Streptomyces specialized metabolites for agricultural applications

by ©Jody-Ann Clarke

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ABSTRACT

Streptomyces biosynthesize a wide variety of specialized metabolites, including volatile organic compounds (VOCs). *Streptomyces* VOCs are diverse and used in different capacities, including competition for resources and intra- and inter-species communication. And so, VOCs may be exploited in farming as inhibitors to plant pests and pathogens. The demand for safer alternatives to synthetic chemicals in agricultural practices makes these naturally occurring compounds ideal for applications. In this study, 133 *Streptomyces* isolates obtained from different locations in St. John's, Newfoundland, were phylogenetically typed using the *rpoB* housekeeping gene, and different strains were selected for fermentation and pooled culture VOC screening. Six of the phylogenetically different isolates (JAC25, JAC45, JAC60, JAC74C, JAC81, and JAC95) were subjected to replicate VOC analysis and phytotoxic effects on plants. These isolates were shortlisted based upon the number and types of VOC they produced, i.e., various VOCs with published bioactivities, including insect repellency making them good targets for pest management in crop farming. Ninety-five bacterially derived compounds were identified among the six isolates in the replicate VOC analysis. One isolate (JAC60) significantly inhibited the development of plant seedlings suggesting its capacity to make a possible natural herbicidal compound.

GENERAL SUMMARY

Streptomyces bacteria use VOCs in nature for intra- and inter-species communication. Sometimes these VOCs may be found in beneficial symbiotic relationships with plants where plant predators are warded off. Therefore, these compounds may be exploited for agricultural applications, wherein *Streptomyces* VOCs may effectively improve plant growth, productivity, and disease resistance. This thesis looked at the genetic relatedness of a collection of soil *Streptomyces* obtained in St. John's, Newfoundland. Genetically different *Streptomyces* were selected for VOC analysis to identify compounds that could be potential pest management agents. The results showed that VOCs are diverse among the *Streptomyces* isolates and that *Streptomyces* may not always be plant-friendly. Future experiments, including insect repellency testing, are encouraged before using *Streptomyces* and derived products directly on plants.

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List of Abbreviations and Symbols

The following abbreviations and acronyms are used throughout this thesis. Acronyms common throughout the life sciences are not included in this list.

Abbreviation	**Meaning**
µM	Micro-meter
BGC	Biosynthetic gene cluster
BLAST	Basic local alignment search tool
Bp	Base pairs
CO_2	Carbon dioxide
CPS	Counts per second
dH_2O	Distilled water
DMSO	Dimethyl sulfoxide
DNA	Deoxyribonucleic acid
GC-MS	Gas chromatography-mass spectrometry
HCl	Hydrochloric acid
KCl	Potassium chloride
KH_2PO_4	Potassium phosphate monobasic
MHA	Muller Hinton agar
Min	Minute
MLSA	Multi-locus sequence analysis
MLST	Multi-locus sequencing type
mm	Millimeter
Na_2HPO_4	Sodium phosphate dibasic
NaCl	Sodium chloride
NIST	National Institute of Standards and Technology
nm	Nanometer
nM	Nano-molar
nt	nucleotide
OTU	Operational taxonomic unit
PBS	Phosphate buffer saline
PCR	Polymerase chain reaction
RI	Kovats retention index
Rpm	Rotation per minute
rpoB	RNA polymerase beta subunit
rRNA	Ribosomal RNA
RT	Retention time
SFM	soy flour mannitol
sec	second
ST	sequence type
VOC	volatile organic compound
WGSA	Whole-genome sequence analysis
YMS	yeast extract-malt extract-starch
YPD	yeast extract-peptone-dextrose
ZOI	Zone of inhibition

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Chapter 1: Introduction

1.1: The genus *Streptomyces*

Streptomyces is the largest genus of Actinobacteria and of the family Streptomycetaceae. The genus comprises sporulating Gram-positive bacteria with filamentous shape and high GC-content in their genomes (Dworkin, 2006). They are ubiquitous soil dwellers occupying various habitats, including the rhizosphere and sometimes as symbionts of plants and animals. *Streptomyces* species life cycles include forming vegetative mycelia under favorable conditions, i.e., when nutrients and water are available. When nutrients become limited, aerial hyphae develop from vegetative mycelia and mature into spores (Chater, 2006). *Streptomyces* spores can remain dormant for long periods and germinate when conditions become favorable once again, and then the cycle repeats. Notably, specialized metabolite production, including antibiotics, occurs in a growth-phase-dependent manner (Demain & Fang, 1995). Specialized metabolic products are not essential for the survival and growth of the producing organism under laboratory conditions; but instead, they enhance the ability of the producer to thrive in its natural habitat (Katz & Baltz, 2016). These molecules offer a selective advantage to compete with other microorganisms for space and nutrients. Specialized metabolite production is theorized to coincide with or slightly precede the development of aerial hyphae in surface-grown cultures. In liquid-grown cultures, it generally occurs in the stationary phase (Bibb, 2005). This event is frequently assumed to result from nutrient limitation, and specialized metabolite biosynthesis during this phase of the life cycle is speculated to be a mechanism by which *Streptomyces* ward off competitors by keeping nutrients and other resources away

from the species (Chater, 2006). Many of these specialized metabolites can be isolated and used to inhibit susceptible species outside of the natural context in which they are used.

Streptomyces are recognized as industrially-relevant because they produce an array of beneficial natural products with uses in medicine and agriculture. Specialized metabolites produced by *Streptomyces* are used in clinical settings and far exceed the use of chemically synthesized ones (Heul et al., 2018). Widely used molecules derived from *Streptomyces* include antifungal, anti-cancer, immunosuppressant, antibacterial, and anthelminthic agents (Barka et al., 2015). Genome mining techniques have revealed that even a single *Streptomyces* species, selected at random, contains an impressive number of biosynthetic gene clusters (BGCs) responsible for producing diverse specialized metabolites (Baltz, 2017; Blin et al., 2019). This diversity of BGCs in *Streptomyces* makes this group of bacteria ideal for the exploitation of novel compounds. When determining *Streptomyces* isolates for specialized metabolite analysis, molecular identification is a valuable tool discussed subsequently.

1.2: Bacterial gene sequences for molecular identification

Several methods have been used to identify bacteria based on phenotypic properties, such as staining, biochemical testing, and molecular methods that employ DNA sequencing. Of the two, modern techniques often use DNA sequencing, as it provides higher resolution and reduces ambiguities often associated with phenotypic tests (Tang et al., 1998). However, even though DNA sequencing is accepted as the gold standard, it has its problems. There is no consensus when selecting DNA sequences to identify bacteria, but some gene sequences are used more often than others. Sequence-based analysis is

usually done with several criteria in mind. First, when selecting genes for identification, one should consider targets that may serve as molecular clocks for phylogeny (Reller et al., 2007). Second, selected genes should have variable and hypervariable regions flanked by conserved segments common to all bacteria. Conserved regions are necessary for universal primers to bind during PCR amplification and sequencing the selected DNA sequence. The variable and hypervariable regions contain nucleotide sequences for species identification (Reller et al., 2007). PCR amplified and sequenced DNA is then compared to reference sequences available in public and proprietary databases to determine relatedness. Relatedness is expressed as a percent identity between two sequences. Depending on the DNA sequence, a specified difference in percent identity is acceptable before classifying a new species (Reller et al., 2007). With these things in mind, one or more gene sequences are selected that will best classify unknown bacterial species into taxonomic groups depending on the desired level of species discrimination required. Methods of DNA identification include using the 16S rRNA gene, protein-coding genes, multilocus, and whole-genome sequencing, which are briefly discussed.

1.2.1: The 16S rRNA gene

The gene most often sequenced for bacterial identification encodes the 16S rRNA (16S rDNA), approximately 1500 bp in size (Johnson et al., 2019). It has been extensively used and has readily available reference databases for comparison, so it is helpful to include it in species identification. Although widely used in the molecular identification of bacteria, there is no consensus regarding which regions of the 16S rDNA are appropriate for species-level resolution (Pollock et al., 2018). The gene consists of regions with different degrees

of conservation and variation, where more conserved sequences have served to create universal 16S rDNA primers for PCR (Table 1.2.1.1). There are nine hypervariable regions (Figure 1.2.1.1), based on the *Escherichia coli* numbering system, which have been identified to be helpful in species identification (Baker et al., 2003). Within the genus *Streptomyces*, the highly variable gamma and alpha regions are thought to be better targets to differentiate between species (Kataoka et al., 1997; Mehling et al., 1995; Song et al., 2004). Select hypervariable regions in the 16S rDNA are typically PCR amplified, sequenced, and compared to reference sequences made available through accessible databases. These include the National Center for Biotechnology Information (NCBI) nucleotide database (Agarwala et al., 2018), which comprises DNA and RNA sequences, and the SILVA rRNA database project (Quast et al., 2013), which has curated ribosomal RNA data including that for 16S rDNA.

Different species of bacteria may contain varying copy numbers of 16S rDNA. When multiple copies of 16S rDNA are present, they may exist as variants accounting for differences in sequences within the same species (Case et al., 2007). Because of these sequence differences within copy variants, species classification using the 16S rDNA sometimes poses interpretation problems and limits the resolution achievable for different species. In addition, the 16S ribosomal subunits are present in all prokaryotes, including the domain archaea, as the subunits are responsible for the conserved function of protein translation, which makes the gene sequence relatively conserved at the genus level, which can obscure inter- and intra-species identification (Fox et al., 1992). Other challenges associated with using 16S rDNA include the lack of a standard where different

Table 1.2.1.1: Bacteria specific 16S universal PCR primers.

Name	Sequence 5'–3'	Length (nt)	Reference
8F/ 27F	AGAGTTTGATCCTGGCTCAG	20	(Reysenbach et al., 1994; Shi et al., 2019)
9F	GAGTTTGATCCTGGCTCAG	19	(Farrelly et al., 1995; Hansen et al., 1998; Inerney et al., 1995)
63F	CAGGCCTAACACATGCAAGTC	21	(Marchesi et al., 1998)
341F	CCTACGGGAGGCAGCAG	17	(Teske et al., 1996)
515F	GTGCCAGCAGCCGCGGTAA	19	(Hansen et al., 1998)
516F	TGCCAGCAGCCGCGGTA	17	(Nagashima et al., 2003; Reysenbach et al., 1994)
806R	GGACTACHVGGGTWTCTAAT	20	(Apprill et al., 2015; Caporaso et al., 2011)
907R	CCCCGTCAATTCCTTTGAGTTT	22	(Teske et al., 1996)
1408R	TGACGGGCGGTGTGTACAAGGC	22	(Hansen et al., 1998; Marchesi et al., 1998)
1492R	ACGGCTACCTTGTTACGACT	20	(Reysenbach et al., 1994; Shi et al., 2019)

Figure 1.2.1.1: Relative location of the 16S rDNA variable regions denoted **V1- V9**. Variable regions are illustrated based on their relative size to each other. The figure was adapted from information made available by Baker et al. (2003).

hypervariable regions, whether alone or in combination, are used to identify a single species or to categorize unidentified bacteria into operational taxonomic units (OTUs). In the case of OTUs, a cut-off percent for sequence identity is used to cluster bacteria with the assumption that they are the same species. However, grouping different species into OTUs increases the potential for false decreased diversity due to the high percent identity of the 16S rDNA sequences among closely related species. Therefore, closely related species with similar 16S rDNA sequences, even within the variable regions, can be mistakenly labelled as the same species when one is trying to identify below the genus level. For instance, the "*Bacillus cereus* group" of bacteria, including *Bacillus cereus, Bacillus thuringiensis,* and *Bacillus anthracis,* cannot be adequately differentiated using their 16S rRNA gene sequences and are distinguished by the plasmids that they carry (Rasko et al., 2005). Likewise, bacterial strains may be more difficult to distinguish based on the 16S rDNA alone. For example, ten *Streptomyces* strains with 16S rDNA identical to the type strain of *Streptomyces cyaneofuscatus* were distinguished into five strains when other analyses including phenotypic, microscopic, and genetic comparisons were used (Antony-Babu et al., 2017). Such analyses suggest that higher resolution of the *Streptomyces* strains is sometimes required; and that 16S rDNA sequence comparison alone will not suffice while studying members of this and other genera.

1.2.2: Protein-coding gene targets

There does not appear to be a universal gene sequence in the literature with sufficient discriminatory power for identifying bacteria below the genus level. The domain bacteria consist of many species with genomes evolving at different rates. Therefore, DNA sequences that provide the best solution for a specific molecular identification need must be selected. Ideally, such targets should include universally conserved and ubiquitous genes for the molecular identification of bacteria across taxa. Protein-coding genes have been chosen recently for such analysis, yet there is no consensus on which ones to use. One study analyzed 143 single-copy genes present in more than 95% of 132 taxonomically diverse bacterial genomes, 39 of which had two conserved regions, for primer design, separated by at least 900 nt (Santos & Ochman, 2004). Ten of these universally conserved bacterial genes are listed in Table 1.2.2.1, among other common protein-coding genes used for the taxonomical analysis of bacteria. Other studies apply a similar approach for identifying phylogenetic markers to divide bacteria into subgroups (Gil et al., 2004; Wu et al., 2013; Zeigler, 2003). A recent study identified 92 bacterial single-copy genes present in more than 95% of the complete genome sequences from 1,429 organisms belonging to 28 phyla (Na et al., 2018). Further analysis of these 92 genes revealed that the majority (n = 67) encodes proteins with roles in cellular processes, including translation, ribosomal structure, and biogenesis.

Many protein-coding genes exist as a single copy, making them easier to work with than the multi-copy and multi-variant 16S rDNA. They can also evolve faster than rDNA genes because of substitutions at the third position of codons that do not change the amino acid sequence of the encoded protein (Han et al., 2012). And because of the faster rate of

Table 1.2.2.1: Some common bacterial protein-coding genes used in species delineation.

Gene	Gene product	Reference
fusA	elongation factor G	(Holmes et al., 2004; Santos & Ochman, 2004)
gyrB	DNA gyrase β subunit	(Han et al., 2012; Holmes et al., 2004; Santos & Ochman, 2004)
ileS	Isoleucine-tRNA ligase	(Santos & Ochman, 2004)
lepA	elongation factor 4	(Qin et al., 2006; Santos & Ochman, 2004)
leuS	leucine tRNA synthetase	(Ribeiro et al., 2015; Santos & Ochman, 2004)
pyrG	cytidine triphosphate synthetase	(Santos & Ochman, 2004)
recA	recombinase A	(Han et al., 2012; Holmes et al., 2004; Santos & Ochman, 2004; Thompson et al., 2005)
recG	ATP-dependent DNA helicase	(Santos & Ochman, 2004)
rplB	ribosomal protein L2	(Mekadim et al., 2018; Santos & Ochman, 2004)
rpoB	RNA polymerase β subunit	(Devulder et al., 2005; Holmes et al., 2004; B. J. Kim et al., 2004; Santos & Ochman, 2004)
atpD	ATP synthase β subunit	(Han et al., 2012)
cpn60	chaperonin 60	(Miñana-Galbis et al., 2009)
hsp65	heat-shock protein 65	(Devulder et al., 2005)
pyrH	Uridylate kinase	(Thompson et al., 2005)
rpoA	RNA polymerase alpha subunit	(Thompson et al., 2005)
trpB	tryptophan synthase β subunit	(Han et al., 2012)
sod	metalloenzyme superoxide dismutase	(Devulder et al., 2005)

evolution, protein-coding genes tend to have less conserved regions when compared across taxonomic groups. Consequently, universal primers for such genes might not be readily available for gene amplification and sequencing for subsequent species identification. Therefore, when a higher level of discrimination is required, details regarding the family and genus of bacteria being analyzed need to be considered for target selection. Due to differential evolution rates, some protein-coding genes are good candidates for intra- and inter-species delineation at taxonomic levels where the 16S rDNA is not sufficiently discriminatory. For example, the *cpn60* gene (also known as *hsp60* or *groEL*) is found in both bacteria and eukaryotes and displays more variability in sequences of inter- and intra-species compared to 16S rDNA, even though they display similar phylogenetic tree topologies (Links et al., 2012). The *Bacillus subtilis* group comprises eight closely related species and strains indistinguishable by 16S rDNA sequence (98.1–99.8 % identity), but they can be distinguished using the *gyrB* gene (75.4–95.0% identity) (Wang et al., 2007). In another example, *Mycobacterium gastri* and *Mycobacterium kansasii,* indistinguishable based on 16S rDNA sequence (Rogall et al., 1990), were successfully typed with 96.2% identity using the *recA* gene (Blackwood et al., 2000). For even greater species and phylogenetic resolution, more than one protein-coding gene sequences can be used (Guo et al., 2008), where the different sequences from the same organism are concatenated, creating sequences that result in more robust phylogenetic trees.

Of the more widely used protein-coding genes used for bacterial identification, the *rpoB* provides better delineation when compared to the 16S rDNA (Khamis et al., 2005; Kim et al., 2004; Vos et al., 2012). The percent cut-off used for *rpoB* gene sequence-based

delineation depends on the portion of the *rpoB* gene used, and for accurate annotation, a hypervariable region (between 2300 and 3300 nt) is recommended for analysis (Adékambi et al., 2009). In such cases, a 300–600 bp fragment of this region requires 94–95% identity, and a 600– 825 bp fragment requires 96–97% identity to be considered the same species (Adékambi et al., 2009). However, when classifying a new bacterial species, it is proposed to sequence the entire *rpoB* gene and use a cut-off of 97.7% identity (Adékambi et al., 2009) and classify a new species strain, using a delineation cut-off of 98.2% identity (Adekambi et al., 2008). The *rpoB* gene was selected along with the 16S rDNA in this study to identify *Streptomyces* isolates.

1.2.3: Multi-locus sequence typing and analysis

For intra-specific level classification, delineation methods include multilocus sequence typing (MLST), which uses allelic mismatches from a small number (usually seven) of housekeeping genes (Enright & Spratt, 1999; Maiden et al., 1998), typically protein-coding like those discussed above (Table 1.2.2.1). PCR amplified DNA from gene sequenced alleles are then assigned arbitrary numbers or codes with a new or unique allelic sequence getting a different number. For each isolate, the combination of assigned codes from each locus defines its sequence type (ST), where isolates with identical sequences are classified as the same ST. Online MLST reference databases for diverse organisms are available, e.g., PubMLST.org (Jolley et al., 2018), which can be used for comparison. Sometimes, more than seven loci are used in the analysis, which might not be necessary, as shown in a study that used six and eleven loci in 107 *Neisseria meningitidis*is isolates to obtain similar levels of discrimination (Maiden et al., 1998). However, MLST is limited in

application to within species and does not work for mixed samples of bacteria from different genera, which would result in allelic mismatches that create false STs (Gevers et al., 2005).

In comparison, multilocus sequencing analysis (MLSA) can use a set of genes present in different species within a genus or genera within a family (Glaeser & Kämpfer, 2015). Unlike MLST, which uses allele profiles to differentiate isolates within a species, MLSA allows for the examination of mixed genera. Gene sequences are generally concatenated, and a phylogenetic tree is prepared to measure relatedness among bacterial isolates. Bacterial MLSA uses 400-500 bp partial sequences of housekeeping genes (Jolley & Maiden, 2014), and as few as three genes (*rpoA*, *recA*, and *pyrH*) have been demonstrated to build more robust phylogenetic trees instead of any one of the single genes in the case of *Vibrio* isolates (Thompson et al., 2005). In a separate report, the sequences of four genes (16S rDNA, *hsp65*, *rpoB*, and *sod*) from 81 *Mycobacterium* isolates provided good results, except that six members of the *M. tuberculosis* group were not resolved using this method (Devulder et al., 2005). In a study of *Streptomyces* with identical 16S rDNA sequences, further delineation was possible using five protein-coding genes, *atpD, gyrB, recA, rpoB,* and *trpD* (Antony-Babu et al., 2017). As many as 93 (Chevrette, Carlson, et al., 2019) and 155 (Alam et al., 2010) genes from genome sequences have been used in MLSA to resolve *Streptomyces* and other closely related species. When using large numbers of genes for multilocus phylogeny, sequencing the genomes is less time-consuming than PCR amplifying and sequencing each gene individually and dramatically streamlines the process.

1.2.4: Whole-genome sequencing

All of the methods described above only examine a small portion of the bacterial genome and miss genetic variations caused by horizontal gene transfer, including the gain and loss of BGCs. It is not uncommon for bacteria to undergo mutation as a means to counter antibiotic susceptibility or for them to pick up resistance genes from the environment (Munita & Arias, 2016). These events pose challenges while examining pathogenic microbes in a clinical setting. For example, multidrug resistance *Klebsiella pneumoniae* isolates classified as a single lineage (ST258) based on MLST, partitioned into two distinct clades following whole-genome sequencing (DeLeo et al., 2014). Analysis of the two ST258 isolates revealed inconsistencies in the number and types of resistant genes present in each strain, indicating the importance of using higher resolution techniques for characterizing pathogenic microbes under clinical settings. These kinds of dilemmas usher in the sequencing of whole genomes to enable the correct sorting of bacterial isolates. It is also important to follow the acquisition of genetic material such as complete BGCs in *Streptomyces*, which are important events that can lead to the production of beneficial specialized metabolites in the new host. Whole-genome sequencing allows for further examination of species with identical single genes sequences or close MLSA percent identity. Information in whole genomes includes the core genome, composing genes common to all studied strains; the dispensable genome, which is shared by a subset of the strains and provides information on diversity and environmental adaptations; and the strain-specific genes that offer insights at below species level (Tian et al., 2016; Vernikos et al., 2015). For example, a comparison of a *Streptomyces* isolate and a reference species

genomes showed 100% identity of their 16S rDNA and 99.92% identity using MLSA, but genome analysis between the two revealed that one of them contained 11 unique genes and is missing 98 genes present in the other (Heinsch et al., 2019). Here, we see that a single gene or a multigene approach misses the variability that a whole-genome method provides.

The increasing affordability of whole-genome sequencing and the availability of bioinformatics tools make it easier to conduct molecular sequencing analyses. Useful for genome studies, the WGSA database (www.wgsa.net) allows the characterization of species genomes, multilocus STs, resistance profiles, and phylogenetic placement among the existing species based on core genes (Balloux et al., 2018). At the time of writing, the WGSA database comprises 43,767 genomes. The Genomes OnLine Database (GOLD) (Mukherjee et al., 2021) has information on 374,599 organisms, with Actinobacteria genome projects accounting for 8.7% of those. The NCBI genome database (Agarwala et al., 2018), which comprises 249,357 prokaryotes genomes, may also be used. The *Streptomyces* specific database, StrepDB (http://strepdb.streptomyces.org.uk/), provides annotated reference genomes of *Streptomyces*. As of July 2021, there were 671 annotated *Streptomyces* species in the List of Prokaryotic Names with Standing in Nomenclature (LPSN) database (Parte et al., 2020), which provides comprehensive information on the nomenclature of prokaryotes.

As it is now recognized that the 16S rDNA alone is insufficient to identify some bacteria to the species level, other genes can be helpful when used in combination with it. However, it is recommended to include the 16S rDNA because it has been extensively used for a longer time and has readily available reference databases for comparison. It is helpful

to use it in complementation with at least one protein-coding gene. In the current study, *rpoB* along with 16S rDNA was used for the molecular identification of select *Streptomyces* isolates. Further testing, including morphology and metabolomics, encourages a more accurate resolution of unknown or unnamed species. Furthermore, it is understood that bacteria can acquire genetic material from the environment, which may play a part in the classification below the species level. Cognisant of these factors, a *rpoB* gene phylogeny was used to determine relatedness and create OTUs for the *Streptomyces* isolates from Newfoundland; and representatives from each OTU were chosen for specialized metabolite analysis.

1.3: *Streptomyces* volatile organic compounds (VOCs)

Generally known for the numerous antibiotics they produce, *Streptomyces* also synthesize an array of VOCs (Citron et al., 2015; Citron, Rabe, et al., 2012). VOCs are described as small odorous molecules (containing up to 20 carbon atoms) with low molecular mass (100–500 Daltons), high vapor pressure, low boiling point, and also containing a lipophilic moiety (Schmidt et al., 2015). These characteristics aid the volatility and diffusion of such molecules to mediate interactions among species in the environment. Bacterial VOCs are grouped into major chemical classes, including hydrocarbons (alkanes, alkenes, alkynes), alcohols, aldehydes, ketones, esters, and terpenes (Figure 1.3.1) (Schulz & Dickschat, 2007). Some VOC classes and members have been more extensively studied than others. VOCs are produced by plants (Vivaldo et al., 2017), animals including humans (Curran et al., 2005; Ni et al., 2012), and fungi (Schnurer et al., 1999). VOCs are often exploited for their aroma in the food, cosmetic, chemical, and pharmaceutical industries

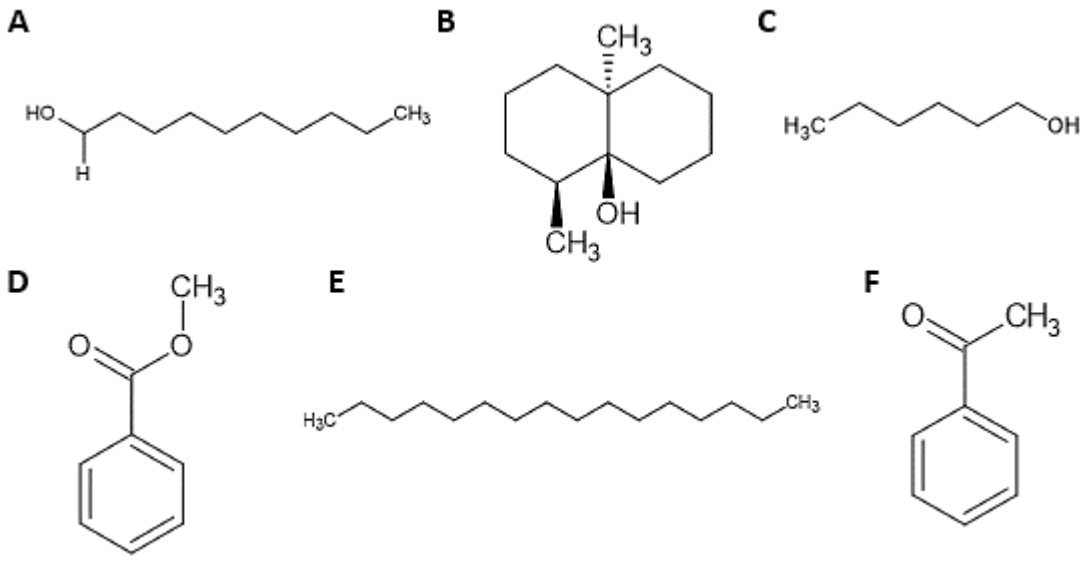

Figure 1.3.1: Representative structures of the major classes of bacterial VOCs **A.** Decanal (aldehyde) **B.** Geosmin (terpene) **C.** 1-Hexanol (alcohol) **D.** Methyl benzoate (ester) **E.** Hexadecane (hydrocarbon) **F.** Acetophenone (ketone)

and are frequently manufactured synthetically for these purposes. However, newer approaches may see microbes as commercial sources for such relevant compounds (Gupta et al., 2015). In addition, VOCs are essential to the sustenance of ecosystems as they regulate a range of functions and behaviours related to the success of a species in its habitat.

VOCs act as information-carrying signals or pheromones from one individual to another, whether intra- or inter-species. This may take on different outcomes in bacteria, including competition and cooperation, as VOCs may be antagonistic or take on supportive roles. For instance, 2,3 butanediol and acetoin are required for full virulence in the plant pathogen, *Pectobacterium carotovorum*. Similarly, the same compounds can increase the production of virulence factors in clinically relevant *Pseudomonas aeruginosa* (Audrain et al., 2015). In some cases, VOCs can modify the behaviours of other bacteria like ammonia, trimethylamine, hydrogen sulfide, nitric oxide, and 2-amino-acetophenone, which can alter biofilm formation or affect the motility of bacteria (Audrain et al., 2015; Raza et al., 2016). Altering motility contains a species and prevents it from acquiring nutrients, thus affecting its survival. Other organisms may exploit bacterial VOCs such as protists, substantial bacterial predators and use volatile signals to locate edible colonies (Schulz-bohm et al., 2017). Bacterial terpene synthase mutants could not mobilize protists (Schulz-bohm et al., 2017), demonstrating that VOCs are directly involved in protist-bacteria interactions.

Streptomyces are sources of valuable specialized metabolites for medicinal use (Emerson de Lima Procópio et al., 2012), suggesting that they might also be good candidates for studying VOCs for agricultural applications. The role of *Streptomyces* VOCs is subsequently discussed, followed by their biosynthesis and potential uses in agriculture.

1.3.1: Role of VOCs in *Streptomyces*

VOCs from *Streptomyces* play essential roles in proliferation, communication, defense, and competition for resources against other microbes. *Streptomyces venezuelae* is shown to perform exploration, a type of motile growth not universal to the genus (Jones et al., 2019), where endogenously produced trimethylamine (TMA, a VOC) increases environmental pH leading to reduced iron availability. In response to TMA, *S. venezuelae* upregulates siderophore biosynthesis and secretion to chelate iron for uptake, which reduces available iron for other bacteria and fungi in the immediate vicinity. Glucose depletion due to growth and a rise in pH due to TMA causes *S. venezuelae* to produce non-branching vegetative hyphae and rapidly cross solid surfaces (Jones et al., 2017). Interestingly, explorer cells can release air-borne VOCs to communicate this exploratory behavior at a distance with other species members to induce their exploratory growth. This behavior is presumably done to escape nutrient-poor conditions and occupy new niches.

Certain VOCs also mediate *Streptomyces* spores dispersal and thus increase their chances of proliferation. The odorous VOCs, geosmin and 2-methylisoborneol, can be sensed by other organisms and may attract or repel them. For example, the two VOCs attract the springtail arthropod (*Folsomia candida*) to induce electrophysiological responses in their antennae (Becher et al., 2020). Upon sensing these VOCs, springtails are attracted to *Streptomyces* colonies where they feed, and spores are then dispersed via the fecal route and by adhering to their hydrophobic cuticles. Because of the nature of VOCs, they are quickly diffused through air and soil to cover relatively short distances. Therefore, VOCs with antimicrobial activities have the added advantage of inhibiting competitors at

a distance. Ammonia is an example of one such naturally occurring chemical released in considerable amounts by some soil *Streptomyces*, which has been shown to inhibit *E. coli* ASD19 in mixed cultures under laboratory conditions (Avalos et al., 2019). Catabolism of the amino acid glycine is required to produce ammonia in *Streptomyces* species, but glycine defective mutants could not synthesize inhibiting amounts of ammonia even when they were grown on increased amounts of the amino acid (Avalos et al., 2019).

Symbiotic relationships between *Streptomyces* and higher animals are not uncommon. For example, the beewolf digger wasp (*Philanthus* spp., Hymenoptera, Crabronidae) incorporates *Streptomyces* into the larval cocoon, protecting larvae against pathogens (Kroiss et al., 2010). It was found that the *Streptomyces* species produce a cocktail of nine antibiotic substances that inhibited pathogenic fungi and bacteria. In addition, VOCs from microbes might account for communication signals that occur in insects and larger animals. Dodecanol/dodecanal are synthesized by soil *Streptomyces* (Citron, Rabe, et al., 2012; Dias et al., 2017), whereas dodecanol was isolated from the codling moth's (*Cydia pomonella*) pheromone gland (Lofstedt & Bengtsson, 1988) and dodecanal from the male ring-tailed lemurs' antebrachial secretions, which mediates attraction of females during mating season (Shirasu et al., 2020). *Streptomyces* were not linked as producers of dodecanol/dodecanal in the codling moths and ring-tailed lemurs, but soil Streptomyces synthesize both molecul*es*. Therefore, these molecules could be of microbial origin. To further understand the roles of *Streptomyces* VOCs and, by extension, their potential application, it is important to understand their biosynthesis.

1.3.2: Biosynthesis of *Streptomyces* VOCs

Understanding the biosynthesis of different VOCs will allow for the genetic manipulation of producers to prepare over-producing strains. Specialized metabolism is not essential to bacteria, and thus, the genes involved are dispensable. As a result, bacterial genome evolution is a dynamic process aided by horizontal gene transfer. In these events, bacteria acquire genetic material through intra- and inter-species transfer (Thomas & Nielsen, 2005). It is hypothesized that the host maintains beneficial DNA sequences for its survival and proliferation in its habitat (González-Torres et al., 2019). Hence, horizontal gene transfer has a role in shaping the metabolome of bacteria. Acquisition and maintenance of DNA that is nonessential to the growth (under laboratory conditions) of a species is often reflected in the *Streptomyces* genus. This group of bacteria is frequently noted for the diversity and number of BGCs present in a given *Streptomyces* genome (Baltz, 2017). Said BGCs will likely function in a beneficial way to the species survival in the face of competitors or sub-optimal environmental conditions. Furthermore, these BGCs may be passed from parent to offspring through vertical transmission, where they are maintained in the species because of often unknown selective pressures.

Because bacteria constantly gain and lose DNA, nonessential BGCs are not necessarily fixed within a population. Therefore, general molecular methods of identifying and classifying *Streptomyces* are not enough when investigating specialized metabolite biosynthesis. If these general methods alone are used, it would be easy to overlook a *Streptomyces* isolate harboring BGCs for novel specialized metabolites. For example, phylogenetic analysis of 287 *Streptomyces* with 100% identity of partial 16S rDNA sequences contained an average of ten unique BGC families each (Chevrette, Carlos-

shanley, et al., 2019). Another study revealed that terpene synthase genes that originated in bacteria were successfully transferred to fungi (Jia et al., 2019), indicating some compatibility in genetic material between the two microbial domains. Hence, bacteria may acquire similar genes from eukaryotes. Eukaryotes, including insects and plants, produce VOCs, whereas it is not uncommon to have symbiotic relations between bacteria and eukaryotic hosts (Crawford & Clardy, 2011; Kim et al., 2019). Therefore, it is possible that bacteria might be responsible for producing some VOCs in their symbiotic hosts. For example, insect pheromones such as methyl 6-methylsalicylate, methyl 6-ethylsalicylate, mellein, pyrrole-2-carboxylate, conophthorin, and chalcogran are among some isolated from actinomycetes (Citron, Rabe, et al., 2012). Further studies are warranted to investigate the role of such symbiotic relations and VOC and genes involved in the process.

