Molecular detection on culture medium of Acidobacteria from Amazon soils

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Abstract
Cultivation and molecular approaches were combined to recover and detect Acidobacteria from Amazon soils on culture medium. The strategy of the cultivation procedure included the following: the use of VL55 growth medium supplemented with 0.05% xylan as the carbon source and solidified with gellan gum; incubation under hypoxic conditions (2% O2 [vol/vol], 2% CO2 [vol/vol], and 96% N2 [vol/vol]) for a relatively long period; inclusion of aluminium potassium sulphate in the growth medium; and soil dilution and plating. Of the 456 colonies recovered on the growth medium and subjected to PCR screening, three colonies belonging to Acidobacteria subdivision 1 and one colony belonging to Acidobacteria subdivision 3 were detected. The use of 16S rRNA gene based clone libraries comprising 437 clones confirmed that members of the phylum Acidobacteria grew primarily on plates on wich acidobacterial colonies were detected by PCR screening. The clones in the libraries consisted predominantly of Proteobacteria (orders Burkholderiales and Xanthomonadales). In summary, this work reports the recovery and molecular detection on VL55 growth medium of representatives of Acidobacteria subdivisions 1 and 3 concomitantly with to other bacterial groups inhabiting pasture and soybean cropland soils from the Amazon region.

Keywords: Soil microbiology, tropical rainforest soils, molecular PCR screening, Acidobacteria subdivisions 1 and 3

Introduction
The existence of large phylogenetic groups of bacteria that are poorly represented by cultivated strains has been revealed by culture-independent molecular surveys. Comparative phylogenetic analyses of the DNA sequences of 16S rRNA genes have shown that bacterial groups, such as the Acidobacteria, are ubiquitous and among the most abundant in different environments, including soil (Barns et al., 1999; Hugenholtz et al., 1998; Janssen, 2006). In spite of their high abundance, however, there are few members of Acidobacteria that have been cultured to date. Of 142,153 high-quality 16S rRNA gene sequences available from bacterial isolates (Ribosomal Database Project (RDP) II v10.4; http://rdp.msu.edu/), only 141 are classified as Acidobacteria, with cultured representatives of only 5 subdivisions [1,2,3,4, and 6] of the current 26 subdivisions (Barns et al., 2007; Hugenholtz et al., 1998; Zimmermann et al., 2005).

The culture-independent approach based on the direct recovery of bacterial 16S rRNA from tropical soils indicated the predominance of Acidobacteria in soils from Western Amazon (Kim et al., 2007; Jesus et al., 2009), Central Amazon (Navarrete et al., 2010), Southeastern Amazon (Navarrete et al., 2013), and the Brazilian Cerrado (Araujo et al., 2012). Among the 26 acidobacterial subdivisions classified, subdivisions [1-7, 10,11,13,16-18,22, and 25] have been detected in Amazon soils using 16S rRNA gene pyrosequencing (Navarrete et al., 2013 and Cannavan, 2012). Acidobacteria subdivisions [1,2, and 3] were reported to be dominant in soils from primary forests, soybean cropland fields, and pasture. In contrast, in the anthrosols associated with pre-Colombian settlements in the Amazonian region – Amazonian Dark Earth – Acidobacteria subdivisions [4 and 6] were dominant members within acidobacterial communities.

Despite the high abundance of acidobacterial 16S rRNA gene sequences recovered from the Amazon soils, there are no cultured representatives of Acidobacteria from this tropical ecosystem. Although many laboratories are attempting to obtain pure cultures of Acidobacteria from different environments worldwide, the taxonomically described diversity within this group remains very limited. More than half of the currently characterised Acidobacteria belong to subdivision [1], and only 18/141 high-quality 16S rRNA gene sequences from bacterial isolates are classified as subdivision [3] (Ribosomal Database Project (RDP) II v10.4; http://rdp.msu.edu/). Members of Acidobacteria subdivision [1] have been isolated from diverse soils (Janssen et al., 2002; Sait et al., 2002; Joseph et al., 2003; Eichorst et al., 2007; Koch et al., 2008; Stott et al., 2008), acidic mineral environments (Kishimoto et al., 1991), the termite hindgut (Eichorst et al., 2007), Sphagnum-dominated wetlands (Pankratov et al., 2008, 2012; Pankratov and Dedys, 2010), decaying wood (Folman et al., 2008; Valášková et al., 2009) and methanotrophic enrichment culture (Koch et al., 2008; Dedys et al., 2012). Acidobacteria subdivision [3] representatives have been isolated from soil (Sait et al., 2002; Joseph et al., 2003;
In this work, we took advantage of the treatments tested in Stevenson et al. (2004) and Davis et al., (2005), combining cultivation and molecular approaches to recover and detect Acidobacteria from Amazon soils on laboratory media. For this purpose, a high carbon concentration was provided in the culture medium, and the samples were maintained under hypoxic conditions (2% O₂, 2% CO₂ [v/v] and 96% N₂ [v/v]) with a long incubation time. We performed a laboratory cultivation experiment using Acidobacteria-positive soils from primary forest, soybean cropland fields, pasture and Amazonian Dark Earth sites located in the Brazilian Amazon region as the inoculum and previously screened for Acidobacteria using 16S rRNA gene amplicon pyrosequencing (Navarrete et al., 2013 and Cannavan, 2012).

