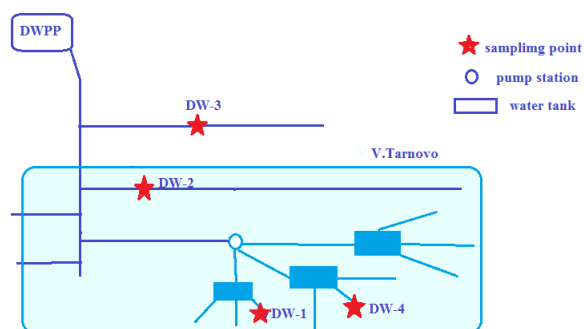


Supplementary Materials

A scheme of the DWDS and the drinking water sampling points



Longitudes and latitude of the DW sampling points:

DW-1 (43.079241N; 25.609019E)

DW-2 (43.073547N; 25.604005E)

DW-3 (43.043731N; 25.620591E)

DW-4 (43.086231N; 25.635262E)

Table S1. Data plotted on Figure 1(a). Relative percentage of the bacteria resistant to the individual ABs in drinking water depending on the DW sampling location at the DWDS

Type of ABs	DW-1	DW-2	DW-3	DW-4
<i>AMP</i>	0.6 (0.1)	0.2 (0.2)	3.1 (0.2)	0.1 (0.003)
<i>TE</i>	0.1 (0.1)	0.2 (0.1)	0.4 (0.1)	0.04 (0.01)
<i>C</i>	14.6 (1.9)	18.0 (2.3)	6.2 (0.4)	1.0 (0.04)
<i>CIP</i>	0.8 (0.2)	<i>nd</i>	3.1 (0.2)	0.1 (0.005)
<i>Sul</i>	0.5 (0.1)	12.6 (2.9)	4.3 (3.1)	0.3 (0.01)
<i>S</i>	27.6 (4.1)	8.3 (2.2)	6.2 (0.4)	9.9 (0.4)

AMP - ampicillin; *TE* - tetracycline; *C* - chloramphenicol; *CIP* - ciprofloxacin; *Sul* - sulfamethoxazole; *S* – streptomycin;
In brackets – standard deviation; *nd* - not detected.

Table S2. Data plotted on Figure 1(b). Relative percentage of the HPC bacteria resistant to the tested ABs in drinking water-associated biofilms depending on DW sampling location at the DWDS

AB, mg/l	DW-1	DW-2	DW-3	DW-4
<i>AMP</i>	0.1 (0.1)	0.03 (0.04)	0.4 (0.3)	0.2 (0.2)
<i>TE</i>	0.002 (0.002)	0.0004 (0)	0.06 (0.05)	0.02 (0.01)
<i>C</i>	8.6 (5.5)	25.4 (22.0)	15.2 (8.0)	2.0 (1.4)
<i>CIP</i>	1.8 (1.5)	0.01 (0.01)	0.3 (0.1)	34.0 (8.7)
<i>Sul</i>	8.6 (7.6)	7.5 (5.6)	1.3 (0.5)	0.2 (0.2)
<i>S</i>	33.2 (14.2)	23.8 (17.8)	24.3 (4.1)	54.9 (13.5)

AMP - ampicillin; *TE* - tetracycline; *C* - chloramphenicol; *CIP* - ciprofloxacin; *Sul* - sulfamethoxazole; *S* – streptomycin;
In brackets – standard deviation.