The amount and composition of VOCs produced by microorganisms can vary according to culture conditions and substrate availability (Garbeva et al., 2014). Other important factors influencing the production of VOCs are the physiological state of the producing microorganism, oxygen availability, moisture, temperature, and pH (Insam & Seewald, 2010). As seen with terpenes that comprise the vast majority of naturally produced VOCs, a small number of substrates are used to synthesize a mixture of molecules by cyclases with similar backbones. Monoterpenes are generated from geranyl diphosphate, diterpenes from geranylgeranyl diphosphate, and sesquiterpenes from farnesyl diphosphate (Dickschat, 2016), where sesquiterpene synthases can sometimes also use geranyl diphosphate as a substrate (Dickschat et al., 2014). Diterpene cyclases are further classified

into type I or type II enzymes based on their mechanism of action (Dickschat, 2016) but, both classes have similar substrate specificities.

Many VOCs are theorized to be side products of metabolic pathways formed during primary metabolism or from various intermediates during specialized metabolism (Korpi et al., 2009). Studies of Actinomyces terpenes biosynthetic pathways reveal that it is common for even highly specific terpene cyclases to produce mixtures of compounds along with their dominant product (Rabe et al., 2013). For instance, the well-studied geosmin biosynthetic pathway has at least 15 side products or deduced derivatives (Rabe et al., 2013). Often, genes encoding cytochrome P450s and methyltransferases are part of operons formed by terpene cyclases and are speculated to catalyze a series of oxidations and methylations of the parent sesquiterpene synthase product, resulting in mixtures of end products (Hu et al., 2011).

Sometimes VOCs are precursors in antibiotic biosynthetic pathways, as shown for the *epi*-isozizaene synthase product identified in *Streptomyces coelicolor* (Zhao et al., 2008). The biosynthesis of the sesquiterpene antibiotic albaflavenone is elicited by two-gene containing cluster (Lin & Cane, 2009). The first gene product catalyzes the cyclization of farnesyl diphosphate to the sesquiterpene hydrocarbon, epi-isozizaene and the second carries out the oxidation of *epi*-isozizaene in a two-step process, leading to albaflavenone. Furthermore, homologs of *epi*-isozizaene synthase and albaflavenone genes are translationally coupled in *Streptomyces avermitilis* (Takamatsu, Lin, et al., 2011), although *epi*-isozizaene or any of its oxidized derivatives, albaflavenols and albaflavenone, were not identified under culture conditions used.

β-Cedrene is a sesquiterpene isolated from *Streptomyces arenae, Streptomyces citreus* (Rabe et al., 2013), and soil *Streptomyces* species present in the rhizosphere of disease suppressive soil (Cordovez et al., 2015). Synthesis of β-Cedrene in actinomycetes is thought to only occur in species capable of synthesizing *epi*-isozizaene, (Rabe et al., 2013), and is proposed to be a side product of the antibiotic albaflavenone biosynthetic pathway. In addition, the change of one amino acid at position 198 of the *epi*-isozizaene synthase converts it to a β-cedrene synthase (Li et al., 2014).

The pentalenolactone antibiotic BGC in *S. avermitilis* contains all of the necessary genes to produce the antibiotic (Quaderer et al., 2006). In the pathway, the sesquiterpene pentalenene is converted to pentalenolactone via a proposed series of intermediates, including 1-deoxypentalenic acid, pentalen-13-ol, and pentalen-13-al whereas, pentalenic acid is a shunt product (Takamatsu, Xu, et al., 2011). The pentalenolactone BGC does not contain any specific gene responsible for the formation of pentalenic acid. It was shown that a cytochrome P450 gene (*sav7469*) located outside the BGC in *S. avermitilis* is responsible for converting 1-deoxypentalenic acid to pentalenic acid (Takamatsu, Xu, et al., 2011). Hence, it is apparent that genes outside of major BGCs encode enzymes that use intermediates from dominant pathways. These are a few cases linking volatile shunt products to biosynthetic pathways of specialized metabolites.

Among the first isolated VOCs from S*treptomyces* are the terpenes geosmin (Gerber & Brunswick, 1965) and 2-methylisoborneol (Gerber, 1969), where the latter is also a widely distributed terpene reported in other actinomycetes, myxobacteria, and cyanobacteria (Citron et al., 2015). The two VOCs are responsible for the characteristic

earthy odor of soil and cause contamination of drinking water and edible fish. 2-methylyisoborneol biosynthesis occurs in a two-step pathway, where geranyl diphosphate is methylated to 2-methyl- geranyl diphosphate by an S-adenosylmethionine-dependent methyltransferase, followed by a catalyzation to 2-methylisoborneol by a terpene synthase (Martín-Sánchez et al., 2019). In *S. coelicolor*, two adjacent genes (*sco7700* and *sco7701*) elicit 2-methylisoborneol biosynthesis (Wang & Cane, 2008), whereas geosmin is produced from farnesyl diphosphate by the geosmin synthase encoded by gene *sco6073* (*cyc2*) in *S. coelicolor* (Gust et al., 2003) and *sav2163* (*geoA*) in *S. avermitilis* (Cane et al., 2006).

Geosmin synthase is a bifunctional enzyme that also catalyzed the formation of another terpene, germacrene D, using the same substrate as for geosmin (Jiang et al., 2007). The enzyme has two active sites that perform the Mg^{2+}-dependent cyclization, where the N-terminal site produces germacradienol and germacrene D from farnesyl diphosphate, and the C-terminal one converts germacradienol to geosmin. Germacrene D is a sesquiterpene isolated from *S. citreus* (Pollak & Berger, 1996), *Streptomyces fimicarius* BWL-H1 (Xing et al., 2018), and various other *Streptomyces* (Citron et al., 2015; Rabe et al., 2013).

The complex network of pathways leading to specialized metabolites reveals the diversity of molecules that arise from the transformation of intermediate products. The terpene cogeijerene is a proposed side product of the geosmin pathway (Citron, Gleitzmann, et al., 2012), where the intermediate (10R)-8,10-dimethyl-8-octalin is oxidized by an unknown enzyme. Among the lesser-studied systems is 1,8-cineole synthase, encoded by *cnsA* in *Streptomyces clavuligerus*, which catalyzes the conversion of geranyl diphosphate to eucalyptol (Rinkel et al., 2016).

Although the terpenes encompass the most produced microbial VOCs from the specialized metabolic class, other VOCs are synthesized using different enzyme families. These families include the cytochrome P450 enzymes that synthesize and metabolize various compounds, including alkanes, alcohols, aldehydes, and acids (Kelly & Kelly, 2013; Nie et al., 2014; Scheller et al., 1998). In other instances, the production of aldehydes, short-chain alkanes, fatty esters, and fatty alcohols like dodecanal and tridecane occurs via the Acyl-CoA reduction pathway by the fatty acyl-CoA/ACP reductases (Choi & Lee, 2013; Lehtinen et al., 2018). Therefore, it is essential to know the biosynthesis for specialized metabolites, especially those produced via multiple pathways. This knowledge is necessary when considering genetic manipulation methods to produce bacterial VOCs for large-scale use in industry and agriculture.

1.3.3: Potential applications of *Streptomyces* VOCs in agriculture

Annual losses in crop production due to pests affect both farmers and consumers. Therefore, finding sustainable solutions that reduce synthetic chemical use is paramount for eco-friendly agriculture. Among the notable green solutions is bioprospecting, where natural products are encouraged as alternatives to toxic chemicals (Kanchiswamy et al., 2015). VOCs are one example of safe biocontrol agents that could improve crop health and yield. Although few studies demonstrate the potential of VOCs in agriculture, the possible uses are promising and deserve attention.

In general, the bioactivities of *Streptomyces* VOCs and their applications are not well studied, but some recent reports linking VOCs to ecological processes (e.g., inhibition of microbes) have revealed some potential applications (Table 1.3.3.1). VOCs collected

Table 1.3.3.1: Some VOCs produced by *Streptomyces* and relevant bioactivities.

VOC	Function	Bacteria
Aldehydes		
Decanal	Beetle (*Scolytus schevyrewi*) repellent (Zhu et al., 2020); Bactericidal (K. Liu et al., 2012)	Various *Streptomyces* (Citron et al., 2015; Citron, Rabe, et al., 2012; Groenhagen et al., 2014)
Nonanal	Beetle (*Scolytus schevyrewi*) repellent (Zhu et al., 2020)	*Streptomyces sp.* FORM5 (Groenhagen et al., 2014)
Dodecanal	In male lemur sex pheromone (Shirasu et al., 2020)	Various *Streptomyces* (Citron, Rabe, et al., 2012)
Ketones		
Acetophenone	Tsetse fly repellent (Olaide et al., 2019); Kissing bug (*Rhodnius prolixus*) repellent (Franco et al., 2018); Western pine beetle repellent (Erbilgin et al., 2007)	Various *Streptomyces* (Citron et al., 2015; P. Xu et al., 2014)
Alcohols		
1-hexanol	Beetle (*Scolytus schevyrewi*) attractant (Zhu et al., 2020)	Various *Streptomyces* (Citron, Rabe, et al., 2012)
Benzyl alcohol	Head lice repellent (Toloza et al., 2006)	Various *Streptomyces* (Citron et al., 2015)
Dodecanol	Inhibits *Aspergillus fumigatus* biofilm formation (Mowat et al., 2010); Coddling moth sex pheromone (Lofstedt & Bengtsson, 1988)	Various *Streptomyces* (Dias et al., 2017)
Esters		
Methyl benzoate	Repel various insects (Feng & Zhang, 2017; Morrison III et al., 2019; Mostafiz et al., 2018)	Various *Streptomyces* (Citron et al., 2015; Cordovez et al., 2015; Groenhagen et al., 2014; Pollak & Berger, 1996)
Hydrocarbons		
Hexadecane	Nematicidal activity (Gu et al., 2007)	Various *Streptomyces* (Citron, Rabe, et al., 2012; X. Li et al., 2020; Schöller et al., 2002)
Heptadecane	Hydrocabon fuel (Schirmer et al., 2010)	Various *Streptomyces* (Citron, Rabe, et al., 2012; X. Li et al., 2020)
Terpenes		

epi-*isozizaene*	Precursor to antibiotic albaflavenone (B. Zhao et al., 2008)	*S. coelicolor* (B. Zhao et al., 2008)
Geosmin	Springtail attractant (Becher et al., 2020); *Drosophila* repellent (Becher et al., 2010; Stensmyr et al., 2012)	Various *Streptomyces* (Becher et al., 2020)
Methylisoborneol	Springtail attractant (Becher et al., 2020); Antifungal (Logrieco et al., 2002; Z. Wang et al., 2013)	Various *Streptomyces* (Becher et al., 2020)
α-himachalene	Antifungal and antibacterial (Chaudhary et al., 2014)	*S. clavuligerus* (Citron, Gleitzmann, et al., 2012)
1-8 cineole	Mosquito repellent (Klocke et al., 1987)	*S. clavuligerus* (Rinkel et al., 2016)
β-Cedrene	Inhibit sudden oak disease pathogen (*Phytophthora ramorum*) (Manter et al., 2007)	*S. citreus, S. arenae* (Rabe et al., 2013), other soil *Streptomyces* (Cordovez et al., 2015)
Geranyl acetone	Cassava mite's natural predator attractant (Pinto-zevallos et al., 2018); Asian larch bark beetles repellent (Q. Zhang et al., 2007); Tsetse flies repellent (Vale et al., 2012) Mosquito (*Anopheles gambiae*) repellent (Meijerink et al., 2001)	*Streptomyces sp.* GWS-BW-H5 (Martens et al., 2005)
Dihydroagarofuran	Reverse multidrug-resistance (Torres-romero et al., 2009)	*S. citreus* (Pollak & Berger, 1996),*Streptomyces yanglinensis* (Lyu et al., 2020)
Germacrene D	Mosquito (*Aedes aegypti* and *Aedes albopictus*) larvicide (Satyal et al., 2019); Chagas disease vector (*Triatoma rubrofasciata*) repellent (Satyal et al., 2019); Mosquito larvicide (Govindarajan et al., 2016)	*S. citreus* (Pollak & Berger, 1996), *S. fimicarius* BWL-H1 (Xing et al., 2018), and other *Streptomyces* (Citron et al., 2015; Rabe et al., 2013)
Other		
Trimethylamine	Promotes *Streptomyces* exploratory growth (Jones et al., 2019)	*S. venezuelae* (Jones et al., 2019)
Ammonia	Anti-bacterial (Avalos et al., 2019)	Soil *Streptomyces* (Avalos et al., 2019)

from *Streptomyces* are typically identified and documented, creating a foundation for future studies; as such, many VOCs have not yet made it to the application phase. This study aims to add knowledge of *Streptomyces* isolates VOCs to a relatively new field that may see VOCs as potential application in agriculture as natural pest deterrents.

Streptomyces VOCs have the potential to alleviate common problems, including *Drosophila* pests (Kirkpatrick et al., 2018; Wallingford et al., 2017); soft rot disease in tomato plants (Dias et al., 2017); and spoilage to litchi fruit (Xing et al., 2018) and other storage crops (Wang et al., 2013; Yang et al., 2019) caused by fungi. Synthesized by multiple *Streptomyces* species (Citron et al., 2015; Pollak & Berger, 1996), phenylethyl alcohol shows antifungal activity against plant pathogens of peanut kernels (Lyu et al., 2020) and post-harvest sweet potato (Li et al., 2020). The hydrocarbon hexadecane has nematicidal activity (Gu et al., 2007) and is also naturally synthesized in multiple *Streptomyces* (Citron, Rabe, et al., 2012; Li et al., 2020; Schöller et al., 2002).

2-methylisoborneol is an antifungal from *Streptomyces alboflavus* TD-1 that inhibits *Fusarium moniliforme* (Z. Wang et al., 2013), a facultative and non-host necrotrophic pathogen implicated in several plant diseases. *Fusarium moniliforme* broadly contaminates corn, sorghum, wheat, tomatoes, cotton, peanuts, bananas, soybeans, and other feeds where it causes diseases such as corn ear rot, wheat scab, and rice bakanae disease (Logrieco et al., 2002). Interestingly, 2-methylisoborneol is also implicated in attracting the fruit fly *Drosophila melanogaster*; however, the producing *Streptomyces* also synthesizes other specialized metabolites that are larvicidal to the *Drosophila* species (Ho et al., 2020).

The antibacterial and antifungal sesquiterpene α-himachalene has a reported presence in the volatile collection headspace of fermented *S. clavuligerus* (Citron, Gleitzmann, et al., 2012). It is active against the mycotoxigenic fungus, *Aspergillus parasiticus* (Chaudhary et al., 2014), implicated in the disease of widely used spices black and white pepper (Madhyasth & Bhat, 1984). Another terpene, geranyl acetone, plays a defensive role against cassava plant mites and is made by the plant in response to herbivory by the insect leading to the attraction of the cassava mite's natural predator (Pinto-zevallos et al., 2018), thereby protecting the plant. Geranyl acetone was isolated from *Streptomyces* strain GWS-BW-H5 (Martens et al., 2005) and the Actinobacteria, *Amycolatopsis alba* and *Amycolatopsis nigrescens* (Citron et al., 2015). In addition, the metabolite inhibits the growth of green algae (Ikawa et al., 2001), indicating its possible use in the prevention and containment of eutrophication in farm irrigation systems. Geranyl acetone may also act as an insect repellent for Asian larch bark beetles (Zhang et al., 2007), making it potentially valuable in the timber industry. Likewise, ketone acetophenone repels the western pine beetle, *Dendroctonus brevicomis*, but not its predator, *Temnochila chlorodia* (Erbilgin et al., 2007).

The ester, methyl benzoate, is synthesized by various *Streptomyces* species (Citron et al., 2015; Cordovez et al., 2015; Groenhagen et al., 2014; Pollak & Berger, 1996), and its insect repellency has been widely examined using brown marmorated stink bug (*Halyomorpha halys*), diamondback moth (*Plutella xylostella*), tobacco hornworm (*Manduca sexta*), the spotted wing *Drosophila* (*Drosophila suzukii*), American wheat weevil (*Rhyzopertha dominica*), and the red flour beetle (*Tribolium castaneum*) (Feng &

Zhang, 2017; Morrison III et al., 2019). Methyl benzoate also inhibits oviposition, nymphal development and causes mortality of adults in the Silverleaf whitefly (*Bemisia tabaci*) that infects tomato plants (Mostafiz et al., 2018), alluding to its potential application as a biopesticide to control various insects.

Geosmin, known for its earthy smell, can be used as a *Drosophila* repellent to prevent losses in small fruit crops. Geosmin acts as a stimulus to activate specific olfactory pathways that warn the flies of the presence of pathogenic fungi (Stensmyr et al., 2012). The researchers suggested that the geosmin detection system might be conserved across the *Drosophila* genus, indicating its potential use as a broad-spectrum eco-friendly *Drosophila* deterrent. Due to the widespread capacity of *Streptomyces* to produce the specialized metabolite, they are ideal choices to pursue for future applications.

The *Streptomyces* have also been shown to protect the strawberry plants and pollinating bees against pathogenic fungi and pathogenic bacteria (Kim et al., 2019). Although it is not yet known the type of specialized metabolite that provides protection, it is accepted that pollinators are attracted to nectars of plants in flowers. Therefore, VOCs may play a role in the interaction of the strawberry plants, *Streptomyces*, and honeybees. In other symbiotic relationships, *Streptomyces* in disease suppressive soils may increase plant growth and productivity. For example, *Streptomyces* VOCs inhibited hyphal growth of fungal root pathogen, *Rhizoctonia solani*, and significantly enhanced plant shoot and root biomass (Cordovez et al., 2015).

1.4: The main objectives of this thesis

Sustainable farming practices rely on natural community-level interactions to help control pest organisms. The heavy use of harsh chemicals and the lack of community-level species diversity in industrial agriculture can disrupt the ability of natural enemies to control pest populations, so it is vital to reduce harmful chemicals so that natural ecological interactions can be promoted in agroecosystems (Gliessman, 1990). As a proposed solution, naturally occurring VOCs may be used to restore and maintain natural functions to agroecosystems. Among the sources of VOCs, the *Streptomyces* is an excellent candidate genus to study. To date, many studies on *Streptomyces* specialized metabolites focus on antibiotic discovery and their biosynthesis. However, *Streptomyces* VOCs are just as bountiful and display potential for agricultural purposes. The objective of this thesis was to analyze a collection of *Streptomyces* isolates capacity for VOC production and add to the database of growing research on *Streptomyces* VOCs. One hundred and thirty-three *Streptomyces* isolates from the northeastern part of the island of Newfoundland were phylogenetically typed using the *rpoB* gene. Phylogenetically distinct isolates were then subjected to VOC analysis, and compounds with reported bioactivities such as insect repellency were noted. Such compounds may make good targets for agricultural applications, and the isolates should be considered for future insect repellency assays. The isolates were tested for bioactivities against six biological indicators (five bacteria and a fungus). A shortlist of six isolates selected on criteria of the number and types of VOCs they produced were subjected to replicate VOC analysis and phytotoxicity testing.

Chapter 2: Materials and Methods

2.1: General equipment and materials

All media and reagents were prepared with distilled water (dH_2O) and were sterilized by autoclaving. All antibiotic solutions were prepared in dH_2O or DMSO and were filter sterilized using 0.2 µm filters in the case of aqueous solutions (161013311, Basix, Fisher Scientific, Canada). Unless otherwise stated, antibiotics, reagents, and dehydrated media were purchased from Sigma Aldrich, Fisher Scientific, or VWR International (Canada). All procedures involving bacterial cultures were performed using aseptic techniques with sterile equipment and reagents. All centrifugations were performed using an Eppendorf 5424 (0012836), or 5418 microfuge-centrifuge (5418ZR715696), or a ThermoFisher Scientific Sorvall ST 16 R centrifuge (75004381) with a TX-400 Swinging Bucket Rotor (75003629). An Implen P300 NanoPhotometer (1777, Montreal Biotech Inc., Canada) or NanoDrop 1000 (I951, Thermo Scientific, USA) were used to measure nucleic acid concentrations. Isolated DNA was stored at -20°C, and bacterial glycerol stocks and culture supernatants were stored at -80°C.

2.2: *Streptomyces* procedures

2.2.1: Maintenance and stock preparation

All *Streptomyces* stocks were prepared by growing strains/ isolates on ISP-4 agar medium (M359-500G, Himedia) for 7 to 14 days and then scraping the growth with an ethanol flame-sterilized steel spatula into 1.5 ml microfuge tubes containing 500- 1000 µl of 20% glycerol. When required, nystatin (50 µg/ml) and nalidixic acid (50 µg/ml) were

included in the growth media. Mycelial stocks were prepared by centrifuging 1 ml cultures in Eppendorf tubes at 4,000 rpm for 5 min, discarding the growth media, and resuspending the cells in 20% glycerol. All *Streptomyces* isolates liquid cultures were grown at 28°C on a rotary shaker at 200 rpm (08988, New Brunswick Scientific, USA), and all cultures on solid media were incubated at 28°C (C2574, Hotpack, Canada).

2.2.2: Reviving of *Streptomyces* isolates from the strain collection

The *Streptomyces* isolates analyzed in this project were collected between 2011 and 2018 from soil samples collected from St John's, Newfoundland, Canada, and processed into spore stocks (K. Tahlan, personal communication). They were kept frozen at -80°C, and each isolate was revived by spotting 10 µl onto nutrient agar [3% w/v nutrient broth (234000, BD, Difco), 2% w/v agar in dH_2O] containing nalidixic acid and nystatin and incubated for 2-3 days.

2.2.2.1: Liquid cultures for mycelial stocks and chromosomal DNA extraction

Following incubation (section 2.2.2), some mycelia for each *Streptomyces* isolate mycelia were scraped off the respective agar plate using an ethanol flame-sterilized stainless-steel spatula and used to inoculate 5 ml of nutrient broth in 50 ml Falcon tubes containing 3 mm Borosilicate glass balls (Salem Specialty Ball, USA) to help break up mycelia during growth. Liquid cultures were then incubated for 3- 5 days, after which 1 ml of each mycelia culture was used to prepare and store mycelial stocks. Another 1 ml of each culture was used for chromosomal DNA extraction, as described later.

2.2.2.2: *Streptomyces* cultures for spore stock preparations

Some mycelia from nutrient agar plates described above (section 2.2.2) were scraped and spotted with ethanol flamed-sterilized stainless-steel spatula onto ISP-4 agar containing nalidixic acid and nystatin. Four isolates were spotted on one agar plate divided into quarters. Inoculated ISP-4 agar plates were incubated to allow for sporulation of the *Streptomyces* isolates. Once the *Streptomyces* isolates had sporulated, the spores from each quarter were scraped and transferred to fresh ISP-4 plates (one isolate per plate) for lawn cultures. The ISP-4 media plates were incubated and used to make spore stocks after sporulation had occurred.

2.2.3: Chromosomal DNA extraction

Genomic DNA extraction from environmental isolates was performed using the Presto mini gDNA Bacteria kit (GBB100, Geneaid Biotech Ltd., Taiwan) with an additional step involving bead beating. The protocol for extracting chromosomal DNA from Gram-negative bacteria was used because a higher DNA yield was obtained. Clean bead beating tubes were prepared with fine silica beads (BAWZ 400-250-35, OPS Diagnostics, USA), and 1 ml of 3-5 days old mycelial cultures grown in nutrient broth (Section 2.2.2.1) were added to appropriately labeled tubes. The tubes were centrifuged for 3 mins at 14,000 rpm, and the growth medium (supernatant) was discarded. According to the manufacturer's instructions, GT buffer containing proteinase K was added, and the tubes were capped, sealed with parafilm, and subjected to two rounds of bead beating using the pre-installed bacteria protocol (10-3280-001-26, SpeedMill plus, Montreal Biotech Inc lab equipment, Canada). Following bead beating, the tubes were centrifuged for 3 mins at 14,000 rpm to separate the lysate (DNA) from cell debris and the silica beads. The

supernatant was carefully transferred (without collecting the silica beads) to clean and appropriately labeled Eppendorf tubes. The remaining steps were followed according to the manufacturer's instructions up to the elution step, where 43 µl of 60°C nuclease-free water was used instead of the elution buffer provided in the kit. The DNA concentrations were measured and the DNA stored for future use.

2.2.4: Liquid cultures for bioassays and VOC collection

Duplicate *Streptomyces* seed cultures for inoculating fermentation media were grown in 5 ml of trypticase soy broth (211825, BD Bacto) in 25 - 50 ml capacity Erlenmeyer flasks, with stainless steel springs to break up the mycelia growth. After 48 hours of growth, 250 µl and 500 µl seeds were used to inoculate 25 ml of fermentation media in 250 ml capacity fermentation flasks with stainless steel springs. The fermentations were set up as follows:

Streptomyces scabies 87-22 (Li et al., 2019) seed (250 µl) was inoculated into oat bran broth (OBB) medium (Johnson et al., 2007), and *Streptomyces* isolates seeds (500 µl) were inoculated into one of three media (Appendix A.2.1): soy flour mannitol (SFM) medium (Citron, Gleitzmann, et al., 2012; Citron, Rabe, et al., 2012; Komatsu et al., 2008; Rabe et al., 2013; Riclea et al., 2012); a synthetic medium (Cane et al., 2006; Jáchymová et al., 2002); or yeast extract-malt extract-starch (YMS) medium (Ikeda et al., 1987).

Following 5 days incubation, 2- 3 ml of each *Streptomyces* culture was transferred to labeled 1.5 ml Eppendorf tubes (1 ml per tube) and stored at -80°C for future antimicrobial and growth assays (aliquots of *S. scabies* 87-22 from OBB were stored and

only used for phytopathogenicity testing). The remainder of each *Streptomyces* isolates culture were used for VOC collection as follows.

2.2.4.1: Liquid cultures for pooled media VOC collection

At any one time, a maximum of four *Streptomyces* isolates seed cultures were used to start fermentation using the described media (SFM, YMS, and synthetic). Un-inoculated media controls were set up using the same conditions for each medium. After incubation for 5 days, 2 ml aliquots were removed and stored for future use and, the approximately remaining 23 ml of each of the three media were pooled (69 ml) for each isolate and mixed well. For VOC collection, an aliquot of 25 ml per Streptomyces isolate was transferred to labeled 8 oz mason jars (Bernardin Ltd., Canada).

2.2.4.2: Liquid cultures for replicate VOC collection

Single *Streptomyces* isolates were used to set up seed cultures for replicate fermentations and VOC collection. The two seed cultures for each isolate were pooled and mixed well, then used to start three flasks of production cultures in SFM medium. After incubation, 3 ml from each replicate culture were drawn and stored for future use. The approximately remaining 22 ml of each culture was poured into 8 oz mason jars for VOC collection. Small, sterilized magnetic stir bars were added to each mason jar to agitate the cultures during VOC collection. The mason jars were placed atop a hot plate (07287218, VWR, USA) to use the stirring feature only (without heating). The same *Streptomyces* isolate was subjected to replicate culture fermentation in YMS and the synthetic media

following fermentation in SFM medium and VOC collection. Un-inoculated media was used under the same conditions as the *Streptomyces* isolates for control purposes.

2.2.5: Media growth profile of *Streptomyces* isolates

Each *Streptomyces* isolate was tested for growth on the three fermentation media used in this study, SFM YMS and synthetic media; each liquid media formulation (section 2.2.4) was supplemented with 2% w/v agar. A single agar plate was divided to accommodate 20 *Streptomyces* isolates. A glycerol stock of each isolate (2 µl) was spotted onto each of the three different agar media. The plates were then incubated for a maximum of 3 days. Following incubation, the plates were observed for the growth of the *Streptomyces* isolates.

2.2.6: Antibiotic susceptibility profiling of *Streptomyces* isolates

Each *Streptomyces* isolate was tested against three antibiotics: apramycin (50 µg/ml), kanamycin (50 µg/ml), and thiostrepton (25 µg/ml). A single nutrient agar plate was divided to accommodate 20 *Streptomyces* isolates. A glycerol stock of each isolate (2 µl) was spotted onto three different agar media containing one of the three antibiotics. These agar plates were incubated for 1-3 days. Following incubation, the plates were observed for the presence of growth of each *Streptomyces* isolates.

2.2.7: DNA assay for *Streptomyces* growth in fermentation media

An indirect assay was used to measure the growth of *Streptomyces* in the fermentation media as described previously (Burton, 1968; Zhao et al., 2013). To prepare the diphenylamine reagent: 1.5% w/v diphenylamine in 150 ml glacial acetic acid, 1.5%

v/v (final) of concentrated sulfuric acid was added to this solution (the solution was stored in the dark). Before use, aqueous acetaldehyde was prepared for addition as follows: 2% v/v of cooled acetaldehyde (> 99.95% purity, kept at 4°C, and in the dark) was pipetted into 49 ml cooled dH_2O. To the 152.25 ml of diphenylamine- glacial acetic acid- sulfuric acid reagent, 0.5 % v/v (final) of the aqueous acetaldehyde was added. This diphenylamine reagent was set aside in the dark for later use.

One milliliter aliquots of *Streptomyces* cultures (Section 2.2.4.2) were centrifuged at 10,000 rpm for 10 min, and the supernatants were removed and transferred to freshly labeled Eppendorf tubes and stored for future use. The cell pellets were washed with 1 ml of PBS buffer (0.8% w/v NaCl, 0.02% w/v KCl, 0.144% w/v Na_2HPO_4, 0.024% w/v KH_2PO_4, adjusted to pH 7.4 with HCl), the suspension was centrifuged at the same speed and time as before, and the supernatant was discarded. The cells pellets were resuspended a second time with 1 ml of PBS. Aliquots (500 µl) of the cell suspensions were transferred to two freshly labeled Eppendorf tubes (duplicate for each culture). The 500 µl cell suspensions were centrifuged, and the supernatants were discarded. The cell pellets were resuspended in 1 ml of diphenylamine reagent, vortexed to break up the cell pellets, and incubated at 60°C for 1 hour (Oven: 07-32353, Binder, U.S.A.). The Eppendorf tubes were removed from 60°C, vortexed once more, and kept in the dark at room temperature overnight. Following overnight incubation, the tubes were centrifuged at 7,000 rpm for 5 min, and 150 µl of the supernatant from each tube was transferred to a well in 96 – well microtiter plates. The absorbance was measured at 595 nm with a multifunctional microtiter plate reader (270789, Synergy Hybrid Reader, BioTek industries, USA).

2.3: DNA procedures

2.3.1: Polymerase chain reaction and agarose gel electrophoresis conditions

Twenty microliter PCRs to amplify 880 bp DNA and 1465 bp DNA fragments from *rpoB* and 16s rDNA gene, respectively, were set up using 20- 250 ng of DNA, 5% v/v DMSO, 0.5 µM forward primer, 0.5 µM reverse primer, 0.2 mM dNTPs, 1× buffer (5× GC or HF) and 1% v/v polymerase from the Phusion® High-Fidelity PCR Kit (E0553L, NEB, Canada), and nuclease-free water to the final volume. PCRs were performed using an Eppendorf VapoProtect Mastercycler (6321AO714802, Fisher Scientific, Canada) or C1000 Touch Thermal cycler (CC003324, Bio-Rad, Canada). The *rpoB* PCR cycles were set up as follows: initial denaturation 98°C for 30 sec; followed by 30 cycles of 98°C for 10 sec, 58°C for 30 sec, and 72°C for 20 sec; and a final extension of 72°C for 5 min. The 16s rDNA PCR cycles were set up as follows: initial denaturation 98°C for 30 sec; followed by 30 cycles of 98°C for 10 sec, 50°C for 30 sec, and 72°C for 40 sec; and a final extension of 72°C for 5 min. DNA template for PCRs consisted of chromosomal DNA (section 2.2.3) or nuclease-free water in the case of negative controls. All primers used in the current study are listed in Table 2.3.1.1.

Two microliters from each PCR were loaded onto a 1% w/v agarose gel using 6× gel loading dye (B7024S, NEB, Canada) alongside 5 µl of 1 kb ladder (DM010-R500F, FroggaBio, Canada) for a band size estimation. Electrophoresis was conducted at 100 V in constant voltage mode using 1× Tris-borate EDTA (TBE) buffer (89 mM Tris base, 89 mM Boric acid, 2 mM EDTA, pH 8) as follows: 45 minutes for *rpoB* gene amplicons and 60 minutes for 16S rDNA gene amplicons. All gels were imaged following staining with

Table 2.3.1.1: Oligonucleotide primers used for PCR amplification and DNA sequencing in the current study.

Primer name	Sequence (5'- 3')	Annealing temperature [+]	Purpose	Reference
27F 1492R	AGAGTTTGATCCTGGCTCAG ACGGCTACCTTGTTACGACT	59	Amplifying 1465 bp of the 16s rDNA gene and sequencing for molecular identification	(Shi et al., 2019)
516F	TGCCAGCAGCCGCGGTA	-	Sequencing 16s rDNA gene amplicons for molecular identification	(Nagashima et al., 2003)
rpoBF1 rpoBR1	TTCATGGACCAGAACAACC CGTAGTTGTGACCCTCCC	58	Amplifying 880 bp of the *rpoB* gene for use in phylogeny	(Guo et al., 2008)
rpoBF2 rpoBR2	CCAGAACAACCCGCT CTCCCACGGCATGAA	-	Sequencing *rpoB* gene amplicons for phylogeny	This Study

[+] Annealing temperatures were calculated using the NEB online Tm calculator (https://tmcalculator.neb.com/#!/main) for the Phusion system.
- means not applicable.

ethidium bromide using a ChemiImager™ Ready (Alpha Innotech Corporation, USA) or a benchtop UV transilluminator (95-0458-01, UVP, USA). The reaction products were purified using the EZ-10 Spin Column PCR Products Purification Kit (Bio Basic Inc., Canada) according to the manufacturer's instructions, except that DNA was eluted using 30 µl nuclease-free water heated to 60°C instead of the elution buffer. The PCR product concentrations were measured, and the DNA was sent for sequencing at The Centre for Applied Genomics (TCAG) sequencing facility (The Hospital for Sick Children, Canada).

