dates in bold.

Site	Sampling day at WWTP	Sampling day at sea	Marine station coordinates
Francavilla al Mare	28 April 2020	28 April 2020	14.275°E; 42.464°N
	29 May 2020	29 May 2020	
	17 June 2020	17 June 2020	
	21 July 2020	21 July 2020	
	28 August 2020	28 August 2020	
	22 September 2020	22 September 2020	
Zadar	30 July 2019	30 July 2019	15.236°E; 44.087°N
	13 September 2019	13 September 2019	
	7 November 2019	7 November 2019	
	22 April 2020	22 April 2020	
	18 May 2020	18 May 2020	
	18 June 2020	18 June 2020	
	27 July 2020	27 July 2020	
	26 August 2020	26 August 2020	
Katalinića Brig	29 September 2020	29 September 2020	16.453°E; 43.490°N
	31 July 2019	31 July 2019	
	27 February 2020	27 February 2020	
	23 April 2020	23 April 2020	
	28 May 2020	28 May 2020	
	26 June 2020	26 June 2020	
	22 July 2020	22 July 2020	
	21 September 2020	21 September 2020	
	31 July 2019	31 July 2019	
	27 February 2020	27 February 2020	
Stobreč	23 April 2020	23 April 2020	16.518°E; 43.482°N
	28 May 2020	28 May 2020	
	26 June 2020	26 June 2020	
	22 July 2020	22 July 2020	
	21 September 2020	21 September 2020	

Table S2. Primer sets used for qPCR.

Target	Primer name	Primer sequence (5'- 3')	Amplicon size (bp)	Annealing T (°C)	Reference
16SrDNA	Bact1369F	CGGTGAATACGTTTCYCGG	142	55	[51]
	Prok1492R	GGHTACCTTGTTACGACTT			
<i>ermB</i>	ermB Fw	CCGAACACTAGGGTTGCTC	139	55	[52]
	ermB Rev	ATCTGGAACATCTGTGGTATG			
<i>tetA</i>	tetA Fw	GCTACATCCTGCTTGCCTTC	210	64	[55]
	tetA Rev	CATAGATCGCCGTGAAGAGG			
<i>sulII</i>	sulII Fw	TCCGGTGGAGGCCGGTATCTGG	191	60	[56]
	sulII Rev	CGGGAATGCCATCTGCCTTGAG			
<i>qnrS</i>	qnrS Fw	GACGTGCTAACTTGCGTGAT	118	62	[57]
	qnrS Rev	TGGCATTGTTGGAAACTTG			
<i>bla</i> _{CTX-M}	blaCTX-M Fw	CTATGGCACCACCAACGATA	103	60	[58]
	blaCTX-M Rev	ACGGCTTTCTGCCTTAGGTT			
<i>mcr-1</i>	mcr-1 qF1	ACACTTATGGCACGGTCTATG	120	63	[59]
	mcr-1 qR1	GCACACCCAAACCAATGATAC			
<i>bla</i> _{TEM}	blaTEM Fw	TTCCTGTTTTTGCTCACCCAG	112	60	[60]
	blaTEM Rev	CTCAAGGATCTTACCGCTGTTG			
<i>bla</i> _{OXA}	Oxa-rt Fw	AGGCACGTATGAGCAAGATG	189	60	[61]
	Oxa-rt Rev	TGGCTTGTTTGACAATACGC			

Supplementary Table S3. qPCR parameters for gene quantification. Melting peaks, efficiencies, and r^2 are the mean of the whole data produced for all runs for each gene \pm standard deviation.

