

Figure S1. Dynamics of the total number of bacteria and FFB in the studied soils, incubation temperature 5°C: I – soil (total cells); II – FFB

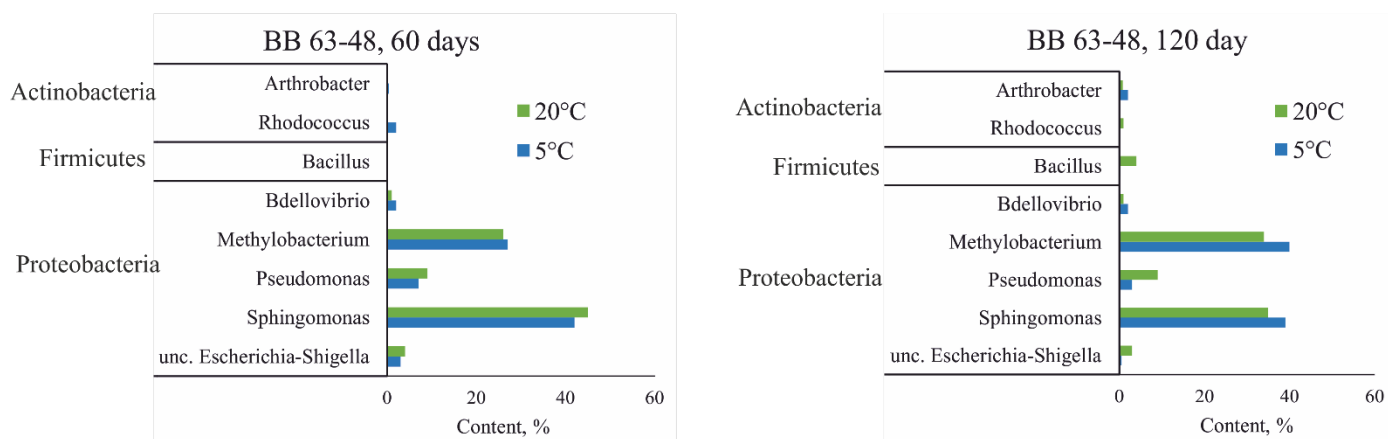


Figure 2. Distribution of dominant phyla in sample BB 63-48

Table S1. OTUs which are present only in the filtrate / in the soil

Phylum	Class	The filtrate	Soil suspension
<i>Proteobacteria</i>	<i>Alpha-proteobacteria</i>	<i>Ochrobactrum</i>	<i>Rhodospirillaceae</i>
		<i>Roseomonas</i>	<i>Polymorphobacter</i>
		<i>Paracoccus</i>	Uncultured (<i>Sphingomonadales</i>)
		<i>Afipia</i>	Uncultured (<i>Rickettsiales</i>)
			Uncultured (Cand. <i>Odyssella</i>)
			Uncultured (<i>Holosporaceae</i>)
			Uncultured (<i>Rickettsiaceae</i>)
			<i>Rhizobiales</i>
			<i>Devosia</i>
			Ambiguous taxa (LWSR-14)
			<i>Rhodoplanes</i>
			<i>Methylocella</i>
			<i>Inquilinus</i>
	<i>Beta-proteobacteria</i>	<i>Achromobacter</i>	Uncultured (<i>Comamonadaceae</i>)
		<i>Polaromonas</i>	<i>Limnobacter</i>
		<i>Delftia</i>	<i>Nitrosomonadales</i>
		<i>Ralstonia</i>	Uncultured (<i>Neisseriales</i>)
		<i>Methylophilaceae</i>	<i>Rhodocyclales</i>
		<i>Hydrogenophilaceae</i>	<i>Noviherbaspirillum</i>
	<i>Delta-proteobacteria</i>	-	Uncultured <i>Alcaligenaceae</i>
			<i>Phaselicystis</i>
			Ambiguous taxa (KD3-10)
			<i>Polyangiaceae</i> (Blrii41)
			Uncultured <i>Desulfovibrionales</i>
	<i>Gamma-proteobacteria</i>	Uncultured (<i>Escherichia-Shigella</i>)	Uncultured <i>Oligoflexaceae</i>
			<i>Rhodanobacter</i>
			<i>Dokdonella</i>
			<i>Coxiella</i>
			<i>Acidiferrobacteraceae</i>
			Ambiguous taxa (HTA4)
<i>Chloroflexi</i>	Ambiguous class	-	Ambiguous taxa (JG37-AG-4)
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Blastococcus</i>	<i>Sporichthyaceae</i>
		<i>Geodermatophilus</i>	Uncultured <i>Micromonosporaceae</i>
		<i>Arthrobacter</i>	
		<i>Micrococcus</i>	
		<i>Agrococcus</i>	
		<i>Rhodococcus</i>	
		<i>Kocuria</i>	
		Uncultured <i>Frankiales</i>	
	<i>Thermoleophilia</i>		<i>Solirubrobacterales</i> (0319-6M6)
<i>Acidobacteria</i>		-	-
<i>Bacteroidetes</i>	<i>Flavobacteriia</i>	<i>Chryseobacterium</i>	
		<i>Flavobacterium</i>	
	<i>Cytophagia</i>	<i>Rufibacter</i>	<i>Sporocytophaga</i>
		<i>Hymenobacter</i>	
	<i>Sphingobacteriia</i>	<i>Pedobacter</i>	<i>Sphingobacterium</i>
<i>Verrucomicrobia</i>	Ambiguous class	-	Ambiguous taxa (OPB35 soil group)
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	-	<i>Gemmatimonadaceae</i> (Uncultured soil bacterium)

