

Supplementary Material

The pangenome of Gram-negative environmental bacteria hides a promising biotechnological potential.

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Figures

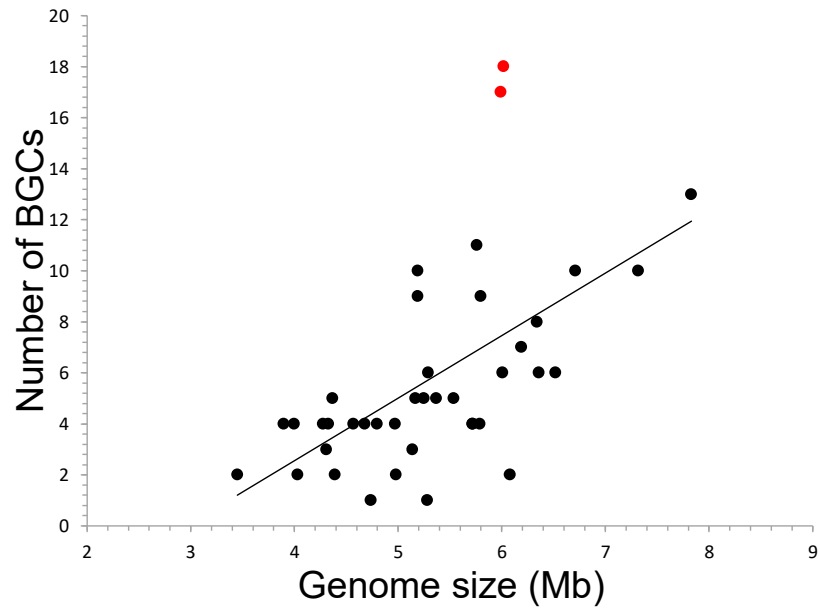


Figure S1: Relation between genome size of *Pedobacter* spp. and the number of BGCs found in each genome. The red points represent *P. cryoconitis* and *P. lusitanus* that are the strains with the highest number of BGCs.

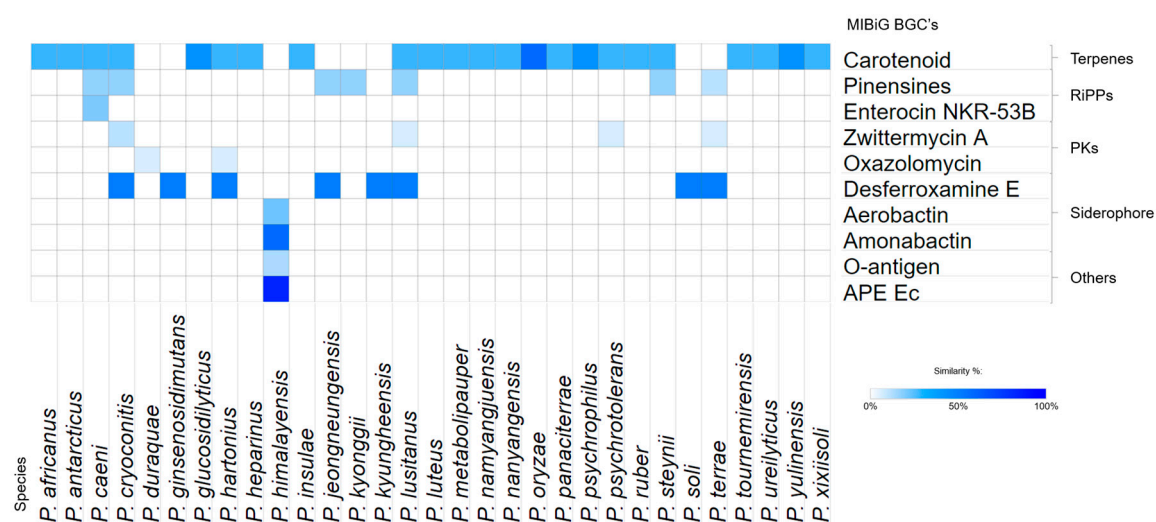


Figure S2: Heatmap of sequence similarity BGCs from *Pedobacter* genus. Columns represent the 31 *Pedobacter* species under study and the rows the MiBiG similarity hits and BGCs classes. The degree of similarity is represented by gradient color and was obtained from antiSMASH (Table S1).

