Antimicrobial potential of actinobacteria isolated from the rhizosphere of the Caatinga biome plant *Caesalpinia pyramidalis* Tul.

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ABSTRACT. Actinobacteria are known to produce various secondary metabolites having antibiotic effects. This study assessed the antimicrobial potential of actinobacteria isolated from the rhizosphere of *Caesalpinia pyramidalis* Tul. from the Caatinga biome. Sixty-eight actinobacteria isolates were evaluated for antimicrobial activity against different microorganisms by disk diffusion and submerged fermentation, using different culture media, followed by determination of minimum inhibitory concentration (MIC) and chemical prospecting of the crude extract. Of the isolates studied, 52.9% of those isolated at 37°C and 47.05% of those isolated at 45°C had activity against *Bacillus subtilis*, *Staphylococcus aureus*, methicillin-resistant *S. aureus* (MRSA), *Fusarium moniliforme*, and *Candida albicans*. When compared with others actinobacteria, the isolate C1.129 stood out with better activity and was identified by 16S rDNA gene analysis as *Streptomyces parvulus*. The crude ethanol extract showed an MIC of 0.97 µg/mL for MRSA and *B. subtilis*, while the ethyl acetate extract showed MIC of 3.9 µg/mL for *S. aureus* and MRSA, showing the greatest potential among the metabolites produced. Chemical prospecting revealed

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the presence of mono/sesquiterpenes, proanthocyanidin, triterpenes, and steroids in both crude extracts. This study evaluates *S. parvulus* activity against multi-resistant microorganisms such as MRSA. Thus, it proves that low-fertility soil, as is found in the Caatinga, may contain important microorganisms for the development of new antimicrobial drugs.

Key words: *Streptomyces*; Bioactive compounds; Antimicrobial activity

INTRODUCTION

The Caatinga biome is located in the northeast of Brazil, covers eight northeastern states and part of Minas Gerais, and is a biological heritage site in the region that exists nowhere else in the world. It is the least protected of all Brazilian biomes, and has been subjected to environmental deterioration. While the Caatinga biome is characterized by its wide species diversity, biodiversity conservation in the region faces major challenges (Gorlach-Lira and Coutinho, 2007). The endemic plant *Caesalpinia pyramidalis* Tul. is one of these diverse species found here. It is used for various purposes, including the treatment of diarrheal processes and dysentery, as well as of respiratory infections.

The rhizosphere is a soil region strongly influenced by plant roots, and has maximum microbial activity and a large microbial diversity, which in most cases is enriched with the byproducts of plant metabolism. Bacteria, fungi, actinobacteria, and plants live in a constant process of symbiosis (Melo and Azevedo, 2008; Berg and Smalla, 2009).

The study of microorganisms from the rhizosphere plants of the Caatinga is extremely important, since they are a means by which low-fertility soil can become a powerful source of biotechnologically important metabolites. The search for products effective against multi-drug resistant bacteria pathogenic to humans is an important goal. The rapid and aggressive development of antimicrobial-resistant bacterial species has motivated scientists to develop novel biomolecules. Microorganisms of the rhizosphere - in particular the actinobacteria - are a promising source of new antibiotics and are of great interest to the pharmaceutical industry and biotechnology (Higginbotham and Murphy, 2010; Choi et al., 2012).

The actinobacteria constitute an important group of bacteria commonly isolated from the rhizosphere. They are Gram-positive and are known to produce several types of antibiotics with practical applications in industry, agriculture, medicine, and veterinary science. The genus *Streptomyces* is the best known among the actinobacteria, and includes over 3000 identified species (Goodfellow et al., 2012). They are in greater abundance in the soil, but may also occur in various other environments. These filamentous bacteria are aerobic and synthesize volatile compounds, such as geosmin, which gives soil its characteristic “wet earth” odor. *Streptomyces* sp are very valuable, as they produce several commercial antibiotics, including streptomycin (Vasconcellos et al., 2010; Madigan et al., 2012). Given this, the aim of the present study was to evaluate the antimicrobial activity of actinobacteria isolated from the rhizosphere of the plant *Caesalpinia pyramidalis* Tul. from the Caatinga biome.

