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Culture dependent analysis of bacterial diversity in Canada’s Raspberry Rising Cave revealed antimicrobial properties

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Abstract: Bacteria and archaea thrive in terrestrial subsurface environments because of their unique physiology. Over time, these unique microorganisms may have adapted to possess specialized metabolic pathways that sustain their continued existence in caves, one of the harshest environments on earth. The present study elucidates cultivation based microbial diversity of the cave sediments and wall scrapings collected from seven different locations in Raspberry Rising Cave located in the Columbia Mountain Range, British Columbia, Canada. A total of 103 cultivable bacteria from the cave were isolated on various agar media including R2A, Hickey-Tresner, and DifcoTM Actinomycetes Isolation agar media. Taxonomical phylogenetic analysis of the 16S rRNA gene of the bacterial isolates identified three major phyla: Proteobacteria (Class: Gammaproteobacteria) (51.45%), Actinobacteria (43.68%) and Bacteroidetes (3.88%). Among them, the major genus was Pseudomonas (48.54%) followed by Rhodococcus (39.80%) and Flavobacterium (3.88%). The genus Janthinobacterium and Arthrobacter contributed about 2.91% each, of the total population. Noteworthy, 0.99% were recognized as endophytic Proteobacteria. Furthermore, these bacterial isolates were evaluated for their potential antimicrobial activities against the multidrug resistant bacterial strains. Two bacterial isolates (RRC23, RRC75) showed antimicrobial activities against multi-drug resistant (MDR) Escherichia coli #15-318 while RRC48 exhibited against methicillin resistant (MRSA) Staphylococcus aureus. The isolates RRC36 and RRC38 were identified to show antimicrobial activities against non-pathogenic isolates of Staphylococcus aureus. To the best of our knowledge, this is the first scientific study conducted and provides the insight in occurrence and distribution of the cultivated bacterial diversity from the Raspberry Rising Cave. Moreover, the antimicrobial properties exhibited by some of the bacterial isolates suggested that this cave system could be a resource for potential antibiotics, drugs or novel biologics of clinical relevance.

Keywords: cave microbial diversity, multi-drug resistant organisms, cultivation-based, antimicrobial activities, Raspberry Rising Cave, marble cave

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INTRODUCTION

Microbial communities are able to exist and thrive in a multitude of environments, including those that are harsher habitats such as caves that were previously thought to be completely devoid of life (Coughlan et al., 2015). Challenging characteristics of some cave habitats include the lack of light, low and limited amounts of organic nutrients, higher humidity and higher concentration of minerals that are normally natural DNA blocking agents. These demanding features contribute to distinctive cave environments (Cheeptham et al., 2013; Ghosh et al., 2016), and each cave has unique characteristics. Hence, cave microorganisms must adapt to possess some specialized metabolic pathways to enable them to survive and thrive within them (Ghosh et al., 2016). The broad diversity of microorganisms within caves encompass members among Proteobacteria, Firmicutes and Actinobacteria.
In particular, cave sediments house interesting microbial communities that include species of *Streptomycetes, Arthrobacter, Leifsonia, Rhodococcus, Bacillus, Paenosporosarcina, Paenibacillus, Pseudomonas, Williamsia, Leifsonia, Nocardia, Devosia* (Ghosh et al., 2016; 2017), and interactions due to the unique conditions of the cave environment (Barron et al., 2010). These bacterial communities exist within caves are able to acquire their energy in a number of ways, that comprises breaking down complex aromatic compounds, fixing volatile organics as well as carbon dioxide and nitrogen from the atmosphere, and oxidizing reduced metals within rocks (Barton & Jurado, 2007; Ghosh et al., 2016). Due to the fact that there is limited and chemically complex nutrients within a cave system, very few microbial species are able to uptake and perform catabolic reactions for growth (Barton & Jurado, 2007). Thus, many microbial communities work in a mutualistic cooperative relationship to overcome this nutrient limitation (Barton & Jurado, 2007). The unique cave environment that possesses a myriad of bacterial communities can be utilized for the potential discovery of new antibiotics (Ghosh et al., 2016; Gosse et al., 2019).

