Microbiome differentiation between ant castes implicates new microbial roles in the fungus-growing ant *Trachymyrmex septentrionalis*

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Supplementary Figure S1. *Pseudonocardia cf. carboxydivorans* morphotypes: (A) light tan, circular growth (B) yellow, circular growth (C) white, irregular growth front (D) dark brown, circular growth. Despite the range of morphology, all of the isolates shared identical partial 16S sequences.
Supplementary Figure S2. Rarefaction analyses of bacterial Operational Taxonomic Units (OTUs) associated with *Trachymyrmex septentrionalis*. OTUs are binned at 3% sequence dissimilarity. Samples from garden workers, outside workers, and reproductives (male and females) appear to reach an asymptote at 1000-5000 sequences sampled, but, as expected, soil samples require much greater sequencing depth (probably more than 10,000-100,000 sequences) to profile the full bacterial diversity. Some of the garden samples reach an asymptote with a sequencing depth between 1000-5000, but bacterial diversity in other gardens was under-sampled.
Supplementary Figure S3. Relative abundances or percent sequence reads of common bacterial orders associated with \textit{T. septentrionalis} ants, its nest environment, and \textit{Pheidole} control ants collected nearby. Relative abundances are percentages calculated by counting the 454-sequences identified to order by BLAST match. Total sequence reads were averaged for each sample type (garden workers, outside workers, reproductive females, males, garden, chamber soil, excavated soil, and \textit{Pheidole} ants). Two orders, Actinomycetales and Solirubrobacterales (both in the class Actinobacteria), had the most sequence reads associated with \textit{T. septentrionalis} garden workers, outside workers, males, and reproductive females. \textit{Pheidole} ants show very different bacterial profiles compared to \textit{Trachymyrmex} ants (common bacteria for \textit{Pheidole} ants are listed in Tables S1 and S2).
Supplementary Table S1. BLAST match to closest taxonomic identity. 454-sequences were identified to their closest taxonomic level from BLAST hits using a high quality 16S reference database curated by the Medical Biofilm Institute. The reference BLAST-assignments are presented according to percent sequence-identity to particular taxonomic levels (i.e., sequences with a greater than 97% sequence-identity match were resolved to species: between 95-97% to genus, between 90-95% to family, between 85-90% to order, 80-85% to class, and 75-80% to phylum).
Supplementary Table S2. BLAST results to nearest forced genus.

BLAST was used to identify raw 454 sequence tags to a reference sequence from the Medical Biofilm Research Institute 16S database. This table presents the data forced to the nearest bacterial genus (matched at a 100-75% hit identity) with an average blast hit having a 93.8% (+/- 4.2) identity match. This forced BLAST table was not intended to be a strict reference assignment, but was useful to compare the variation of sequence reads observed within samples.
Supplementary Table S3. Bacterial genera found in ants and soils per nest. To evaluate possible ecological links between ant-associated microbes and microbes in the soil, we counted the number of shared bacterial genera identified in ant samples (not including the garden) and soil samples of the same nest. 65% of the bacterial genera found in the ant samples were shared with the bacterial genera found in the soil, suggesting possible ecological connectivity between bacterial communities associated with ants and with soil.