**Materials and methods**

Cultivation and molecular approaches were combined to recover and detect Acidobacteria from Amazon soils on culture medium according to the procedure shown in the methodological flow chart illustrated in (Figure 1). A detailed description of the methodology is shown in the subsequent sections of this paper.

**Soil collection and manipulation**

The soil samples were collected in November 2011 from six different sampling sites located at three different municipalities in the Brazilian Amazon region: (1) Porto dos Gaúchos municipality (-15°13'39" S and -54°04'31" W), state of Mato Grosso, in primary forest (PF-1) and soybean cropland fields (SC-1); (2) Ipiranga do Norte municipality (-13°21'57" S and -54°54'24" W), state of Mato Grosso, in primary forest (PF-2), soybean cropland fields (SC-2), and pasture (*Brachiaria brizantha*) (PA); and (3) Iranduba municipality (03°18'25" S and 60°32'05" W), state of Amazonas, in an anthropogenic soil site characterised as Amazonian Dark Earth (ADE). Oxisol is the predominant soil order in the field sites located in Mato
soil bacteria used in this study. The gas mixture (2% O₂ [vol/vol], 2% CO₂ [vol/vol], and 96% N₂ [vol/vol]) inside the cylinder was pulsed into the system daily after electric vacuum aspiration. The pressure control inside the anaerobic jars was based on a manometer located in the opening of the gas cylinder.

Figure 2. Cartoon representing the cultivation system for soil bacteria used in this study. The gas mixture (2% O₂ [vol/vol], 2% CO₂ [vol/vol], and 96% N₂ [vol/vol]) inside the cylinder was pulsed into the system daily after electric vacuum aspiration. The pressure control inside the anaerobic jars was based on a manometer located in the opening of the gas cylinder.

Grosso (SEPLAN, 2001); the soil at the ADE site is classified as Hortic Anthrosol according to the World Reference Base for Soil Resources (FAO, 1998).

Five soil cores (5 cm in diameter, 0- to 20-cm topsoil layer) were collected from each sampling site using a cylindrical soil corer aseptically and transported to the laboratory in a sealed polyethylene bag at ambient temperature and stored overnight at 4 °C. The soil samples were collected from five sampling points at each site, with one central sampling point and other four sampling points (at least 50 m away from the central point) directed toward the north, south, east, and west of the central point. An accurately weighed aliquot of soil (6 g fresh weight) from each of the five soil samples per sampling site was suspended in 100 mL sterile salt solution (3.9 g 2-[N-morpholino]ethanesulphonic acid, 0.4 mM MgSO₄, 0.6 mM CaCl₂, and 0.4 mM (NH₄)₂HPO₄ per litre) and mixed using a Teflon-coated magnetic bar for 15 min at approximately 200 r.p.m. The resulting suspensions were serially diluted in 10-fold steps by the addition of 1 mL of the previous dilution to 9 mL sterile salt solution, stirring for 5 min between dilutions. Volumes of 100 mL from the 10⁻⁵ and 10⁻⁶ dilutions of the soil were spread onto plates of VL55 medium (see below) using a sterile glass spreader.