			<i>Gemmatirosa</i>
<i>Firmicutes</i>	<i>Clostridia</i>	-	<i>Anaerococcus</i>
			<i>Clostridium</i>
	<i>Bacilli</i>		<i>Paenibacillus</i>
			<i>Streptococcus</i>

Table S2. The number of bacteria grown on agar nutrient media (thousand CFU in 1 g of soil)

Sample	T	Media	Succession points, number of days							
			0	3	7	14	30	60	90	120
BB 63-48	5°C	TSA	0	0	0	0	0	0	0	0
		R-2A	0	0	0	0	0	0	0	0
	20°C	TSA	0	19	10	0	13	35	14	4
		R-2A	0	15	0	0	16	29	3	8
BB 63-58 (AT)	5°C	TSA	15	55	220	100	179	100	287	950
		R-2A	78	130	280	190	184	350	480	670
	20°C	TSA	15	130	180	210	340	80	240	670
		R-2A	78	100	450	320	530	135	570	930
BB 63-58 (AB)	5°C	TSA	40	10	36	10	88	17	18	8
		R-2A	35	15	36	180	222	8	29	6
	20°C	TSA	40	80	1090	840	1050	1000	570	200
		R-2A	35	520	820	1325	900	1500	610	300

Table 3. Taxonomic structure of the heterotrophic bacterial complex along the course of succession

Succession points	Sample	5°C		20°C	
		TSA	R-2A	TSA	R-2A
0	BB 63-48	-	-	-	-
	BB 63-58 (AT)	<i>Variovorax ginsengisoli</i>	<i>Variovorax ginsengisoli</i>	-	<i>Cellulomonas sp.</i> <i>Sphingomonas sp.</i> <i>Mesorhizobium australicum</i> <i>Blastococcus aggregatus</i>
	BB 63-58 (AB)	<i>Pseudomonas sp.</i>	<i>Pseudomonas sp.</i>	-	<i>Arthrobacter sp.</i>
3 days	BB 63-48	-	-	<i>Chryseobacterium montanum</i> <i>Micrococcus endophyticus</i> <i>Gordonia didemni</i> <i>Gordonia hongkongensis/terrae</i> <i>Dietzia maris</i> <i>Methylobacterium podarium</i>	<i>Rhodococcus sp.</i>
	BB 63-58 (AT)	-	<i>Variovorax ginsengisoli</i>	-	<i>Variovorax ginsengisoli</i>
	BB 63-58 (AB)	<i>Pseudomonas sp.</i>	<i>Pseudomonas sp.</i>	<i>Pseudomonas sp.</i>	<i>Sphingomonas sp.</i> <i>Micrococcus sp.</i> <i>Arthrobacter sp.</i> <i>Pseudomonas sp.</i>
7 days	BB 63-48	-	-	<i>Arthrobacter sp.</i>	-
	BB 63-58 (AT)	<i>Pseudomonas sp.</i>	<i>Pseudomonas sp.</i>	<i>Pseudomonas sp.</i>	<i>Brevundimonas vesicularis</i>
	BB 63-58 (AB)	<i>Pseudomonas sp.</i>	<i>Pseudomonas sp.</i>	<i>Bacillus halosaccharovorans</i> <i>Pseudomonas sp.</i>	<i>Pseudomonas sp.</i>
14 days	BB 63-48	-	-	-	-
	BB 63-58 (AT)	<i>Pseudomonas sp.</i>	<i>Pseudomonas sp.</i>	<i>Pseudomonas sp.</i> <i>Pseudoarthrobacter sp.</i>	<i>Pseudomonas sp.</i> <i>Mesorhizobium australicum</i>
	BB 63-58 (AB)	<i>Pseudomonas sp.</i>	<i>Pseudomonas sp.</i>	<i>Pseudomonas sp.</i> <i>Pseudoarthrobacter sp.</i>	<i>Pseudomonas sp.</i>
30 days	BB 63-48	-	-	<i>Methylobacterium extorquens</i> <i>Arthrobacter sp.</i> <i>Pseudomonas sp.</i>	<i>Methylobacterium extorquens</i> <i>Arthrobacter sp.</i> <i>Moraxella osloensis</i> <i>Sphingomonas sp.</i>
	BB 63-58 (AT)	<i>Pseudomonas sp.</i>	<i>Pseudomonas sp.</i>	<i>Pseudomonas sp.</i>	<i>Pseudomonas sp.</i> <i>Rhizobacter profundi</i> <i>Mesorhizobium australicum</i> <i>Bacillus sp.</i>

