Electronic supplementary information

Manuscript title: Isolation and characterization of psychrotolerant denitrifying bacteria for improvement of nitrate removal in woodchip bioreactors treating agricultural drainage water at low temperature

Authors: Arnaud Jéglot, Kirk Matthew Schnorr, Sebastian Reinhold Sørensen, Lars Elsgaard

Figure S1. Biomass growth (optical density at 600 nm, OD600) of the isolated bacterial strains *Pseudomonas chlororaphis* PSS4, *P. proteolytica* WBRS105, *P. veronii* WBRS70, *P. brenneri* WBRS 96, J*anthinobacterium lividum* WBRS30, and *Kluyvera intermedia* WBRS56. An inoculum of 10% (v/v) of a growing pure culture was transferred to fresh minimal denitrifying medium and incubated at 10°C under anoxic conditions. Data are shown as means and standard errors (*n* = 3). Doubling times (Td) were calculated from biomass growth during the exponential phase.

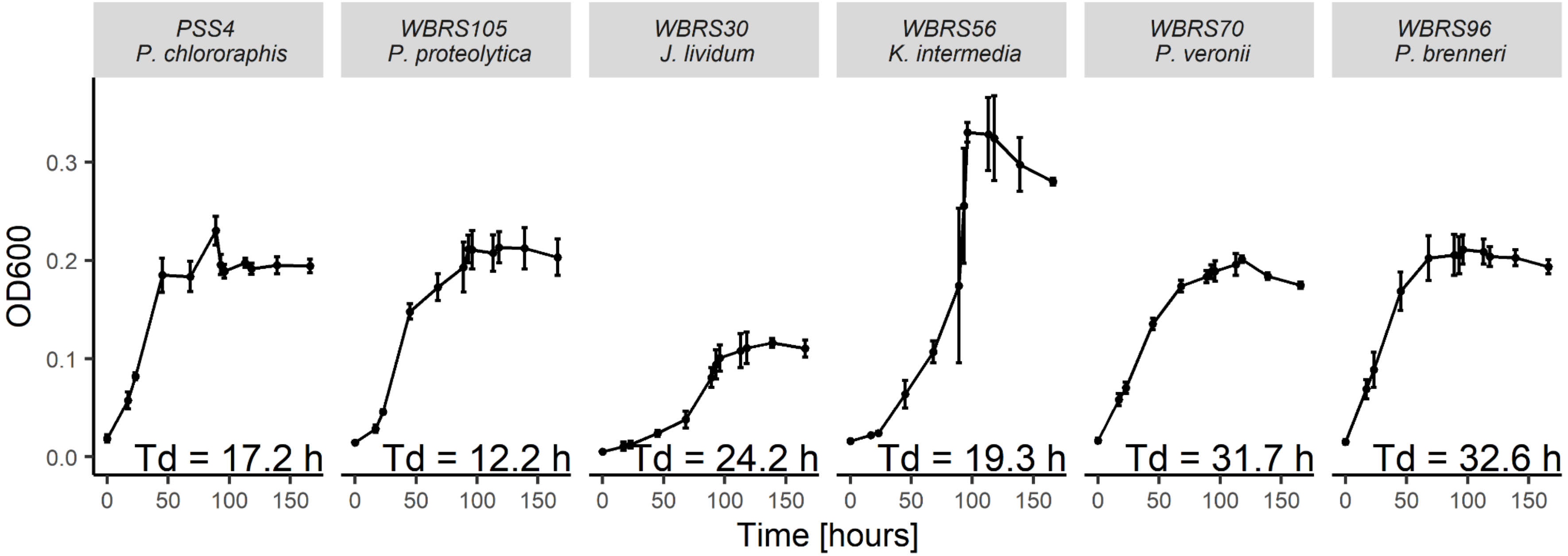

Table S1. Denitrification genes identified in the whole-genome sequenced bacterial strains. Components of genes coding for nitrate reductases (NAR/NAP), nitrite reductases (NIR), nitric oxide reductases (NOR) and nitrous oxide reductases (NOS) are shown by their codes in the protein families (Pfam) database.