| Nest | # Bacterial Genera in Ants | # Bacterial Genera in Soils | Genera Shared between Ants & Soil | % Shared/Ant | % Shared/Soil |
|------|---------------------------|-----------------------------|----------------------------------|--------------|--------------|
| J0201 | 63                        | 180                         | 37                               | 58.7         | 20.6         |
| J0303 | 78                        | 255                         | 58                               | 74.4         | 22.7         |
| J0304 | 55                        | 277                         | 40                               | 72.7         | 14.4         |
| J032A | 133                       | 227                         | 79                               | 59.4         | 34.8         |
| J032B | 151                       | 359                         | 123                              | 81.5         | 34.3         |
| J0401 | 82                        | 263                         | 59                               | 72.0         | 22.4         |
| J0402 | 106                       | 247                         | 64                               | 60.4         | 25.9         |
| J0403 | 103                       | 275                         | 58                               | 56.3         | 21.1         |
| J0404 | 78                        | 272                         | 59                               | 75.6         | 21.7         |
| J0501 | 87                        | 248                         | 62                               | 71.3         | 25           |
| J0502 | 63                        | 308                         | 41                               | 65.1         | 13.3         |
| J0503 | 77                        | 318                         | 50                               | 64.9         | 15.7         |
| J0504 | 99                        | 292                         | 76                               | 76.8         | 26           |
| J0601 | 82                        | 295                         | 57                               | 69.5         | 19.3         |
| J0602 | 88                        | 210                         | 58                               | 65.9         | 27.6         |
| J0603 | 65                        | 262                         | 44                               | 67.7         | 16.8         |
| J0630-03 | 73                    | 226                         | 38                               | 52.1         | 16.8         |
| J0701 | 96                        | 181                         | 43                               | 44.8         | 23.8         |
| J0702 | 80                        | 185                         | 39                               | 48.8         | 21.1         |
| J0704 | 113                       | 216                         | 69                               | 61.1         | 31.9         |
| J0801 | 78                        | 372                         | 59                               | 75.6         | 15.9         |
| J0802 | 46                        | 245                         | 28                               | 60.9         | 11.4         |
| J0803 | 103                       | 215                         | 49                               | 47.6         | 22.8         |
| J1-7  | 145                       | 260                         | 106                              | 73.1         | 40.8         |
| J8-12 | 68                        | 280                         | 49                               | 72.1         | 17.5         |
| Average | 88.5                   | 258.7                       | 57.8                             | 65.1         | 22.5         |
| Standard Deviation | 26.3                | 49.5                        | 21.2                             |              |              |
Supplementary Table S4. BLAST results according to two 16S reference databases. Sample subset comparison of BLAST results using two different 16S reference databases: Ribosomal Database Project (RDP) Classifier and a high-quality 16S database curated by the Medical Biofilm Research Institute (MBRI). We performed a BLAST on all of the 454-sequences using the two reference databases, but a subset of the results are shown in the table from collection months February and June. This table illustrates some of the differences between BLAST hits from two different reference databases. Both databases identified the most abundant genera found in all samples as Solirubrobacter and Pseudonocardia with a 93% and 98% similarity, respectively. However, much of the rare bacterial strains did not match between the databases. Overall, this comparison served to increase our confidence in the common bacteria, but any rare genera results should be interpreted with caution.