Target	Melting peak	Efficiency (%)	r^2	Standard curve (copies μL^{-1})	LOQ (copies μL^{-1})
16SrDNA	85.3 \pm 0.7	100.1 \pm 2.7	0.998 \pm 0.001	4.23 $\times 10^5$	430
				4.23 $\times 10^4$	
				4.23 $\times 10^3$	
				4.23 $\times 10^2$	
<i>sulII</i>	90.7 \pm 0.3	98.7 \pm 1.1	0.998 \pm 0.001	3.36 $\times 10^5$	34
				3.36 $\times 10^4$	
				3.36 $\times 10^3$	
				3.36 $\times 10^2$	
<i>tetA</i>	89.5 \pm 0.2	97.0 \pm 0.4	0.999 \pm 0.001	3.36 $\times 10^1$	13
				1.23 $\times 10^5$	
				1.23 $\times 10^4$	
				1.23 $\times 10^3$	
<i>bla_{OXA}</i>	83.5 \pm 0.0	90.0 \pm 0.04	0.999 \pm 0.000	1.23 $\times 10^2$	31
				1.23 $\times 10^1$	
				3.05 $\times 10^5$	
				3.05 $\times 10^4$	
<i>mcr-1</i>	82.8 \pm 0.3	101.7 \pm 3.8	0.999 \pm 0.001	3.05 $\times 10^3$	9
				3.05 $\times 10^2$	
				3.05 $\times 10^1$	
				8.91 $\times 10^4$	
<i>bla_{TEM}</i>	81.9 \pm 0.4	99.2 \pm 2.0	0.999 \pm 0.001	8.91 $\times 10^3$	41
				8.91 $\times 10^2$	
				8.91 $\times 10^1$	
				8.91 $\times 10^0$	
<i>bla_{CTX-M}</i>	84.6 \pm 0.03	99.2 \pm 1.9	0.999 \pm 0.001	4.10 $\times 10^5$	14
				4.10 $\times 10^4$	
				4.10 $\times 10^3$	
				4.10 $\times 10^2$	
<i>ermB</i>	81.6 \pm 0.04	100.5 \pm 0.4	1.000 \pm 0.001	4.10 $\times 10^1$	25
				1.37 $\times 10^5$	
				1.37 $\times 10^4$	
				1.37 $\times 10^3$	
<i>qnrS</i>	82.5 \pm 0.4	100.2 \pm 2.4	0.998 \pm 0.001	1.37 $\times 10^2$	23
				1.37 $\times 10^1$	
				2.45 $\times 10^5$	
				2.45 $\times 10^4$	
				2.45 $\times 10^3$	
				2.45 $\times 10^2$	
				2.45 $\times 10^1$	
				2.29 $\times 10^5$	
				2.29 $\times 10^4$	
				2.29 $\times 10^3$	
				2.29 $\times 10^2$	
				2.29 $\times 10^1$	