2.3.2: Primer design for sequencing the *rpoB* gene amplicon

Primers for the sequencing of the *rpoB* gene amplicon (Table 2.3.1.1) were designed in this study by creating a multiple sequence alignment in the Molecular Evolutionary Genetics Analysis version ten software (MEGA-X) (Kumar et al., 2018) of six *Streptomyces* species *rpoB* genes, *Streptomyces lividans, Streptomyces avermitillis, Streptomyces clavuligerus, Streptomyces coelicolor, Streptomyces scabies, and Streptomyces venezuelae*. These sequences were obtained from the National Center for Biotechnology Information (NCBI) or the StrepDB database. The consensus sequence (Appendix A.2.3.2.1) was compared against the NCBI non-redundant nucleotide collection database, specific to *Streptomyces* (taxid:1883), using the Basic Local Alignment Search Tool (BLAST). The top hits were selected and downloaded via the multiple sequence alignment viewer in aln file format (102 *rpoB* gene sequences including the query). The aln file was converted to fasta file format using the HIV sequence database format converter (https://www.hiv.lanl.gov/content/sequence/FORMAT_CONVERSION/form.html) then aligned using ClustalW in MEGA-X. One sequence (Accession CP040941.1 for

Streptomyces variabilis) was removed as it was not of sufficient length, leaving 101 sequences inclusive of the query (Appendix A.2.3.2.2). Two primer sequences were then selected from conserved regions of the alignment, flanking a variable 880 bp region. Primers were designed and then purchased from Integrated DNA Technologies, Inc. (USA).

2.3.3: Phylogeny for determining relatedness of *Streptomyces* isolates

rpoB gene phylogenetic trees of all *Streptomyces* isolates from the current study and those from *Streptomyces* genome assemblies available in the NCBI database as of April 8, 2021 (n = 282) were used to determine relatedness. Only one strain per *Streptomyces* species downloaded from NCBI genome assemblies was included in the phylogenetic analyses (n = 211). Each *Streptomyces* isolate *rpoB* gene sequence was compiled by aligning the DNA sequences for the forward and reverse sequencing primers in the online Benchling software (https://www.benchling.com/). The sequences were manually curated using the respective Sanger sequencing chromatograms (peak height, width, and periodicity) to correct any ambiguities, i.e., only one nucleotide (A, G, C, or T) was included at a given position in the alignment. The target *rpoB* gene segments of the NCBI genome assemblies were extracted with the *rpoB* primers created in this study. All *Streptomyces* and isolates *rpoB* sequences were made into two multiple sequence alignments, one with isolates from this study and reference sequences from the NCBI genome database (Appendix A.2.3.3.1) and one with only isolates from this study (Appendix A.2.3.3.2), using the Benchling software MAFFT program, which was downloaded in FASTA format for evolutionary analyses in MEGA-X.

The multiple sequence alignments obtained above were trimmed, and the evolutionary history was inferred using the Maximum Likelihood method and General Time Reversible model (Nei & Kumar, 2000). The trees with the highest log-likelihood were selected. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using the Maximum Composite Likelihood (MCL) approach and then selecting the topology with a superior log-likelihood value. The trees were drawn to scale, with branch lengths measured in the number of substitutions per site. The analyses involved 345 and 134 nucleotide sequences for *Streptomyces* species and isolates phylogeny (211 *Streptomyces* species and 133 isolates sequences) and isolates only phylogeny (133 isolates sequences) with *M. tuberculosis* as an outgroup for both trees. There were 623 and 618 positions in the final datasets, respectively. Both trees were run using 100 bootstrap replicates, and a minimum of 50% consensus cut-off value was used to create branches. The isolates phylogenetic tree was used to define OTUs for this thesis, where isolates with identical *rpoB* sequences were clustered together. The multiple sequence alignment was checked to ensure that all isolates in an OTU had 100% identity of *rpoB* sequences.

2.3.4: 16S rDNA identification of *Streptomyces* isolates

Select *Streptomyces* isolates were identified using 16S rDNA and *rpoB* sequences. Following the curation of 16S rDNA sequences as described above, each *Streptomyces* isolate sequence was compared against the NCBI 16S rRNA sequences (Bacteria and Archaea) database using BLASTN. The top hit was selected as the species ID, and if there were more than one species with the same percent identity to the query (the isolate's 16S

rDNA sequence) in the top hits, the *rpoB* sequence was then used for further resolution. In this case, the species in the 16S rDNA search top hits respective *rpoB* sequences were pulled from NCBI available genome sequences (accession numbers in Table 3.5.1) using *rpoB* primers in this study (Table 2.3.1.1) and then compared to the *Streptomyces* isolate *rpoB* sequence (Table 3.5.1) in a multiple sequence alignment using Benchling. A minimum recommended 96–97% identity for a 600– 825 bp fragment of *rpoB* between the isolate and the reference sequences (Adékambi et al., 2009) was used to determine the isolate's ID.

2.3.5: AntiSMASH analysis of JAC60 possible species IDs

An antiSMASH (Blin et al., 2021) analysis was done to predict specialized metabolites BGCs in the genomes of two shortlisted species ID for JAC60, *Streptomyces griseofuscus* and *Streptomyces murinus* (NCBI accession numbers NZ_CP051006.1 and NZ_CP0066774.1, respectively). The NCBI accession numbers for the two *Streptomyces* genomes sequences were inputted into the antiSMASH online analysis software (https://antismash.secondarymetabolites.org), and the results were downloaded following completion of the analyses.

2.4: Bioactivity screening of culture supernatants

Fermented culture supernatants (section 2.2.4) were tested against several indicator organisms (Table 2.4.1). Growth conditions and a description of each indicator organism are provided. Bioassays were performed within two months of supernatant collection. One milliliter of each supernatant (thawed from the frozen culture aliquots) was centrifuged at

Table 2.4.1: Indicator organisms used for bioactivity assessment of culture supernatants.

Indicator organism	Testing media and incubation conditions	Description/ Relevant features	Source
Saccharomyces cerevisiae ATCC 208352	YPD[e]; 28ºC, 24-48 hours	Yeast or single-celled fungus	ATCC[g]
Bacillus subtilis ATCC 23857[a]	MHA[f]; 28ºC, 24-48 hours	Gram-positive, rod-shape	ATCC[g]
Escherichia coli ESS	MHA[f]; 37ºC, 24 hours	Gram-negative, rod-shape; β-lactam sensitive	(Jensen et al., 1983)
Pseudomonas fluorescens ATCC 13525[b]	MHA[f]; 28ºC, 24-48 hours	Gram-negative, rod-shape,	ATCC[g]
Micrococcus luteus ATCC 4698[c]	MHA[f]; 28ºC, 24-48 hours	Gram-positive, coccus	ATCC[g]
Staphylococcus epidermidis ATCC 14990[d]	MHA[f]; 37ºC, 24-48 hours	Gram-positive, coccus	ATCC[g]

ATCC conditions for indicators are like those used except as follows:

[a] Grows on potato extract agar, 26°C for 18 to 24 hours.

[b] Grows on nutrient agar, 26ºC for 24-48 hours.

[c] Grows on tryptic soy agar, 28ºC for 24-48 hours.

[d] Grows on nutrient agar, 37ºC for 24-48 hours.

[e]YPD- yeast extract-peptone-dextrose agar.

[f]MHA- Mueller Hinton agar.

[g]ATCC- American Type Culture Collection.

14,000 rpm for 3 minutes, and the supernatants were collected and separated from the cell pellet and debris. Two hundred and ten milliliters of Muller Hinton agar (MHA) (V310937, Mikrobiologie, Thermo Fisher, Canada) were inoculated with 2 ml of *B. subtilis, E. coli, M. luteus, P. fluorescence, or S. epidermidis* glycerol stock. Similarly, 210 ml of yeast extract-peptone-dextrose agar (YPD) was inoculated with 2 ml of *Saccharomyces cerevisiae* glycerol stock. Inoculated media were poured into sterile 22 × 22 cm plastic bioassay trays, and 42 sterile 6 mm Whatman filter paper discs (prepared using a hole punch) were then placed on top of the agar plate. *Streptomyces* supernatants (10 µl) were spotted onto individual discs, after which the plates were incubated under conditions listed in Table 2.4.1, at 28°C or 37°C (01050214, VWR, USA). Following incubation, the zones of inhibitions were measured in millimeters.

2.5: VOC collection and GC-MS analysis procedures

2.5.1: VOC collection, including apparatus set-up and cleaning

VOC collection was performed according to the method described by Light et al. (Light et al., 2020) with some modifications. After fermentation of *Streptomyces* (section 2.2.4), a total of four mason jars containing ~25 ml of cultures each were connected to a pump (PVAS22, portable Volatile Assay System [VAS], USA) that pushed unsterile air into the headspace of each jar and simultaneously pulled that air through pre-cleaned divinylbenzene polymer VOC traps (HayeSep-Q 80/100 mesh, 27+ mg; VAS, USA). The traps were pre-cleaned using established protocols (Light et al., 2020), which involved flushing sequentially with methanol, acetone, and HPLC-grade hexane. The jars were connected to the pump with polypropylene tubing made airtight at connecting junctions as

best as possible. Plastic nuts and bolts wrapped with ½ inch Teflon tape (PS6036, PlumbShop, Canada) were used to connect tubing through two holes made in the lids of each jar. One hole linked tubing with air being pushed into the jar, and the other connected tubing with air being pulled through a trap to collect VOCs emitted from the cultures. A continuous airflow through hydrocarbon filters (PN10033.00, VAS, USA) was passed through each mason jar (0.3 L/min push and 0.1L/min pull).

The first VOC collection set-up included two fermented *Streptomyces* and two controls. One jar was left empty, and one contained uninoculated media treated the same as the test samples for control purposes. Following overnight (~17 hours) VOC trapping, the tubing was disassembled for cleaning, first with tap water, then with 95-100% ethanol. The mason jars were washed with unscented soap (043204, Sparkleen, Fisher Scientific, Canada). The traps were sealed at both ends with Teflon tape, labeled accordingly, and stored at -80°C before being sent for gas chromatography-mass spectrometry (GC-MS) analysis by Dr. Hillier's group (Acadia University, NS, Canada).

2.5.2: VOC collection trap processing

At Acadia University, GC-MS (Scion 456 Gas Chromatograph–Single Quad Mass Spectrometer, SCION Instruments, UK) was used to determine the composition of VOCs collected in the VOC traps (section 2.5.1). VOCs in the traps were eluted with 200 µl of hexane (CHROMASOLV, >98.5% purity, Sigma-Aldrich, USA) under a flow of nitrogen into 1.5 ml vials. Aliquots of 40 µl per eluted samples were transferred to 250 µl limited volume glass inserts within septum-capped autosampler vials. Ten microliters of 50 ng/µl racemic menthol (Sigma-Aldrich) was added as an internal standard to each of these

aliquots. Autosampler vials were capped, sealed with Teflon tape, and stored at 4°C before further analysis.

A non-polar capillary Rxi®-5silMS column (30 m x 0.25 mm, film thickness 0.25 mm; Restek Corporation, USA) linked to a Bruker mass spectrometer (Bruker Daltonics Ltd., UK) was used for analysis. Samples underwent splitless injection for 1 min, followed by a 20:1 split state after that (injector held at 250°C). The oven temperature was maintained for 1 min at 40°C then increased to 100°C at 6°C/ min and held for 1 min, then increased to 250°C at 10°C/ min, and the temperature held for 5 min. The injector and transfer line were maintained at 250°C. Helium was used as a carrier gas at a flow of 1 ml/min.

2.5.3: Identification of VOCs

Peaks from GC-MS analysis were identified using the Bruker-supplied MS Data Review software (version 8.0.1, Bruker Daltonics Ltd., UK) using a detection threshold of 2000 CPS, a maximum peak width of 6.0 sec, a slope sensitivity of 20, and a tangent of 10%. VOCs were identified using standards and NIST Mass Spectral Search Program for the NIST/EPA/NIH Mass Spectral Library Version 2.0g built in 2011 (abbreviated as NIST library) (Scion Instruments UK Ltd, UK).

Spectrum lists of VOCs (libraries of compound IDs) were created for each *Streptomyces* isolate and control chromatogram in the MS Data review software. An empty jar and uninoculated media subjected to the same conditions of volatile trapping, sampling, and analysis served as controls. Text files of the integrated peaks were made, and spectrum

lists were saved as MSP files. Compound tables saved as MSP files in the MS Data review software were imported in the Bruker supplied Method Builder software (version 8.0.1, Bruker Daltonics Ltd., UK). The compound tables were then copied and saved as Microsoft excel CSV files. R-studio (version 1.3.1093, RStudio, USA) was used to calculate integrations and combine the Microsoft excel CSV files and the previously created text file of the spectrum list (Appendices A.2.5.3.1a and A.2.5.3.1b). VOC matches suggested by the NIST library were then evaluated based on spectral similarity and comparing their Kovats retention indices (RI) to published values.

Compounds from the bacterial samples detected in control samples were considered media-derived or artifacts of the collection and sampling procedure, thus not of bacterial origin. The compounds with good spectral matches to the NIST library references and subsequent injection of authentic standards or supported by published RI data (absolute difference ≤ 10) (Linstrom & Mallard, 2001) were considered high confidence matches. If no authentic standards were available and the published RI could not support a NIST library suggested compound ID, or there was no NIST library suggested compound ID, the VOC was deemed a low confidence match or unknown, respectively. A further classification assigned the identified compounds with a functional group and putative origin (bacterial or control-derived).

2.6: Phytopathogenicity screening of select *Streptomyces* isolates

Six *Streptomyces* isolates selected for replicate culture analysis were tested for phytotoxic effects along with the known plant pathogen, *S. scabies* 87-22 (Li et al., 2019). Inoculants for the procedure were prepared as follows: *Streptomyces* spores (~200 µl) from

glycerol stocks were used to inoculate ISP-4 plates, one plate per *Streptomyces* isolate. The spores were spread as lawns with sterilized spreaders to cover the agar plates. The *Streptomyces* isolates and *S. scabies* 87-22 were incubated for 10 days, following which a sterile spatula was used to scrape the spores from each plate and transfer them into 2 ml of sterile dH_2O in 50 ml Falcon tubes. JAC45 was suspended in 1.5 ml of sterile dH_2O as it sporulated less than the other *Streptomyces* isolates. The spores were then vortexed to prepare a homogenous suspension to inoculate the germinated radish seeds described below. Supernatants were drawn from 1 ml aliquots of fermented *S. scabies* 87-22 in OBB (section 2.2.4) and two replicate cultures of the six isolates in SFM (section 2.2.4.2) were also used as inoculum for the germinated seeds.

Radish seeds (White Icicle, The Seed Company by EW Gaze, Canada) were placed into a 50 ml Falcon tube containing 70% v/v ethanol. The seeds were incubated for 5 min with gentle agitation on a gyro shaker (13687705, Fisher Scientific, EU). The ethanol was then poured off, 40 ml of 15% v/v bleach solution added (099-5345-6, Old Dutch, Canada), and the seeds were incubated for 10 min with gentle agitation using the gyro shaker. Following this, the seeds were rinsed 8-10 times with 40 ml of sterile dH_2O to remove all bleach. The seeds were then placed into a sterile deep Petri-dish containing sterile Whatman filter paper prewetted with 2 ml sterile dH_2O. The plate was then sealed with parafilm, and the seeds were left to germinate for 36-48 hours at room temperature in the dark.

2.6.1: Phytotoxicity assessment of *Streptomyces* isolates

Approximately 50 ml of sterile 1.5% w/v agar in dH_2O was poured into eight sterile deep Petri-dishes, 20 mm thick/deep and 140 mm wide. Petri-dishes were labeled to

accommodate one *Streptomyces* isolate per plate. Six wells (or five when the supernatant inoculum was used) per plate were generated in the agar using a sterile test tube with a mouth diameter of 13 mm. The agar plugs were removed with sterile forceps, placed into a sterile beaker, remelted in a microwave, and 200 µl was used to seal the bottom of each well. Once the agar in the wells had set, individual germinated seeds were transferred aseptically to each well using sterile forceps. Two hundred microliters of freshly prepared *Streptomyces* isolate spore suspension or supernatant were pipetted into each agar well containing one germinated seed. *Streptomyces scabies* 87-22 was used as a positive control and sterile dH_2O as a negative control. The plates were sealed with parafilm and incubated at room temperature (~23°C) under a 16-hour photoperiod for 7 days. Following the incubation period, the plates were photographed for a qualitative assessment (spores treated seedlings), or the seedlings were measured for a quantitative evaluation (supernatant treated seedlings). The shortest and longest seedling in each treatment was discarded for the quantitative assessment, and the remaining three were used to calculate an average length. The experiment was repeated using the *Streptomyces* spores.

Chapter 3: Results and Discussion

In this study, a collection of 133 *Streptomyces* isolates from St. John's, Newfoundland, were phylogenetically typed to determine relatedness using the *rpoB* gene. Thirty-seven representative *Streptomyces* isolates from different OTUs were selected for fermentation, VOC collection, and subsequent GC-MS analysis. A shortlist of six *Streptomyces* isolates was further typed using 16S rDNA and was tested for phytotoxic effects on plants. The following sections present and discuss the results obtained.

3.1: The collection of *Streptomyces* isolates is phylogenetically diverse

All isolates used in this study were obtained using soil samples from the vicinity of St. John's, located on the Avalon Peninsula of the island of Newfoundland. These soils have developed from materials derived from the underlying slate, siltstone, sandstone, shale, limestone, conglomerate, and granitic and volcanic rocks (Heringa, 1981). Most of the mineral soils are coarse to moderately coarse-textured, stony, acidic to highly acidic in pH, and low in natural fertility. The ocean heavily influences the climate, with July temperatures ranging from 13-16 °C and winter temperatures ranging from -4–2 °C in December to February.

A specific region of *rpoB* (position 1347 to 2207) from the *Streptomyces* isolates was amplified by PCR using custom primers (Table 2.3.1.1). For comparison, all *Streptomyces* genome assemblies available in the NCBI genome database (n = 282) as of April 2021 were downloaded, and *rpoB* sequences were extracted. However, only one strain per species was included in a phylogenetic analysis (211 reference *Streptomyces*

species) to remove over-represented strains. Phylogenetic analysis with the *Streptomyces* species showed that the *Streptomyces* isolates were distributed throughout the phylogenetic tree, indicating diversity in the isolates collection (Appendix A.3.1.1).

A closer examination of *rpoB* sequences of the 133 isolates from the current study showed that they could be clustered into 31 OTUs, where isolates in an OTU have 100% identity of *rpoB* sequence (Figure 3.1.1). Each isolate *rpoB* sequence was run against the NCBI non-redundant database, and it was assumed that the *rpoB* provided resolution below the genus level. One OTU contained two *Dermacoccus* species, a genus belonging to the class Actinobacteria (Parte et al., 2020; Stackebrandt et al., 1995) and was not included in further analyses. The remaining 30 OTUs contained *Streptomyces* isolates. One clade contained 25 isolates closely related to *Streptomyces pratensis* (Shirling & Gottlieb, 1969). *Streptomyces pratensis* contains a cryptic clavulanic acid-like BGC, which might produce a β-lactamase inhibitor (Álvarez-Álvarez et al., 2013). Other OTUs had one to ten *Streptomyces* isolates, and seven OTUs contained one isolate each.

It is believed that phylogeny, a reliable tool to examine evolutionary relationships, may be used to predict natural product biosynthesis (Adamek et al., 2019). Phylogenetic application may differentiate between orthologous (homologues created through speciation) and paralogous (homologues created through duplication) genes. Orthologous genes are assumed to retain equivalent functions in different species (Gabaldón & Koonin, 2013), which is also applicable for specialized metabolite BGCs.

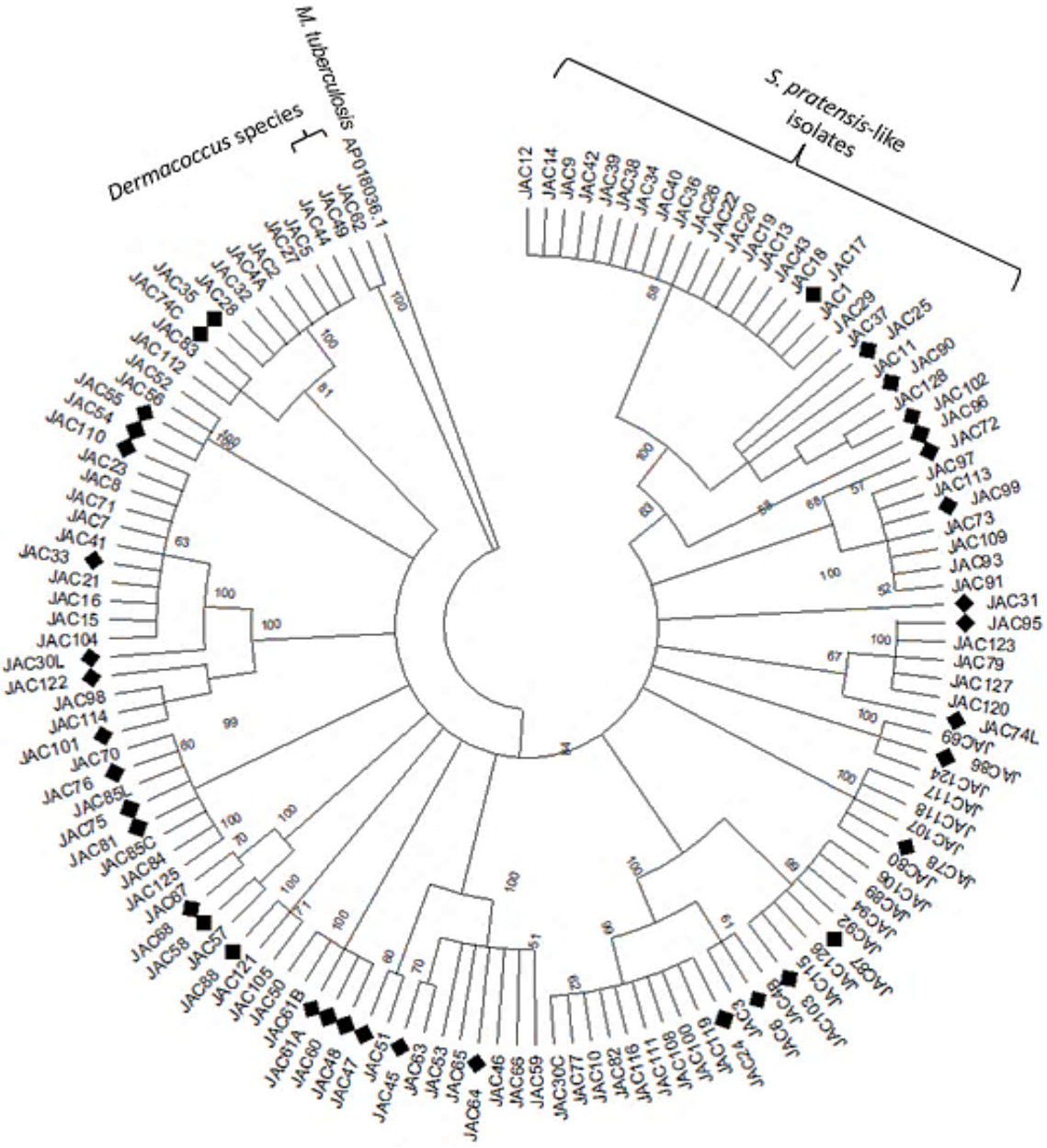

Figure 3.1.1: Phylogenetic comparison of *Streptomyces* isolates in this study. The tree consists of 133 *Streptomyces* isolates *rpoB* gene sequences condensed into 31 OTUs. The tree was constructed with 618 nucleotide sequence lengths using 100 bootstraps replicates. A minimum of 50% consensus cut-off value was used to create the tree branches. Isolates defined as one OTU *rpoB* sequences were verified to be 100% identity. ♦ denotes isolates selected for VOC analysis. *Mycobacterium tuberculosis* served as an outgroup.

3.2: The *Streptomyces* isolates had various phenotypes

The lawn morphology of each *Streptomyces* isolates grown on ISP-4 medium was determined, and they were tested on nutrient agar for apramycin, kanamycin, and thiostrepton susceptibility (Table 3.2.1). The isolates that displayed resistance to the respective antibiotics probably harbour antibiotic resistance genes (Van Hoek et al., 2011), which may allude to their ability to produce similar or related antibiotics (Peterson & Kaur, 2018).

The growth of the *Streptomyces* isolates on solid fermentation media used in this study was also tested. All *Streptomyces* grew successfully on the three media except for a few (Table 3.2.1). The media included SFM, used to encourage VOC production by *Streptomyces* species in other studies (Citron, Gleitzmann, et al., 2012; Citron, Rabe, et al., 2012; Komatsu et al., 2008; Rabe et al., 2013; Riclea et al., 2012); a synthetic and minimal medium used previously to promote geosmin production (Cane et al., 2006; Jáchymová et al., 2002); and YMS (Ikeda et al., 1987), a general *Streptomyces* specialized metabolite test medium.

Thirty-seven *Streptomyces* isolates representing each OTU were selected for VOC analysis (Figure 3.1.1). A maximum of three Streptomyces isolates was chosen from one OTU in a few cases as bacteria with identical *rpoB* gene sequences might have differences in specialized metabolism (Antony-Babu et al., 2017). Bacteria from OTUs containing single isolates were selected for VOC analysis regardless of their growth on all three-fermentation media used in the study. Growth on at least one of the fermentation media was sufficient for the selection of such isolates. Therefore, all phylogenetically different

Table 3.2.1: Characteristics of *Streptomyces* isolates from this study.

Isolate	Growth on ISP-4 medium				Antibiotic resistance	Growth on fermentation media		
	Growth	Sporul-ation	lawn color	diffusible pigment		SFM	Synthetic	YMS
JAC1	+++	+++	white	-	-	**	**	**
JAC2	++	+	cream	-	-	**	**	**
JAC3	+++	+++	cream	red-brown	-	**	**	**
JAC4A	+++	+++	white	-	-	**	**	**
JAC4B	+++	+++	dark yellow and mucoid	red-brown	-	**	**	**
JAC5	+	+	translucent	-	-	-	-	-
JAC6	+++	+++	cream	red-brown	-	**	**	**
JAC7	++	+	cream and translucent	brown	-	**	**	**
JAC8	+++	+	cream	-	-	**	*	**
JAC9	+++	+++	white	-	-	**	**	**
JAC10	+++	+++	cream	red-brown	-	**	**	**
JAC11	+++	+++	white	-	-	**	**	**
JAC12	+++	+++	white	-	-	**	**	**
JAC13	+++	+++	white	-	-	**	**	**
JAC14	+++	++	white	-	-	**	**	**
JAC15	++	+	cream	brown	-	**	**	**
JAC16	++	+	cream	brown	-	**	**	**
JAC17	+++	+++	white	-	-	**	**	**
JAC18	+++	++	white	-	-	**	**	**
JAC19	+++	++	white	-	-	**	**	**
JAC20	+++	+++	white	-	-	**	**	**
JAC21	+++	+	cream	brown	-	-	-	*
JAC22	+++	+++	white	-	-	**	**	**
JAC23	+++	+++	cream	brown	-	**	**	**
JAC24	+++	+++	cream	brown	-	**	**	**
JAC25	+++		white	-	-	**	**	**
JAC26	+++	+++	white	-	-	**	**	**
JAC27	+++	+++	white	-	-	**	**	**
JAC28	+++	+++	white	-	-	**	**	**
JAC29	+++	+++	white	-	-	**	**	**
JAC30C	+++	+++	purple	dark purple	-	**	**	**
JAC30L	+++	+	white	-	-	**	**	**

JAC31	+++		cream	-	-	**	**	**
JAC32	+++	+++	grey	-	-	**	**	**
JAC33	+++	+	white	-	-	**	**	**
JAC34	+++	+++	grey	-	-	**	**	**
JAC35	+++	+++	white	slight orange	-	**	**	**
JAC36	+++	+++	grey	-	-	**	**	**
JAC37	+++	+++	grey	-	-	**	**	**
JAC38	+++	+++	grey	-	-	**	**	**
JAC39	+++	+++	grey	-	-	**	**	**
JAC40	+++	+++	grey	-	-	**	**	**
JAC41	+++	+++	white	dark purple	-	**	**	**
JAC42	+++	+++	white with grey spores	-	-	**	**	**
JAC43	+++	+++	white with grey spores	-	-	**	**	**
JAC44	+++	+++	white	-	-	**	**	**
JAC45	+++	+++	white with grey spores	pink	-	**	**	**
JAC46	+++	+++	white with grey spores	pink	-	**	**	**
JAC47	+++	+++	white with grey spores	pink	-	**	**	**
JAC48	+++	+++	black	golden yellow	-	**	**	**
JAC49	+++	+++	yellow and mucoid	-	thio	**	**	**
JAC50	+++	+++	white with grey spores	golden yellow	-	**	**	**
JAC51	+++	+	grey	pink	-	**	**	**
JAC52	+++	++	grey	-	-	**	**	**
JAC53	+++	++	white	slight pink	-	**	**	**
JAC54	+++	++	grey	-	-	**	**	**
JAC55	+++	++	grey	-	-	**	**	**
JAC56	+++	++	grey	-	-	**	**	**
JAC57	+++	++	grey	-	-	**	**	**
JAC58	+++	+++	grey	-	-	**	**	**
JAC59	+++	+++	grey	slight pink	-	**	**	**
JAC60	+++	+++	slight pink with grey spores	golden yellow	-	**	**	**
JAC61A	+++	+++	brown	yellow	-	**	**	**
JAC61B	+++	-	orange, sporulation not obvious	orange	-	**	**	**

JAC62	+++	+	orange and mucoid	-	apra, kan, thio	**	**	**
JAC63	+++	++	grey	slight pink	-	**	**	**
JAC64	+++	+++	grey	slight	-	**	**	**
JAC65	+++	+++	white with grey spores	slight orange/pink	-	**	**	**
JAC66	+++	+++	white with grey spores	slight orange/pink	-	**	**	**
JAC67	+++	+++	grey	-	-	**	**	**
JAC68	+++	+++	grey	-	-	**	**	**
JAC69	+++	++	white	-	-	**	**	**
JAC70	+++	+++	grey	dark green/brown	-	**	**	**
JAC71	+++	+	grey	brown/slight orange	-	**	**	**
JAC72	+++	+++	white	slight yellow	-	**	**	**
JAC73	+++	+++	white with grey spores	yellow	-	**	**	**
JAC74C	+++	+++	dark grey	dark green	-	**	**	**
JAC74L	+++	+++	light grey	-	-	**	**	**
JAC75	+++	+++	green with grey spores	brown	-	**	**	**
JAC76	+++	+++	white with grey spores	-	-	**	**	**
JAC77	+++	+++	grey	dark purple	-	**	**	**
JAC78	+++	+++	white	-	-	**	**	**
JAC79	++	+	white and translucent	brown	-	**	**	**
JAC80	+++	+++	white and translucent	-	-	-	-	**
JAC81	+++	++	grey	brown	-	**	**	**
JAC82	+++	+++	grey	dark purple	-	**	**	**
JAC83	+++	+++	grey	black/ dark green	-	**	**	**
JAC84	+++	++	white with grey spores	brown	-	**	**	**
JAC85C	++	++	white	brown	-	**	**	**
JAC85L	+++	+++	dark grey with light grey spores	dark green	-	**	**	**
JAC86	+++	+++	black with grey spores	slight pink	-	**	**	**
JAC87	+++	+++	dark grey	black/ grey	-	**	**	**
JAC88	++	+	white and translucent	-	-	**	**	**
JAC89	+++	+++	black and mucoid	black/ grey	-	**	**	**

JAC90	++	+++	dark grey	-	-	**	**	**
JAC91	+++	+++	white with grey spores	yellow	-	**	**	**
JAC92	+++	+++	dark grey	grey/ black	-	**	**	**
JAC93	+++	+++	white with grey spores	yellow	-	**	**	**
JAC94	+++	+++	grey and translucent	grey	-	**	**	**
JAC95	++	+	white and translucent	-	-	**	**	**
JAC96	++	+	white	-	-	-	*	**
JAC97	+++	++	white	yellow	-	**	**	**
JAC98	+	+	translucent	-	-	**	*	*
JAC99	+++	++	white	yellow	-	**	**	**
JAC100	+++	+++	dark grey	dark purple	-	**	**	**
JAC101	+	+	grey	-	-	**	**	**
JAC102	+++	+++	grey	-	-	**	**	**
JAC103	+++	+++	translucent	brown	-	**	**	**
JAC104	+	+	white and translucent	-	-	**	**	**
JAC105	+++	+++	white	slight pink	-	**	**	**
JAC106	+++	+++	dark grey	dark green/ black	-	**	**	**
JAC107	+++	+++	grey	slight orange	-	**	**	**
JAC108	+++	+	red and mucoid	dark purple	thio	**	**	**
JAC109	+++	++	white	yellow	-	**	**	**
JAC110	+++	+++	grey	-	thio	**	**	**
JAC111	+++	+++	red and mucoid	dark purple	thio	**	**	**
JAC112	+++	+++	grey	black/ grey	-	**	-	**
JAC113	+++	++	white	yellow	-	**	**	**
JAC114	++	+	grey	-	-	**	*	**
JAC115	+++	+++	dark grey	black grey	-	**	**	**
JAC116	+++	+++	red	dark purple	kan, thio	**	**	**
JAC117	+++	+++	white	slight orange	-	-	-	**
JAC118	+++	+++	white	slight orange	-	-	-	**
JAC119	+++	+	brown and translucent	brown	-	**	**	**
JAC120	+++	+++	dark grey	yellow	apra	**	**	**
JAC121	+++	+	translucent	-	-	**	**	**
JAC122	+++	+	yellow and mucoid	yellow	kan	**	**	**

JAC123	+++	+++	grey	red-brown	-	**	**	**
JAC124	+++	+++	white	slight yellow	-	*	-	**
JAC125	+++	+++	light grey	slight brown	-	**	**	**
JAC126	+++	+	white	slight yellow	-	**	**	**
JAC127	+++	+++	white	-	-	**	**	**
JAC128	+++	++	translucent	slight green	-	**	**	**

\+ poor growth or sporulation on ISP-4 medium.
++ some (not good but not poor) growth or sporulation on ISP-4 medium.
+++ good growth or sporulation on ISP-4 medium.
\- antibiotic susceptibility, no diffusible pigment, or no growth on selected fermentation media.
** good growth observed on select fermentation media.
* poor growth on select fermentation media.
apra means resistance to apramycin antibiotic at 50 µg/ml.
kan means resistance to kanamycin antibiotic at 50 µg/ml.
thio means resistance to thiostrepton antibiotic at 25 µg/ml.

