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ISOLATION AND CHARACTERIZATION OF ENDOPHYTIC BACTERIA ISOLATED FROM THE LEAVES OF THE COMMON BEAN (*PHASEOLUS VULGARIS*)

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ABSTRACT

The common bean is one of the most important legumes in the human diet, but little is known about the endophytic bacteria associated with the leaves of this plant. The objective of this study was to characterize the culturable endophytic bacteria of common bean (*Phaseolus vulgaris*) leaves from three different cultivars (Vermelhinho, Talismã, and Ouro Negro) grown under the same field conditions. The density of endophytic populations varied from 4.5×10^2 to 2.8×10^3 CFU g^{-1} of fresh weight. Of the 158 total isolates, 36.7% belonged to the Proteobacteria, 32.9% to Firmicutes, 29.7% to Actinobacteria, and 0.6% to Bacteroidetes. The three *P. vulgaris* cultivars showed class distribution differences among Actinobacteria, Alphaproteobacteria and Bacilli. Based on 16S rDNA sequences, 23 different genera were isolated comprising bacteria commonly associated with soil and plants. The genera *Bacillus*, *Delftia*, *Methylobacterium*, *Microbacterium*, *Paenibacillus*, *Staphylococcus* and *Stenotrophomonas* were isolated from all three cultivars. To access and compare the community structure, diversity indices were calculated. The isolates from the Talismã cultivar were less diverse than the isolates derived from the other two cultivars. The results of this work indicate that the cultivar of the plant may contribute to the structure of the endophytic community associated with the common bean. This is the first report of endophytic bacteria from the leaves of *P. vulgaris* cultivars. Future studies will determine the potential application of these isolates in biological control, growth promotion and enzyme production for biotechnology.

Key words: Endophytic bacteria, common bean, *Phaseolus vulgaris*, 16S rDNA, diversity indices.

INTRODUCTION

The phyllosphere is the habitat for a large diversity of microorganisms. Although bacteria are the predominant microorganisms present in phyllospheres, others such as filamentous fungi are also important members. Phyllosphere bacteria may be found on the surface of plants (epiphytes) as well as in the interior of plant tissues (endophytes) (3, 32, 40). Endophytic bacteria can be defined as those that can be isolated from healthy, superficially disinfected plant tissues and do not cause any damage to the host plant (15, 17).

The population density of endophytic bacteria can vary

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from 10^2 to 10^9 (6, 12, 25, 39, 44) and depends on many factors, including the plant being studied, the part under analysis (31, 46), the developmental stage of the plant (17, 44), the plant cultivar (genotype) (15, 44) and the interaction with other organisms, as well as other environmental-related factors (17).

The interaction between endophytic bacteria and their host plants is not completely understood. However, many isolates seem to have beneficial effects on their hosts (58). These beneficial effects include promoting host growth and biological control of phytopathogens (17, 21).

The common bean (*Phaseolus vulgaris*) is one of the most important legumes in the human diet and serves as a significant source of proteins (10). The relationship between *Rhizobium* and other nitrogen-fixing bacteria in the root nodules of beans has been extensively studied (13, 37, 38). Recently, López-López *et al*. (34) reported the isolation of endophytic bacteria from the seeds and roots of the common bean. However, little is known about endophytic bacteria inhabiting the aerial tissues of the common bean. Therefore, the objective of this study was to isolate the culturable, endophytic bacteria from the leaves of three different common bean cultivars growing in field conditions and characterize the community of culturable bacteria. To our knowledge, this is the first report on endophytic bacteria from the leaves of different cultivars of the common bean.

MATERIALS AND METHODS

Plant materials

Samples were collected from three common bean cultivars during the winter of 2007: Talismã (TAL), Ouro Negro (ONG), and Vermelhinho (VER). The cultivars were planted in an experimental field in the town of Coimbra – MG (altitude: 690 m; latitude: 20º 45’ S; longitude 42º 51’ W). During sowing, 350 kg ha^{-1} of the 8-28-16 NPK (percentage of nitrogen, phosphorus and potassium) formula was applied, and 25 days after their emergence, the plants were covered in 150 kg ha^{-1} of ammonium sulfate. The leaves of the superior portion of the plant (20 cm above the soil) were collected in the vegetative phase 45 days after sowing.

Sample preparation and bacterial isolation

The collected leaves were washed in running water and those with superficial injury that was visible to the naked eye were excluded. Each isolation procedure was done in triplicate for each cultivar. Each triplicate was composed of approximately 2 g of leaves belonging to two different plants being evaluated, totaling six plants per cultivar. The disinfection and isolation were performed according to Araujo *et al.* (1) with minor modifications. Briefly, the leaves were disinfected superficially through the following protocol: 70% alcohol for 1 min, sodium hypochlorite (2.5% Cl^-) for 4 min, ethanol for 30 s, and finally 3 rinses in sterile, distilled water. To confirm the disinfection protocol, aliquots of the sterile water used in the final rinse were plated in 10% TSA (1.5 g/L of triptone, 0.5 g/L of soy peptone, 1.5 g/L of NaCl, 15 g/L of agar, pH 7.3) at 28 ºC for 15 days and the plates are examined for the presence or absence of microorganismal growth colony.

Initially, the leaves were ground with 6 mL of aqueous solution (0.9 % NaCl) using a sterile mortar and pestle. The tissue extract was subsequently incubated at 28 ºC for 3 hours to allow the complete release of endophytic microorganisms from the host tissue. For the isolation of endophytic bacteria, the tissue extract was diluted in an aqueous solution (0.9 % NaCl) and plated on five 10% TSA plates for each dilution (10^{-1} and 10^{-2}). The plates were incubated for up to 15 days at 28ºC. Colonies were selected on days 2, 5, 10, and 15 of incubation and purified in 10% TSA. For each petri dish evaluated, the colonies were selected according to their time of growth and morphology (color, size, shape). After 15 days of incubation, all of the colonies were counted and expressed as CFU per gram of fresh tissue.

Identification and phylogenetic analysis of endophytic bacteria

DNA from each isolate was extracted using the following protocol: 1.5 ml of a 48-hour bacterial culture was centrifuged for 5 minutes at 14000 *g* and resuspended in 1 ml of TE buffer (mM Tris-HCl, 1 mM EDTA, pH 8.0), centrifuged, resuspended in 500 µl of TE buffer and finally adding 0.5 g of glass pearls (0.1 mm in diameter) (Sigma-Aldrich, USA) and 15 µl of 20% SDS. The cells were then homogenized for 30 s in a vortex mixer (AP56 – Phoenix), 500 µl of buffered phenol was added, and the solution was mixed and centrifuged for 5 min at 14000 *g*. The aqueous phase was extracted once with phenol-chloroform (1:1) and once more with chloroform. Following the extraction of the aqueous phase, 20 µl of 5M NaCl was added, the DNA was precipitated with isopropanol (5 min at room temperature) and collected by centrifugation for 10 min at 14000 *g*. The DNA pellet was washed with 70% ethanol, air dried and resuspended in 30 µl of autoclaved, ultrapure water.