The need for discovery of new antibiotics is on the rise, since pathogens continuously becoming resistant to antibiotics, and those currently available either not having specific inhibitory activities or pose concerned side effects (Cheeptham et al., 2013; Ghosh et al., 2016). In terms of the cave microbiome, a number of studies have been explored for its diversity and has exhibited a wide range of antimicrobial properties (Cheeptham, et al., 2013; Ghosh et al., 2017; Gosse et al., 2019). For instance, in a recent study from Iron Curtain Cave, Canada, two bacterial isolates were identified ICC1 and ICC4, that exhibited antagonistic properties against the multidrug resistant *E. coli* strains (Ghos et al., 2017). Further genomic and metabolome analysis revealed that though the isolates are highly homologous with the terrestrial bacteria *Streptomycyes lavendulae* but there were not the same, and possess expanded metabolic potentials (Gosse et al., 2019). These results have extended potential scopes from the caves and more extreme environments to be an effective resource for novel biologics and antibiotics (Ghos et al., 2016).

In this study, we investigated the diversity of cultivated bacteria from seven different locations within the Raspberry Rising Cave, Canada, which has never been reported earlier. The phylogenetic analysis of 16S rRNA gene sequences of the cultivable bacteria were performed and furthermore, antimicrobial properties of these cultivated bacteria against the multidrug resistant bacterial strains were assessed. The Tupper-Raspberry cave system has fairly demonstrated us that it could be a potential source for some crucial microbes, such as phyla belonging to *Actinomycetes, Proteobacteria, Firmicutes, Bacteroidetes*, and novel biomolecules.

### MATERIALS AND METHODS

**Cave description: The Tupper-Raspberry cave system**

In Glacier National Park of Canada, a large sink takes meltwater from the Tupper Glacier. Known as Tupper Sink, water entering it was dye-traced by Ford and others from the Karst Research Group at McMaster University (Ford, 1967). The waters were positively traced to a spring 483 m lower and 1940 m distant. This spring, known as Cascade Cave, or Raspberry Rising, has been known for over a hundred years. This spring had been explored by cavers and open cave passages characterized by a flowing streamway were explored for 70 m to a sump. The sump was first passed by cave diving methods in 1972, where the passage rose from the water and emerged into an air-filled room with the water flow emanating from a high waterfall (Rollins, 2004). This waterfall obstacle remained unpassed until modern explorations began in 2012 (Graham & Stenner, 2019).

The system is obstructed by water at both ends, by the sump 70 m after the entrance and by the sink at the top taking the meltwater from the Tupper Glacier. Exploration of the cave is limited to the winter months, due to dangerous flow rates which prevent diving through the sump and contribute to high water levels within the remainder of the cave. In between the sump and the Tupper Sink, an open, vadose cave system is present. Once past the waterfall, a mixture of open cave passages and large rooms have been explored, in a cave system with multiple levels. Five flooded sumps have been discovered and explored, so far, and the cave system has proven to be remarkable due to the quantity and quality of unique speleothems (Graham & Stenner, 2019). The cave system is confined to a 20-60 m wide marble band sandwiched between calcareous slates and garnet schist identified this system as a classic Type 1 stripe-karst hydrology (Yonge, 2013).

The system has now been explored to 5,495 m in length and a vertical range of 219 m. As of January 2019, it is the longest marble cave system in Canada, the tenth longest and 26th deepest overall cave in Canada and is the second longest cave in all of Canada’s National Parks (Graham & Stenner, 2019).

The system had only been explored to the waterfall immediately after the sump, resulting in 76 m of surveyed cave passage (Rollins, 2004). The remainder of the cave passages, having only been explored since 2012, had been devoid of human contact. The majority of passages, outside of the main route within the cave, were only visited during initial surveying and have not otherwise seen human traffic. This represents a unique opportunity for cave sediments and speleothem sample collections in a cave system while it underwent initial exploration.