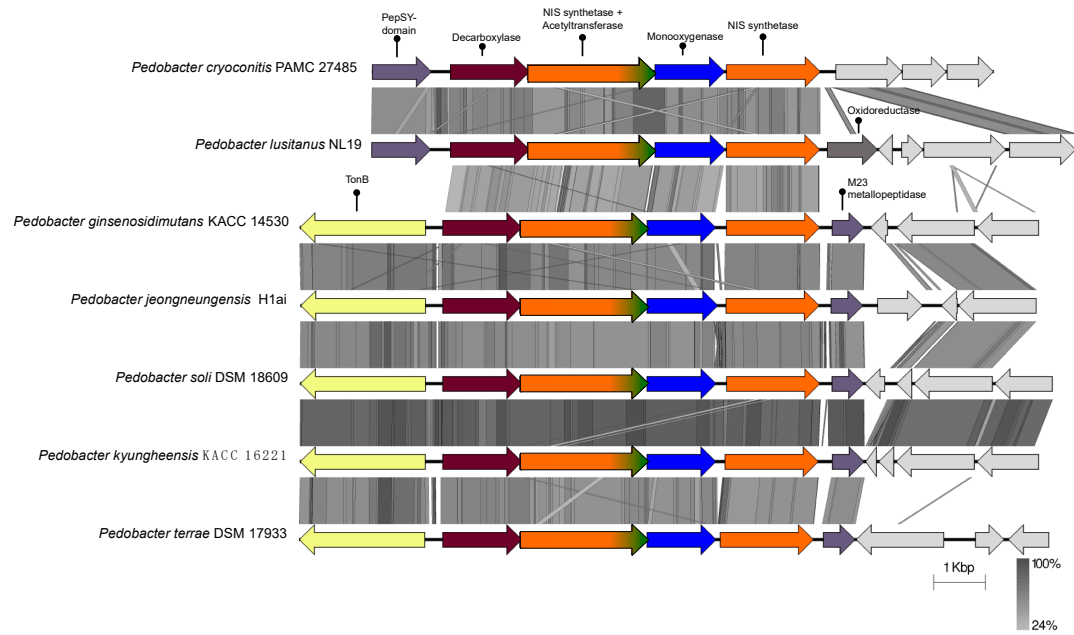


Figure S3: Genetic comparison between seven siderophore's gene clusters encoding the NIS synthase C-terminally fused to an acetyltransferase together with a decarboxylase and a monooxygenase identified in this study in *P. cryoconitis*, *P. lusitanus* and other *Pedobacter* species. Grey shadowing indicates regions of shared similarity according to the legend.

Table S1: Biosynthetic gene cluster identified in the *Pedobacter* species genome by antiSMASH and BiG-SCAPE tools. GCF: gene cluster family. GS: Genome size. GCF singleton and in network were written in black and red, respectively.

Clusters	BGC type	BGC class	GCF	Most similar known cluster	MIBiG BGC-ID	GS (Mb)
<i>P. africanus</i> DSM 12126 ^T						5.72287
Cluster 1	Terpene	Terpene	FAM00122	Carotenoid_biosynthetic_gene_cluster (28% of genes show similarity)	BGC0000650_c1	
Cluster 2	Bacteriocin	RiPPs	FAM00123	-	-	
Cluster 3	T3pks	PK	FAM00124	-	-	
Cluster 4	NRPS-T1pks	Hybrid	FAM00125	-	-	
<i>P. agri</i> PB92 ^T						5.14155
Cluster 1	Terpene	Terpene	FAM00030	-	-	
Cluster 2	Bacteriocin	RiPPs	FAM00184	-	-	
Cluster 3	T3pks	PK	FAM00185	-	-	
<i>P. antarcticus</i> 4BY ^T						4.56632
Cluster 1	T3pks	PK	FAM00009	-	-	
Cluster 2	NRPS-T1pks	Hybrid	FAM00010	-	-	
Cluster 3	Terpene	Terpene	FAM00011	-	-	
Cluster 4	Terpene	Terpene	FAM00012	Carotenoid_biosynthetic_gene_cluster (28% of genes show similarity)	BGC0000650_c1	
<i>P. borealis</i> DSM 19626 ^T						5.54492
Cluster 1	T3pks-Bacteriocin	Hybrid	FAM00128	-	-	
Cluster 2	Lanthipeptide	RiPPs	FAM00129	-	-	
Cluster 3	Bacteriocin	RiPPs	FAM00130	-	-	
Cluster 4	Linaridin	RiPPs	FAM00070	-	-	
Cluster 5	Terpene	Terpene	FAM00030	-	-	
<i>P. caeni</i> DSM 16990 ^T						7.82878
Cluster 1	Bacteriocin	RiPPs	FAM00107	-	-	
Cluster 2	Terpene	Terpene	FAM00108	-	-	
Cluster 3	Terpene	Terpene	FAM00109	Carotenoid_biosynthetic_gene_cluster (28% of genes show similarity)	BGC0000650_c	
Cluster 4	Resorcinol	Others	FAM00110	-	-	
Cluster 5	NRPS-T1pks	Hybrid	FAM00111	-	-	
Cluster 6	T1pks-hgIE-KS	Hybrid RiPPs	FAM00112	-	-	