MATERIAL AND METHODS

Isolation of actinobacteria

Isolations were performed from 10 g rhizosphere in 90 mL PBS buffer. The sample was

pretreated by homogenization in vortex for 20 min and by placing in a 50°C water bath for 15 min. Samples were serially diluted from 10^{-3} to 10^{-5} in saline solution, and 0.1 mL of each dilution was inoculated into AY modified media (AYM) (Nomomura and Ohara 1969a); MC (Nomomura and Ohara, 1969b), and ISP-4 (Shirling and Gottlieb, 1966). The plates were incubated in a greenhouse B.O.D. (biochemical oxygen demand) at 37°C and 45°C for 20 days.

Determination of antimicrobial activity

Preliminary assay

Seeding of actinobacteria was performed following the method of Ichikawa et al. (1971). Strains were cultivated in a carpet at 37°C and 45°C. After 120 h, an agar block diffusion assay was performed using test microorganisms strains from the Microorganism Culture Collection of Departamento de Antibióticos, Universidade Federal de Pernambuco (UFPEDA). Species included for testing were: *Fusarium moniliforme* UFPEDA-2456; *Malassezia furfur* UFPEDA-1320; *Candida albicans* UFPEDA-1007; *Bacillus subtilis* UFPEDA-86; *Staphylococcus aureus* UFPEDA-02; methicillin-resistant *S. aureus* (MRSA) UFPEDA-700; *Escherichia coli* UFPEDA-224; *Klebsiella pneumoniae* UFPEDA-416; and *Pseudomonas aeruginosa* UFPEDA-396 (Vasconcelos et al., 2015).

Secondary assay

The actinobacteria was cultivated in the media ISP-4, modified AYM, M1, and MPE (Kawamura et al., 1976) and stirred at 180 rpm for 120 h. After this period, 10% (v/v) were transferred to Erlenmeyer flasks containing 50 mL medium. Every 24 h, a 1-mL aliquot was taken to evaluate the dry weight, antimicrobial activity, and pH. For evaluating the antimicrobial activity of secondary metabolites, a disc diffusion test was performed. Fifty-microliter aliquots fermented liquid were placed on Mueller Hinton (MH) plates containing the test microorganisms strains and incubated at 37°C for 24 h. The disc diffusion test was performed in triplicate and the results were determined through the arithmetic average of the inhibition zone diameters in millimeters (CLSI, 2014).

Extraction of bioactive metabolites

Streptomyces C1.129 was cultivated in the M1 medium at 37°C for 96 h at 180 rpm. Extraction of metabolites from the cell mass and liquid was then performed. The cell mass was treated with acetone, ethanol, and pure methanol at pH 2.0, 7.0, and 9.0, and for the metabolic liquid we used ethyl acetate, chloroform, and pure petroleum ether at the same pH values mentioned above. The pH was then adjusted to 7.0, and the antimicrobial activity was assessed using the disc diffusion test (Lyra et al, 1964; CLSI, 2014)

Determination of minimum inhibitory concentration (MIC)

Antimicrobial activity was determined by microdilution in multiwell plates, according to the methods prescribed by the Clinical and Laboratory Standards Institute (CLSI, 2014). MH broth was distributed in wells and extract was added at concentrations ranging from 1000 to 3.9 µg/mL. Then, standardized microbial inoculum, containing 1.5 x 10^8 *S. aureus* UFPEDA-02, MRSA UFPEDA-700, and *B. subtilis* UFPEDA-86, was added. Microplates were cultured at 37°C for 18 to 24

h. Ethanol and ethyl acetate extracts were tested for activity against Gram-positive bacteria, using as a standard control oxacillin, which has an MIC of 4 μg/mL for *S. aureus*. Microplates were then stained with 0.01% resazurin and incubated for 1 to 3 h to observe color changes in the wells (blue to pink). The bactericidal minimum concentration was determined by establishing subculture wells on Petri dishes containing the solid medium MH and incubating at 37°C for 24 h.