The Tupper cave system is designated as an Environmentally-Sensitive Site within Parks Canada Zone 2 Wilderness. Entry into an Environmentally-Sensitive Site requires the highest level of care in order to protect sensitive geological resources and ensure minimal intervention in ecological processes.
Exploration and research in Raspberry Rising were made possible by Parks Canada via “Tupper Cave System (Tupper Sink/Raspberry Rising) Exploration” Research and Collection Permit GLA-2016-23196.

Sample sites and site selection

Sample sites within the cave were chosen for their diversity and consisted of locations within the cave that had distinctly different features from one another. These sites were of varying distances from the entrance, cave sediment types, and speleothem types. Cave sediment samples were collected aseptically from seven different sampling areas from locations in the cave beyond the initial sump 70 m from the entrance (Fig. 1). The average cave sediment temperatures measured was 4.8°C.

Samples 1 and 2

During the exploration of the cave on 9 April 2017, a squeeze between breakdown rocks revealed a small unexplored room connecting two known passages approximately 750 m from the entrance. This room was home to a sloping floor of loose sediment. With this opportunity to collect cave sediments which unequivocally had not been disturbed by humans at this time samples were collected of both top cave sediments and cave sediments from a dig of one-ft depth (Fig. 1) (Supplementary Table 1).

Samples 3 and 4

These samples of cave sediments were located in passage characterized by an active stream flow 123 m from the entrance. The cave sediments were in a sandbar like deposit to the side of the flowing water. This sandbar is expected to have increased water saturation or even could be submerged every summer due to increased flow rates from the meltwater of the Tupper Glacier entering the sink. Top cave sediments and cave sediments from ½ ft deep were separately sampled, deeper cave sediments were unobtainable due to the dig hitting a layer of bedrock (Fig. 1) (Supplementary Table 1).

Sample 5, 6, and 7

Samples 5, 6, and 7 were all co-located in a rift passage, high on a ledge approximately 4 meters above the active stream way and 119 m from the entrance. This area is expected to remain dry during summer floods. On the wall of the ledge a patch of multicolored loose flaky material approximately 50 cm by 30 cm was located. This material was scraped from the wall using sterile instruments and captured as Sample 5. Sample 7 was from the same patch of material on the wall but a specifically loose and powdery section that was all orange colored. Sample 6 consisted of scrapings, in the form of powder, from a vein of orange material on the ceiling close to the wall mat (Fig. 1) (Supplementary Table 1).

Sample collection and bacterial isolation

Approximately 10 g of cave sediment samples (Sample #1-4) and cave wall scrapings (Sample #5-7) (Fig. 2) were placed in sterile 250 mL volumetric flask. The samples were rinsed with sterile deionized water on a shaking incubator at 8°C, 150 rpm overnight. One hundred microliter of the undiluted and decimally diluted (10⁰, 10⁻¹, 10⁻², 10⁻³) cave sediment washings were plated on the three different media plates, namely R2A (Teknova, Hollister, CA, USA), Hickey-Tresner (HT) (Yeast extract 0.1%, Beef extract 0.1%, N-Z Amine 0.2%, Dextrin 1%, pH 7.3) (Cheeptham et al., 2013) (Campbell Company, Toronto, ON, Canada), and Difco™ Actinomycetes Isolation (AI) Agar media (Thermo Fisher Scientific Inc., Waltham, MA, USA). The plates were incubated at 8°C till 7–8 weeks/until the visible colonies were observed. Morphologically distinguishable colonies were selected and re-streaked.
on the same media plates to obtain pure cultures. Each of the pure bacterial isolates were further inoculated in 3 mL volume of the respective broth media (R2A, HT, AI), incubated for a period of 1-2 weeks, followed by bacterial genomic DNA extraction. An aliquot of the grown cultures was stored in 20% (v/v) glycerol at -80°C.

