SUPPLEMENTARY DATA

Characterization of microbial communities associated with ceramic raw materials as potential contributors for the improvement of ceramic rheological properties

Angela M. Garcia-Sanchez [1], Bernardino Machado-Moreira [2], Mário Freire [3], Ricardo Santos [3], Sílvia Monteiro [3], Diamantino Dias [4], Orquídia Neves [2], Amélia Dionísio [2] and Ana Z. Miller [5]*

[1] Department of Microbiology and Parasitology, Faculty of Pharmacy, University of Seville. Profesor García González 2, 41012 Seville, Spain;
[2] CERENA, Instituto Superior Técnico, Universidade de Lisboa, Av. Rovisco Pais, 1, 1049-001, Lisboa, Portugal;
[3] Laboratorio de Análises do Instituto Superior Técnico, Universidade de Lisboa, Av. Rovisco Pais 1, 1049-001 Lisboa, Portugal;
[4] Rauschert Portuguesa, SA., Estrada Nacional 249-4, Trajouce, 2785-653 São Domingos de Rana, Portugal;
[5] Instituto de Recursos Naturales y Agrobiologia de Sevilla (IRNAS-CSIC), Av. Reina Mercedes 10, 41012 Sevilla, Spain;
[6] HERCULES Laboratory, University of Évora, Largo Marquês de Marialva 8, 7000-809 Évora, Portugal.

* Correspondence: anamiller@irnas.csic.es

The Supplementary data include:

Figure S1. Rarefaction curves.

Table S1. Phylogenetic affiliations of the 16S rRNA gene sequences of total bacteria obtained from sample 1A (74 sequences, 64 OTUs).

Table S2. Phylogenetic affiliations of the 16S rRNA gene sequences of total bacteria obtained from sample 2B (69 sequences, 51 OTUs).

Table S3. Phylogenetic affiliations of the 16S rRNA gene sequences of total bacteria obtained from sample 4D (80 sequences, 54 OTUs).

Table S4. Phylogenetic affiliations of the 16S rRNA gene sequences of total bacteria obtained from sample 6F (86 sequences, 38 OTUs).

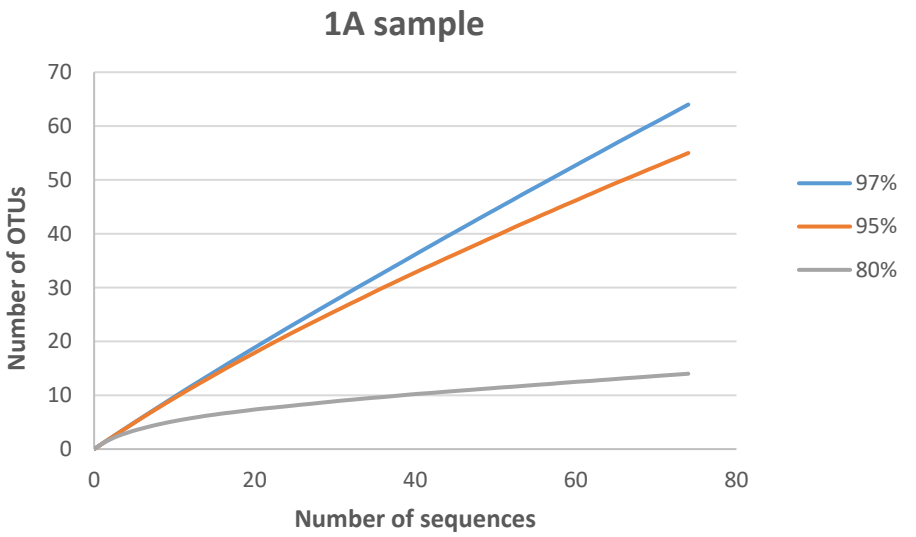
Table S5. Phylogenetic affiliations of the 16S rRNA gene sequences of total bacteria obtained from sample 7G (79 sequences, 48 OTUs).

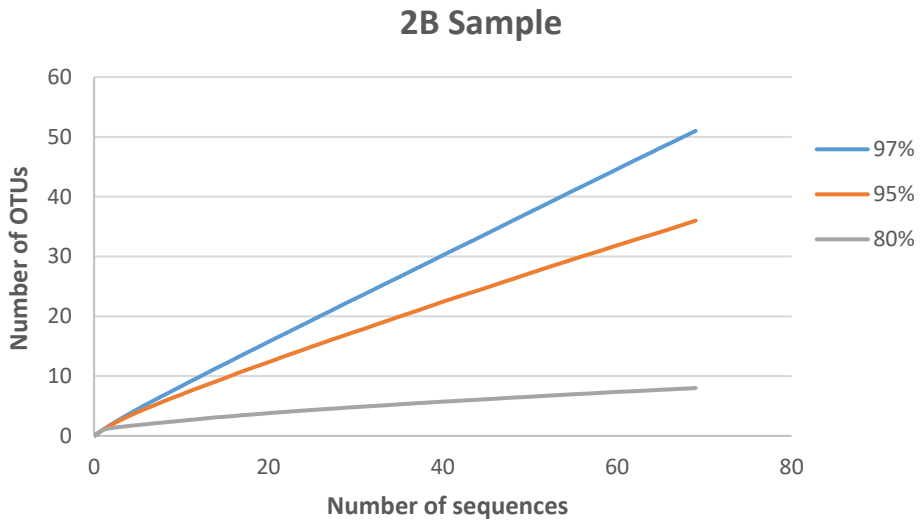
Table S6. Phylogenetic affiliations of the 16S rRNA gene sequences of total bacteria obtained from sample 8H (65 sequences, 38 OTUs).

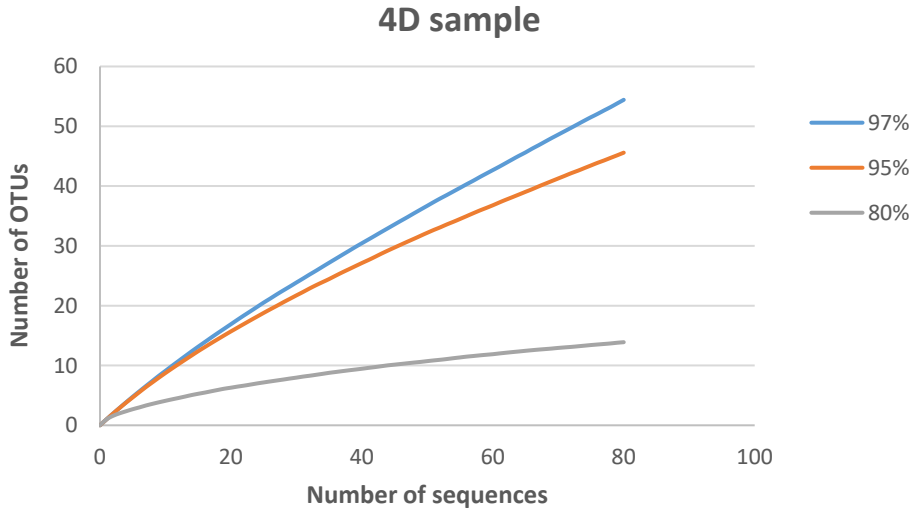
Table S7. Phylogenetic affiliations of the OTUs obtained from the ITS fungal sequences of sample 7GF**.**

Table S8. Phylogenetic affiliations of the bacterial strains isolated from samples 1A, 2B, 3C, 4D, 7G and 8H.

Table S9: Taxonomy of fungi isolated from samples 1A, 2B, 3C and 7G.


1A sample
Number of OTUs
70
60
50
40
30
20
10
0
0
20
40
60
80
Number of sequences
97%
95%
80%


2B Sample
Number of OTUs
60
50
40
30
20
10
0
0
20
40
60
80
Number of sequences
97%
95%
80%


4D sample
Number of OTUs
60
50
40
30
20
10
0
0
20
40
60
80
100
Number of sequences
97%
95%
80%