Strain	Pfam reference[†] Species	NAR/NAP			NIR				NOR		NOS		
		PF14710	PF03892	PF02665	PF13442	PF00394	PF05940	PF03460	PF00115	PF00034	PF00116	PF18764	PF18793
WBRS105	*Pseudomonas proteolytica*	+	+	-	+	+	+	+	+	+	+	+	+
WBRS96	*Pseudomonas brenneri*	+	-	+	+	+	+	+	+	+	+	+	+
WBRS70	*Pseudomonas veronii*	+	+	+	+	+	+	+	+	+	+	+	+
PSS4	*Pseudomonas chlororaphis*	+	+	+	+	+	+	+	+	+	+	+	+
WBRS30	*Janthinobacterium lividum*	+	-	+	+	+	+	+	+	+	+	+	+
WBRS56	*Kluyvera intermedia*	+	-	+	+	+	+	+	+	+	+	+	+

[†] PF14710, respiratory nitrate reductase alpha N-terminal; PF03892, nitrate reductase cytochrome c-type subunit (*NapB*); PF02665, nitrate reductase gamma subunit; PF13442, cytochrome C oxidase, cbb3-type, subunit III; PF00394, copper-containing nitrite reductase (*nirK*); PF05940, protein (*NnrS*); PF03460, nitrite/sulfite reductase ferredoxin-like half domain; PF00115, main subunit of cytochrome C oxidase; PF00034, COX1; PF00116, cytochrome c oxidase subunit II (COX2); PF18764, nitrous oxide reductase propeller repeat; PF18793, nitrous oxide reductase propeller repeat 2.

Table S2. Identification of genes related to wood degradation found in the genomes of the two strains *Pseudomonas proteolytica* WBRS105 and *P. chlororaphis* PSS4. The '+' sign means that the protein families database (Pfam) reference was detected in the genome and the '-' sign means that it was not. KEGG, Kyoto Encyclopedia of Genes and Genomes.

Function	Product	KEGG reference	Pfam reference	Strain	
				WBRS105	PSS4
Cellulose degradation	4-alpha-glucanotransferase	EC 2.4.1.25	PF02446	+	+
	1,3-beta-glucanase	EC 3.2.1.39	PF16483	-	-
	alpha-glucosidase	EC 3.2.1	GH97_N	-	-
	6-phospho-beta-glucosidase	EC 3.2.1.86	P46320	-	-
	endocellulase	EC 3.2.1.4	PF01270	-	-
	exocellulase	EC 3.2.1.176, EC 3.2.1.91, EC 3.2.1.74	PF02011	-	-
	β-glucosidases	EC 3.2.1.21	PF12215	-	-
Xylan degradation	1,4-beta-xylanase	EC 3.2.1.8	PF00457	-	-
Starch/glycogen degradation	alpha-amylase	EC 3.2.1.1	PF00128	+	+
	glucoamylase	EC 3.2.1.3	PF10091	-	-
Lignin degradation	Laccases	EC 1.10.3.2	PF02578	+	+
	Peroxydases	EC 1.11.1.26	PF00141	+	-
Hemicellulose degradation	xyloglucanases	EC 3.2.1.151	PF06955	-	-
	endoxylanases	EC 3.2.1.8	PF00457	-	-
	xylosidases	EC 3.2.1.37	PF03512	-	-
	mannosidases	EC 3.2.1.25	PF09261	-	-
	fucosidases	EC 3.2.1.63	PF16757	-	-
	arabinofuranosidases	EC 3.2.1.55	PF06964	-	-
	glucuronidases	EC 3.2.1.31	PF03648	-	-
	glycosidases	EC 3.2.1.21	PF02449	+	-
	xylan esterases	EC 3.1.1.72	PF05448	-	-
	ferulic acid esterase	EC 3.1.1.73	PF01764	+	+
	lignin peroxidases	EC 1.11.1.14	PF00141	+	-
	manganese peroxidase	EC 1.11.1.13	PF00141	+	-
	versatile peroxidases	EC 1.11.1.16	PF04261	+	+
	pectin methyl esterases	EC 3.1.1.11	PF01095	-	-
	exopolygalacturonases	EC 3.2.1.	P49063	-	-
	pectate lyases and oligouronide lyases	EC 4.2.2.	PF00544	-	-