**MOLECULAR TAXONOMY**

**Genomic DNA extraction and sequencing**

Genomic DNA (gDNA) extraction from the bacterial isolates were performed as per previous studies (Hoffman & Winston, 1987; Ghosh et al., 2017). Following the extraction, the gDNA was subjected to
polymerized chain reaction amplification of the 16S rRNA gene as described previously (Ghosh et al., 2017). The 27F (5'-AGAGTTTGATCMTGGCTCAG-3') and 1492R (5'-TACGGYTACCTTGTTCAGACTT-3') primers were used for the amplification reaction. The PCR amplicons obtained were further resolved on an Ethidium bromide –Agarose (0.8%) gel in order to confirm their amplification. The unpurified amplicons were sent to Macrogen, Seoul, South Korea for nucleotide sequencing. The DNA sequences obtained were analyzed using the BLAST algorithm with the available sequences in the GenBank at the National Center for Biotechnology Information (NCBI) [http://www.ncbi.nlm.nih.gov/genebank/index.html](http://www.ncbi.nlm.nih.gov/genebank/index.html) (Altschul, et al., 1997). 16S rRNA gene sequences were identified with the >98% identity and >80% coverage to the closest homologue in the GenBank and DNA Data Bank of Japan and were assigned with gene accession numbers (Supplementary Table 3). The sequences that were not allotted with the GenBank or DDBJ number will be considered for further analysis.

**Molecular Phylogenetic analysis**

The evolutionary history was inferred using the Neighbor-Joining method (Saitou & Nei, 1987). The optimal tree with the sum of branch length = 2.09133087 is shown. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches (Felsenstein, 1985). The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Maximum Composite Likelihood method (Tamura et al., 2004) and are in the units of the number of base substitutions per site. The analysis involved 103 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All positions containing gaps and missing data were eliminated. There was a total of 250 positions in the final dataset. Evolutionary analyses were conducted in MEGA6 (Tamura et al., 2013).

**Antimicrobial activity determination**

The cave bacterial isolates were subjected for antimicrobial activities screening against the multidrug resistant (MDR) and regular non-resistant bacterial strains. The MDR *E. coli* (New Delhi strain) #15-318, *E. coli* #15-102 and methicillin-resistant *Staphylococcus aureus* (MRSA)-43300 while the regular non-resistant strains *E. coli*-33 and *S. aureus* were chosen. All the test strains used were procured from our previous studies (Ghosh et al., 2017; Ghosh et al., 2018). The bacterial strains were inoculated in 3 mL of the nutrient broth (Criterion™Dehydrated CultureMedia, Hardy Diagnostics, CA, USA) and incubated overnight on a shaking test tube rotator overnight at 37°C. The antimicrobial activities assay was conducted employing seeded agar method. All the tested bacterial strains were inoculated at a concentration of 10⁸ cfu/mL in 250 mL molten agar media with a gentle shaking and poured in a Nunc® Bioassay Dish (245 mm x 245 mm x 25 mm) (Cole-Parmer Scientific Experts, Montreal, QC, Canada). Two screening techniques, the plug and the toothpick assays, were adopted to screen the cave bacterial isolates against the tested bacterial strains. The former technique involved aseptically cutting of the agar plugs (0.5 square centimeter) using sterile scalpel from each of the cave bacterial culture plate, while the latter include aseptically picking up of the cave bacterial colony using sterile tooth picks. Both agar plugs and the bacterial isolate were finally placed on to the tested microbe’s-seeded agar plates. The antimicrobial assay plates were prepared in duplicates and incubated at 8°C for a period of 2-3 days. The antimicrobial activities were determined as the zone of inhibition around each bacterial colony. The diameter of the zone of the inhibition was measured manually with electronic Vernier caliper (Guilin, Guangxi, China).

**RESULTS**

**Bacterial diversity**

A total of 103 bacteria, based on their colony characteristics on the specific culture growth media, were isolated from cave sediments and wall scrapping samples of the Raspberry Rising Cave. A set of 34 bacteria each were isolated on isolated on R2A- and HT- agar media while 35 bacteria were cultivated on Al-agar (Table 1).