Cultivation experiment
Four replicate plates per soil dilution and sampling site were incubated under hypoxic conditions (2% O₂ [vol/vol], CO₂ (2% [vol/vol], and 96% N₂ [vol/vol]) at room temperature in a cultivation system, as illustrated in Figure 2. All the cultures were maintained under low light conditions at room temperature (24 to 26 °C) for six weeks, and the number of colonies was then counted per plate the colonies used to determine the colony counts were visible using a colony counter fitted with a 1.5x magnifying lens. The VL55 base contained 3.9 g 2-[N-morpholino]ethanesulphonic acid, 0.4 mM MgSO₄, 0.6 mM CaCl₂, 0.4 mM (NH₄)₂HPO₄, 2 mL of selenite/tungstate solution (Tschech and Pfennig, 1984), and 0.8% gellan gum per litre. Gellan gum provides a more transparent medium than agar, facilitating the visualisation of the colonies. The pH was adjusted to 5.5 with a mixture of 200 mM NaOH plus 100 mM KOH. This medium base was autoclaved at 121 °C for 20 min and cooled to 56 °C. A 10 mL aliquot of 5% (w/v) xylan from beechwood (Fluka), 2 mL vitamin solution (see below), and 2 mL of a trace element solution SL-10 (Widdel et al., 1983) with inclusion of aluminium potassium sulphate (0.01 g/L) were added per litre of medium base. The selenite/tungstate, vitamin, and trace element solutions were added after membrane filtration. The vitamin solution contained (per litre of H₂O) 2 mg (+)-biotin, 2 mg folic acid, 10 mg pyridoxamine hydrochloride, 5 mg thiamine chloride, 5 mg riboflavin, 5 mg nicotinic acid, 5 mg hemicalcium D(+)-pantothenate, 0.1 mg cyanocobalamin, 5 mg 4-aminobenzoate and 5 mg DL-6,8-thiotoic acid. Cycloheximide 1 µg/mL was added as antifungal agent. This medium was used for both enumeration and subcultivation.

PCR screening for Acidobacteria on culture plates and subcultivation
After six weeks of incubation, screening for acidobacterial colonies was performed with Acidobacteria-specific primers and Acidobacterium capsulatum (DSM 11244) as a positive control in the PCR reactions. A total of 456 individual colonies were subjected to screening for Acidobacteria by PCR. For picking individual colonies, the plates were viewed with illumination from a cool white light. Unreplicated PCR reaction was performed for each individual colony after cells lysis in 50 µL 1x Tris-EDTA (TE) buffer (10 mM Tris-HCl and 1 mM EDTA, pH 8.0) using a thermal cycler (Applied Biosystems, CA, USA) for 10 min at 96 °C. Each 25-µL PCR reaction contained approximately 50 ng template DNA, 1x reaction buffer (Invitrogen, CA, USA), 1.5 mM MgCl₂, 0.25 mM each deoxynucleoside triphosphate, 0.2 µM each forward Acid31F (5’-GATCCTGGCGTCAGATC-3’) (Barns et al., 1999) and reverse 1492R (5’-TACGGYTACCTTGTTACGACTT-3’) (Lane, 1991) primer, and 1.0 U Taq DNA polymerase (Invitrogen, CA, USA). The PCR mixtures were incubated in a GeneAmp PCR System 9700 thermal cycler (Applied Biosystems, CA, USA) for the following amplification cycles: 3 min at 95 °C; 30 cycles of 1.5 min at 95 °C, 1 min at 52 °C, and 1.5 min at 72 °C; followed by 10 min at 72 °C.

The PCR products were analysed by electrophoresis of 5 µL of the reaction mixture on 1% agarose gels at 100 V in 0.5x Tris-borate-EDTA, visualised by UV illumination after staining with GelRed (Biotium Inc., CA, USA), and photographed. Based on the A. capsulatum-positive product, four individual colonies of Acidobacteria were detected, and the cell lysis material obtained from these colonies and A. capsulatum-positive colony was used as the template in PCR reactions separately performed with the universal bacterial primers 27F (5’-AGAGTTTGATCCTGCTGAG-3’) and 1492R