	BB 63-58 (AB)	<i>Pseudomonas</i> sp. <i>Agreia</i> sp.	<i>Leifsonia</i> sp. <i>Pseudomonas</i> sp.	<i>Pseudomonas</i> sp.	<i>Pseudomonas</i> sp. <i>Pseudarthrobacter</i> sp.
60 days	BB 63-48	-	-	<i>Pseudomonas</i> sp. <i>Brevundimonas</i> <i>vesicularis</i>	<i>Pseudomonas</i> sp. <i>Arthrobacter oryzae</i> <i>Sphingobium xenophagum</i> <i>Sphingomonas</i> sp. <i>Roseomonas</i> sp.
	BB 63-58 (AT)	<i>Pseudomonas</i> sp.	<i>Pseudomonas</i> sp.	<i>Pseudomonas</i> sp.	<i>Pseudomonas</i> sp.
	BB 63-58 (AB)	<i>Pseudomonas</i> sp.	<i>Pseudomonas</i> sp. <i>Blastococcus</i> <i>aggregatus</i>	<i>Pseudomonas</i> sp.	<i>Pseudomonas</i> sp.
90 days	BB 63-48	-	-	<i>Pseudomonas</i> sp. <i>Methylobacterium</i> <i>extorquens</i>	<i>Pseudomonas</i> sp.
	BB 63-58 (AT)	<i>Pseudomonas</i> sp.	<i>Pseudomonas</i> sp.	<i>Pseudomonas</i> sp. <i>Bacillus</i> sp.	<i>Pseudomonas</i> sp. <i>Mesorhizobium</i> <i>australicum</i>
	BB 63-58 (AB)	<i>Pseudomonas</i> sp. <i>Arthrobacter</i> sp.	<i>Pseudomonas</i> sp. <i>Variovorax</i> <i>boronicumulans</i>	<i>Pseudomonas</i> sp.	<i>Pseudomonas</i> sp.
120 days	BB 63-48	-	-	<i>Pseudomonas</i> sp.	<i>Pseudomonas</i> sp. <i>Sphingobium xenophagum</i> <i>Variovorax ginsengisoli</i> <i>Brevundimonas vesicularis</i> <i>Roseomonas</i> sp.
	BB 63-58 (AT)	<i>Pseudomonas</i> sp.	<i>Pseudomonas</i> sp.	<i>Pseudomonas</i> sp.	<i>Pseudomonas</i> sp. <i>Mesorhizobium</i> <i>australicum</i>
	BB 63-58 (AB)	<i>Pseudomonas</i> sp.	<i>Pseudomonas</i> sp. <i>Rhodopseudomonas</i> sp.	<i>Pseudomonas</i> sp. <i>Arthrobacter oryzae</i>	<i>Pseudomonas</i> sp.

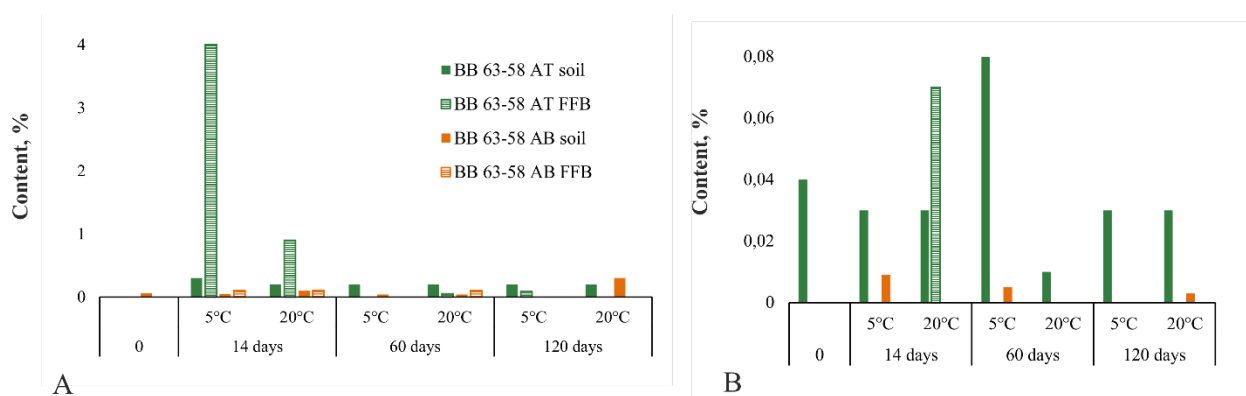


Figure 3. Content (%) of (A) phylum *Saccharibacteria*; (B) genus *Opitutus*