Genomic DNA extraction were performed from each the cultivated bacterial isolates followed by the 16S rRNA gene amplification. The PCR amplification revealed that the amplicons ranging from 1300-1500 bp. Based on the nucleotide sequencing of each of the rDNA amplicons, the bacterial isolates were categorized into three major phyla of *Proteobacteria*, *Actinobacteria* and *Bacteroidetes*. Further investigations, revealed the genera of *Pseudomonas* (48.54%) exhibited the majority of the population followed by *Rhodococcus* (39.80%) and *Flavobacterium* (3.88%). The genus *Janthinobacterium* and *Arthrobacter* contributed about 2.91% each, of the total population while, 0.99% bacterial population were recognized as endophytic *Proteobacteria* (Fig. 3) (Supplementary Table 2, Supplementary Table 3). Noteworthy, 5.82% of the bacterial population exhibited ≤ 98% when compared to the available 16S rRNA gene sequences and could not be assigned with the Gene Accession numbers neither from the GenBank nor from the DNA Data Bank of Japan (DDBJ) (Supplementary Table 2, Supplementary Table 3).

The *Pseudomonas* and *Rhodococcus* were found to be widely distributed in all the sampling points that includes sampling points 1,2,3,4,5,7 and 2,3,4,5,6,7 respectively while *Flavobacterium* and *Janthinobacterium lividum* were distributed at two and three sampling points respectively. *Paeniglutamicibacter* sp. and *Arthrobacter* sp. were scarcely distributed and only observed at a single sampling point (Fig. 3).

**Phylogenetic analysis**

Dendogram deduced from the 16S rRNA gene sequences of these bacteria revealed that *Proteobacteria*...
Table 1. Sampling locations with their respective characteristics in the Raspberry Rising Cave (RRC). Also, denoting the isolation media used to cultivate the bacterial isolates.

<table>
<thead>
<tr>
<th>Samples</th>
<th>Sampling locations</th>
<th>Location characteristics</th>
<th>Isolation culture media</th>
<th>Bacterial isolates</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Wall of No Return</td>
<td>Cave sediments 1FT depth</td>
<td>R2A</td>
<td>RRC1-RRC5</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>HT</td>
<td>RRC6-RRC7</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Act</td>
<td>RRC8-RRC14</td>
</tr>
<tr>
<td>2</td>
<td>Wall of No Return</td>
<td>Top Cave sediments</td>
<td>R2A</td>
<td>RRC15-RRC20</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>HT</td>
<td>RRC21-RRC25</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Act</td>
<td>RRC26-RRC29</td>
</tr>
<tr>
<td>3</td>
<td>Station 44</td>
<td>Top Cave sediments</td>
<td>R2A</td>
<td>RRC30-RRC34</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>HT</td>
<td>RRC35-RRC39</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Act</td>
<td>RRC40-RRC45</td>
</tr>
<tr>
<td>4</td>
<td>Station 44</td>
<td>Cave sediments 1/2FT depth</td>
<td>R2A</td>
<td>RRC46-RRC49</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>HT</td>
<td>RRC50-RRC54</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Act</td>
<td>RRC55-RRC59</td>
</tr>
<tr>
<td>5</td>
<td>Station 17</td>
<td>Wall Scraping</td>
<td>R2A</td>
<td>RRC60-RRC65</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>HT</td>
<td>RRC66-RRC71</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Act</td>
<td>RR72-RR76</td>
</tr>
<tr>
<td>6</td>
<td>Station 17</td>
<td>Wall Scraping</td>
<td>R2A</td>
<td>RRC77-RRC80</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>HT</td>
<td>RRC81-RRC85</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Act</td>
<td>RRC86-RRC88</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>R2A</td>
<td>RRC89-RRC92</td>
</tr>
<tr>
<td>7</td>
<td>Station 17</td>
<td>Wall Scraping</td>
<td>R2A</td>
<td>RRC93-RRC98</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>HT</td>
<td>RRC99-RRC103</td>
</tr>
</tbody>
</table>