Prospection chemical of the extracts

Ethanolic and ethyl acetate crude extracts were analyzed by thin-layer chromatography (TLC) in aluminum TLC sheets containing silica gel 60 F254 (Merck). For the identification of classes of secondary metabolites, various mobile phases were used and specific revealing (Robertson et al., 1956; Metz, 1961; Sharma and Darwra, 1991; Wagner and Bladt, 1996; Harbone, 1998).

Bioautography

The antimicrobial fraction was characterized using the TCL bioautography technique described by Scher et al. (2004). The crude extract of biomass and metabolic liquid was applied to a silica gel plate 60 F254 (Merck), and the chromatographic run performed using the solvent system $CHCl_3$:MeOH (9:1 v/v). Organic revelation was performed using MH culture medium inoculated with a suspension of *S. aureus* (UFPEDA 02) with a density in the range of 0.5 by the MacFarland scale (1.5 UFC/mL) and incubated at 37°C for 24 h. Revelation was conducted with an aqueous solution of 2,3,5-triphenyltetrazolium chloride (20 mg/mL) and maintained at 37°C for 2 to 4 h.

Classical taxonomic characterization

Micromorphological analysis was performed using the method followed by Shirling and Gottlieb (1966). Actinobacteria were inoculated as a wide streak on ISP-4 culture medium; coverslips were inserted at a 45° inclination on the streak to induce growth of aerial mycelia on the coverslip. The culture medium was then incubated at 37°C for 5 to 10 days, after which the coverslip was removed to observe the formation of spore-sporophore chains using an optical microscope with a 40X objective (Medilux, MDL-150-BAI).

The actinobacterial cell wall was studied by assessing isomers of diaminopimelic acid (DAP), LL-diaminopimelic acid or meso-diaminopimelic acid, according to the methodology of Staneck and Roberts (1974). The bacterial cell wall was hydrolyzed and evaluated by TLC with a mobile phase consisting of methanol:water:hydrochloric acid 6N:pyridine (80:26:4:10 v/v) and fixed-layer cellulose plates Merck No. 5716, 20 x 20 (Merck Millipore Corporation, Darmstadt, Germany). *Streptomyces regensis* (UFPEDA-3053) and *Nocardia asteroides* (UFPEDA-3503), which show LL-DAP and Meso-DAP isomers, respectively, were used as standards. Visualization was performed using 0.2% ninhydrin and heating at 100°C for 5 min to visualize the isomers.

Molecular characterization

DNA was extracted from the bacterial strain C1.129 using culture grown in ISP-2 liquid medium for 16 h at 37°C. Subsequently, the sample was centrifuged for 3 min at 9168 *g*, and DNA extraction performed using the Wizard genomic DNA purification kit according to the manufacturer instructions (Promega Biotecnologia). The extracted DNA was assessed using electrophoresis on

an agarose gel, and host 16S ribosomal RNA (rRNA) was amplified by polymerase chain reaction (PCR) using universal oligonucleotides.

The reaction mixture, in 25 µL final volume, comprised 50 ng DNA; 5 pmol each oligonucleotide (fD1; 5'-AGAGAGTTTGATCCTGGCTCAG-3' and rD1 5'-CGGTGTGTACAAGGCCCGGGGAACG-3'); 200 mM dNTP; 1.5 mM $MgCl_2$; 1X buffer; and 1 U Platinum Taq DNA polymerase (Invitrogen Life Technologies, Carlsbad, CA, USA). Reaction conditions were as follows: 5 min denaturation at 94°C; 25 cycles of 1 min at 94°C, 30 s at 52°C, and 2 min at 72°C, and a final extension of 10 min at 72°C (Weisburg et al., 1991). The amplified product was analyzed by electrophoresis on a 1.2% agarose (w/v) gel, and the sample sequenced by Macrogen (Seoul, Korea). This sequence was compared with those in GenBank, using the BLAST software from the National Center for Biotechnology Information (www.ncbi.nlm.nih.gov). Sequence alignment was performed using the Clustal software (www.ebi.ac.uk/tools/msa/clustaw2), and phylogenetic tree construction was carried out using Mega 5.5. Topology assessed by bootstrap analysis (1000 resamplings).