Supplementary Table S5. Abundance of *Pseudonocardia* strains of *T. septentrionalis* and their phylogenetic placement. Hits from a custom BLAST of *Pseudonocardia* 454-sequences to a *Pseudonocardia* reference database were grouped for each sample type into the 10 subclades of *Pseudonocardia* identified previously in the phylogenetic analysis of ¹. Total number of different sequences (second to last row) indicates the number of *Pseudonocardia* sequences generated by 454-sequencing. Because some of the 454 sequences BLAST to the same reference sequence in the *Pseudonocardia* phylogeny, we also list the total number of distinct strains placed into each clade, defined as the number of unique BLAST hits to one of the 116 sequences included in our *Pseudonocardia* database. BLAST hits for all 26,965 sequences are shown in Supplementary Table S8. The genus *Pseudonocardia* is split basally into two main subgroups, one containing clades 1-5, the other containing clades 6-10 ¹. Although all ant samples combined (garden worker, outside worker, reproductive females, and males) carried *Pseudonocardia* from most of the ten clades (except strains from clades 2, 4, and 5 were not found on ants), the majority of the ant-associated *Pseudonocardia* sequences were placed into clade 3 (the so-called nitrificans/alni/carboxydivorans clade sensu ¹). The garden and soil samples also contained *Pseudonocardia* from almost all the clades, but the majority of these sequences are found in clades 6-10, which are *Pseudonocardia* types found more frequently in soil (see Fig. 2b in ¹).
| Samples screened | Garden Worker | Outside Worker | Reproductive Female | Male | Garden Chamber soil | Excavated Soil | Pheidole An | Clades | Name | seq | strains | seq | strains | seq | strains | seq | strains | seq | strains | seq | strains | seq | strains | seq | strains | seq | strains | seq | strains |
|------------------|---------------|----------------|---------------------|------|---------------------|---------------|-------------|---------|------|-----|--------|-----|---------|-----|---------|-----|---------|-----|---------|-----|---------|-----|---------|-----|---------|-----|---------|
| lade 1           | 4             | 3              | 3                   | 2    | 0                   | 0             | 0           | 0       | 0    | 0   | 47     | 5   | 25       | 6   | 0       | 0   | 0       | 0   | 0       | 0   | 0       | 0   | 0       | 0   | 0       |
| lade 2           | 0             | 0              | 0                   | 0    | 0                   | 0             | 0           | 0       | 0    | 0   | 0      | 0   | 0        | 0   | 1       | 1   | 0       | 0   | 0       | 0   | 0       | 0   | 0       | 0   | 0       |
| lade 3           | 7,281         | 3              | 2,879               | 3    | 12,070              | 3             | 2,088       | 2       | 50   | 1   | 13     | 1   | 3        | 1   | 0       | 0   | 0       | 0   | 0       | 0   | 0       | 0   | 0       |
| lade 4           | 0             | 0              | 0                   | 0    | 0                   | 0             | 0           | 2       | 1    | 1   | 1      | 1   | 3        | 1   | 0       | 0   | 0       | 0   | 0       | 0   | 0       | 0   | 0       |
| lade 5           | 0             | 0              | 0                   | 0    | 0                   | 0             | 0           | 2       | 2    | 8   | 3      | 0   | 0        | 0   | 0       | 0   | 0       | 0   | 0       | 0   | 0       | 0   | 0       |
| lade 6           | 4             | 2              | 3                   | 3    | 1                   | 2             | 3           | 2       | 50   | 1   | 13     | 1   | 3        | 1   | 0       | 0   | 0       | 0   | 0       | 0   | 0       | 0   | 0       | 0   | 0       |
| lade 7           | 7             | 2              | 3                   | 1    | 1                   | 1             | 0           | 0       | 0    | 0   | 28     | 3   | 1        | 1   | 0       | 0   | 0       | 0   | 0       | 0   | 0       | 0   | 0       | 0   | 0       |
| lade 8           | 2             | 1              | 2                   | 1    | 0                   | 0             | 2           | 2       | 20   | 2   | 463    | 9   | 319      | 8   | 2       | 1   | 0       | 0   | 0       | 0   | 0       | 0   | 0       | 0   | 0       |
| lade 9           | 8             | 2              | 2                   | 2    | 0                   | 0             | 6           | 5       | 4    | 44  | 131    | 6   | 968      | 2   | 0       | 0   | 0       | 0   | 0       | 0   | 0       | 0   | 0       | 0   | 0       |
| lade 10          | 2             | 1              | 6                   | 2    | 0                   | 0             | 0           | 0       | 2    | 2   | 10     | 2   | 14       | 3   | 0       | 0   | 0       | 0   | 0       | 0   | 0       | 0   | 0       | 0   | 0       |