(51.45%), were the major phylum followed by **Actinobacteria** (43.68%) and **Bacteroidetes** (3.88%). Remarkably, only the class **Gammaproteobacteria** was identified as the major class (94.44%) among the **Proteobacteria** population followed by **Betaproteobacteria** (5.55%) (Supplementary Table 3). Furthermore, the five antimicrobial bacterial isolates RRC48 (**Pseudomonas** sp.), RRC23 (**Pseudomonas frederiksbergen**), RRC36 (**Flavobacterium** sp.), RRC38 (**Rhodococcus** sp.) and RRC75 (**Rhodococcus** sp.) were identified under the phylum **Proteobacteria**, **Bacteroidetes** and **Actinobacteria**, respectively (Fig. 4).

**Antimicrobial activities of cave bacteria**

Five bacterial isolates were observed to exhibit antimicrobial activities. RRC23 (close homologue: **Pseudomonas frederiksbergen**, 99.77% identity) and RRC75 (close homologue: **Rhodococcus** sp., 99.85% identity) showed antimicrobial activities against **Escherichia coli** #15-318 while RRC48 (close homologue: **Pseudomonas** sp., 84.58% identity) exhibit against **Staphylococcus aureus** (MRSA). RRC36 (close homologue: **Flavobacterium** sp., 99.70% identity) and RRC38 (close homologue: **Rhodococcus** sp., 100% identity) showed antimicrobial activities against the non-pathogenic **Staphylococcus aureus** strain (Table 2). Intriguingly, RRC48 showed a low identity (84.58%) and query coverage (68%) to its close homologue **Pseudomonas** sp. and therefore was not deposited to the Genbank or DDBJ.

All these bacteria that exhibited antimicrobial activities were isolated from sample location 2 (RRC23), sample location 3 (RRC36 and RRC38), sample location 4 (RRC48) and sample location 7 (RRC75). Notably, all these sampling sites, besides sample location 2 at the Station 108, were from Station 17 and Station 44, adjacent to the cave entrance (Fig. 1) (Table 1).

**DISCUSSION**

Raspberry Rising Cave is karstic cave, located in the Glacier National Park’s Tupper mountain system in British Columbia, Canada. Seven locations in the cave were identified from where cave sediments/wall scrapings were sampled. The samples were processed and a cultivation-/PCR-based study were carried out for the first time to elucidate the bacterial diversity of this cave that revealed 103 bacterial isolates. Notably, the samples were incubated at 8°C, although, the temperature of the cave was measured as 4.8°C. A higher incubation temperature was employed as cave bacteria can exhibit confluent growth at temperatures in the range of 5-45°C (Laiz Trobajo et al., 2003).

The cave typically showed the presence of yellow mat/microbial communities (Fig. 2), commonly observed both in karstic and lava caves (Porca et al., 2012; Velikonja et al., 2014; Riquelme et al., 2015). Our study, though preliminary, has identified different bacterial strains with **Proteobacteria** as the major phylum followed by **Actinobacteria** and **Bacteroidetes**. These findings were in consistent to a few previous cultivation-based studies on bacterial phylogenetic diversity of the karstic caves where **Proteobacteria** was recognized as a predominant bacterial population (Barton et al., 2004; Lu et al.,...
2018; Yasir, 2018). Proteobacteria phylum was dominated by the class Gammaproteobacteria with Pseudomonas sp. observed as the major genera in accordance to previous studies (Barton et al., 2004; Banerjee & Joshi, 2016; Yasir, 2018). Proteobacterial population seldom observed to be the dominant class in most of the cave bacterial diversity studies with the majority of the bacterial population has been shown as Actinobacteria (Axenov-Gribanov et al., 2016; Ghosh et al., 2016, 2017; Lavoie et al., 2017). However, a few studies have reported Proteobacteria as the most abundant phylum (Sauro et al., 2018; Yasir, 2018; Barron et al., 2010). Our study has revealed 94.44% of the proteobacterial community was represented by the class Gammaproteobacteria. These findings were consistent with the previous cultivation-based studies where class Gammaproteobacteria were shown to constitute the major bacterial population (Banerjee & Joshi, 2016; Yasir, 2018). For instance, bacterial diversity study on the Meghalayan caves in North-East India, exposed thirty-two different cultivable bacterial species belonging to sixteen different genera where majority belongs to Pseudomonas and Bacillus (Banerjee & Joshi, 2016). Furthermore, we have reported Betaproteobacteria as the less abundant class representing Janthinobacterium sp. (2.91% of the total population) as the only genus (Fig. 4). These observations were in line with previous studies where paired end Illumina was conducted on the bacterial diversity using the V3 region of the 16S DNA from five unknown and unexplored caves of Mizoram, the Northeast India, showing Alpha- and Gammaproteobacteria, the dominant phylotypes while Betaproteobacteria constitute the minor population (De Mandal et al., 2017). Likewise, another study conducted on the microbial diversity and functionality on silica mobility in orthoquartzite caves also reported Janthinobacterium as the less abundant genus among the betaproteobacterial population (Sauro et al., 2018). Our study has reflected a previous literature that has shown Rhodococcus to be the abundant genera among the Actinobacteria (De Mandal et al., 2015), although, in most of the cases Rhodococcus is a rare Actinobacteria (Groth et al., 1999, Adam et al., 2018). Phylum Bacteroidetes with the genus Flavobacterium has been identified as the minor population in our study as stated in the previous findings (Rusznyak et al., 2012; Carmichael et al., 2013).