Table S3. Data plotted on Figure 3 (a). Biomass amount of the single-species biofilms of the isolated bacteria in R2A broth

Strain №	Bacterial taxon	Biofilm, OD _{590nm}	Plankton, OD _{620nm}
4-1	<i>Sphingomonas</i> spp.	0.64 (0.07)	0.76 (0.12)
4-2	<i>Sphingomonas</i> spp.	0.31 (0.06)	0.39 (0.01)
4-4	<i>Sphingomonas</i> spp.	0.47 (0.06)	0.54 (0.05)
124	<i>Sphingomonas paucimobilis</i>	0.07 (0.0)	1.16 (0.05)
2-90	<i>Embedobacter brevis</i>	2.65 (0.79)	0.34 (0.01)
2-91	<i>Embedobacter brevis</i>	2.56 (0.26)	0.82 (0.39)
11	<i>Pseudomonas</i> spp.	0.32 (0.03)	1.11 (0.08)
12	<i>Pseudomonas</i> spp.	0.41 (0.02)	0.82 (0.04)
64	<i>Pseudomonas</i> spp.	0.23 (0.08)	1.51 (0.06)
56	<i>P. fluorescens</i>	0.98 (0.44)	1.04 (0.11)
51	<i>P. fluorescens</i>	0.75 (0.04)	0.75 (0.13)
65	<i>P. putida</i>	0.09 (0.01)	1.43 (0.09)
57	<i>Stenotrophomonas maltophilia</i>	0.07 (0.01)	0.90 (0.10)
2-78	<i>Methylobacterium exorquens</i>	0.24 (0.06)	0.15 (0.01)
77	<i>Methylobacterium</i> spp.	0.10 (0.07)	1.24 (0.11)
3-70	<i>Lysinibacillus sphaericus</i>	0.12 (0.01)	0.54 (0.06)
3-25	<i>Bacillus</i> spp.	0.30 (0.05)	0.75 (0.14)
3-52	<i>B. thuringiensis</i>	0.19 (0.01)	1.46 (0.23)
2-94	<i>Staphylococcus cohnii</i>	0.06 (0.02)	0.32 (0.15)
2-61	<i>Micrococcus luteus</i>	2.47 (0.17)	0.22 (0.04)

Table S4. Data plotted on Figure 3 (b). Biomass amount of the single-species biofilms of the isolated bacteria in M63 medium

Strain №	Bacterial taxon	Biofilm, OD _{590nm}	Plankton, OD _{620nm}
4-1	<i>Sphingomonas</i> spp.	0.37 (0.06)	0.44 (0.06)
4-2	<i>Sphingomonas</i> spp.	0.47 (0.14)	0.51 (0.03)
4-4	<i>Sphingomonas</i> spp.	0.44 (0.08)	1.20 (0.01)
124	<i>Sphingomonas paucimobilis</i>	0.26 (0.07)	1.34 (0.08)
2-90	<i>Embedobacter brevis</i>	0.42 (0.13)	0.04 (0.01)
2-91	<i>Embedobacter brevis</i>	0.40 (0.02)	0.13 (0.02)
11	<i>Pseudomonas</i> spp.	0.40 (0.15)	1.90 (0.21)
12	<i>Pseudomonas</i> spp.	0.35 (0.12)	1.98 (0.27)
64	<i>Pseudomonas</i> spp.	0.34 (0.07)	2.23 (0.03)
56	<i>P. fluorescens</i>	3.05 (0.05)	1.28 (0.11)
51	<i>P. fluorescens</i>	2.91 (0.04)	1.07 (0.02)
65	<i>P. putida</i>	0.16 (0.06)	1.96 (0.06)
57	<i>Stenotrophomonas maltophilia</i>	0.10 (0.02)	0.06 (0.004)
2-78	<i>Methylobacterium exorquens</i>	0.34 (0.07)	0.70 (0.15)
77	<i>Methylobacterium</i> sp.	0.18 (0.02)	0.12 (0.02)
3-70	<i>Lysinibacillus sphaericus</i>	0.13 (0.03)	0.05 (0.01)
3-25	<i>Bacillus</i> spp.	0.14 (0.03)	0.06 (0.01)
3-52	<i>B. thuringiensis</i>	0.14 (0.02)	0.06 (0.01)
2-94	<i>Staphylococcus cohnii</i>	0.13 (0.04)	0.024 (0.006)
2-61	<i>Micrococcus luteus</i>	0.68 (0.03)	0.008 (0.002)

*In brackets - standard deviations for the replicates