Statistical analysis

Statistical analysis was performed by one-way analysis of variance (ANOVA) with a Tukey-Kramer test (Sokal & Rohlf, 1995), using Excel 2010 (Microsoft® Office) software and Minitab version 15 (Minitab®).

RESULTS

Isolation of actinobacteria

Sixty-eight strains of actinobacteria were isolated from the rhizosphere of *C. pyramidalis* Tul. from the Caatinga biome. Of these, 36 (52.9%) were isolated at 37°C and 32 (47.05%) at 45°C. The culture medium with the largest number of colonies was MC, which yielded 60.3% of the isolates, followed by ISP-4 (23.5%) and AYM (16.2%) at 37°C (Figure 1A). The majority of actinobacteria was isolated in MC medium (Figure 1B).

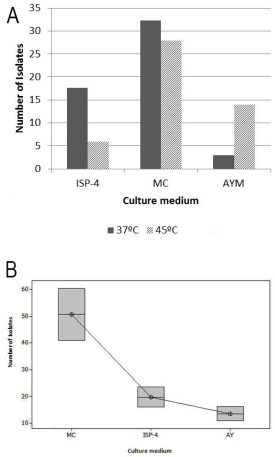

Figure 1. A. Isolation of actinobacteria in different culture media (MC, ISP-4 and AYM) and at different temperatures (37° and 45°C). **B.** Statistical analysis comparing isolation of actinobacteria in various culture media.

Taxonomic characterization

Micromorphology of the 68 isolates showed spore chains spiral-shaped and long, short or verticillate, as reported by Goodfellow et al. (2012).

The evaluation of micromorphology showed that all strains belonging to the genus *Streptomyces* presented short spiral sporophores, while others showed short chains of straight and slightly curved spores. Despite variations, analysis of LL-DAP confirmed that these isolates belonged to the genus *Streptomyces*.

Molecular characterization of 16S rRNA

The amplification product generated from strain C1.129 was 1649 bp in length. Comparison with 16S rDNA in the GenBank database revealed a 98% similarity to *Streptomyces parvulus* S2-SC26 (accession No. KP339491.1; Figure 2).

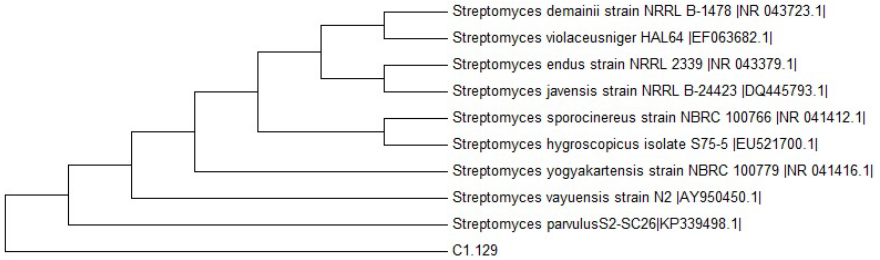

Figure 2. Neighbor-joining tree showing the phylogenetic relationships based on the 16S rRNA gene sequence of the strain C1.129 and the closest species.

Antimicrobial activity

Evaluation of antimicrobial activity revealed that only 16% (11) of the 68 isolates showed antimicrobial activity against some of the microorganisms tested; the remaining 84% (57) showed no antimicrobial activity. Of 36 strains isolated at 37°C, 25% (9) showed inhibition zones greater than 15 mm, while of 32 strains isolated at 45°C, only 9.4% (3) showed similar antimicrobial activity. Strains with antimicrobial activity are presented in Figure 3. The C1.129 strain showed the largest inhibition zones in the primary test for *S. aureus* (UFPEDA-02), *B. subtilis* (UFPEDA-86), and MRSA (UFPEDA-700); following fermentation for 96 h in medium M1, halos of up to 28 mm diameter were observed (Table 1).

