

Supporting Information

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SI Methods

Isolation of Actinomycete Test Species. Actinomycetes were isolated on chitin-medium described by (1) and (2). Our basic protocol replicated the isolation protocol of these previous studies, with 2 exceptions. The 2 exceptions in our study were: (a) use of a saline buffer (rather than distilled water) to suspend bacteria when dislodging microbes from the ants through vortexing and (b) use of antibiotic-free medium for actinomycete isolation. Previous studies had supplemented isolation plates with antibiotics (nystatin and cycloheximide) to suppress growth of fungi during bacterial isolation, but we used antibiotic-free medium to permit simultaneous isolation of integument-inhabiting fungi (e.g., entomopathogens) that could be useful for testing of the antifungal properties of attine actinomycetes. Because all microbes grow very slowly on the minimum-carbon chitin medium, and because actinomycetes grew abundantly on culture plates, actinomycetes could be readily isolated from the chitin plates on the first attempt.

Buffer for Suspension of Bacteria During Vortexing. The saline buffer contained the same salt concentrations as the chitin-medium (0.7g K₂HPO₄, 0.5g MgSO₄, 0.3g KH₂PO₄, 0.01g FeSO₄, 0.001g ZnSO₄ dissolved in 1 liter ultrapure water).

PCR Conditions and Sequencing. Bacterial isolates were characterized by sequencing a segment of the 16S rDNA gene using the primer pair U519F and 1406R (3) (1 μ l 10x buffer, 0.8 μ l MgCl₂ 25 mM, 0.8 μ l dNTP mix [2.5 mM each nucleotide], 0.8 μ l 100x BSA, 0.6 μ l of each primer at 2 mM, 0.1 μ l Taq polymerase, 1 μ l template, and ddH₂O to a total volume of 10 μ l). The PCR temperature profile was 94 °C for 1 min, 50 °C for 1 min, 72 °C for 2 min; repeat for 35 cycles; followed by a final extension step of 72 °C for 10 min. All PCR products were cycle-sequenced with the ABI Big Dye Terminator Kit (version 3.1) on an ABI PRISM 3100 automated sequencer.

Bacterial Tag-Encoded Titanium Amplicon Pyrosequencing. DNA was extracted from ants and gardens after dry ice methanol freezing and mortar and pestle grinding to a fine powder using methods detailed previously (4). Homogenized powder was resuspended in 500 μ l RLT buffer (QIAGEN) (with β -mercaptoethanol). A sterile 5 mm steel bead (QIAGEN) and 500 μ l 0.1 mm glass beads (Scientific Industries, Inc.) were added for complete bacterial lyses in a Qiagen TissueLyser (QIAGEN), run at 30 Hz for 5 min. Samples were centrifuged briefly, and 100 μ l 100% ethanol were added to a 100 μ l aliquot of the sample supernatant. This mixture was added to a DNA spin column, and DNA recovery protocols were followed as instructed in the QIAamp DNA Mini Kit (QIAGEN) starting at step 5 of the Tissue Protocol. DNA was eluted from the column with 30 μ l water and samples were diluted accordingly to a final concentration of 20 ng/ μ l for use with SYBR Green RT-PCR (Qiagen). DNA samples were quantified using a Nanodrop spectrophotometer (Nyxor Biotech). Bacterial tag-encoded titanium amplicon pyrosequencing and data processing were performed as described previously (5, 6). In short, raw data from bTEFAP was screened and trimmed based upon quality scores and binned into individual sample collections. Sequence collections were then depleted of chimeras using B2C2. The resulting files were then depleted of short reads (<200 bp) and bacterial species identified using BLASTn comparison to a curated high quality 16S database derived from National Center for Biotechnology In-

formation (NCBI). Data were compiled and relative percentages of a given bacterial species were determined for each sample. Data were also compiled at each individual taxonomic level according to the NCBI taxonomy criteria as described previously (5, 6). Collection and sequence information is deposited at GenBank under accessions SRA008625.9.

Isolation of Ecologically-Relevant Test Fungi. To accumulate a set of fungi (Table S4) for the testing of antifungal activities of the actinomycete isolates, attine cultivars and “weed” microfungi were isolated from attine gardens of the same nests from which actinomycetes had been obtained. Fungi were isolated from gardens about 6 weeks after the first actinomycete isolation (see SI Methods S5 for isolation procedure). Isolations were performed by carefully placing 8 garden fragments (2–4 mm diameter) with sterilized forceps on potato dextrose agar (PDA), using the methods of (7) for isolations of cultivars and using the methods of (8) for the isolation of noncultivar garden microfungi. Cultivars were obtained from all of the 7 nests, but noncultivar microfungi were obtained only from 5 of the 7 nests (Table S4). All microfungi obtained from attine gardens were used for testing except for 2 *Penicillium* isolates, which were excluded because of the great risk of contaminating the work environment with spores. One *Escovopsis* strain was isolated from the experimental nest of *C. wheeleri*. Two additional *Escovopsis* strains (one from *T. zeteki* from Panama, one from *T. turrifex* from Texas) that had been obtained in previous *Escovopsis* surveys were added to the set of test-fungi. These 2 strains had been stored under glycerol at –80 °C since isolation in 2003 and 2006, respectively, but were revived 3 weeks before testing in 2008. Three filamentous fungi obtained from the chitin plates (see above; vortex of whole workers of *M. smithii*, *T. turrifex*, and *C. wheeleri*) were also added to the set of test-fungi. One facultatively entomopathogenic fungus, *Fusarium solani*, was isolated from an *Atta texana* queen that had died in an incipient lab nest during spring 2008. One additional entomopathogenic fungus (*Acrodontium* sp.) was isolated from a diseased queen of *Acromyrmex versicolor* that had been collected from a mating flight in Arizona in 2007, then reared in a lab nest. Apart for the exclusion of the 2 *Penicillium* isolates mentioned above, the complete set of 14 noncultivar test fungi (Table S4) represents an unbiased selection of filamentous fungi available in the Mueller Lab shortly after isolation of the actinomycete species in 2008. Because these filamentous fungi were all isolated from attine gardens or from attine ants, the set of 14 test-fungi should be more representative for the problem fungi that ants encounter than standard laboratory species used traditionally for antibiotic testing. To increase the number of entomopathogenic test fungi, we added 5 *Beauveria* and one *Metarhizium* strains from the collection of Department of Agriculture–Agriculture Research Service (USDA-ARS) Plant Protection Research Unit, U.S. Plant, Soil and Nutrition Laboratory, Ithaca, NY 14853-2901.

Test-fungi were identified by sequencing of the ITS rDNA region using the universal primers ITS4 x ITS5 (9) and the LSU rDNA region using the universal primers LR5 x LROR (10). Sequences were compared via the BLASTn with information available at GenBank in September 2008. BLASTn results are listed in Table S4.

SI Results

Presence of Diverse Pseudonocardia Bacteria in Single Attine Nests. Tag-encoded 454-pyrosequencing yielded a total of 41,561 16S-sequences from 4 ant samples and 4 gardens (from *M.*

smithii, 2 nests; *C. wheeleri*, and *T. septentrionalis*) with an average sequence length of 457 bp. The garden sample of *T. septentrionalis* had to be discarded because it consistently yielded inadequate reads (fewer than 30 reads) in repeat 454-sequencing attempts. For the remaining samples, an average of about 5,400 16S-amplicons were characterized for worker-associated bacterial communities and an average of 6,600 amplicons for garden-associated bacterial communities. Rarefaction analyses indicate that this sampling regime of about 5,000 16S-amplicons per community appears sufficient to capture a significant proportion (if not most) of the bacterial diversities (Table S1, Figs. S1 and S2). Under the most stringent definition of Operational Taxonomic Units (OTUs; at least 1% sequence difference between OTUs), accumulation curves reveal 200–300 OTUs (observed) and 300–600 OTUs (predicted with additional sampling) for worker-associated bacterial communities, and 200–500 OTUs (observed) and 200–1000 OTUs (predicted) for garden-associated communities (Fig. S1, Table S1). Compared to other known bacterial communities (e.g., ref. 11), attine-associated bacterial communities emerge as moderately species-rich, even when using a stringent definition of OTUs (1% sequence difference). Additional diversity and richness indices [Shannon

diversity, Chao1 richness, ACE richness; Table S2] indicate that bacterial communities in the 2 gardens of *M. smithii* were moderately richer and more diverse (by about a factor of 2) than the corresponding communities on worker ants, whereas ant-associated bacterial communities were richer and more diverse than garden-associated communities in *C. wheeleri*. Because of the small number of samples screened, these diversity patterns should not be over-interpreted.

Amycolatopsis Identification in the Present Versus Previous Studies.

Previous culture-dependent studies had failed to identify *Amycolatopsis* from attine workers, for several reasons: First, *Amycolatopsis* was present only in *Mycocepurus smithii* samples, a species which had been screened only in one previous study (12). Second, because *Amycolatopsis* colonies exhibit mycelia-like fuzzy growth on the minimum-carbon isolation medium (unlike the button-like growth morphology typical for *Pseudonocardia*), previous researchers may have failed to recognize this growth form as an actinomycete. Third, fungicidal supplements in previous isolations could have precluded *Amycolatopsis* isolation on fungicidal medium but allowed such isolation on our antibiotic-free medium.