Clusters	BGC type	BGC class	GCF	Most similar known cluster	MIBiG BGC-ID	GS (Mb)
Cluster 7	Lanthipeptide		FAM00113			
Cluster 8	Bacteriocin	RiPPs	FAM00114	-	-	
Cluster 9	T3pks	PK	FAM00115	-	-	
Cluster 10	Lanthipeptide	RiPPs	FAM00054	Pinensins_biosynthetic_gene_cluster (17% of genes show similarity)	BGC0001392_c	
Cluster 11	Terpene	Terpene	FAM00117	-	-	
Cluster 12	NRPS-like	Others	FAM00118	Enterocin_NKR-53B_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0001291_c	
Cluster 13	Bacteriocin	RiPPs	FAM00119	-	-	
<i>P. cryoconitis</i> PAMC 27485 ^T						6.01539
Cluster 1	T1pks-hgIE-KS	Hybrid	FAM00037	-	-	
Cluster 2	NRPS-T1pks	Hybrid	FAM00038	-	-	
Cluster 3	Siderophore	Siderophore	FAM00039	Desferrioxamine_E_biosynthetic_gene_cluster (50% of genes show similarity)	BGC0001572_c1	
Cluster 4	NRPS-T1pks	Hybrid	FAM00040	Pinensins_biosynthetic_gene_cluster (17% of genes show similarity)	BGC0001392_c1	
Cluster 5	Terpene	Terpene	FAM00041	-	-	
Cluster 6	Lanthipeptide	RiPPs	FAM00042	-	-	
Cluster 7	Linaridin	RiPPs	FAM00043	-	-	
Cluster 8	Terpene	Terpene	FAM00044	Carotenoid_biosynthetic_gene_cluster (28% of genes show similarity)	BGC0000650_c1	
Cluster 9	NRPS-like	Others	FAM00045	-	-	
Cluster 10	NRPS	NRP	FAM00046	-	-	
Cluster 11	NRPS	NRP	FAM00047	-	-	
Cluster 12	T3pks	PK	FAM00048	-	-	
Cluster 13	Lanthipeptide-T1pks-NRPS	Hybrid	FAM00049	Zwittermycin_A_biosynthetic_gene_cluster (11% of genes show similarity)	BGC0001059_c1	
Cluster 14	Siderophore	Siderophore	FAM00050	-	-	
Cluster 15	NRPS	NRP	FAM00051	-	-	
Cluster 16	Siderophore	Siderophore	FAM00147	-	-	
Cluster 17	Lanthipeptide	RiPPs	FAM00053	-	-	
Cluster 18	Lanthipeptide	RiPPs	FAM00054	Pinensins_biosynthetic_gene_cluster (17% of genes show similarity)	BGC0001392_c1	
<i>P. duraquae</i> DSM 10034 ^T						5.28826
Cluster 1	NRPS-like	Others	FAM00217	-	-	
Cluster 2	Terpene	Terpene	FAM00218	-	-	

Clusters	BGC type	BGC class	GCF	Most similar known cluster	MIBiG BGC-ID	GS (Mb)
Cluster 3	T3pks	PK	FAM00219	-	-	BGC0001106_c1
Cluster 4	Bacteriocin	RiPPs	FAM00220	-	-	
Cluster 5	Terpene	Terpene	FAM00221	-	-	
Cluster 6	NRPS-T1pks	Hybrid	FAM00222	Oxazolomycin_biosynthetic_gene_cluster (6% of genes show similarity)	-	
<i>P. ginsengisoli</i> T01R-27 ^T						5.37336
Cluster 1	Lanthipeptide	RiPPs	FAM00065	-	-	6.51755
Cluster 2	NRPS-T1pks	Hybrid	FAM00166	-	-	
Cluster 3	T3pks	PK	FAM00067	-	-	
Cluster 4	Bacteriocin	RiPPs	FAM00163	-	-	
Cluster 5	hglE-KS	Hybrid	FAM00069	-	-	
<i>P. ginsenosidimutans</i> KACC 14530 ^T						6.51755
Cluster 1	Bacteriocin	RiPPs	FAM00028	-	-	BGC0001572_c1
Cluster 2	Linaridin	RiPPs	FAM00070	-	-	
Cluster 3	T3pks-Bacteriocin	Hybrid	FAM00128	-	-	
Cluster 4	Siderophore	siderophore	FAM00029	Desferrioxamine_E_biosynthetic_gene_cluster (50% of genes show similarity)	-	
Cluster 5	T1pks-hglE-KS	Hybrid	FAM00207	-	-	
Cluster 6	Terpene	Terpene	FAM00030	-	-	
<i>P. glucosidilyticus</i> DD6b ^T						3.9019
Cluster 1	Arylpolyene	Others	FAM00133	-	-	BGC0000650_c1
Cluster 2	Terpene	Terpene	FAM00134	Carotenoid_biosynthetic_gene_cluster (42% of genes show similarity)	-	
Cluster 3	Terpene	Terpene	FAM00135	-	-	
Cluster 4	T3pks	PK	FAM00136	-	-	
<i>P. hartonius</i> DSM 19033 ^T						5.18872
Cluster 1	T3pks	PK	FAM00091	-	-	BGC0001106_c1
Cluster 2	NRPS-like	Others	FAM00092	Oxazolomycin_biosynthetic_gene_cluster (6% of genes show similarity)	-	
Cluster 3	Siderophore	siderophore	FAM00093	Desferrioxamine_E_biosynthetic_gene_cluster (50% of genes show similarity)	-	BGC0001572_c1
Cluster 4	Bacteriocin	RiPPs	FAM00094	-	-	-
Cluster 5	Terpene	Terpene	FAM00095	-	-	
Cluster 6	Lanthipeptide	RiPPs	FAM00096	-	-	