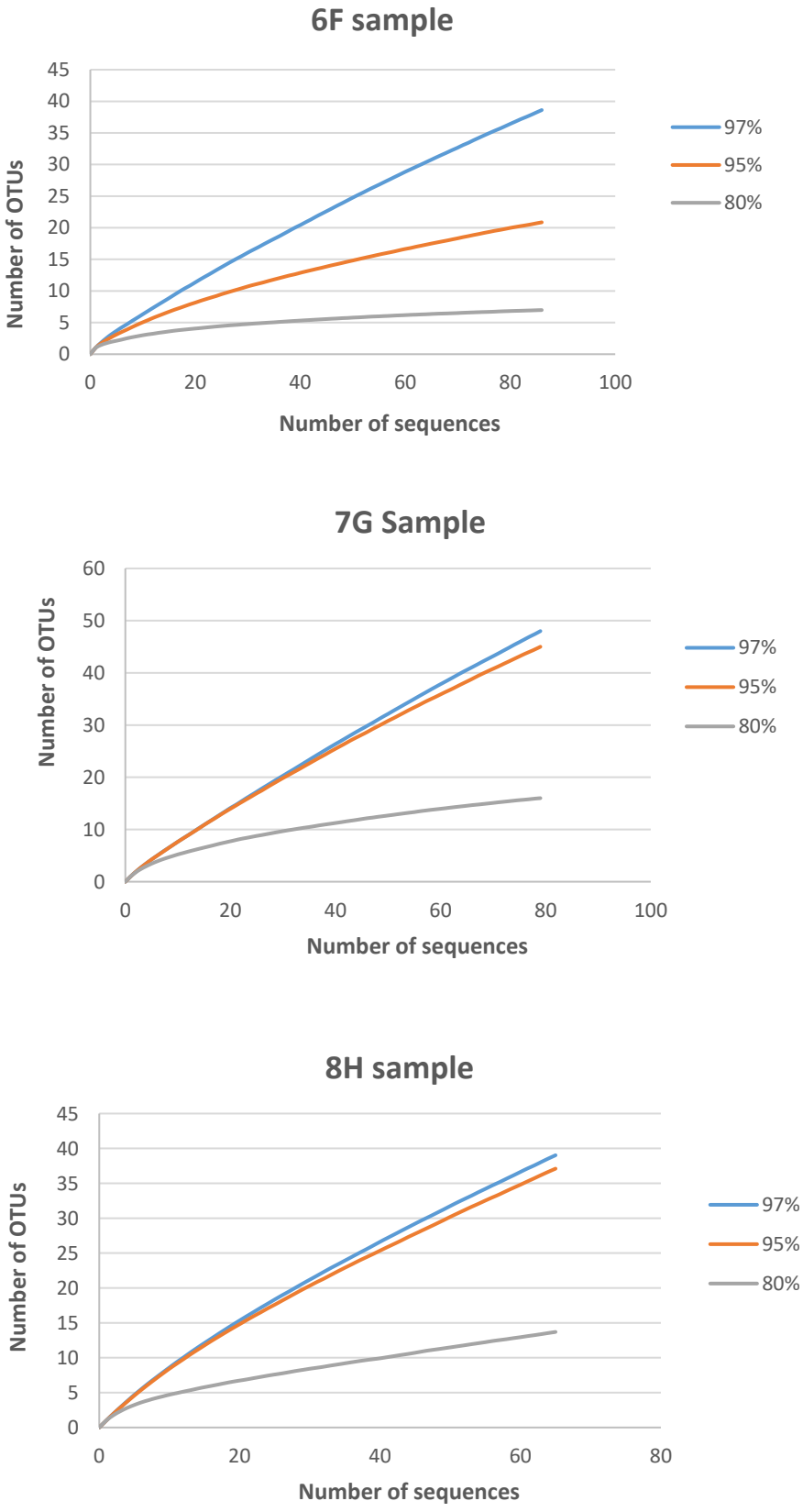


Figure S1. Rarefaction curves.

Table S1. Phylogenetic affiliations of the 16S rRNA gene sequences of total bacteria obtained from sample 1A (74 sequences, 64 OTUs).

Representative clone	No. of clones	Closest match to uncultured clones (Accession no.)	Isolation source	Similarity (%)	Closest match to isolates (Accession no.)	Similarity (%)
Actinobacteria						
LR216298	1	*Brachybacterium rhamnosum* (MF467815)	Mudboil	95	*Brachybacterium rhamnosum* (AJ415376)	93
LR216299	1	*Micrococcus* sp. (MH777904)	Ascidiaceae	89	*Micrococcus aloeverae* (KF524364)	89
LR216300	1	*Micrococcus* sp. (KF648896)	*Pteris multifida*	97	*Micrococcus yunnanensis* (FJ214355)	98
LR216301	1	*Nocardioides glacieisoli* (NR_145916)	Soil	99	*Nocardioides glacieisoli* (JQ673418)	99
Cyanobacteria						
LR216302	2	Uncultured bacterium (JX226767)	Polymetallic nodules	99	*Gloeobacter violaceus* (BA000045)	83
LR216303	1	Uncultured bacterium (JX226767)	Polymetallic nodules	97	*Gloeobacter violaceus* (BA000045)	83
LR216304	1	Uncultured bacterium (JX226767)	Polymetallic nodules	97	*Gloeobacter violaceus* (BA000045)	81
Firmicutes						
LR216305	1	*Bacillus* sp. (KU131261)	Mangrove rhizosphere	99	*Bacillus altitudinis* (ASJC01000029)	99
Alphaproteobacteria						
LR216306	2	*Rhizobium cellulosilyticum* (JQ660020)	Plant tissue	99	*Rhizobium cellulosilyticum* (DQ855276)	99
LR216307	1	*Bradyrhizobium* sp. (KF933594)	Acid soils	98	*Bradyrhizobium huanghuaihaiense* (jgi.1041381)	97
LR216308	1	Uncultured *Methylobacterium* sp. (LN614862)	Green biofilm from an Etruscan tomb	95	*Methylobacterium goesingense* (AY364020)	95
LR216309	1	Uncultured bacterium (DQ228360)	Bench Glacier	93	*Mesorhizobium alhagi* (AHAM01000052)	93
LR216310	1	*Mesorhizobium* sp. (MF949008)	*Lebeckia ambigua*	95	*Mesorhizobium opportunistum* (ACZA01000068)	95
LR216311	1	*Mesorhizobium* sp. (MF949008)	*Lebeckia ambigua*	99	*Mesorhizobium shonense* (GQ847890)	99
LR216312	1	*Novosphingobium* sp. (KP236402)	Coastal area	91	*Novosphingobium colocasiae* (HF548595)	90
LR216313	1	*Roseomonas hibiscisoli* (NR_157795)	Soil	98	*Roseomonas hibiscisoli* (KX456186)	98
LR216314	1	*Sphingomonas* sp. (KT984987)	*Salix sitchensis* branch endosphere	98	*Sphingobium yanoikuyae* (JH992904)	99
LR216315	1	*Sphingomonas* sp. (KT984987)	*Salix sitchensis* branch endosphere	98	*Sphingobium yanoikuyae* (JH992904)	98
Betaproteobacteria						
LR216316	1	*Paraburkholderia ferrariae* (NR_043890)	Iron ore	99	*Paraburkholderia ferrariae* (BAYB01000079)	100
LR216317	1	Uncultured bacterium (KY609367)	Fe-Si-rich precipitates	98	*Schlegelella aquatica* (DQ417336)	97
LR216318	1	*Schlegelella aquatica* (MG282291)	Mineral substrates	95	*Schlegelella aquatica* (DQ417336)	95
LR216319	1	Uncultured *Ralstonia* sp. (LN624415)	Tinto River sediment	97	*Ralstonia solanacearum* (EF016361)	95
LR216320	1	Uncultured *Ralstonia* sp. (LN624415)	Tinto River sediment	98	*Ralstonia solanacearum* (EF016361)	96

Table S1 (Continued)

Representative clone	No. of clones	Closest match to uncultured clones (Accession no.)	Isolation source	Similarity (%)	Closest match to isolates (Accession no.)	Similarity (%)
LR216321	1	Uncultured *Ralstonia* sp. (LN624415)	Tinto River sediment	95	*Ralstonia solanacearum* (EF016361)	93
LR216322	1	Uncultured *Ralstonia* sp. (LN624415)	Tinto River sediment	99	*Ralstonia syzygii* (KC757057)	97
Gammaproteobacteria						
LR216323	6	*Stenotrophomonas rhizophila* (MH144280)	Freshwater lake	99	*Stenotrophomonas rhizophila* (CP007597)	99
LR216324	1	*Stenotrophomonas rhizophila* (MH144280)	Freshwater lake	95	*Stenotrophomonas rhizophila* (CP007597)	95
LR216325	1	*Stenotrophomonas* sp. (KF263571)	Cow dung	96	*Stenotrophomonas rhizophila* (CP007597)	95
LR216326	1	*Stenotrophomonas rhizophila* (KJ395362)	Surface water	97	*Stenotrophomonas rhizophila* (CP007597)	94
LR216327	1	*Stenotrophomonas* sp. (FR828806)	Rhizosphere	92	*Stenotrophomonas rhizophila* (CP007597)	90
LR216328	1	Uncultured *Stenotrophomonas* sp. (HM438645)	Contaminated soil	93	*Stenotrophomonas rhizophila* (CP007597)	88
LR216329	2	*Acinetobacter johnsonii* (MG581287)	Pond	98	*Acinetobacter oryzae* (GU954428)	97
LR216330	1	Uncultured *Acinetobacter* sp. (FJ192369)	Spacecraft assembly clean room	96	*Acinetobacter oryzae* (GU954428)	95
LR216331	1	Uncultured *Acinetobacter* sp. (JN082603)	Room air	97	*Acinetobacter oryzae* (GU954428)	96
LR216332	1	*Acinetobacter schindleri* (JN644622)	Midgut	98	*Acinetobacter schindleri* (APPQ01000011)	97
LR216333	1	Uncultured bacterium (KC666558)	Lake	98	*Acinetobacter schindleri* (APPQ01000011)	97
LR216334	1	Uncultured bacterium (HM559045)	Microbiome	97	*Acinetobacter schindleri* (APPQ01000011)	96
LR216335	1	*Acinetobacter schindleri* (JQ039984)	Root	96	*Acinetobacter schindleri* (APPQ01000011)	95
LR216336	1	*Acinetobacter schindleri* (JQ039984)	Root	98	*Acinetobacter schindleri* (APPQ01000011)	96
LR216337	1	Uncultured bacterium (HQ860682)	Stream water	99	*Acinetobacter lwoffii* (AIEL01000120)	99
LR216338	1	*Acinetobacter lwoffii* (JF935111)	*Sturnira lilium*	96	*Acinetobacter lwoffii* (AIEL01000120)	98
LR216339	1	Uncultured bacterium (HQ860455)	Stream water	96	*Acinetobacter lwoffii* (AIEL01000120)	98
LR216340	1	Uncultured bacterium (KJ643952)	Saline mine	97	*Acinetobacter lwoffii* (AIEL01000120)	97
LR216341	1	*Acinetobacter lwoffii* (MG208860)	Liver	95	*Acinetobacter lwoffii* (AIEL01000120)	97
LR216342	1	*Acinetobacter lwoffii* (MH298336)	*Pinus pinea* root	98	*Acinetobacter lwoffii* (AIEL01000120)	97
LR216343	1	Uncultured *Acinetobacter* sp. (MF615138)	Microplastics biofilm	96	*Acinetobacter lwoffii* (AIEL01000120)	96
LR216344	1	Uncultured bacterium (JF218021)	Skin	91	*Acinetobacter lwoffii* (AIEL01000120)	92
LR216345	1	Uncultured bacterium (KF841211)	As contaminated groundwater	93	*Acinetobacter lwoffii* (AIEL01000120)	91