Number of 454-sequences generated: 7,308
Number of distinct strains among all sequences: 14
Supplementary Table S6. 16S primers for amplification and sequencing of cultured isolates.

Primer combinations used to amplify partial 16S rDNA sequences for culture-dependent 16S-sequence identification of isolated bacterial morphotypes.

| Primer – Forward 5’-3’ | Tm | Source | Primer – Reverse 5’-3’ | Tm | Source | Bacterial genera that amplified with primer combination |
|------------------------|----|--------|------------------------|----|--------|-------------------------------------------------------|
| 8F - AGA GTT TGA TCC TGG CTC AG | 61 | 2 | 897R_hdi- GGT AAG GTT CTT CGC GTT GC | 66 | Developed by H. Ishak | some Streptomyces |
| 133F_hdi - GAGTAA CAC GTG GGY GAC CTG C | 68 | Developed by H. Ishak | 897R_hdi- GGT AAG GTT CTT CGC GTT GC | 66 | Developed by H. Ishak | All bacteria from our survey except Nonomuraea. |
| 261F_hdi - CTG GGA CTG AGA CAC GGC | 65 | Developed by H. Ishak | 897R_hdi- GGT AAG GTT CTT CGC GTT GC | 66 | Developed by H. Ishak | All bacteria from our survey except Nonomuraea. Main primer set used. Kribbella, Nocardia, Pseudonocardia spinospora, P. carboxydivorans, and some Streptomyces |
| AMP2- GTG GAA AGT TTT TTC GGC TGG GG | 53 | 5 | AMP3- GCG GCA CAG AGA CCG TGG AAT | 53 | 5 | Kribbella, Nocardia, Nonomuraea, and some Streptomyces |
| U519F- CAG CMG CCG TGG TAA TWC | 54 | 4 | U1406R- GAC GGG CGG TGT GTR CA | 52 | 5 | Pseudonocardia alni and P. carboxydivorans |
| U519F_Psadj - CAG CWG CCG CGG TAA YAC | 64 | 4 | U1406R- GAC GGG CGG TGT GTR CA | 52 | 5 | Pseudonocardia alni and P. carboxydivorans |
Supplementary Table S7. Raw output from the Medical Biofilm Research Institute BLAST. The BLAST output report includes the raw sequence read, the % identity score, and the genus reference assignments. The sequence identity scores range from 100-75% with higher scores indicating a better match.
Supplementary Table S8. Raw output for the *Pseudonocardia*-specific BLAST. The BLAST used a comprehensive *Pseudonocardia* reference database derived from the phylogenetic analysis in \(^1\)
Supplementary Methods

The Study System

The fungus-growing ant *Trachymyrmex septentrionalis* is a suitable study system for a phenological survey of bacterial-community associations because (a) colony sizes are large enough to permit repeat sampling of single nests in the field, but small enough for easy sampling of an entire colony; (b) nests occur at high densities in most populations, so many nests can be studied in the same habitat; (c) nests occur in sandy soil, facilitating nest excavation; (d) nest architecture is simple, with 2-5 gardens total (mode of 2-3 gardens), topmost garden chambers are found in spring at a depth of 5-15 cm, and the deepest garden chambers almost never exceed 80 cm depth in central Texas; (e) most importantly, colonies undergo an annual cycle where garden sizes are greatly reduced during winter (gardens are sometimes reduced to small fragments carried by a few workers; 6,7), foraging ceases during the coldest months, gardens are reactivated in spring, and gardens reach the largest sizes throughout summer when alates are produced. *T. septentrionalis* is the only fungus-growing ant known with such extreme changes in garden size between seasons 6. *T. septentrionalis* alates will wait in the nest until rains stimulate mating flights. The study site experienced drought conditions in 2009, according to nearby precipitation data from the National Climate Data Center for Austin Bergstrom public database (http://www.nws.noaa.gov/climate/index.php?wfo=ewx) there were only three days between June and September with >1” precipitation (July 22, August 12, and Aug 27), which may have stimulated mating flights.

Culture-dependent isolation

Samples for culture-dependent isolation were collected in vials containing 1-mL of autoclaved saline buffer (0.7g K₂HPO₄, 0.5g MgSO₄, 0.3g KH₂PO₄, 0.01g FeSO₄, 0.001g ZnSO₄ in 1 L
ultrapure water). Samples in saline vials were vortexed for 10 min to dislodge microbes, and then 50µL aliquots of the vortexed saline were spread on two replicate chitin plates containing a minimum-carbon medium that favors growth of autotrophic bacteria. In addition, ants housed individually in sterile, blank vials (i.e. vials without ethanol or saline buffer) were separated into head, mesosoma, and metasoma using flame-sterilized forceps, and then each body segment was streaked directly onto chitin plates (streaking the body part over the medium surface). Growth of the first actinomycete colonies was visible on the chitin plates after 8-10 days incubation at room temperature. A subset of representative actinomycete colonies visible 7-14 days after inoculation were transferred to potato dextrose agar (PDA) and maintained as pure live cultures for morphotyping and 16S rDNA Sanger-sequencing. After 14 days, chitin plates generally became overgrown with contaminant fungi and isolation of actinomycete bacteria was terminated.

