

Supplementary Information

Deterioration of an Etruscan tomb by bacteria from the order *Rhizobiales*

M. Diaz-Herraiz, V. Jurado, S. Cuezva, L. Laiz, P. Pallecchi, P. Tiano, S. Sanchez-Moral & C. Saiz-Jimenez*

*To whom correspondence should be addressed. E-mail: saiz@irnase.csic.es (C.S.J.)

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Rarefaction curves
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Rarefaction curves

Rarefaction curves (Fig. S1) indicated that the full extent of diversity was not reached, suggesting that a greater diversity of bacteria was present in the samples. Due to the sampling restrictions imposed by the protection of cultural heritage site guidelines, the number and size of samples was limited and a deep coverage of the bacterial communities in the samples from this historical site was not possible.

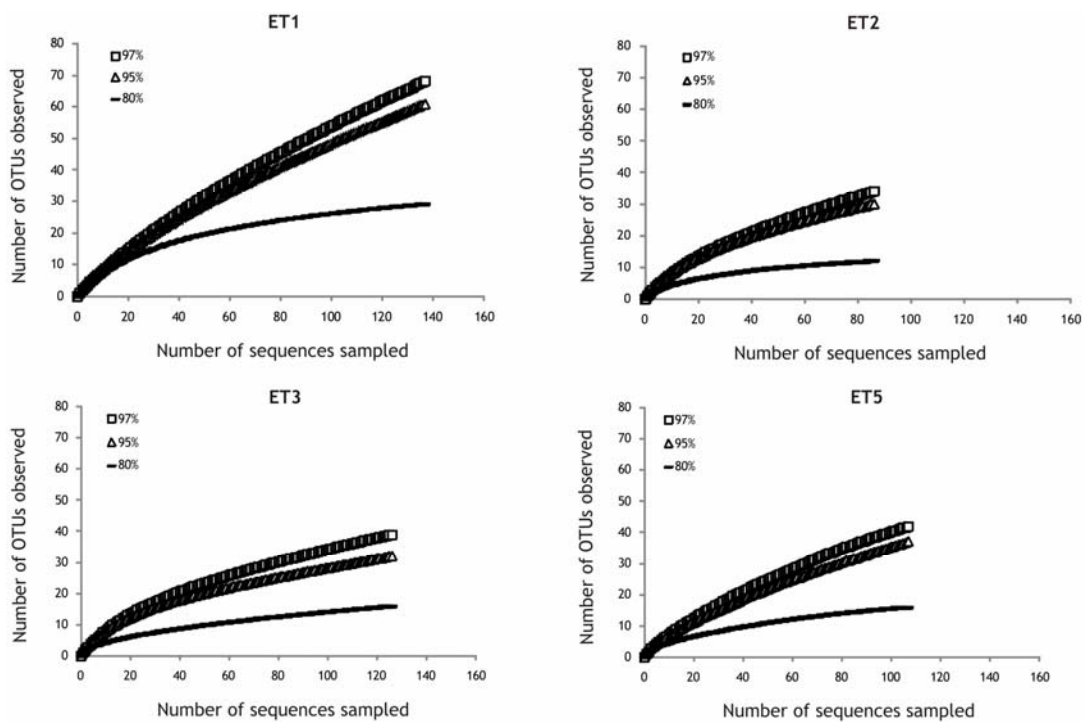


Figure S1. Rarefaction curves of 16S rDNA gene sequences of the bacteria clones from *Tomba del Colle*.

Table S1. Phylogenetic affiliations of the 16S rRNA sequences obtained from the bacteria in the ET1 sample

Representative clone (accession number)	No. of clones	Similarity (%)	Nearest published relative	Source	Similarity (%)	Eztaxon affiliation (accession number)
Acidobacteria						
HG379790	1	97	<i>Acidobacteria</i> bacterium (GU187029)	Surface soil	84	<i>Terriglobus saanensis</i> (CP002467)
HG379791	2	98	Uncultured <i>Acidobacteria</i> bacterium (HQ729805)	Grassland soil	82	<i>Acanthopleuribacter pedis</i> (AB303221)
HG379792	1	91	Uncultured <i>Acidobacteria</i> bacterium (AM934751)	Contaminated soil	84	<i>Acidicapsa borealis</i> (FR774763)
HG379793	4	99	Uncultured <i>Acidobacteria</i> bacterium (GQ120659)	Mine tailings	84	<i>Candidatus</i> Chloracidobacterium thermophilus (CP002514)
HG379794	3	99	Uncultured <i>Acidobacteria</i> bacterium (JN037860)	Saline-alkaline soil	85	<i>Candidatus</i> Chloracidobacterium thermophilus (CP002514)
HG379795	1	98	Uncultured <i>Acidobacteria</i> bacterium (HM062376)	Agricultural soil	80	<i>Candidatus</i> Chloracidobacterium thermophilus (CP002514)
HG379796	1	95	Uncultured <i>Acidobacteria</i> bacterium (JQ957800)	Rhizosphere soil	80	<i>Candidatus</i> Chloracidobacterium thermophilus (CP002514)
HG379797	1	96	Uncultured <i>Acidobacteria</i> bacterium (HF584585)	White spots from Etruscan tombs mural paintings	85	<i>Candidatus</i> Chloracidobacterium thermophilus (CP002514)
HG379798	1	99	Uncultured <i>Acidobacteria</i> bacterium (HQ597108)	Grassland soil	83	<i>Geothrix fermentans</i> (U41563)
HG379799	1	97	Uncultured <i>Acidobacteriaceae</i> bacterium (AM935189)	Hydrocarbon-contaminated soil	87	<i>Solibacter usitatus</i> (CP000473)
HG379800	2	91	Uncultured bacterium (JN850206)	Lava tube wall	82	<i>Acidicapsa ligni</i> (EU780204)
HG379801	4	97	Uncultured bacterium (JF266297)	White microbial mat lava tube walls	83	<i>Acidicapsa ligni</i> (EU780204)
HG379802	1	95	Uncultured bacterium (HM186317)	Saturated zone of the Hanford Site	88	<i>Acidobacterium capsulatum</i> (AB561884)
HG379803	3	97	Uncultured bacterium (JF266297)	White microbial mat lava tube walls	85	<i>Candidatus</i> Koribacter versatilis (CP000360)
Actinobacteria						
HG379804	1	90	Uncultured actinobacterium (HF584587)	White spots from Etruscan tombs mural paintings	87	<i>Actinoallomurus spadix</i> (AF163120)
HG379805	1	97	Uncultured actinobacterium (HF584505)	White spots from Etruscan tombs mural paintings	91	<i>Crosiella cryophila</i> (AF114806)
HG379806	1	85	Uncultured actinobacterium (HF584587)	White spots from Etruscan tombs mural paintings	82	<i>Crossiella cryophila</i> (A114806)
HG379807	1	97	Uncultured actinobacterium (HM480640)	Meadow soil, basalt bedrock	93	<i>Ilumatobacter fluminis</i> (AB360343)
HG379808	1	88	Uncultured actinobacterium (HF584648)	White spots from Etruscan tombs mural paintings	88	<i>Jiangella muralis</i> (FN645214)
HG379809	1	91	Uncultured actinobacterium (HF584587)	White spots from Etruscan tombs mural paintings	87	<i>Jiangella muralis</i> (FN645214)
HG379810	33	99	Uncultured actinobacterium (HF584587)	White spots from Etruscan tombs mural paintings	95	<i>Pseudonocardia saturnea</i> (AJ252829)