Figure 2. Cartoon representing the cultivation system for soil bacteria used in this study. The gas mixture (2% O₂ [vol/vol], 2% CO₂ [vol/vol], and 96% N₂ [vol/vol]) inside the cylinder was pulsed into the system daily after electric vacuum aspiration. The pressure control inside the anaerobic jars was based on a manometer located in the opening of the gas cylinder.
16S rRNA gene of the detected acidobacterial colonies – PA (2.6) and SC-2 (3.2) – were deposited in the GenBank Database (http://www.ncbi.nlm.nih.gov/genbank/). Partial sequences (1000 - 1488 bp) for the 16S rRNA gene was performed for each clone using the primers 27F, 1492R, 518F (5’-CCAGCAGCCGCGGTAATACG-3’), and 800R (5’-TACCAAGGTATCTAATCC-3’), the BigDye Terminator v3.1 cycle sequencing kit (Applied Biosystems, CA, USA), and an ABI 3730xl DNA Analyzer capillary sequencer (Applied Biosystems, CA, USA) (Macrogen Inc. Company, South Korea). Taxonomy was assigned to the sequences using Ribosomal Database Project (RDP) 2 classifier (release 10.4) (http://rdp.cme.msu.edu/). The sequences were grouped into operational taxonomic units (OTUs) using MOTHUR software (Schloss et al., 2009). An OTU was defined as a group of sequences exhibiting ≥ 97% similarity to each other using the average neighbour algorithm. A representative sequence for each OTU was determined using MOTHUR software as the sequence that has the minimum distance from all other sequences within the same OTU. In addition, representative sequences for each OTU were assigned to a phylogenetic tree containing mostly related nucleotide sequences available from databases (GenBank and Ribosomal Database Project). The sequences were aligned using ClustalX2 (Larkin et al., 2007) and further clustered using neighbour-joining analysis with Kimura-2 parameters from a study conducted using MEGA version 4.0 (Tamura et al., 2007), determining the preferred phylogenetic tree, as supported by bootstrap values, based on an analysis of 1,000 subsamples.

**Results and Discussion**

The recalcitrance of acidobacterial taxa members to growth on culture media has been extensively reported during the past decade. However, new cultivation strategies have been considered in combination with classical microbiology methods to improve the culturability of Acidobacteria in the laboratory. Culturing techniques that have contributed to the successful isolation of Acidobacteria include the following: media with a low pH (Sait et al., 2006); increased headspace CO₂ concentrations (Stevenson et al., 2004); substrate amendments (Pankratov et al., 2008); random selection of a wide variety of growth substrates (Joseph et al., 2003); the use of a diffusion chamber (Bollmann et al., 2007); and the extension of the by gel electrophoresis. The PCR products were ligated into the pGEM-T easy vector (Promega, WI, USA) and transformed into competent E. coli DH5α cells. Six different clone libraries were constructed, one for each soil type. A total of 437 clones were randomly selected and sequenced using the vector primer M13F (5’-GGCAGGTTTTCAGCAGC-3’) (Huey and Hall, 1989), the BigDye Terminator v3.1 cycle sequencing kit (Applied Biosystems, CA, USA), and an ABI 3730xl DNA Analyzer capillary sequencer (Applied Biosystems, CA, USA). The libraries were constructed for the DNA samples from the isolation plates inoculated with PF soils (PF-1 GenBank accession nos. JX574664 - JX574723 and PF-2 GenBank accession nos. JX574724 - JX574770), SC soils (SC-1 GenBank accession nos. JX574771 - JX574828 and SC-2 GenBank accession nos. JX574829 - JX574911), PA soil (GenBank accession nos. JX574912 - JX574988), and ADE soil (GenBank accession nos. JX574989 - JX575075).

**Clustering clones into operational taxonomic units and phylogenetic analysis**

The 16S rRNA gene sequences were edited using Phred/Phrap (Ewing et al., 1998). Taxonomy was assigned to the sequences using Ribosomal Database Project (RDP) 2 classifier (release 10.4) (http://rdp.cme.msu.edu/). The sequences were grouped into operational taxonomic units (OTUs) using MOTHUR software (Schloss et al., 2009). An OTU was defined as a group of sequences exhibiting ≥ 97% similarity to each other using the average neighbour algorithm. A representative sequence for each OTU was determined using MOTHUR software as the sequence that has the minimum distance from all other sequences within the same OTU. In addition, representative sequences for each OTU were assigned to a phylogenetic tree containing mostly related nucleotide sequences available from databases (GenBank and Ribosomal Database Project). The sequences were aligned using ClustalX2 (Larkin et al., 2007) and further clustered using neighbour-joining analysis with Kimura-2 parameters from a study conducted using MEGA version 4.0 (Tamura et al., 2007), determining the preferred phylogenetic tree, as supported by bootstrap values, based on an analysis of 1,000 subsamples.