Five bacterial isolates (RRC23, RRC36, RRC38, RRC48, RRC75) exhibited antagonistic activities against the multidrug resistant strains of E. coli and Staphylococcus aureus revealed in our study. Most of
Fig. 4. Maximum Likelihood tree showing the phylogenetic position of the Raspberry Rising Cave bacterial isolates. The 16S ribosomal operons were obtained from the NCBI database, aligned by MUSCLE with default parameters and the phylogenetic dendrogram was constructed using MEGA6 by neighbor-joining method. Bootstrap confidence levels of 1000 re-samplings were indicated at the nodes. The alphanumeric characters in the parenthesis specifies the gene accession numbers. The isolates marked with a single asterisk indicate lower homology towards their closest relatives (accession numbers were not assigned) while the double asterisks exhibit the isolates with antimicrobial properties. RRC is the abbreviation used for Raspberry Rising Cave.
these isolates belonged to the phylum *Actinobacteria* and *Proteobacteria*. RRC38 and RRC75 were both identified as the closest homologues to *Actinobacteria* (Genus: *Rhodococcus* sp.) while RRC 23 and RRC 48 as Gammaproteobacteria (Genus: *Pseudomonas*). Earlier studies have shown that *Actinobacteria* to be a promising resource for the bioactive compounds (Ghosh et al., 2016, 2017; Rangseekaew & Pathom-Aree, 2019). The genera *Streptomyces* predominantly exhibited antagonistic effect against bacteria and fungi (Ghosh et al., 2017, Rangseekaew & Pathom-Aree, 2019). For instance, a study on an Italian cave, Grotta dei Cervi, have shown bioactive compounds Cervimycin A, B, C, and D, extracted from *Streptomyces tendae* strain HKI 0179, exhibited antagonistic effect against Gram-positive bacteria (*B. subtilis* and *S. aureus*) as well as multidrug resistant *S. aureus* (MRSA), vancomycin-resistant *Enterococcus faecalis* (VRE) and efflux-resistant *S. aureus* EIS4 (Herold et al., 2005). However, the genera *Rhodococcus* were not reported expansively from the cave habitat to possess antimicrobial activities. An earlier study has demonstrated isolation of *Rhodococcus* sp. from the limestone deposit sites in Hundung, Manipur, India, that only showed biocontrol activity against the rice fungal pathogen (Nimaichand et al., 2015). *Pseudomonas* sp. was rarely identified to exhibit antimicrobial activities from the cave environment. For instance, a previous study has reported *Pseudomonas fluorescens*, isolated from the Magura Cave, Bulgaria, has exhibited antimicrobial effect against *P. aeruginosa* and *Rhodotorula mucilaginosa* displaying 20 mm and 16 mm as the zone of inhibition respectively (Tomova et al., 2013; Ghosh et al., 2016). Our study has identified RRC 36 (close homologue: *Flavobacterium* sp.) to exhibit antibacterial activities against *S. aureus*. There is no study accounted until date for the antibacterial activities of *Flavobacterium* from the cave environment. However, a cultivation-based study from the Antarctic environments has reported anticyanobacterial activities of *Flavobacterium against Mycobacterium smegmatis* and *M. tuberculosis* (Mojib, et al., 2010). Notably, it has also been observed that all the five isolates exhibited antimicrobial activities were retrieved from all the three stations of the cave (17, 44, and 108) implying that the antimicrobial properties were relatively wide spread in terms of sampling areas and characteristics of the cave sediments within the cave. In addition, the antimicrobial activities were observed at 8°C. However, a previous study has shown Antarctic bacteria produce antimicrobials at low temperature during their growth cycle for their competitive survival (O’Brien et al., 2004).