2. Supplementary figures

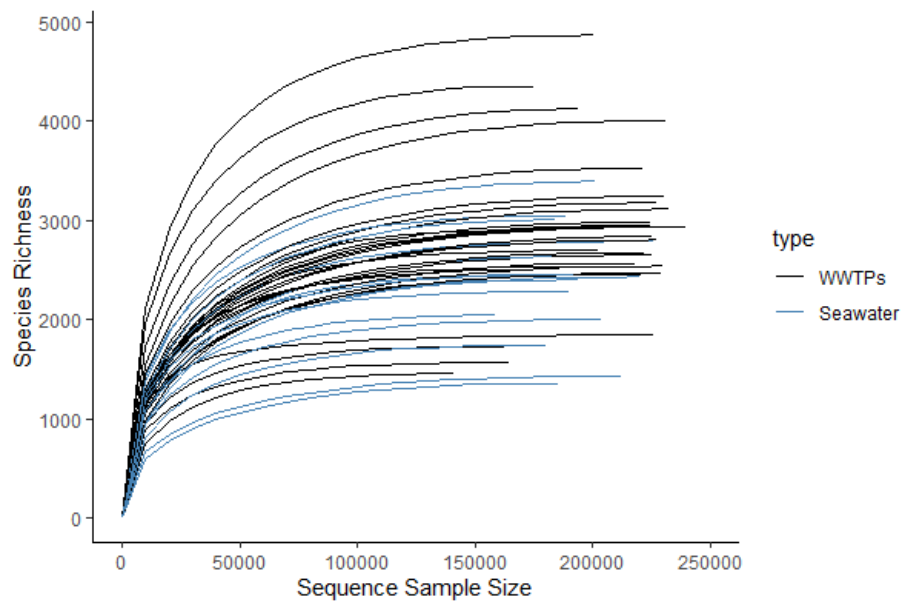


Figure S1. Rarefaction curves of treated sewage (WWTPs) and seawater communities based on 16S rDNA amplicon sequencing. Curves were built before performing any filtration.