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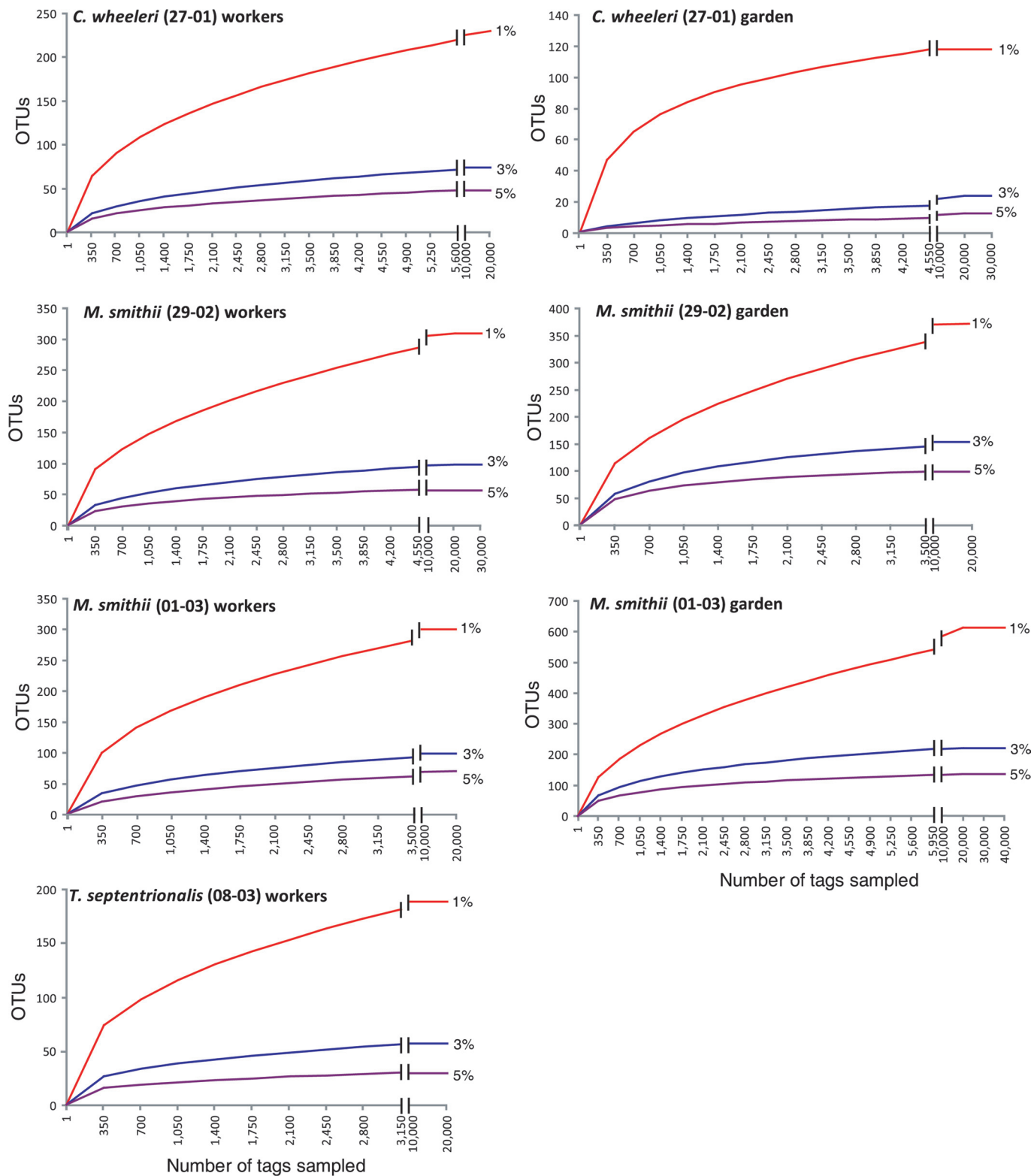


Fig. S1. Operational taxonomic unit (OTU)-accumulation curves and rarefaction predictions of OTU-diversity for each of the 7 bacterial communities screened. For each community, accumulation curves and rarefaction predictions are shown for 3 different stringency levels of defining OTUs (at least 1%, 3%, or 5% sequence difference between OTUs).

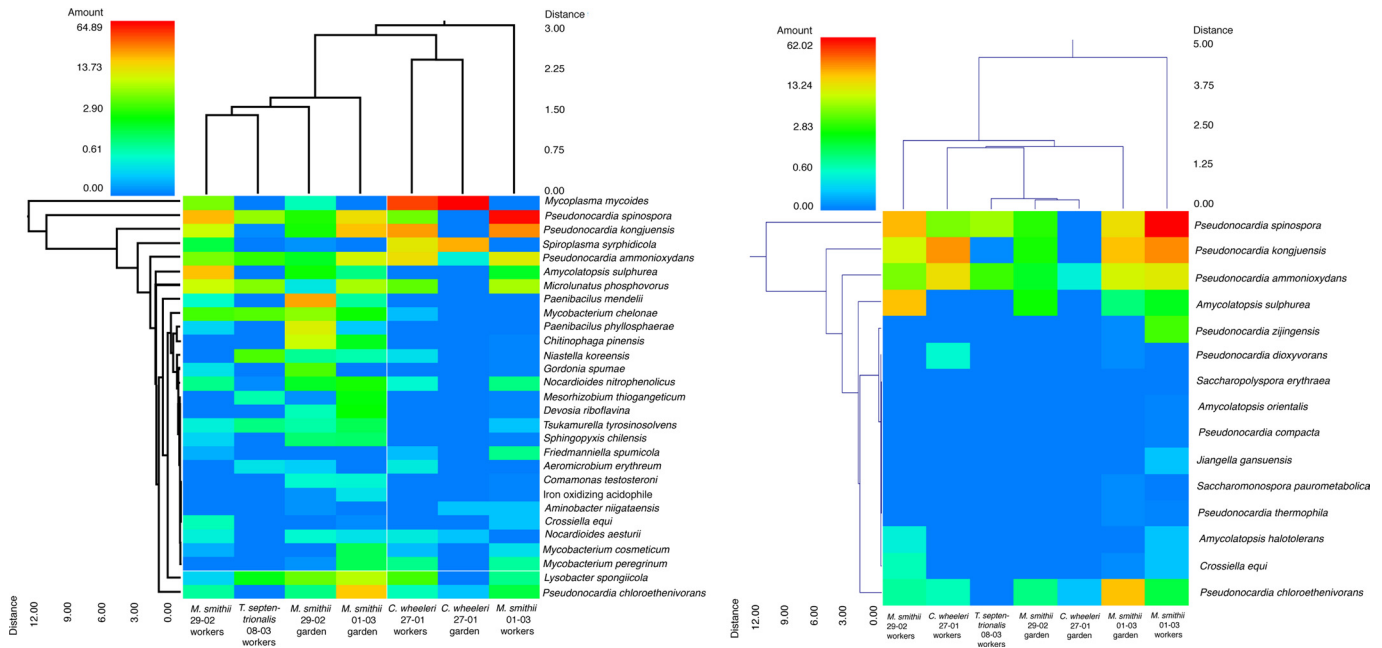


Fig. S2. Bacterial species identification and community composition obtained from 16S rDNA pyrosequencing of worker-associated and garden-associated bacteria species (*Left*) and pseudonocardioaceae species (*Right*) in 4 attine ant colonies. Bacteria from the same source are depicted in individual columns. The dendrograms do not depict phylogenetic relationships; rather, dendrograms cluster bacteria and communities by relative bacterial abundances. Contribution percentage of each bacteria is given in [Table S1](#).