Table S1 (Continued)

Representative clone	No. of clones	Closest match to uncultured clones (Accession no.)	Isolation source	Similarity (%)	Closest match to isolates (Accession no.)	Similarity (%)
LR216346	1	Uncultured bacterium (FN296331)	Atmospheric dust deposition	90	*Acinetobacter lwoffii* (AIEL01000120)	91
LR216347	3	*Pseudomonas* sp. (KJ452338)	As contaminated soil	99	*Pseudomonas xanthomarina* (jgi.1021496)	99
LR216348	1	*Pseudomonas* sp. (KJ452338)	As contaminated soil	97	*Pseudomonas xanthomarina* (jgi.1021496)	96
LR216349	1	*Pseudomonas* sp. (KJ452337)	As contaminated soil	95	*Pseudomonas xanthomarina* (jgi.1021496)	94
LR216350	1	Uncultured *Pseudomonas* sp. (JQ994165)	Crypts	84	*Pseudomonas koreensis* (AF468452)	85
LR216351	1	*Pseudomonas* sp. (EU449117)	Water from oil seep	95	*Pseudomonas koreensis* (AF468452)	96
LR216352	1	Uncultured bacterium (FJ618868)	Intestinal tract	97	*Pseudomonas stutzeri* (CP002881)	94
LR216353	1	*Pseudomonas* sp. (KY945805)	Soil	84	*Pseudomonas oryzihabitans* (BBIT01000012)	81
LR216354	1	Uncultured *Pseudoxanthomonas* sp. (HF912285)	Process white water of a paper mill	98	*Pseudoxanthomonas taiwanensis* (AF427039)	98
LR216355	1	*Pseudomonas* sp. (AY936495)	Rhizosphere	90	*Pseudomonas fulva* (BBIQ01000036)	89
LR216356	1	*Dyella* sp. (KY194795)	Forest soil	94	*Dyella caseinilytica* (KU296960)	92
LR216357	1	*Dyella* sp. (KY194795)	Forest soil	97	*Dyella lipolytica* (KX430827)	97
LR216358	1	*Dyella* sp. (KY194795)	Forest soil	92	*Dyella lipolytica* (KX430827)	92
Unclassified bacteria*						
LR216359	1	Uncultured bacterium (AJ583205)	Ground waters	93	-	-
LR216360	1	Uncultured bacterium (AJ583205)	Ground waters	95	-	-
LR216361	1	Uncultured bacterium (AJ583205)	Ground waters	96	-	-

* OTUs with less than 80% of similarity with their closest cultured match when compared using EzBioCould database were not shown in Table S1.

Table S2. Phylogenetic affiliations of the 16S rRNA gene sequences of total bacteria obtained from sample 2B (69 sequences, 51 OTUs).

Representative clone	No. of clones	Closest match to uncultured clones (Accession no.)	Isolation source	Similarity (%)	Closest match to isolates (Accession no.)	Similarity (%)
Actinobacteria						
LR216362	1	*Rhodococcus* sp. (MK241968)	Soil	97	*Rhodococcus kronopolitis* (KF887492)	96
LR216363	1	*Rhodococcus* sp. (MH392665)	Soil	95	*Rhodococcus kronopolitis* (KF887492)	95
LR216364	1	*Rhodococcus* sp. (MH392665)	Soil	96	*Rhodococcus kronopolitis* (KF887492)	95
LR216365	1	*Rhodococcus* sp. (MK241968)	Soil	95	*Rhodococcus kronopolitis* (KF887492)	94
LR216366	1	*Rhodococcus* sp. (MK241968)	Soil	95	*Rhodococcus kronopolitis* (KF887492)	94
LR216367	1	*Glutamicibacter ardleyensis* (AJ551162)	Deep sea sediment	90	*Glutamicibacter ardleyensis* (AJ551163)	86
LR216368	1	*Glutamicibacter arilaitensis* (LN774350)	Air sample from a cave	91	*Glutamicibacter ardleyensis* (AJ551163)	86
LR216369	1	*Knoellia* sp. (DQ812538)	Baltic Sea	90	*Knoellia locipacati* (HQ171909)	82
LR216370	1	Uncultured bacterium (JQ427755)	Alkaline saline soil	89	*Nocardioides intraradicalis* (KU940252)	81
Alphaproteobacteria						
LR216371	18	*Phyllobacterium* sp. (MF977588)	Soil	99	*Phyllobacterium brassicacearum* (AY785319)	100
LR216372	2	*Phyllobacterium* sp. (MF977588)	Soil	93	*Phyllobacterium brassicacearum* (AY785319)	94
LR216373	1	*Phyllobacterium* sp. (MF977588)	Soil	96	*Phyllobacterium brassicacearum* (AY785319)	98
LR216374	1	*Phyllobacterium* sp. (MF977588)	Soil	97	*Phyllobacterium brassicacearum* (AY785319)	98
LR216375	1	*Phyllobacterium* sp. (HM467181)	Marine sediment	98	*Phyllobacterium brassicacearum* (AY785319)	98
LR216376	1	*Phyllobacterium* sp. (MF977588)	Soil	98	*Phyllobacterium brassicacearum* (AY785319)	98
LR216377	1	*Phyllobacterium* sp. (HM467181)	Marine sediment	97	*Phyllobacterium brassicacearum* (AY785319)	97
LR216378	1	*Phyllobacterium* sp. (MF977588)	Soil	98	*Phyllobacterium brassicacearum* (AY785319)	97
LR216379	1	*Phyllobacterium* sp. (MF977588)	Soil	97	*Phyllobacterium brassicacearum* (AY785319)	97
LR216380	1	*Phyllobacterium* sp. (MF977588)	Soil	97	*Phyllobacterium brassicacearum* (AY785319)	97
LR216381	1	*Phyllobacterium* sp. (MF977588)	Soil	97	*Phyllobacterium brassicacearum* (AY785319)	97
LR216382	1	*Phyllobacterium* sp. (MF977588)	Soil	95	*Phyllobacterium brassicacearum* (AY785319)	95
LR216383	1	*Phyllobacterium* sp. (MF977588)	Soil	97	*Phyllobacterium brassicacearum* (AY785319)	96
LR216384	1	*Phyllobacterium* sp. (MF977588)	Soil	94	*Phyllobacterium brassicacearum* (AY785319)	96
LR216385	1	*Phyllobacterium* sp. (HM467181)	Marine sediment	95	*Phyllobacterium brassicacearum* (AY785319)	96
LR216386	1	*Phyllobacterium* sp. (HM467181)	Marine sediment	94	*Phyllobacterium brassicacearum* (AY785319)	96
LR216387	1	*Phyllobacterium* sp. (MF977588)	Soil	96	*Phyllobacterium brassicacearum* (AY785319)	96
LR216388	1	*Phyllobacterium* sp. (MF977588)	Soil	96	*Phyllobacterium brassicacearum* (AY785319)	96
LR216389	1	*Phyllobacterium* sp. (MF977588)	Soil	94	*Phyllobacterium brassicacearum* (AY785319)	94
LR216390	1	*Phyllobacterium* sp. (MF977588)	Soil	92	*Phyllobacterium brassicacearum* (AY785319)	94