Streptomyces isolates were selected to capture the full range of VOCs that the collection of bacteria could produce.

3.3: VOC analysis

3.3.1: Screening of VOC production by select *Streptomyces* isolates

The 37 *Streptomyces* isolates representing each OTU were grown in the three fermentation media, SFM, YMS, and the synthetic medium. The cultures were pooled together for VOC collection and GC-MS analysis. The VOCs identifications were primarily based on spectra availability in the NIST library, and the stereochemistry assigned should be interpreted with caution. It was assumed that not all compounds present in the samples were identified due to limitations in the identification procedure. One hundred and sixty-three bacterially derived VOCs were detected from the 37 *Streptomyces* isolates and were further classified based on the level of confidence in their identities (Figure 3.3.1.1 and Table 3.3.1.1). Those compounds with a high confidence level identity were further divided into major VOC classes, of which the alcohols were the most common (Table 3.3.1.2). There were more unknown compounds than those identified with high or low confidence, where 116 VOCs did not have published RI values for comparison. Therefore, there may be novel VOCs in the 116 unknown compounds with potentially useful bioactivities. Forty-nine of the bacterially derived VOCs were produced by isolates from more than one OTU, and 22 of those were from two of the 30 OTUs in the current study. Geosmin, [4a(2H)-Naphthalenol, octahydro-4,8a-dimethyl-,(4.alpha.,4a.alpha.,8a.beta.)- or trans-1,10-Dimethyl-trans-9-decalol], was the most common VOCs detected in 23 isolates (VOC 27 in Table 3.3.1.1). Compounds detected in single OTUs totalled 114 (Table 3.3.1.2),

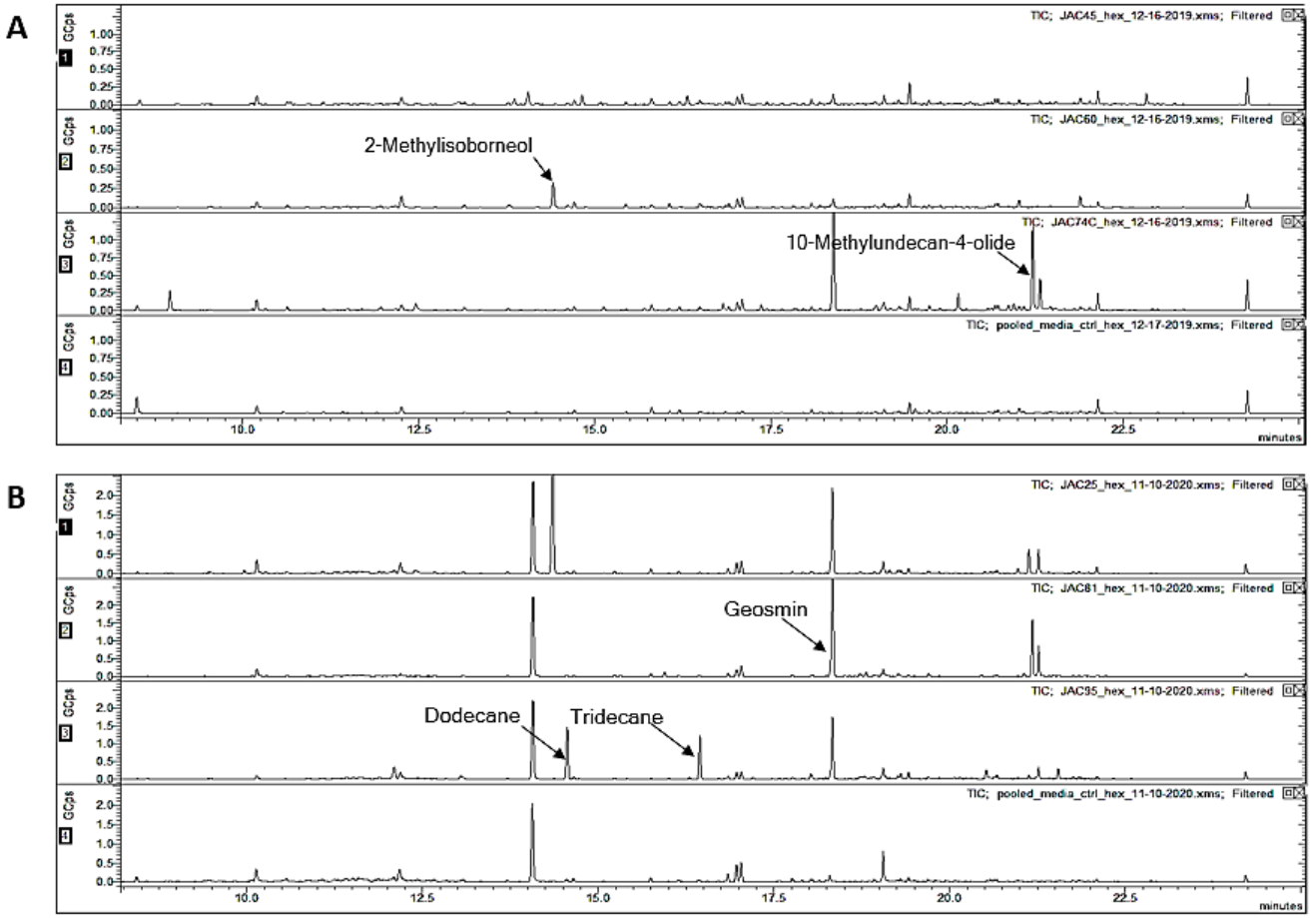

Figure 3.3.1.1: Example view (~9- 23 min) of pooled culture GC-MS chromatograms for six *Streptomyces* isolates. Some prominent peaks with >38% identity to NIST reference spectra are labelled. GC-MS analysis was done for cultures fermented in two batches of media for isolates (top to bottom) **A.** JAC45, JAC60, JAC74C, and a pooled media control **B.** JAC25, JAC81, JAC95, and a pooled media control.

Table 3.3.1.1: Bacterially derived compounds detected in pooled culture VOC analysis.

No.	VOC [a]	IUPAC name	RT	RT Stdev [b]	Detected in	Confidence in the VOC ID [c]	Detected in >1 OTU [d]
1	(R)-(+)-3-Methylcyclopentanone	(3*R*)-3-methylcyclopentan-1-one	5.742	0.000	JAC6	high	no
2	1-Hexanol	hexan-1-ol	6.223	0.034	JAC60, JAC61A	high	no
3	1-Octen-3-ol	oct-1-en-3-ol	8.963	0.000	JAC74C	high	no
4	3-Octanone	octan-3-one	9.038	0.000	JAC122	high	no
5	Ethanol, 2-(2-ethoxyethoxy)-	2-(2-ethoxyethoxy)ethanol	9.425	0.000	JAC17	high	no
6	2-Methyl-2-bornene	1,2,7,7-tetramethylbicyclo[2.2.1]hept-2-ene	9.964	0.000	JAC25	high	no
7	2,6-Octadienoic acid, 3,7-dimethyl-, methyl ester	methyl (2E)-3,7-dimethylocta-2,6-dienoate	16.820	0.000	JAC74C	high	no
8	2,4-Furandicarboxylic acid, dimethyl ester	dimethyl furan-2,4-dicarboxylate	17.364	0.000	JAC74C	high	no
9	1H-Benzocycloheptene, 2,4a,5,6,7,8,9,9a-octahydro-3,5,5-trimethyl-9-methylene-, (4aS-cis)- Alpha-Himachalene [e]	3,5,5-trimethyl-9-methylidene-2,4a,6,7,8,9a-hexahydro-1H-benzo[7]annulene	18.341	0.000	JAC102	high	no
10	1-Dodecanol	dodecan-1-ol	19.054	0.000	JAC68	high	no
11	Dodecanoic acid, methyl ester	methyl dodecanoate	19.695	0.000	JAC35	high	no
12	Cyclohexanemethanol, 4-ethenyl-.alpha.,.alpha.,4-trimethyl-3-(1-methylethenyl)-, [1R-(1.alpha.,3.alpha.,4.beta.)]- Elemol group [e]	2-(4-ethenyl-4-methyl-3-prop-1-en-2-ylcyclohexyl)propan-2-ol	20.162	0.000	JAC74C	high	no

13	Pentanoic acid, 2,2,4-trimethyl-3-carboxyisopropyl, isobutyl ester	1-O-(2-methylpropyl) 4-O-propan-2-yl 2,2-dimethyl-3-propan-2-ylbutanedioate	20.535	0.000	JAC122	high	no
14	Cetene	hexadec-1-ene	20.633	0.000	JAC47	high	no
15	DL-2,3-Butanediol	butane-2,3-diol	4.894	0.003	JAC17, JAC47	high	yes
16	Hexanenitrile	hexanenitrile	6.403	0.025	JAC60, JAC78, JAC61A	high	yes
17	Pyrazine, 2,5-dimethyl-	2,5-dimethylpyrazine	7.230	0.012	JAC17, JAC24, JAC31, JAC33, JAC47, JAC64, JAC78, JAC74C, JAC25, JAC35, JAC96, JAC110, JAC74L, JAC61A, JAC30L, JAC87, JAC81	high	yes
18	Methyl 2-methylhexanoate	methyl 2-methylhexanoate	8.537	0.001	JAC45, JAC64	high	yes
19	Benzyl alcohol	phenylmethanol	10.290	0.027	JAC17, JAC58, JAC25, JAC122, JAC30L	high	yes
20	1-Octanol	octan-1-ol	11.282	0.002	JAC99, JAC101, JAC64	high	yes
21	Undecane	Undecane	12.099	0.001	JAC95, JAC6, JAC122	high	yes
22	Phenylethyl Alcohol	2-phenylethanol	12.432	0.032	JAC17, JAC31, JAC86, JAC101, JAC33, JAC58, JAC74C, JAC25, JAC110, JAC74L, JAC30L	high	yes
23	Cyclopropane, pentyl-	pentylcyclopropane	12.917	0.001	JAC99, JAC101	high	yes

24	2-Methylisoborneol	1,2,7,7-tetramethylbicyclo[2.2.1]heptan-2-ol	14.380	0.032	JAC102, JAC99, JAC31, JAC101, JAC60, JAC78, JAC25, JAC72, JAC55, JAC54, JAC61A, JAC90	high	yes
25	Dodecane	dodecane	14.560	0.001	JAC95, JAC6, JAC122, JAC68	high	yes
26	heptylcyclohexane	heptylcyclohexane	17.204	0.000	JAC95, JAC6, JAC122, JAC68	high	yes
27	4a(2H)-Naphthalenol, octahydro-4,8a-dimethyl-,(4.alpha.,4a.alpha.,8a.beta.)- trans-1,10-Dimethyl-trans-9-decalol Geosmin [e]	(4S,4aS,8aR)-4,8a-dimethyl-1,2,3,4,5,6,7,8-octahydronaphthalen-4a-ol	18.356	0.014	JAC95, JAC35, JAC88, JAC55, JAC110, JAC74L, JAC54, JAC61A, JAC75, JAC90, JAC87, JAC78, JAC25, JAC81, JAC102, JAC31, JAC86, JAC101, JAC33, JAC76, JAC47, JAC64, JAC74C	high	yes
28	1,6-Cyclodecadiene, 1-methyl-5-methylene-8-(1-methylethyl)-, [S-(E,E)]- Germacrene D [e]	(1Z,6Z)-1-methyl-5-methylidene-8-propan-2-ylcyclodeca-1,6-diene	19.270	0.002	JAC25, JAC81	high	yes
29	epi-cubenol	(1S,4R,4aS,8aR)-4,7-dimethyl-1-propan-2-yl-2,3,4,5,6,8a-hexahydro-1H-naphthalen-4a-ol	21.128	0.001	JAC25, JAC95, JAC90, JAC87	high	yes

30	1-Naphthalenol, 1,2,3,4,4a,7,8,8a-octahydro-1,6-dimethyl-4-(1-methylethyl)-, [1R-(1.alpha.,4.beta.,4a.beta.,8a.beta.)]- Cadinol [e]	(1R,4S)-1,6-dimethyl-4-propan-2-yl-3,4,4a,7,8,8a-hexahydro-2H-naphthalen-1-ol	21.182	0.003	JAC17, JAC102, JAC24, JAC86	high	yes
31	cubenol	(1S,4R,4aR,8aR)-4,7-dimethyl-1-propan-2-yl-2,3,4,5,6,8a-hexahydro-1H-naphthalen-4a-ol	21.277	0.024	JAC47, JAC25, JAC110, JAC74L, JAC81	high	yes
32	2-Naphthalenemethanol, decahydro-α,α,4a-trimethyl-8-methylene-, [2R-(2α,4aα,8aβ)]- β-Selinenol [e]	2-(4*a*-methyl-8-methylidene-1,2,3,4,5,6,7,8*a*-octahydronaphthalen-2-yl)propan-2-ol	21.320	0.001	JAC86, JAC101, JAC33, JAC76, JAC74C	high	yes
33	Methyl tetradecanoate	methyl tetradecanoate	22.094	0.001	JAC35, JAC110, JAC74L	high	yes
34	Toluene-Dup1 [f]	[g]	4.322	0.000	JAC103	low	no
35	3-Hexanone, 5-methyl-	5-methylhexan-3-one	5.486	0.000	JAC64	low	no
36	Cyclohexane, 1,1,2-trimethyl-	1,1,2-trimethylcyclohexane	6.691	0.000	JAC99	low	no
37	7-Tetradecene	(E)-tetradec-7-ene	19.307	0.000	JAC35	low	no
38	10-Methylundecan-4-olide	5-(6-methylheptyl)oxolan-2-one	21.220	0.000	JAC74C	low	no
39	7-epi-.alpha.-eudesmol	2-[(2S,4aR)-4a,8-dimethyl-2,3,4,5,6,8a-hexahydro-1H-naphthalen-2-yl]propan-2-ol	21.599	0.000	JAC86	low	no
40	10-epi-.gamma.-Eudesmol	2-(4a,8-dimethyl-2,3,4,5,6,7-hexahydro-1H-naphthalen-2-yl)propan-2-ol	21.655	0.000	JAC31	low	no
41	10-Methyldodecan-5-olide	6-(5-methylheptyl)oxan-2-one	22.831	0.000	JAC45	low	no
42	3-Hexanone	hexan-3-one	4.493	0.030	JAC99, JAC76, JAC48, JAC6	low	yes

43	Cyclopentanol, 1-methyl-	1-methylcyclopentan-1-ol	4.676	0.012	JAC99, JAC103, JAC76, JAC48	low	yes
44	Dodecane, 2,6,10-trimethyl-	2,6,10-trimethyldodecane	18.875	0.001	JAC6, JAC68, JA95	low	yes
	Farnesane [e]						
45	Alloaromadendrene	1,1,7-trimethyl-4-methylidene-2,3,4a,5,6,7,7a,7b-octahydro-1aH-cyclopropa[e]azulene	21.265	0.002	JAC88, JAC75, JAC87	low	yes
46	7-epi-.alpha.-selinene	5,8a-dimethyl-3-prop-1-en-2-yl-2,3,4,4a,7,8-hexahydro-1H-naphthalene	21.544	0.000	JAC95, JAC87	low	yes
47	1-Nonadecene	nonadec-1-ene	21.757	0.000	JAC110, JAC74L	low	yes
48	Propanedioic acid, (bromomethyl)methyl-, bis(1,1-dimethylethyl) ester	ditert-butyl 2-(bromomethyl)-2-methylpropanedioate	4.019	0.000	JAC61A	unknown	no
49	t-Butyl cyclopentaneperoxycarboxylate	tert-butyl cyclopentanecarboperoxoate	4.026	0.000	JAC96	unknown	no
50	t-Butyl cyclopentaneperoxycarboxylate-Dup1 [f]	[g]	4.057	0.000	JAC96	unknown	no
51	1-n-Butoxy-2,3-dimethyldiaziridine	1-butoxy-2,3-dimethylaziridine	4.065	0.000	JAC75	unknown	no
52	(S)-3,4-Dimethylpentanol	(3S)-3,4-dimethylpentan-1-ol	4.129	0.000	JAC122	unknown	no
53	1-Heptene, 3-methoxy-	3-methoxyhept-1-ene	4.268	0.000	JAC74C	unknown	no
54	Propanoic acid, 2-methyl-, 2-ethyl-1-propyl-1,3-propanediyl ester	[2-ethyl-3-(2-methylpropanoyloxy)hexyl] 2-methylpropanoate	4.273	0.000	JAC64	unknown	no
55	2-Hexanone, 6-methoxy-	6-methoxyhexan-2-one	4.290	0.000	JAC6	unknown	no
56	2-Buten-1-ol, 2-methyl-	(E)-2-methylbut-2-en-1-ol	4.316	0.000	JAC74C	unknown	no
57	Sulfurous acid, isobutyl pentyl ester	2-methylpropyl pentyl sulfite	4.485	0.000	JAC103	unknown	no

58	2-Hexanone	hexan-2-one	4.523	0.000	JAC6	unknown	no
59	(2,3,3-Trimethyloxiranyl)methanol	(2,3,3-trimethyloxiran-2-yl)methanol	4.714	0.000	JAC88	unknown	no
60	meso-3,4-Hexanediol	hexane-3,4-diol	4.724	0.000	JAC30L	unknown	no
61	(S)-3,4-Dimethylpentanol	(3S)-3,4-dimethylpentan-1-ol	4.744	0.000	JAC87	unknown	no
62	2-Methyl-2,3-pentanediol	2-methylpentane-2,3-diol	4.757	0.000	JAC17	unknown	no
63	2-Hexanol	hexan-2-ol	4.766	0.000	JAC88	unknown	no
64	DL-2,3-Butanediol	butane-2,3-diol	4.798	0.000	JAC103	unknown	no
65	Methyl 2-methoxypropenoate	methyl 2-methoxyprop-2-enoate	4.824	0.000	JAC30L	unknown	no
66	Propanoic acid, 2,2-dimethyl-, 2,4-dinitrophenyl ester	(2,4-dinitrophenyl) 2,2-dimethylpropanoate	5.488	0.000	JAC45	unknown	no
67	2-Furanmethanol	furan-2-ylmethanol	5.826	0.000	JAC30L	unknown	no
68	2-Butenoic acid, 2-methyl-, methyl ester	methyl (E)-2-methylbut-2-enoate	6.158	0.000	JAC74C	unknown	no
69	Butanedioic acid, phenyl-	2-phenylbutanedioic acid	6.733	0.000	JAC88	unknown	no
70	Vinyl butyrate	ethenyl butanoate	6.751	0.000	JAC61A	unknown	no
71	Carbonic acid, bis(1-methylethyl) ester	dipropan-2-yl carbonate	6.791	0.000	JAC33	unknown	no
72	4-Octanol, 2-methyl-	2-methyloctan-4-ol	6.918	0.000	JAC99	unknown	no
73	1,6:3,4-Dianhydro-2-deoxy-.beta.-d-ribo-hexopyranose	3,7,9-trioxatricyclo[4.2.1.02,4]nonane	8.253	0.000	JAC88	unknown	no
74	Dimethyl trisulfide	(methyltrisulfanyl)methane	8.636	0.000	JAC90	unknown	no
75	Formic acid, heptyl ester	heptyl formate	8.714	0.000	JAC99	unknown	no
76	3(2H)-Thiophenone, dihydro-2-methyl-	2-methylthiolan-3-one	9.139	0.000	JAC96	unknown	no
77	3-Octanol	octan-3-ol	9.342	0.000	JAC122	unknown	no
78	4-Octene, 2,3,7-trimethyl-, [S-(E)]-	(E,3S)-2,3,7-trimethyloct-4-ene	9.601	0.000	JAC25	unknown	no

79	Tricyclo[2.2.1.0(1,4)]heptan-2-one, 6-nitro-	6-nitrotricyclo[2.2.1.01,4]heptan-2-one	9.615	0.000	JAC58	unknown	no
80	4-Nonene, 3-methyl-, (Z)-	3-methylnon-4-ene	10.026	0.000	JAC31	unknown	no
81	Tricyclo[3.2.1.0(2,4)]octane, 8-methylene-, (1.alpha.,2.alpha.,4.alpha.,5.alpha.)-	8-methylidenetricyclo[3.2.1.02,4]octane	10.075	0.000	JAC35	unknown	no
82	6-Azabicyclo[3,2,0]heptan-7-one	6-azabicyclo[3.2.0]heptan-7-one	10.079	0.000	JAC61A	unknown	no
83	Cyclopropane, 1-butyl-2-(2-methylpropyl)-	1-butyl-2-(2-methylpropyl)cyclopropane	10.337	0.000	JAC87	unknown	no
84	Propanoic acid, 3-chloro-, 4-formylphenyl ester	(4-formylphenyl) 3-chloropropanoate	10.547	0.000	JAC54	unknown	no
85	DL-4,5-Octanediol	octane-4,5-diol	11.475	0.000	JAC17	unknown	no
86	6-Dodecene, (E)-	(E)-dodec-6-ene	12.024	0.000	JAC87	unknown	no
87	1-Octanol, 2-butyl-	2-butyloctan-1-ol	12.098	0.000	JAC35	unknown	no
88	Hydrazine, (phenylmethyl)-	benzylhydrazine	12.396	0.000	JAC55	unknown	no
89	Bicyclo[3.2.0]hepta-2,6-diene	bicyclo[3.2.0]hepta-2,6-diene	12.400	0.000	JAC90	unknown	no
90	Cyclopropane, 1-butyl-2-(2-methylpropyl)-	1-butyl-2-(2-methylpropyl)cyclopropane	13.103	0.000	JAC86	unknown	no
91	Iron, tricarbonyl[(2,3,4,5-.eta.)-2,4-cycloheptadien-1-ol]-	[g]	13.856	0.000	JAC45	unknown	no
92	Benzene, (iodomethyl)-	iodomethylbenzene	13.969	0.000	JAC30L	unknown	no
93	Benzene, [(methylsulfonyl)methyl]-	methylsulfonylmethylbenzene	14.023	0.000	JAC58	unknown	no
94	Iron, tricarbonyl[(2,3,4,5-.eta.)-2,4-cycloheptadien-1-ol]--Dup1 [f]	[g]	14.818	0.000	JAC45	unknown	no
95	Sydnone, 3-(phenylmethyl)-	3-benzyl-2H-oxadiazol-3-ium-5-one	14.820	0.000	JAC64	unknown	no
96	Benzothiazole	1,3-benzothiazole	15.082	0.000	JAC61A	unknown	no

97	6-Octen-1-ol, 3,7-dimethyl-, formate	3,7-dimethyloct-6-enyl formate	15.123	0.000	JAC74C	unknown	no
98	(2S,4R)-p-Mentha-[1(7),8]-diene 2-hydroperoxide	2-hydroperoxy-1-methylidene-4-prop-1-en-2-ylcyclohexane	15.292	0.000	JAC86	unknown	no
99	(1,2,2-trimethyl-3-cyclopenten-1-yl)acetaldehyde	2-(1,2,2-trimethylcyclopent-3-en-1-yl)acetaldehyde	15.315	0.000	JAC81	unknown	no
100	Phenol, 4-[2-(methylamino)ethyl]-	4-[2-(methylamino)ethyl]phenol	15.317	0.000	JAC25	unknown	no
101	Bicyclo[3.1.1]heptane, 6,6-dimethyl-2-methylene-, (1S)- β-pinene [e]	6,6-dimethyl-2-methylidenebicyclo[3.1.1]heptane	15.528	0.000	JAC122	unknown	no
102	2-Hydroxy-5-ethyl-5-methylcyclopent-2-en-1-one	5-ethyl-2-hydroxy-5-methylcyclopent-2-en-1-one	15.944	0.000	JAC81	unknown	no
103	3-Hexadecene, (Z)-	(Z)-hexadec-3-ene	16.299	0.000	JAC122	unknown	no
104	1-Tridecene	tridec-1-ene	16.300	0.000	JAC6	unknown	no
105	Tricyclo[4.1.0.0(2,7)]heptane	tricyclo[4.1.0.02,7]heptane	16.311	0.000	JAC47	unknown	no
106	Phenylacetaldehyde N-methyl-N-formylhydrazone	N-methyl-N-[(E)-2-phenylethylideneamino]formamide	16.707	0.000	JAC25	unknown	no
107	1-Methylene-2b-hydroxymethyl-3,3-dimethyl-4b-(3-methylbut-2-enyl)-cyclohexane	[2,2-dimethyl-4-(3-methylbut-2-enyl)-6-methylidenecyclohexyl]methanol	18.507	0.000	JAC81	unknown	no
108	1-Methylene-2b-hydroxymethyl-3,3-dimethyl-4b-(3-methylbut-2-enyl)-cyclohexane-Dup1 [f]	[g]	18.575	0.000	JAC81	unknown	no
109	(3R,2E)-2-(Hexadec-15-ynylidene)-3-hydroxy-4-methylenebutanolide	(3E,4R)-3-hexadec-15-ynylidene-4-hydroxy-5-methylideneoxolan-2-one	18.654	0.000	JAC81	unknown	no
110	1,4-Dimethyladamantane #	1,4-dimethyladamantane	18.726	0.000	JAC95	unknown	no

111	Cyclobutaneacetonitrile, 1-methyl-2-(1-methylethylidene)-	2-(1-methyl-2-propan-2-ylidenecyclobutyl)acetonitrile	18.780	0.000	JAC86	unknown	no
112	Pyrrol-2(5H)-one, 4-acetyl-3-hydroxy-5-(3-nitrophenyl)-1-[2-(1-piperazinyl)ethyl]-	3-acetyl-4-hydroxy-2-(3-nitrophenyl)-1-(2-piperazin-1-ylethyl)-2H-pyrrol-5-one	18.795	0.000	JAC87	unknown	no
113	4,7-Methanoazulene, 1,2,3,4,5,6,7,8-octahydro-1,4,9,9-tetramethyl-, [1S-(1.alpha.,4.alpha.,7.alpha.)]- β-Patchoulene [e]	1,5,11,11-tetramethyltricyclo[6.2.1.02,6]undec-2(6)-ene	18.812	0.000	JAC81	unknown	no
114	n-Hexyl methylphosphonofluoridate	1-[fluoro(methyl)phosphoryl]oxyhexane	18.841	0.000	JAC86	unknown	no
115	trans,trans- and trans,cis-1,8-Dimethylspiro[5.5]undecane	4,11-dimethylspiro[5.5]undecane	18.950	0.000	JAC86	unknown	no
116	3-Isopropoxy-1,1,1,7,7,7-hexamethyl-3,5,5-tris(trimethylsiloxy)tetrasiloxane	propan-2-yl bis(trimethylsilyl) tris(trimethylsilyloxy)silyl silicate	18.960	0.000	JAC87	unknown	no
117	5,10-Pentadecadiyn-1-ol	pentadeca-5,10-diyn-1-ol	18.969	0.000	JAC81	unknown	no
118	tert-Butyl 3-methylbutyl disulfide	1-(tert-butyldisulfanyl)-3-methylbutane	18.977	0.000	JAC33	unknown	no
119	2H-Benzocyclohepten-2-one, decahydro-4a-methyl-, trans-	4a-methyl-3,4,5,6,7,8,9,9a-octahydro-1H-benzo[7]annulen-2-one	19.147	0.000	JAC25	unknown	no
120	6-Tridecene	(E)-tridec-6-ene	19.307	0.000	JAC88	unknown	no
121	Dichlorphen, O,O'-bis(4-fluoro-2-trifluoromethylbenzoyl)-	[4-chloro-2-[[5-chloro-2-[4-fluoro-2-(trifluoromethyl)benzoyl]oxyphenyl]methyl]phenyl] 4-fluoro-2-(trifluoromethyl)benzoate	19.496	0.000	JAC61A	unknown	no

122	Benzoic acid, 4-ethoxy-, ethyl ester	ethyl 4-ethoxybenzoate	19.728	0.000	JAC88	unknown	no
123	Cyclohexanol, 4-ethyl-4-methyl-3-(1-methylethyl)-, (1.alpha.,3.alpha.,4.beta.)-	4-ethyl-4-methyl-3-propan-2-ylcyclohexan-1-ol	20.279	0.000	JAC87	unknown	no
124	2,7-Octadiene-1,6-diol, 2,6-dimethyl-, (E)-	(2E)-2,6-dimethylocta-2,7-diene-1,6-diol	20.454	0.000	JAC81	unknown	no
125	Naphthalene, 1,2,4a,5,6,8a-hexahydro-4,7-dimethyl-1-(1-methylethyl)- α-Amorphene [e]	4,7-dimethyl-1-propan-2-yl-1,2,4a,5,6,8a-hexahydronaphthalene	20.502	0.000	JAC25	unknown	no
126	1-Hexyl-2-nitrocyclohexane	1-hexyl-2-nitrocyclohexane	20.947	0.000	JAC74C	unknown	no
127	Hexanethioic acid, S-methyl ester	S-methyl hexanethioate	21.058	0.000	JAC81	unknown	no
128	Dihydro-cis-.alpha.-copaene-8-ol-Dup1 [f]	[g]	21.267	0.000	JAC95	unknown	no
129	3,4-Nonadien-6-yne, 5-ethyl-3-methyl-	5-Ethyl-3-methyl-3,4-nonadien-6-yne	21.482	0.000	JAC81	unknown	no
130	1-Allyl-cyclohexane-1,2-diol	1-prop-2-enylcyclohexane-1,2-diol	21.544	0.000	JAC81	unknown	no
131	10-Heneicosene (c,t)	(E)-henicos-10-ene	21.758	0.000	JAC25	unknown	no
132	Cyclohexene, 1,5,5-trimethyl-6-(2-propenylidene)-	(6Z)-1,5,5-trimethyl-6-prop-2-enylidenecyclohexene	21.921	0.000	JAC81	unknown	no
133	Benzoic acid, 3-fluoro-, 2-oxo-2-phenylethyl ester	phenacyl 3-fluorobenzoate	21.976	0.000	JAC25	unknown	no
134	Cyclohexanol, 1-ethyl-2,2-dimethyl-6-methylene-	1-ethyl-2,2-dimethyl-6-methylidenecyclohexan-1-ol	22.219	0.000	JAC81	unknown	no
135	5,6-Decadien-3-yne, 5,7-diethyl-	[g]	24.274	0.000	JAC35	unknown	no
136	1-Nitrosoadamantane	1-nitrosoadamantane	24.376	0.000	JAC35	unknown	no
137	5,10-Pentadecadien-1-ol, (Z,Z)-	(5Z,10Z)-pentadeca-5,10-dien-1-ol	25.467	0.000	JAC102	unknown	no
138	Hexanedioic acid, mono(2-ethylhexyl)ester	6-(2-ethylhexoxy)-6-oxohexanoic acid	28.637	0.000	JAC81	unknown	no

139	Phthalic acid, di(hept-3-yl) ester	diheptan-3-yl benzene-1,2-dicarboxylate	30.506	0.000	JAC81	unknown	no
140	Butane, 2-azido-2,3,3-trimethyl-	2-azido-2,3,3-trimethylbutane	4.022	0.000	JAC72, JAC75, JAC81	unknown	yes
141	3-Pentanol, 3-methyl-	3-methylpentan-3-ol	4.036	0.005	JAC99, JAC48	unknown	yes
142	Cyclobutanone, 2,3-dimethyl-, trans-	(2S,3R)-2,3-dimethylcyclobutan-1-one	4.061	0.006	JAC88, JAC30L	unknown	yes
143	Butanoic acid, 2-methyl-, methyl ester	methyl 2-methylbutanoate	4.359	0.005	JAC45, JAC47	unknown	yes
144	Propanoic acid, 2,2-dimethyl-, 2,4-dinitrophenyl ester	(2,4-dinitrophenyl) 2,2-dimethylpropanoate	4.361	0.001	JAC60, JAC64	unknown	yes
145	2-Hydroxy-3-pentanone	2-hydroxypentan-3-one	4.856	0.007	JAC88, JAC30L	unknown	yes
146	Acetamidoacetaldehyde	N-(2-oxoethyl)acetamide	7.523	0.000	JAC110, JAC74L	unknown	yes
147	Ether, 3-butenyl propyl	4-propoxybut-1-ene	7.524	0.002	JAC6, JAC88, JAC55	unknown	yes
148	(S)-3-Ethyl-4-methylpentanol	3-ethyl-4-methylpentan-1-ol	9.462	0.053	JAC25, JAC88, JAC61A	unknown	yes
149	Formic acid, 2-ethylhexyl ester	2-ethylhexyl formate	11.490	0.003	JAC99, JAC101, JAC64	unknown	yes
150	Benzoyl bromide	benzoyl bromide	11.954	0.004	JAC86, JAC76	unknown	yes
151	1,3-Methanopentalene, octahydro-	tricyclo[5.1.1.02,6]nonane	14.053	0.001	JAC45, JAC64	unknown	yes
152	Tricyclo[3.3.1.1(3,7)]decanone, 4-iodo-, (1.alpha.,3.beta.,4.beta.,5.alpha.,7.beta.)-	[g]	15.236	0.000	JAC25, JAC81	unknown	yes
153	6-Tridecene, (Z)-	(Z)-tridec-6-ene	16.301	0.001	JAC95, JAC68	unknown	yes
154	Bicyclo[3.2.0]hept-2-en-6-one, 7-chloro-	7-chlorobicyclo[3.2.0]hept-2-en-6-one	16.313	0.000	JAC45, JAC64	unknown	yes
155	Dodecanal	dodecanal	18.199	0.001	JAC24, JAC33	unknown	yes
156	trans-1,10-Dimethyl-trans-9-decalinol	8,8a-dimethyl-2,3,4,4a,5,6,7,8-octahydro-1H-naphthalen-1-ol	18.385	0.001	JAC24, JAC60, JAC58, JAC45	unknown	yes

157	3-Heptyne, 5-methyl-	5-methylhept-3-yne	18.726	0.001	JAC25, JAC81	unknown	yes
158	Cyclopentane, nonyl-	nonylcyclopentane	18.755	0.002	JAC95, JAC6, JAC122	unknown	yes
159	n-Heptyl methylphosphonofluoridate	1-[fluoro(methyl)phosphoryl]oxyheptane	18.818	0.032	JAC78, JAC95	unknown	yes
160	n-Heptadecylcyclohexane	heptadecylcyclohexane	20.143	0.000	JAC95, JAC6, JAC122, JAC68	unknown	yes
161	Dihydro-cis-.alpha.-copaene-8-ol	2,8-dimethyl-5-propan-2-yltricyclo[4.4.0.02,7]decan-4-ol	20.549	0.031	JAC24, JAC86, JAC95, JAC87	unknown	yes
162	β-Vatirenene	2-Isopropylidene-8,8a-dimethyl-1,2,3,7,8,8a-hexahydronaphthalene	21.177	0.002	JAC72, JAC75, JAC81	unknown	yes
163	5,10-Pentadecadiyn-1-ol	pentadeca-5,10-diyn-1-ol	21.247	0.025	JAC76, JAC90	unknown	Yes

[a] Compound names were assigned by the NIST library. This was used in conjunction with the retention time for more accurate identification of compounds, i.e., VOCs with the same name but different RT should be interpreted cautiously.