Representative clone (accession number)	No. of clones	Similarity (%)	Nearest published relative	Source	Similarity (%)	Eztaxon affiliation (accession number)
HG379811	1	94	Uncultured bacterium (FR871558)	Greenhouse soil	83	<i>Fodinicola feengrottensis</i> (EF490376)
HG379812	1	84	Uncultured bacterium (JF829544)	Soil	83	<i>Pseudonocardia mongoliensis</i> (AB521676)
Firmicutes						
HG379813	1	89	Uncultured bacterium (HE602920)	Cave wall biofilm	82	<i>Clostridium sordelli</i> (AB075771)
HG379814	4	96	Uncultured bacterium (JN616158)	Organic ooze from lava tube wall	82	<i>Thermolithobacter ferrireducens</i> (AF282253)
Gemmatimonadetes						
HG379815	1	95	Uncultured <i>Gemmatimonadales</i> bacterium (EU665102)	Agricultural soil	81	<i>Gemmatimonas aurantiaca</i> (AP009153)
HG379816	1	99	Uncultured bacterium (JN672056)	White microbial mat from lava tube wall	84	<i>Gemmatimonas aurantiaca</i> (AP009153)
Nitrospirae						
HG379817	3	94	Uncultured bacterium (EU287098)	Arctic surface sediment	84	<i>Methylomirabilis oxyfera</i> (FP565575)
HG379818	5	99	Uncultured bacterium (HM445369)	White microbial mat from lava tube walls	95	<i>Nitrospira moscoviensis</i> (X82558)
HG379819	1	99	Uncultured bacterium (HE653874)	Cave	95	<i>Nitrospira moscoviensis</i> (X82558)
HG379820	1	99	Uncultured bacterium (HM545202)	White microbial mat from lava tube walls	95	<i>Nitrospira moscoviensis</i> (X82558)
Planctomycetes						
HG379821	1	95	Uncultured <i>Planctomycetales</i> bacterium (JN825597)	Alkaline lake	80	<i>Anammoxoglobus propionicus</i> (DQ317601)
HG379822	1	98	Uncultured <i>Planctomycetes</i> bacterium (CU925416)	Sludge	87	<i>Blastopirellula marina</i> (AANZ01000021)
HG379823	1	97	Uncultured <i>Planctomycetales</i> bacterium (JN825608)	Microbialites from alkaline lake	87	<i>Planctomyces brasiliensis</i> (AEICO1000055)
HG379824	1	93	Uncultured bacterium (FN659098)	Host gut <i>Lumbricus terrestris</i>	86	<i>Blastopirellula marina</i> (AANZ01000021)
HG379825	1	88	Uncultured bacterium (EU135128)	Soil	83	<i>Pirellula staleyii</i> (CP001848)
Alphaproteobacteria						
HG379826	1	99	Alphaproteobacterium (EF612344)	Mine tailings	91	<i>Rhodobium orientis</i> (D30792)
HG379827	1	95	Uncultured alphaproteobacterium (FN594637)	Biofilm from gold mine in Zloty Stok	89	<i>Geminicoccus roseus</i> (AM403172)
HG379828	1	98	Uncultured alphaproteobacterium (HE614837)	Arsenic and gold mine	90	<i>Geminicoccus roseus</i> (AM403172)
HG379829	1	91	Uncultured <i>Hyphomicrobiaceae</i> bacterium (HQ183835)	Leachate sediment	93	<i>Hyphomicrobium hollandicum</i> (Y14303)
HG379830	1	98	Uncultured bacterium (JF265753)	White microbial mat lava tube wall	93	<i>Filomicrobium fusiforme</i> (Y14313)
HG379831	1	97	Uncultured bacterium (JN606987)	White microbial mat from lava tube wall	88	<i>Microvirga aerophila</i> (GQ421848)
HG379832	1	98	Uncultured bacterium (FN659225)	Soil	96	<i>Rhodoplanes roseus</i> (D25313)