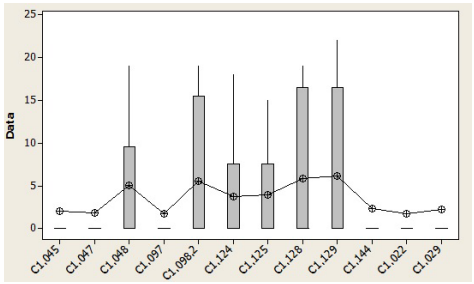

Figure 3. Statistical analysis of relationships between actinobacteria activity against different microorganisms.

Table 1. Inhibition halos (mm) of the antimicrobial activity assay of C1.129 strain over 120 h of fermentation.

Microorganism	M1					MPE					AYM					ISP-4				
	24 h	48 h	72 h	96 h	120 h	24 h	48 h	72 h	96 h	120 h	24 h	48 h	72 h	96 h	120 h	24 h	48 h	72 h	96 h	120 h
S. aureus UFPEDA 02	21.6 ± 0.47	24 ± 0.81	26 ± 0.81	29	25.3 ± 0.47	20	20.6 ± 0.47	22.6 ± 0.47	25 ± 0.81	22.3 ± 0.47	14.66 ± 0.94	13.6 ± 0.47	12.6 ± 0.94	13.3 ± 0.47	11.6 ± 0.94	18.6 ± 0.47	21.3 ± 0.47	20.3 ± 0.47	20.3 ± 0.47	20.3 ± 0.94
S. aureus MRSA UFPEDA 1099	0	22.3 ± 0.47	27.3 ± 0.47	24.6 ± 0.47	24 ± 1.4	0	22.6 ± 1.24	28 ± 0.81	24.6 ± 0.47	26.3 ± 0.94	0	4 ± 5.6	12.6 ± 0.47	6.6 ± 4.7	0	0	28 ± 0.81	28	28.3 ± 0.47	22.3 ± 0.94
B. subtilis UFPEDA 86	24.6 ± 0.47	26.6 ± 0.47	28.6 ± 0.94	29.3 ± 0.47	28.6 ± 1.24	23 ± 0.81	24.6± 0.47	25.6 ± 0.47	26.3 ± 0.47	25 ± 0.81	19 ± 0.81	18.3 ± 0.47	17.6 ± 0.94	17.3 ± 0.47	17.3 ± 0.94	21.6 ± 0.47	24.3 ± 0.47	23.3 ± 0.47	23.6 ± 0.47	23.3 ± 0.47

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Antibiotic extraction and MIC determination

The bioactive metabolite of biomass from fermentation of *S. parvulus* C1.129 (UFPEDA-3408) was extracted using ethanol and showed zones of inhibition above 20 mm for various microorganisms, such as *S. aureus*, *B. subtilis*, and MRSA. The most effective extraction of bioactive compounds from the metabolic liquid was achieved using ethyl acetate, with inhibition zones of up to 28 mm diameter for to the same microorganisms.

Crude ethanolic extract showed a good antimicrobial activity against the Gram-positive bacteria tested, with MIC values equal to or below 3.9 µg/mL. The crude ethyl acetate extract of the liquid metabolic, however, showed MIC values equal to or below 15.62 µg/mL. The crude ethanolic extract of biomass showed the best MIC values (0.97 µg/mL) when tested against MRSA (UFPEDA-700) and *B. subtilis* (UFPEDA-86). The crude ethyl acetate extract of liquid metabolic showed higher MIC values, inhibiting the growth of *S. aureus* (UFPEDA-02) and MRSA (UFPEDA-700) at 3.9 µg/mL (Table 2).

Table 2. Minimum inhibitory concentration of crude extracts of biomass and metabolic net of *Streptomyces parvulus* C1.129 (UFPEDA-3408) compared to that of other microorganisms.