[b] Standard deviation from the average retention time (RT) for a given VOC.

[c] The level of confidence assigned to the identity of the VOC. High confidence means there was a good spectral match to the NIST library reference and a Kovats retention index (RI) within 10 points of a literature value available on the NIST WebBook (https://webbook.nist.gov/chemistry/name-ser/), low confidence means the difference in RI of a NIST library suggested VOC to that of the literature value is greater 10 points, and unknown means that a literature RI value could not be found for a NIST library suggested compound.

[d] Indicates if the VOC was from one or more isolates/OTU.

[e] common name for the given VOC.

[f] Dup1 suffix means a NIST reference spectra with close identity to the given VOC was not available in the library used in this study.

[g] not applicable, or the IUPAC name is not available.

Table 3.3.1.2: The numbers of bacterially derived VOCs detected in the pooled cultures.

Confidence in VOC identity	**No. of VOCs present in 1 OTU**	**No. of VOCs Present in >1 OTU**	**Total**
High	**14**	**19**	**33**
Alcohol	*4*	*4*	*8*
Aldehyde	*0*	*0*	*0*
Ketone	*2*	*0*	*2*
Ester	*4*	*2*	*6*
Hydrocarbon	*1*	*4*	*5*
Terpene	*2*	*1*	*3*
Terpenoid	*1*	*6*	*7*
Other	*0*	*2*	*2*
Low	**8**	**6**	**14**
Unknown	**92**	**24**	**116**
Total	**114**	**49**	**163**

indicating differences in the VOC production profiles of phylogenetically different isolates.

There was variability in VOCs produced among the isolates. For example, JAC81 produced the most (14) VOCs that were not produced by the other isolates, while nine isolates did not produce any unique VOCs (Table 3.3.1.3). Variability was also evident within the OTUs, where two or more isolates were selected for analysis. For example, OTU-22 comprising JAC75, JAC76, and JAC81 shows notable differences in the number of unique VOCs produced by each mentioned *Streptomyces* isolates. JAC81 produced 14 unique VOCs, while JAC75 and JAC76 produced one and no unique VOCs, respectively (Table 3.3.1.3). This event might mean that genes or BGCs for VOCs are present in JAC81 but absent in the others, though all three *Streptomyces* are from the same OTU. However, there could be variability in the growth of the isolates during fermentation. Similar results were seen for OTUs 13, 21, and 28, where the VOC production profiles by the isolates were inconsistent with each other.

Table 3.3.1.3: The number of VOCs detected from each *Streptomyces* isolate in pooled culture VOC analysis.

***Streptomyces* isolate**	**OTU [a]**	**Empty jar VOCs [b]**	**Medium VOCs [c]**	**Bacteria VOCs [d]**	**Total VOC**	**Unique bacteria VOCs [e]**
Empty jar (Dec 2019)	[g]	26	[g]	[g]	26	[g]
empty jar (2020)	[g]	83	[g]	[g]	83	[g]
Medium (Dec 2019)	[g]	15	2	[g]	17	[g]
Medium (2020)	[g]	38	13	[g]	51	[g]
Medium_2 (2020)	[g]	40	12	[g]	52	[g]
JAC17	1	22	0	8	30	3
JAC25 [f]	2	46	11	20	77	8
JAC90	3	50	6	6	62	2
JAC102	4	20	1	5	26	2
JAC96	5	51	8	6	65	3
JAC72	6	42	7	4	53	0
JAC99	7	21	2	11	34	3
JAC31	8	22	2	12	36	2
JAC95 [f]	9	22	6	15	43	2
JAC74L	10	38	6	7	51	0
JAC86	11	20	1	12	33	5
JAC78	12	27	1	5	33	0
JAC87	13	60	3	12	75	4
JAC103	13	25	2	3	30	3
JAC6	14	21	5	13	39	4
JAC24	15	32	2	5	39	0
JAC64	16	20	0	12	32	3
JAC45 [f]	17	22	2	9	33	3
JAC47	18	29	2	7	38	2
JAC61A	19	50	6	12	68	5
JAC48	19	19	2	3	24	0
JAC60 [f]	19	20	1	5	26	0
JAC88	20	59	4	12	75	6
JAC58	21	22	2	5	29	2
JAC68	21	20	6	8	34	1
JAC81 [f]	22	33	4	22	59	14
JAC75	22	36	4	4	44	1
JAC76	22	14	1	5	20	0
JAC101	23	24	2	8	34	0
JAC122	24	25	4	13	42	5
JAC30L	25	43	11	10	64	4

JAC33	26	23	2	8	33	2
JAC110	27	38	6	7	51	0
JAC54	28	37	4	4	45	1
JAC55	28	52	6	4	62	1
JAC74C [f]	29	22	2	18	42	10
JAC35	30	32	5	8	45	6

[a] The OTU that the isolate was assigned.

[b] The total VOCs determined as coming from the empty jar control (the VOC collection system).

[c] The total VOCs determined as coming from the pooled media control.

[d] The total VOCs that were not present in the controls but detected from the *Streptomyces* isolate.

[e] VOCs detected from only the *Streptomyces* isolate in question and not the others.

[f] *Streptomyces* isolates selected for replicate culture VOC analysis.

[g] means not applicable.

3.3.2: Six isolates selected for replicate VOC analysis

Six of the 37 isolates (JAC25, JAC45, JAC60, JAC74C, JAC81, and JAC95) were selected for replicate VOC analysis (fermentation of isolates in triplicate followed by VOC collection and subsequent GC-MS analysis) based on the numbers and types of VOCs they produced during the pooled culture screens (Figure 3.3.1.1 and Table 3.3.1.3). Those VOCs identified with high confidence in the pooled culture screen were noted, and published bioactivities were reported (Table 3.3.2.1), which aided in selecting the six isolates for further analysis. Some of these VOCs were described in the literature as insect repellents, making them target candidates for future studies. Phenylethyl alcohol detected in JAC25 and JAC74C has mosquito repellency (Zeng et al., 2019) and antifungal activity (Li et al., 2020; Lyu et al., 2020). 1-hexanol produced by JAC60 suppresses mosquito CO_2 sensing receptors (Turner et al., 2011) and plays a role in oriental fruit moth (*Grapholita molesta*) signaling (Chen et al., 2019). 1-octen-3-ol detected in JAC74C has a variety of bioactivities, including nematicidal activity (Hummadi et al., 2020; Khoja et al., 2020), and it is produced by the foreign grain beetle (*Ahasverus advena*) (Pierce et al., 1990) and bont ticks (*Amblyomma variegatum* and *Amblyomma hebraeum*) (Mcmahon et al., 2001) and has a role in attracting the insects. Dodecane, heptylcyclohexane, and undecane produced by JAC95 are used in various insect communication systems (El-Sayed, 2007; Minaeimoghadam et al., 2017). Cubenol detected in JAC25 and JAC81 was found in plant essential oils that repel berry pests (Espinoza et al., 2016) and has larvicidal and adulticidal activity against various mosquito species (Dua et al., 2008). Geosmin detected in JAC25, JAC74C, JAC81, and JAC95 has various bioactivities, including springtail insect

Table 3.3.2.1: VOCs identified with high confidence in the pooled culture screen and their published bioactivities.

VOC	IUPAC name	Functional Group	Present in	Reported in plants	Bioactivities	Reported in *Streptomyces*
Alcohol						
Phenylethyl Alcohol	2-phenylethanol	aromatic alcohol	JAC17, JAC31, JAC86, JAC101, JAC33, JAC58, JAC74C, JAC25, JAC110, JAC74L, JAC30L	[b]	Mosquito repellent (Zeng et al., 2019); Antifungal (Li et al., 2020; Lyu et al., 2020)	(X. Li et al., 2020; Schöller et al., 2002)
DL-2,3-Butanediol	butane-2,3-diol	diol	JAC17, JAC47	[b]	[b]	[b]
1-Dodecanol	dodecan-1-ol	alcohol	JAC68	[b]	[b]	[b]
1-Hexanol	hexan-1-ol	alcohol	JAC60, JAC61A	Prickly pear (Andreu-Coll et al., 2020), mangos (Haocheng et al., 2020), korla fragrant pears (J. Chen et al., 2020)	Suppresses mosquito CO_2 receptors (Turner et al., 2011); beetle attractant (Zhu et al., 2020); role in the oriental fruit moth signaling & attractant (L. H. Chen et al., 2019)	(Cheng et al., 2020)
1-Octen-3-ol	oct-1-en-3-ol	fatty alcohol	JAC74C	orange essence (Högnadóttir & Rouseff, 2003) ; Kiwi fruit essence and Kiwi fruit puree, (El-Sayed, 2007); edible Korean chamchwi (Chung et al., 1993)	Nematicidal (Hummadi et al., 2020; Khoja et al., 2020); produced by and attract foreign grain beetle (Pierce et al., 1990); produced by and attract bont ticks (Mcmahon et al., 2001)	[b]
1-Octanol	octan-1-ol	fatty alcohol	JAC99, JAC101, JAC64	[b]	multiple insects use in their communication system – (El-Sayed, 2007)	[b]

Benzyl alcohol	phenylmethanol	aromatic alcohol	JAC17, JAC58, JAC25, JAC122, JAC30L	In climbing shrub essential oil (Thangadurai et al., 2002)	Head lice repellent (Toloza et al., 2006)	(Cheng et al., 2020; Narayana et al., 2008)
Ester						
Methyl 2-methylhexanoate	methyl 2-methylhexanoate	fatty ester	JAC45, JAC64	[b]	[b]	[b]
Dodecanoic acid, methyl ester	methyl dodecanoate	fatty ester	JAC35		Drosophila sex pheromone (Dweck et al., 2015)	(Cheng et al., 2020)
Methyl tetradecanoate	methyl tetradecanoate	fatty ester	JAC35, JAC110, JAC74L	emitted by multiple plant species – (El-Sayed, 2007)	Multiple insects use in their communication system (El-Sayed, 2007); ant repellent allomone (Posy et al., 1984)	[b]
Hydrocarbon						
Dodecane	dodecane	alkane	JAC95, JAC6, JAC122, JAC68	Released by tomato plants when exposed to pests (Errard et al., 2015)	clearwing moth sex pheromone (Minaeimoghadam et al., 2017)	(El-Din Mohamed & Zaki, 2019)
heptylcyclohexane	heptylcyclohexane	cyclic alkane	JAC95, JAC6, JAC122, JAC68	[b]	used in insect communication systems (El-Sayed, 2007)	[b]
Cetene	hexadec-1-ene	alkene	JAC47	[b]	[b]	[b]
Cyclopropane, pentyl-	pentylcyclopropane	cyclic alkane	JAC99, JAC101	in Persian Hogweed essential oil (Ehsani et al., 2019)	[b]	[b]
Undecane	undecane	alkane	JAC95, JAC6, JAC122	From herbaceous fern-root exudate (K. mei Zhang et al., 2019)	Ant sex and alarm pheromone (Monnin et al., 2018)	[b]
Ketone						

(R)-(+)-3-Methylcyclopentanone	(3R)-3-methylcyclopentan-1-one	cyclic ketone	JAC6	[b]	In the territorial marking fluid of Siberian tigers (Soso & Koziel, 2016)	[b]
3-Octanone	octan-3-one	ketone	JAC122	[b]	[b]	[b]
Terpene					[b]	
1,6-Cyclodecadiene, 1-methyl-5-methylene-8-(1-methylethyl)-, [S-(E,E)]- Germacrene D [a]	(1Z,6Z)-1-methyl-5-methylidene-8-propan-2-ylcyclodeca-1,6-diene	sesquiterpene	JAC25, JAC81	Synthase gene in grapevine (Lücker et al., 2004)	[b]	(Cheng et al., 2020; Pollak & Berger, 1996; Rabe et al., 2013);
2-Methyl-2-bornene	1,2,7,7-tetramethylbicyclo[2.2.1]hept-2-ene	monoterpene	JAC25	[b]	[b]	(Cheng et al., 2020; Rabe et al., 2013)
1H-Benzocycloheptene, 2,4a,5,6,7,8,9,9a-octahydro-3,5,5-trimethyl-9-methylene-, (4aS-cis)- α-Himachalene [a]	3,5,5-trimethyl-9-methylidene-2,4a,6,7,8,9a-hexahydro-1H-benzo[7]annulene	sesquiterpene	JAC102	In various plant extracts (Alves et al., 2019; Chaudhary et al., 2009; Joycharat et al., 2014; Ogunbinua et al., 2009; Paoli et al., 2011)	In essential oil that repels Mediterranean Fruit Fly (Alves et al., 2019)	(Cheng et al., 2020; Citron, Gleitzmann, et al., 2012)
Terpenoid						
1-Naphthalenol, 1,2,3,4,4a,7,8,8a-octahydro-1,6-dimethyl-4-(1-methylethyl)-, [1R-(1.alpha.,4.beta.,4a.beta.,8a.beta.)]- Cadinol [a]	(1R,4S)-1,6-dimethyl-4-propan-2-yl-3,4,4a,7,8,8a-hexahydro-2H-naphthalen-1-ol	sesquiterpene, alcohol	JAC17, JAC102, JAC24, JAC86	In giant Tangier fennel essential oil (Elghwaji et al., 2017)	[b]	[b]

cubenol	(1S,4R,4aR,8aR)-4,7-dimethyl-1-propan-2-yl-2,3,4,5,6,8a-hexahydro-1H-naphthalen-4a-ol	sesquiterpene, alcohol	JAC47, JAC25, JAC110, JAC74L, JAC81	floral compound emitted by various plants (El-Sayed, 2007); in various plant essential oil (Ciccarelli et al., 2016; Jirovetz et al., 2002; Mulyaningsih et al., 2010)	In essential oil that repels berry pests (Espinoza et al., 2016); in an essential oil that has larvicidal and adulticidal activity against various mosquito species (Dua et al., 2008)	(Cheng et al., 2020)
epi-cubenol	(1S,4R,4aS,8aR)-4,7-dimethyl-1-propan-2-yl-2,3,4,5,6,8a-hexahydro-1H-naphthalen-4a-ol	sesquiterpene, alcohol	JAC25, JAC95, JAC90, JAC87	[b]	[b]	(Rabe et al., 2013)
Geosmin	(4S,4aS,8aR)-4,8a-dimethyl-1,2,3,4,5,6,7,8-octahydronaphthalen-4a-ol	monoterpene, alcohol	JAC102, JAC31, JAC86, JAC101, JAC33, JAC76, JAC47, JAC64, JAC78, JAC74C, JAC25, JAC95, JAC35, JAC88, JAC55, JAC110, JAC74L, JAC54, JAC61A, JAC75, JAC90, JAC87, JAC81	[b]	Springtail insect attractant (Becher et al., 2020); Drosophila repellent (Stensmyr et al., 2012)	(Pollak & Berger, 1996; Rabe et al., 2013; Schöller et al., 2002)
2-Methylisoborneol	1,2,7,7-tetramethylbicyclo[2.2.1]heptan-2-ol	monoterpene, alcohol	JAC102, JAC99, JAC31, JAC101, JAC60, JAC78, JAC25, JAC72, JAC55, JAC54, JAC61A, JAC90	[b]	Springtail insect attractant (Becher et al., 2020); *Drosophila* attractant (Ho et al., 2020) ; Antifungal (Z. Wang et al., 2013)	(Becher et al., 2020; Rabe et al., 2013; Schrader et al., 2015)
2,6-Octadienoic acid, 3,7-dimethyl-, methyl ester	methyl (2E)-3,7-dimethylocta-2,6-dienoate	monoterpene, ester	JAC74C	[b]	[b]	[b]

Cyclohexanemethanol, 4-ethenyl-.alpha.,.alpha.,4-trimethyl-3-(1-methylethenyl)-, [1R-(1.alpha.,3.alpha.,4.beta.)]- elemol group [a]	2-(4-ethenyl-4-methyl-3-prop-1-en-2-ylcyclohexyl)propan-2-ol	sesquiterpene, alcohol	JAC74C	[b]	used in insect communication systems (El-Sayed, 2007)	(Cheng et al., 2020)
2-Naphthalenemethanol, decahydro-α,α,4a-trimethyl-8-methylene-, [2R-(2α,4aα,8aβ)]- β-Eudesmol ; β-Selinenol [a]	2-[(2R,4aR,8aS)-4a-methyl-8-methylidene-1,2,3,4,5,6,7,8a-octahydronaphthalen-2-yl]propan-2-ol	sesquiterpene, alcohol	JAC86, JAC101, JAC33, JAC76, JAC74C	In perennial medicinal plant extract (Tsusaka et al., 2020)	Insecticidal to *Drosophila* species (Chu et al., 2011)	(Cheng et al., 2020)
Other						
Pentanoic acid, 2,2,4-trimethyl-3-carboxyisopropyl, isobutyl ester	1-O-(2-methylpropyl) 4-O-propan-2-yl 2,2-dimethyl-3-propan-2-ylbutanedioate	ester	JAC122	[b]	[b]	[b]
Ethanol, 2-(2-ethoxyethoxy)- Carbitol [a]	2-(2-ethoxyethoxy)ethanol	alcohol, ether	JAC17	[b]	[b]	[b]
Pyrazine, 2,5-dimethyl-	2,5-dimethylpyrazine	pyrazine	JAC17, JAC24, JAC31, JAC33, JAC47, JAC64, JAC78, JAC74C, JAC25, JAC35, JAC96, JAC110, JAC74L, JAC61A, JAC30L, JAC87, JAC81	[b]	[b]	[b]
2,4-Furandicarboxylic acid, dimethyl ester	dimethyl furan-2,4-dicarboxylate	[b]	JAC74C	[b]	[b]	[b]
Hexanenitrile	hexanenitrile	cyanide	JAC60, JAC78, JAC61A	[b]	Used in aphid insect communication system (Pope et al., 2004)	[b]

[a] common name for the given VOC.

[b] means no relevant publications were found.

attractancy (Becher et al., 2020) and *Drosophila* repellency (Stensmyr et al., 2012). 2-Methylisoborneol detected in JAC25 and JAC60 attracts the springtail insect (Becher et al., 2020) and *Drosophila* (Ho et al., 2020) and has antifungal activity (Z. Wang et al., 2013). The terpene, β-Eudesmol detected in JAC74C, is insecticidal to *Drosophila* species (Chu et al., 2011). JAC45 did not produce any notable VOCs (Table 3.3.2.1). JAC45 and JAC60 produced the least number of VOCs, 9 and 5, respectively, while JAC81 produced the most VOCs (Table 3.3.1.3). The six isolates were confirmed for further analysis by Dr. Sean McCann (Hillier Lab, Acadia University). A total of seventy-one VOCs were detected in the six isolates during the pooled culture screens (Table 3.3.2.2), where there were more unknown compounds (low and unknown confidence level VOCs) than known compounds (high confidence VOCs) except for JAC74C (Figure 3.3.2.1). Further analysis is needed to identify the unknown VOCs, where potentially useful ones could be present.

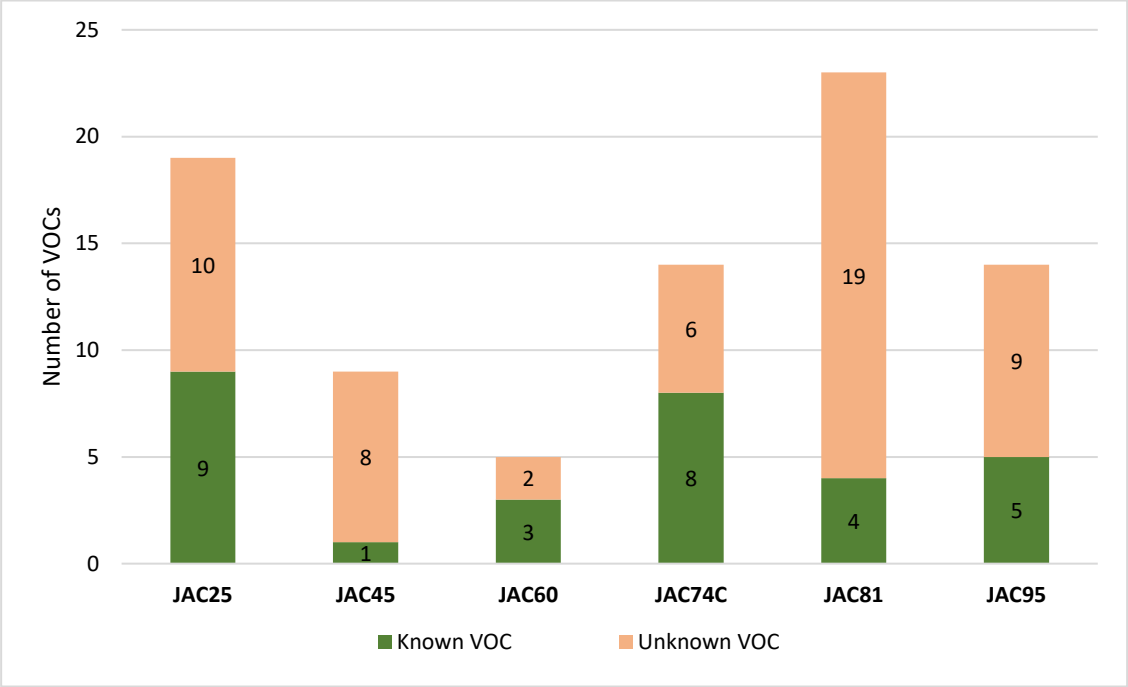

Figure 3.3.2.1: Number of VOCs detected in the pooled culture screens for the six *Streptomyces* isolates selected for replicate VOC analysis. Known VOCs were identified with a high confidence level, and unknown VOCs were identified with a low and unknown confidence level.

Table. 3.3.2.2: VOCs detected in the pooled culture screen for the six *Streptomyces* isolates selected for replicate VOC analysis.

No.	VOC [a]	IUPAC name	RT	RT Stdev [b]	Detected in [c]	Confidence in the VOC ID [d]	Detected in >1 OTU [e]
1	Hexanenitrile	hexanenitrile	6.403	0.025	JAC60,	high	yes
2	Pyrazine, 2,5-dimethyl-	2,5-dimethylpyrazine	7.230	0.012	JAC25, JAC74C, JAC81	high	yes
3	Methyl 2-methylhexanoate	methyl 2-methylhexanoate	8.537	0.001	JAC45	high	yes
4	Benzyl alcohol	phenylmethanol	10.290	0.027	JAC25	high	yes
5	Undecane	Undecane	12.099	0.001	JAC95	high	yes
6	Phenylethyl Alcohol	2-phenylethanol	12.432	0.032	JAC25, JAC74C	high	yes
7	2-Methylisoborneol	1,2,7,7-tetramethylbicyclo[2.2.1]heptan-2-ol	14.380	0.032	JAC25, JAC60	high	yes
8	Dodecane	dodecane	14.560	0.001	JAC95	high	yes
9	heptylcyclohexane	heptylcyclohexane	17.204	0.000	JAC95	high	yes
10	geosmin	(4S,4aS,8aR)-4,8a-dimethyl-1,2,3,4,5,6,7,8-octahydronaphthalen-4a-ol	18.356	0.014	JAC25, JAC74C, JAC81, JAC95	high	yes
11	1,6-Cyclodecadiene, 1-methyl-5-methylene-8-(1-methylethyl)-, [S-(E,E)]-	(1Z,6Z)-1-methyl-5-methylidene-8-propan-2-ylcyclodeca-1,6-diene	19.270	0.002	JAC25, JAC81	high	yes
12	epi-cubenol	(1S,4R,4aS,8aR)-4,7-dimethyl-1-propan-2-yl-2,3,4,5,6,8a-hexahydro-1H-naphthalen-4a-ol	21.128	0.001	JAC25, JAC95	high	yes
13	cubenol	(1S,4R,4aR,8aR)-4,7-dimethyl-1-propan-2-yl-2,3,4,5,6,8a-hexahydro-1H-naphthalen-4a-ol	21.277	0.024	JAC25, JAC81	high	yes

14	2-Naphthalenemethanol, decahydro-α,α,4a-trimethyl-8-methylene-, [2R-(2α,4aα,8aβ)]-	2-(4*a*-methyl-8-methylidene-1,2,3,4,5,6,7,8*a*-octahydronaphthalen-2-yl)propan-2-ol	21.320	0.001	JAC74C	high	yes
15	1-Hexanol	hexan-1-ol	6.223	0.034	JAC60	high	no
16	1-Octen-3-ol	oct-1-en-3-ol	8.963	0.000	JAC74C	high	no
17	2-Methyl-2-bornene	1,2,7,7-tetramethylbicyclo[2.2.1]hept-2-ene	9.964	0.000	JAC25	high	no
18	2,6-Octadienoic acid, 3,7-dimethyl-, methyl ester	methyl (2E)-3,7-dimethylocta-2,6-dienoate	16.820	0.000	JAC74C	high	no
19	2,4-Furandicarboxylic acid, dimethyl ester	dimethyl furan-2,4-dicarboxylate	17.364	0.000	JAC74C	high	no
20	Cyclohexanemethanol, 4-ethenyl-.alpha.,.alpha.,4-trimethyl-3-(1-methylethenyl)-, [1R-(1.alpha.,3.alpha.,4.beta.)]-	2-(4-ethenyl-4-methyl-3-prop-1-en-2-ylcyclohexyl)propan-2-ol	20.162	0.000	JAC74C	high	no
21	7-epi-.alpha.-selinene	5,8a-dimethyl-3-prop-1-en-2-yl-2,3,4,4a,7,8-hexahydro-1H-naphthalene	21.544	0.000	JAC95	low	yes
22	10-Methylundecan-4-olide	5-(6-methylheptyl)oxolan-2-one	21.220	0.000	JAC74C	low	no
23	10-Methyldodecan-5-olide	6-(5-methylheptyl)oxan-2-one	22.831	0.000	JAC45	low	no
24	Butane, 2-azido-2,3,3-trimethyl-	2-azido-2,3,3-trimethylbutane	4.022	0.000	JAC81	unknown	yes
25	Butanoic acid, 2-methyl-, methyl ester	methyl 2-methylbutanoate	4.359	0.005	JAC45	unknown	yes
26	Propanoic acid, 2,2-dimethyl-, 2,4-dinitrophenyl ester	(2,4-dinitrophenyl) 2,2-dimethylpropanoate	4.361	0.001	JAC60	unknown	yes
27	(S)-3-Ethyl-4-methylpentanol	3-ethyl-4-methylpentan-1-ol	9.462	0.053	JAC25	unknown	yes
28	1,3-Methanopentalene, octahydro-	tricyclo[5.1.1.02,6]nonane	14.053	0.001	JAC45	unknown	yes
29	Tricyclo[3.3.1.1(3,7)]decanone, 4-iodo-,	[g]	15.236	0.000	JAC25, JAC81	unknown	yes

	(1.alpha.,3.beta.,4.beta.,5.alpha.,7.beta.)-						
30	6-Tridecene, (Z)-	(Z)-tridec-6-ene	16.301	0.001	JAC95	unknown	yes
31	Bicyclo[3.2.0]hept-2-en-6-one, 7-chloro-	7-chlorobicyclo[3.2.0]hept-2-en-6-one	16.313	0.000	JAC45	unknown	yes
32	trans-1,10-Dimethyl-trans-9-decalinol	8,8a-dimethyl-2,3,4,4a,5,6,7,8-octahydro-1H-naphthalen-1-ol	18.385	0.001	JAC45, JAC60	unknown	yes
33	3-Heptyne, 5-methyl-	5-methylhept-3-yne	18.726	0.001	JAC25, JAC81	unknown	yes
34	Cyclopentane, nonyl-	nonylcyclopentane	18.755	0.002	JAC95	unknown	yes
35	n-Heptyl methylphosphonofluoridate	1-[fluoro(methyl)phosphoryl]oxyheptane	18.818	0.032	JAC95	unknown	yes
36	n-Heptadecylcyclohexane	heptadecylcyclohexane	20.143	0.000	JAC95	unknown	yes
37	Dihydro-cis-.alpha.-copaene-8-ol	2,8-dimethyl-5-propan-2-yltricyclo[4.4.0.02,7]decan-4-ol	20.549	0.031	JAC95	unknown	yes
38	β-Vatirenene	2-Isopropylidene-8,8a-dimethyl-1,2,3,7,8,8a-hexahydronaphthalene	21.177	0.002	JAC81	unknown	yes
39	1-Heptene, 3-methoxy-	3-methoxyhept-1-ene	4.268	0.000	JAC74C	unknown	no
40	2-Buten-1-ol, 2-methyl-	(E)-2-methylbut-2-en-1-ol	4.316	0.000	JAC74C	unknown	no
41	Propanoic acid, 2,2-dimethyl-, 2,4-dinitrophenyl ester	(2,4-dinitrophenyl) 2,2-dimethylpropanoate	5.488	0.000	JAC45	unknown	no
42	2-Butenoic acid, 2-methyl-, methyl ester	methyl (E)-2-methylbut-2-enoate	6.158	0.000	JAC74C	unknown	no
43	4-Octene, 2,3,7-trimethyl-, [S-(E)]-	(E,3S)-2,3,7-trimethyloct-4-ene	9.601	0.000	JAC25	unknown	no
44	Iron, tricarbonyl[(2,3,4,5-.eta.)-2,4-cycloheptadien-1-ol]-	[g]	13.856	0.000	JAC45	unknown	no
45	Iron, tricarbonyl[(2,3,4,5-.eta.)-2,4-cycloheptadien-1-ol]--Dup1 [f]	[g]	14.818	0.000	JAC45	unknown	no

46	6-Octen-1-ol, 3,7-dimethyl-, formate	3,7-dimethyloct-6-enyl formate	15.123	0.000	JAC74C	unknown	no
47	(1,2,2-trimethyl-3-cyclopenten-1-yl)acetaldehyde	2-(1,2,2-trimethylcyclopent-3-en-1-yl)acetaldehyde	15.315	0.000	JAC81	unknown	no
48	Phenol, 4-[2-(methylamino)ethyl]-	4-[2-(methylamino)ethyl]phenol	15.317	0.000	JAC25	unknown	no
49	2-Hydroxy-5-ethyl-5-methylcyclopent-2-en-1-one	5-ethyl-2-hydroxy-5-methylcyclopent-2-en-1-one	15.944	0.000	JAC81	unknown	no
50	Phenylacetaldehyde N-methyl-N-formylhydrazone	N-methyl-N-[(E)-2-phenylethylideneamino]formamide	16.707	0.000	JAC25	unknown	no
51	1-Methylene-2b-hydroxymethyl-3,3-dimethyl-4b-(3-methylbut-2-enyl)-cyclohexane	[2,2-dimethyl-4-(3-methylbut-2-enyl)-6-methylidenecyclohexyl]methanol	18.507	0.000	JAC81	unknown	no
52	1-Methylene-2b-hydroxymethyl-3,3-dimethyl-4b-(3-methylbut-2-enyl)-cyclohexane-Dup1 [f]	[g]	18.575	0.000	JAC81	unknown	no
53	(3R,2E)-2-(Hexadec-15-ynylidene)-3-hydroxy-4-methylenebutanolide	(3E,4R)-3-hexadec-15-ynylidene-4-hydroxy-5-methylideneoxolan-2-one	18.654	0.000	JAC81	unknown	no
54	1,4-Dimethyladamantane #	1,4-dimethyladamantane	18.726	0.000	JAC95	unknown	no
55	4,7-Methanoazulene, 1,2,3,4,5,6,7,8-octahydro-1,4,9,9-tetramethyl-, [1S-(1.alpha.,4.alpha.,7.alpha.)]-	1,5,11,11-tetramethyltricyclo[6.2.1.02,6]undec-2(6)-ene	18.812	0.000	JAC81	unknown	no
56	Dodecane, 2,6,10-trimethyl-	2,6,10-trimethyldodecane	18.876	0.000	JAC95	unknown	no
57	5,10-Pentadecadiyn-1-ol	pentadeca-5,10-diyn-1-ol	18.969	0.000	JAC81	unknown	no
58	2H-Benzocyclohepten-2-one, decahydro-4a-methyl-, trans-	4a-methyl-3,4,5,6,7,8,9,9a-octahydro-1H-benzo[7]annulen-2-one	19.147	0.000	JAC25	unknown	no

59	2,7-Octadiene-1,6-diol, 2,6-dimethyl-, (E)-	(2E)-2,6-dimethylocta-2,7-diene-1,6-diol	20.454	0.000	JAC81	unknown	no
60	Naphthalene, 1,2,4a,5,6,8a-hexahydro-4,7-dimethyl-1-(1-methylethyl)-	4,7-dimethyl-1-propan-2-yl-1,2,4a,5,6,8a-hexahydronaphthalene	20.502	0.000	JAC25	unknown	no
61	1-Hexyl-2-nitrocyclohexane	1-hexyl-2-nitrocyclohexane	20.947	0.000	JAC74C	unknown	no
62	Hexanethioic acid, S-methyl ester	S-methyl hexanethioate	21.058	0.000	JAC81	unknown	no
63	Dihydro-cis-.alpha.-copaene-8-ol-Dup1 [f]	[g]	21.267	0.000	JAC95	unknown	no
64	3,4-Nonadien-6-yne, 5-ethyl-3-methyl-	5-Ethyl-3-methyl-3,4-nonadien-6-yne	21.482	0.000	JAC81	unknown	no
65	1-Allyl-cyclohexane-1,2-diol	1-prop-2-enylcyclohexane-1,2-diol	21.544	0.000	JAC81	unknown	no
66	10-Heneicosene (c,t)	(E)-henicos-10-ene	21.758	0.000	JAC25	unknown	no
67	Cyclohexene, 1,5,5-trimethyl-6-(2-propenylidene)-	(6Z)-1,5,5-trimethyl-6-prop-2-enylidenecyclohexene	21.921	0.000	JAC81	unknown	no
68	Benzoic acid, 3-fluoro-, 2-oxo-2-phenylethyl ester	phenacyl 3-fluorobenzoate	21.976	0.000	JAC25	unknown	no
69	Cyclohexanol, 1-ethyl-2,2-dimethyl-6-methylene-	1-ethyl-2,2-dimethyl-6-methylidenecyclohexan-1-ol	22.219	0.000	JAC81	unknown	no
70	Hexanedioic acid, mono(2-ethylhexyl)ester	6-(2-ethylhexoxy)-6-oxohexanoic acid	28.637	0.000	JAC81	unknown	no
71	Phthalic acid, di(hept-3-yl) ester	diheptan-3-yl benzene-1,2-dicarboxylate	30.506	0.000	JAC81	unknown	No

[a] VOC names were assigned by the NIST library. This was used in conjunction with the retention time for more accurate identification of compounds, i.e., VOCs with the same name but different RT should be interpreted cautiously.