Clusters	BGC type	BGC class	GCF	Most similar known cluster	MIBiG BGC-ID	GS (Mb)
Cluster 7	Terpene	Terpene	FAM00097	-	-	
Cluster 8	NRPS-T1pks	Hybrid	FAM00038	-	-	
Cluster 9	T1pks- hglE-KS Oligosaccharide	Hybrid	FAM00099	-	-	
Cluster 10	Terpene	Terpene	FAM00100	Carotenoid_biosynthetic_gene_cluster (28% of genes show similarity)	BGC0000650_c1	
<i>P. heparinus</i> DSM 2366 ^T						5.16945
Cluster 1	Lanthipeptide	RiPPs	FAM00017	-	-	
Cluster 2	T3pks	PK	FAM00018	-	-	
Cluster 3	NRPS-T1pks	Hybrid	FAM00019	-	-	
Cluster 4	Terpene	Terpene	FAM00020	Carotenoid_biosynthetic_gene_cluster (28% of genes show similarity)	BGC0000650_c1	
Cluster 5	Bacteriocin	RiPPs	FAM00021	-	-	
<i>P. himalayensis</i> HHS 22 ^T						4.67912
Cluster 1	Thiopeptide	RiPPs	FAM00013	O-antigen_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000781_c1	
Cluster 2	NRPS	NRP	FAM00014	Amonabactin P750 biosynthetic_gene_cluster (57% of genes show similarity)	BGC0001502_c1	
Cluster 3	Aryl polyene	Others	FAM00015	APE_Ec_biosynthetic_gene_cluster (84% of genes show similarity)	BGC0000836_c1	
Cluster 4	Siderophore	siderophore	FAM00016	Aerobactin_biosynthetic_gene_cluster (22% of genes show similarity)	BGC0000939_c1	
<i>P. insulae</i> DSM 18684 ^T						4.388
Cluster 1	Terpene	Terpene	FAM00105	Carotenoid_biosynthetic_gene_cluster (28% of genes show similarity)	BGC0000650_c1	
Cluster 2	T3pks	PK	FAM00106	-	-	
<i>P. jejuensis</i> TNB23 ^T						4.79581
Cluster 1	T3pks	PK	FAM00196	-	-	
Cluster 2	NRPS	NRP	FAM00197	-	-	
Cluster 3	Terpene	Terpene	FAM00198	-	-	
Cluster 4	NRPS-T1pks	Hybrid	FAM00199	-	-	
<i>P. jeongneungensis</i> H1ai ^T						6.70808