Microorganisms	Crude biomass extract (µg/mL)		Crude extract of liquid metabolic (µg/mL)		Oxacilin (µg/mL)	
	MIC	BMC	MIC	BMC	MIC	BMC
S. aureus UFPEDA 02	3.9	15.62	3.9	15.62	0.156	0.39
S. aureus MRSA UFPEDA 700	0.97	1.95	3.9	31.25	256	512
B. subtilis UFPEDA 86	0.97	31.25	15.62	31.25	0.156	0.156

MIC = minimal inhibitory concentration; BMC = bactericidal minimum concentration.

Bioautography

Chromatography of the crude extract of biomass revealed two fractions with Rfs of 0.37 and 0.68, whereas the crude extract of liquid metabolic revealed three fractions with Rfs of 0.2, 0.37, and 0.58 (Figure 4). These early results indicate that the fraction of biomass with Rf 0.37 is similar to the fraction of metabolic liquid with the same Rf.

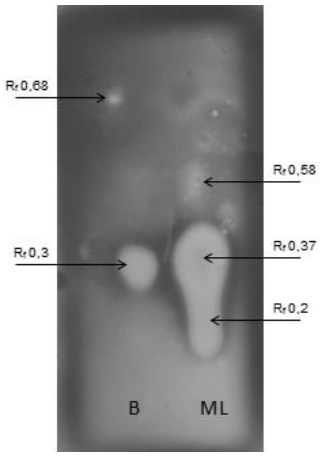

Figure 4. Bioautography of crude extracts of biomass (B) and metabolic liquid (ML) of *Streptomyces parvulus*. Arrows indicate R_fs of bioactive metabolites.

Chemical prospection of crude extracts

Aliquots of each sample were analyzed by TLC to identify the class of secondary metabolites. In the crude extract of the biomass, it was possible to verify the presence of reducing sugars, mono/sesquiterpenes, proanthocyanidin, triterpenes, and steroids. In the crude extract of the metabolic liquid, the presence of mono/sesquiterpenes, proanthocyanidin, triterpenes, and steroids was confirmed. However, the reducing sugars are the only metabolites, which differs the substance of biomass from the metabolic liquid, indicating that the antibiotic substance in such extracts could be the same.

DISCUSSION

Actinobacteria are microorganism that produce numerous secondary metabolites, many of which have already been successfully isolated and some of which have provided important antibiotics with broad medical, veterinary and pharmaceutical applications (Raja and Prabakarana, 2011). Actinobacteria from soil and marine sediments have shown high antimicrobial activity against Gram-positive and -negative bacteria and fungi (Laidi et al., 2008; Zhao et al., 2009).

The predominance of the genus *Streptomyces* in soil is justified by it is being an actinobacterial group that does not have many nutritional requirements. Other genera may be isolated using more complex culture media with different carbon sources or nitrogen or even at different temperatures than those used in this study. As emphasized by Sanchez and Demain (2002), the carbon source may interfere with growth and the yields of bioactive metabolites. The predominance of the genus *Streptomyces* in soil has also been reported by researchers worldwide (Velho-Pereira and Kamat, 2011; Manimaran et al., 2015). These findings are in accordance with those of our study.

We observed a high antimicrobial activity against Gram-positive bacteria, which may be due to the cell wall composition of these bacteria being 90% peptidoglycan, unlike the wall of Gram-negative bacteria, which are much more complex and thus more resistant to antibiotics. Higginbotham and Murphy (2010) evaluated actinobacteria and observed that these exhibited antimicrobial activity against MRSA, with inhibition halos of 22 mm in diameter (Trabulsi and Alterthum, 2008).

The strain C1.129 showed the best activity against *S. aureus* (UFPEDA-02), MRSA (UFPEDA-700) and *B. subtilis* (UFPEDA-86) and was used in the secondary assay. This strain was identified as *S. parvulus* C1.129 and was deposited at the Microorganism Culture Collection of UFPEDA with accession No. UFPEDA-3408.

The isolates that showed no antimicrobial activity on solid medium may still produce antibiotics. The percentage of carbon in the environment and starch concentration are factors that can influence the production of secondary metabolites, and hence it cannot be categorically stated that these isolates do not produce antibiotics. New assays using other culture media and other microorganism tests may detect such antibiotic activity (Matsuura, 2004).