[b] Standard deviation from the average retention time (RT) of a VOC.

[c] Only the six isolates selected for replicate VOC analysis are included here. A complete list of isolates a VOC was detected in can be found in Table 3.3.1.1 if the VOC is listed as detected in more than one OTU.

[d] The level of confidence assigned to the identity of the VOC. High confidence means there was a good spectral match to the NIST library reference and a Kovats retention index (RI) within 10 points of a literature value available on the NIST WebBook (https://webbook.nist.gov/chemistry/name-ser/), low confidence means the difference in RI of a NIST library suggested VOC to that of the literature value is greater 10 points, and unknown means that a literature RI value could not be found for a NIST library suggested compound.

[e] Indicates if the VOC was from one or more isolates/OTU.

[f] Dup1 suffix means a NIST reference spectra with close identity to the given VOC was not available in the library used in this study.

[g] not applicable, or the IUPAC name is not available.

3.3.3: VOC production profiles for replicate cultures of the six selected *Streptomyces* isolates

Six *Streptomyces* isolates described above were chosen from the 37 phylogenetically different ones used in pooled culture VOC analysis. These six were fermented in triplicate in the three media for replicate VOC analysis. Ninety-five VOCs were identified (Table 3.3.3.1), where VOCs present in at least two of three replicate cultures were considered produced by a *Streptomyces* isolate (Figure 3.3.3.1). JAC81 fermented in SFM produced VOCs that elute at RTs 21.056, 21.177, and 21.266 with relatively prominent peaks (Figure 3.3.3.1). However, the confidence in their identity is not high. That is to say that the published literature or standards were not available to confirm that these VOCs elute at the RTs mentioned above. VOCs were considered unknown because the reference spectra were not available to identify them unambiguously. In these instances, more than one VOCs eluted at the same RTs (Table 3.3.3.1) and could not be distinguished with the spectra alone. Therefore, they should be interpreted cautiously.

Replicate VOC analysis revealed that some compounds detected in the pooled VOC screen were only produced in certain fermentation media (Table 3.3.3.1 and Figure 3.3.3.2). Overall, the isolates produced the highest number of VOCs in SFM medium and the least number in the synthetic medium, except for JAC25 and JAC74C, where the numbers were the same or more in the YMS medium, respectively (Figure 3.3.3.2). JAC81 and JAC95 were relatively the most productive in the three media regarding the numbers of VOCs (Figure 3.3.3.2).

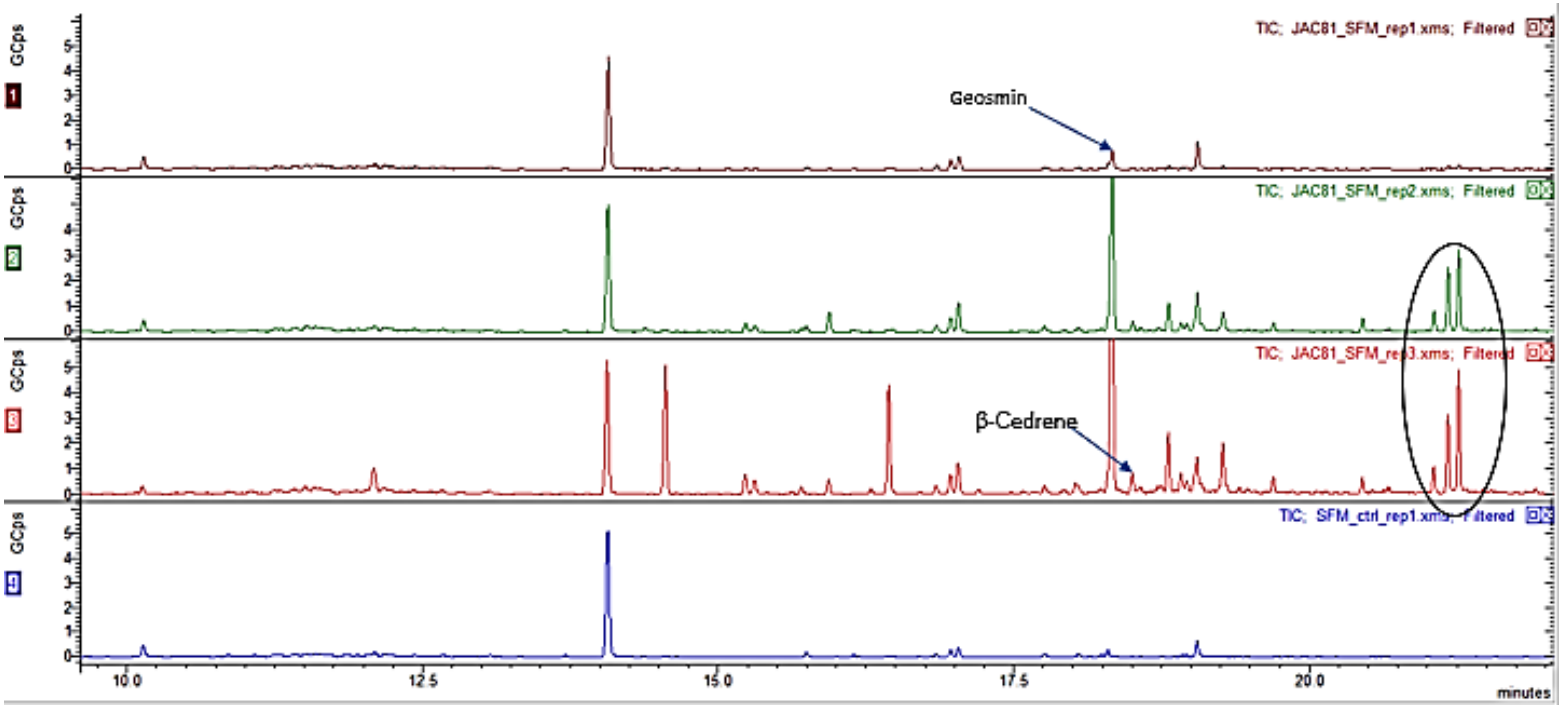

Figure 3.3.3.1: Example (~10- 22 min) of GC-MS chromatogram for JAC81 replicate cultures (x3) fermented in SFM medium. Two peaks with >40% probability match to the reference spectra are labeled. JAC81 chromatograms are compared to the SFM medium chromatogram used as a control. Only peaks common to at least two of JAC81 replicate cultures are considered VOC products of said bacteria. Peaks at RT 21.056 to 21.266 (circled) were identified with an "unknown" confidence level.

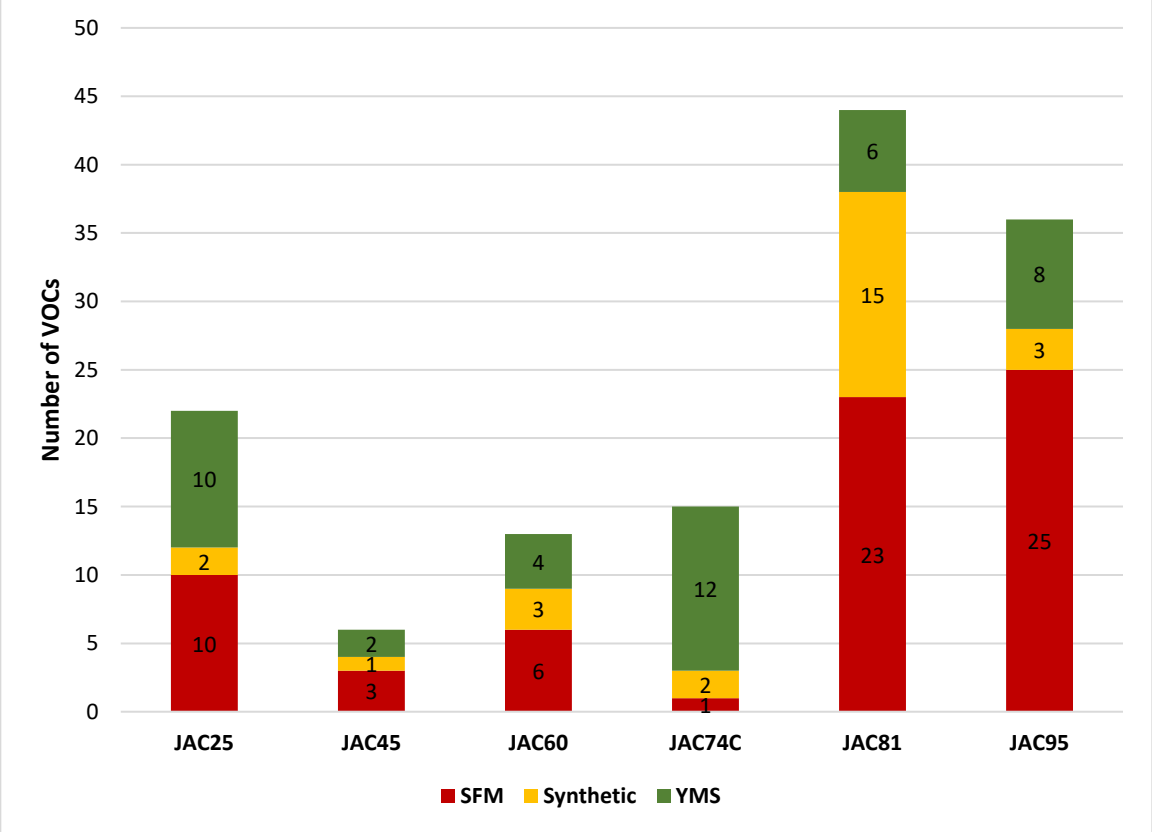

Figure 3.3.3.2: The numbers of VOCs produced by the *Streptomyces* isolates in replicate culture analysis. VOCs were counted if they were present in at least two replicate cultures of a given isolate.

Table 3.3.3.1: Bacterially derived compounds identified in replicate VOC analysis.

No.	VOC [a]	IUPAC name	Confidence in VOC ID [b]	RT	Stdev from the RT [c]	Medium	Isolate	Present in total replicates [d]
1	(1,2,2-trimethyl-3-cyclopenten-1-yl)acetaldehyde	2-(1,2,2-trimethylcyclopent-3-en-1-yl)acetaldehyde	low	15.711	0.001	SFM	JAC25	2
				15.714	0.002	SFM	JAC95	3
				15.707	0.004	SFM	JAC81	2
2	(S)-3,4-Dimethylpentanol	(3S)-3,4-dimethylpentan-1-ol	unknown	6.257	0.045	YMS	JAC95	2
3	.alfa.-Copaene	1,3-dimethyl-8-propan-2-yltricyclo[4.4.0.02,7]dec-3-ene	unknown	21.130	0.001	SFM	JAC95	3
4	1,5-Cyclodecadiene, 1,5-dimethyl-8-(1-methylethenyl)-, [S-(Z,E)]-	(1E,5Z,8S)-1,5-dimethyl-8-prop-1-en-2-ylcyclodeca-1,5-diene	unknown	17.933	0.001	SFM	JAC95	3
				17.930	0.002	YMS	JAC74C	2
5 [a]	1,5-Cyclodecadiene, 1,5-dimethyl-8-(1-methylethenyl)-, [S-(Z,E)]--Dup1 [f]	[g]	unknown	20.109	0.001	YMS	JAC74C	3
	1-Methylene-2b-hydroxymethyl-3,3-dimethyl-4b-(3-methylbut-2-enyl)-cyclohexane	[2,2-dimethyl-4-(3-methylbut-2-enyl)-6-methylidenecyclohexyl]methanol						
6 [a]	1,6:3,4-Dianhydro-2-deoxy-.beta.-d-ribo-hexopyranose	3,7,9-trioxatricyclo[4.2.1.02,4]nonane	unknown	5.499	0.001	YMS	JAC25	2
	Oxalic acid, cyclohexyl tetradecyl ester	2-O-cyclohexyl 1-O-tetradecyl oxalate						

7	1,6-Cyclodecadiene, 1-methyl-5-methylene-8-(1-methylethyl)-, [S-(E,E)]-	(1Z,6Z)-1-methyl-5-methylidene-8-propan-2-ylcyclodeca-1,6-diene	high	19.273	0.000	SFM	JAC25	2
	Germacrene D [e]							
				19.274	0.001	SFM	JAC95	3
				19.271	0.001	SFM	JAC81	3
				19.271	0.002	synthetic	JAC81	3
				19.274	0.002	YMS	JAC74C	2
8 [a]	1,8-Nonanediol, 8-methyl-	8-methylnonane-1,8-diol	unknown	4.722	0.014	YMS	JAC25	2
	2-Methyl-2,3-pentanediol	2-methylpentane-2,3-diol		4.720	0.004	YMS	JAC60	2
9	10-Methylundecan-4-olide	5-(6-methylheptyl)oxolan-2-one	low	21.155	0.004	synthetic	JAC74C	2
				21.157	0.002	YMS	JAC74C	3
10	1H-3a,7-Methanoazulene, octahydro-3,8,8-trimethyl-6-methylene-, [3R-(3.alpha.,3a.beta.,7.beta.,8a.alpha.)]-	2,6,6-trimethyl-8-methylidenetricyclo[5.3.1.01,5]undecane	high	18.506	0.003	SFM	JAC81	3
	β-Cedrene [e]							
11	1-Hexanol	hexan-1-ol	high	6.197	0.002	synthetic	JAC60	3
12 [a]	1-Hexyl-2-nitrocyclohexane	1-hexyl-2-nitrocyclohexane	unknown	19.803	0.001	SFM	JAC95	2
	Hexadecen-1-ol, trans-9-	(E)-hexadec-9-en-1-ol						
13 [a]	1-Hexyl-2-nitrocyclohexane-Dup1 [f]	[g]	unknown	27.638	0.001	YMS	JAC25	3
	Oxiraneoctanoic acid, 3-octyl-, methyl ester	methyl 8-[(2S,3R)-3-octyloxiran-2-yl]octanoate						
	3-Methyl-2-(2-oxopropyl)furan	1-(3-methylfuran-2-yl)propan-2-one						

14	1H-Indene, 1-ethylideneoctahydro-7a-methyl-, (1E,3aα,7aβ)-	(1E)-1-Ethylidene-7a-methyloctahydro-1H-indene	unknown	15.626	0.005	SFM	JAC81	2
15	1H-Indene, 1-ethylideneoctahydro-7a-methyl-, (1Z,3aα,7aβ)-	(1E)-1-Ethylidene-7a-methyloctahydro-1H-indene	unknown	15.316	0.003	SFM	JAC25	2
				15.317	0.000	SFM	JAC95	3
				15.311	0.002	SFM	JAC81	2
				15.314	0.003	synthetic	JAC81	2
16	1H-Indene, 1-ethylideneoctahydro-7a-methyl-, cis-	[g]	unknown	15.234	0.003	SFM	JAC60	3
				15.235	0.001	SFM	JAC25	2
				15.237	0.001	SFM	JAC95	3
				15.234	0.005	SFM	JAC81	3
				15.233	0.003	synthetic	JAC81	3
				15.237	0.001	YMS	JAC74C	2
17 [a]	1-Methyl-4-isopropyl-cyclohexyl 2-hydroperfluorobutanoate-Dup1 [f]	[g]	unknown	21.836	0.001	YMS	JAC45	2
	4-[(Bicyclo[2.2.1]hepta-2,5-dien-7-yl)oxy]benzonitrile-Dup1 [f]	[g]						
18	1-Methylene-2b-hydroxymethyl-3,3-dimethyl-4b-(3-methylbut-2-enyl)-cyclohexane	[2,2-dimethyl-4-(3-methylbut-2-enyl)-6-methylidenecyclohexyl]methanol	unknown	18.421	0.001	SFM	JAC95	2
				18.505	0.001	synthetic	JAC81	3
19	1-Methylene-2b-hydroxymethyl-3,3-dimethyl-	[g]	unknown	18.507	0.002	YMS	JAC81	2

	4b-(3-methylbut-2-enyl)-cyclohexane-Dup1 [f]							
20 [a]	1-Methylene-2b-hydroxymethyl-3,3-dimethyl-4b-(3-methylbut-2-enyl)-cyclohexane-Dup1 [f]	[g]	unknown	21.479	0.001	SFM	JAC81	2
	10-Pentadecen-5-yn-1-ol, (E)-	(E)-pentadec-10-en-5-yn-1-ol						
21 [a]	1-Methylene-2b-hydroxymethyl-3,3-dimethyl-4b-(3-methylbut-2-enyl)-cyclohexane-Dup1 [f]	[g]	unknown	21.479	0.002	synthetic	JAC81	3
	5,10-Pentadecadiyn-1-ol ; 1,5-Diphenylhex-3-ene-Dup1 [f]	[g]						
22 [a]	1-Methylene-2b-hydroxymethyl-3,3-dimethyl-4b-(3-methylbut-2-enyl)-cyclohexane-Dup1 [f]	[g]	unknown	21.266	0.001	YMS	JAC74C	3
	Dihydro-cis-.alpha.-copaene-8-ol	2,8-dimethyl-5-propan-2-yltricyclo[4.4.0.02,7]decan-4-ol		21.263	0.002	synthetic	JAC81	3
				21.266	0.001	SFM	JAC25	2
				21.266	0.002	SFM	JAC95	3
	5,10-Pentadecadiyne, 1-chloro-	1-chloropentadeca-5,10-diyne						
23	1-Phenyl-2-methyl-oct-1-ene	[(E)-2-methyloct-1-enyl]benzene	unknown	21.177	0.002	SFM	JAC81	3
				21.177	0.002	synthetic	JAC81	3
				21.177	0.001	YMS	JAC81	2
24 [a]	2(5H)-Furanone, 5-(bromomethyl)-5-phenyl-	5-(bromomethyl)-5-phenylfuran-2-one	unknown	21.060	0.003	synthetic	JAC81	2

	3-[4-Hydroxyisopent-2(Z)-enyl]-4-hydroxyacetophenone	1-[4-hydroxy-3-[(Z)-4-hydroxy-3-methylbut-2-enyl]phenyl]ethanone						
25 [a]	2,3,4-Trifluorobenzoic acid, 2,6-dimethylnon-1-en-3-yn-5-yl ester	2,6-dimethylnon-1-en-3-yn-5-yl 2,3,4-trifluorobenzoate	unknown	18.967	0.002	synthetic	JAC81	3
	1-Phenyl-2-methyl-oct-1-ene	[(E)-2-methyloct-1-enyl]benzene						
26 [a]	2,5-Octadiyne, 4,4-diethyl-	4,4-diethylocta-2,5-diyne	unknown	21.914	0.001	SFM	JAC81	2
	Cyclohexene, 1,5,5-trimethyl-6-(2-propenylidene)-	(6Z)-1,5,5-trimethyl-6-prop-2-enylidenecyclohexene		21.916	0.001	synthetic	JAC81	3
27	2,6-Octadienoic acid, 3,7-dimethyl-, methyl ester	methyl (2E)-3,7-dimethylocta-2,6-dienoate	high	16.772	0.001	YMS	JAC74C	2
	Methyl geranate [e]							
28 [a]	2-Furanol, tetrahydro-2-methyl-	2-methyloxolan-2-ol	unknown	4.020	0.003	synthetic	JAC81	2
	propanoic acid, 2-methyl- ethyl ester	ethyl 2-methylpropanoate						
	Propanedioic acid, oxo-, bis(1-methylethyl) ester	dipropan-2-yl 2-oxopropanedioate		4.027	0.005	SFM	JAC81	2
	Butane, 2,2'-[methylenebis(oxy)]bis[2-methyl-	2-methyl-2-(2-methylbutan-2-yloxymethoxy)butane		4.022	0.002	SFM	JAC95	3
29	2H-3,9a-Methano-1-benzoxepin, octahydro-2,2,5a,9-tetramethyl-, [3R-(3.alpha.,5a.alpha.,9.alpha.,9a.alpha.)]-	(2S,6R,9S)-2,6,10,10-tetramethyl-11-oxatricyclo[7.2.1.01,6]dodecane	low	19.699	0.001	SFM	JAC81	2
	Dihydroagarofuran [e]							

30	2H-Pyran-2-one, 6-hexyltetrahydro-	6-hexyloxan-2-one	unknown	18.799	0.005	SFM	JAC95	3
31 [a]	2-Hydroxy-3-pentanone	2-hydroxypentan-3-one	low	4.854	0.001	YMS	JAC95	2
	DL-2,3-Butanediol	butane-2,3-diol		4.856	0.006	YMS	JAC60	2
32 [a]	2-Hydroxy-5-ethyl-5-methylcyclopent-2-en-1-one	5-ethyl-2-hydroxy-5-methylcyclopent-2-en-1-one	unknown	15.940	0.006	SFM	JAC81	3
	Bicyclo[2.2.1]heptan-2-ol, 2-(2-cyclopenten-1-yl)-	2-cyclopent-2-en-1-ylbicyclo[2.2.1]heptan-2-ol						
33	2-Methyl-2,3-pentanediol	2-methylpentane-2,3-diol	unknown	4.720	0.004	YMS	JAC60	2
34	2-Methyl-2-bornene	1,2,7,7-tetramethylbicyclo[2.2.1]hept-2-ene	high	9.966	0.002	SFM	JAC60	3
				9.965	0.001	SFM	JAC25	2
35	2-Methyl-3-(3-methyl-but-2-enyl)-2-(4-methyl-pent-3-enyl)-oxetane	2-methyl-3-(3-methylbut-2-enyl)-2-(4-methylpent-3-enyl)oxetane	unknown	18.724	0.001	SFM	JAC81	2
36	2-Methylisoborneol	1,2,7,7-tetramethylbicyclo[2.2.1]heptan-2-ol	high	14.348	0.001	SFM	JAC60	3
				14.349	0.001	SFM	JAC25	2
				14.347	0.004	synthetic	JAC25	2
				14.351	0.002	YMS	JAC25	2
37 [a]	2R-Acetoxymethyl-1,3,3-trimethyl-4t-(3-methyl-2-buten-1-yl)-1t-cyclohexanol	[6-hydroxy-2,2,6-trimethyl-3-(3-methylbut-2-enyl)cyclohexyl]methyl acetate	unknown	18.918	0.002	SFM	JAC81	2
	Dihydro-cis-.alpha.-copaene-8-ol-Dup1 [f]	[g]						
38	3-Heptyne, 5-methyl-	5-methylhept-3-yne	low	18.729	0.001	SFM	JAC95	3
39	3-Isopropoxy-1,1,1,7,7,7-hexamethyl-3,5,5-tris(trimethylsiloxy)tetrasiloxane	propan-2-yl bis(trimethylsilyl) tris(trimethylsilyloxy)silyl silicate	unknown	18.965	0.002	SFM	JAC81	2

40 [a]	4,4-Dimethyl-3-(3-methylbut-3-enylidene)-2-methylenebicyclo[4.1.0]heptane	(3E)-4,4-dimethyl-3-(3-methylbut-3-enylidene)-2-methylidenebicyclo[4.1.0]heptane	unknown	18.578	0.001	synthetic	JAC81	3
	Benzene, 1-(5,5-dimethyl-1-cyclopenten-1-yl)-2-methoxy-	1-(5,5-dimethylcyclopenten-1-yl)-2-methoxybenzene		18.576	0.002	SFM	JAC81	2
	1-Phenyl-2-methyl-oct-1-ene	[(E)-2-methyloct-1-enyl]benzene						
41	4-Acetylbenzoic acid	4-Acetylbenzoic acid	unknown	14.294	0.002	YMS	JAC95	3
42	4-Methyl-2,4-bis(4'-trimethylsilyloxyphenyl)pentene-1-Dup1 [f]	[g]	unknown	4.862	0.003	synthetic	JAC60	3
43	5,6-Decadien-3-yne, 5,7-diethyl-	[g]	unknown	21.126	0.001	synthetic	JAC25	3
44 [a]	5,6-Decadien-3-yne, 5,7-diethyl-	[g]	unknown	18.811	0.002	synthetic	JAC81	3
	Cadina-1(10),6,8-triene	2,5-dimethyl-8-propan-2-yl-1,2,3,4-tetrahydronaphthalene		18.812	0.002	YMS	JAC81	2
45	5-Hepten-3-one, 5-ethyl-2-methyl-	(E)-5-ethyl-2-methylhept-5-en-3-one	unknown	20.451	0.004	SFM	JAC81	2
46	6,7-Dodecanedione	dodecane-6,7-dione	unknown	21.056	0.003	SFM	JAC81	3
47	7-epi-.alpha.-eudesmol	2-[(2S,4aR)-4a,8-dimethyl-2,3,4,5,6,8a-hexahydro-1H-naphthalen-2-yl]propan-2-ol	low	21.547	0.001	SFM	JAC95	3
48 [a]	Acetamide, N,N'-ethylenebis(N-nitro-	N-[2-[acetyl(nitro)amino]ethyl]-N-nitroacetamide	unknown	4.579	0.021	YMS	JAC81	2
	Pentane, 1-bromo-3,4-dimethyl-	1-bromo-3,4-dimethylpentane						
49	Acetic acid, (dodecahydro-7-hydroxy-1,4b,8,8-tetramethyl-10-oxo-2(1H)-	2-(dimethylamino)ethyl (2E)-2-(7-hydroxy-1,4b,8,8-tetramethyl-10-oxo-1,3,4,4a,5,6,7,8a,9,10a-	unknown	19.482	0.002	SFM	JAC81	2

	phenanthrenylidene)-,2-(dimethylamino)ethyl ester	decahydrophenanthren-2-ylidene)acetate						
50 [a]	Benzene, (propoxymethyl)-	propoxymethylbenzene	unknown	4.231	0.002	SFM	JAC45	3
	1-Heptene, 3-methoxy-	3-methoxyhept-1-ene						
51	Benzoic acid, methyl ester	methyl benzoate	high	11.889	0.001	SFM	JAC95	2
52	Benzyl alcohol	phenylmethanol	high	10.269	0.001	SFM	JAC95	2
53 [a]	Bicyclo[3.2.0]hepta-2,6-diene	bicyclo[3.2.0]hepta-2,6-diene	unknown	12.398	0.010	YMS	JAC95	2
	3-Methoxyamphetamine	1-(3-methoxyphenyl)propan-2-amine						
54	Butane, 2-azido-2,3,3-trimethyl-	2-azido-2,3,3-trimethylbutane	unknown	5.683	0.017	synthetic	JAC95	3
55 [a]	Butanedioic acid, phenyl-	2-phenylbutanedioic acid	unknown	6.730	0.001	synthetic	JAC60	3
	Oxalic acid, pentyl propyl ester	2-O-pentyl 1-O-propyl oxalate						
	(SS)- or (RR)-4-methyl-2,3-pentanediol	4-methylpentane-2,3-diol						
56 [a]	Butanoic acid, 2-methyl-, methyl ester	methyl 2-methylbutanoate	unknown	4.314	0.000	SFM	JAC45	3
				4.314	0.001	synthetic	JAC45	2
	Propanoic acid, 2,2-dimethyl-, 2,4-dinitrophenyl ester	(2,4-dinitrophenyl) 2,2-dimethylpropanoate		4.310	0.004	SFM	JAC60	3
57	Butanoic acid, 3-methyl-	3-methylbutanoic acid	high	5.582	0.007	synthetic	JAC95	3
58	Butanoic acid, 3-methyl-	3-methylbutanoic acid	low	5.634	0.002	synthetic	JAC95	2
59 [a]	Butanoic acid, 3-methyl-	3-methylbutanoic acid	unknown	6.112	0.002	YMS	JAC74C	2
	Methyl tiglate	methyl (E)-2-methylbut-2-enoate						
60	Cadina-1(10),6,8-triene	2,5-dimethyl-8-propan-2-yl-1,2,3,4-tetrahydronaphthalene	low	18.812	0.003	SFM	JAC81	3
61	Caryophyllenyl alcohol	(3Z)-4,8,11,11-tetramethylbicyclo[7.2.0]undec-3-en-5-ol	unknown	20.523	0.001	SFM	JAC95	3

62 [a]	cis-muurola-3,5-diene	(1R,4R,4aS)-4,7-dimethyl-1-propan-2-yl-1,2,3,4,4a,5-hexahydronaphthalene	unknown	21.129	0.001	SFM	JAC25	2
	5,6-Decadien-3-yne, 5,7-diethyl-	[g]						
63 [a]	Cyclobutaneacetonitrile, 1-methyl-2-(1-methylethylidene)-	[g]	unknown	19.031	0.001	YMS	JAC74C	2
	2H-3,9a-Methano-1-benzoxepin, octahydro-2,2,5a,9-tetramethyl-, [3R-(3.alpha.,5a.alpha.,9.alpha.,9a.alpha.)]-	(2S,6R,9S)-2,6,10,10-tetramethyl-11-oxatricyclo[7.2.1.01,6]dodecane						
64 [a]	Cyclobutaneacetonitrile, 1-methyl-2-(1-methylethylidene)--Dup1 [f]	[g]	unknown	19.855	0.002	SFM	JAC95	3
	Nonadecane	nonadecane						
65 [a]	Cyclobutanone, 2-methyl-	2-methylcyclobutan-1-one	unknown	4.562	0.002	SFM	JAC45	3
	Cyclopentanone, 2-(1-methylpropyl)-	2-butan-2-ylcyclopentan-1-one						
66 [a]	Cyclohexanol, 1,3,3-trimethyl-2-(3-methyl-2-methylene-3-butenylidene)-, (Z)-	(2*Z*)-1,3,3-trimethyl-2-(3-methyl-2-methylidenebut-3-enylidene)cyclohexan-1-ol	unknown	21.836	0.004	YMS	JAC60	2
	Cyclohexanone, 3-ethenyl-3-methyl-2-(1-methylethenyl)-6-(1-methylethylidene)-, cis-	[g]						
67	Cyclohexanol, 1-ethyl-2,2-dimethyl-6-methylene-	1-ethyl-2,2-dimethyl-6-methylidenecyclohexan-1-ol	unknown	22.103	0.002	SFM	JAC81	2
68 [a]	Cyclohexanol, 4-ethyl-4-methyl-3-(1-methylethyl)-, (1.alpha.,3.beta.,4.alpha.)-	4-ethyl-4-methyl-3-propan-2-ylcyclohexan-1-ol	unknown	19.704	0.001	SFM	JAC95	3

	2H-3,9a-Methano-1-benzoxepin, octahydro-2,2,5a,9-tetramethyl-, [3R-(3.alpha.,5a.alpha.,9.alpha.,9a.alpha.)]--Dup1 [f]	[g]						
	11,12-Dihydroxyseychellane	2-(hydroxymethyl)-3,6,8-trimethyltricyclo[5.3.1.03,8]undecan-2-ol						
69 [a]	Decane, 3-bromo-	3-bromodecane	unknown	16.709	0.002	SFM	JAC74C	2
	Nonadecane	nonadecane						
70 [a]	Diacetyl sulphide	S-acetyl ethanethioate	low	4.313	0.003	YMS	JAC45	2
	(S)-3,4-Dimethylpentanol	(3S)-3,4-dimethylpentan-1-ol						
71	Diethyl Phthalate	diethyl benzene-1,2-dicarboxylate	high	20.523	0.001	YMS	JAC25	3
				20.522	0.002	YMS	JAC81	3
				20.523	0.001	YMS	JAC74C	2
72	Dihydro-cis-.alpha.-copaene-8-ol-Dup1 [f]	[g]	unknown	18.387	0.002	SFM	JAC81	3
73	Dihydro-cis-.alpha.-copaene-8-ol	2,8-dimethyl-5-propan-2-yltricyclo[4.4.0.02,7]decan-4-ol	unknown	21.263	0.002	synthetic	JAC81	3
				21.266	0.001	SFM	JAC25	2
				21.266	0.002	SFM	JAC95	3
74 [a]	Dihydro-cis-.alpha.-copaene-8-ol-Dup1 [f]	[g]	unknown	19.482	0.001	SFM	JAC95	3
	Selina-3,7(11)-diene	5,8a-dimethyl-3-propan-2-ylidene-1,2,4,4a,7,8-hexahydronaphthalene						
75 [a]	Ethaneperoxoic acid, 1-cyano-1-[2-(2-phenyl-1,3-dioxolan-2-yl)ethyl]pentyl ester	[3-cyano-1-(2-phenyl-1,3-dioxolan-2-yl)heptan-3-yl] ethaneperoxoate	unknown	20.523	0.001	YMS	JAC74C	2