Table S2 (Continued)

Representative clone	No. of clones	Closest match to uncultured clones (Accession no.)	Isolation source	Similarity (%)	Closest match to isolates (Accession no.)	Similarity (%)
LR216391	1	*Phyllobacterium* sp. (MF977588)	Soil	94	*Phyllobacterium brassicacearum* (AY785319)	94
LR216392	1	*Phyllobacterium* sp. (MF977588)	Soil	95	*Phyllobacterium brassicacearum* (AY785319)	94
LR216393	1	*Phyllobacterium* sp. (MF977588)	Soil	93	*Phyllobacterium brassicacearum* (AY785319)	93
LR216394	1	*Phyllobacterium* sp. (MF977588)	Soil	93	*Phyllobacterium brassicacearum* (AY785319)	93
LR216395	1	*Phyllobacterium* sp. (MF977588)	Soil	93	*Phyllobacterium brassicacearum* (AY785319)	93
LR216396	1	*Phyllobacterium* sp. (MF977588)	Soil	95	*Phyllobacterium brassicacearum* (AY785319)	92
LR216397	1	*Phyllobacterium* sp. (MF977588)	Soil	95	*Phyllobacterium brassicacearum* (AY785319)	92
LR216398	1	*Phyllobacterium* sp. (MF977588)	Soil	92	*Phyllobacterium brassicacearum* (AY785319)	92
LR216399	1	Uncultured bacterium (EU335152)	Soil aggregate	91	*Phyllobacterium brassicacearum* (AY785319)	91
LR216400	1	*Phyllobacterium* sp. (MF977588)	Soil	95	*Phyllobacterium brassicacearum* (AY785319)	91
LR216401	1	*Phyllobacterium* sp. (MF977588)	Soil	89	*Phyllobacterium brassicacearum* (AY785319)	90
LR216402	1	*Phyllobacterium* sp. (HM467181)	Marine sediment	91	*Phyllobacterium brassicacearum* (AY785319)	90
LR216403	1	*Phyllobacterium* sp. (MF977588)	Soil	92	*Phyllobacterium brassicacearum* (AY785319)	89
LR216404	1	*Phyllobacterium* sp. (HM467181)	Marine sediment	91	*Phyllobacterium brassicacearum* (AY785319)	88
LR216405	1	*Phyllobacterium* sp. (MF977588)	Soil	89	*Phyllobacterium brassicacearum* (AY785319)	87
LR216406	1	*Phyllobacterium* sp. (HM467181)	Marine sediment	89	*Phyllobacterium brassicacearum* (AY785319)	86
LR216407	1	*Phyllobacterium* sp. (HM467181)	Marine sediment	88	*Phyllobacterium brassicacearum* (AY785319)	86
LR216408	1	*Mesorhizobium* sp. (MF949008)	*Lebeckia ambigua*	91	*Mesorhizobium shonense* (GQ847890)	92
LR216409	1	Uncultured bacterium (AY328581)	Water distribution system simulator	97	*Sphingorhabdus arenilitoris* (KJ452169)	96
Gammaproteobacteria						
LR216410	1	Uncultured bacterium (KF878227)	Waste ores in a mine	98	*Dyella acidisoli* (KX430826)	95
Rhodothermaeota						
LR216411	1	Uncultured bacterium (EU133663)	Soil, prairie	90	*Rhodothermus marinus* (CP001807)	83
Unclassified bacteria*						
LR216412	1	*Nocardioides* sp. (LC203063)	Rhizosphere soil	85	-	-

* OTUs with less than 80% of similarity with their closest cultured match when compared using EzBioCloud database were not shown in Table S2.

Table S3. Phylogenetic affiliations of the 16S rRNA gene sequences of total bacteria obtained from sample 4D (80 sequences, 54 OTUs).

Representative clone	No. of clones	Closest match to uncultured clones (Accession no.)	Isolation source	Similarity (%)	Closest match to isolates (Accession no.)	Similarity (%)
Actinobacteria						
LR216413	9	*Amycolatopsis nigrescens* (NR_043880)	Roman catacomb	98	*Amycolatopsis nigrescens* (ARVW01000001)	98
LR216414	1	*Amycolatopsis* sp. (MH930453)	Plant root	94	*Amycolatopsis nigrescens* (ARVW01000001)	95
LR216415	1	*Amycolatopsis* sp. (MH930453)	Plant root	95	*Amycolatopsis nigrescens* (ARVW01000001)	94
LR216416	1	*Amycolatopsis* sp. (MH930453)	Plant root	92	*Amycolatopsis nigrescens* (ARVW01000001)	90
LR216417	1	*Amycolatopsis* sp. (MH930453)	Plant root	90	*Amycolatopsis nigrescens* (ARVW01000001)	85
LR216418	1	*Amycolatopsis* sp. (MH930453)	Plant root	93	*Amycolatopsis saalfeldensis* (DQ792500)	89
LR216419	6	Uncultured bacterium (JQ428697)	Alkaline saline soil	99	*Nocardioides albus* (AF004988)	99
LR216420	1	*Nocardioides* sp. (HF954400)	Soil	99	*Nocardioides albus* (AF004988)	100
LR216421	1	Uncultured bacterium (JQ428697)	Soil	95	*Nocardioides albus* (AF004988)	95
LR216422	1	Uncultured bacterium (JQ428697)	Soil	95	*Nocardioides albus* (AF004988)	95
LR216423	2	*Nocardioides* sp. (AJ244657)	Mediterranean Sea	99	*Nocardioides alpinus* (GU784866)	98
LR216424	1	Uncultured bacterium (KY190639)	Polluted soil	99	*Nocardioides ganghwensis* (AY423718)	98
LR216425	1	Uncultured bacterium (DQ643751)	Agricultural soil	92	*Nocardioides ungokensis* (KP893899)	93
LR216426	1	Uncultured bacterium (EU218637)	High arctic	95	*Nocardioides pakistanensis* (LC065367)	89
LR216427	1	*Nocardia cummidelens* (FJ547136)	Soil	99	*Nocardia lasii* (KP784803)	99
LR216428	1	*Nocardia cummidelens* (FJ547136)	Soil	97	*Nocardia lasii* (KP784803)	96
LR216429	4	*Pseudonocardia spinosispora* (NR_025367)	Soil	99	*Pseudonocardia spinosispora* (AJ249206)	99
LR216430	1	*Pseudonocardia spinosispora* (NR_025367)	Soil	93	*Pseudonocardia spinosispora* (AJ249206)	93
LR216431	4	Uncultured bacterium (EF516465)	Grassland soil	99	*Pseudonocardia seranimata* (FJ817379)	99
LR216432	1	Uncultured bacterium (EF516465)	Grassland soil	94	*Pseudonocardia seranimata* (FJ817379)	96
LR216433	1	Uncultured bacterium (EF516465)	Grassland soil	93	*Pseudonocardia seranimata* (FJ817379)	96
LR216434	1	Uncultured *Pseudonocardia* sp. (KP675985)	Ancient tomb mural paintings	93	*Pseudonocardia seranimata* (FJ817379)	95
LR216435	1	*Pseudonocardia sediminis* (NR_118632)	Marine sediments	98	*Pseudonocardia sediminis* (KF564279)	98
LR216436	1	*Pseudonocardia* sp. (HM001291)	Marine sponge	95	*Pseudonocardia petroleophila* (X80596)	95
LR216437	1	Uncultured bacterium (KC331725)	Lava tuve wall	99	*Pseudonocardia bannensis* (FJ817375)	95
LR216438	1	Uncultured bacterium (KC331725)	Lava tuve wall	97	*Pseudonocardia bannensis* (FJ817375)	94
LR216439	1	*Pseudonocardia spinosa* (NR_104698)	Unknown	96	*Pseudonocardia spinosa* (AB547126)	97
LR216440	1	*Microbacterium flavum* (NR_041562)	Marine environments	99	*Microbacterium flavum* (AB286029)	99
LR216441	1	*Rhodococcus* sp. (MH392665)	Soil	97	*Rhodococcus kronopolitis* (KF887492)	96

Table S3 (Continued)