Representative clone (accession number)	No. of clones	Similarity (%)	Nearest published relative	Source	Similarity (%)	Eztaxon affiliation (accession number)
HG379833	1	99	Uncultured bacterium (JN616000)	White microbial mat lava tube wall	91	<i>Skermanella aerolata</i> (DQ672568)
Betaproteobacteria						
HG379834	8	99	Uncultured betaproteobacterium (EF612412)	Soil	90	<i>Cupriavidus gilardii</i> (EU024163)
HG379835	2	97	Uncultured betaproteobacterium (EF612412)	Soil	89	<i>Cupriavidus gilardii</i> (EU024163)
HG379836	1	96	Uncultured betaproteobacterium (EF612412)	Soil	89	<i>Cupriavidus gilardii</i> (EU024163)
HG379837	1	98	Uncultured <i>Burkholderiales</i> bacterium (EU449561)	Agricultural soil	89	<i>Cupriavidus gilardii</i> (EU024163)
HG379838	1	98	Uncultured bacterium (FJ152869)	Alkaline saline soil	97	<i>Piscinibacter aquaticus</i> (DQ664244)
Gammaproteobacteria						
HG379839	2	97	Gammaproteobacterium (AB663506)	Dechlorinating process	94	<i>Panacagrimonas perspica</i> (AB257722)
HG379840	1	98	Uncultured gammaproteobacterium (HF584687)	White spots from Etruscan tombs mural paintings	88	<i>Fontimonas thermophila</i> (JN415769)
HG379841	1	99	Uncultured gammaproteobacterium (HF584627)	White spots from Etruscan tombs mural paintings	89	<i>Panacagrimonas perspica</i> (AB257722)
HG379842	1	99	Uncultured gammaproteobacterium (AY922146)	Farm soil	95	<i>Steroidobacter denitrificans</i> (EF605262)
HG379843	2	99	Uncultured gammaproteobacterium (HF584625)	White spots from Etruscan tombs mural paintings	98	<i>Steroidobacter denitrificans</i> (EF605262)
HG379844	1	96	Uncultured bacterium (JN801134)	Tan microbial mat from lava tube wall	87	<i>Steroidobacter denitrificans</i> (EF605262)
HG379845	1	93	Uncultured bacterium (EU801093)	Delaware Bay, NJ	89	<i>Steroidobacter denitrificans</i> (EF605262)
HG379846	1	94	Uncultured bacterium (HM187301)	Saturated zone of the Hanford Site	88	<i>Steroidobacter denitrificans</i> (EF605262)
Deltaproteobacteria						
HG379847	4	98	Uncultured deltaproteobacterium (AM935293)	Contaminated soil	81	<i>Desulfohalobium utahense</i> (DQ067421)
HG379848	1	94	Uncultured deltaproteobacterium (FJ535064)	Cave wall biofilm	81	<i>Desulfosalsimonas propionica</i> (DQ067422)
HG379849	1	99	Uncultured deltaproteobacterium (HF584635)	White spots from Etruscan tombs mural paintings	86	<i>Desulfacinum hydrothermale</i> (AF170417)
HG379850	1	99	Uncultured <i>Desulfuromonadales</i> bacterium (AM935314)	Contaminated soil	82	<i>Desulfacinum infernum</i> (L27426)
HG379851	1	99	Uncultured bacterium (JN606997)	White microbial mat from lava tube wall	84	<i>Desulfosalsimonas propionica</i> (DQ067422)
HG379852	4	99	Uncultured bacterium (JF265699)	White microbial mat lava tube wall	84	<i>Desulfovibrio sulfodismutans</i> (Y17764)
HG379853	1	98	Uncultured bacterium (JN615842)	Yellow microbial mat from lava tube wall	83	<i>Desulfopila inferna</i> (AM774321)
HG379854	1	98	Uncultured bacterium (HM558628)	Garden	85	<i>Geoalkalibacter ferrihydriticus</i> (DQ309326)
HG379855	1	98	Uncultured bacterium (JN672401)	White microbial mat from lava tube wall	88	<i>Haliangium tepidum</i> (AB062751)

Representative clone (accession number)	No. of clones	Similarity (%)	Nearest published relative	Source	Similarity (%)	Eztaxon affiliation (accession number)
HG379856 Unclassified bacterium	1	98	Uncultured bacterium (JF265710)	White microbial mat lava tube wall	82	<i>Hippea jasoniae</i> (FR754498)
HG379857	1	97	Uncultured bacterium (EU133899)	Grass prairie	79	<i>Aciditerrimonas ferrireducens</i> (AB517669)

Table S2. Phylogenetic affiliations of the 16S rRNA sequences obtained from the bacteria in the ET2 sample