	Diethyl Phthalate	diethyl benzene-1,2-dicarboxylate						
76	Geosmin	(4S,4aS,8aR)-4,8a-dimethyl-1,2,3,4,5,6,7,8-octahydronaphthalen-4a-ol	high	18.331	0.001	SFM	JAC60	3
				18.332	0.002	SFM	JAC25	2
				18.337	0.005	SFM	JAC95	3
				18.334	0.001	SFM	JAC81	3
				18.331	0.002	synthetic	JAC81	3
				18.333	0.002	YMS	JAC74C	3
				18.330	0.003	YMS	JAC81	2
77 [a]	Heptacosane	heptacosane	unknown	25.901	0.000	YMS	JAC25	3
	Dodecane, 2,6,10-trimethyl-	2,6,10-trimethyldodecane						
78 [a]	Hexacosane	hexacosane	unknown	19.854	0.001	YMS	JAC95	2
	Decane, 2,4,6-trimethyl-	2,4,6-trimethyldecane						
79 [a]	Hexadecanoic acid, 15-methyl-, methyl ester	methyl 15-methylhexadecanoate	unknown	26.128	0.001	YMS	JAC25	3
	Methyl stearate	methyl octadecanoate						
80 [a]	Hexane, 2,3-dimethyl-	2,3-dimethylhexane	unknown	20.282	0.001	SFM	JAC95	3
	n-Hexyl methylphosphonofluoridate	1-[fluoro(methyl)phosphoryl]oxyhexane						
81	Hexane, 3,4-bis(1,1-dimethylethyl)-2,2,5,5-tetramethyl-	3,4-ditert-butyl-2,2,5,5-tetramethylhexane	unknown	4.864	0.002	SFM	JAC95	2
82	Hexanedioic acid, bis(2-ethylhexyl) ester	bis(2-ethylhexyl) hexanedioate	unknown	28.636	0.001	YMS	JAC25	3
83	Hexanoic acid, 5-methyl-, methyl ester	methyl 5-methylhexanoate	high	9.322	0.001	SFM	JAC60	2

84 [a]	Naphthalene, 1,2,3,4,4a,5,6,8a-octahydro-4a,8-dimethyl-2-(1-methylethenyl)-, [2R-(2.alpha.,4a.alpha.,8a.beta.)]-	(3S,8aS)-5,8a-dimethyl-3-prop-1-en-2-yl-2,3,4,4a,7,8-hexahydro-1H-naphthalene	unknown	21.268	0.001	SFM	JAC95	3
	Dihydro-cis-.alpha.-copaene-8-ol-Dup1 [f]	[g]						
85 [a]	Naphthalene, 1,2,3,4,4a,7-hexahydro-1,6-dimethyl-4-(1-methylethyl)-	1,6-dimethyl-4-propan-2-yl-1,2,3,4,4a,7-hexahydronaphthalene	unknown	19.933	0.001	SFM	JAC95	2
	5,6-Decadien-3-yne, 5,7-diethyl-	[g]						
86 [a]	Naphthalene, 1,2,3,4,4a,7-hexahydro-1,6-dimethyl-4-(1-methylethyl)-	1,6-dimethyl-4-propan-2-yl-1,2,3,4,4a,7-hexahydronaphthalene	unknown	21.128	0.001	YMS	JAC25	3
	5,6-Decadien-3-yne, 5,7-diethyl-	[g]						
87 [a]	Phenol, 4-[2-(methylamino)ethyl]-	4-[2-(methylamino)ethyl]phenol	unknown	15.712	0.000	YMS	JAC74C	2
	indene-4(1H-indene, 1-ethylideneoctahydro-7a-methyl-,cis-	[g]						
88 [a]	Phenylacetaldehyde N-methyl-N-formylhydrazone	N-methyl-N-[(E)-2-phenylethylideneamino]formamide	unknown	21.391	0.001	YMS	JAC95	2
	Ethanone, 1-(3-ethyloxiranyl)-	1-(3-ethyloxiran-2-yl)ethanone						
89	Phenylethyl Alcohol	2-phenylethanol	high	12.393	0.002	SFM	JAC95	3
				12.388	0.002	YMS	JAC60	2
90	photocitral B	1,6,6-trimethylbicyclo[2.1.1]hexane-5-carbaldehyde	unknown	19.699	0.001	synthetic	JAC81	3

91 [a]	Propanoic acid, 2-methyl-, anhydride	2-methylpropanoyl 2-methylpropanoate	unknown	5.111	0.001	YMS	JAC95	2
	4-Methyl-2,4-bis(4'-trimethylsilyloxyphenyl)pentene-1-Dup1 [f]	[g]						
92 [a]	Pyrazine, 2-methyl-5-(1-methylethyl)-	2-methyl-5-propan-2-ylpyrazine	unknown	10.541	0.007	YMS	JAC95	2
	Acetamide, N,N'-ethylenebis(N-nitro-	N-[2-[acetyl(nitro)amino]ethyl]-N-nitroacetamide						
93 [a]	Pyrimidine-2,4(1H,3H)-dione, 5-amino-6-nitroso-	5-amino-6-nitroso-1H-pyrimidine-2,4-dione	unknown	4.021	0.001	SFM	JAC25	2
	Pentane, 1-propoxy-	1-propoxypentane						
94	Sulfurous acid, cyclohexylmethyl heptadecyl ester	cyclohexylmethyl heptadecyl sulfite	unknown	4.923	0.001	YMS	JAC25	2
95 [a]	Tetrahydrofuran, 2-propyl-	2-propyloxolane	unknown	4.024	0.004	synthetic	JAC74C	2
	2,2,5,5,6-Pentamethyl-4,7,9-trioxabicyclo[4.2.1]nonane	1,2,2,5,5-pentamethyl-3,8,9-trioxabicyclo[4.2.1]nonane						

[a] VOC names should be interpreted with caution where more than one VOCs have similar retention time (RT).

[b] The level of confidence assigned to the identity of the VOC. High confidence means there was a good spectral match to the NIST library reference and a Kovats retention index (RI) within 10 points of a literature value available on the NIST WebBook (https://webbook.nist.gov/chemistry/name-ser/), low confidence means the difference in RI of a NIST library suggested VOC to that of the literature value is greater 10 points, and unknown means that a literature RI value could not be found for a NIST library suggested compound.

[c] Standard deviation from the average retention time (RT).

[d] The number of replicates of an isolate fermented in each medium that had the VOC in question. Only VOCs present in at least 2 of 3 media replicate cultures are listed as produced by the *Streptomyces* isolate in question.

[e] common name for the given VOC.

[f] Dup1 suffix means a NIST reference spectra with close identity to the given VOC was not available in the library used in this study.

[g] not applicable or IUPAC name not available.

1-hexanol produced by JAC60 was only detected in the synthetic medium and has various bioactivities (Table 3.3.2.1), including attracting the beetle, *Scolytus schevyrewi*, a pest to apricot trees (producer of 1-hexanol) that promote the death of the host trees (Zhu et al., 2020). Other insects that pose a threat to small fruits have found a way to evolve and sense 1-hexanol. For example, the oriental fruit fly, *Grapholita molesta*, has honed its receptors to sense plant volatiles, including 1-hexanol (L. H. Chen et al., 2019). The same compound disrupts CO_2-mediated activation and host-finding behaviour in *Ades aegypti* mosquitoes (Turner et al., 2011). Geosmin was detected from four of the six isolates (JAC25, JAC60, JAC81, and JAC95) fermented in SFM, one of the six (JAC81) fermented in the synthetic medium, and two of the six (JAC74C and JAC81) fermented in YMS (VOC No. 76, Table 3.3.3.1). Geosmin attracts springtails insects (Becher et al., 2020) but repels *Drosophila* (Stensmyr et al., 2012). Other VOCs function similarly (Table 1.3.3.1); hence, it is crucial to not categorize VOCs as having only one mechanism of action, e.g., insect repellency. A species that uses a given VOC as a communication signal evolve to either be repelled or attracted to the location of that VOC, e.g., a predator to avoid or a food source for nourishment, respectively. Therefore, when selecting VOCs for agricultural uses, one needs to do extensive experiments, including insect repellency testing, to investigate the effects of candidate compounds on pests and their natural predators. In addition, the fermentation media used will determine the VOCs produced.

3.3.4: There was no direct relationship between *Streptomyces* growth and VOC production

An indirect DNA assay (Burton, 1968; Zhao et al., 2013) was performed to determine the growth in the fermentation media of the six isolates selected for replicate VOC analysis. DNA content in the cultures was measured and used to correlate with growth. The DNA was treated with a diphenylamine reagent creating products with typical absorbance at 595 nm. Absorbance was then compared for the cultures with a higher absorbance indicating more growth. Comparison of the amount of VOCs produced and the growth of the six isolates showed no direct relationship across the three media (Figure 3.3.3.2 and Figure 3.3.4.1). Only JAC81 out of six isolates showed that more growth equalled more VOCs produced.

Furthermore, JAC74C showed the least growth in YMS (Figure 3.3.4.1) but produced the most VOCs in YMS (Figure 3.3.3.2). JAC45 and JAC60 grew the most in YMS compared to the other two media (Figure 3.3.4.1). However, the number of VOCs produced by each of the two isolates in YMS was less than those made in SFM and not notably more than those produced in the synthetic medium (Figure 3.3.3.2). The results showed that it might not have been the growth of the isolates but other conditions like the ingredients in the media that determined VOC production. Therefore, optimal conditions for specialized metabolite production are not the same for different species (VanderMolen et al., 2013). More growth may not be more ideal for VOC production. Moreover, variations existed within replicates of the same isolate, i.e., VOC production was not the same across replicate cultures (Table 3.3.3.1), and only VOCs produced in at least two replicate cultures were considered. It should also be noted that VOC collection was done after five days of

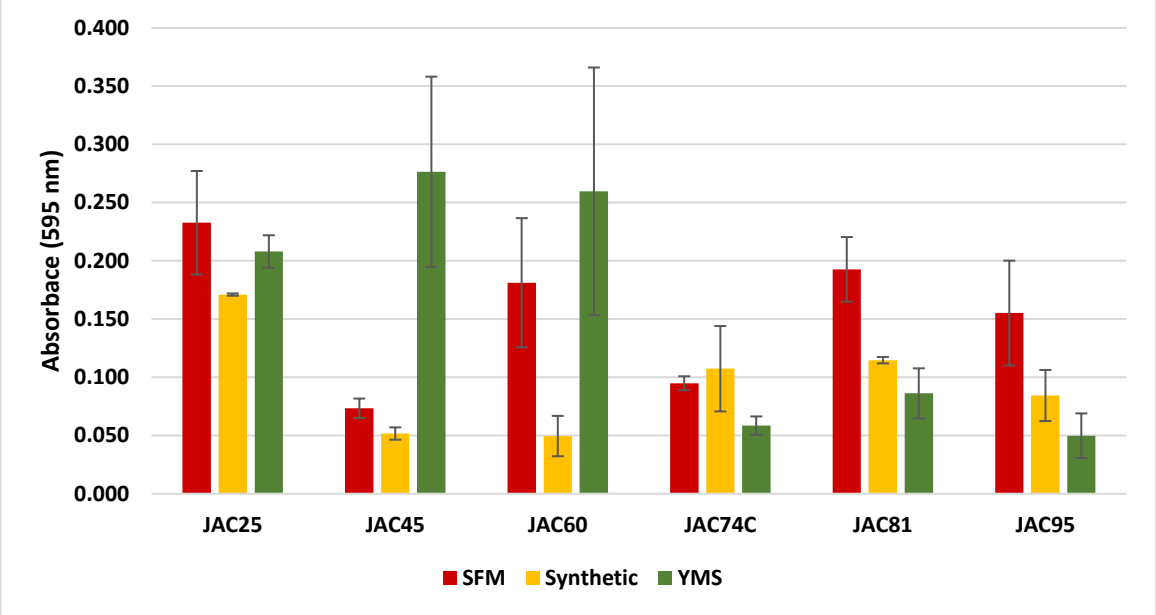

Figure 3.3.4.1: Growth of the *Streptomyces* isolates fermented in SFM, YMS, and the synthetic media. DNA content in the cultures was measured and used to correlate with growth. DNA from the cultures was treated with a diphenylamine reagent creating products with typical absorbance at 595 nm. Error bars represent the standard deviation from the mean calculated for three replicate cultures of the same *Streptomyces* isolate for each medium. Duplicate absorbances for each replicate culture were measured and averaged before calculating the average absorbances for the *Streptomyces* isolates.

fermentation, and VOCs emitted before collection were not trapped for GC-MS analysis. Therefore, cultures that grew the most may have emitted most of their VOCs earlier in the fermentation period and have entered the death phase of its growth closer to the time of collection. At this point, the nutrients in the media would have been primarily used up (Kolter et al., 1993), and VOCs produced are expected to be less.

3.4: Bioassay typing of selected *Streptomyces* isolates

3.4.1: Antibiotic bioactivities varied for phylogenetically different isolates

The 37 *Streptomyces* isolates selected from different OTUs were tested for bioactivities against several indicator organisms, including Gram-positive and Gram-negative bacteria and a fungus (Figure 3.4.1.1). Twelve isolates (JAC24, JAC30L, JAC31, JAC33, JAC45, JAC58, JAC74C, JAC74L, JAC86, JAC101, JAC103, and JAC110) displayed no bioactivity against any of the biological indicators. The remaining 25 isolates produced antibacterials, with ten isolates (JAC25, JAC54, JAC55, JAC68, JAC72, JAC81, JAC88, JAC96, JAC99, JAC122) having activities against Gram-negative bacteria and 19 isolates (JAC17, JAC25, JAC35, JAC47, JAC48, JAC54, JAC55, JAC60, JAC61A, JAC64, JAC68, JAC75, JAC78, JAC81, JAC87, JAC88, JAC90, JAC96, JAC102) having activities against Gram-positive bacteria. Eight isolates (JAC6, JAC35, JAC54, JAC55, JAC75, JAC76, JAC81, and JAC95) had anti-fungal activity.

The isolates produced diverse bioactivities across the three media. For example, supernatant from JAC35 grown in SFM had activity against all indicators except *E. coli* and *P. fluorescence*. JAC35 supernatant from the synthetic medium had similar results to

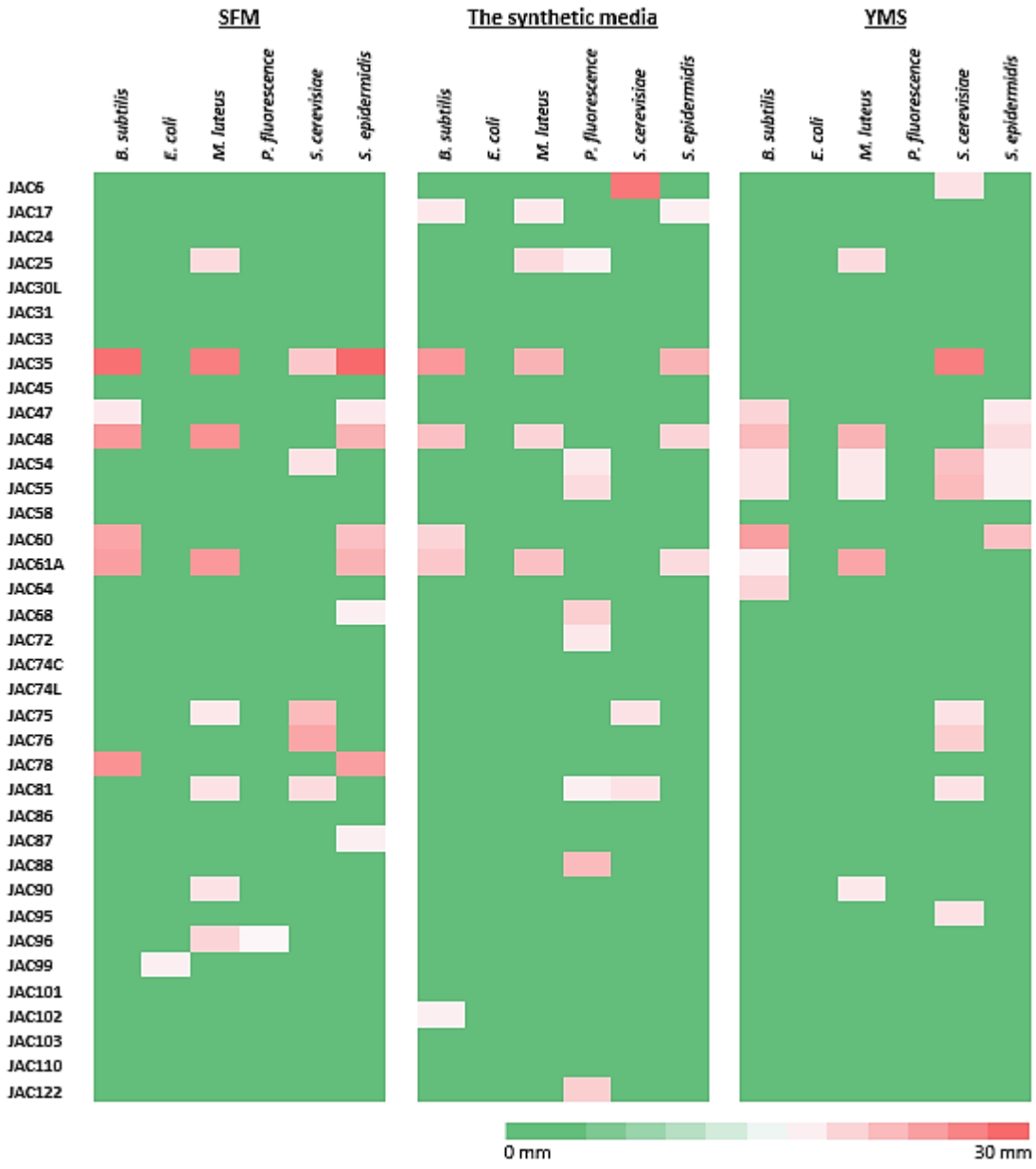

Figure 3.4.1.1: Comparative single-culture supernatant bioassay against six indicator organisms. Supernatants were from the 37 *Streptomyces* isolates representing different OTUs and fermented in SFM, YMS, and the synthetic medium. The data available was for one replicate bioassay analysis. Zones of inhibitions (ZOIs) were measured in mm.

SFM but showed no inhibition against *S. cerevisiae,* while only *S. cerevisiae* was inhibited when exposed to JAC35 supernatant grown on YMS. Only one medium had supernatants showing bioactivities in some cases, e.g., JAC72, JAC102, and JAC122 grown in the synthetic medium, and JAC78, JAC87 JAC96, and JAC99 grown in SFM, and the indicators were not necessarily the same ones inhibited as seen with JAC54.

The six *Streptomyces* isolates used in replicate VOC analysis were fermented in triplicate and tested for bioactivity against the same indicator organisms mentioned above (Figure 3.4.1.2). There were some differences when the results were compared for the bioassays first done with one culture supernatant of each isolate (Figure 3.4.1.1) and subsequently with replicate culture supernatants (Figure 3.4.1.2). JAC25 replicate cultures did not show bioactivity against any biological indicators contrasting with the results obtained before, where *M. luteus* was inhibited with supernatants from the three media and *P. fluorescence* was inhibited by supernatant from the synthetic medium (Figure 3.4.1.1). JAC45 replicate culture supernatants from the synthetic medium displayed bioactivity against *E. coli* and *P. fluorescence* (Figure 3.4.1.2), though the isolate did not show bioactivity when first tested (Figure 3.4.1.1). Likewise, the JAC74C replicate culture supernatants from YMS displayed antibacterial activity against *M. luteus* (Figure 3.4.1.2), but not so when tested at first with one culture supernatant (Figure 3.4.1.1). JAC81 replicate culture supernatants from the synthetic medium did not show bioactivity against *P. fluorescence* and *S. cerevisiae* (Figure 3.4.1.2) but did so when tested at first with supernatant from the same medium (Figure 3.4.1.1). JAC95 replicate culture supernatants from the synthetic medium showed bioactivity against *E. coli* and *P. fluorescence*

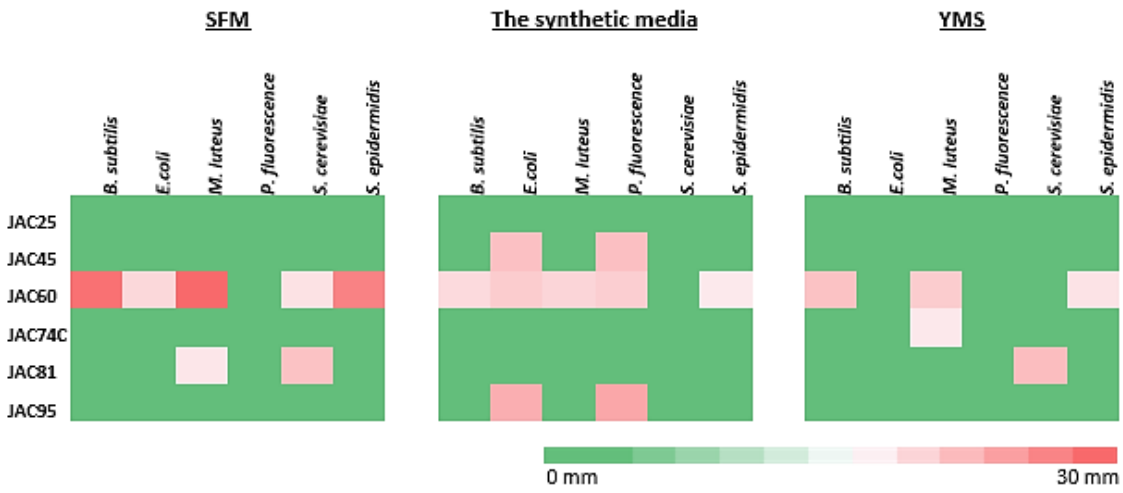

Figure 3.4.1.2: Comparative replicate supernatant bioassay against six indicator organisms. Supernatants were from six *Streptomyces* isolates fermented in triplicate in SFM, YMS, and the synthetic medium. Zones of inhibitions (ZOIs) measured in mm were averaged for the three replicates and used to construct the heat map.

(Figure 3.4.1.2), while only supernatant from YMS inhibited *S. cerevisiae* when JAC95 was first tested (Figure 3.4.1.1). JAC60 replicate culture supernatants inhibited all biological indicators (Figure 3.4.1.2), but only *B. subtilis* and *S. epidermidis* were inhibited by JAC60 single-culture supernatant when tested first (Figure 3.4.1.1).

One should be aware that variability can occur in replicate cultures of the same bacteria as local conditions within a fermentation flask may differ from those of other flasks treated under the same laboratory conditions (Siebenberg et al., 2010). Therefore, these events were not unexpected because slight changes (e.g., the concentration of oxygen in the fermentation flasks) can affect specialized metabolite production, including the volume produced and whether it is enough to cause inhibition of a biological indicator.

Apart from external conditions and uncontrollable circumstances, it is established that media formulation and growth conditions should be considered when targeting a specialized metabolite for production. In the "one strain many compounds" technique, one bacterial strain can produce many different compounds by changing media composition and cultivation conditions (Pan et al., 2019). Hence, one should keep this in mind to capture a bacterial strain's total specialized metabolic capacity.

3.4.2: Phytopathogenicity testing of select *Streptomyces* isolates

The six *Streptomyces* isolates selected for replicate VOC analysis were tested for toxic effects on plants in a simple radish seedlings assay. The *Streptomyces* isolates were compared to a known plant pathogen, *S. scabies* 87-22 (Li et al., 2019), using the respective isolates spores as inoculants to the seedlings. The results (Figure 3.4.2.1) showed that only

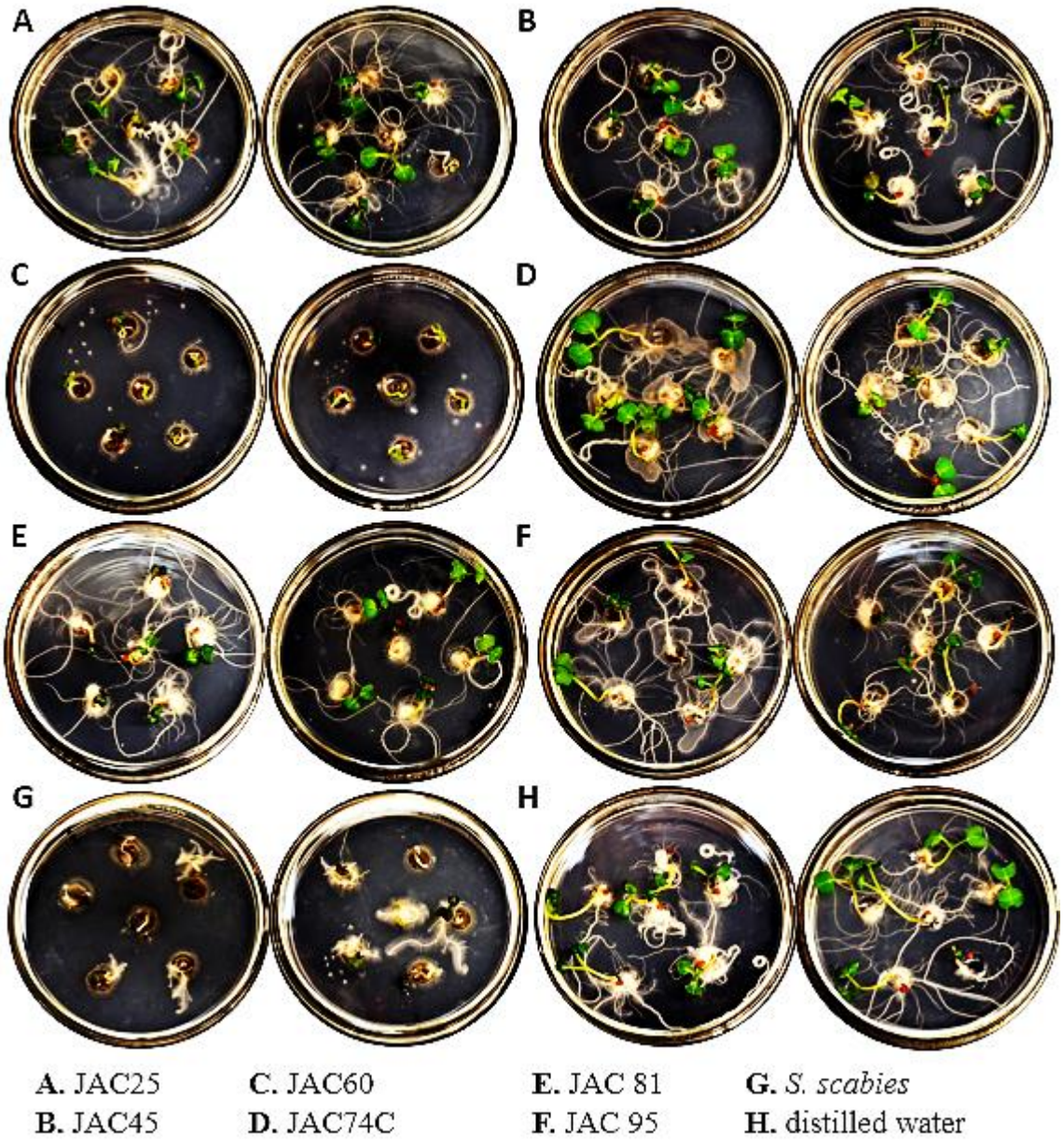

Figure 3.4.2.1: Phytotoxic effects of *Streptomyces* isolates spores on radish seedlings. *S. scabies* 87-22 was used as a positive control and sterile distilled water as a negative control. The test was done in duplicate.

JAC60 significantly hindered the growth of the radish seedlings. The roots and shoots of the seedlings were not well developed compared to the seedlings treated with the other *Streptomyces* spores.

Supernatants collected from the six isolates fermented in the SFM medium were tested for plant toxicity. The average for three of the five seedlings in each treatment (the longest and shortest seedlings were removed) was taken. An ANOVA test was used to compare the radish seedling lengths treated with the SFM supernatants from the isolates and the SFM medium control (Table 3.4.2.1). The ANOVA showed that the p-values for both replicates are less than an alpha value of 0.05. Likewise, the F-values for both the replicates are greater than the critical F-statistics, indicating significant results. When considering both replicate experiments, JAC60 and JAC95 hindered the radish seedlings' growth compared to the SFM medium control, though JAC60 caused the most considerable reduction in plant height (Table 3.4.2.1 and Figure 3.4.2.2). JAC45 and JAC74C appeared to enhance the growth of the radish seedlings (Table 3.4.2.1 and Figure 3.4.2.2) though further analysis is necessary to confirm this. *Streptomyces scabies* 87-22 known to produce phytotoxins in OBB (Johnson et al., 2007) was used to verify that the supernatant test worked, where *S. scabies* 87-22 supernatant from fermented OBB hindered the growth of the radish seedlings when compared to the OBB medium (Table 3.4.2.1 and Figure 3.4.2.2).

It should be noted that there is not a big difference in the variance between the lengths of seedlings treated with *S. scabies* 87-22 OBB supernatant and the OBB control. However, *S. scabies* 87-22 OBB supernatant caused shorter heights in the radish seedlings.

Table 3.4.2.1: Radish seedlings height after treatment with the *Streptomyces* isolates and *S. scabies* 87-22 supernatants from the SFM and OBB media, respectively.

		Replicate1			**Replicate2**		
SUMMARY							
Groups	*Count*	*Sum*	*Average*	*Variance*	*Sum*	*Average*	*Variance*
JAC25	3	124	41.33	56.33	91	30.33	14.33
JAC45	3	146	48.67	158.33	150	50.00	273.00
JAC60	3	65	21.67	12.33	57	19.00	4.00
JAC74C	3	143	47.67	58.33	145	48.33	70.33
JAC81	3	79	26.33	14.33	78	26.00	36.00
JAC95	3	118	39.33	8.33	126	42.00	12.00
SFM-ctrl	3	146	48.67	41.33	115	38.33	20.33
OBB-ctrl	3	81	27.00	1.00			
S. scabies 87-22	3	68	22.67	4.33			

ANOVA	**Replicate1**						**Replicate2**					
Source of Variation	*SS*	*df*	*MS*	*F*	*P-value*	*F crit*	*SS*	*df*	*MS*	*F*	*P-value*	*F crit*
Between Groups	2185.14	6	364.19	7.29	0.001096	2.85	2430.29	6	405.05	6.59	0.001787	2.85
Within Groups	698.67	14	49.90				860	14	61.43			
Total	2883.81	20					3290.29	20				

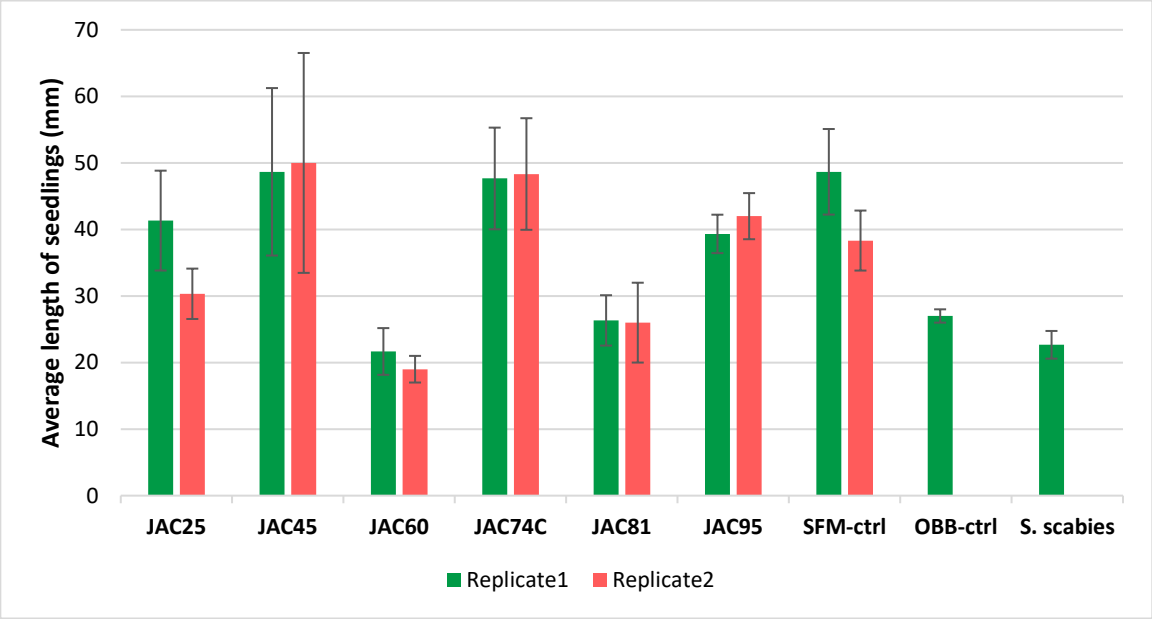

Figure 3.4.2.2: Phytotoxic effects of *Streptomyces* isolates supernatants on radish seedlings. The *Streptomyces* isolates supernatants were drawn from the SFM medium following fermentation. A detailed comparison of the treatments is shown in the ANOVA table (Table 3.4.2.1). The graph depicts averages of technical replicates for the length of seedlings in each supernatant treatment (n=3). The experiment was done in duplicate. Error bars are standard deviations from the means. SFM and Oat-bran broth (OBB) were used as negative controls and *S. scabies* 87-22 supernatant from OBB as a positive control to show that the test worked. There was no positive control for the use of the SFM medium. Only *S. scabies* 87-22 was grown in OBB to collect the supernatant.