Representative clone	No. of clones	Closest match to uncultured clones (Accession no.)	Isolation source	Similarity (%)	Closest match to isolates (Accession no.)	Similarity (%)
LR216442	1	*Rhodococcus* sp. (MH392665)	Soil	96	*Rhodococcus kronopolitis* (KF887492)	96
LR216443	1	*Cryobacterium psychrotolerans* (JN662519)	Soil of a glacier forefield	99	*Cryobacterium psychrotolerans* (jgi.1076200)	100
LR216444	1	Uncultured bacterium (KF110031)	Human skin	99	*Cutibacterium acnes* (AWZZ01000008)	99
LR216445	1	Uncultured actinobacterium (HM480654)	Meadow soil, basalt bedrock	95	*Aquihabitans daechungensis* (JN033775)	93
LR216446	1	Uncultured actinobacterium (HM480654)	Meadow soil, basalt bedrock	92	*Aquihabitans daechungensis* (JN033775)	91
LR216447	1	Uncultured actinobacterium (HM480654)	Meadow soil, basalt bedrock	93	*Aquihabitans daechungensis* (JN033775)	91
LR216448	1	Uncultured bacterium (EU421859)	Soil under a glacier	90	*Aquihabitans daechungensis* (JN033775)	80
Bacteroidetes						
LR216449	3	Uncultured bacterium (JQ072726)	Brewery wastewater	99	*Prevotella massiliensis* (KQ960595)	89
LR216450	1	Uncultured bacterium (JQ072726)	Brewery wastewater	95	*Prevotella maculosa* (EF534314)	85
Firmicutes						
LR216451	2	Uncultured bacterium (GU107015)	Human feces	95	*Gemmiger formicilis* (GU562446)	93
LR216452	1	*Clostridium xylanolyticum* (AB601065)	Italian ryegrass silage	96	*Clostridium xylanolyticum* (X71855)	95
LR216453	1	Uncultured *Desulfosporosinus* sp. (KJ650779)	Mine tailing dump	93	*Desulfosporosinus nitroreducens* (KX822013)	94
Alphaproteobacteria						
LR216454	4	*Phyllobacterium* sp. (MF977588)	Soil	99	*Phyllobacterium brassicacearum* (AY785319)	100
LR216455	1	*Phyllobacterium* sp. (MF977588)	Soil	95	*Phyllobacterium brassicacearum* (AY785319)	97
LR216456	1	*Phyllobacterium* sp. (MF977588)	Soil	96	*Phyllobacterium brassicacearum* (AY785319)	96
LR216457	1	*Phyllobacterium* sp. (MF977588)	Soil	95	*Phyllobacterium brassicacearum* (AY785319)	93
LR216458	1	*Phyllobacterium* sp. (MF977588)	Soil	94	*Phyllobacterium brassicacearum* (AY785319)	92
LR216459	1	Uncultured bacterium (JF432941)	Rhizosphere	94	*Methyloceanibacter marginalis* (LPWD01000072)	92
LR216460	1	Uncultured bacterium (KF494674)	Permafrost soil	98	*Tardiphaga robiniae* (FR753034)	91
Betaproteobacteria						
LR216461	1	Uncultured bacterium (DQ123737)	Contaminated soil	99	*Thiobacillus thioparus* (ARDU01000017)	98
LR216462	1	Uncultured bacterium (EU676423)	Contaminated soil	99	*Thiobacillus thioparus* (ARDU01000017)	95
LR216463	1	*Sulfuriferula multivorans* (LC005593)	Freshwater lake	94	*Sulfuriferula multivorans* (LC005593)	95

Table S3 (Continued)

Representative clone	No. of clones	Closest match to uncultured clones (Accession no.)	Isolation source	Similarity (%)	Closest match to isolates (Accession no.)	Similarity (%)
Gammaproteobacteria						
LR216464	1	*Pseudomonas veronii* (MK028129)	Unknown	99	*Pseudomonas veronii* (JYLL01000074)	100
LR216465	1	*Acinetobacter bereziniae* (JX035952)	*Gynostemma pentaphyllum*	96	*Acinetobacter bereziniae* (AIEI01000248)	95
Unclassified bacteria*						
LR216466	1	Uncultured bacterium (EU755078)	Contaminated soil	98	-	-

* OTUs with less than 80% of similarity with their closest cultured match when compared using EzBioCloud database were not shown in Table S3.

Table S4. Phylogenetic affiliations of the 16S rRNA gene sequences of total bacteria obtained from sample 6F (86 sequences, 38 OTUs).

Representative clone	No. of clones	Closest match to uncultured clones (Accession no.)	Isolation source	Similarity (%)	Closest match to isolates (Accession no.)	Similarity (%)
Actinobacteria						
LR216467	3	*Nocardia* sp. (JQ838093)	Rhizosphere soils	99	*Nocardia ignorata* (BDBI01000064)	98
LR216468	1	*Nocardia* sp. (JQ838093)	Rhizosphere soils	98	*Nocardia ignorata* (BDBI01000064)	97
LR216469	1	*Nocardia* sp. (JQ838093)	Rhizosphere soils	94	*Nocardia ignorata* (BDBI01000064)	95
LR216470	1	Uncultured bacterium (EF516465)	Grassland soil	97	*Pseudonocardia seranimata* (FJ817379)	97
LR216471	1	*Rhodococcus* sp. (MH392665)	Soil	98	*Rhodococcus kronopolitis* (KF887492)	97
LR216472	1	Uncultured bacterium (GQ008834)	Human skin	99	*Cutibacterium acnes* (AWZZ01000008)	99
LR216473	1	Uncultured bacterium (GQ067471)	Human skin	97	*Cutibacterium acnes* (AWZZ01000008)	97
LR216474	1	Uncultured bacterium (GQ093637)	Human skin	96	*Cutibacterium acnes* (AWZZ01000008)	96
Cyanobacteria						
LR216475	2	Uncultured bacterium (KP143922)	Freshwater biofilms	98	*Anabaenopsis nadsonii* (FM177481)	82
Deinococcus-Thermus						
LR216476	1	*Thermus scotoductus* (KF279363)	Bioreacter treating odors	94	*Thermus scotoductus* (AF032127)	94
Alphaproteobacteria						
LR216477	40	*Phyllobacterium* sp. (MF977588)	Soil	99	*Phyllobacterium brassicacearum* (AY785319)	100
LR216478	2	*Phyllobacterium* sp. (MF977588)	Soil	97	*Phyllobacterium brassicacearum* (AY785319)	99
LR216479	1	*Phyllobacterium* sp. (MF977588)	Soil	96	*Phyllobacterium brassicacearum* (AY785319)	99
LR216480	1	*Phyllobacterium* sp. (MF977588)	Soil	96	*Phyllobacterium brassicacearum* (AY785319)	99
LR216481	1	*Phyllobacterium* sp. (MF977588)	Soil	96	*Phyllobacterium brassicacearum* (AY785319)	98
LR216482	1	*Phyllobacterium* sp. (MF977588)	Soil	95	*Phyllobacterium brassicacearum* (AY785319)	98
LR216483	1	*Phyllobacterium* sp. (MF977588)	Soil	96	*Phyllobacterium brassicacearum* (AY785319)	98
LR216484	1	*Phyllobacterium* sp. (MF977588)	Soil	96	*Phyllobacterium brassicacearum* (AY785319)	98
LR216485	1	*Phyllobacterium* sp. (MF977588)	Soil	95	*Phyllobacterium brassicacearum* (AY785319)	98
LR216486	1	*Phyllobacterium* sp. (MF977588)	Soil	95	*Phyllobacterium brassicacearum* (AY785319)	98
LR216487	1	*Phyllobacterium* sp. (MF977588)	Soil	95	*Phyllobacterium brassicacearum* (AY785319)	97
LR216488	2	*Phyllobacterium* sp. (MF977588)	Soil	95	*Phyllobacterium brassicacearum* (AY785319)	97
LR216489	2	*Phyllobacterium* sp. (MF977588)	Soil	97	*Phyllobacterium brassicacearum* (AY785319)	97
LR216490	1	*Phyllobacterium brassicacearum* (EF581126)	Unknown	97	*Phyllobacterium brassicacearum* (AY785319)	97
LR216491	1	*Phyllobacterium* sp. (MF977588)	Soil	95	*Phyllobacterium brassicacearum* (AY785319)	97
LR216492	1	*Phyllobacterium* sp. (MF977588)	Soil	97	*Phyllobacterium brassicacearum* (AY785319)	97
LR216493	1	*Phyllobacterium* sp. (MF977588)	Soil	95	*Phyllobacterium brassicacearum* (AY785319)	95
LR216494	1	*Phyllobacterium* sp. (MF977588)	Soil	94	*Phyllobacterium brassicacearum* (AY785319)	94

Table S4 (Continued)

Representative clone	No. of clones	Closest match to uncultured clones (Accession no.)	Isolation source	Similarity (%)	Closest match to isolates (Accession no.)	Similarity (%)
LR216495	1	Uncultured *Sphingopyxis* sp. (MF351948)	Seawater	99	*Sphingopyxis fribergensis* (CP009122)	99
LR216496	1	*Methylobacterium platani* (LC025994)	Seeds of rice	99	*Methylobacterium platani* (LWHQ01000067)	98
LR216497	1	*Methylobacterium* sp. (CP029553)	Soil	96	*Methylobacterium platani* (LWHQ01000067)	95
LR216498	1	Uncultured bacterium (JX112928)	Rice paddy soil	98	*Bradyrhizobium jicamae* (LLXZ01000092)	97
Betaproteobacteria						
LR216499	1	Uncultured *Ralstonia* sp. (LN624415)	Tinto River sediment	99	*Ralstonia syzygii* (KC757057)	98
LR216500	1	Uncultured bacterium (KX507875)	Rainwater	97	*Aquabacterium commune* (AF035054)	97
Gammaproteobacteria						
LR216501	3	*Pseudomonas* sp. (MH769579)	Mulberry	99	*Pseudomonas oryzihabitans* (BBIT01000012)	99
LR216502	2	*Pseudomonas* sp. (MH769579)	Mulberry	97	*Pseudomonas oryzihabitans* (BBIT01000012)	98
LR216503	1	*Pseudomonas oryzihabitans* (KY194718)	Desert, dry land	97	*Pseudomonas oryzihabitans* (BBIT01000012)	97
LR216504	1	*Pseudomonas* sp. (MH769579)	Mulberry	93	*Pseudomonas oryzihabitans* (BBIT01000012)	91

Table S5. Phylogenetic affiliations of the 16S rRNA gene sequences of total bacteria obtained from sample 7G (79 sequences, 48 OTUs).