The amplification of 16S rDNA was carried out in a reaction with a final volume of 25 µl containing 1 µl (0.5-10 ng) of total DNA, 2.5 µl (0.2 µM) of the P027F primer (5'-GAGAGTTTGATCCTGGCTAG-3'), 2.5 µl (0.2 µM) of the 1378R primer (5'-CGGTGTGTACSSGGCCCGGGAACG-3'), 1.6 µl (200 µM) of each dNTP, 2.5 µl of 5x IB buffer (Phoneutria; Belo Horizonte, Brazil); 1µl (1U) of Taq DNA polymerase (Phoneutria; Belo Horizonte, Brazil), and 2.5 µl (25 µg) of BSA (Promega). A negative control (PCR mix without DNA) was included in all PCR experiments. The PCR reaction conditions were as follows: 94ºC for 4 min, followed by 30 cycles of denaturation at 94ºC for 30 s, annealing at 63ºC for 1 min and extension at 72ºC for 1 min, before a final extension at 72ºC for 7 min. The PCR products were purified and sequenced by Macrogen Inc. (Seoul, South Korea) using an ABI3730 XL automatic DNA sequencer and the primers P027F and 1378R.

The identification of the isolates was performed using the Ribosomal Database Project (14, 61) and BLAST (http://blast.ncbi.nlm.nih.gov/blast/Blast.cgi) in NCBI. We used the Sequence Match application and BLAST to verify the similarity of experimental sequences with the reference sequences in the databases (14) and classified them at the genus level.

The DNA sequences of 34 reference strains ("type strain"), 2 strains obtained from the Ribosomal Database Project, and 34 representative strains from experimental isolates were aligned using the Ribosomal Database Project. Phylogenetic trees were constructed using the Neighbor-Joining (NJ) algorithm in *MEGA* version 4 (56), the Maximum Parsimony (MP) and Maximum Likelihood (ML) algorithm in Paup* (52), and the Bayesian Analysis (BA) algorithm in MrBayes 3.1 (23). The Neighbor Joining method was corrected by the Tamura-Nei multiple base substitution model (55) and by the GAMA distribution (0.4899) established by Modeltest 3.7. The parameters for Maximum Likelihood (GTR+I+G) were selected by AIC in Modeltest 3.7 (45). The Bayesian parameters (GTR+I+G) were selected by AIC in MrModeltest 2.3 (42). A total of 1000 replications were used for the bootstrap tests of the NJ and MP methods, while the ML test had 100 replications. The MB was performed in two independent runs with four Markov chain Monte Carlo (MCMC). A total of 10,000,000 generations were run, with trees being sampled every 1000 generations and the first 1,000,000 trees being discarded. Non-rooted trees were calculated using the 16S rDNA sequence of *Methanocaldococcus jannaschii* DSM 2661 as an outgroup. The 16S rDNA sequences of each isolate were deposited in the NCBI GENBANK database under the accession numbers HM355592 to HM355749.

Diversity indices

The diversity indices were calculated in the PAST program version 2.01(20), and the expected number of genotypes in the R program version 2.11.1 (47) using the Vegan library (43).

RESULTS

Endophytic bacteria isolation and identification

The density of endophytic populations recovered in 10%

TSA medium varied from 4.5 x 10^2 to 2.8 x 10^3 CFU g^{-1} per fresh weight. A total of 158 (about 40 % of the total counted) isolates was obtained, of which 31.01% (49) were isolated from the Talismã cultivar, 37.34% (59) from the Ouro Negro cultivar and 31.65% (50) from the Vermelhinho cultivar (Table 1).

Table 1. Endophytic isolates obtained from three *Phaseolus vulgaris* cultivars.

Identified taxum	**Cultivar***		
	TAL	**ONG**	**VER**
Actinobacteria	25	13	9
Actinobacteria (class)	25	13	9
Agromyces (A. mediolanus; *Agromyces* sp.*)*	0	2	3
Dietzia (D. cinnamea)	0	0	1
Frigoribacterium (*F. faeni*)	0	3	0
Kocuria (*K. palustris*)	1	0	0
Microbacterium (*M. foliorum*; *M. phyllosphaerae*; *Microbacterium sp.*; *M. testaceum*)	20	7	5
Micrococcus (*M. luteus*)	4	0	0
Rhodococcus (*R. erythropolis*)	0	1	0
Bacteroidetes	0	0	1
Sphingobacteria	0	0	1
Sphingobacterium (*S. multivorum*)	0	0	1
Firmicutes	11	23	18
Bacilli	11	22	18
Bacillus (*B. amyloliquefaciens; B. bataviensis; B. muralis; B. niacini, Bacillus sp.; B. subtilis; B. thuringiensis*)	7	3	5
Brevibacillus (*B. agri*)	0	1	1
Lysinibacillus (*Lysinibacillus sphaericus*)	0	0	1
Paenibacillus (*P. cineris; P. lautus; Paenibacillus sp.*)	1	2	1
Sporosarcina (*S. aquimarina; Sporosarcina sp.*)	0	1	1
Staphylococcus (*S. caprae; S. epidermidis; S. kloosii; S. saprophyticus; Staphylococcus sp.; S. warneri;*)	3	16	9
Proteobacteria	13	23	22
Alphaproteobacteria	5	14	7
Brevundimonas (*B. vesicularis*)	1	0	0
Methylobacterium (*M. populi*)	3	8	7
Rhizobium (*R. larrymoorei*)	1	4	0
Sphingomonas (*S. dokdonensis; S. sanguinis*)	0	2	0
Betaproteobacteria	1	2	1
Delftia (*D. tsuruhatensis*)	1	2	1
Gammaproteobacteria	7	7	14
Acinetobacter (*A. radioresistens; Acinetobacter sp.*)	0	0	2
Enterobacter (*E. asburiae; E. hormaechei*)	4	0	0
Stenotrophomonas (*S. maltophilia; Stenotrophomonas sp.*)	2	7	10
Pseudomonas (*P. aeruginosa*)	1	0	2
Total	49	59	50

* TAL = Talismã; ONG = Ouro Negro; VER = Vermelhinho.

Identification and phylogenetic analyses of endophytic bacteria

Sequencing of 16S rDNA was performed in all 158 isolates. Based on the nucleotide sequences each of the isolates was assigned to 23 different genera (Table 1). In terms of phylum, most isolates belonged to Proteobacteria (36.7% of the total number of isolates), followed by Firmicutes (32.9%) and lastly Actinobacteria (29.7%). Isolates from phylum Bacteroidetes comprised only 0.6% of the total and only a single isolate was found from the Sphingobacteria

(Sphingobacteriaceae) of the genus *Sphingobacterium*. The highest number of isolates belonged to the Bacilli class (32.9%), comprised of bacteria from the families Staphylococcaceae (17.7%), Bacillaceae (10.1%), Paenibacillaceae (3.8%) and Planococcaceae (1.3%). The second most prevalent class in isolates was Actinobacteria (29.7%), which includes Microbacteriaceae (24.7%), Micrococcaceae (3.1%), Nocardiaceae (0.6%) and Dietziaceae (0.6%). Among the isolates identified as Proteobacteria, the dominant class in the isolate collection was Gammaproteobacteria (17.71%), with isolates belonging to the families Xanthomonadaceae (12.0%), Enterobacteriaceae (2.5%), Pseudomonadaceae (1.9%) and two (1.3%) isolates from the family Moraxellaceae. Isolates from the Alphaproteobacteria (16.5%) comprised representatives from the families Methylobacteriaceae (11.4%), Rhizobiaceae (3.2%), Sphingomonadaceae (1.3%) and one isolate from the family Caulobacteraceae. Betaproteobacteria (2.5%) contains only members from the family Comamonadaceae (2.5%).