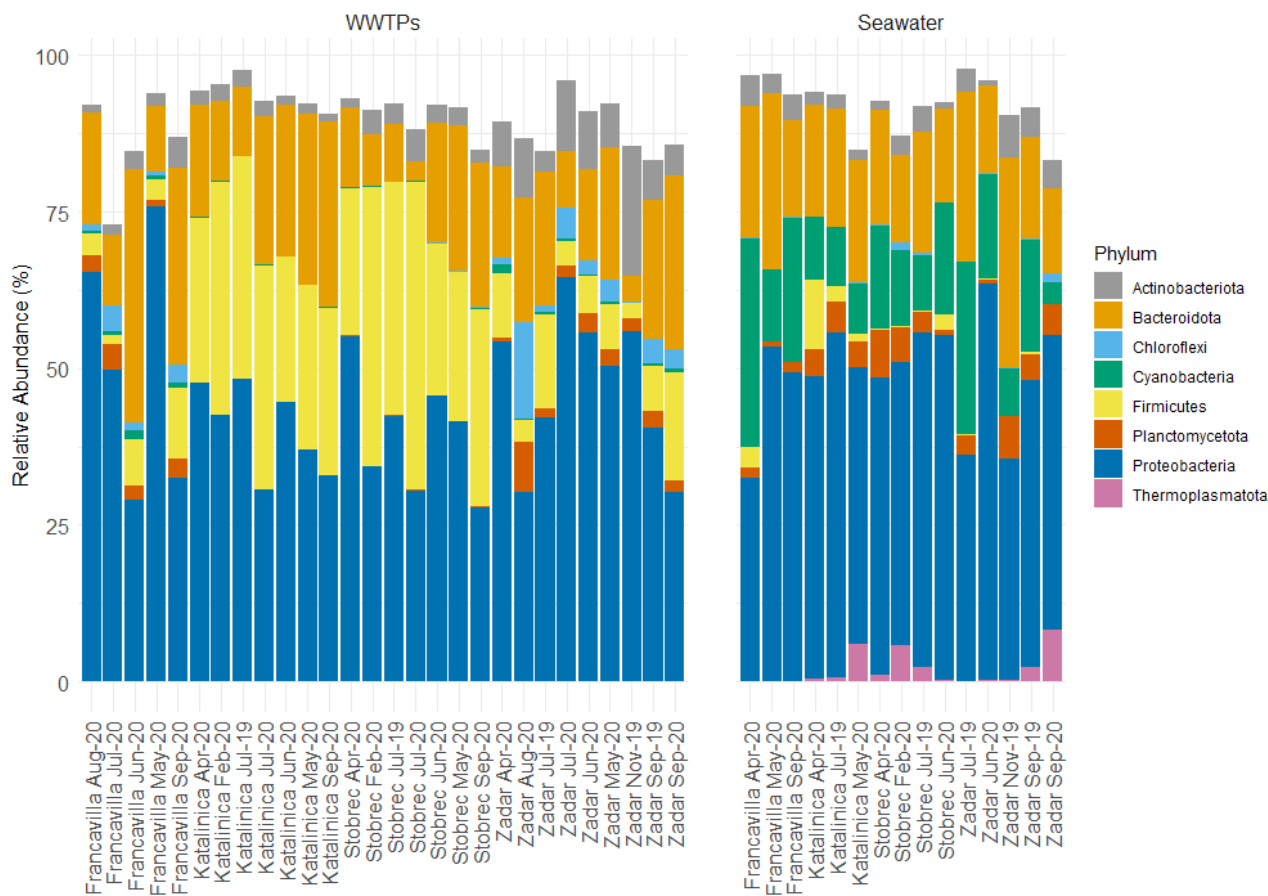


Figure S2. Bacterial community composition at phylum level of treated sewage (WWTPs) and seawater samples based on 16S rDNA amplicon sequencing. Only top phyla are depicted.

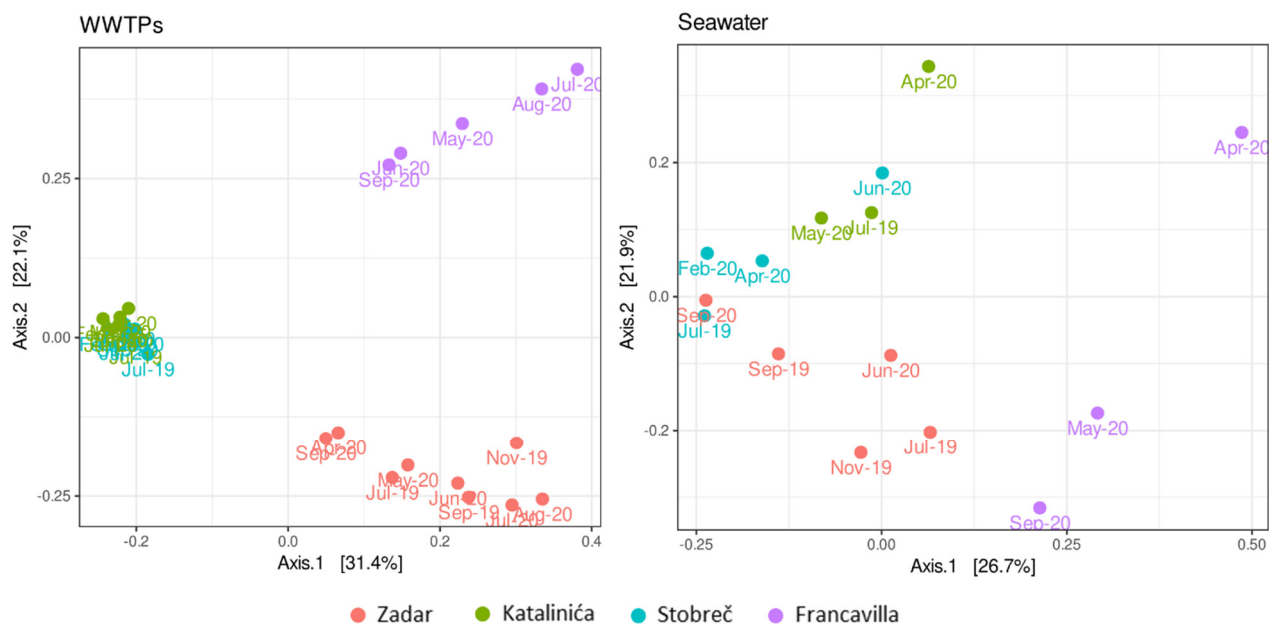


Figure S3. Sample ordination by PCoA of Bray-Curtis distances. In Katalinića and Stobreč WWTPs, sewage undergoes only basic mechanical treatments (i.e., "primary treatments"). Zadar and Francavilla WWTPs perform activated sludge treatment subsequently to primary treatments. Only in the case of Francavilla WWTP treated sewage undergoes a final disinfection step.