Clusters	BGC type	BGC class	GCF	Most similar known cluster	MIBiG BGC-ID	GS (Mb)
Cluster 1	Lanthipeptide	RiPPs	FAM00027	-	-	BGC0001572_c1
Cluster 2	Bacteriocin	RiPPs	FAM00028	-	-	
Cluster 3	Siderophore	siderophore	FAM00029	Desferrioxamine_E_biosynthetic_gene_cluster (50% of genes show similarity)	-	
Cluster 4	Terpene	Terpene	FAM00030	-	-	BGC0001392_c1
Cluster 5	Lanthipeptide	RiPPs	FAM00031	Pinensins_biosynthetic_gene_cluster (17% of genes show similarity)	-	
Cluster 6	Bacteriocin	RiPPs	FAM00032	-	-	-
Cluster 7	T1pks-hgIE-KS	Hybrid	FAM00033	-	-	
Cluster 8	T3pks	PK	FAM00185	-	-	
Cluster 9	Linaridin	RiPPs	FAM00035	-	-	-
Cluster 10	Lanthipeptide	RiPPs	FAM00036	-	-	-
<i>P. Kyonggii</i> K-4-11-1 ^T					6.18618	
Cluster 1	Bacteriocin	RiPPs	FAM00028	-	-	BGC0001392_c1
Cluster 2	NRPS	NRP	FAM00202	-	-	
Cluster 3	T3pks	PK	FAM00203	-	-	
Cluster 4	Terpene	Terpene	FAM00030	-	-	Pinensins_biosynthetic_gene_cluster (17% of genes show similarity)
Cluster 5	Lanthipeptide	RiPPs	FAM00031	-	-	
Cluster 6	Linaridin	RiPPs	FAM00206	-	-	-
Cluster 7	T1pks-hgIE-KS	Hybrid	FAM00207	-	-	-
<i>P. kyungheensis</i> KACC 16221 ^T						6.35864
Cluster 1	Terpene	Terpene	FAM00137	-	-	BGC0001572_c1
Cluster 2	Terpene	Terpene	FAM00030	-	-	
Cluster 3	Siderophore	siderophore	FAM00029	Desferrioxamine_E_biosynthetic_gene_cluster (50% of genes show similarity)	-	
Cluster 4	Bacteriocin	RiPPs	FAM00184	-	-	-
Cluster 5	T1pks-hgIE-KS	Hybrid	FAM00207	-	-	
Cluster 6	Linaridin	RiPPs	FAM00070	-	-	-
<i>P. lusitanus</i> NL19 ^T						5.98819
Cluster 1	Siderophore	siderophore	FAM00143	Desferrioxamine_E_biosynthetic_gene_cluster (50% of genes show similarity)	BGC0001572_c1	
Cluster 2	NRPS-T1pks	Hybrid	FAM00038	-	-	
Cluster 3	T1pks-hgIE-KS	Hybrid	FAM00145	-	-	

Clusters	BGC type	BGC class	GCF	Most similar known cluster	MIBiG BGC-ID	GS (Mb)	
Cluster 4	NRPS-Terpene	Hybrid	FAM00146	Carotenoid_biosynthetic_gene_cluster (28% of genes show similarity)	BGC0000650_c1	4.02864	
Cluster 5	Siderophore	siderophore	FAM00147	-	-		
Cluster 6	T3pks	PK	FAM00048	-	-		
Cluster 7	Lanthipeptide	RiPPs	FAM00149	-	-		
Cluster 8	NRPS	NRP	FAM00150	-	-		
Cluster 9	Bacteriocin	RiPPs	FAM00151	-	-		
Cluster 10	NRPS	NRP	FAM00152	Pinensins_biosynthetic_gene_cluster (17% of genes show similarity)	BGC0001392_c1		
Cluster 11	NRPS	NRP	FAM00153	-	-		
Cluster 12	Lanthipeptide	RiPPs	FAM00154	-	-		
Cluster 13	Lanthipeptide	RiPPs	FAM00155	-	-		
Cluster 14	Linaridin	RiPPs	FAM00156	-	-		
Cluster 15	Lanthipeptide	RiPPs	FAM00054	Pinensins_biosynthetic_gene_cluster (17% of genes show similarity) (Caetano et al., 2020)	BGC0001392_c1		
Cluster 16	NRPS-like	Others	FAM00158	-	-		
Cluster 17	NRPS	NRP	FAM00159	Zwittermycin_A_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0001059_c1		
<i>P. luteus</i> DSM 22385 ^T							
Cluster 1	Terpene	Terpene	FAM00120	Carotenoid_biosynthetic_gene_cluster (28% of genes show similarity)	BGC0000650_c1		
Cluster 2	T3pks	PK	FAM00121	-	-		
<i>P. metabolipauper</i> DSM 19035 ^T					5.25114		
Cluster 1	Terpene	Terpene	FAM00223	-	-		
Cluster 2	Resorcinol	Others	FAM00224	-	-		
Cluster 3	Terpene	Terpene	FAM00225	Carotenoid_biosynthetic_gene_cluster (28% of genes show similarity)	BGC0000650_c1		
Cluster 4	Bacteriocin	RiPPs	FAM00184	-	-		
Cluster 5	T3pks	PK	FAM00227	-	-		
<i>P. namyangjuensis</i> 5G38 ^T						4.33013	
Cluster 1	NRPS-T1pks	Hybrid	FAM00192	-	-		
Cluster 2	Bacteriocin	RiPPs	FAM00184	-	-		
Cluster 3	Terpene	Terpene	FAM00194	Carotenoid_biosynthetic_gene_cluster (28% of genes show similarity)	BGC0000650_c1		