The relative composition of the bacterial isolates by cultivars is shown in Figure 1 according to class. Differences in the proportions of the classes Actinobacteria, Alphaproteobacteria and Bacilli were observed between the three *P. vulgaris* cultivars. Sphingobacteria were isolated only from the Vermelhinho cultivar, which also exhibited differences in the proportion of isolates belonging to Gammaproteobacteria compared to isolates from the other two cultivars. The proportion of Betaproteobacteria was the same in all cultivars and all isolates of this class belonged to the genus *Delftia*.

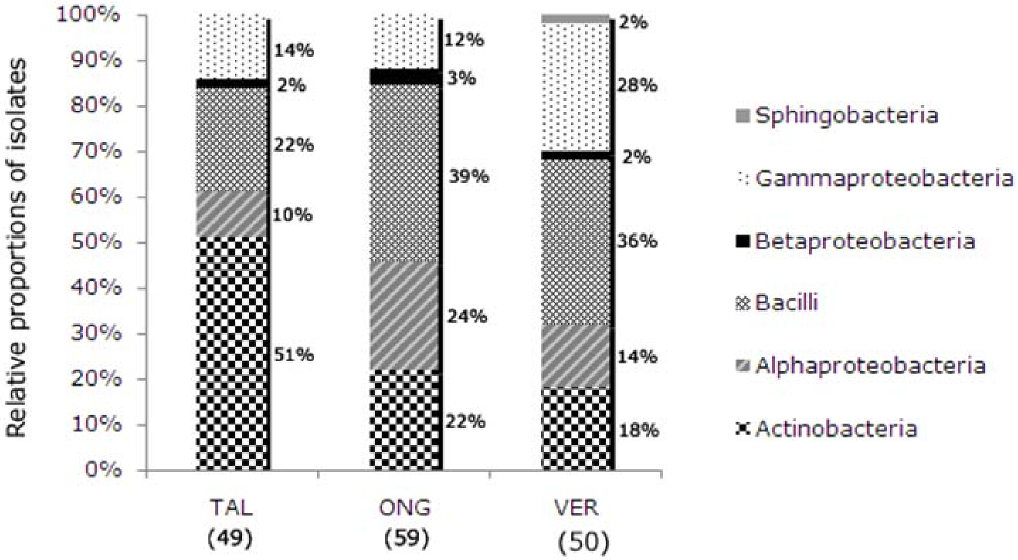

Figure 1. Bacterial class distribution of the culturable endophytic isolates obtained from three *Phaseolus vulgaris* cultivars: Talismã cultivar (TAL); Ouro Negro cultivar (ONG); Vermelhinho cultivar (VER).

Partial 16S rDNA gene sequences (approximately 1200 bp) from the isolates were used together with sequences taken from the Ribosomal Database Project for construction of phylogenetic trees using four different methods (Neighbor-Joining, Maximum Parsimony, Maximum Likelihood and Bayesian). The tree obtained by the Bayesian method is shown in Figure 2.

Two major clades were formed with a posterior probability of 0.50: the first is comprised of Gram positive bacteria and the second of Gram-negative bacteria. The terminal nodes containing isolates BAC2078 and BAC3048 had bootstrap values below 90 as determined by the ML method; the terminal node that contained the isolate BAC3114 had bootstrap values below 90 for both the ML and NJ methods. The terminal node that contained the isolate BAC2073 had bootstrap values below 90 for the methods MP, ML and NJ. The phylum Bacteroidetes aligned with bacteria from the phylum Proteobacteria.

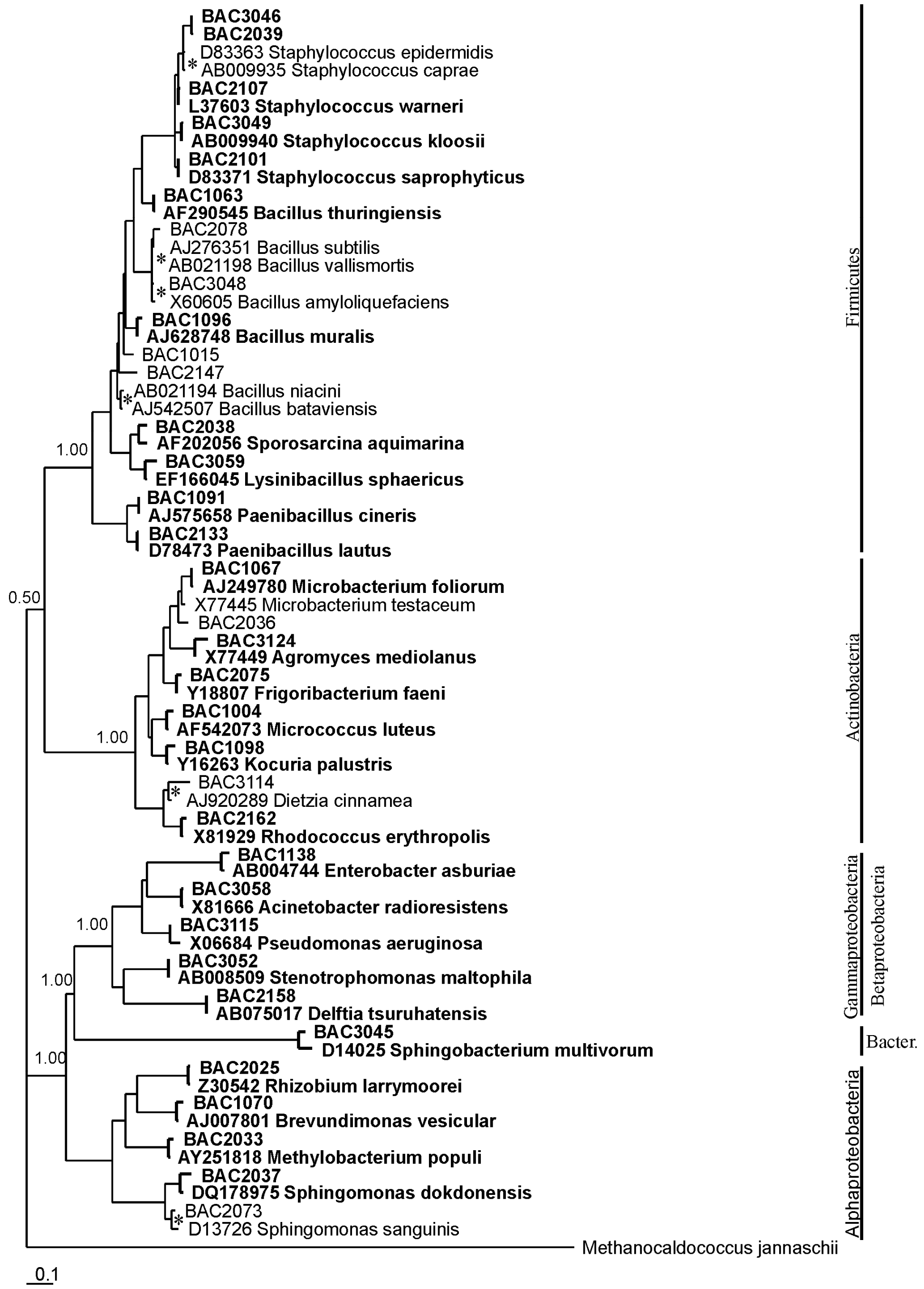

Figure 2. Phylogenetic tree showing the relationship between the 16S rDNA gene sequences from representative isolates of endophytic bacteria from three *P. vulgaris* cultivars. Terminal nodes in bold have bootstrap values greater than or equal to 94 in the three methods used (NJ, MP, ML) and presented *a posteriori* probabilities greater than or equal to 0.99. Terminal nodes with *a posteriori* probabilities equal to 1.00 and with bootstrap values under 90 in any of the other methods are marked with an *. Bacter. = Bacteroidetes.