Table S3. European Nucleotide Archive accession numbers for microbiomes and isolates sequences.

Name	Sample	Accession	Type
Control_Ini	ERS7641076	ERR6800859	Microbiome
Control_Ini	ERS7641077	ERR6800884	Microbiome
Control_Ini	ERS7641078	ERR6800897	Microbiome
Control_Fin_5C	ERS7641079	ERR6800927	Microbiome
Control_Fin_5C	ERS7641080	ERR6800930	Microbiome
Control_Fin_10C	ERS7641081	ERR6800910	Microbiome
Control_Fin_10C	ERS7641082	ERR6800913	Microbiome
Control_Fin_10C	ERS7641083	ERR6800916	Microbiome
Bio_WBRS105_5C	ERS7641084	ERR6800932	Microbiome
Bio_WBRS105_5C	ERS7641085	ERR6800934	Microbiome
Bio_WBRS105_5C	ERS7641086	ERR6800936	Microbiome
Bio_PSS4_5C	ERS7641087	ERR6800939	Microbiome
Bio_PSS4_5C	ERS7641088	ERR6801482	Microbiome
Bio_PSS4_5C	ERS7641089	ERR6801484	Microbiome
Bio_WBRS105_10C	ERS7641090	ERR6800874	Microbiome
Bio_WBRS105_10C	ERS7641091	ERR6800901	Microbiome
Bio_WBRS105_10C	ERS7641092	ERR6800907	Microbiome
Bio_PSS4_10C	ERS7641093	ERR6800919	Microbiome
Bio_PSS4_10C	ERS7641094	ERR6800921	Microbiome
Bio_PSS4_10C	ERS7641095	ERR6800925	Microbiome
WBRS105	ERS7641070	ERR6800832	Isolate
WBRS70	ERS7641072	ERR6800834	Isolate
WBRS56	ERS7641074	ERR6800835	Isolate
WBRS96	ERS7641071	ERR6800837	Isolate
WBRS30	ERS7641073	ERR6800833	Isolate
PSS4	ERS7641075	ERR6800838	Isolate

Table S4. PCR2 primers for analysis of the development of the microbiome composition in woodchip enrichments at 5 and 10^{o}C with and without bioaugmentation (first bioaugmentation assay). Highlighted in yellow the linker sequences, in blue the barcode sequences and in green the primer sequences.