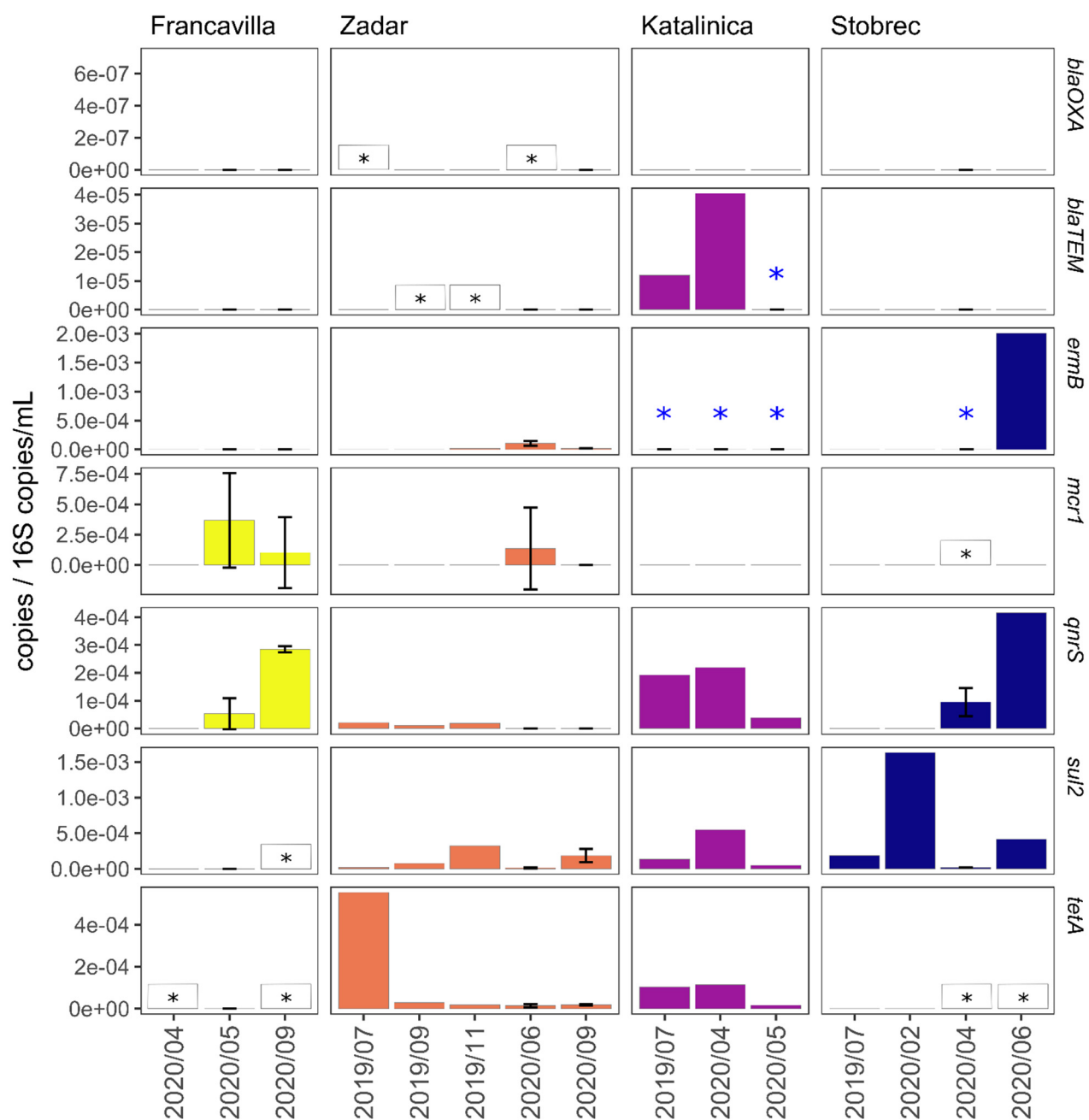


Figure S4. Content of ARGs in seawater samples over time. Black stars in white boxes are <LOQ values. Blue stars indicate not quantifiable samples due to primer-specificity issues. Error bars show the standard deviation between biological replicates (n.2).