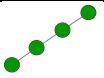















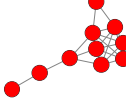
Clusters	BGC type	BGC class	GCF	Most similar known cluster	MIBiG BGC-ID	GS (Mb)
Cluster 4	T3pks	PK	FAM00195	-	-	
<i>P. nanyangensis</i> Q-4 ^T						
Cluster 1	Terpene	Terpene	FAM00191	Carotenoid_biosynthetic_gene_cluster (28% of genes show similarity)	BGC0000650_c1	4.73626
<i>P. nutrimenti</i> DSM 27372 ^T						5.71699
Cluster 1	T3pks	PK	FAM00187	-	-	
Cluster 2	NRPS-T1pks	Hybrid	FAM00188	-	-	
Cluster 3	Bacteriocin	RiPPs	FAM00189	-	-	
Cluster 4	Bacteriocin	RiPPs	FAM00190	-	-	
<i>P. nyackensis</i> DSM 19625 ^T						6.07711
Cluster 1	NRPS-like	Others	FAM00126	-	-	
Cluster 2	T3pks	PK	FAM00127	-	-	
<i>P. oryzae</i> DSM 19973 ^T						3.44577
Cluster 1	T3pks	PK	FAM00025	-	-	BGC0000650_c1
Cluster 2	Terpene	Terpene	FAM00026	Carotenoid_biosynthetic_gene_cluster (57% of genes show similarity)		
<i>P. panaciterrae</i> O48 ^T						6.3428
Cluster 1	Terpene	Terpene	FAM00160	Carotenoid_biosynthetic_gene_cluster (28% of genes show similarity)	BGC0000650_c1	
Cluster 2	T1pks-hgIE-KS	Hybrid	FAM00161	-	-	
Cluster 3	T1pks-hgIE-KS	Hybrid	FAM00161	-	-	
Cluster 4	Bacteriocin	RiPPs	FAM00163	-	-	
Cluster 5	NRPS-like	Others	FAM00164	-	-	
Cluster 6	T3pks	PK	FAM00067	-	-	
Cluster 7	NRPS-T1pks	Hybrid	FAM00166	-	-	
Cluster 8	NRPS	NRP	FAM00167	-	-	
<i>P. psychrophilus</i> CCM 8644 ^T						3.99914
Cluster 1	Terpene	Terpene	FAM00174	Carotenoid_biosynthetic_gene_cluster (42% of genes show similarity)	BGC0000650_c1	
Cluster 2	Resorcinol	Others	FAM00175	-	-	


Clusters	BGC type	BGC class	GCF	Most similar known cluster	MIBiG BGC-ID	GS (Mb)
Cluster 3	T3pks	PK	FAM00176	-	-	
Cluster 4	Terpene	Terpene	FAM00177	-	-	
<i>P. psychrotolerans</i> DSM 103236 ^T					5.19395	
Cluster 1	T3pks	PK	FAM00208	-	-	
Cluster 2	Terpene	Terpene	FAM00209	Carotenoid_biosynthetic_gene_cluster (28% of genes show similarity)	BGC0000650_c1	
Cluster 3	T1pks-hgIE-KS	Hybrid	FAM00210	-	-	
Cluster 4	NRPS	NRP	FAM00211	Zwittermycin_A_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0001059_c1	
Cluster 5	Siderophore	siderophore	FAM00212	-	-	
Cluster 6	Terpene	Terpene	FAM00213	-	-	
Cluster 7	NRPS	NRP	FAM00214	Zwittermycin_A_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0001059_c1	
Cluster 8	NRPS	NRP	FAM00215	-	-	
Cluster 9	NRPS-T1pks	Hybrid	FAM00216	-	-	
<i>P. rhizosphaerae</i> DSM 18610 ^T						5.7893
Cluster 1	Terpene	Terpene	FAM00101	-	-	
Cluster 2	Terpene	Terpene	FAM00102	-	-	
Cluster 3	T1pks-hgIE-KS	Hybrid	FAM00103	-	-	
Cluster 4	Bacteriocin	RiPPs	FAM00104	-	-	
<i>P. ruber</i> DSM 24536 ^T						4.27928
Cluster 1	T3pks	PK	FAM00087	-	-	
Cluster 2	Bacteriocin	RiPPs	FAM00088	-	-	
Cluster 3	Terpene	Terpene	FAM00120	Carotenoid_biosynthetic_gene_cluster (28% of genes show similarity)	BGC0000650_c1	
Cluster 4	NRPS-T1pks	Hybrid	FAM00090	-	-	
<i>P. steynii</i> D14 ^T						7.32118
Cluster 1	T3pks	PK	FAM00055	-	-	
Cluster 2	Lanthipeptide	RiPPs	FAM00054	Pinensins_biosynthetic_gene_cluster (17% of genes show similarity)	BGC0001392_c1	
Cluster 3	Bacteriocin	RiPPs	FAM00057	-	-	
Cluster 4	T1pks-hgIE-KS	Hybrid	FAM00058	-	-	
Cluster 5	NRPS-T1pks	Hybrid	FAM00059	-	-	
Cluster 6	Terpene	Terpene	FAM00060	-	-	