Diversity indices

The diversity index that was calculated in the PAST program and the expected number of genotypes for each cultivar estimated in the R program can be visualized in Table 2.

Table 2. Number of taxa, individuals, diversity index and expected number of genotypes for each cultivar.

Diversity indices/Parameters	**Formula**[††]	**Cultivar**		
		TAL	**ONG**	**VER**
Taxa (S)	-	13	14	15
Individuals (n)	-	49	59	50
Dominance (D)	$D = Sum(n_i/n)^2$	0.212	0.135	0.122
Shannon (H)	$H = Sum((n_i/n)ln(n_i/n))$	2.002	2.282	2.340
Simpson (1-D)	$1 – D = 1 - Sum(n_i/n)^2$	0.788	0.865	0.878
Evenness (E)	$E = e^H/S$	0.570	0.700	0.692
Menhinick (db)	$Db = S/\sqrt{n}$	1.857	1.823	2.121
Margalef (Ma)	$Ma = (S-1)/\ln(n)$	3.083	3.188	3.579
Equitability (J)	$J = H/Hmax$	0.781	0.865	0.864
Fisher alpha (FA)	$S = \alpha*ln(1+n/\alpha)$	5.781	5.801	7.265
Berger-Parker (d)	$d = n/nT$	0.408	0.271	0.200
Expected number of genotypes[†]	-	13	13.38	14.86

† Calculated in R program version 2.11.1

†† n = number of individuals; ni = number of individuals of taxon i; S = number of taxa; Nt = number of individuals in the dominant taxon; Hmax = log S.

* Fisher´s alpha.

DISCUSSION

Isolation and identification of endophytic bacteria was performed from the leaves of three common bean (*P. vulgaris*) cultivars grown under the same field conditions in Minas Gerais during the winter season. The population densities of culturable bacteria in this study were similar to the population density of isolates obtained from soybean leaves growing in herbicide-free soil by Kuklinsky-Sobral *et al.* (30).

All identified isolates corresponded to genera commonly isolated from either the rhizosphere or bacteria associated with plants. Species from the genera *Agromyces*, *Bacillus*, *Brevibacillus*, *Delftia*, *Dietzia*, *Enterobacter*, *Methylobacterium*, *Microbacterium*, *Micrococcus*, *Paenibacillus*, *Pseudomonas*, *Rhizobium*, *Rhodococcus*, *Sphingobacterium* and *Stenotrophomonas* have already been isolated from rhizospheric soil and as endophytic bacteria in many previous studies (4, 5, 8, 18, 19, 24, 27–30, 36, 48–51, 54, 57–60). Additionally, species from the genera *Acinetobacter*, *Brevundimonas*, *Frigoribacterium*, *Kocuria*, *Sphingomonas*, *Sporosarcina* and *Staphylococcus* have been isolated or reported in studies of culturable and non-culturable endophytic bacteria (5, 8, 27, 29, 30, 48, 50, 51, 58).

Many of the bacterial genera encountered in this work were previously reported by Lopez-Lopez *et al.*, (34), and many species of genera *Bacillus* were found by Walker *et al.* (63) in bean seeds. However, some of the species are not the same. The presence of certain genera in different bean cultivars suggest that they are better adapted to live as endophytic bacteria in *P. vulgaris* than other genera. The genera isolated in this work that have not been previously reported for *P. vulgaris* are as follows: *Agromyces*, *Brevibacillus*, *Brevundinomonas*, *Delftia*, *Dietzia*, *Frigoribacterium*, *Lysinibacillus*, *Sphingobacterium*, *Sporosarcina* and *Stenotrophomonas*.

Differences in the composition of the endophytic population according to cultivar or clone of plant have been documented for citrus plants, poplar trees, potato, salix and soybean (2, 11, 29, 41, 44, 58). The results of this study suggest that the cultivar of the plant contributes to the structure of the endophytic community associated with common bean plants or that the observed differences between common bean cultivars could be due to the use of only one sample collected in the Winter of 2007. First, some specific genera were only isolated from a single studied cultivar (Table 1). Second, isolate analyses also indicated that the cultivar of the plant may contribute to the determination of associated bacteria. Some of the genera had been isolated with greater frequency from a particular cultivar, for example, the genus *Microbacterium* from TAL, the genus *Staphylococcus* from ONG and *Stenotrophomonas* from VER. The differences between the number and type of isolates in each cultivar may suggest distinct endophytic communities in each cultivar. The differences in diversity of the endophytic communities of the cultivars may also be observed by the comparison of the relative class percentages presented in Figure 1.

To better visualize the community structure of the three common bean cultivars studied, diversity indices (Table 2) were calculated. The diversity indices obtained show that the diversity of bacterial isolates from cultivar Talismã was lower than the diversity of isolates obtained from the other two cultivars while the diversity of bacterial isolates from the cultivar Vermelhinho was the highest. Moreover, the indices Dominance_D and Berger-Parker clearly show that a single *taxa* of the cultivar Talismã is more abundant in the community, and the number of isolates shown in Table 1 reveal that this is the genus *Microbacterium*.

Bacteria usually associated with common bean leaf diseases belong to the genera *Curtobacterium* (22), *Pseudomonas* (33) and *Xanthomonas* (62). None of the isolates belong to *Curtobacterium* or *Xanthomonas*, while all the isolates belonging to *Pseudomonas* aligned with different strains of *Pseudomonas aeruginosa* with scores of 0.999.

The levels of NPK and ammonium sulfate applied to the plants were in accordance with the recommendations for producers in Brazil. However, this high level of nitrogen probably inhibited the nodulation of the bean roots and the association with other nitrogen-fixing bacteria. A few *Rhizobium*, *Pseudomonas*, *Methylobacterium* and *Enterobacter* species have already been described in the literature as nitrogen-fixing and nodule-forming organisms in the roots of many Leguminosae (7, 26, 37, 53). The five *Rhizobium* isolates aligned with sequences of *Rhizobium larrymoorei*, which was originally isolated from tumors affecting aerial parts of *Ficus benjamina* (9). Some bacterial species considered pathogenic for certain plant species have been isolated as endophytic in other species; from the polar tree, Ulrich *et al.* (58) isolated endophytes with high similarity to known plant pathogens, such as *Clavibacter michiganensis*, *Pseudomonas syringae* and *Xanthomonas populi.* Maes *et. al.* (35) also showed that *Brenneria salicis* could be isolated as an endophyte from poplar (*Populus*) and alder (*Alnus*). It is unclear whether these endophytic bacterial species confer some benefit to the host plant or if they merely use the host as a survival strategy in the environment to reach plants on which they can develop disease.