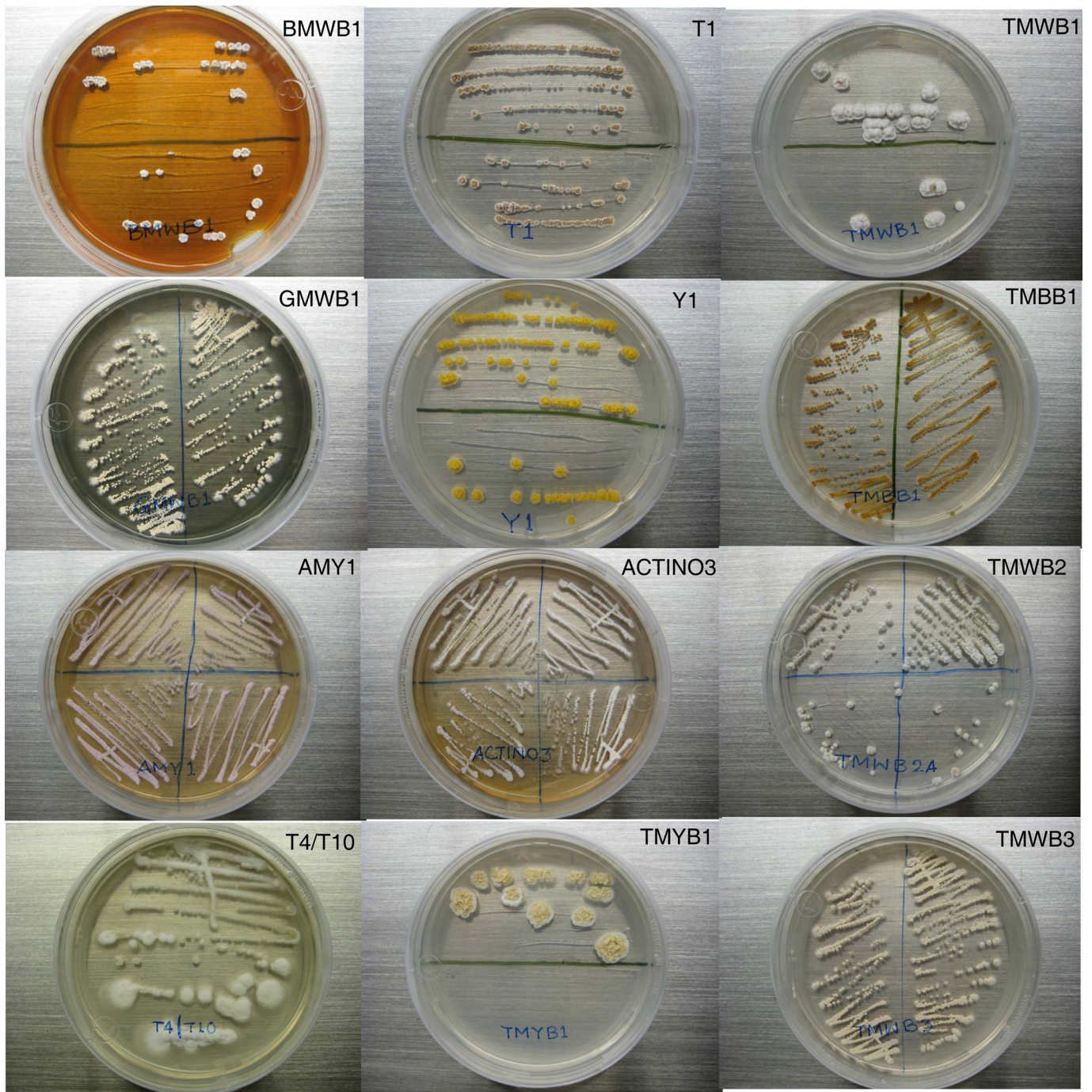


Fig. S3. Bacterial morphotypes growing on PDA agar at room temperature (see Table 2 for sources of isolation).

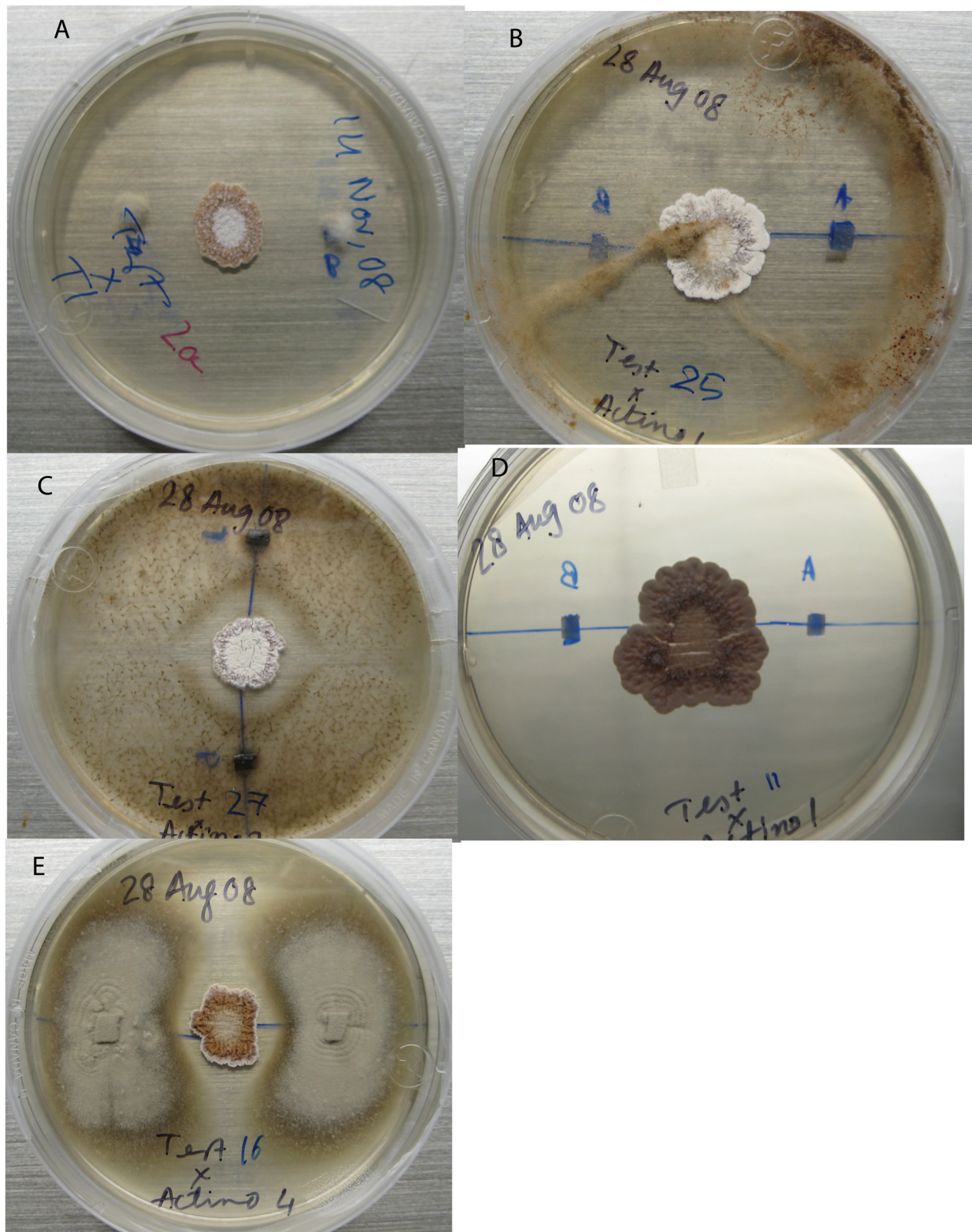


Fig. 54. (A–E). Assays testing antibiotic activity of *Pseudonocardia* (center of plate) against the same test fungus inoculated at 2 sides on the same plate. All photos were taken 28 days after inoculating the respective test fungus. (A) *Pseudonocardia*T1 vs. *Escovopsis*; (B) *Pseudonocardia*1 vs. *Escovopsis*; (C) *Pseudonocardia*2 vs. *Phoma*; (D) *Pseudonocardia*1 vs. cultivar; (E) *Pseudonocardia* vs. entomopathogen.