Representative clone (accession number)	No. of clones	Similarity (%)	Nearest published relative	Source	Similarity (%)	Eztaxon affiliation (accession number)
Acidobacteria						
HG379858	1	99	Uncultured <i>Acidobacteria</i> bacterium (DQ139452)	Roman catacombs	91	<i>Solibacter usitatus</i> (CP000473)
Actinobacteria						
HG379859	7	96	<i>Catelliglobospora koreensis</i> (NR_028758)	Gold-mine cave	96	<i>Catelliglobospora koreensis</i> (AF171700)
HG379860	2	99	<i>Jiangella muralis</i> (FN645214)	Indoor environment	99	<i>Jiangella muralis</i> (FN645214)
HG379861	1	95	<i>Jiangella muralis</i> (FN645214)	Indoor environment	95	<i>Jiangella muralis</i> (FN645214)
HG379862	6	96	<i>Streptosporangium</i> sp. (EF216362)	Shallow water sediment	97	<i>Streptosporangium anatoliense</i> (HQ157194)
HG379863	1	91	Uncultured actinobacterium (HF584512)	White spots from Etruscan mural paintings	91	<i>Marmoricola scoriae</i> (FN386750)
HG379864	3	99	Uncultured actinobacterium (HF584605)	White spots from Etruscan mural paintings	96	<i>Nocardioides salaries</i> (DQ401092)
HG379865	1	97	Uncultured bacterium (EU132756)	Soil	91	<i>Aciditerrimonas ferrireducens</i> (AB517669)
HG379866	1	85	Uncultured bacterium (AM697552)	Indoor dust	88	<i>Saccharopolyspora cebuensis</i> (EF030715)
HG379867	1	87	Uncultured <i>Pseudonocardiaceae</i> bacterium (FM209144)	Contaminated soil	89	<i>Yuhushiella deserti</i> (FJ526746)
HG379868	1	99	Uncultured <i>Rubrobacter</i> sp. (FN689575)	Fragment of historical paper	99	<i>Rubrobacter xylanophilus</i> (CP000386)
Bacteroidetes						
HG379869	5	96	Uncultured <i>Bacteroidetes</i> bacterium (CU921989)	Sludge	94	<i>Flavitalea gansuensis</i> (GU295962)
Planctomycetes						
HG379870	1	90	Uncultured <i>Planctomycetaceae</i> bacterium (FJ543048)	Gut	80	<i>Blastopirellula marina</i> (AANZ01000021)
HG379871	1	84	Uncultured <i>Planctomycetales</i> bacterium (AY360646)	Oxic rice field soil	86	<i>Singulisphaera acidiphila</i> (AM850678)
Alphaproteobacteria						
HG379872	1	99	<i>Phyllobacterium</i> sp. (DQ431466)	Soil	99	<i>Phyllobacterium trifolii</i> (AY786080)
HG379873	1	93	<i>Phyllobacterium</i> sp. (DQ431466)	Soil	95	<i>Phyllobacterium trifolii</i> (AY786080)
HG379874	1	98	Alphaproteobacterium (DQ123619)	Hospital water network	95	<i>Rhodoplanes roseus</i> (D25313)
HG379875	1	96	Uncultured alphaproteobacterium (GQ302527)	Cold spring	94	<i>Filomicrobium fusiforme</i> (Y14313)
HG379876	2	98	Uncultured alphaproteobacterium (HE614776)	Arsenic and gold mine	90	<i>Geminicoccus roseus</i> (AY428766)
HG379877	14	99	Uncultured alphaproteobacterium (GQ302527)	Cold spring	95	<i>Pedomicrobium manganicum</i> (X97691)

Representative clone (accession number)	No. of clones	Similarity (%)	Nearest published relative	Source	Similarity (%)	Eztaxon affiliation (accession number)
HG379878	1	95	Uncultured alphaproteobacterium (GQ302527)	Cold spring	92	<i>Pedomicrobium manganicum</i> (X97691)
HG379879	2	95	Uncultured alphaproteobacterium (GQ302527)	Cold spring	94	<i>Phyllobacterium trifolii</i> (AY786080)
HG379880	1	97	Uncultured bacterium (FJ478824)	Soil	90	<i>Dongia mobilis</i> (FJ455532)
HG379881	1	87	Uncultured bacterium (AM949497)	Oxic zone of flooded paddy soil	87	<i>Hyphomicrobium aestuarii</i> (Y14304)
HG379882	10	94	Uncultured bacterium (JF166737)	Skin	94	<i>Prosthecomicrobium pneumaticum</i> (AB017203)
HG379883	3	96	Uncultured bacterium (JF166737)	Skin	94	<i>Prosthecomicrobium pneumaticum</i> (AB017203)
HG379884	1	99	Uncultured bacterium (HQ218506)	PAH-contaminated soil	98	<i>Sphingomonas sanxanigenens</i> (DQ789172)
HG379885	1	93	Uncultured <i>Phyllobacteriaceae</i> bacterium (AM936593)	Contaminated soil	91	<i>Prosthecomicrobium pneumaticum</i> (AB017203)
HG379886	5	99	Uncultured sludge bacterium (AF234724)	Sludge	99	<i>Hyphomicrobium aestuarii</i> (Y14304)
HG379887	1	91	Uncultured sludge bacterium (AF234703)	Sludge	94	<i>Hyphomicrobium aestuarii</i> (Y14304)
HG379888	1	91	Uncultured <i>Xanthobacter</i> sp. (FJ542975)	Gut <i>Eisenia foetida</i>	92	<i>Xanthobacter agilis</i> (X94198)
HG379889	2	93	Uncultured <i>Xanthobacter</i> sp. (FJ542975)	High ergovaline treatment gut	94	<i>Xanthobacter agilis</i> (X94198)
Gammaproteobacteria						
HG379890	1	90	Uncultured bacterium (HQ385560)	Activated sludge	90	<i>Luteimonas aquatica</i> (EF626688)
HG379891	4	94	Uncultured <i>Xanthomonadaceae</i> bacterium (AY360613)	Oxic rice field soil	93	<i>Lysobacter thermophilus</i> (JQ746036)

Table S3. Phylogenetic affiliations of the 16S rRNA sequences obtained from the bacteria in the ET3 sample