Representative clone	No. of clones	Closest match to uncultured clones (Accession no.)	Isolation source	Similarity (%)	Closest match to isolates (Accession no.)	Similarity (%)
Acidobacteria						
LR216505	1	Uncultured Acidobacteria (AM935546)	Bioremediation process	98	*Vicinamibacter silvestris* (KP761690)	90
Actinobacteria						
LR216506	3	Uncultured actinobacterium (JN038203)	Petroleum-contaminated soil	99	*Aquihabitans daechungensis* (JN033775)	91
LR216507	1	Uncultured Acidimicrobidae (AM935533)	Bioremediation process	97	*Aquihabitans daechungensis* (JN033775)	91
LR216508	1	Uncultured bacterium (JQ825121)	Soil	99	*Aquihabitans daechungensis* (JN033775)	91
LR216509	3	*Rhodococcus* sp. (MG980183)	Moonmilk speleothem	99	*Rhodococcus kronopolitis* (KF887492)	99
LR216510	2	Uncultured bacterium (DQ125846)	U contaminated soil	98	*Gaiella occulta* (JF423906)	94
LR216511	1	Uncultured bacterium (MF314812)	PAHs contaminated soil	96	*Gaiella occulta* (JF423906)	95
LR216512	1	Uncultured bacterium (EU335305)	Soil aggregate	98	*Gaiella occulta* (JF423906)	93
LR216513	1	Uncultured bacterium (EU335437)	Soil aggregate	96	*Gaiella occulta* (JF423906)	93
LR216514	1	Uncultured bacterium (KX771402)	Periglacial environment	98	*Gaiella occulta* (JF423906)	92
LR216515	2	Uncultured actinobacterium (JN002821)	Serpentinized dunite	99	*Streptomyces albulus* (AB024440)	88
LR216516	1	*Streptomyces* sp. (KT581339)	Plant rhizosphere soil	98	*Streptomyces gardneri* (AB249908)	98
LR216517	1	*Streptomyces* sp. (KJ690941)	Sea sediments	99	*Streptomyces tateyamensis* (AB473555)	98
LR216518	1	*Streptomyces* sp. (MG711818)	Plant	92	*Streptomyces camponoticapitis* (KP784807)	95
LR216519	1	Uncultured actinobacterium (EF018262)	Trembling aspen rhizosphere	95	*Streptomyces thermoautotrophicus* (JYIJ01000013)	88
LR216520	1	*Saccharopolyspora endophytica* (NR_132591)	Root	99	*Saccharopolyspora endophytica* (EU814512)	100
LR216521	1	*Nonomuraea* sp. (CP017717)	Soil	99	*Nonomuraea bangladeshensis* (AB274966)	99
LR216522	1	Uncultured bacterium (KC554674)	Soil	98	*Modestobacter multiseptatus* (Y18646)	98
LR216523	1	Uncultured bacterium (JF417829)	Coalbed	99	*Arthrobacter flavus* (AB537168)	98
LR216524	1	*Nocardioides sediminis* (NR_044228)	Soil	99	*Nocardioides sediminis* (EF466110)	100
LR216525	1	Uncultured bacterium (KC554708)	Soil	99	*Nocardioides furvisabuli* (DQ411542)	98
LR216526	1	Uncultured bacterium (HE985049)	Soil	99	*Nocardioides aquiterrae* (AF529063)	97
LR216527	1	Uncultured bacterium (KC554754)	Soil	97	*Nocardioides pelophilus* (KY287247)	97
LR216528	1	*Nocardioides* sp. (MG800321)	Karst cave soil	99	*Nocardioides allogilvus* (MG800321)	99

Table S5 (Continued)

Representative clone	No. of clones	Closest match to uncultured clones (Accession no.)	Isolation source	Similarity (%)	Closest match to isolates (Accession no.)	Similarity (%)
LR216529	1	Uncultured actinobacterium (JN038203)	Petroleum-contaminated soil	91	*Nocardioides allogilvus* (MG800321)	90
LR216530	1	Uncultured bacterium (KF494737)	Permafrost soil	98	*Angustibacter speluncae* (LT719160)	97
LR216531	1	Uncultured Actinomycetales bacterium (HM565047)	Concrete	99	*Aciditerrimonas ferrireducens* (AB517669)	93
LR216532	1	Uncultured bacterium (AB672281)	Rice paddy field soil	97	*Conexibacter arvalis* (AB597950)	93
LR216533	1	Uncultured bacterium (AB821162)	Soil	99	*Actinoallomurus purpureus* (AB364588)	94
LR216534	1	Actinomycetales bacterium (KY386569)	Soil	98	*Frankia elaeagni* (KB893676)	94
LR216535	1	Uncultured bacterium (KC554214)	Soil	98	*Solirubrobacter ginsenosidimutans* (EU332825)	93
LR216536	1	Uncultured bacterium (JQ377231)	Soil sample	98	*Acidothermus cellulolyticus* (CP000481)	85
Chloroflexi						
LR216537	1	Uncultured bacterium (JX489842)	Soil	99	*Kallotenue papyrolyticum* (JAGA01000002)	82
Firmicutes						
LR216538	1	Uncultured bacterium (JX112942)	Rice paddy soil	97	*Marinithermofilum abyssi* (KM368341)	81
Gemmatimonadetes						
LR216539	1	Uncultured bacterium (GQ396892)	Soil	99	*Gemmatimonas aurantiaca* (AP009153)	90
Alphaproteobacteria						
LR216540	25	Uncultured *Mesorhizobium* sp. (DQ303368)	*Tuber magnatum*	99	*Phyllobacterium brassicacearum* (AY785319)	99
LR216541	1	Uncultured bacterium (KU886651)	Epilithic biofilm from limestone	99	*Methylobacterium iners* (EF174497)	98
LR216542	1	Uncultured proteobacterium (EF018792)	Rhizosphere	98	*Rhizomicrobium palustre* (AB081581)	92
Betaproteobacteria						
LR216543	1	Uncultured *Ralstonia* sp. (LN624415)	Tinto River sediment	99	*Ralstonia syzygii* (KC757057)	98
LR216544	1	Uncultured bacterium (EU589304)	Rice paddy field soil	99	*Ramlibacter solisilvae* (CP010951)	98
Gammaproteobacteria						
LR216545	2	Uncultured bacterium (KC255281)	Moonmilk	98	*Cavicella subterranea* (JX458449)	97
LR216546	1	Uncultured bacterium (KJ809234)	Mycorrhizal fungi	99	*Acidibacter ferrireducens* (JX412366)	95
LR216547	1	Uncultured bacterium (EU335183)	Soil aggregate	99	*Lysobacter rhizophilus* (KT962171)	98

Table S5 (Continued)

Representative clone	No. of clones	Closest match to uncultured clones (Accession no.)	Isolation source	Similarity (%)	Closest match to isolates (Accession no.)	Similarity (%)
Unclassified bacteria*						
LR216548	1	Uncultured bacterium (EF515915)	Grassland soil	98	-	-
LR216549	1	Uncultured bacterium (MG641145)	Subtropics forest soil	94	-	-
LR216550	1	Uncultured bacterium (FJ479410)	Tall grass prairie	98	-	-
LR216551	1	Uncultured bacterium (DQ297983)	Hydrocarbon contaminated soil	99	-	-
LR216552	1	Uncultured bacterium (DQ297986)	Hydrocarbon contaminated soil	97	-	-

* OTUs with less than 80% of similarity with their closest cultured match when compared using EzBioCloud database were not shown in Table S5.

Table S6. Phylogenetic affiliations of the 16S rRNA gene sequences of total bacteria obtained from sample 8H (65 sequences, 38 OTUs).