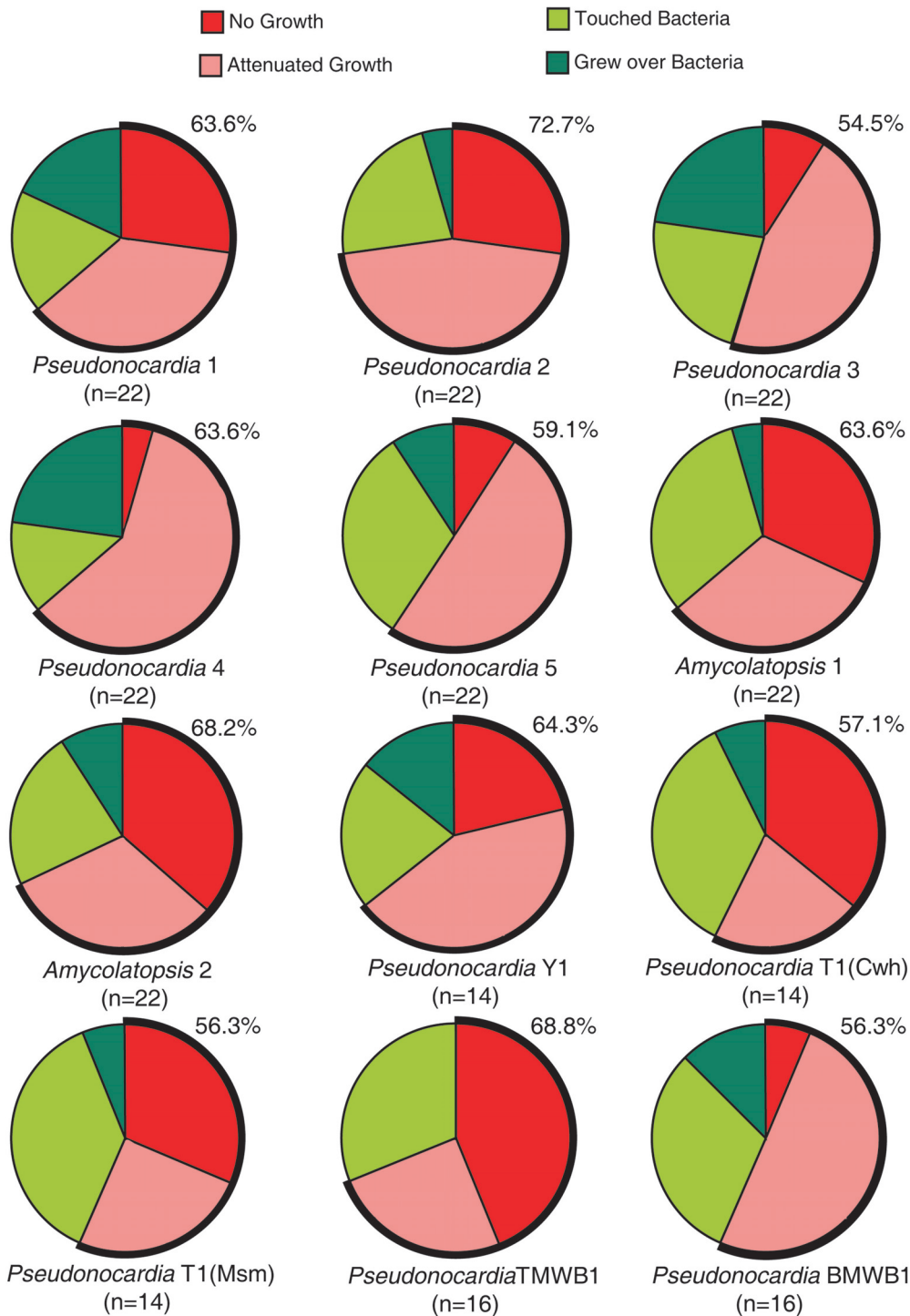


Fig. S5. Inhibition profile of *Pseudonocardia* and *Amycolatopsis* confronted with attine cultivars or different types of problem fungi. The extent of inhibition was scored as complete inhibition (no growth of test fungi), attenuated growth compared to control growth, and 2 types of no inhibition (fungi grew up to and touched the test bacterium but did not grow over the bacterium; test fungi grew over the test bacterium). The pie charts represent percentages of different growth responses by test fungi when challenged with a particular pseudonocardiaceous bacterium. Red sectors represent inhibited growth (total percentage given on the right side of each pie chart), green sectors unaffected growth; n is the number of fungi tested against each bacterium. (see [Tables S3](#) and [S4](#) for sources of isolation of bacteria and fungi, respectively). Authors will be able to provide raw data for each challenge upon request.

Table S1. Percent contribution of bacterial species to attine bacterial communities, surveyed by 454 16S-amplicon pyrosequencing

Species	<i>Myc. smithii</i> 29–02 Worker	<i>Myc. smithii</i> 29–02 Garden	<i>Myc. smithii</i> 01–03 Worker	<i>Myc. smithii</i> 01–03 Garden	<i>Cypho.</i> <i>wheeleri</i> 27–01 Worker	<i>Cypho.</i> <i>wheeleri</i> 27–01 Garden	<i>Trachy. septen-</i> <i>trionalis</i> 08–03 Worker
<i>Achromobacter cf. xylooxidans</i>	0.000	0.119	0.000	0.000	0.000	0.000	0.000
<i>Acidovorax cf. avenae</i>	0.000	0.278	0.000	0.000	0.000	0.000	0.000
<i>Acinetobacter cf. calcoaceticus</i>	0.055	0.000	0.000	0.000	0.000	0.000	0.000
<i>Acinetobacter cf. junii</i>	3.324	0.000	0.000	0.000	0.000	0.000	0.000
<i>Actinotalea cf. fermentans</i>	0.027	0.040	0.000	0.254	0.000	0.000	0.036
<i>Aeromicrobium cf. alkaliterrae</i>	0.027	0.000	0.000	0.000	0.000	0.000	0.000
<i>Aeromicrobium cf. erythreum</i>	0.027	0.079	0.000	0.000	0.128	0.000	0.109
<i>Aeromicrobium cf. marinum</i>	0.027	0.000	0.000	1.050	0.000	0.000	0.615
<i>Afipia cf. felis</i>	0.000	0.119	0.000	0.000	0.000	0.000	0.000
<i>Afipia cf. massiliensis</i>	0.000	0.119	0.000	0.000	0.000	0.000	0.000
<i>Agrococcus cf. jenensis</i>	0.000	0.000	0.000	0.000	0.096	0.000	0.471
<i>Agromyces cf. italicus</i>	0.027	1.626	0.000	0.000	0.000	0.000	0.000
<i>Agromyces cf. ramosus</i>	0.000	0.000	0.000	0.036	0.000	0.000	0.000
<i>Agromyces cf. ulmi</i>	0.027	1.705	0.000	0.000	0.000	0.000	0.000
<i>Alcaligenes cf. faecalis</i>	0.000	0.357	0.000	0.000	0.000	0.000	0.217
<i>Alistipes cf. putredinis</i>	0.027	0.000	0.000	0.000	0.000	0.000	0.000
<i>Amaricoccus cf. kaplicensis</i>	0.000	0.000	0.033	0.797	0.000	0.000	0.000
<i>Amaricoccus cf. macauensis</i>	0.027	0.040	0.000	20.029	0.000	0.000	0.000
<i>Aminobacter cf. niigataensis</i>	0.000	0.040	0.065	0.000	0.000	0.066	0.000
<i>Amycolatopsis cf. halotolerans</i>	0.137	0.000	0.065	0.000	0.000	0.000	0.000
<i>Amycolatopsis cf. orientalis</i>	0.000	0.000	0.033	0.000	0.000	0.000	0.000
<i>Amycolatopsis cf. sulphurea</i>	12.802	0.991	0.717	0.326	0.000	0.000	0.000
<i>Aurantimonas cf. coralicida</i>	0.000	0.000	0.000	0.036	0.000	0.000	0.000
<i>Azospirillum cf. brasilense</i>	0.000	0.000	0.000	0.036	0.000	0.000	0.000
<i>Bacillus cf. caldolyticus</i>	0.000	0.159	0.000	0.362	0.000	0.000	0.000
<i>Bacillus cf. mannilyticus</i>	0.000	0.000	0.000	0.036	0.000	0.000	0.000
<i>Bacteroides cf. splanchnicus</i>	0.000	0.000	0.065	0.036	0.000	0.133	0.109
<i>Bacteroides cf. vulgatus</i>	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<i>Blastochloris cf. sulfovridis</i>	0.000	0.000	0.000	0.036	0.000	0.000	0.000
<i>Bordetella cf. hinzii</i>	0.027	0.317	0.000	0.000	0.000	0.000	0.000
<i>Bosea cf. minatitlanensis</i>	0.000	0.040	0.000	0.109	0.000	0.000	0.109
<i>Bosea cf. vestrisii</i>	0.027	0.040	0.000	0.000	0.000	0.000	0.000
<i>Brachybacterium cf. nesterenkovi</i>	0.000	0.000	0.033	0.217	0.000	0.000	0.000
<i>Brachybacterium cf. sacelli</i>	0.000	0.000	0.033	0.616	0.000	0.000	0.000
<i>Bradyrhizobium cf. group</i>	0.000	0.040	0.000	0.435	0.000	0.000	0.000
<i>Bradyrhizobium cf. japonicum</i>	0.000	0.000	0.000	1.014	0.000	0.000	0.000
<i>Bradyrhizobium cf. liaoningense</i>	0.000	0.198	0.000	0.000	0.000	0.000	0.000
<i>Brevibacillus cf. borstelensis</i>	0.000	0.000	0.000	0.072	0.000	0.000	0.000
<i>Brevibacillus cf. formosus</i>	0.000	0.000	0.000	0.109	0.000	0.000	0.000
<i>Brevibacillus cf. levickii</i>	0.000	0.000	0.000	0.036	0.000	0.000	0.000
<i>Brooklawnia cf. cerclae</i>	0.000	0.000	0.000	0.000	0.000	0.000	0.036
<i>Burkholderia cf. ambifaria</i>	0.000	0.000	0.000	0.072	0.000	0.000	0.000
<i>Burkholderia cf. cenocepacia</i>	0.000	0.278	0.000	0.072	0.000	0.000	0.072
<i>Burkholderia cf. cepacia</i>	0.000	0.079	0.000	0.072	0.000	0.000	0.000
<i>Burkholderia cf. pyrrocinia</i>	0.000	0.000	0.000	0.036	0.000	0.000	0.000
<i>Burkholderia cf. thailandensis</i>	0.000	0.000	0.000	0.036	0.000	0.000	0.000
<i>Candidatus cf. Nostocoida</i>	0.000	0.000	0.000	0.036	0.000	0.000	0.109
<i>Candidatus cf. Protochlamydia</i>	0.000	0.040	0.000	0.000	0.000	0.000	0.000
<i>Candidatus cf. Reyranelia</i>	0.000	0.000	0.000	0.109	0.000	0.000	0.000
<i>Candidatus cf. Rhizobium</i>	0.000	0.238	0.000	0.000	0.000	0.000	0.000
<i>Candidatus cf. Xiphinematobacter</i>	0.000	0.159	0.000	0.000	0.000	0.000	0.000
<i>Cellulomonas cf. denverensis</i>	0.000	0.000	0.000	0.036	0.000	0.000	0.000
<i>Cellulosimicrobium cf. funkei</i>	0.000	0.198	0.000	0.942	0.000	0.000	0.000
<i>CFB cf. group</i>	0.027	0.000	0.033	0.217	0.000	0.000	0.000
<i>Chitinophaga cf. pinensis</i>	0.027	5.115	0.033	0.724	0.000	0.000	0.000
<i>Chryseobacterium cf. joostei</i>	0.604	0.000	0.000	0.000	0.000	0.000	52.009
<i>Clostridium cf. propionicum</i>	0.000	0.000	0.033	0.000	0.000	0.000	0.000
<i>Comamonas cf. testosteroni</i>	0.000	0.159	0.033	0.145	0.000	0.000	0.000
<i>Conexibacter cf. woesei</i>	0.055	0.278	0.000	0.217	0.000	0.000	0.651