Representative clone (accession number)	No. of clones	Similarity (%)	Nearest published relative	Source	Similarity (%)	Eztaxon affiliation (accession number)
Acidobacteria						
HG379892	1	96	Uncultured <i>Acidobacteria</i> bacterium (DQ139453)	Roman catacombs	84	<i>Granulicella pectinivorans</i> (AM887757)
HG379893	3	99	Uncultured <i>Acidobacteria</i> bacterium (DQ139452)	Roman catacombs	92	<i>Solibacter usitatus</i> (CP000473)
Actinobacteria						
HG379894	11	96	<i>Catelliglobospora koreensis</i> (NR_028758)	Gold-mine cave	96	<i>Catelliglobospora koreensis</i> (AF171700)
HG379895	5	99	<i>Jiangella muralis</i> (FN645214)	Indoor environment	99	<i>Jiangella muralis</i> (FN645214)
HG379896	1	82	<i>Jiangella muralis</i> (FN645214)	Indoor environment	82	<i>Jiangella muralis</i> (FN645214)
HG379897	1	94	<i>Jiangella muralis</i> (FN645214)	Indoor environment	95	<i>Jiangella muralis</i> (FN645214)
HG379898	6	97	<i>Streptosporangium</i> sp. (EF216357)	Shallow water sediment	97	<i>Streptosporangium longisporum</i> (X89944)
HG379899	5	99	Uncultured actinobacterium (HF584605)	White spots from Etruscan tombs mural paintings	96	<i>Marmoricola scoriae</i> (FN386750)
HG379900	1	94	Uncultured actinobacterium (HM480664)	Soil	94	<i>Micromonospora lupine</i> (AJ783996)
HG379901	1	96	Uncultured bacterium (HM295827)	Skin	97	<i>Nocardia transvalensis</i> (BAGL01000037)
Bacteroidetes						
HG379902	1	94	<i>Chitinophaga japonensis</i> (NR_028638)	Environmental sample	95	<i>Chitinophaga japonensis</i> (AB078055)
HG379903	5	96	Uncultured <i>Bacteroidetes</i> bacterium (CU921989)	Sludge	94	<i>Flavitalea gansuensis</i> (GU295962)
Planctomycetes						
HG379904	1	95	Uncultured <i>Planctomycetaceae</i> bacterium (FJ543047)	Gut	87	<i>Blastopirellula marina</i> (AANZ01000021)
HG379905	4	96	Uncultured <i>Planctomycetes</i> (EF188522)	Altamira Cave	86	<i>Gemmata obscuriglobus</i> (ABGO01000325)
HG379906	1	97	Uncultured bacterium (EF516253)	Grass land soil	93	<i>Singulisphaera rosea</i> (FN391026)
Alphaproteobacteria						
HG379907	9	93	<i>Xanthobacter</i> sp. (AB636292)	Forest soil	93	<i>Xanthobacter tagetidis</i> (X99469)
HG379908	1	99	Uncultured alphaproteobacterium (EF612404)	Soil	96	<i>Afipia birgiae</i> (CAJQ01000091)
HG379909	1	89	Uncultured alphaproteobacterium (EF188662)	Altamira Cave	90	<i>Agaricicola taiwanensis</i> (FJ594057)
HG379910	1	93	Uncultured alphaproteobacterium (AY921815)	Farm soil	89	<i>Azospirillum oryzae</i> (AB185396)
HG379911	1	86	Uncultured alphaproteobacterium (CU921531)	Sludge	86	<i>Bauldia consociata</i> (FJ560750)

Representative clone (accession number)	No. of clones	Similarity (%)	Nearest published relative	Source	Similarity (%)	Eztaxon affiliation (accession number)
HG379912	1	97	Uncultured alphaproteobacterium (GQ302527)	Cold spring	96	<i>Hyphomicrobium aestuarii</i> (Y14304)
HG379913	2	99	Uncultured alphaproteobacterium (EF188462)	Altamira Cave	99	<i>Phyllobacterium ifriqiyense</i> (AY785325)
HG379914	1	95	Uncultured alphaproteobacterium (GQ302527)	Cold spring	94	<i>Phyllobacterium ifriqiyense</i> (AY785325)
HG379915	16	99	Uncultured alphaproteobacterium (GQ302527)	Cold spring	95	<i>Pedomicrobium manganicum</i> X97691)
HG379916	1	88	Uncultured alphaproteobacterium (GQ302527)	Cold spring	85	<i>Pedomicrobium manganicum</i> (X97691)
HG379917	1	93	Uncultured alphaproteobacterium (CU923974)	Sludge	91	<i>Rhodoplanes roseus</i> (D25313)
HG379918	3	94	Uncultured alphaproteobacterium (CU921531)	Sludge	94	<i>Xanthobacter autotrophicus</i> (X94201)
HG379919	1	97	Uncultured bacterium (FJ478824)	Grass prairie	89	<i>Dongia mobilis</i> (FJ455532)
HG379920	1	84	Uncultured bacterium (GQ264219)	Waste site	81	<i>Filomicrobium insigne</i> (EF117253)
HG379921	11	99	Uncultured bacterium (AY424825)	Mobile Cave	99	<i>Hyphomicrobium aestuarii</i> (Y14304)
HG379922	2	99	Uncultured bacterium (JN052226)	<i>Citrus</i> rhizosphere	95	<i>Hyphomicrobium hollandicum</i> (Y14303)
HG379923	1	90	Uncultured bacterium (AY963442)	Soil	86	<i>Pedomicrobium australicum</i> (X97693)
HG379924	12	94	Uncultured bacterium (JF166737)	Skin	93	<i>Prosthecomicrobium pneumaticum</i> (AB017203)
HG379925	2	99	Uncultured bacterium (FJ479056)	Tall grass prairie	99	<i>Rhizobium lupini</i> (X87273)
Gammaproteobacteria						
HG379926	7	94	Uncultured <i>Xanthomonadaceae</i> bacterium (AY360613)	Oxic rice field soil	93	<i>Lysobacter thermophilus</i> (JQ746036)
HG379927	1	89	Uncultured <i>Xanthomonadaceae</i> bacterium (AY360613)	Oxic rice field soil	88	<i>Lysobacter thermophilus</i> (JQ746036)
HG379928	1	90	Uncultured <i>Xanthomonadaceae</i> bacterium (AY360613)	Oxic rice field soil	89	<i>Lysobacter thermophilus</i> (JQ746036)
HG379929	1	87	Uncultured bacterium (AB672310)	Rice paddy field soil	86	<i>Silanimonas mangrovi</i> (HE573756)
Unclassified bacterium						
HG379930	1	80	Alphaproteobacterium (DQ123619)	Water network	78	<i>Rhodoplanes piscinae</i> (AM712913)