**DNA Isolation, amplification, and construction of 16S rRNA gene clone libraries**

Colonies were partially kept on the surface of the plates after picking colonies procedure for PCR screening as described above. For construction of the 16S rRNA gene clone libraries, the surface of these plates was flooded with 2 mL of bead solution from the Power Soil DNA Isolation Kit (MO BIO Laboratories Inc., CA, USA), and a sterile spreader was used to suspend as much of the colony material as possible. The colony material was pooled from isolation plates for each of the six soil types. The bead solution with suspended cells was transferred to a dry bead tube from the DNA kit, 50 µL of lysozyme solution (50 mg/mL; Sigma-Aldrich) was added, and the tube was incubated for 30 min in a 37 °C water bath. DNA isolation was then performed according to the manufacturer’s protocol. The 16S rRNA gene fragments were amplified using the PCR universal bacterial primers 27F and 1492R (Weisburg et al., 1991) as described. The PCR products were purified using the Qiagen PCR purification kit (Qiagen, CA, USA) after analysis
A total of 456 colonies from the plates containing $10^5$ and $10^6$ soil dilutions as the inoculum were picked and subjected to PCR screening with primers targeting a region of the 16S rRNA-encoding gene specific to Acidobacteria. Only four acidobacterial colonies were detected by PCR from the total number of screened colonies. Three acidobacterial colonies were positively detected from the plates inoculated with PA soil (colonies PA(1.5), PA(2.1), and PA(2.6)), and one acidobacterial colony was detected from a plate inoculated with SC-2 soil (colony SG-2(3.2)). Although the plates for the initial isolation experiment were incubated for six weeks, subcultures of the acidobacterial colonies PA(1.5) and PA(2.1) were able to decrease the pH of the medium to 3.1, and hydrolysing the gellan gum within three weeks and, thus, rendering the plates unusable. Therefore, these two acidobacterial colonies could not be isolated. The PA(1.5) colony was identified as Acidobacteria subdivision [1] (100% identity with 16S rRNA gene sequences) and the PA(2.1) colony as belonging to Acidobacteria subdivision [3] (100% identity with 16S rRNA gene sequences) (Figure 4). Based on the partial sequencing of the 16S rRNA gene (1488 bp), the acidobacterial colonies PA(2.6) and SC-2(3.2) were identified as Acidobacteria subdivision [1] (100% identity with 16S rRNA gene sequences) (Figure 4), and both were isolated and preserved by lyophilisation and mineral oil. All the four acidobacterial colonies did not grow when inoculated in liquid VL55 medium; however, PA(2.6) and SC-2(3.2) were able to grow on solid medium under atmosphere-unamended air. The subdivision [1] isolates (PA (2.6)) formed smooth and semi-transparent colonies, generally with an irregular margin at a later stage of development (> 2 months of incubation) (Figure 5).

Assessment based on the 16S rRNA gene clone libraries
The ability to obtain visible colonies is a factor that may limit the apparent culturability of some microorganisms. All colonies on a growth medium do not develop at the same rate, even in pure cultures (Ishikuri and Hattori, 1985; Mochizuki and Hattori, 1986), and after extraction from the soil, some cells develop into microcolonies of just a few cells (Winding et al., 1994). Furthermore, it is not clear whether micro- or minicolonies would form visible colonies if incubated for a sufficient amount of time, or whether they have a self-limiting growth phenotype (Davis et al., 2011). However, to avoid the situation in which acidobacterial colonies would not be detected by picking isolated colonies, we used 16S rRNA gene clone libraries to identify growth of Acidobacteria on the growth medium.

Of the bacterial 16S rRNA genes present on the growth medium after six weeks of incubation, 437 sequences were recovered from samples of the Amazon soils from the PF, SC, PA, and ADE sites. The taxonomy assignment showed that acidobacterial clones (≥ 97% identity with 16S rRNA gene sequences) were recovered only from plates inoculated with the SC and PA soils (Table 1, Figure 4). Sequences belonging

![Figure 3](http://www.hoajonline.com/journals/pdf/2052-6180-1-1.pdf)