The study of endophytic microorganisms is important to comprehend their interaction with their host plants. Additionally, endophytic microorganisms may have biotechnological applications. The potential of the isolated endophytic bacteria to promote bean plant growth and their biocontrol potential in diseases that affect the aerial parts of this important legume for the human diet will be addressed in future studies.

Table S1. Identity of the 16S rDNA gene sequences of the isolates with the sequences deposited in the database.

Isolate	Ribossomal Database Project		NCBI	
	Similarity score	Sequence name	Sequence name	% identity
BAC1001	1.00	*Bacillus thuringiensis* (T); ATCC10792; AF290545	Bacillus thuringiensis strain ODPY 16S; HM770098.1	100
BAC1002	1.00	*Micrococcus luteus* (T); ATCC 4698; AF542073	Micrococcus luteus strain EHFS1_S04Ha 16S; EU071593.1	100
BAC1003	1.00	*Microbacterium testaceum* (T); DSM 20166; X77445	Microbacterium testaceum StLB037; AP012052.1	99
BAC1004	1.00	*Micrococcus luteus* (T); ATCC 4698; AF542073	Micrococcus luteus strain SV21 16S; GU143803.1	99
BAC1005	1.00	*Micrococcus luteus* (T); ATCC 4698; AF542073	Micrococcus sp. 185 16S ribosomal RNA gene; EU714334.1	99
BAC1006	1.00	*Microbacterium testaceum* (T); DSM 20166; X77445	Microbacterium testaceum StLB037; AP012052.1	99
BAC1007	1.00	*Enterobacter asburiae* (T); JCM6051; AB004744	Enterobacter asburiae strain E53; HQ407230.1	99

Table S1. Continuation

Isolate	Ribossomal Database Project		NCBI	
	Similarity score	**Sequence name**	**Sequence name**	**% identity**
BAC1008	1.00	*Microbacterium testaceum* (T); DSM 20166; X77445	Microbacterium testaceum strain ESS21; EF602568.1	99
BAC1009	0.98	*Microbacterium testaceum* (T); DSM 20166; X77445	Microbacterium testaceum strain PCSB7 16S; HM449703.1	98
BAC1010	1.00	*Enterobacter hormaechei* (T); CIP 103441; AJ508302	Enterobacter hormaechei strain Ni-1 16S; HM446004.1	99
BAC1011	1.00	*Rhizobium larrymoorei* (T); 3-10; Z30542	Agrobacterium larrymoorei strain 13638E 16S; EU741094.1	100
BAC1012	1.00	*Stenotrophomonas maltophilia* (T); ATCC 13637T; AB008509	Stenotrophomonas maltophilia strain AhsB4 16S; HM143858.1	100
BAC1013	1.00	*Microbacterium testaceum* (T); DSM 20166; X77445	Microbacterium testaceum StLB037; AP012052.1	99
BAC1014	1.00	*Microbacterium testaceum* (T); DSM 20166; X77445	Stenotrophomonas maltophilia strain AhsB4 16S; HM143858.1	100
BAC1015	0.98	*Bacillus niacini* (T); IFO15566; AB021194	Bacillus sp. DL006 16S; GQ355276.1	98
BAC1016	1.00	*Staphylococcus epidermidis* (T); ATCC 14990; D83363	Staphylococcus epidermidis strain LCR40 16S; FJ976549.1	100
BAC1017	1.00	*Bacillus thuringiensis* (T); ATCC10792; AF290545	Bacillus thuringiensis strain ODPY 16S; HM770098.1	100
BAC1018	1.00	*Microbacterium testaceum* (T); DSM 20166; X77445	Microbacterium testaceum StLB037; AP012052.1	99
BAC1019	1.00	*Microbacterium testaceum* (T); DSM 20166; X77445	Microbacterium testaceum strain ESS21 16S; EF602568.1	99
BAC1020	1.00	*Microbacterium testaceum* (T); DSM 20166; X77445	Microbacterium testaceum StLB037; AP012052.1	99
BAC2021	1.00	*Rhizobium larrymoorei* (T); 3-10; Z30542	Agrobacterium larrymoorei strain 13638E 16S; EU741094.1	99
BAC2022	1.00	*Microbacterium testaceum* (T); DSM 20166; X77445	Microbacterium testaceum StLB037; AP012052.1	99
BAC2023	0.99	*Methylobacterium populi* (T); BJ001; ATCC BAA-705; NCIMB 13946; AY251818	Methylobacterium sp. SuP10 16S; EU912450.1	100
BAC2024	1.00	*Stenotrophomonas maltophilia* (T); ATCC 13637T; AB008509	Stenotrophomonas maltophilia strain AhsB4 16S; HM143858.1	100
BAC2025	1.00	*Rhizobium larrymoorei* (T); 3-10; Z30542	Agrobacterium larrymoorei strain 13638E 16S; EU741094.1	100
BAC2026	1.00	*Staphylococcus epidermidis* (T); ATCC 14990; D83363	Staphylococcus epidermidis strain F71028 16S; HQ908659.1	100
BAC2027	1.00	*Brevibacillus agri* (T); NRRL NRS-1219; D78454	Brevibacillus agri partial 16S strain R-20121; AJ586388.1	99
BAC2028	0.99	*Methylobacterium populi* (T); BJ001; ATCC BAA-705; NCIMB 13946; AY251818	Methylobacterium populi BJ001 16S; CP001029.1	99
BAC2029	1.00	*Microbacterium testaceum* (T); DSM 20166; X77445	Microbacterium testaceum StLB037; AP012052.1	99
BAC2030	1.00	*Staphylococcus warneri* (T); L37603	Staphylococcus warneri strain FUA2075 16 S; HQ694734.1	99
BAC2031	1.00	*Stenotrophomonas maltophilia* (T); ATCC 13637T; AB008509	Stenotrophomonas maltophilia strain AhsB4 16S; HM143858.1	99
BAC2032	1.00	*Staphylococcus warneri* (T); L37603	Staphylococcus warneri strain FUA2075 16 S; HQ694734.1	99
BAC2033	0.99	*Methylobacterium populi* (T); BJ001; ATCC BAA-705; NCIMB 13946; AY251818	Methylobacterium populi BJ001; CP001029.1	99
BAC2034	1.00	*Staphylococcus epidermidis* (T); ATCC 14990; D83363	Staphylococcus epidermidis gene for 16S; AB617573.1	100
BAC2035	1.00	*Staphylococcus epidermidis* (T); ATCC 14990; D83363	Staphylococcus epidermidis strain NM62-4 16S; HM218280.1	100
BAC2036	0.98	*Microbacterium testaceum* (T); DSM 20166; X77445	Microbacterium hominis strain 1P10AE; EU977655.1	99
BAC2037	0.98	*Sphingomonas dokdonensis* (T); DS-4; DQ178975	Sphingomonas dokdonensis strain 2P01AE; EU977661.1	99
BAC2038	0.98	*Sporosarcina aquimarina* (T); SW28(T); AF202056	Sporosarcina luteola gene for 16S; AB473560.1	99
BAC2039	1.00	*Staphylococcus caprae* (T); ATCC 35538T; AB009935	Staphylococcus capitis strain EHFS2_AU1Hc 16S; EU071603.1	100
BAC2040	0.99	*Methylobacterium populi* (T); BJ001; ATCC BAA-705; NCIMB 13946; AY251818	Methylobacterium extorquens AM1; CP001510.1	99
BAC3041	1.00	*Staphylococcus epidermidis* (T); ATCC 14990; D83363	Staphylococcus epidermidis strain NM62-4 16S; HM218280.1	100
BAC3042	1.00	*Bacillus thuringiensis* (T); ATCC10792; AF290545	Bacillus thuringiensis serovar colmeri 16S; EU429660.1	100
BAC3043	1.00	*Microbacterium foliorum* (T); DSM 12966; P 333/02; AJ249780	Microbacterium foliorum strain 720 16S; EU714376.1	99
BAC3044	0.97	*Bacillus bataviensis* (T); type strain: LMG 21832; AJ542507	Bacillus sp. R-30632 partial 16S; AM910246.1	99
BAC3045	0.98	*Sphingobacterium multivorum* (T); IFO 14947; D14025	Sphingobacterium sp. G-2-27-2 16S; EF102865.1	99
BAC3046	1.00	*Staphylococcus epidermidis* (T); ATCC 14990; D83363	Staphylococcus epidermidis strain F71028 16S; HQ908659.1	100
BAC3047	1.00	*Microbacterium testaceum (T); DSM 20166; X77445*	Microbacterium sp. Fek04 16S; EU741023.1	99
BAC3048	1.00	*Bacillus amyloliquefaciens (T); CR-502; AY603658*	Bacillus amyloliquefaciens LL3; CP002634.1	100
BAC3049	1.00	*Staphylococcus kloosii (T); ATCC 43959T; AB009940*	Staphylococcus kloosii strain FR2_36con 16S; EU934080.1	100
BAC3050	0.99	*Microbacterium phyllosphaerae (T); DSM 13468; P 369/06; AJ277840*	Microbacterium foliorum strain 720 16S; EU714376.1	99
BAC3051	0.99	*Methylobacterium populi (T); BJ001; ATCC BAA-705; NCIMB 13946; AY251818*	Methylobacterium sp. SuP10 16S; EU912450.1	99
BAC3052	1.00	*Stenotrophomonas maltophilia (T); ATCC 13637T; AB008509*	Stenotrophomonas maltophilia strain AhsB4 16S; HM143858.1	100