Table S4. Phylogenetic affiliations of the 16S rRNA sequences obtained from the bacteria in the ET5 sample

Representative clone (accession number)	No. of clones	Similarity (%)	Nearest published relative	Source	Similarity (%)	Eztaxon affiliation (accession number)
Acidobacteria						
HG379931	2	94	Uncultured Acidobacteria bacterium (JN037860)	Saline-alkaline soil	83	<i>Candidatus Chloracidobacterium thermophilus</i> (CP002514)
Actinobacteria						
HG379932	1	97	<i>Catelliglobospora koreensis</i> (NR_028758)	Gold-mine cave	98	<i>Catelliglobospora koreensis</i> (AF171700)
HG379933	1	98	<i>Kribbella antibiotica</i> (NR_029048)	Soil	99	<i>Kribbella antibiotica</i> (AY082063)
HG379934	1	92	<i>Kribbella antibiotica</i> (NR_029048)	Soil	92	<i>Kribbella antibiotica</i> (AY082063)
HG379935	2	99	Uncultured actinobacterium (HF584605)	White spots from Etruscan mural paintings	95	<i>Nocardioides salaries</i> (DQ401092)
HG379936	2	96	Uncultured bacterium (FJ479385)	Grass prairie	91	<i>Aciditerrimonas ferrireducens</i> (JN033775)
HG379937	1	97	Uncultured bacterium (FJ479385)	Undisturbed tall grass prairie	91	<i>Iamia majanohamensis</i> (JN033775)
HG379938	3	95	Uncultured bacterium (HM557659)	Fungus garden	99	<i>Jiangella muralis</i> (FN645214)
HG379939	1	95	Uncultured bacterium (HM295827)	Skin	95	<i>Nocardia transvalensis</i> (BAGL01000037)
HG379940	4	96	Uncultured soil bacterium (DQ643735)	Agricultural soil	96	<i>Streptosporangium anatoliense</i> (HQ157194)
Bacteroidetes						
HG379941	1	99	<i>Chitinophaga niabensis</i> (NR_044559)	Soil	99	<i>Chitinophaga niabensis</i> (EU714259)
Planctomycetes						
HG379942	1	90	<i>Isosphaera pallida</i> (NR_074534)	Algal mat from Kah-nee-tah hot spring	90	<i>Isosphaera pallida</i> (CP002353)
HG379943	2	97	<i>Singulisphaera acidiphila</i> (AM902527)	<i>Sphagnum</i> peat bog	97	<i>Singulisphaera acidiphila</i> (AM850678)
HG379944	2	96	Uncultured <i>Planctomycetes</i> (EF188522)	Altamira Cave	86	<i>Zavarzinella formosa</i> (AM162406)
HG379945	1	99	Uncultured sludge bacterium (AF234736)	Sludge	85	<i>Pirellula staleyi</i> (CP001848)
Alphaproteobacteria						
HG379946	1	93	<i>Xanthobacter</i> sp. (AB636292)	Forest soil	94	<i>Xanthobacter tagetidis</i> (X99469)
HG379947	1	99	Uncultured <i>Hyphomicrobium</i> sp. (AM935308)	Hydrocarbon-contaminated soil	96	<i>Hyphomicrobium denitrificans</i> (ACVL01000012)
HG379948	1	98	Alphaproteobacterium (DQ123619)	Hospital water network	93	<i>Rhodoplanes roseus</i> (D25313)
HG379949	1	95	Uncultured <i>Hyphomicrobiaceae</i> bacterium (EU266918)	Tar-oil contaminated aquifer sediments	92	<i>Filomicrobium fusiforme</i> (Y14313)
HG379950	1	98	Uncultured <i>Phyllobacteriaceae</i> bacterium (EF019808)	Trembling aspen rhizosphere	94	<i>Mesorhizobium chacoense</i> (AJ278249)