Clusters	BGC type	BGC class	GCF	Most similar known cluster	MIBiG BGC-ID	GS (Mb)
Cluster 7	Terpene	Terpene	FAM00061	Carotenoid_biosynthetic_gene_cluster (28% of genes show similarity)	BGC0000650_c1	6.00642
Cluster 8	Resorcinol	Others	FAM00062	-	-	
Cluster 9	NRPS	NRP	FAM00063	-	-	
Cluster 10	NRPS-T1pks	Hybrid	FAM00166	-	-	
<i>P. soli</i> DSM 18609 ^T						6.00642
Cluster 1	Linaridin	RiPPs	FAM00070	-	-	5.80383
Cluster 2	Terpene	Terpene	FAM00030	-	-	
Cluster 3	Bacteriocin	RiPPs	FAM00075	-	-	
Cluster 4	Siderophore	Siderophore	FAM00029	Desferrioxamine_E_biosynthetic_gene_cluster (50% of genes show similarity)	BGC0001572_c1	
Cluster 5	T1pks-hgIE-KS	Hybrid	FAM00207	-	-	5.80383
Cluster 6	Bacteriocin	RiPPs	FAM00028	-	-	
<i>P. suwonensis</i> DSM 18130 ^T						5.80383
Cluster 1	Lanthipeptide	RiPPs	FAM00000	-	-	5.7551
Cluster 2	T3pks	PK	FAM00185	-	-	
Cluster 3	Linaridin	RiPPs	FAM00002	-	-	
Cluster 4	NRPS	NRP	FAM00003	-	-	
Cluster 5	Terpene	Terpene	FAM00030	-	-	
Cluster 6	NRPS-like	Others	FAM00005	-	-	
Cluster 7	NRPS-T1pks	Hybrid	FAM00006	-	-	
Cluster 8	NRPS	NRP	FAM00007	-	-	
Cluster 9	NRPS	NRP	FAM00008	-	-	
<i>P. terrae</i> DSM 17933 ^T						5.7551
Cluster 1	Lanthipeptide	RiPPs	FAM00031	Pinensins_biosynthetic_gene_cluster (11% of genes show similarity)	BGC0001392_c1	5.7551
Cluster 2	Terpene	Terpene	FAM00030	-	-	
Cluster 3	Siderophore	siderophore	FAM00029	Desferrioxamine_E_biosynthetic_gene_cluster (50% of genes show similarity)	BGC0001572_c1	
Cluster 4	Terpene	Terpene	FAM00079	-	-	
Cluster 5	T3pks	PK	FAM00185	-	-	
Cluster 6	Lanthipeptide	RiPPs	FAM00081	-	-	
Cluster 7	NRPS	NRP	FAM00082	Zwittermycin_A_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0001059_c1	
Cluster 8	NRPS	NRP	FAM00083	-	-	