Identification of actinomycete morphotypes

Each actinomycete colony was morphotyped according to color and growth morphology on the PDA medium. The actinomycete morphotypes were each identified by sequencing a portion of the 16S rDNA gene. DNA was extracted from a small sample of actinomycete growth taken from a pure live culture using a standard 10% Chelex protocol (Sigma-Aldrich). A fragment of the 16S gene was amplified and then sequenced on an ABI 3100 automated sequencer (16S primers are listed in Supplementary Table S5). All primer pairs used the following PCR cycling profile: 94°C for 4 min; 35 cycles of 94°C for 1 min, 50°C for 1 min, 70°C for 2 min; final 72°C incubation for 10 min. 264 total sequences obtained from the isolated bacteria were assigned to genus or species in fall 2009 according to their closest hit via nucleotide BLAST at the Core Nucleotide Collection deposited in the National Center for Biotechnology Information (NCBI). Once we had identified at least three cultures of each morphotype through 16S sequencing (e.g.,
*Amycolatopsis, Kribbella, Streptomyces, Pseudonocardia,* etc.), the remaining cultures were classified by their respective morphotype appearance on PDA plates.

454 Sequencing Fast UniFrac Analyses

For community comparison analysis, we used a custom Perl script to randomly sub-sample 1000 sequences from each bacterial community sequenced. In four samples, less than 1000 sequences had been generated, so we used all the respective sequences from these four samples. Garden sample J0304-G had a failed 454-pyrosequencing run and therefore had to be excluded from the analyses. The randomly-sampled sequences were clustered by sequence similarity using the web-based program cd-hit-est with a minimum identity of 97% within each cluster. The longest sequence read from each cluster was selected as a representative sequence for that cluster for further analysis. These representative sequences were aligned using the sequence pipeline in Mothur with the SILVA alignment as a template (www.mothur.org). The final alignment consisted of 1,787 total sequences with an average sequence length of 445 base pairs (bp) and a range of 300 bp to 510 bp. An approximate maximum-likelihood phylogenetic tree was generated by FastTree. We used Fast Unifrac to assess the differences between the bacterial communities associated with ants, gardens, and the two types of soil sampled. UniFrac distances are based on the phylogenetic tree branch lengths shared between two communities. A large UniFrac distance between two communities implies that they are not similar, and therefore members of the compared bacterial communities tend to be more distantly related. We used an abundance-weighted principal coordinate analysis (PCoA) to evaluate differences in bacterial community composition. All 454-sequencing data can be found at NCBI in the short read archive (SRP008669) with the exception of samples J1-J12 whose .sff files were lost. A complete data set in fasta format can be requested from the authors.

List of sequences selected for the custom Pseudonocardia BLAST
116 sequences were used for the custom BLAST derived from the recently published global *Pseudonocardia* phylogenetic analysis. These 116 sequences were chosen from the complete dataset (n=334) by removing redundant sequences (i.e., sequences with at least 99.5% sequence similarity) and removing sequences that did not cover the complete V1-V3 region of the 16S gene. The below sequence names retain their original name as it appeared in, but the clade numbers were added for clarity. Note that respective GenBank accessions are incorporated within each taxon name.