Representative clone (accession number)	No. of clones	Similarity (%)	Nearest published relative	Source	Similarity (%)	Eztaxon affiliation (accession number)
HG379951	2	94	Uncultured <i>Rhizobiales</i> bacterium (AM936561)	Contaminated soil	91	<i>Prosthecomicrobium pneumaticum</i> (AB017203)
HG379952	1	99	Uncultured <i>Sphingomonadaceae</i> bacterium (EF019685)	Trembling aspen rhizosphere	96	<i>Sphingomonas sediminicola</i> (AB258386)
HG379953	2	99	Uncultured alphaproteobacterium (FJ535080)	Cave wall biofilm	89	<i>Hyphomicrobium hollandicum</i> (IFAMKB-677)
HG379954	1	99	Uncultured alphaproteobacterium (HF584615)	White spots from Etruscan mural paintings	88	<i>Paracoccus rhizosphaerae</i> (JN662389)
HG379955	3	98	Uncultured alphaproteobacterium (GQ302527)	Cold spring	94	<i>Pedomicrobium manganicum</i> (X97691)
HG379956	5	99	Uncultured alphaproteobacterium (GQ302527)	Cold spring	95	<i>Pedomicrobium manganicum</i> (X97691)
HG379957	1	99	Uncultured alphaproteobacterium (GQ302524)	Cold spring	95	<i>Pseudolabrys taiwanensis</i> (DQ062742)
HG379958	1	99	Uncultured bacterium (JN850318)	Yellow microbial mat from lava tube wall	89	<i>Dongia mobilis</i> (FJ455532)
HG379959	26	98	Uncultured bacterium (AY424825)	Movile Cave	99	<i>Hyphomicrobium aestuarii</i> (Y14304)
HG379960	1	98	Uncultured bacterium (AY424825)	Movile Cave	98	<i>Hyphomicrobium aestuarii</i> (Y14304)
HG379961	1	86	Uncultured bacterium (AY424825)	Movile Cave	86	<i>Hyphomicrobium zavarzinii</i> (Y14305)
HG379962	1	93	Uncultured bacterium (AB280306)	Methane-consuming sludge	93	<i>Hyphomicrobium zavarzinii</i> (Y14305)
HG379963	1	90	Uncultured bacterium (AY424825)	Movile Cave	88	<i>Hyphomicrobium zavarzinii</i> (Y14305)
HG379964	1	99	Uncultured bacterium (DQ304805)	Root from <i>Lasiurus sindicus</i>	97	<i>Inquilingus ginsengisoli</i> (AB245352)
HG379965	1	96	Uncultured sludge bacterium (AF234724)	Sludge	93	<i>Hyphomicrobium aestuarii</i> (Y14304)
Betaproteobacteria						
HG379966	1	99	<i>Achromobacter</i> sp. (HE613446)	Humans	95	<i>Achromobacter spanius</i> (AY170848)
Gammaproteobacteria						
HG379967	1	99	<i>Pseudomonas alcaligenes</i> (AY835998)	Marine	99	<i>Pseudomonas alcaligenes</i> (Z76653)
HG379968	2	95	Uncultured <i>Xanthomonadaceae</i> bacterium (AY360613)	Oxic rice field soil	93	<i>Lysobacter thermophilus</i> (JQ746036)
HG379969	20	94	Uncultured <i>Xanthomonadaceae</i> bacterium (AY360613)	Oxic rice field soil	93	<i>Lysobacter thermophilus</i> (JQ746036)
HG379970	3	94	Uncultured <i>Xanthomonadaceae</i> bacterium (AY360613)	Oxic rice field soil	93	<i>Lysobacter thermophilus</i> (JQ746036)
HG379971	1	94	Uncultured <i>Xanthomonadaceae</i> bacterium (AY360613)	Oxid rice field soil	91	<i>Lysobacter thermophilus</i> (JQ746036)
Deltaproteobacteria						
HG379972	1	99	Uncultured bacterium (GQ263899)	Waste site	86	<i>Desulfuromonas thiophila</i> (Y11560)

Table S5. Phylogenetic affiliations of the 16S rRNA sequences obtained from the potentially active bacteria in the ET3 sample

Representative clone (accession number)	No. of clones	Similarity (%)	Nearest published relative	Source	Similarity (%)	Eztaxon affiliation (accession number)
Acidobacteria						
HG379973	1	93	Uncultured <i>Acidobacteria</i> bacterium (HF584585)	White spots from Etruscan tombs mural paintings	83	<i>Candidatus</i> Chloracidobacterium thermophilum (CP002514)
Actinobacteria						
HG379974	1	96	<i>Catelliglobospora koreensis</i> (NR_028758)	Gold-mine cave	96	<i>Catelliglobospora koreensis</i> (AF171700)
HG379975	1	95	<i>Catelliglobospora koreensis</i> (NR_028758)	Gold-mine cave	92	<i>Catelliglobospora koreensis</i> (AF171700)
HG379976	4	98	<i>Jiangella muralis</i> (FN645214)	Wall material of an indoor environment	99	<i>Jiangella muralis</i> (FN645214)
HG379977	3	95	<i>Streptosporangium</i> sp. (GQ924528)	Vegetable garden soil	96	<i>Streptosporangium oxazolinicum</i> (AB594818)
HG379978	4	97	<i>Streptosporangium</i> sp. (EF216357)	Shallow water sediment	97	<i>Streptosporangium longisporum</i> (X89944)
HG379979	6	99	Uncultured actinobacterium (HF584605)	White spots from Etruscan tombs mural paintings	95	<i>Marmoricola scoriae</i> (FN386750)
HG379980	1	98	Uncultured actinobacterium (HF584605)	White spots from Etruscan tombs mural paintings	91	<i>Nocardioides fonticola</i> (EF626689)
HG379981	1	99	Uncultured actinobacterium (HF584644)	White spots from Etruscan tombs mural paintings	99	<i>Rubrobacter xylanophilus</i> (CP000386)
HG379982	2	97	Uncultured bacterium (FJ479385)	Undisturbed tall grass prairie	89	<i>Iamia majanohamensis</i> (AB360448)
HG379983	1	99	Uncultured bacterium (HM297992)	Skin	98	<i>Janibacter anophelis</i> (AY837752)
HG379984	1	99	Uncultured bacterium (GQ091279)	Skin	95	<i>Propionibacterium acnes</i> (AE017283)
Bacteroidetes						
HG379985	1	95	Uncultured bacterium (JN367229)	Soil	90	<i>Adhaeribacter terreus</i> (EU682684)
HG379986	1	97	Uncultured bacterium (HM186161)	Hanford Site 300 Area Surface	95	<i>Chitinophaga niabensis</i> (EU714259)
HG379987	3	96	Uncultured <i>Bacteroidetes</i> bacterium (CU921989)	Wastewater sludge	94	<i>Flavitalea gansuensis</i> (GU295962)
Firmicutes						
HG379988	1	98	<i>Lactobacillus crispatus</i> (NR_074986)	Ephitelial cells	99	<i>Lactobacillus crispatus</i> (Y17362)
Alphaproteobacteria						
HG379989	3	99	<i>Hyphomicrobium aestuarii</i> (Y14304)	Brackish water, Elbe river	99	<i>Hyphomicrobium aestuarii</i> (Y14304)
HG379990	1	99	<i>Hyphomicrobium aestuarii</i> (Y14304)	Brackish water, Elbe river	97	<i>Hyphomicrobium aestuarii</i> (Y14304)
HG379991	7	99	<i>Hyphomicrobium zavarzinii</i> (Y14306)	Peaty and moist soil	99	<i>Hyphomicrobium zavarzinii</i> (Y14306)
HG379992	1	96	<i>Hyphomicrobium zavarzinii</i> (Y14306)	Peaty and moist soil	93	<i>Hyphomicrobium zavarzinii</i> (Y14306)