Representative clone	No. of clones	Closest match to uncultured clones (Accession no.)	Isolation source	Similarity (%)	Closest match to isolates (Accession no.)	Similarity (%)
Actinobacteria						
LR216553	2	*Microbacterium lacusdiani* (NR_149217)	Mucilaginous sheath of *Microcystis*	99	*Microbacterium lacusdiani* (KP986565)	99
LR216554	1	Uncultured bacterium (HM124392)	Tar ponds sediment	99	*Mycobacterium montefiorense* (AF330038)	99
LR216555	1	Uncultured actinobacterium (HG379940)	White spots, Etruscan mural paintings	99	*Streptosporangium roseum* (CP001814)	96
LR216556	1	*Isoptericola variabilis* (CP002810)	Hindgut of termite	89	*Isoptericola variabilis* (AJ298873)	87
Cyanobacteria						
LR216557	4	Uncultured bacterium (JX226767)	Polymetallic nodules	99	*Gloeobacter violaceus* (BA000045)	84
LR216558	2	Uncultured bacterium (JX226767)	Polymetallic nodules	99	*Gloeobacter violaceus* (BA000045)	84
LR216559	1	Uncultured bacterium (JX226767)	Polymetallic nodules	97	*Gloeobacter violaceus* (BA000045)	83
LR216560	1	Uncultured bacterium (JX226767)	Polymetallic nodules	94	*Gloeobacter violaceus* (BA000045)	80
LR216561	1	Uncultured cyanobacterium (LN615256)	Roman tomb	99	*Atelocyanobacterium thalassa* (CP001842)	91
Firmicutes						
LR216562	1	*Streptococcus sanguinis* (KF933773)	Oral cavity	98	*Streptococcus sanguinis* (AFAZ01000011)	97
Alphaproteobacteria						
LR216563	9	Uncultured *Mesorhizobium* sp. (DQ303368)	*Tuber magnatum*	99	*Phyllobacterium brassicacearum* (AY785319)	99
LR216564	3	*Mesorhizobium* sp. (CP034447)	Root nodule	99	*Mesorhizobium shonense* (GQ847890)	99
LR216565	1	*Mesorhizobium* sp. (CP034447)	Root nodule	99	*Mesorhizobium shonense* (GQ847890)	100
LR216566	1	Uncultured bacterium (KU514787)	Rainwater	99	*Sphingomonas aerolata* (AJ429240)	100
LR216567	1	*Bradyrhizobium* sp. (FJ418915)	Soil	93	*Bradyrhizobium arachidis* (jgi.1071222)	93
LR216568	1	Uncultured alpha-proteobacterium (AJ583167)	Water, deep-well monitoring site	99	*Aliidongia dinghuensis* (KX426600)	88
LR216569	1	Uncultured alpha-proteobacterium (AJ583167)	Water, deep-well monitoring site	99	*Aliidongia dinghuensis* (KX426600)	87
LR216570	1	Uncultured bacterium (JQ906077)	Disinfected water	88	*Phreatobacter cathodiphilus* (MH032761)	84
Betaproteobacteria						
LR216571	7	Uncultured *Ralstonia* sp. (LN624415)	Tinto River sediment	99	*Ralstonia syzygii* (KC757057)	98
LR216572	1	Uncultured bacterium (KC682291)	Substrate mineral chips	96	*Ralstonia syzygii* (KC757057)	95
LR216573	1	Uncultured bacterium (KC682291)	Substrate mineral chips	92	*Ralstonia syzygii* (KC757057)	92
LR216574	6	*Schlegelella* sp. (FR774567)	Paper mill	99	*Schlegelella aquatica* (DQ417336)	99

Table S6 (Continued)

Representative clone	No. of clones	Closest match to uncultured clones (Accession no.)	Isolation source	Similarity (%)	Closest match to isolates (Accession no.)	Similarity (%)
LR216575	1	*Schlegelella* sp. (FR774567)	Paper mill	94	*Schlegelella aquatica* (DQ417336)	94
LR216576	1	*Schlegelella* sp. (FR774567)	Paper mill	94	*Schlegelella aquatica* (DQ417336)	94
LR216577	1	*Schlegelella* sp. (FR774567)	Paper mill	94	*Schlegelella aquatica* (DQ417336)	93
LR216578	1	*Schlegelella* sp. (AY538706)	Hot compost	92	*Schlegelella aquatica* (DQ417336)	93
LR216579	1	Uncultured *Schlegelella* sp. (JN082687)	Room air	88	*Schlegelella aquatica* (DQ417336)	88
LR216580	1	*Schlegelella* sp. (FR774567)	Paper mill	85	*Schlegelella aquatica* (DQ417336)	85
LR216581	1	Uncultured bacterium (EF208659)	Sandy carbonate sediment	99	*Acidovorax soli* (jgi.1085893)	99
LR216582	1	Uncultured bacterium (KM453919)	Freshwaters	99	*Curvibacter gracilis* (AB109889)	99
LR216583	1	Uncultured bacterium (JX227522)	Polymetallic nodules	99	*Paraburkholderia kururiensis* (BAMQ01000301)	98
LR216584	1	*Burkholderia* sp. (JN872505)	Floral nectar	99	*Paraburkholderia kururiensis* (BAMQ01000301)	98
LR216585	1	Uncultured bacterium (AY570632)	Biodegraded oil reservoir	95	*Thauera chlorobenzoica* (jgi.1084690)	94
LR216586	1	Uncultured *Bordetella* sp. (MF449384)	Rhizosphere	88	*Bordetella petrii* (AM902716)	88
Deltaproteobacteria						
LR216587	1	Uncultured bacterium (KC432541)	Wetland	99	*Desulfococcus biacutus* (AJ277887)	80
Gammaproteobacteria						
LR216588	2	*Dyella* sp. (MH393407)	Forest soil	98	*Dyella caseinilytica* (KU296960)	98
LR216589	1	Uncultured bacterium (DQ823220)	Oregon Caves National Monument	99	*Thiohalomonas denitrificans* (FMWD01000026)	93
Unclassified bacteria*						
LR216590	1	Uncultured bacterium (FJ478842)	Tall grass prairie	99	-	-

* OTUs with less than 80% of similarity with their closest cultured match when compared using EzBioCloud database were not shown in Table S6.

Table S7. Phylogenetic affiliations of the OTUs obtained from the ITS fungal sequences of sample 7G-F.

Representative clone (accesion number)	No. of clones	Nearest relative (Accession no.)	Isolation source	Similarity (%)
Ascomycota				
LR216591	1	*Ascochyta* sp. (MG065755)	Plant (*Ballota hirsuta*)	99
LR216592	1	*Acrostalagmus luteoalbus* (KT824244)	Apple leaf	98
LR216593	1	*Acrostalagmus luteoalbus* (KT824244)	Apple leaf	94
LR216594	1	*Acrostalagmus luteoalbus* (KP216977)	Bat guanos of Heshang cave (China)	94
LR216595	3	*Hypocreales* sp. (HQ649990)	Rhizospheric soil	96
LR216596	2	*Hypocreales* sp. (MG733749)	Bioaerosols	99
LR216597	1	*Leotiaceae* sp. (KU057814)	Lichens	99
LR216598	3	*Talaromyces minioluteus* (LC195248)	Soil in an ancient circular tomb (Japan)	96
LR216599	1	*Talaromyces verruculosus* (HQ607791)	Ants (*Atta texana*) nest	99
LR216600	1	*Talaromyces rugulosus* (MH858378)	Jute	97
LR216601	1	*Ascomycota* sp. (KC180737)	Hair root, root mycobionts	96
LR216602	1	*Diaporthales* sp. (KF428538)	Washed and surface-sterilized roots	99
LR216603	1	*Cladosporium angustisporum* (MK271397)	South African indoor environments	99
LR216604	1	*Doratomyces* sp. (AJ608985)	Plasticized polyvinyl chloride (pPVC)	99
LR216605	1	*Humicola fuscoatra* (LT993580)	Soil	99
LR216606	1	*Fusarium merismoides* (KU214553)	Seawater-saturated wood	96
LR216607	1	*Fusarium oxysporum* (MK212364)	Soybean cotyledon	99
LR216608	1	*Nectriella pironii* (MH861261)	Plant (*Aphelandra squarrosa*)	98
LR216609	1	*Penicillium* sp. (GU566206)	Rhizosphere	100
LR216610	1	*Penicillium thomii* (MH858993)	Soil	99
LR216611	1	*Penicillium* sp. (KT264421)	Root (*Pinus edulis*)	95
LR216612	3	*Penicillium citrinum* (MH059538)	Entomogenous fungus (*Isaria cicadae*)	99
LR216613	1	*Penicillium* sp. (KY681453)	Pasture soil	99
LR216614	1	*Penicillium ochrochloron* (KY977590)	Soil	92
LR216615	1	*Penicillium* sp. (KF428217)	Washed and surface-sterilized roots	95
LR216616	1	*Penicillium tularense* (NR_121251)	Soil under *Pinus ponderosa* and *Quercus kelloggii*	98
LR216617	1	*Penicillium radiatolobatum* (MF803948)	House dust	97
LR216618	1	*Acremonium persicinum* (NR_131260)	Coastal sand under *Ammophila arenaria*	99
LR216619	1	*Aspergillus brasiliensis* (KM491891)	Surface water	99
LR216620	1	*Aspergillus tubingensis* (KJ028003)	Unknown	99
LR216621	1	*Trichoderma viride* (MK290390)	Rhizosphere soil	96
LR216622	1	*Chrysosporium lobatum* (HQ914933)	Marine macroalgae	97