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<i>Crassostrea cf. virginica</i>	0.000	0.000	0.033	0.000	0.000	0.000	0.000
<i>Crossiella cf. equi</i>	0.192	0.000	0.065	0.036	0.000	0.000	0.000
<i>Cupriavidus cf. basileus</i>	0.000	0.000	0.000	0.254	0.000	0.000	0.000
<i>Cupriavidus cf. necator</i>	0.000	0.000	0.000	0.616	0.000	0.000	0.000
<i>Demetria cf. terrigena</i>	0.000	0.000	0.000	0.000	0.000	0.000	2.063
<i>Dermabacter cf. hominis</i>	0.000	0.000	0.000	0.109	0.000	0.000	0.000
<i>Dermatophilus cf. congolensis</i>	0.000	0.000	0.000	0.036	0.000	0.000	0.000
<i>Desulfovibrio cf. piger</i>	0.000	0.000	0.033	0.000	0.000	0.000	0.000
<i>Devosia cf. limi</i>	0.000	0.000	0.033	0.435	0.000	0.000	0.000
<i>Devosia cf. riboflavina</i>	0.027	0.198	0.033	0.942	0.000	0.000	0.000
<i>Dokdonella cf. fugitiva</i>	0.000	3.370	0.000	0.398	0.000	0.000	0.000
<i>Dokdonella cf. koreensis</i>	0.000	0.079	0.000	0.000	0.000	0.000	0.000
<i>Dyadobacter cf. fermentans</i>	0.000	0.000	0.033	0.000	0.000	0.000	0.000
<i>Enhygromyxa cf. salina</i>	0.000	0.040	0.000	0.000	0.000	0.000	0.000
<i>Ensifer cf. adhaerens</i>	0.000	0.159	0.000	0.000	0.000	0.000	0.000
<i>Entomoplasma cf. freundtii</i>	0.000	0.000	0.000	0.000	0.000	0.000	0.109
<i>Eubacterium cf. desmolans</i>	0.000	0.000	0.000	0.000	0.032	0.000	0.000
<i>Eubacterium cf. eligens</i>	0.000	0.000	0.000	0.036	0.000	0.000	0.000
<i>Exiguobacterium cf. aestuarii</i>	0.000	0.119	0.000	0.000	0.000	0.000	0.000
<i>Exiguobacterium cf. aurantiacum</i>	0.000	0.040	0.000	0.000	0.000	0.000	0.000
<i>Faecalibacterium cf. prausnitzii</i>	0.000	0.000	0.033	0.000	0.000	0.000	0.000
<i>Finegoldia cf. magna</i>	0.000	0.079	0.000	0.000	0.000	0.000	0.000
<i>Flavobacterium cf. weaverense</i>	0.000	0.000	0.000	0.036	0.000	0.000	0.000
<i>Friedmanniella cf. spumicola</i>	0.055	0.000	0.293	0.000	0.064	0.000	0.000
<i>Gordonia cf. namibiensis</i>	0.000	0.040	0.000	0.000	0.000	0.000	0.000
<i>Gordonia cf. polyisoprenivorans</i>	1.264	9.080	0.033	0.000	0.000	0.000	0.072
<i>Gordonia cf. sinesedis</i>	0.000	0.357	0.000	0.000	0.000	0.000	0.000
<i>Gordonia cf. spumae</i>	0.110	1.745	0.033	0.000	0.000	0.000	0.000
<i>Gordonia cf. terrae</i>	0.000	0.040	0.000	0.000	0.000	0.000	0.000
<i>Haemophilus cf. parainfluenzae</i>	0.000	0.000	0.000	0.036	0.000	0.000	0.000
<i>Haliangium cf. tepidum</i>	0.000	0.000	0.000	0.072	0.000	0.000	0.000
<i>Hespellia cf. porcina</i>	0.000	0.000	0.000	0.036	0.000	0.000	0.000
<i>Hydrocarboniphaga cf. effusa</i>	0.000	0.000	0.033	0.000	0.032	0.000	0.000
<i>Hydrocoleum cf. lyngbyaceum</i>	0.000	0.000	0.000	0.072	0.000	0.000	0.000
<i>Hydrogenophaga cf. intermedia</i>	0.000	1.229	0.000	0.000	0.000	0.000	0.000
<i>Hyphomicrobium cf. hollandicum</i>	0.000	0.000	0.000	0.145	0.000	0.000	0.000
<i>Hyphomicrobium cf. zavarzinii</i>	0.000	0.040	0.000	0.109	0.032	0.000	0.000
<i>iron-oxidizing cf. acidophile</i>	0.000	0.040	0.033	0.109	0.000	0.000	0.000
<i>Jiangella cf. gansuensis</i>	0.000	0.000	0.065	0.000	0.000	0.000	0.000
<i>Kaistia cf. adipata</i>	0.000	0.000	0.000	0.036	0.000	0.000	0.000
<i>Kartchner cf. Caverns</i>	0.000	0.000	0.000	0.036	0.000	0.000	0.000
<i>Klebsiella cf. pneumoniae</i>	0.000	0.793	0.000	1.050	0.000	0.000	0.000
<i>Kribbella cf. antibiotica</i>	0.000	0.000	0.000	0.000	0.225	0.000	0.000
<i>Kribbella cf. swartbergensis</i>	0.000	0.000	0.098	0.507	0.000	0.000	0.000
<i>Lactobacillus cf. acidophilus</i>	0.000	0.040	0.000	0.000	0.000	0.000	0.000
<i>Legionella-like cf. amoebal</i>	0.000	0.079	0.000	0.000	0.000	0.000	0.000
<i>Leifsonia cf. xyli</i>	0.000	0.119	0.000	0.000	0.000	0.000	0.036
<i>Leptospira cf. meyeri</i>	0.000	0.079	0.000	0.000	0.000	0.000	0.000
<i>Lysobacter cf. spongiicola</i>	0.082	2.220	0.293	4.346	1.670	0.000	0.796
<i>Marmoricola cf. aurantiacus</i>	0.000	0.000	0.000	0.000	0.000	0.000	0.072
<i>Mesoplasma cf. chauliocola</i>	0.000	0.000	0.000	0.000	0.514	1.064	0.000
<i>Mesoplasma cf. lactucae</i>	0.000	0.000	0.000	0.000	0.000	0.000	22.222
<i>Mesoplasma cf. tabanidae</i>	0.000	0.000	0.000	0.000	15.382	17.354	0.000
<i>Mesorhizobium cf. amorphae</i>	0.000	0.079	0.000	0.109	0.032	0.000	0.036
<i>Mesorhizobium cf. chacoense</i>	0.000	0.079	0.065	0.290	0.000	0.000	0.000
<i>Mesorhizobium cf. loti</i>	0.000	0.079	0.000	0.580	0.000	0.000	0.000
<i>Mesorhizobium cf. plurifarum</i>	0.000	0.040	0.000	1.340	0.000	0.000	0.000
<i>Mesorhizobium cf. temperatum</i>	0.000	0.040	0.000	0.290	0.000	0.000	0.000
<i>Mesorhizobium cf. thioangeticum</i>	0.000	0.040	0.033	0.869	0.000	0.000	0.217