Table S1. Continuation

Isolate	Ribossomal Database Project		NCBI	
	Similarity score	**Sequence name**	**Sequence name**	**% identity**
BAC3053	0.97	*Bacillus bataviensis* (T); type strain: LMG 21832; AJ542507	Bacillus sp. R-30632 partial 16S; AM910246.1	98
BAC3054	0.99	*Methylobacterium populi* (T); BJ001; ATCC BAA-705; NCIMB 13946; AY251818	Methylobacterium sp. SuP10 16S; EU912450.1	100
BAC3055	0.99	*Staphylococcus warneri* (T); L37603	Staphylococcus warneri strain FUA2075 16S; HQ694734.1	98
BAC3056	0.92	Sporosarcina koreensis F73; DQ073393	Sporosarcina ginsengisoli strain CR5 16S; HQ331532.1	90
BAC3057	0.82	*Acinetobacter radioresistens* INBS1; AM495259	Acinetobacter radioresistens strain TY37SsD 16S; HQ406757.1	81
BAC3058	1.00	*Acinetobacter radioresistens* (T); DSM 6976; X81666	Acinetobacter radioresistens strain S13 16S; GU145275.1	99
BAC3059	0.98	*Lysinibacillus sphaericus*; KNUC228; EF166045	Lysinibacillus sphaericus strain IMAU80223 16S; GU125639.1	97
BAC1061	0.92	*Microbacterium testaceum* (T); DSM 20166; X77445	Microbacterium sp. CSBd gene for 16S; AB552874.1	91
BAC1062	1.00	*Staphylococcus epidermidis* (T); ATCC 14990; D83363	Staphylococcus epidermidis strain NM62-4 16S; HM218280.1	100
BAC1063	1.00	*Bacillus thuringiensis* (T); ATCC10792; AF290545	Bacillus thuringiensis strain ODPY 16S; HM770098.1	100
BAC1064	0.99	*Methylobacterium populi* (T); BJ001; ATCC BAA-705; NCIMB 13946; AY251818	Methylobacterium extorquens DM4 str. DM4; FP103042.2	100
BAC1065	1.00	*Microbacterium testaceum* (T); DSM 20166; X77445	Microbacterium testaceum strain DSM 20166 16S; NR_026163.1	99
BAC1066	1.00	*Microbacterium testaceum* (T); DSM 20166; X77445	Microbacterium testaceum StLB037; AP012052.1	99
BAC1067	1.00	*Microbacterium foliorum* (T); DSM 12966; P 333/02; AJ249780	Microbacterium foliorum strain 720 16S; EU714376.1	99
BAC1068	0.99	*Methylobacterium populi* (T); BJ001; ATCC BAA-705; NCIMB 13946; AY251818	Methylobacterium extorquens AM1; CP001510.1	99
BAC1069	0.99	*Methylobacterium populi* (T); BJ001; ATCC BAA-705; NCIMB 13946; AY251818	Methylobacterium extorquens AM1; CP001510.1	100
BAC1070	0.99	*Brevundimonas vesicularis* (T); ATCC 11426 (T); AJ007801	Brevundimonas vesicularis DNA for 16S strain LMG 11141; AJ227781.1	99
BAC2071	1.00	*Staphylococcus epidermidis* (T); ATCC 14990; D83363	Staphylococcus epidermidis strain LCR40 16S; FJ976549.1	100
BAC2072	1.00	*Frigoribacterium faeni* (T); 801; Y18807	Frigoribacterium sp. PDD-24b-20 16S; HQ256793.1	99
BAC2073	0.99	*Sphingomonas sanguinis* (T); IFO 13937; D13726	Sphingomonas pseudosanguinis partial 16S; AM412238.1	99
BAC2074	0.98	*Staphylococcus warneri* (T); L37603	Staphylococcus pasteuri partial 16S strain PSM NO.15; FR846535.1	98
BAC2075	0.99	*Frigoribacterium faeni* (T); 801; Y18807	Frigoribacterium sp. 301 16S; AF157479.1	99
BAC2076	1.00	*Rhizobium larrymoorei* (T); 3-10; Z30542	Agrobacterium larrymoorei strain 2R46 16S; EF178437.1	100
BAC2077	1.00	*Staphylococcus epidermidis* (T); ATCC 14990; D83363	Staphylococcus epidermidis strain F71028 16S; HQ908659.1	100
BAC2078	1.00	*Bacillus subtilis* subsp. subtilis (T); DSM10; AJ276351	Bacillus subtilis strain M-15 16S; HQ401271.1	100
BAC2079	1.00	*Microbacterium testaceum* (T); DSM 20166; X77445	Microbacterium sp. CSBd gene for 16S; AB552874.1	100
BAC2080	1.00	*Microbacterium testaceum* (T); DSM 20166; X77445	Microbacterium sp. Fek04 16S; EU741023.1	99
BAC3081	1.00	*Brevibacillus agri* (T); NRRL NRS-1219; D78454	Brevibacillus agri strain PLIV 16S; HQ166189.1	100
BAC3082	0.99	*Methylobacterium populi* (T); BJ001; ATCC BAA-705; NCIMB 13946; AY251818	Methylobacterium sp. SuP10 16S; EU912450.1	99
BAC3083	0.99	*Methylobacterium populi* (T); BJ001; ATCC BAA-705; NCIMB 13946; AY251818	Methylobacterium sp. SuP10 16S; EU912450.1	99
BAC3084	1.00	*Paenibacillus cineris* (T); type strain:LMG 18439; AJ575658	Paenibacillus sp. 3492BRRJ 16S; JF309261.1	100
BAC3085	1.00	*Staphylococcus epidermidis* (T); ATCC 14990; D83363	Staphylococcus epidermidis strain NM62-4 16S; HM218280.1	100
BAC3087	1.00	*Microbacterium foliorum* (T); DSM 12966; P 333/02; AJ249780	Microbacterium foliorum strain 720 16S; EU714376.1	99
BAC3088	0.99	*Methylobacterium populi* (T); BJ001; ATCC BAA-705; NCIMB 13946; AY251818	Methylobacterium sp. DC2c-19 gene for 16S; AB552870.1	99
BAC3089	1.00	*Staphylococcus warneri* (T); L37603	Staphylococcus warneri strain FUA2075 16S; HQ694734.1	99
BAC3090	0.99	*Methylobacterium populi* (T); BJ001; ATCC BAA-705; NCIMB 13946; AY251818	Methylobacterium sp. SuP10 16S; EU912450.1	99
BAC1091	1.00	*Paenibacillus cineris* (T); type strain:LMG 18439; AJ575658	Paenibacillus cineris partial 16S; AJ575658.1	99
BAC1092	1.00	*Microbacterium testaceum* (T); DSM 20166; X77445	Microbacterium testaceum strain 4CAJ3 16S; GQ383916.1	99
BAC1093	1.00	*Microbacterium testaceum* (T); DSM 20166; X77445	Microbacterium sp. CSBd gene for 16S; AB552874.1	99
BAC1094	0.99	*Microbacterium phyllosphaerae* (T); DSM 13468; P 369/06; AJ277840	Microbacterium sp. CSBd gene for 16S	99
BAC1095	1.00	*Micrococcus luteus* (T); ATCC 4698; AF542073	Micrococcus luteus strain EHFS1_S04Ha 16S; EU071593.1	100
BAC1096	1.00	*Bacillus muralis* (T); type strain: LMG 20238; AJ628748	Bacillus muralis strain REG126 16S; GQ844961.1	100
BAC1097	0.93	*Microbacterium* sp. S15-M4; AM234160	Microbacterium sp. HY14(2010) 16S; HM579805.1	92