Table S7 (Continued)

Representative clone (accesion number)	No. of clones	Nearest relative (Accession no.)	Isolation source	Similarity (%)
LR216623	1	*Embellisia* sp. (KJ935004)	Bryophyte crust	97
LR216624	1	*Xylariaceae* sp. (AB741591)	Living leaf	90
LR216625	1	*Sarocladium strictum* (MF077236)	Deep root plant rhizosphere	97
LR216626	1	*Chaetosphaeronema* sp. (KT268592)	Roots	99
Basidiomycota				
LR216627	1	*Rhodotorula mucilaginosa* (MK156304)	Marine sediment	99
LR216628	1	*Ustilago tritici* (MH115003)	Plant (Poaceae Family)	99
LR216629	3	*Scleroderma* sp. (MK300689)	Unknown	98
LR216630	1	*Scleroderma* sp. (MK300689)	Unknown	89
LR216631	1	*Pholiota* sp. (LN901138)	Extremely Acidic Soils	94
Muromycota				
LR216632	1	*Mucor plumbeus* (EU484261)	Different ecological habitats and climatic regions	93
LR216633	2	*Mortierella* sp. (KC007188)	Plant roots	99
LR216634	1	*Mortierella* sp. (MF565377)	Alpine plant (*Saxifraga stellaris* ssp. *alpigena*)	99
LR216635	1	*Mortierella alpina* (KX343151)	Mycorrhiza of *Tuber melanosporum*	99
Unclassified Eukaryota				
LR216636	1	Uncultured fungus (KF297160)	Soil	96
LR216637	1	Uncultured fungus (HG328094)	Arable soil	96
LR216638	1	Uncultured fungus (DQ421069)	Soil	100
LR216639	1	Uncultured fungus (EU516714)	Soil	95

Table S8. Phylogenetic affiliations of the bacterial strains isolated from samples 1A, 2B, 3C, 4D, 7G and 8H.

Sample	Strain (Accesion no.)	Nº of clones	Nearest relative (Accession no.)	Isolation source	Similarity (%)	Closest match to isolates (Accession no.)	Similarity (%)
1A	**Actinobacteria**						
	LR536330	2	*Microbacterium* sp. (KM376509)	Soil	100	*Microbacterium lacusdiani* (KP986565)	99
	LR536331	1	*Brachybacterium* sp. (MH298681)	*Camellia sinensis*	99	*Brachybacterium rhamnosum* (AJ415376)	100
	LR536332	1	*Kocuria* sp. (MK205171)	Salted Chinese herring	99	*Kocuria palustris* (Y16263)	100
	Firmicutes						
	LR536333	1	*Bacillus aryabhattai* (MK110364)	Sediments from a lake	100	*Bacillus aryabhattai* (EF114313)	100
	Betaproteobacteria						
	LR536334	5	*Hydrogenophaga* sp. (LT009510)	Lagoon water	99	*Hydrogenophaga bisanensis* (EF532793)	100
	Gammaproteobacteria						
	LR536335	1	*Pseudomonas stutzeri* (MH010320)	Slop water	99	*Pseudomonas stutzeri* (CP002881)	99
2B	**Actinobacteria**						
	LR536336	1	*Kocuria rosea* (JQ649405)	Marble monuments	100	*Kocuria rosea* (X87756)	99
	LR536337	2	*Glutamicibacter bergerei* (KT983988)	Soil	100	*Glutamicibacter bergerei* (AJ609630)	99
	LR536338	1	*Pseudarthrobacter sulfonivorans* (KF923412)	Permafrost soil	96	*Pseudarthrobacter sulfonivorans* (AF235091)	97
	Firmicutes						
	LR536339	1	*Oceanobacillus* sp. (MG893163)	Sandy soil, desert	100	*Oceanobacillus picturae* (AJ315060)	100
3C	**Actinobacteria**						
	LR536340	1	*Arthrobacter tumbae* (KJ575034)	Deep sea sediments	100	*Arthrobacter tumbae* (AJ315069)	99
	Firmicutes						
	LR536341	1	Uncultured *Bacillus* sp. (JQ793428)	Rhizospheric soil	99	*Bacillus pocheonensis* (AB245377)	98
	LR536342	1	*Bacillus* sp. (MH071747)	Rice root soil	100	*Bacillus aryabhattai* (EF114313)	99
4D	**Actinobacteria**						
	LR536343	1	*Arthrobacter* sp. (MG708155)	Rhizosphere potted in PCB-contaminated soil	99	*Arthrobacter sulfonivorans* (AF235091)	98
	LR536344	10	*Arthrobacter* sp. (KY906997)	Oil-contaminated soil	99	*Arthrobacter humícola* (AB279890)	99
	LR536345	1	*Arthrobacter* sp. (KJ190984)	Sediment of high-arsenic groundwater	96	*Arthrobacter pascens* (X80740)	95
	LR536346	1	*Arthrobacter* sp. (KT183561)	Rhizospheric soil	99	*Arthrobacter ramosus* (AM039435)	99
	LR536347	3	*Microbacterium flavum* (NR_041562)	Marine environments	99	*Microbacterium flavum* (AB286029)	99
	Gammaproteobacteria						
	LR536348	11	*Pseudomonas* sp. (MK140954)	Unknown	100	*Pseudomonas caspiana* (LOHF01000033)	99
	LR536349	3	*Pseudomonas* sp. (KJ659071)	Forest soil	99	*Pseudomonas kilonensis* (LHVH01000037)	99

Table S8 (Continued)

Sample	Strain (Accesion no.)	Nº of clones	Nearest relative (Accession no.)	Isolation source	Similarity (%)	Closest match to isolates (Accession no.)	Similarity (%)
7G	**Actinobacteria**						
	LR536350	2	*Nocardioides* sp. (KM035951)	Forest soil	99	*Nocardioides kongjuensis* (DQ218275)	98
	Betaproteobacteria						
	LR536351	1	*Herbaspirillum* sp. (FN386764)	Volcanic ash	99	*Herbaspirillum canariense* (HQ830496)	99
8H	**Actinobacteria**						
	LR536352	5	*Microbacterium flavum* (NR_041562)	Marine environments	99	*Microbacterium flavum* (AB286029)	100
	LR536353	1	*Microbacterium flavum* (NR_041562)	Marine environments	96	*Microbacterium flavum* (AB286029)	95
	LR536354	3	*Microbacterium* sp. (KM376509)	Soil	99	*Microbacterium lacusdiani* (KP986565)	99
	Alphaproteobacteria						
	LR536355	1	*Brevundimonas* sp. (KU557513)	Root	100	*Brevundimonas diminuta* (GL883089)	99
	LR536356	4	*Agrobacterium* sp. (MK241871)	Tailing	99	*Rhizobium radiobacter* (AJ389904)	99
	Betaproteobacteria						
	LR536357	1	*Delftia* sp. (MG755255)	Activated sludge	99	*Delftia lacustris* (jgi.1102360)	100
	LR536358	5	*Acidovorax* sp. (JX949427)	Glacier	99	*Acidovorax facilis* (AF078765)	99
	LR536359	1	*Hydrogenophaga* sp. (EU379017)	Wastewater treatment plant	99	*Hydrogenophaga luteola* (KM598239)	99
	Gammaproteobacteria						
	LR536360	1	*Stenotrophomonas rhizophila* (KM524119)	Estuarine sediment	99	*Stenotrophomonas rhizophila* (CP007597)	99
	LR536361	2	*Pseudomonas chengduensis* (MK108035)	Sludge	100	*Pseudomonas chengduensis* (EU307111)	99
	LR536362	1	*Pseudomonas* sp. (MG967453)	Heavy metal contaminated soil	99	*Pseudomonas reidholzensis* (LT009707)	99
	LR536363	1	*Pseudomonas stutzeri* (KU131277)	Mangrove rhizosphere	97	*Pseudomonas stutzeri* (CP002881)	99
	LR536364	1	*Pseudomonas stutzeri* (CP025149)	Air	99	*Pseudomonas stutzeri* (CP002881)	99
	LR536365	1	*Pseudomonas* sp. (JF740047)	Antimony mined soil	96	*Pseudomonas stutzeri* (CP002881)	97

Table S9. Taxonomy of fungi isolated from samples 1A, 2B, 3C and 7G.

Sample	Phylum	Number of isolated strains
1A	Ascomycota	1
2B	Ascomycota	17
	Mucoromycotina	3
3C	Ascomycota	10
	Mucoromycotina	5
7G	Ascomycota	7
	Mucoromycotina	3