Primer ID	Full Primer sequence
P2F1	AATGATACGGCGACCACCGAGATCTACACAACGTTAGACACTCTTTCCCTACACGACG
P2F2	AATGATACGGCGACCACCGAGATCTACACCATTCTAAACACTCTTTCCCTACACGACG
P2F3	AATGATACGGCGACCACCGAGATCTACACGCTCTACCACACTCTTTCCCTACACGACG
P2F4	AATGATACGGCGACCACCGAGATCTACACTGGAGGCCACACTCTTTCCCTACACGACG
P2F5	AATGATACGGCGACCACCGAGATCTACACAGAAGCGGACACTCTTTCCCTACACGACG
P2F6	AATGATACGGCGACCACCGAGATCTACACCCGGACTGACACTCTTTCCCTACACGACG
P2F7	AATGATACGGCGACCACCGAGATCTACACGTCTAACCACACTCTTTCCCTACACGACG
P2F8	AATGATACGGCGACCACCGAGATCTACACTTACCGGTACACTCTTTCCCTACACGACG
P2F09	AATGATACGGCGACCACCGAGATCTACACAATAATGCACACTCTTTCCCTACACGACG
P2F10	AATGATACGGCGACCACCGAGATCTACACACCGTCCAACACTCTTTCCCTACACGACG
P2F11	AATGATACGGCGACCACCGAGATCTACACCAGATTCCACACTCTTTCCCTACACGACG
P2F12	AATGATACGGCGACCACCGAGATCTACACCGCTCAATACACTCTTTCCCTACACGACG
P2F13	AATGATACGGCGACCACCGAGATCTACACGCAGCTTGACACTCTTTCCCTACACGACG
P2F14	AATGATACGGCGACCACCGAGATCTACACGGTCAAGTACACTCTTTCCCTACACGACG
P2F15	AATGATACGGCGACCACCGAGATCTACACTTATGAAGACACTCTTTCCCTACACGACG
P2F16	AATGATACGGCGACCACCGAGATCTACACTTGCGTCAACACTCTTTCCCTACACGACG
P2R1	CAAGCAGAAGACGGCATACGAGATCGTTGGTTGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT
P2R2	CAAGCAGAAGACGGCATACGAGATGTCCGTTGGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT
P2R3	CAAGCAGAAGACGGCATACGAGATCAAGCTGCGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT
P2R4	CAAGCAGAAGACGGCATACGAGATGCATCCGAGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT
P2R5	CAAGCAGAAGACGGCATACGAGATGTTCAATTGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT
P2R6	CAAGCAGAAGACGGCATACGAGATACCTTGCGGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT
P2R7	CAAGCAGAAGACGGCATACGAGATTACGAACCGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT
P2R8	CAAGCAGAAGACGGCATACGAGATTGACGCAAGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT
P2R9	CAAGCAGAAGACGGCATACGAGATGCGATCGTGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT
P2R10	CAAGCAGAAGACGGCATACGAGATCTGATGCGGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT
P2R11	CAAGCAGAAGACGGCATACGAGATAGGTCTACGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT
P2R12	CAAGCAGAAGACGGCATACGAGATCATGCCAAGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT
P2R13	CAAGCAGAAGACGGCATACGAGATAACGCATCGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT
P2R14	CAAGCAGAAGACGGCATACGAGATAATAATGCGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT
P2R15	CAAGCAGAAGACGGCATACGAGATACGATCGCGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT
P2R16	CAAGCAGAAGACGGCATACGAGATATGGCCATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT
P2R17	CAAGCAGAAGACGGCATACGAGATCAAGTCAAGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT
P2R18	CAAGCAGAAGACGGCATACGAGATCTATCTCGGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT
P2R19	CAAGCAGAAGACGGCATACGAGATGCGAGTTCGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT
P2R20	CAAGCAGAAGACGGCATACGAGATGGACGTAGGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT
P2R21	CAAGCAGAAGACGGCATACGAGATGGCGAATGGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT
P2R22	CAAGCAGAAGACGGCATACGAGATGGTCAAGTGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT
P2R23	CAAGCAGAAGACGGCATACGAGATTCTATGACGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT
P2R24	CAAGCAGAAGACGGCATACGAGATTTCTGGCTGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT

Table S5. List of bacterial isolates obtained from wetland soil and woodchip bioreactor samples. Strains are referred to as "sp." when we were not able to find a match to a type strain with a similarity above 98.7% on the 16S rRNA gene. NCBI, National Center for Biotechnology Information.