Taken together, our study has expanded a new understanding to the Canada’s underground. To the best of our knowledge, this is the first attempt that intend to provide the in situ cultured bacterial diversity and antimicrobial activities from the Raspberry Rising Cave. Moreover, the antimicrobial activities exhibited by lesser studied genera such as *Rhodococcus, Pseudomonas* and *Flavobacterium* rather than the commonly studied *Streptomyces* has further opened new frontiers in antimicrobial research studies. Further investigations should emphasize to reveal the whole genome sequences, functional genomics, biochemical assays, fermentation structure elucidation, active component extraction and mode of action of these bacterial isolates in order to understand the underpinning mechanisms of their antimicrobial activities. However, our study gave a smaller snapshot of this cave habitat. Therefore, future study should focus on the metagenomic approaches to have holistic taxonomical and functional profiles of Raspberry Rising Cave microbiomes, in a way to bio-prospect antimicrobial genes/molecules of biotechnological and pharmaceutical relevance and further to elucidate the molecular mechanisms related to microbe-mineral interactions in cave.

**ACKNOWLEDGEMENTS**

Charlene Barker for assisting with sample collections and Kathleen Graham for coordinating exploration of the cave and permit with Parks Canada. Parks Canada for allowing the exploration and research in Raspberry Rising via “Tupper Cave System (Tupper Sink/Raspberry Rising) Exploration” Research and Collection Permit GLA-2016-23196. Comments from two anonymous reviews improved the content of this paper.

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**Table 2. Antimicrobial activity screening of the RRC isolates against the MDR and normal bacterial strains. ‘+’ and ‘-’ denotes ‘antimicrobial’ activities and ‘no antimicrobial’ activities respectively.**

<table>
<thead>
<tr>
<th>Bacterial isolates</th>
<th>Growth media</th>
<th>Location description/sample type</th>
<th>Test microorganisms</th>
</tr>
</thead>
<tbody>
<tr>
<td>RRC23</td>
<td>HT</td>
<td>Station 108/Wall of no return/cave sediments</td>
<td>E. coli #15-102</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>E. coli #15-318</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>S. aureus MRSA-43300</td>
</tr>
<tr>
<td>RRC36</td>
<td>HT</td>
<td>Station 44/ Sandbar in streamway below S. 17/ cave sediments</td>
<td>-</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>-</td>
</tr>
<tr>
<td>RRC38</td>
<td>HT</td>
<td>Station 44/ Sandbar in stream way below S. 17/ cave sediments</td>
<td>-</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>-</td>
</tr>
<tr>
<td>RRC48</td>
<td>R2A</td>
<td>Station 44/ Sandbar in stream way below S. 17/ cave sediments</td>
<td>-</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>+</td>
</tr>
<tr>
<td>RRC75</td>
<td>Actinomyces media</td>
<td>Station 17/ Up climb into low chamber above S.17 stream/wall scrapings</td>
<td>-</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>+</td>
</tr>
</tbody>
</table>

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REFERENCES