Table S1. Continuation

Isolate	Ribossomal Database Project		NCBI	
	Similarity score	**Sequence name**	**Sequence name**	**% identity**
BAC1098	1.00	*Kocuria palustris* (T); TAGA27 (DSM 11925, type strain); Y16263	Kocuria palustris strain cT220 16S; JF303036.1	99
BAC1099	1.00	*Microbacterium testaceum* (T); DSM 20166; X77445	Staphylococcus warneri strain FUA2075 16S; HQ694734.1	100
BAC1100	1.00	*Microbacterium testaceum* (T); DSM 20166; X77445	Staphylococcus saprophyticus strain OTUC3 16S; FJ210844.1	100
BAC2101	1.00	*Staphylococcus saprophyticus* subsp. saprophyticus (T); ATCC 15305 (= MAFF 911473); D83371	Staphylococcus saprophyticus strain OTUC3 16S; FJ210844.1	100
BAC2102	1.00	*Staphylococcus warneri* (T); L37603	Staphylococcus warneri strain FUA2075 16S; HQ694734.1	100
BAC2103	0.99	*Methylobacterium populi* (T); BJ001; ATCC BAA-705; NCIMB 13946; AY251818	Methylobacterium extorquens gene for 16S rRNA; AB298401.1	99
BAC2104	1.00	*Delftia tsuruhatensis* (T); T7; AB075017	Delftia tsuruhatensis strain IPPBC R15 16S; HQ436355.1	100
BAC2105	0.99	*Methylobacterium populi* (T); BJ001; ATCC BAA-705; NCIMB 13946; AY251818	Methylobacterium extorquens gene for 16S; AB298401.1	99
BAC2106	0.86	*Bacillus cereus* me-5; EU652058	Bacillus cereus partial 16S; FR749846.1	85
BAC2107	1.00	*Staphylococcus warneri* (T); L37603	Staphylococcus warneri strain FUA2075 16S; HQ694734.1	99
BAC2108	0.99	*Methylobacterium populi* (T); BJ001; ATCC BAA-705; NCIMB 13946; AY251818	Methylobacterium extorquens gene for 16S rRNA; AB298401.1	99
BAC2109	1.00	*Staphylococcus warneri* (T); L37603	Staphylococcus warneri strain FUA2075 16S; HQ694734.1	99
BAC2110	1.00	*Frigoribacterium faeni* (T); 801; Y18807	Frigoribacterium faeni partial 16S; AM410686.1	99
BAC3111	0.99	*Pseudomonas aeruginosa* (T); DSM50071; X06684	Pseudomonas aeruginosa strain CRC5 16S; HQ995502.1	100
BAC3112	1.00	*Staphylococcus warneri* (T); L37603	Staphylococcus warneri strain FUA2075 16S; HQ694734.1	100
BAC3113	0.99	*Methylobacterium populi* (T); BJ001; ATCC BAA-705; NCIMB 13946; AY251818	Methylobacterium chloromethanicum gene for 16S; AB175630.1	99
BAC3114	0.97	*Dietzia cinnamea* (T); type strain:IMMIB RIV-399; AJ920289	Dietzia timorensis gene for 16S; AB377289.1	100
BAC3115	0.99	*Pseudomonas aeruginosa* (T); DSM50071; X06684	Pseudomonas aeruginosa strain MTH8 16S; HQ202541.1	100
BAC3116	0.95	*Staphylococcus warneri* (T); L37603	Staphylococcus warneri strain FUA2075 16S; HQ694734.1	94
BAC3117	1.00	*Agromyces mediolanus* (T); DSM 20152; X77449	Agromyces mediolanus gene for 16S; D45054.1	99
BAC3118	1.00	*Agromyces mediolanus* (T); DSM 20152; X77449	Agromyces mediolanus strain c18 16S; FJ950540.1	100
BAC3119	1.00	*Staphylococcus warneri* (T); L37603	Staphylococcus warneri strain FUA 3088 16S; GQ222399.1	99
BAC3120	0.88	*Stenotrophomonas maltophilia*; AY484506	Stenotrophomonas maltophilia strain AhsB4 16S; HM143858.1	87
BAC3121	1.00	*Stenotrophomonas maltophilia* (T); ATCC 13637T; AB008509	Stenotrophomonas maltophilia strain AhsB4 16S; HM143858.1	100
BAC3122	1.00	*Stenotrophomonas maltophilia* (T); ATCC 13637T; AB008509	Stenotrophomonas maltophilia strain AhsB4; HM143858.1	100
BAC3123	0.99	*Stenotrophomonas maltophilia* (T); ATCC 13637T; AB008509	Stenotrophomonas maltophilia strain AhsB4 16S; HM143858.1	99
BAC3124	0.98	*Agromyces mediolanus* (T); DSM 20152; X77449	Agromyces mediolanus strain c18 16S; FJ950540.1	97
BAC3125	1.00	*Stenotrophomonas maltophilia* (T); ATCC 13637T; AB008509	Stenotrophomonas maltophilia strain JKR32b 16S; HQ671069.1	100
BAC2126	0.99	*Microbacterium testaceum* (T); DSM 20166; X77445	Microbacterium trichotecenolyticum strain 3370 16S; EU714362.1	99
BAC2127	0.99	*Stenotrophomonas maltophilia* (T); ATCC 13637T; AB008509	Stenotrophomonas maltophilia strain AhsB4 16S; HM143858.1	99
BAC2128	1.00	*Stenotrophomonas maltophilia* (T); ATCC 13637T; AB008509	Stenotrophomonas maltophilia strain AhsB4 16S; HM143858.1	100
BAC2129	1.00	*Agromyces mediolanus* (T); DSM 20152; X77449	Agromyces mediolanus strain c18 16S; FJ950540.1	100
BAC2130	0.92	*Agromyces mediolanus* DSM 20152; X77449	Agromyces mediolanus strain c70 16S; FJ950561.1	91
BAC2131	1.00	*Staphylococcus epidermidis* (T); ATCC 14990; D83363	Staphylococcus epidermidis gene for 16S; AB617573.1	100
BAC2132	0.99	*Methylobacterium populi* (T); BJ001; ATCC BAA-705; NCIMB 13946; AY251818	Methylobacterium populi strain TNAU10 16S; EF116588.1	98
BAC2133	0.99	*Paenibacillus lautus* (T); NRRL NRS-666T; D78473	Paenibacillus lautus strain DS19 16S; EU834247.1	99
BAC2134	1.00	*Stenotrophomonas maltophilia* (T); ATCC 13637T; AB008509	Stenotrophomonas maltophilia strain JKR32b 16S; HQ671069.1	99
BAC2135	1.00	*Stenotrophomonas maltophilia* (T); ATCC 13637T; AB008509	Stenotrophomonas maltophilia strain AhsB4 16S; HM143858.1	100
BAC1136	0.99	*Stenotrophomonas maltophilia* (T); ATCC 13637T; AB008509	Stenotrophomonas maltophilia strain AhsB4 16S; HM143858.1	98
BAC1137	0.99	*Pseudomonas aeruginosa* (T); DSM50071; X06684	Pseudomonas aeruginosa strain MTH8 16S; HQ202541.1	100
BAC1138	1.00	*Enterobacter asburiae* (T); JCM6051; AB004744	Enterobacter hormaechei strain Ni-1 16S; HM446004.1	99
BAC1139	1.00	*Enterobacter hormaechei* (T); CIP 103441; AJ508302	Enterobacter cancerogenus strain M119 16S; HQ407292.1	99