Most antibiotics are produced by genetically distinct species via different pathways, and environmental conditions may therefore have a significant effect on antibiotic production during fermentation. Variable parameters involved in the fermentation process, such as pH, temperature, nutrient composition of the medium, and fermentation time are factors which should be evaluated for characterization of secondary metabolites produced by the strain under study (Pfefferle et al., 2000).

Krishnaveni et al. (2011) have used acetone and chloroform to extract bioactive metabolites from the mycelial mass and the fermented metabolic liquid, respectively, of *Streptomyces noursei*. In accordance with the results of our studies, crude extracts of the *S. noursei* strain exhib-

ited antibacterial activity against Gram-positive bacteria, including resistant clinical isolates. Vimal et al. (2009) evaluated the antimicrobial activity of bioactive metabolites from a marine actinobacteria of genus *Nocardiopsis*.The efficiency of extraction was verified by antimicrobial assays and it was observed that the petroleum ether extract obtained from the isolate showed significant antimicrobial activity against Gram-positive and -negative bacteria; the ethyl acetate extract also showed antifungal activity, and the chloroform extract was observed to be effective against yeast. Thus, ethyl acetate was shown to be an effective solvent for the extraction of bioactive metabolites produced by different actinobacteria, retaining high antimicrobial activity, and studies with such solvents corroborate results of our studies (Arasu et al., 2009; Vimal et al., 2009).

Arasu et al. (2009) evaluated the antimicrobial activity of *Streptomyces* spp ERI-3, isolated from the rocky soil of the forests of the Western Ghats in India. There, as in this study, microorganisms were observed to produce bioactive metabolites, which could be extracted from the supernatant (metabolic liquid) using ethyl acetate. The extract thus obtained inhibited the growth of *B. subtilis* (MIC = 0.25 mg/mL) and *S. aureus* (MIC = 0.5 to 1 mg/mL) considerably more than what was observed in this study. Khieu et al. (2015) purified compounds from *S. parvulus*, and one of them presented an MIC of 62.5 µg/mL for MRSA, lower than the values observed in our study. These studies corroborate our findings, and also report the action of bioactive metabolites of *Streptomyces* against Gram-positive and multidrug-resistant bacteria.

It is noteworthy that bioautography is effective for the detection of antimicrobials present in the extracts, which generally occur as complex mixtures of compounds, albeit in small quantities. However, the technique restricts the identification of the fraction that has antimicrobial activity. The ethyl acetate extract yielded components that had an Rf value of 0.37, which is similar to the Rf value of actinomycin-D (Sousa et al., 2002). Actinomycin-D, produced by *S. parvulus*, is a potent antineoplastic drug molecule and is used to inhibit cell proliferation in tumor cells (Rahman et al., 2010). Moreover, several studies report that most antibacterial compounds produced by the genus *Streptomyces* detected by bioautography method have Rfs similar to those found in our study (Hozzein et al., 2011; Krishnaveni et al., 2011). Purification of these antibiotics may further elucidate whether this antibiotic is a new bioactive metabolite, or has already been described in the literature.

Chemical prospection is generally performed with extracts from medicinal plants to identify compounds with therapeutic potential. Flavonoids, alkaloids, triterpenes, sesquiterpenes, tannins, and lignans have been extensively studied and found to possess these properties. Studies have reported the presence of these and other active compounds in various plants, in both plant and root extracts (Lôbo et al., 2010). Thus, it is important to consider that the rhizosphere has a high concentration of organic nutrients derived from the roots, influencing microorganisms to produce similar compounds (Melo and Azevedo, 2008).

Our results indicated the huge potential of species of *S. parvulus* as a useful and powerful source for the production of bioactive natural compounds owing to the production of metabolites with antimicrobial activity against multidrug-resistant bacteria. The literature has little information about this microorganism, which makes our study pioneering in this matter, since this actinobacteria produces bioactive metabolites with activity against Gram-positive and multi-drug resistant microorganisms.

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