**Figure 3.** Distribution of colony forming units (CFUs) in the different soils used for the cultivation experiment. Each CFU count represents the mean of four plates at one dilution level and was calculated based on the dry weight of the soil and dilution factors. The standard deviations are indicated as error bars. PF-1, Primary forest 1; PF-2, Primary forest 2; SC-1, Soybean cropland 1; SC-2, Soybean cropland 2; PA, Pasture; ADE, Amazonian Dark Earth.
Figure 4. Phylogenetic relationships based on the partial 16S rRNA gene sequences of detected acidobacterial colonies on growth medium and representative clones from libraries constructed to assess the total bacterial community on growth medium inoculated with Amazon soils from different origins (PF, primary forest areas; SC, soybean cropland fields; PA, pasture; and ADE, Amazonian Dark Earth sites) with their best matches in the databases searched (GenBank and Ribosomal Database Project). A bootstrap analysis was performed with 1,000 repetitions, and the values indicate the percentage of clustering matches. The scale bar at the bottom of the figure displays the number of differences in the base composition among the sequences. The values and abbreviations in brackets indicate the number of clones in each OTU (3% cutoff point of dissimilarity) and their origins, respectively. The soil samples (PF and SC) were collected from sites located at Porto dos Gaúchos municipality (1) and Ipiranga do Norte municipality (2).
Acidobacteria subdivision 1 accounted for 10% and 23% of the total number of clones from plates inoculated with SC-2 and PA soils, respectively. One sequence belonging Acidobacteria subdivision 3 was recovered from a plate inoculated with the SC-1 soil (Table 1, Figure 4), a result that expands that obtained with PCR screening using specific primers showing the detection of an Acidobacteria subdivision 3 representative only from the plate inoculated with the PA soil.

Although a comparative phylogenetic analysis of DNA sequences of the 16S rRNA genes revealed that subdivisions 1 and 3 are dominant in the primary forest and cropland field soils evaluated in this study (Navarrete et al., 2013), representatives of these group were recovered only from the isolation plates inoculated with the soybean cropland and pasture soils (Table 1, Figure 4). Eichorst et al., (2011) also detected members of Acidobacteria subdivisions 1 and 3 in agricultural and managed grassland soils in Michigan using molecular and cultivation-based approaches. These authors suggested that members of these two acidobacterial subdivisions have the potential to play an active role in the degradation of plant polymers in bulk soil and to utilise sugars from plant root exudates at various concentrations in the rhizosphere.

Several growth conditions have been considered in cultivation experiments to allow a better representation of acidobacterial diversity into laboratory culture. Sait et al., (2006) identified moderately acidic pH values as an important factor for their success in isolating many members of subdivision 1. This condition fits with the abundance of members of this group in different soils in which they form relatively larger parts of the total community as the soil pH decreases (Sait et al., 2006). Pure cultures also display growth
Additionally, taxonomically unclassified bacteria were found (Actinomycetales) and Acidobacteria (Table 1, Figure 3). For the isolation plates inoculated with the ADE soil, the clones were majority related to phylum Proteobacteria (orders Burkholderiales and Rhizobiales) (Table 1, Figure 4). Among the clones in the SC-2 library but not in the SC-1 library, the clones derived from the isolation plates inoculated with the PA soils were mostly affiliated with Proteobacteria (order Burkholderiales), followed by Acidobacteria subdivision [1]. For the isolation plates inoculated with the ADE soil, the clones were majority related to phylum Proteobacteria (orders Burkholderiales and Rhizobiales) (Table 1, Figure 4). Additionally, taxonomically unclassified bacteria were found in all the libraries, except that for PF-2. Considering the differential occurrence of Acidobacteria on isolation plates in contrast to the growth of other bacterial groups (Table 1), it is interesting to note that, based on the cultivation strategy employed in this study, acidobacterial colonies were detected on those plates a lower number of colonies and an increased time for visible growth (Table 1, Figure 3). These slow-growing microorganisms may have been inhibited by products from more rapidly growing colonies (Janssen, 2008; Vartoukian et al., 2010), which may be a reason why most used cultivation methods failed to capture the full extent of the phylogenetic diversity of bacteria present in environmental samples (Hugenholtz et al., 1998). This situation has been particularly apparent in attempts to culture soil bacteria, whereby both the number (Conn, 1918) and diversity (Janssen, 2006) are greatly underestimated by the most traditional cultivation-based techniques.

**Conclusion**

In summary, this work reports the recovery and the molecular detection on VLSS growth medium of representatives of Acidobacteria subdivisions [1 and 3] from Amazon soils under soybean cropland and pasture. The results serve as the first indication of the potential of combining cultivation and molecular approaches to grow and to detect Acidobacteria from Amazon soils on culture medium.

**Competing interests**

The authors declare that they have no competing interests.

**Authors’ contributions**

AAN made substantial contributions to the conception and design of the study and acquisition, analysis, and interpretation of the data. CCB participated in the design of the study and helped to define the strategy for the cultivation procedure. MA participated in the cultivation experiment. SMT participated in the design and coordination of the study and helped to draft the manuscript. All authors read and approved the final manuscript.

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