Species	<i>Myc. smithii</i> 29–02 Worker	<i>Myc. smithii</i> 29–02 Garden	<i>Myc. smithii</i> 01–03 Worker	<i>Myc. smithii</i> 01–03 Garden	<i>Cypho.</i> <i>wheeleri</i> 27–01 Worker	<i>Cypho.</i> <i>wheeleri</i> 27–01 Garden	<i>Trachy. septen-</i> <i>trionalis</i> 08–03 Worker
<i>Mesorhizobium cf.</i> <i>tianshanense</i>	0.000	0.000	0.000	0.036	0.000	0.000	0.000
<i>Methylobacterium cf. specialis</i>	0.000	0.000	0.000	0.000	0.032	0.133	0.036
<i>Microbacterium cf. aurantiacum</i>	0.000	0.000	0.033	0.326	0.000	0.000	0.000
<i>Microbacterium cf. aurum</i>	0.000	0.040	0.000	0.000	0.000	0.000	0.000
<i>Microbacterium cf. chocolateum</i>	0.000	0.079	0.000	0.000	0.000	0.000	0.000
<i>Microbacterium cf.</i> <i>esteraromaticum</i>	0.000	0.000	0.000	0.000	0.000	0.000	0.145
<i>Microbacterium cf. flavescens</i>	0.000	0.278	0.000	0.000	0.000	0.000	0.000
<i>Microbacterium cf. foliorum</i>	0.000	0.040	0.000	0.000	0.000	0.000	0.000
<i>Microbacterium cf. hominis</i>	0.000	0.000	0.000	0.109	0.000	0.000	0.398
<i>Microbacterium cf.</i> <i>keratanolyticum</i>	0.027	0.000	0.000	0.000	0.000	0.000	0.000
<i>Microbacterium cf. koreense</i>	0.000	0.119	0.000	0.000	0.000	0.000	0.000
<i>Microbacterium cf. resistens</i>	0.027	0.278	0.000	0.290	0.000	0.000	0.000
<i>Microbacterium cf. thalassium</i>	0.000	0.040	0.000	0.000	0.000	0.000	0.000
<i>Microbacterium cf.</i> <i>xylanilyticum</i>	0.000	0.000	0.000	0.471	0.000	0.000	0.072
<i>Microlunatus cf. phosphovorus</i>	5.110	0.119	3.876	3.875	2.119	0.000	2.787
<i>Mycobacterium cf. brisbanense</i>	0.000	0.000	0.000	0.072	0.000	0.000	0.000
<i>Mycobacterium cf. chelonae</i>	1.593	3.053	0.000	1.014	0.064	0.000	1.846
<i>Mycobacterium cf.</i> <i>chlorophenolicum</i>	0.000	0.000	0.033	0.036	0.000	0.000	0.000
<i>Mycobacterium cf.</i> <i>conceptionense</i>	0.000	0.000	0.000	0.688	0.000	0.000	0.000
<i>Mycobacterium cf. conspicuum</i>	0.000	0.000	0.000	0.036	0.000	0.000	0.000
<i>Mycobacterium cf. cosmeticum</i>	0.055	0.000	0.098	0.471	0.064	0.000	0.000
<i>Mycobacterium cf. elephantis</i>	0.000	0.000	0.163	0.217	0.000	0.000	0.000
<i>Mycobacterium cf. mageritense</i>	0.000	0.000	0.033	0.217	0.000	0.000	0.000
<i>Mycobacterium cf. parmense</i>	0.000	0.000	0.033	0.036	0.000	0.000	0.000
<i>Mycobacterium cf. peregrinum</i>	0.027	0.040	0.261	0.471	0.289	0.000	0.000
<i>Mycobacterium cf. phocaicum</i>	0.000	1.190	0.098	0.036	0.000	0.000	0.217
<i>Mycobacterium cf. poriferae</i>	0.000	0.000	0.000	0.326	0.000	0.000	0.000
<i>Mycobacterium cf.</i> <i>psychrotolerans</i>	0.000	0.000	0.065	0.000	0.000	0.000	0.000
<i>Mycobacterium cf. smegmatis</i>	0.027	0.119	0.000	0.109	0.000	0.000	0.000
<i>Mycoplasma cf. cottewii</i>	0.110	0.000	0.000	0.000	0.032	0.000	0.000
<i>Mycoplasma cf. mycoides</i>	2.582	0.198	0.000	0.000	39.338	64.894	0.000
<i>Nakamurella cf. multipartita</i>	0.000	0.000	0.000	0.435	0.193	0.000	0.000
<i>Neisseria cf. animalis</i>	0.000	0.040	0.000	0.000	0.000	0.000	0.000
<i>Niastella cf. koreensis</i>	0.027	0.278	0.033	0.217	0.096	0.000	1.701
<i>Nitratireductor cf.</i> <i>aquibiodomus</i>	0.000	0.000	0.000	0.072	0.000	0.000	0.000
<i>Nitrobacter cf. winogradskyi</i>	0.000	0.000	0.000	0.036	0.000	0.000	0.000
<i>Nitrosococcus cf. oceani</i>	0.000	0.040	0.000	0.000	0.000	0.000	0.000
<i>Nocardia cf. harenosa</i>	0.000	0.000	0.033	0.000	0.000	0.000	0.000
<i>Nocardia cf. neocaledoniensis</i>	0.000	0.000	0.065	0.072	0.000	0.000	0.000
<i>Nocardia cf. paucivorans</i>	0.000	0.000	0.065	0.000	0.000	0.000	0.000
<i>Nocardiooides cf. aestuarii</i>	0.137	0.159	0.000	0.109	0.128	0.066	0.000
<i>Nocardiooides cf. alkalitolerans</i>	0.000	0.040	0.000	0.000	0.000	0.000	0.000
<i>Nocardiooides cf. aquiterrae</i>	0.000	0.079	0.000	0.036	0.096	0.000	0.253
<i>Nocardiooides cf. dubius</i>	0.000	0.000	0.000	0.036	0.000	0.000	0.000
<i>Nocardiooides cf. ganghwensis</i>	0.000	0.198	0.000	0.000	0.064	0.000	0.072
<i>Nocardiooides cf. kribbensis</i>	0.000	0.040	0.000	0.072	0.000	0.000	0.000
<i>Nocardiooides cf.</i> <i>nitrophenolicus</i>	0.302	0.714	0.326	1.123	0.161	0.000	0.036
<i>Novosphingobium cf.</i> <i>pentaromativorans</i>	0.000	0.000	0.000	0.036	0.000	0.000	0.000
<i>Ochrobactrum cf. anthropi</i>	0.000	0.198	0.000	0.000	0.000	0.000	0.036
<i>Ornithinococcus cf. hortensis</i>	0.000	0.000	0.000	0.000	0.000	0.000	0.109
<i>Paenibacillus cf. chitinolyticus</i>	0.000	0.000	0.000	0.254	0.000	0.000	0.000
<i>Paenibacillus cf. mendelii</i>	0.165	16.336	0.000	0.254	0.000	0.000	0.000
<i>Paenibacillus cf. phyllosphaerae</i>	0.082	6.661	0.000	0.072	0.000	0.000	0.000

Species	<i>Myc. smithii</i> 29-02 Worker	<i>Myc. smithii</i> 29-02 Garden	<i>Myc. smithii</i> 01-03 Worker	<i>Myc. smithii</i> 01-03 Garden	<i>Cypho.</i> <i>wheeleri</i> 27-01 Worker	<i>Cypho.</i> <i>wheeleri</i> 27-01 Garden	<i>Trachy. septen-</i> <i>trionalis</i> 08-03 Worker
<i>Papillibacter cf. cinnamivorans</i>	0.000	0.000	0.000	0.036	0.000	0.000	0.036
<i>Parachlamydia cf. acanthamoebae</i>	0.000	0.079	0.000	0.000	0.000	0.000	0.000
<i>Paracoccus cf. denitrificans</i>	0.000	0.000	0.033	0.000	0.000	0.000	0.000
<i>Paracoccus cf. pantotrophus</i>	0.000	0.000	0.033	0.000	0.000	0.000	0.000
<i>Pelomonas cf. saccharophila</i>	0.000	0.079	0.000	0.000	0.000	0.000	0.000
<i>Peptoniphilus cf. harei</i>	0.027	0.000	0.000	0.000	0.000	0.000	0.000
<i>Peptoniphilus cf. ivorii</i>	0.000	0.198	0.000	0.145	0.000	0.000	0.000
<i>Phenylobacterium cf. falsum</i>	0.000	0.000	0.000	0.036	0.000	0.000	0.000
<i>Phenylobacterium cf. koreense</i>	0.000	0.000	0.000	0.072	0.000	0.000	0.000
<i>Phyllobacterium cf. bourgognense</i>	0.000	0.634	0.000	0.000	0.000	0.000	0.000
<i>Pigmentiphaga cf. kullae</i>	0.000	0.079	0.000	0.000	0.000	0.000	0.000
<i>Planococcus cf. antarcticus</i>	0.000	0.040	0.000	0.000	0.000	0.000	0.000
<i>Prevotella cf. oulorum</i>	0.000	0.040	0.033	0.000	0.000	0.000	0.000
<i>Prevotella cf. veroralis</i>	0.000	0.079	0.000	0.000	0.000	0.000	0.000
<i>Promicromonospora cf. aerolata</i>	0.000	0.000	0.000	0.072	0.000	0.000	0.000
<i>Propionibacterium cf. acnes</i>	0.000	0.515	0.000	0.181	0.000	0.000	0.036
<i>Propionicicella cf. superfundia</i>	0.000	0.000	0.000	0.000	0.706	0.000	1.773
<i>Propioniferax cf. innocua</i>	0.000	0.000	0.000	0.000	0.128	0.000	0.000
<i>Pseudaminobacter cf. salicylatoxidans</i>	0.000	0.000	0.000	0.036	0.000	0.000	0.000
<i>Pseudomonas cf. aeruginosa</i>	40.440	3.569	0.000	0.000	0.000	0.000	0.000
<i>Pseudomonas cf. alcaligenes</i>	0.000	0.040	0.000	0.000	0.000	0.000	0.000
<i>Pseudomonas cf. alcaliphila</i>	0.000	0.000	0.000	0.036	0.000	0.000	0.000
<i>Pseudomonas cf. gessardii</i>	0.027	0.000	0.000	0.000	0.000	0.000	0.000
<i>Pseudomonas cf. hibiscicola</i>	1.429	0.198	0.000	0.000	0.000	0.000	0.000
<i>Pseudomonas cf. mendocina</i>	0.027	0.000	0.000	0.000	0.000	0.000	0.000
<i>Pseudomonas cf. otitidis</i>	0.000	0.040	0.000	0.000	0.000	0.000	0.000
<i>Pseudonocardia cf. ammonioxydans</i>	2.500	0.674	6.938	5.976	8.863	0.133	1.412
<i>Pseudonocardia cf. chloroethenivorans</i>	0.247	0.317	0.554	12.351	0.193	0.066	0.000
<i>Pseudonocardia cf. compacta</i>	0.000	0.000	0.033	0.000	0.000	0.000	0.000
<i>Pseudonocardia cf. dioxanivorans</i>	0.000	0.000	0.000	0.036	0.161	0.000	0.000
<i>Pseudonocardia cf. kongjuensis</i>	5.275	1.071	20.782	12.966	18.369	0.000	0.036
<i>Pseudonocardia cf. spinospora</i>	13.874	1.229	62.020	8.982	2.473	0.000	3.330
<i>Pseudonocardia cf. thermophila</i>	0.000	0.000	0.033	0.036	0.000	0.000	0.000
<i>Pseudonocardia cf. zijingensis</i>	0.000	0.000	1.564	0.036	0.000	0.000	0.000
<i>Pseudoxanthomonas cf. mexicana</i>	0.000	9.794	0.033	0.000	0.000	0.000	0.000
<i>Pseudoxanthomonas cf. spadix</i>	0.000	10.151	0.000	0.000	0.000	0.000	0.000
<i>Pseudoxanthomonas cf. suwonensis</i>	0.000	0.040	0.000	0.000	0.000	0.000	0.000
<i>Ralstonia cf. insidiosa</i>	0.000	0.000	0.000	0.036	0.000	0.000	0.000
<i>Ralstonia cf. mannitolilytica</i>	0.000	0.000	0.000	0.000	0.000	0.000	0.760
<i>Ralstonia cf. pickettii</i>	0.000	0.159	0.000	0.000	0.000	0.000	0.000
<i>Ralstonia cf. syzygii</i>	0.000	0.000	0.000	0.072	0.000	0.000	0.000
<i>Rhizobium cf. gallicum</i>	0.000	0.000	0.000	0.036	0.000	0.000	0.000
<i>Rhizobium cf. huautlense</i>	0.000	0.040	0.000	0.000	0.000	0.000	0.000
<i>Rhizobium cf. loessense</i>	0.000	0.000	0.000	0.036	0.000	0.000	0.000
<i>Rhodanobacter cf. spathiphylli</i>	0.000	0.040	0.000	0.000	0.000	0.000	0.000
<i>Rhodobium cf. orientis</i>	0.000	0.198	0.000	0.580	0.000	0.000	0.000
<i>Rhodoblastus cf. sphagnicola</i>	0.000	0.000	0.000	0.036	0.000	0.000	0.000
<i>Rhodococcus cf. equi</i>	0.000	0.000	0.033	0.036	0.000	0.000	0.000
<i>Rhodoplanes cf. elegans</i>	0.000	0.079	0.033	0.072	0.000	0.000	0.000
<i>Rhodopseudomonas cf. faecalis</i>	0.000	0.000	0.000	0.000	0.000	0.000	0.072
<i>Rhodopseudomonas cf. palustris</i>	0.000	0.119	0.033	0.000	0.000	0.000	0.072
<i>Rubritalea cf. spongiae</i>	0.000	1.665	0.000	0.000	0.000	0.000	0.000
<i>Rubrivivax cf. gelatinosus</i>	0.000	0.040	0.000	0.000	0.000	0.000	0.000