Code	**Scientific Name (NCBI)**	**Source**
PSS1	*Aeromonas molluscorum*	Wetland soil
PSS2	*Klebsiella aerogenes*	Wetland soil
PSS3	*Lelliottia amnigena*	Wetland soil
PSS4	*Pseudomonas chlororaphis* subsp. *aurantiaca*	Wetland soil
PSS5	*Pseudomonas chlororaphis* subsp. *aurantiaca*	Wetland soil
PSS6	*Pseudomonas veronii*	Wetland soil
PSS7	*Pseudomonas veronii*	Wetland soil
PSS8	*Pseudomonas veronii*	Wetland soil
PSS9	*Pseudomonas veronii*	Wetland soil
PSS10	*Pseudomonas veronii*	Wetland soil
WBRS1	*Aeromonas bestiarum*	Woodchip bioreactor
WBRS2	*Aeromonas hydrophila*	Woodchip bioreactor
WBRS3	*Aeromonas salmonicida*	Woodchip bioreactor
WBRS4	*Aeromonas salmonicida*	Woodchip bioreactor
WBRS5	*Aeromonas salmonicida* subsp. *pectinolytica*	Woodchip bioreactor
WBRS6	*Aeromonas salmonicida* subsp. *pectinolytica*	Woodchip bioreactor
WBRS7	*Aeromonas salmonicida* subsp. *pectinolytica*	Woodchip bioreactor
WBRS8	*Aeromonas salmonicida* subsp. *salmonicida*	Woodchip bioreactor
WBRS9	*Aeromonas* sp.	Woodchip bioreactor
WBRS10	*Arcobacter venerupis*	Woodchip bioreactor
WBRS11	*Bacillus thuringiensis*	Woodchip bioreactor
WBRS12	*Bacillus thuringiensis*	Woodchip bioreactor
WBRS13	*Burkholderia sp.*	Woodchip bioreactor
WBRS14	*Buttiauxella gaviniae*	Woodchip bioreactor
WBRS15	*Buttiauxella gaviniae*	Woodchip bioreactor
WBRS16	*Buttiauxella gaviniae*	Woodchip bioreactor
WBRS17	*Buttiauxella izardii*	Woodchip bioreactor
WBRS18	*Buttiauxella izardii*	Woodchip bioreactor
WBRS19	*Carnobacterium maltaromaticum*	Woodchip bioreactor
WBRS20	*Carnobacterium maltaromaticum*	Woodchip bioreactor
WBRS21	*Carnobacterium maltaromaticum*	Woodchip bioreactor
WBRS22	*Carnobacterium maltaromaticum*	Woodchip bioreactor
WBRS23	*Chryseobacterium piscium*	Woodchip bioreactor
WBRS24	*Citrobacter freundii*	Woodchip bioreactor
WBRS25	*Citrobacter freundii*	Woodchip bioreactor
WBRS26	*Dyella japonica*	Woodchip bioreactor
WBRS27	*Dyella japonica*	Woodchip bioreactor