>Clade1PyroSequGQ082333nbw1151a06c1humanskinUSA
>Clade1PyroSequGQ008081nbw113d01c1humanskinUSA
>Clade1PyroSequGQ009429nbw776e01c1humanskinUSA
>Clade1PendophyticaCulturedDQ887489YIM56035endophyteChina
>Clade1simtoPendophyticaCulturedEF216352TFS701fjordsedimentNorway
>Clade1PyroSequGQ002479nbu177h11c1humanskinUSA
>Clade1simtoPendophyticaCulturedX87314SR244aleaflitterAustralia
>Clade1CulturedAY376892ApdentigerumA38workerPanama
>Clade1CulturedFJ948117MyssmithiiumG01040103T1workerlabnestUSA
>Clade1CulturedAY944264S07marinespongeChinaSea
>Clade1PkongjuensisCulturedAJ252833LM157cavesoilSouthKorea
>Clade1simtoPammonioxydansCulturedEU925632JSM074014anemonesymbiontChina
>Clade1PammonioxydansCulturedAY500143H9AS41877coastalsedimentChina
>Clade1CulturedFJ490529Ao19Acocctosinosus
>Clade2ParietisCulturedFM86370304St002mouldywallGermany
>Clade2PficiCulturedEU200678YIM56250endophyteChina
>Clade3PtropicaspnovCulturedGQ906587YIM61452endophyteChina
>Clade3CulturedEF588222AcspSP030940501workerArgentina
>Clade3CulturedFJ490549Ao2AcocctosinosusPanama
>Clade3PnitrificansCulturedNEWGENBANKNRRLB1664soilUSA
>Clade4PacaciaeEU921261GMKU095plantrootThailand
>Clade4 Cultured FJ805426 EUM374 endophyte Australia
>Clade5 Cultured FJ948115 Cywheeleri UGM03042701 Y1 worker lab nest
>Clade5 Cultured AJ007000 LAA2 compost biofilter Canada
>Clade5 Cultured AF131480 IM6067 rainforest soil Singapore
>Clade5 Pailaonensis Cultured DQ344632 YIM45505 soil China
>Clade5 Cultured AJ006999 LAA1 compost biofilter Canada
>Clade5 Cultured FJ817397 YIM63638 endophyte China
>Clade5 Phalophobica Cultured AJ252827 IMSNU21327 Type Strain soil
>Clade5 Phalophobica Cultured GQ179660 S4201 endophyte Thailand
>Clade6 Pbabensis sp nov Cultured AB514449 VN05A0561 plant litter Vietnam
>Clade6 Cultured sp EU722523 S053 source unknown
>Clade6 Cloned AJ400508 Hb1K67 deteriorating painting Austria
>Clade6 Cultured DQ344633 YIM45552
>Clade6 Xinjiangensis Cultured EU722520 XJ45 Type Strain soil China
>Clade6 Cultured EU81088001 Q8 Scavewall Spain
>Clade6 Cultured FJ887905 swalm 1229 spring sediment China
>Clade6 Psaturnea Cultured AJ252829 IMSNU20052 air Germany
>Clade6 Cultured EU677789 FXJ2021 soil China
>Clade6 Ppetroleophila Cultured AJ252828 IMSNU22072 soil Germany
>Clade6 Cloned EF516465 FCPP410 grassland soil CA USA
>Clade6 Cloned AB074634 APe452 aposymbioticaphid Japan
>Clade6 Cloned EF540540 M26 oil shale waste Estonia
>Clade6 Cultured EF216350 TFS575 fjord sediment Norway
>Clade6 Cloned FM872941 FB04 H09 flood dust Finland
>Clade6 Cultured FJ937942 LS288 marinesponge China Sea
>Clade6 Cloned GQ263688 FW385 C waste ID USA
>Clade6 Cultured FJ817379 YIM63233 endophyte China
>Clade6 Cloned EF507108 CZ52 H03 contaminated soil Czech Republic
Clade 6
- Cloned FJ893767 nbt35b02 mouseskin USA
- Cultured FJ214340 YIM61043 endophyte China
- Cloned GQ263538FW299B waste USA
- Pzijingensis AF3257256330 Type Strain soil China
- Cloned EU841604 HBUM174915 China
- Paurantiaca Cultured AF325727 AS41537 soil China