Species	<i>Myc. smithii</i> 29-02 Worker	<i>Myc. smithii</i> 29-02 Garden	<i>Myc. smithii</i> 01-03 Worker	<i>Myc. smithii</i> 01-03 Garden	<i>Cypho.</i> <i>wheeleri</i> 27-01 Worker	<i>Cypho.</i> <i>wheeleri</i> 27-01 Garden	<i>Trachy. septen-</i> <i>trionalis</i> 08-03 Worker
<i>Ruminococcus cf. albus</i>	0.000	0.040	0.000	0.000	0.000	0.000	0.000
<i>Saccharomonospora cf. paurometabolica</i>	0.000	0.000	0.000	0.036	0.000	0.000	0.000
<i>Saccharopolyspora cf. erythraea</i>	0.027	0.000	0.000	0.000	0.000	0.000	0.000
<i>Serinicoccus cf. marinus</i>	0.000	0.000	0.000	0.000	0.000	0.000	2.751
<i>Shinella cf. granuli</i>	0.000	0.119	0.000	0.109	0.000	0.000	0.000
<i>Shinella cf. zoogloeoides</i>	0.000	0.000	0.033	0.978	0.000	0.000	0.000
<i>Sinorhizobium cf. americanum</i>	0.000	0.000	0.000	0.036	0.000	0.000	0.000
<i>Skermania cf. piniformis</i>	0.000	0.000	0.000	0.145	0.000	0.000	0.000
<i>Solibacter cf. usitatus</i>	0.000	0.119	0.000	0.036	0.000	0.000	0.000
<i>Solirubrobacter cf. pauli</i>	0.000	0.000	0.000	0.000	0.000	0.000	0.688
<i>Sphingomonas cf. aquatilis</i>	0.000	0.000	0.000	0.036	0.000	0.000	0.000
<i>Sphingomonas cf. panni</i>	0.027	0.000	0.000	0.036	0.000	0.000	0.000
<i>Sphingopyxis cf. chilensis</i>	0.082	0.357	0.033	0.398	0.000	0.000	0.000
<i>Sphingopyxis cf. wittflariensis</i>	0.000	0.000	0.000	0.435	0.000	0.000	0.000
<i>Spiroplasma cf. insolitum</i>	0.027	0.000	0.000	0.000	0.161	0.532	0.000
<i>Spiroplasma cf. syrphidicola</i>	0.549	0.040	0.000	0.000	7.836	15.559	0.000
<i>Staphylococcus cf. aureus</i>	0.000	0.000	0.000	0.072	0.000	0.000	0.000
<i>Staphylococcus cf. capitis</i>	0.000	0.040	0.000	0.000	0.000	0.000	0.036
<i>Stella cf. humosa</i>	0.000	0.000	0.000	0.036	0.000	0.000	0.000
<i>Stenotrophomonas cf. maltophilia</i>	5.934	3.132	0.000	0.000	0.000	0.000	0.000
<i>Streptococcus cf. mitis</i>	0.000	0.040	0.000	0.109	0.000	0.000	0.072
<i>Streptococcus cf. pyogenes</i>	0.000	0.119	0.000	0.000	0.000	0.000	0.000
<i>Streptococcus cf. thermophilus</i>	0.000	0.159	0.000	0.000	0.000	0.000	0.000
<i>Streptomyces cf. cinereoruber</i>	0.000	0.000	0.000	0.036	0.000	0.000	0.000
<i>Streptomyces cf. cinnabarinus</i>	0.027	0.198	0.000	0.000	0.000	0.000	0.000
<i>Streptomyces cf. macrosporus</i>	0.000	0.000	0.000	0.217	0.000	0.000	0.000
<i>Streptomyces cf. olivoreticuli</i>	0.000	0.000	0.000	0.326	0.032	0.000	0.000
<i>Streptomyces cf. resistomyticificus</i>	0.000	0.159	0.000	0.000	0.000	0.000	0.000
<i>Streptomyces cf. viridobrunneus</i>	0.000	0.000	0.065	0.833	0.000	0.000	0.000
<i>Terrimonas cf. ferruginea</i>	0.000	0.000	0.000	0.109	0.032	0.000	0.688
<i>Tetrasphaera cf. australiensis</i>	0.000	0.000	0.000	0.000	0.000	0.000	0.036
<i>Thermomonas cf. haemolytica</i>	0.000	0.040	0.000	0.000	0.161	0.000	0.000
<i>thin cf. bent</i>	0.000	0.000	0.000	0.072	0.000	0.000	0.000
<i>Thioalkalivibrio cf. denitrificans</i>	0.000	0.000	0.000	0.290	0.000	0.000	0.000
<i>Tsukamurella cf. tyrosinosolvans</i>	0.137	0.238	0.065	0.471	0.000	0.000	0.326
<i>Variovorax cf. dokdonensis</i>	0.000	0.317	0.000	0.000	0.000	0.000	0.000
<i>Veillonella cf. dispar</i>	0.000	0.000	0.000	0.072	0.000	0.000	0.000
<i>Woodsholea cf. maritima</i>	0.000	0.040	0.000	0.000	0.000	0.000	0.000
<i>Xanthomonas cf. campestris</i>	0.000	0.079	0.000	0.000	0.000	0.000	0.000
<i>Xanthomonas cf. group</i>	0.027	0.000	0.000	0.000	0.000	0.000	0.000
<i>Xenophilus cf. azovorans</i>	0.000	0.000	0.033	0.254	0.000	0.000	0.000

Table S2. Richness and diversity indices for each of the seven bacterial communities screened (OTU = Operational Taxonomic Unit; ACE = Abundance-based Coverage Estimator). Advantages and disadvantages of each index are explained in ref. 1

Ant species, sample type	#sequences	OTUs observed			Rarefaction			Chao1 Richness			ACE Richness			Shannon Diversity		
		1%	3%	5%	1%	3%	5%	1%	3%	5%	1%	3%	5%	1%	3%	5%
<i>M. smithii</i> 29-02, workers	4602	288	95	58	286.5	94.6	57.8	584.1	165.3	82.4	556.8	149.8	81.4	4.22	2.54	2.24
<i>M. smithii</i> 29-02, garden	3643	344	147	100	338.1	145.4	99.1	620.2	176.3	136.1	567.9	177.8	116.9	4.58	3.28	3.09
<i>M. smithii</i> 01-03, workers	3741	290	95	63	281.9	92.8	61.5	482.4	140.8	86.0	487.5	136.8	84.6	4.37	2.55	1.62
<i>M. smithii</i> 01-03, garden	6038	544	219	135	540.2	217.8	134.5	1054.1	334.6	190.5	1001.1	309.6	169.7	4.73	3.46	2.86
<i>C. wheeleri</i> 27-01, workers	5659	220	72	48	219.1	71.7	47.8	331.6	117.1	82.2	347.3	114.9	78.8	3.47	1.71	0.99
<i>C. wheeleri</i> 27-01, garden	4715	119	18	10	117.8	17.7	12.2	163.0	23.6	12.0	148.7	29.4	16.1	2.44	0.27	0.25
<i>T. septentrionalis</i> . 08-03, workers	3431	188	58	46	181.5	56.4	44.8	302.0	85.1	67.0	315.5	87.1	69.3	3.87	2.02	1.85

1. Hughes JB, Hellmann JJ, Ricketts TH, JM Bohannan BJM (2001) Counting the uncountable: Statistical approaches to estimating microbial diversity. *Appl Environ Microbiol* 67:4399-4406.