WBRS28	*Flavobacterium* sp.	Woodchip bioreactor
WBRS29	*Humibacter* sp.	Woodchip bioreactor
WBRS30	*Janthinobacterium lividum*	Woodchip bioreactor
WBRS31	*Janthinobacterium* sp.	Woodchip bioreactor
WBRS32	*Klebsiella aerogenes*	Woodchip bioreactor
WBRS33	*Klebsiella aerogenes*	Woodchip bioreactor
WBRS34	*Klebsiella aerogenes*	Woodchip bioreactor
WBRS35	*Klebsiella aerogenes*	Woodchip bioreactor
WBRS36	*Klebsiella aerogenes*	Woodchip bioreactor
WBRS37	*Klebsiella aerogenes*	Woodchip bioreactor
WBRS38	*Klebsiella aerogenes*	Woodchip bioreactor
WBRS39	*Klebsiella aerogenes*	Woodchip bioreactor
WBRS40	*Kluyvera cryocrescens*	Woodchip bioreactor
WBRS41	*Kluyvera intermedia*	Woodchip bioreactor
WBRS42	*Kluyvera intermedia*	Woodchip bioreactor
WBRS43	*Kluyvera intermedia*	Woodchip bioreactor
WBRS44	*Kluyvera intermedia*	Woodchip bioreactor
WBRS45	*Kluyvera intermedia*	Woodchip bioreactor
WBRS46	*Kluyvera intermedia*	Woodchip bioreactor
WBRS47	*Kluyvera intermedia*	Woodchip bioreactor
WBRS48	*Kluyvera intermedia*	Woodchip bioreactor
WBRS49	*Lelliottia amnigena*	Woodchip bioreactor
WBRS50	*Lelliottia amnigena*	Woodchip bioreactor
WBRS51	*Lelliottia amnigena*	Woodchip bioreactor
WBRS52	*Luteibacter yeojuensis*	Woodchip bioreactor
WBRS53	*Macellibacteroides* sp.	Woodchip bioreactor
WBRS54	*Massilia* sp.	Woodchip bioreactor
WBRS55	*Massilia* sp.	Woodchip bioreactor
WBRS56	*Kluyvera intermedia*	Woodchip bioreactor
WBRS57	*Morganella*	Woodchip bioreactor
WBRS58	*Morganella psychrotolerans*	Woodchip bioreactor
WBRS59	*Mucilaginibacter* sp.	Woodchip bioreactor
WBRS60	*Mucilaginibacter* sp.	Woodchip bioreactor
WBRS61	*Pelomonas* sp.	Woodchip bioreactor
WBRS62	*Polaromonas ginsengisoli*	Woodchip bioreactor
WBRS63	*Pseudomonas baetica*	Woodchip bioreactor
WBRS64	*Pseudomonas baetica*	Woodchip bioreactor
WBRS65	*Pseudomonas baetica*	Woodchip bioreactor
WBRS66	*Pseudomonas baetica*	Woodchip bioreactor
WBRS67	*Pseudomonas baetica*	Woodchip bioreactor
WBRS68	*Pseudomonas baetica*	Woodchip bioreactor
WBRS69	*Pseudomonas cedrina* subsp. *fulgida*	Woodchip bioreactor
WBRS70	*Pseudomonas veronii*	Woodchip bioreactor
WBRS71	*Pseudomonas fluorescens*	Woodchip bioreactor

WBRS72	*Pseudomonas fluorescens*	Woodchip bioreactor
WBRS73	*Pseudomonas fluorescens*	Woodchip bioreactor
WBRS74	*Pseudomonas gessardii*	Woodchip bioreactor
WBRS75	*Pseudomonas gessardii*	Woodchip bioreactor
WBRS76	*Pseudomonas gessardii*	Woodchip bioreactor
WBRS77	*Pseudomonas gessardii*	Woodchip bioreactor
WBRS78	*Pseudomonas jessenii*	Woodchip bioreactor
WBRS79	*Pseudomonas libanensis*	Woodchip bioreactor
WBRS80	*Pseudomonas mandelii*	Woodchip bioreactor
WBRS81	*Pseudomonas migulae*	Woodchip bioreactor
WBRS82	*Pseudomonas migulae*	Woodchip bioreactor
WBRS83	*Pseudomonas migulae*	Woodchip bioreactor
WBRS84	*Pseudomonas migulae*	Woodchip bioreactor
WBRS85	*Pseudomonas migulae*	Woodchip bioreactor
WBRS86	*Pseudomonas migulae*	Woodchip bioreactor
WBRS87	*Pseudomonas migulae*	Woodchip bioreactor
WBRS88	*Pseudomonas migulae*	Woodchip bioreactor
WBRS89	*Pseudomonas migulae*	Woodchip bioreactor
WBRS90	*Pseudomonas migulae*	Woodchip bioreactor
WBRS91	*Pseudomonas migulae*	Woodchip bioreactor
WBRS92	*Pseudomonas migulae*	Woodchip bioreactor
WBRS93	*Pseudomonas migulae*	Woodchip bioreactor
WBRS94	*Pseudomonas migulae*	Woodchip bioreactor
WBRS95	*Pseudomonas migulae*	Woodchip bioreactor
WBRS96	*Pseudomonas brenneri*	Woodchip bioreactor
WBRS97	*Pseudomonas proteolytica*	Woodchip bioreactor
WBRS98	*Pseudomonas proteolytica*	Woodchip bioreactor
WBRS99	*Pseudomonas proteolytica*	Woodchip bioreactor
WBRS100	*Pseudomonas proteolytica*	Woodchip bioreactor
WBRS101	*Pseudomonas proteolytica*	Woodchip bioreactor
WBRS102	*Pseudomonas proteolytica*	Woodchip bioreactor
WBRS103	*Pseudomonas vancouverensis*	Woodchip bioreactor
WBRS104	*Pseudomonas vancouverensis*	Woodchip bioreactor
WBRS105	*Pseudomonas proteolytica*	Woodchip bioreactor
WBRS106	*Pseudomonas veronii*	Woodchip bioreactor
WBRS107	*Pseudomonas veronii*	Woodchip bioreactor
WBRS108	*Pseudomonas veronii*	Woodchip bioreactor
WBRS109	*Pseudomonas veronii*	Woodchip bioreactor
WBRS110	*Pseudomonas veronii*	Woodchip bioreactor
WBRS111	*Pseudomonas veronii*	Woodchip bioreactor
WBRS112	*Pseudomonas veronii*	Woodchip bioreactor
WBRS113	*Pseudomonas veronii*	Woodchip bioreactor
WBRS114	*Pseudomonas veronii*	Woodchip bioreactor
WBRS115	*Rhodopseudomonas palustris*	Woodchip bioreactor