Clade 7
- Paurantiaca Cultured AF325727 AS41537 soil China
- Pchloroethenivorans Cultured AF454510 SL1 soil
- Pzijingensis EU841604 HBUM174915 China
- Cultured EU841604 HBUM174915 China
- Cloned EF589993A21 polluted driversediment China
- Cultured EF588213 Trzeteki CC03040404 worker Panama
- Cultured EF588226 Trzeteki CC03010505 worker Panama
- AM936575CM1D11 contaminated soil France
- Pspinosispora Cultured AJ249206 LM141 Type Strain caves soil South Korea
- Cloned EU979047 g38 rhizospheres soil China
- Cultured DQ448726 CNS139 PL04 marine sediment Palau
- Cultured FJ948122 Mysmithii UGM01040208 Actino3 worker
- Cloned EU527120 zd430 glaciers snow Tibet
- Pthermophilia Cultured AJ252830 IMSNU20112 compost Switzerland
- Pkhuvsgulensis spp nov Cultured AB521672 MN08 A0297 Type Strain soil Mongolia
- Cultured FJ948118 Mysmithii UGM01040103 TMWB 1 worker nest
- Cloned DQ643700 W4 Ba36 agricultural soil Germany
- Direct PCR EU718355 Trzeteki RMMA0501052841 worker nest
- Direct PCR EU718354 Trzeteki RMMA0501052840 worker nest
- Direct PCR EU718334 Cywheeleri UGM0304290148 worker nest
- Cloned AM935373 AMGB8 contaminated soil France
- Cultured FJ948123 Mysmithii AGH01041701 TMWB 2 worker nest
- Cultured JESSICA2 Tr septentrio nalis worker field nest garden TX USA
- Cloned FJ661791 P aAD11 nitrate enriched soil MI USA
>Clade9ClonedDQ643691W4Ba27agriculturalsoilGermany
>Clade9ClonedFJ568357A19YB03RMalpinesoilFrance
>Clade9ClonedFJ661792AaAC12nitrateenrichedsoilMIUSA
>Clade9PyroSequGQ002521nbu178d12c1humanskinUSA
>Clade9ClonedFJ570491A6YM19RMalpinesoilFrance
>Clade9PyroSequGQ099352nbw509f04c1humanskinUSA
>Clade9ClonedEU052164C3AA07savannahsoilTXUSA
>Clade9ClonedAM992500A44forestsoilOHUSA
>Clade9ClonedFJ568422A19YE18RMalpinesoilFrance
>Clade9ClonedAY921961AKYG1573farmsoilMNUSA
>Clade9PyroSequGQ062989nbw96c07c1humanskinUSA
>Clade9ClonedFJ616000F12C11agriculturalfieldMIUSA
>Clade9ClonedAY555622Act9sandsoilMDUSA
>Clade9ClonedDQ129564AKIW476aerosolTXUSA
>Clade9PasaccharolyticaY08536DSM44247TypeStrainwastegasbiofilterGermany
>Clade9ClonedEU132741FFCH12016prairiesoilOKUSA
>Clade10CulturedAF118130DB1refinerywastewaterGermany
>Clade10CulturedFJ711205KCITH6stalactitecavernAZUSA
>Clade10PbenzenivoransCulturedAJ556156B5soilGermany
>Clade10PhydrocarbonoxydansCulturedAJ252826IMSNU22140TypeStrainairGermany
>betweenClade9&10CulturedGQ924573ACT0146rootSolomonIslands
>betweenClade9&10PyroSequGQ021408nbw277g01c1humanskinUSA
>betweenClade9&10CulturedEU722525W101sourceunknown
>betweenClade9&10PyunnanensisCulturedAJ252822IMSNU22019TypeStrainsoilChina
>betweenClade9&10ClonedEU132625FFCH10433soilUSA
>betweenClade9&10ClonedGQ264114WC345wasteIDUSA
>betweenClade9&10CulturedFJ3817406YIM63646endophyteChina
>betweenClade9and10PmongoliensisspCulturedAB521671MN08A0270TypeStrainsoilMongolia
>betweenClade9&10ClonedEF220405FI2FC12soilFalkland
>betweenClade9&10CulturedAF131481IM6071rainforestsoilSingapore
>ActinokineosporaenzanensisAB058395IFO16517
>ActinokineosporaterraeNR024774IFO15668
>CrossiellacryophilaNR024964NRRLB16238
>CrossiellaequiNR025088NRRLB24104
>KibdelosporangiumaridumAJ311174DSM43828
>KibdelosporangiumphilippinenseAJ512464DSM44226
>AmycolatopsisalbaNR024888DSM44262
>AmycolatopsisdecaplaninaNR025562DSM44594
>AmycolatopsiskeratiniphilaNR025563DSM44586
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