Table S3. Taxonomic placement and sources of pseudonocardiaecous isolates tested for antifungal activity

Tested species (code)	Source	Source colony ID	Organism	GenBank accession number
<i>Pseudonocardia</i> 1 (P1)	<i>Trachymyrmex zeteki</i> worker	RMMA050816-03	<i>Pseudonocardia</i> sp.	FJ948108
<i>Pseudonocardia</i> 2 (P2)	<i>Trachymyrmex zeteki</i> worker	RMMA050818-12	<i>Pseudonocardia</i> sp.	FJ948109
<i>Pseudonocardia</i> 3 (P3)	<i>Trachymyrmex turrifex</i> worker	AGH000427-01	<i>Pseudonocardia</i> sp.	FJ948110
<i>Pseudonocardia</i> 4 (P4)	<i>Trachymyrmex septentrionalis</i> worker	AMG040508-03	<i>Pseudonocardia</i> sp.	FJ948111
<i>Pseudonocardia</i> 5 (P5)	<i>Cyphomyrmex wheeleri</i> worker	UGM030427-01	<i>Pseudonocardia</i> sp.	FJ948112
<i>Amycolatopsis</i> 1 (Amy1)	<i>Mycocephurus smithii</i> worker	UGM030329-02	<i>Amycolatopsis</i> sp.	FJ948113
<i>Amycolatopsis</i> 2 (Amy2)	<i>Mycocephurus smithii</i> worker	UGM010402-08A	<i>Amycolatopsis</i> sp.	FJ948114
<i>Pseudonocardia</i> (PY1)	<i>Cyphomyrmex wheeleri</i> worker	UGM030427-01	<i>Pseudonocardia</i> sp.	FJ948115
<i>Pseudonocardia</i> (PT1)	<i>Cyphomyrmex wheeleri</i> male	UGM030427-01	<i>Pseudonocardia</i> sp.	FJ948116
<i>Pseudonocardia</i> (PT1)	<i>Mycocephurus smithii</i> worker	UGM010401-03	<i>Pseudonocardia</i> sp.	FJ948117
<i>Pseudonocardia</i> (TMWB1)	<i>Mycocephurus smithii</i> worker	UGM010401-03	<i>Pseudonocardia</i> sp.	FJ948118
<i>Pseudonocardia</i> (BMW1)	<i>Mycocephurus smithii</i> worker	UGM010401-03	<i>Pseudonocardia</i> sp.	FJ948119

Table S4. Taxonomic placement and source of test fungi used in antibiotic challenges with pseudonocardiaecous secretions (GP = garden pathogen; AP = attine-ant pathogen; S = saprotroph fungus; EP = endophytic fungus; C = cultivar fungus; GE = general entomopathogen)

Test Fungus	Type	Taxonomic Name, Genbank Accessions	Order, Family	Source of Test Fungus
Garden Pathogen				
Test 1	GP	<i>Syncephalastrum racemosum</i> accessions FJ948130, FJ948146	Mucorales, Syncephalastraceae	Garden of <i>Trachymyrmex zeteki</i> (colony RMMMA050818–12)
Test 2	GP	<i>Escovopsis</i> sp. (cf. <i>weberi</i>) accessions FJ948131, FJ948147	Hypocreales, Hypocreaceae	Garden of <i>Cyphomyrmex wheeleri</i> (colony UGM030427–01)
Test 23	GP	<i>Escovopsis</i> sp. accession FJ948162	Hypocreales, Hypocreaceae	Garden of <i>Trachymyrmex turrifex</i> (colony UGM051119–01; RC005)
Test 25	GP	<i>Escovopsis</i> sp. (cf. <i>weberi</i>) accessions FJ948163	Hypocreales, Hypocreaceae	Garden of <i>Trachymyrmex zeteki</i> (colony SES020522–02)
Attine Ant Pathogen				
Test 3	AP	<i>Simplicillium lanosoniveum</i> accessions FJ948132, FJ948148	Hypocreales, Cordycipitaceae	Worker cuticle, <i>Mycocepurus smithii</i> (colony UGM030329–02)
Test 4	AP	<i>Fusarium solani</i> accessions FJ948133, FJ948149	Hypocreales, Hypocreaceae	Diseased queen, <i>Atta texana</i> (colony UGM080525–01)
Test 16	AP	<i>Acrodontium</i> sp. ¹ accessions FJ948141, FJ948158	mitosporic Ascomycota, incertae sedis	Diseased queen, <i>Acromyrmex versicolor</i> (colony UGM070721-U)
General Entomopathogen				
5465	GE	<i>Beauveria bassiana</i>	Hypocreales, Clavicipitaceae	Overwintering adult, <i>Galerucella</i> sp. (Coleoptera: Chrysomelidae)
2575	GE	<i>Metarhizium anisopliae</i>	Hypocreales, Clavicipitaceae	<i>Curculio caryae</i> (Coleoptera: Curculionidae)
6147	GE	<i>Beauveria bassiana</i>	Hypocreales, Clavicipitaceae	Pupa, <i>Galleria mellonella</i> (Lepidoptera: Pyralidae)
3288	GE	<i>Beauveria bassiana</i>	Hypocreales, Clavicipitaceae	<i>Spodoptera frugiperda</i> (Lepidoptera: Noctuidae)
5991	GE	<i>Beauveria bassiana</i>	Hypocreales, Clavicipitaceae	Earwig (Dermaptera)
6907	GE	<i>Beauveria bassiana</i>	Hypocreales, Clavicipitaceae	<i>Coptotermes formosanus</i> (Isoptera: Rhinotermitidae)
Endophyte / Saprotroph				
Test 5	S	<i>Cyphellophora</i> sp. accessions FJ948134, FJ948150	Chaetothyriales, Herpotrichiellaceae	Garden of <i>Trachymyrmex turrifex</i> (colony AGH000427–01)
Test 7	S	<i>Eucasphaeria/Niesslia</i> (cf. <i>exilis</i>) ² accessions FJ948135, FJ948152	Hypocreales incertae sedis	Garden of <i>Mycocepurus smithii</i> (colony UGM010402–08A)
Test 18	S/EP	<i>Acremonium murorum</i> accessions FJ948143, FJ948160	Hypocreales, mitosporic Hypocreales	Worker of <i>Cyphomyrmex wheeleri</i> (colony UGM030427–01)
Test 19	EP/S	<i>Alternaria tenuissima</i> accessions FJ948144, FJ948161	Pleosporales, Pleosporaceae	Garden of <i>Atta texana</i> (colony UGM070317–04)
Test 17	S/AP	<i>Verticillium leptobactrum</i> ³ accessions FJ948142, FJ948159	Hypocreales, mitosporic Hypocreales	Worker of <i>Trachymyrmex turrifex</i> (colony AGH000427–01)
Test 27	EP	<i>Phoma</i> sp. (cf. <i>glomerata</i>) accessions FJ985694, FJ985695	mitosporic Ascomycota	Garden of <i>Atta texana</i> (colony UGM070317–04)
Attine Cultivar				
Test 6	C	<i>Leucocoprinus</i> sp. accession FJ948151	Agaricales, Agaricaceae	Garden of <i>Trachymyrmex turrifex</i> (colony AGH000427–01)
Test 8	C	<i>Leucocoprinus</i> sp. accessions FJ948136, FJ948153	Agaricales, Agaricaceae	Garden of <i>Mycocepurus smithii</i> (colony UGM010402–08A)
Test 9	C	<i>Leucocoprinus</i> sp. accessions FJ948137, FJ948154	Agaricales, Agaricaceae	Garden of <i>Trachymyrmex zeteki</i> (colony RMMMA050816–03)
Test 11	C	<i>Leucocoprinus</i> sp. accessions FJ948138, FJ948155	Agaricales, Agaricaceae	Garden of <i>Mycocepurus smithii</i> (colony UGM030329–02)
Test 13	C	<i>Leucocoprinus</i> sp. accessions FJ948139, FJ948156	Agaricales, Agaricaceae	Garden of <i>Cyphomyrmex wheeleri</i> (colony UGM030427–01)
Test 15	C	<i>Leucocoprinus</i> sp. accessions FJ948140, FJ948157	Agaricales, Agaricaceae	Garden of <i>Trachymyrmex septentrionalis</i> (colony AMG040508–03)
Test 22	C	<i>Leucocoprinus</i> sp. accession FJ948145	Agaricales, Agaricaceae	Garden of <i>Trachymyrmex zeteki</i> (colony RMMMA050818–12)

¹*Acrodontium* is classified here as an attine pathogen because we have repeatedly isolated it from diseased *Acromyrmex* and *Trachymyrmex* queens kept in lab colonies.

²Crous et al. (1) discuss the close proximity of *Eucasphaeria* and *Niesslia*.

³*Verticillium leptobactrum* is classified here as a saprotroph because it is most frequently isolated from rotting plant material or soil, but less commonly from insect sources.

1. Crous PW, Mohammed C, Glen M, Verkley G, Groenewald JZ (2007) Eucalyptus microfungi known from culture. *Fungal Diversity* 25:19–36.