Table S1. Continuation

Isolate	Ribossomal Database Project		NCBI	
	Similarity score	**Sequence name**	**Sequence name**	**% identity**
BAC1140	1.00	*Bacillus thuringiensis* (T); ATCC10792; AF290545	Bacillus thuringiensis strain ODPY 16S; HM770098.1	100
BAC1141	1.00	*Bacillus thuringiensis* (T); ATCC10792; AF290545	Bacillus thuringiensis strain ODPY 16S; HM770098.1	100
BAC2142	1.00	*Rhizobium larrymoorei* (T); 3-10; Z30542	Agrobacterium larrymoorei strain 13638E 16S; EU741094.1	100
BAC2143	0.95	*Staphylococcus warneri* (T); L37603	Staphylococcus warneri strain FUA2075 16S; HQ694734.1	95
BAC2144	0.88	*Staphylococcus saprophyticus* ATCC 15305; AP008934	Staphylococcus saprophyticus strain T86 16S; HQ407261.1	88
BAC2145	0.81	*Paenibacillus lautus* JCM 9073; AB073188	Paenibacillus lactis strain ZYb1 16S; FJ445392.1	80
BAC2147	0.98	*Bacillus bataviensis* (T); type strain: LMG 21832; AJ542507	Bacillus circulans strain RIGLD BC1 16S; HQ315829.1	98
BAC3148	1.00	*Stenotrophomonas maltophilia* (T); ATCC 13637T; AB008509	Stenotrophomonas sp. 2A9S2 16S; HQ246220.1	100
BAC3149	1.00	*Stenotrophomonas maltophilia* (T); ATCC 13637T; AB008509	Stenotrophomonas sp. 2A9N6 16S; HQ246302.1	100
BAC3150	1.00	*Stenotrophomonas maltophilia* (T); ATCC 13637T; AB008509	Stenotrophomonas maltophilia strain AhsB4 16S; HM143858.1	100
BAC3151	1.00	*Bacillus thuringiensis* (T); ATCC10792; AF290545	Bacillus thuringiensis strain NBB6 16S; HQ256544.1	100
BAC1152	1.00	*Staphylococcus warneri* (T); L37603	Staphylococcus warneri strain FUA2075 16S; HQ694734.1	100
BAC2153	1.00	*Microbacterium testaceum* (T); DSM 20166; X77445	Microbacterium testaceum strain BAC2153 16S; HM355741.1	100
BAC3154	1.00	*Microbacterium testaceum* (T); DSM 20166; X77445	Microbacterium testaceum strain BAC3154 16S; HM355742.1	100
BAC3155	1.00	*Stenotrophomonas maltophilia* (T); ATCC 13637T; AB008509	Stenotrophomonas sp. 2A9N6 16S; HQ246302.1	100
BAC1156	0.92	*Delftia tsuruhatensis* (T); T7; AB075017	Delftia tsuruhatensis strain BN-HKY6 16S; HQ731453.1	92
BAC1157	1.00	*Microbacterium foliorum* (T); DSM 12966; P 333/02; AJ249780	Microbacterium foliorum strain DS42 16S; EU834263.1	99
BAC2158	1.00	*Delftia tsuruhatensis* (T); T7; AB075017	Delftia tsuruhatensis strain BN-HKY6 16S; HQ731453.1	100
BAC3159	1.00	*Delftia tsuruhatensis* (T); T7; AB075017	Delftia tsuruhatensis strain BN-HKY6 16S; HQ731453.1	100
BAC2160	1.00	*Stenotrophomonas maltophilia* (T); ATCC 13637T; AB008509	Stenotrophomonas maltophilia strain BAC3148 16S; HM355736.1	100
BAC2162	1.00	*Rhodococcus erythropolis* (T); ATCC 4277T; X81929	Rhodococcus erythropolis strain BAC2162 16S; HM355749.1	100

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