WBRS116	*Shewanella putrefaciens*	Woodchip bioreactor
WBRS117	*Shewanella putrefaciens*	Woodchip bioreactor
WBRS118	*Staphylococcus pasteuri*	Woodchip bioreactor
WBRS119	*Staphylococcus pasteuri*	Woodchip bioreactor
WBRS120	*Staphylococcus pasteuri*	Woodchip bioreactor
WBRS121	*Staphylococcus pasteuri*	Woodchip bioreactor
WBRS122	*Staphylococcus pasteuri*	Woodchip bioreactor
WBRS123	*Streptomyces thermoviolaceus*	Woodchip bioreactor
WBRS124	*Variovorax ginsengisoli*	Woodchip bioreactor

Table S6. List of identified OTUs (*n* = 113) during the microbiome analysis of woodchip enrichment cultures used for bioaugmentation experiments (first bioaugmentation assay). In the OTU designation, “g” stands for genus, “f” stands for family and “k” stands for kingdom.

Names
OTU1_g__Pusillimonas
OTU2_g__Pusillimonas
OTU3_g__Arcobacter
OTU4_g__Pseudomonas
OTU5_g__Pseudomonas
OTU6_g__Pseudomonas
OTU7_g__Pseudomonas
OTU8_g__Herminiimonas
OTU9_g__Pseudomonas
OTU10_g__Microvirgula
OTU11_g__Citrobacter
OTU12_g__Ochrobactrum
OTU13_g__Aeromonas
OTU14_g__Kluyvera
OTU15_g__Aeromonas
OTU16_g__Bacillus
OTU17_g__Pseudomonas
OTU18_g__Listeria
OTU19_g__Pseudomonas
OTU20_g__Staphylococcus
OTU21_f__Aeromonadaceae
OTU22_f__Oxalobacteraceae
OTU23_g__Lactobacillus
OTU24_g__Enterococcus
OTU25_g__Chryseobacterium
OTU26_g__Enterobacter
OTU27_g__Pseudomonas
OTU28_g__Salmonella
OTU29_g__Escherichia
OTU30_f__Aeromonadaceae
OTU31_g__Aeromonas
OTU32_g__Kluyvera
OTU33_g__Shewanella
OTU34_g__Kluyvera
OTU35_g__Morganella
OTU36_g__Ochrobactrum
OTU37_g__Citrobacter
OTU38_g__Pseudomonas