Representative clone (accession number)	No. of clones	Similarity (%)	Nearest published relative	Source	Similarity (%)	Eztaxon affiliation (accession number)
HG379993	1	97	Uncultured bacterium (JX271904)	Seed sludge	89	<i>Hyphomicrobium zavarzinii</i> (Y14305)
HG379994	1	98	<i>Inquilingus ginsengisoli</i> (GU201848)	Nodules of the <i>Sphaerophysa salsula</i>	99	<i>Inquilingus ginsengisoli</i> (AB245352)
HG379995	1	99	<i>Paracoccus</i> sp. (EU418724)	Endophytic bacteria from copper-tolerant plants	98	<i>Paracoccus aminovorans</i> (D32240)
HG379996	2	98	<i>Sphingomonas sanxanigenens</i> (NR_043962)	Soil	98	<i>Sphingomonas sanxanigenens</i> (DQ789172)
HG379997	1	99	<i>Sphingomonas</i> sp. (EU337119)	Cattle milk	98	<i>Sphingomonas alpine</i> (GQ161989)
HG379998	1	85	Uncultured alphaproteobacterium (CU921531)	Wastewater sludge	83	<i>Blastochloris sulfovirdis</i> (D86514)
HG379999	1	95	Uncultured alphaproteobacterium (HF584671)	White spots from Etruscan tombs mural paintings	89	<i>Dongia mobilis</i> (FJ455532)
HG380000	1	99	Uncultured alphaproteobacterium (HF584663)	White spots from Etruscan tombs mural paintings	99	<i>Sphingomonas echinoides</i> (JH584237)
HG380001	1	98	Uncultured alphaproteobacterium (JN020189)	Chernobyl concrete microbial biofilm	96	<i>Sphingomonas rubra</i> (FJ834325)
HG380002	1	94	Uncultured bacterium (JF166737)	Skin	93	<i>Amorphus coralli</i> (DQ097300)
HG380003	1	93	Uncultured bacterium (JF166737)	Skin	88	<i>Amorphus orientalis</i> (FJ998414)
HG380004	1	92	Uncultured bacterium (EU133367)	Soil	86	<i>Azospirillum halopraeferens</i> (Z29618)
HG380005	1	99	Uncultured bacterium (DQ088788)	Crustal biotome	95	<i>Filomicrobium fusiforme</i> (Y14313)
HG380006	1	99	Uncultured bacterium (JX271904)	Seed sludge	94	<i>Hyphomicrobium zavarzinii</i> (Y14305)
HG380007	1	96	Uncultured bacterium (GQ264456)	Simulated low level waste site	96	<i>Hyphomicrobium aestuarii</i> (Y14304)
HG380008	1	97	Uncultured bacterium (JX271904)	Seed sludge	92	<i>Hyphomicrobium zavarzinii</i> (Y14306)
HG380009	1	99	Uncultured bacterium (GQ264219)	Simulated low level waste site	96	<i>Pedomicrobium manganicum</i> (X97691)
HG380010	1	98	Uncultured bacterium (HM331997)	Skin	96	<i>Sphingomonas jaspsi</i> (AB264131)
HG380011	1	99	Uncultured <i>Bradyrhizobium</i> sp. (FJ193014)	Spacecraft assembly clean room	98	<i>Afipia massiliensis</i> (AY029562)
HG380012	2	93	Uncultured <i>Phyllobacteriaceae</i> bacterium (AM936593)	Contaminated soil	90	<i>Amorphus orientalis</i> (FJ998414)
HG380013	3	98	Uncultured <i>Phyllobacteriaceae</i> bacterium (EF019808)	Trembling aspen rhizosphere	97	<i>Mesorhizobium robiniae</i> (EU849582)
HG380014	30	94	Uncultured <i>Phyllobacteriaceae</i> bacterium (AM936593)	Contaminated soil	93	<i>Prosthecomicrobium pneumaticum</i> (AB017203)
HG380015	1	96	Uncultured soil bacterium (DQ643686)	Agricultural soil	89	<i>Candidatus Alysiosphaera europaea</i> (AY4287566)
HG380016	10	93	Uncultured <i>Xanthobacter</i> sp. (HE575387)	Reverse osmosis membrana	93	<i>Xanthobacter tagetidis</i> (X99469)

Representative clone (accession number)	No. of clones	Similarity (%)	Nearest published relative	Source	Similarity (%)	Eztaxon affiliation (accession number)
Gammaproteobacteria						
HG380017	1	99	Uncultured bacterium (JX105534)	Ornamental fish aquarium	91	<i>Aeromonas taiwanensis</i> (FJ320077)
HG380018	1	99	Uncultured bacterium (JN832961)	Seawater from coral reef	99	<i>Acinetobacter lwoffii</i> (AIEL01000120)
HG380019	1	97	Uncultured <i>Luteimonas</i> sp. (FJ609383)	River sediment	97	<i>Luteimonas cucumeris</i> (HQ874629)
HG380020	2	94	Uncultured <i>Xanthomonadaceae</i> bacterium (AY360613)	Oxic rice field soil	92	<i>Dokdonella fugitiva</i> (AJ969432)