Clusters	BGC type	BGC class	GCF	Most similar known cluster	MIBiG BGC-ID	GS (Mb)
Cluster 9	NRPS	NRP	FAM00084	-	-	
Cluster 10	NRPS	NRP	FAM00085	-	-	
Cluster 11	NRPS-like	Others	FAM00086	-	-	
<i>P. tournemirensis</i> R1 ^T					5.27684	
Cluster 1	Terpene	Terpene	FAM00200	Carotenoid_biosynthetic_gene_cluster (28% of genes show similarity)	BGC0000650_c1	
<i>P. ureilyticus</i> THGT11 ^T					4.97619	
Cluster 1	Terpene	Terpene	FAM00228	-		
Cluster 2	Terpene	Terpene	FAM00229	Carotenoid_biosynthetic_gene_cluster (28% of genes show similarity)	BGC0000650_c1	
<i>P. yonginense</i> KCTC 22721 ^T						4.37242
Cluster 1	Terpene	Terpene Hybrid	FAM00030	-	-	
			FAM00183	-	-	
Cluster 2	NRPS-T1pks	RiPPs	FAM00184	-	-	
Cluster 3	Bacteriocin	PK	FAM00185	-	-	
Cluster 4	T3pks	RiPPs	FAM00186	-	-	
Cluster 5	Lanthipeptide					
<i>P. yulinensis</i> YL28-9 ^T						4.31077
Cluster 1	Lanthipeptide	RiPPs	FAM00230	-	-	
Cluster 2	Terpene	Terpene	FAM00231	Carotenoid_biosynthetic_gene_cluster (42% of genes show similarity)	BGC0000650_c1	
Cluster 3	Terpene	Terpene	FAM00232	-	-	
<i>P. xixiisoli</i> CGMCC1.12803 ^T						4.9747
Cluster 1	Terpene	Terpene	FAM00178	Carotenoid_biosynthetic_gene_cluster (28% of genes show similarity)	BGC0000650_c1	
Cluster 2	Lanthipeptide	RiPPs	FAM00179	-	-	
Cluster 3	NRPS-T1pks	Hybrid	FAM00180	-	-	
Cluster 4	Bacteriocin	RiPPs	FAM00181	-	-	

Table S2: Additional information regarding all the species that compose the GCFs shown in Error! Reference source not found.. The prefixes HY, PK, RP, SD and TP represent hybrid, PK, RiPPs, siderophore and terpene, respectively.

BGC class	Cytoscape networks	<i>Pedobacter</i> species	Product prediction	GCF
hybrids		<i>P. soli</i> <i>P. kyungheensis</i> <i>P. kyonggii</i> <i>P. ginsenosidimutans</i>	hglE-KS-T1pks	HY_GCF1 FAM00207
		<i>P. hartonius</i> <i>P. cryoconitis</i> <i>P. lusitanus</i>	NRPS-T1pks	HY_GCF2 FAM00038
		<i>P. ginsengisoli</i> <i>P. panaciterrae</i> <i>P. steynii</i>	NRPS-T1pks	HY_GCF3 FAM00166
		<i>P. ginsenosidimutans</i> <i>P. borealis</i>	T3pks- Bacteriocin	HY_GCF4 FAM00128
		<i>P. panaciterrae</i> <i>P. panaciterrae</i>	hglE-KS-T1pks	HY_GCF5 FAM00161
PKs		<i>P. jeongneungensis</i> <i>P. suwonensis</i> <i>P. yonginense</i> <i>P. agri</i> <i>P. terrae</i>	T3pks	PK_GCF1 FAM00185
		<i>P. ginsengisoli</i> <i>P. panaciterrae</i>		PK_GCF2 FAM00067
		<i>P. cryoconitis</i> <i>P. lusitanus</i>		PK_GCF3 FAM00048
RiPPs		<i>P. soli</i> <i>P. kyungheensis</i> <i>P. borealis</i> <i>P. ginsenosidimutans</i>	linaridin	RP_GCF1 FAM00070
		<i>P. agri</i> <i>P. namyangjuensis</i> <i>P. metabolipauver</i> <i>P. yonginense</i> <i>P. kyungheensis</i>	bacteriocin	RP_GCF2 FAM00184
		<i>P. caeni</i> <i>P. cryoconitis</i> <i>P. lusitanus</i> <i>P. steynii</i>	lanthipeptide	RP_GCF3 FAM00054
		<i>P. terrae</i> <i>P. jeongneungensis</i> <i>P. kyonggii</i>	lanthipeptide	RP_GCF4 FAM00031
		<i>P. ginsengisoli</i> <i>P. panaciterrae</i>	bacteriocin	RP_GCF5 FAM00163
		<i>P. kyonggii</i> <i>P. soli</i> <i>P. ginsenosidimutans</i> <i>P. jeongneungensis</i>	bacteriocin	RP_GCF6 FAM00028
siderophores		<i>P. ginsenosidimutans</i> <i>P. jeongneungensis</i> <i>P. kyungheensis</i> <i>P. terrae</i> <i>P. soli</i>	siderophore	SD_GCF1 FAM00029
		<i>P. cryoconitis</i> <i>P. lusitanus</i>		SD_GCF2 FAM00147
terpenes		<i>P. suwonensis</i> <i>P. terrae</i> <i>P. jeongneungensis</i> <i>P. ginsenosidimutans</i> <i>P. kyonggii</i> <i>P. yonginense</i> <i>P. agri</i> <i>P. borealis</i>	terpene	TP_GCF1 FAM00030

		<i>P. soli</i> <i>P. kyungheensis</i>		
		<i>P. ruber</i> <i>P. luteus</i>	terpene	TP_GCF2 FAM00120