OTU39_ g__Shewanella
OTU40_ g__Pseudomonas
OTU41_ g__Kluyvera
OTU42_ f__Aeromonadaceae
OTU43_ g__Acidovorax
OTU44_ g__Enterobacter
OTU45_ g__Staphylococcus
OTU46_ g__Acidovorax
OTU47_ f__Aeromonadaceae
OTU48_ g__Dysgonomonas
OTU49_ g__Aeromonas
OTU50_ g__Pseudomonas
OTU51_ g__Carnobacterium
OTU52_ g__Lactobacillus
OTU53_ g__Pseudomonas
OTU54_ g__Aeromonas
OTU55_ g__Simplicispira
OTU56_ g__Escherichia
OTU57_ g__Dysgonomonas
OTU58_ g__Acidovorax
OTU59_ g__Salmonella
OTU60_ g__Aeromonas
OTU61_ g__Enterobacter
OTU62_ g__Enterobacter
OTU63_ g__Aeromonas
OTU64_ g__Rahnella
OTU65_ f__Aeromonadaceae
OTU66_ g__Rahnella
OTU67_ g__Pseudomonas
OTU68_ g__Aeromonas
OTU69_ g__Dysgonomonas
OTU70_ g__Chryseobacterium
OTU72_ g__Providencia
OTU73_ g__Enterobacter
OTU74_ f__Cellulomonadaceae
OTU75_ g__Gluconacetobacter
OTU76_ g__Yersinia
OTU77_ g__Gluconacetobacter
OTU79_ g__Tepidimonas
OTU81_ g__Simplicispira
OTU82_ g__Providencia
OTU83_ g__Pseudomonas
OTU84_ g__Thermosphaera
OTU85_ g__Ochrobactrum

OTU86_ g__Yersinia
OTU87_ g__Pseudomonas
OTU89_ g__Vagococcus
OTU90_ g__Dysgonomonas
OTU92_ f__Aeromonadaceae
OTU93_ g__Clostridium
OTU95_ g__Simplicispira
OTU96_ g__Pyrococcus
OTU97_ g__Acidovorax
OTU98_ g__Simplicispira
OTU99_ f__Alcaligenaceae
OTU100_ g__Paenibacillus
OTU101_ g__Chryseobacterium
OTU102_ g__Clostridium
OTU103_ g__Caldiarchaeum
OTU104_ g__Cohnella
OTU105_ g__Enterobacter
OTU106_ g__Shewanella
OTU107_ g__Glaucocystis
OTU108_ g__Paenibacillus
OTU109_ g__Providencia
OTU110_ g__Planomonospora
OTU111_ g__Clostridium
OTU112_ g__Proteiniphilum
OTU113_k__Bacteria
OTU116_ g__Pyropia
OTU117_ g__Chryseobacterium
OTU118_ f__Simkaniaceae
OTU119_ g__Halobacteriaceae
OTU120_ g__Porphyra
OTU121_ g__Pseudomonas

Table S7. *P* values for pairwise ADONIS test of similarity in microbiome composition after growth of enrichment cultures without (control) or with bioaugmentation using the strains *Pseudomonas proteolytica* WBRS105 and *P. chlororaphis* PSS4. The pairwise ADONIS test was conducted with the whole data set and followed by tests with subsets of the dataset as related to the incubation temperatures of 5 and 10°C.

Data	Pairs		F.Model	R^2	p.value	p.adjusted
All	Control	WBRS105	5.92	0.33	0.007	0.021
	Control	PSS4	6.64	0.36	0.002	0.006
	WBRS105	PSS4	5.79	0.37	0.020	0.060
5°C	Control	WBRS105	32.46	0.84	0.018	0.054
	Control	PSS4	20.29	0.77	0.018	0.054
	WBRS105	PSS4	28.91	0.88	0.100	0.300
10°C	WBRS105	Control	3.60	0.47	0.100	0.300
	WBRS105	PSS4	8.79	0.69	0.100	0.300
	Control	PSS4	25.31	0.86	0.100	0.300