In addition, only one replicate treatment was done using the *S. scabies* 87-22 OBB supernatant and the OBB control. The next step would be to repeat the experiment using replicates and with the *Streptomyces* isolates supernatants from OBB, YMS, and the synthetic media.

By and large, the use of SFM supernatants and the *Streptomyces* isolates spores showed comparable results, e.g., JAC60 spores hindered the seedlings' growth the most, as did JAC60 SFM supernatant (Table 3.4.2.1 and Figure 3.4.2.2). These findings suggest that the responsible metabolite(s) produced in SFM medium may also be made when the isolates spores were used as the test substance. Therefore, using supernatants from the fermentation of media or spores for some isolates may not be safe for direct use on plants. Further studies are encouraged to ensure plant safety or VOCs of interest may be isolated for use. One could exploit the plant growth-inhibiting action of JAC60 as a herbicidal strategy, but likewise, further study of the isolate is encouraged.

3.5: *Streptomyces* isolates identification required more than the 16S rDNA in some cases

DNA sequences for the molecular identification of the six isolates used in replicate VOC analysis and phytopathogenicity testing include 16S rDNA and the *rpoB* gene. The six isolates were identified as members of the genus *Streptomyces* from a 16S rDNA search against the NCBI 16S rRNA database. The top hit for a query (the isolate's 16S rDNA sequence) was taken as the species ID for the isolate if it had the highest percent identity to the query sequence. However, if there was more than one top hit with the same percent identity to the query, the *rpoB* gene sequences of those top hits were manually extracted

from the *Streptomyces* species whole-genome sequences obtained from NCBI (accession numbers in Tabe 3.5.1), using *rpoB* primers from this study (Table 2.3.1.1). The top hits *rpoB* sequences were then compared to that of the *Streptomyces* isolate *rpoB* sequence to determine the *Streptomyces* species with the highest percent identity above the recommended minimum of 96–97% percent identity (Adékambi et al., 2009) to the isolate's *rpoB* sequence to determine its ID (Table 3.5.1). The 16S rDNA sequence did not resolve the species identification of four of the six *Streptomyces* isolates (JAC25, JAC60, JAC81, and JAC95). Therefore, their *rpoB* gene sequences were included in determining the species-level IDs (Table 3.5.1).

JAC25 16S rDNA and *rpoB* gene sequences most resemble *S. pratensis*, formerly called *Streptomyces flavogriseus*, and was first named *Actinomyces flavogriseus* by Duché in 1934 (Shirling & Gottlieb, 1969). Following its first isolation, *S. pratensis* has been studied relatively extensively. One study showed that *S. pratensis* was isolated from diseased tomato plants and inhibited pathogenic fungus, *Botrytis cinerea*, infecting the host plant (Lian et al., 2017). Another study showed that *S. pratensis* inhibits the wheat scab causing fungus, *Fusarium graminearum* (Zhang et al., 2020).

JAC45 was identified as *Streptomyces griseoaurantiacus*, first named *Actinomyces griseoaurantiacus* by Krasil'nikov and Yuan in 1965, and then *S. griseoaurantiacus* by Pridham in 1970 (Shirling & Gottlieb, 1972). JAC74C was identified as *Streptomyces xiamenensis*, a *Streptomyces* first isolated from mangrove sediments in the Fujian Province, China (Xu et al., 2009). JAC81 was identified as *Streptomyces sampsonii*, first isolated from garden soil in India (Jain & Jain, 2007). One study reported using *S. sampsonii* to

Table 3.5.1: Molecular identification of select *Streptomyces* isolates.

Isolate	Gene	Query length (nucleotides)	NCBI, BLAST hit [a]	Query cover to reference (%)	Identity to reference (%)	Species ID proposed
JAC25	16S rDNA	1342	*Streptomyces* species: *S. cyaneofuscatus* (NR_115383.1), *S. anulatus* (NR_112527.1), *S. praecox* (NR_115437.1), *S. pratensis* (NR_125616.1)	100	100	*S. pratensis*
	rpoB	709	*Streptomyces* species:			
			S. cyaneofuscatus (NZ_JOEM01000001.1)	100	91.68	
			S. anulatus (NZ_CM003601.1)	100	92.24	
			S. praecox (JF424013.1)	100	92.10	
			S. pratensis (NZ_CP051486.1)	100	98.87	
JAC45	16S rDNA	1372	*Streptomyces griseoaurantiacus* (NR_115231.1)	100	100	*S. griseoaurantiacus*
	rpoB	738	*S. griseoaurantiacus* (NZ_JACERG010000019.1)	100	99.86	
JAC60	16S rDNA	1348	*Streptomyces* species: *S. graminearus* (NR_112461.1), *S. murinus* (NR_112445.1), *S. costaricanus* (NR_041414.1), *S. griseofuscus* (NR_041084.1)	100	100	*S. griseofuscus*
	rpoB	764	*S. murinus* (NZ_MUNF01000071.1)	100	99.21	
			S. griseofuscus (NZ_CP051006.1)	100	99.35	
			S. graminearus (KJ996369.1)	70.68	95.56	
JAC74C	16S rDNA	1354	*Streptomyces xiamenensis* (NR_044035.1)	100	99.41	*S. xiamenensis*
	rpoB	761	*S. xiamenensis* (NZ_CP009922.3)	100	99.60	
JAC81	16S rDNA	1357	*Streptomyces* species: *S. griseochromogenes* (NR_042102.1)	100	100	*S. sampsonii*

			S. resistomycificus (NR_042100.1)			
			S. coelicolor (NR_112305.1)			
			S. sampsonii (NR_112362.1)			
			S. limosus (NR_112279.1)			
			S. felleus (NR_112266.1)			
	rpoB	751	*Streptomyces* sp. GF20			
			S. griseochromogenes (CP016279.1)	100	90.19	
			S. resistomycificus (NZ_KQ948999.1)	100	91.51	
			S. coelicolor (AL645882.2)	100	91.78	
			S. sampsonii (NZ_CP016824.1)	100	99.73	
			S. limosus (KJ996775.1)	72.02	100	
			S. felleus (KT844524.1)	72.02	100	
JAC95	16S rDNA	1345	*Streptomyces* species:	100	100	*S. halstedii*
			S. cyaneus (NR_114820.1)			
			S. griseolus (NR_112493.1)			
			S. halstedii (NR_112275.1)			
	rpoB	743	*S. cyaneus* (NZ_RQJW01000006.1)	100	89.23	
			S. griseolus (NZ_JOFC01000040.1)	100	99.60	
			S. halstedii (NZ_JAAGLQ010000138.1)	100	100	

[a] The accession numbers are provided for *Streptomyces* species obtained using NCBI BLAST against the 16S ribosomal RNA database. The *rpoB* gene sequences of each isolate's 16S ribosomal RNA database top hits were manually extracted from available NCBI whole-genome sequences. Accession numbers of species used for extraction of *rpoB* gene sequences are provided.

degrade poultry feathers to make a fertilizer that improved wheat seed germination and significantly increased plant height (Jain et al., 2016), demonstrating the indirect use of the *Streptomyces* and products.

JAC95 was identified as *Streptomyces halstedii*, a reported producer of compounds that inhibit the growth of fungi, including *Aspergillus fumigatus, Mucor hiemalis, Penicillium roqueforti,* and *Paecilomyces variotii* (Frandberg et al., 2000). Another study showed that red-pepper seeds soaked in a cell-free culture broth (or supernatant) of *S. halstedii* inhibited the fungal phytopathogen, *Phytophthora capsica*, that causes Phytophthora blight in the peppers (Joo, 2005).

JAC60's was identified as *Streptomyces griseofuscus* (Table 3.5.1). Only JAC60 showed severe growth inhibition to the radish seedlings in this study (Table 3.4.2.1, Figure 3.4.2.1, and Figure 3.4.2.2). An antiSMASH analysis to predict specialized metabolite BGCs in the genome of JAC60 species ID, *S. griseofuscus* (Appendix A.3.5.1), and the species with the following closest *rpoB* percent identity, *S. murinus* (Appendix A.3.5.2), was done. A predicted BGC in *S. murinus* had 89% identity to actinomycin D, an antibiotic implicated in inhibiting auxin-induced elongation in oats seedlings (Cleland, 1965). *Streptomyces murinus* was classified as the same species as *S. costaricanus*, by MLSA of five protein-coding genes, including the *rpoB* gene (Komaki, 2021). Actinomycin D was identified in *S. costaricanus* (Liu et al., 2019). Therefore, if actinomycin D was produced by JAC60 and caused the inhibition of the radish seedlings development (Table 3.4.2.1, Figure 3.4.2.1 and Figure 3.4.2.2), *S. murinus* may be the correct ID, or the *S. griseofuscus* strain in this study (JAC60) may have a BGC that produce a plant growth-inhibiting

specialized metabolite. It should be noted that the *rpoB* percent identities between JAC60 and *S. griseoufuscus,* and JAC60 and *S. murinus* were close (99.35% and 99.21%, respectively). Therefore, it is good to use another protein-coding gene like those mentioned in Table 1.2.2.1 to concatenate with the *rpoB* to confirm JAC60's species ID. The same is encouraged for JAC95.

3.6: Concluding remarks

Streptomyces continues to be a resource for relevant natural products. In this study, 133 *Streptomyces* isolates obtained from St. John's, Newfoundland, Canada, showed diversity in the specialized metabolites they produced. It was discussed that VOC biosynthesis is often linked to specialized metabolic pathways, and along these pathways, intermediate products are transformed into new compounds by enzymes to create shunt products. Many other VOCs are yet to be discovered from the *Streptomyces* genus as relatively few are studied to date, suggesting the need for future research of bacteria VOCs that could replace chemicals for sustainable farming practices. For those *Streptomyces* studied, their detected VOCs were not tested for bioactivity in the scope of this thesis. However, some VOCs detected from the *Streptomyces* isolates were described elsewhere (Table 1.3.3.1 and Table 3.3.2.1); nevertheless, these compounds are the same, so reported activities are assumed to be equivalent. Extensive studies must be done when selecting *Streptomyces* or derived products for agriculture because the effects of a given VOC or other specialized metabolite vary across plant and insect species.

This thesis provided new knowledge of *Streptomyces* isolates from Newfoundland and the VOCs they produce. It is vital to determine the effects of the *Streptomyces* spores

or supernatant on the agricultural crop in question. To apply these VOCs in farming practices, experiments including plant and insect assays should be done. Depending on the crop and insect that predates on that plant, bioassays using those specific seedlings and insects are encouraged. In cases where an isolate produces a VOC that repels a predatory insect yet is phytopathogenic, isolating the VOC for use is an alternative. Other solutions include sequencing the genomes of such isolates and identifying BGCs linked to specialized metabolites of interest. These BGCs may then be heterologously expressed in "generally regarded as safe" species to produce the desired compounds. JAC60 could be used as an antiweed strategy. However, plant assays with the weed of interest should be conducted to ensure that only the weed is negatively impacted during application.

References

Adamek, M., Alanjary, M., & Ziemert, N. (2019). Applied evolution: Phylogeny-based approaches in natural products research. *Natural Product Reports*, *36*(9), 1295–1312. https://doi.org/10.1039/c9np00027e

Adékambi, T., Drancourt, M., & Raoult, D. (2009). The rpoB gene as a tool for clinical microbiologists. *Trends in Microbiology*, *17*(1), 37–45. https://doi.org/10.1016/j.tim.2008.09.008

Adekambi, T., Shinnick, T. M., Raoult, D., & Drancourt, M. (2008). Complete rpoB gene sequencing as a suitable supplement to DNA – DNA hybridization for bacterial species and genus delineation. *International Journal of Systematic and Evolutionary Microbiology*, 1807–1814. https://doi.org/10.1099/ijs.0.65440-0

Agarwala, R., Barrett, T., Beck, J., Benson, D. A., Bollin, C., Bolton, E., Bourexis, D., Brister, J. R., Bryant, S. H., Canese, K., Cavanaugh, M., Charowhas, C., Clark, K., Dondoshansky, I., Feolo, M., Fitzpatrick, L., Funk, K., Geer, L. Y., Gorelenkov, V., … Zbicz, K. (2018). Database resources of the National Center for Biotechnology Information. *Nucleic Acids Research*, *46*(D1), D8–D13. https://doi.org/10.1093/nar/gkx1095

Alam, M. T., Merlo, M. E., Takano, E., & Breitling, R. (2010). Genome-based phylogenetic analysis of Streptomyces and its relatives. *Molecular Phylogenetics and Evolution*, *54*(3), 763–772. https://doi.org/10.1016/j.ympev.2009.11.019

Álvarez-Álvarez, R., Martínez-Burgo, Y., Pérez-Redondo, R., Braña, A. F., Martín, J. F., & Liras, P. (2013). Expression of the endogenous and heterologous clavulanic acid cluster in Streptomyces flavogriseus: Why a silent cluster is sleeping. *Applied Microbiology and Biotechnology*, *97*(21), 9451–9463. https://doi.org/10.1007/s00253-013-5148-7

Alves, T. J. S., Murcia, A., Wanumen, A. C., Wanderley-Teixeira, V., Teixeira, Á. A. C., Ortiz, A., & Medina, P. (2019). Composition and Toxicity of a Mixture of Essential Oils Against Mediterranean Fruit Fly, Ceratitis capitata (Wiedemann) (Diptera: Tephritidae). *Journal of Economic Entomology*, *112*(1), 164–172. https://doi.org/10.1093/jee/toy275

Andreu-Coll, L., Noguera-Artiaga, L., Carbonell-Barrachina, Á. A., Legua, P., & Hernández, F. (2020). Volatile composition of prickly pear fruit pulp from six Spanish cultivars. *Journal of Food Science*, *85*(2), 358–363. https://doi.org/10.1111/1750-3841.15001

Antony-Babu, S., Stien, D., Eparvier, V., Parrot, D., Tomasi, S., & Suzuki, M. T. (2017). Multiple Streptomyces species with distinct secondary metabolomes have identical 16S rRNA gene sequences. *Scientific Reports*, *September 2016*, 1–8. https://doi.org/10.1038/s41598-017-11363-1

Apprill, A., Mcnally, S., Parsons, R., & Weber, L. (2015). Minor revision to V4 region SSU rRNA 806R gene primer greatly increases detection of SAR11 bacterioplankton. *Aquatic Microbial Ecology*, *75*(2), 129–137. https://doi.org/10.3354/ame01753

Audrain, B., Farag, M. A., Ryu, C., & Ghigo, J. (2015). Role of bacterial volatile compounds in bacterial biology. *FEMS Microbiology Reviews*, *39*, 222–233. https://doi.org/10.1093/femsre/fuu013

Avalos, M., Garbeva, P., Raaijmakers, J. M., & van Wezel, G. P. (2019). Production of ammonia as a low-cost and long-distance antibiotic strategy by Streptomyces species. *ISME Journal*. https://doi.org/10.1038/s41396-019-0537-2

Baker, G. C., Smith, J. J., & Cowan, D. A. (2003). Review and re-analysis of domain-specific 16S primers. *Journal of Microbiological Methods*, *55*(3), 541–555. https://doi.org/10.1016/j.mimet.2003.08.009

Balloux, F., Brønstad Brynildsrud, O., van Dorp, L., Shaw, L. P., Chen, H., Harris, K. A., Wang, H., & Eldholm, V. (2018). From Theory to Practice: Translating Whole-Genome Sequencing (WGS) into the Clinic. *Trends in Microbiology*, *26*(12), 1035–1048. https://doi.org/10.1016/j.tim.2018.08.004

Baltz, R. H. (2017). Gifted microbes for genome mining and natural product discovery. *Journal of Industrial Microbiology & Biotechnology*, *44*(4), 573–588. https://doi.org/10.1007/s10295-016-1815-x

Barka, E. A., Vatsa, P., Sanchez, L., Gaveau-Vaillant, N., Jacquard, C., Klenk, H.-P., Clement, C., Ouhdouch, Y., & Wezel, G. P. Van. (2015). Taxonomy, Physiology, and Natural Products of Actinobacteria. *American Society for Microbiology*, *80*(1), 1–43. https://doi.org/10.1128/MMBR.00019-15.Address

Becher, P. G., Bengtsson, M., Hansson, B. S., & Witzgall, P. (2010). Flying the fly: Long-range flight behavior of drosophila melanogaster to attractive odors. *Journal of Chemical Ecology*, *36*(6), 599–607. https://doi.org/10.1007/s10886-010-9794-2

Becher, P. G., Verschut, V., Bibb, M. J., Bush, M. J., Molnár, B. P., Barane, E., Al-bassam, M. M., Chandra, G., Song, L., Challis, G. L., Buttner, M. J., & Flärdh, K. (2020). Developmentally regulated volatiles geosmin and 2-methylisoborneol attract a soil arthropod to Streptomyces bacteria promoting spore dispersal. *Nature Microbiology*. https://doi.org/10.1038/s41564-020-0697-x

Bibb, M. J. (2005). Regulation of secondary metabolism in streptomycetes. *Current Opinion in Microbiology*, *8*, 208–215. https://doi.org/10.1016/j.mib.2005.02.016

Blackwood, K. Y. M. S., He, C., Gunton, J., Turenne, C. Y., Wolfe, J., & Kabani, A. M. (2000). Evaluation of recA Sequences for Identification of Mycobacterium Species. *Journal of Clinical Microbiology*, *38*(8), 2846–2852.

Blin, K., Shaw, S., Kloosterman, A. M., Charlop-Powers, Z., Van Wezel, G. P., Medema,

M. H., & Weber, T. (2021). AntiSMASH 6.0: improving cluster detection and comparison capabilities. *Nucleic Acids Research*, *49*(W1), W29–W35. https://doi.org/10.1093/nar/gkab335

Blin, K., Shaw, S., Steinke, K., Villebro, R., Ziemert, N., Lee, S. Y., Medema, M. H., & Weber, T. (2019). antiSMASH 5.0: updates to the secondary metabolite genome mining pipeline. *Nucleic Acids Research*, *47*(W1), W81–W87. https://doi.org/10.1093/nar/gkz310

Burton, K. (1968). [105] Determination of DNA concentration with diphenylamine. *Methods in Enzymology*, *12*(PART B), 163–166. https://doi.org/10.1016/0076-6879(67)12127-7

Cane, D. E., He, X., Kobayashi, S., Mura, S. O., & Ikeda, H. (2006). Geosmin Biosynthesis in Streptomyces avermitilis. Molecular Cloning, Expression, and Mechanistic Study of the Germacradienol/Geosmin Synthase. *Journal of Antibiotics*, *59*(8), 471–479.

Caporaso, J. G., Lauber, C. L., Walters, W. A., Berg-Lyons, D., Lozupone, C. A., Turnbaugh, P. J., Fierer, N., & Knight, R. (2011). Global patterns of 16S rRNA diversity at a depth of millions of sequences per sample. *PNAS*, *108*(SUPPL. 1), 4516–4522. https://doi.org/10.1073/pnas.1000080107

Case, R. J., Boucher, Y., Dahllöf, I., Holmström, C., Doolittle, W. F., & Kjelleberg, S. (2007). Use of 16S rRNA and rpoB genes as molecular markers for microbial ecology studies. *Applied and Environmental Microbiology*, *73*(1), 278–288. https://doi.org/10.1128/AEM.01177-06

Chater, K. F. (2006). Streptomyces inside-out: a new perspective on the bacteria that provide us with antibiotics. *Philosophical Transactions of the Royal Society B*, *361*, 761–768. https://doi.org/10.1098/rstb.2005.1758

Chaudhary, A., Kaur, P., Singh, B., & Pathania, V. (2009). Chemical Composition of Hydrodistilled and Solvent Volatiles Extracted from Woodchips of Himalayan Cedrus: Cedrus deodara (Roxb.) Loud. *Natural Product Communications*, *4*(9), 1257–1260.

Chaudhary, A., Sood, S., Das, P., Kaur, P., Mahajan, I., Gulati, A., & Singh, B. (2014). Synthesis of novel antimicrobial aryl himachalene derivatives from naturally occurring himachalenes. *Experimental and Clinical Sciences*, *13*, 1216–1225.

Chen, J., Lü, J., He, Z., Zhang, F., Zhang, S., & Zhang, H. (2020). Investigations into the production of volatile compounds in Korla fragrant pears (Pyrus sinkiangensis Yu). *Food Chemistry*, *302*(April 2019), 125337. https://doi.org/10.1016/j.foodchem.2019.125337

Chen, L. H., Tian, K., Wang, G. R., Xu, X. L., He, K. H., Liu, W., & Wu, J. X. (2019). The general odorant receptor GmolOR9 from Grapholita molesta (Lepidoptera: Tortricidae) is mainly tuned to eight host-plant volatiles. *Insect Science*, *6*, 1–11.

https://doi.org/10.1111/1744-7917.12725

Cheng, Z., McCann, S., Faraone, N., Clarke, J. A., Hudson, E. A., Cloonan, K., Hillier, N. K., & Tahlan, K. (2020). Production of plant-associated volatiles by select model and industrially important streptomyces spp. *Microorganisms*, *8*(11), 1–20. https://doi.org/10.3390/microorganisms8111767

Chevrette, M. G., Carlos-shanley, C., Louie, K. B., Bowen, B. P., Northen, T. R., & Currie, C. R. (2019). Taxonomic and Metabolic Incongruence in the Ancient Genus Streptomyces. *Frontiers in Microbiology*, *10*, 1–12. https://doi.org/10.3389/fmicb.2019.02170

Chevrette, M. G., Carlson, C. M., Ortega, H. E., Thomas, C., Ananiev, G. E., Barns, K. J., Book, A. J., Cagnazzo, J., Carlos, C., Flanigan, W., Grubbs, K. J., Horn, H. A., Hoffmann, F. M., Klassen, J. L., Knack, J. J., Lewin, G. R., Mcdonald, B. R., Muller, L., Melo, W. G. P., … Currie, C. R. (2019). The antimicrobial potential of Streptomyces from insect microbiomes. *Nature Communications*, *16*, 1–11. https://doi.org/10.1038/s41467-019-08438-0

Choi, Y. J., & Lee, S. Y. (2013). Microbial production of short-chain alkanes. *Nature*, *502*. https://doi.org/10.1038/nature12536

Chu, S. S., Jiang, G. H., & Liu, Z. L. (2011). Insecticidal compounds from the essential oil of Chinese medicinal herb Atractylodes chinensis. *Pest Management Science*, *67*(10), 1253–1257. https://doi.org/10.1002/ps.2180

Chung, T. Y., Eiserich, J. P., & Shibamoto, T. (1993). Volatile Compounds Isolated from Edible Korean Chamchwi (Aster scaber Thunb). *Journal of Agricultural and Food Chemistry*, *41*(10), 1693–1697. https://doi.org/10.1021/jf00034a033

Ciccarelli, D., Giovanelli, S., & Pistelli, L. (2016). Essential Oils from Anthemis maritima Flowers: Infraspecific Variability along the Adriatic Coast (Italy). *Chemistry and Biodiversity*, *13*(5), 561–570. https://doi.org/10.1002/cbdv.201500184

Citron, C. A., Barra, L., Wink, J., & Dickschat, J. S. (2015). Volatiles from nineteen recently genome sequenced actinomycetes. *Organic and Biomolecular Chemistry*, *13*(9), 2673–2683. https://doi.org/10.1039/c4ob02609h

Citron, C. A., Gleitzmann, J., Laurenzano, G., Pukall, R., & Dickschat, J. S. (2012). Terpenoids are Widespread in Actinomycetes : A Correlation of Secondary Metabolism and Genome Data. *Chembiochem*, *13*, 202–214. https://doi.org/10.1002/cbic.201100641

Citron, C. A., Rabe, P., & Dickschat, J. S. (2012). The Scent of Bacteria: Headspace Analysis for the Discovery of Natural Products. *Journal of Natural Products*, *75*, 1765–1776. https://doi.org/10.1021/np300468h

Cleland, R. (1965). Auxin-induced cell wall loosening in the presence of actinomycin D.

Plant Physiology, *40*(4), 595–600. https://doi.org/10.1104/pp.40.4.595

Cordovez, V., Carrion, V. J., Etalo, D. W., Mumm, R., Zhu, H., van Wezel, G. P., & Raaijmakers, J. M. (2015). Diversity and functions of volatile organic compounds produced by Streptomyces from a disease-suppressive soil. *Frontiers in Microbiology*, *6*, 1–13. https://doi.org/10.3389/fmicb.2015.01081

Crawford, J. M., & Clardy, J. (2011). Bacterial symbionts and natural products. *Chemical Communications*, *47*, 7559–7566. https://doi.org/10.1039/c1cc11574j

Curran, A. M., Rabin, S. I., Prada, P. A., & Furton, K. G. (2005). Comparison of the volatile organic compounds present in human odor using SPME-GC/MS. *Journal of Chemical Ecology*, *31*(7), 1607–1619. https://doi.org/10.1007/s10886-005-5801-4

DeLeo, F. R., Chen, L., Porcella, S. F., Martens, C. A., Kobayashi, S. D., Porter, A. R., Chavda, K. D., Jacobs, M. R., Mathema, B., Olsen, R. J., Bonomo, R. A., Musser, J. M., & Kreiswirth, B. N. (2014). Molecular dissection of the evolution of carbapenem-resistant multilocus sequence type 258 Klebsiella pneumoniae. *Pnas*, *111*(13), 4988–4993. https://doi.org/10.1073/pnas.1321364111

Demain, A. L., & Fang, A. (1995). Emerging concepts of secondary metabolism in Actinomycetes. *Actinomycetologica*, *9*(2), 98–117.

Devulder, G., Perouse de Montclos, M., & Flandrois, J. P. (2005). A multigene approach to phylogenetic analysis using the genus Mycobacterium as a model. *International Journal of Systematic and Evolutionary Microbiology*, *55*, 293–302. https://doi.org/10.1099/ijs.0.63222-0

Dias, M. P., Bastos, M. S., Xavier, V. B., Cassel, E., Astarita, L. V., & Santarém, E. R. (2017). Plant growth and resistance promoted by Streptomyces spp. in tomato. *Plant Physiology and Biochemistry*, *118*, 479–493. https://doi.org/10.1016/j.plaphy.2017.07.017

Dickschat, J. S. (2016). Bacterial terpene cyclases. *Natural Product Reports*, *33*, 87–110. https://doi.org/10.1039/c5np00102a

Dickschat, J. S., Pahirulzaman, K. A. K., Rabe, P., & Klapschinski, T. A. (2014). An Improved Technique for the Rapid Chemical Characterisation of Bacterial Terpene Cyclases. *Chembiochem Communications*, *15*, 810–815. https://doi.org/10.1002/cbic.201300763

Dua, V. K., Alam, M. F., Pandey, A. C., Rai, S., Chopra, A. K., Kaul, V. K., & Dash, A. P. (2008). Insecticidal activity of Valeriana jatamansi (Valerianaceae) against mosquitoes. *Journal of the American Mosquito Control Association*, *24*(2), 315–318. https://doi.org/10.1649/0010-065x(2003)057[0114:antfcg]2.0.co;2

Dweck, H. K. M., Ebrahim, S. A. M., Thoma, M., Mohamed, A. A. M., Keesey, I. W., Trona, F., Lavista-Llanos, S., Svato, A., Sachsea, S., Knadena, M., & Hanssona, B. S. (2015). Pheromones mediating copulation and attraction in Drosophila. *PNAS*,

112(21), E2829–E2835. https://doi.org/10.1073/pnas.1504527112

Dworkin, M. (2006). *The Prokaryotes: A Handbook on the Biology of Bacteria* (M. Dworkin (ed.); 3rd ed.). Springer.

Ehsani, A., Rezaeiyan, A., Hashemi, M., Aminzare, M., Jannat, B., & Afshari, A. (2019). Antibacterial activity and sensory properties of Heracleum persicum essential oil, nisin, and Lactobacillus acidophilus against Listeria monocytogenes in cheese. *Veterinary World*, *12*(1), 90–96. https://doi.org/10.14202/vetworld.2019.90-96

El-Din Mohamed, W. S., & Zaki, D. F. A. (2019). Evaluation of antagonistic actinomycetes isolates as biocontrol agents against wastewater-associated bacteria. *Water Science and Technology*, *79*(12), 2310–2317. https://doi.org/10.2166/wst.2019.231

El-Sayed, A. M. (2007). *The Pherobase: Database of Insect Pheromones and Semiochemicals.* http://www.pherobase.net

Elghwaji, W., El-Sayed, A. M., El-Deeb, K. S., & ElSayed, A. M. (2017). Chemical Composition, Antimicrobial and Antitumor Potentiality of Essential Oil of Ferula tingitana L. Apiaceae Grow in Libya. *Pharmacognosy Magazine*, *13*. https://doi.org/10.4103/pm.pm

Emerson de Lima Procópio, R., Reis da Silva, I., Martins, M. K., Lucio de Azevedo, J., & Magali de Araújo, J. (2012). Antibiotics produced by Streptomyces. *Brazilian Journal of Infectious Diseases*, *16*(5), 466–471. https://doi.org/10.1016/j.bjid.2012.08.014

Enright, M. C., & Spratt, B. G. (1999). Multilocus sequence typing. *Trends in Microbiology*, *7*(12), 482–487.

Erbilgin, N., Gillette, N. E., Mori, S. R., Stein, J. D., Owen, D. R., & Wood, D. L. (2007). Acetophenone as an Anti-attractant for the Western Pine Beetle, Dendroctonus Brevicomis LeConte (Coleoptera: Scolytidae). *Journal of Chemical Ecology*, *33*, 817–823. https://doi.org/10.1007/s10886-007-9267-4

Errard, A., Ulrichs, C., Kühne, S., Mewis, I., Drungowski, M., Schreiner, M., & Baldermann, S. (2015). Single- versus Multiple-Pest Infestation Affects Differently the Biochemistry of Tomato (Solanum lycopersicum 'Ailsa Craig'). *Journal of Agricultural and Food Chemistry*, *63*(46), 10103–10111. https://doi.org/10.1021/acs.jafc.5b03884

Espinoza, J., Urzúa, A., Tampe, J., Parra, L., & Quiroz, A. (2016). Repellent Activity of the Essential Oil from the Heartwood of Pilgerodendron uviferum (D. Don) Florin against Aegorhinus superciliosus (Coleoptera: Curculionidae). *Molecules*, *21*(4), 1–7. https://doi.org/10.3390/molecules21040533

Farrelly, V., Rainey, F. A., & Stackebrandt, E. (1995). Effect of Genome Size and rrn Gene Copy Number on PCR Amplification of 16S rRNA Genes from a Mixture of

Bacterial Species. *American Society for Microbiology*, *61*(7), 2798–2801.

Feng, Y., & Zhang, A. (2017). A Floral Fragrance, Methyl Benzoate, Is An Efficient Green Pesticide. *Scientific Reports*, *7*(42168), 1–9. https://doi.org/10.1038/srep42168

Fox, G. E., Wisotzkey, J. D., & Jurtshuk, JR, P. (1992). How Close Is Close : 1 s rRNA Sequence Identity May Not Be Sufficient To Guarantee Species Identity. *International Journal of Systematic Bacteriology*, *42*(1), 166–170.

Franco, T. A., Xu, P., Brito, N. F., Oliveira, D. S., Wen, X., Moreira, M. F., Unelius, C. R., Leal, W. S., & Melo, A. C. A. (2018). Reverse Chemical Ecology-Based Approach Leading to the Accidental Discovery of Repellents for Rhodnius Prolixus, a Vector of Chagas Diseases Refractory to DEET. *Insect Biochemistry and Molecular Biology*, *103*, 46–52. https://doi.org/10.1016/j.ibmb.2018.10.004

Frandberg, E., Petersson, C., Lundgren, L. N., & Schnurer, J. (2000). Streptomyces halstedii K122 produces the antifungal compounds bafilomycin B1 and C1. *Canadian Journal of Microbiology*, *46*(8), 753–758. https://doi.org/10.1139/cjm-46-8-753

Gabaldón, T., & Koonin, E. V. (2013). Functional and evolutionary implications of gene orthology. *Nature Reviews Genetics*, *14*(5), 360–366. https://doi.org/10.1038/nrg3456

Garbeva, P., Hordijk, C., Gerards, S., & Boer, W. De. (2014). Volatile-mediated interactions between phylogenetically different soil bacteria. *Frontiers in Microbiology*, *5*. https://doi.org/10.3389/fmicb.2014.00289

Gerber, N., & Brunswick, N. (1965). Geosmin , Earthy-Smelling Substance Isolated from Actinomycetes. *American Society for Microbiology*, *13*(6), 935–938.

Gerber, N. N. (1969). A Volatile Metabolite of Actinomycetes, 2-methylisoborneol. *The Journal of Antibiotics*, 508–509.

Gevers, D., Cohan, F. M., Lawrence, J. G., Spratt, B. G., Coenye, T., Feil, E. J., Stackebrandt, E., Peer, Y. Van De, Vandamme, P., Thompson, F. L., & Swings, J. (2005). Opinion: Re-evaluating prokaryotic species. *Nature Reviews Microbiology*, *3*(September), 733–740.

Gil, R., Silva, F. J., Pereto, J., & Moya, A. (2004). Determination of the Core of a Minimal Bacterial Gene Set. *American Society for Microbiology*, *68*(3), 518–537. https://doi.org/10.1128/MMBR.68.3.518

Glaeser, S. P., & Kämpfer, P. (2015). Multilocus sequence analysis (MLSA) in prokaryotic taxonomy. *Systematic and Applied Microbiology*, *38*(4), 237–245. https://doi.org/10.1016/j.syapm.2015.03.007

Gliessman, S. R. (1990). Agroecology: Researching the Ecological Basis for Sustainable Agriculture. In S. R. Gliessman (Ed.), *Angewandte Chemie International Edition,*

6(11), 951–952. (1st ed., Vol. 13, Issue April). Springer-Verlag. https://doi.org/10.1007/978-1-4612-3252-0

González-Torres, P., Rodríguez-Mateos, F., Antón, J., & Gabaldón, T. (2019). Impact of Homologous Recombination on the Evolution of Prokaryotic Core Genomes. *MBio*, *10*(1), 1–17.

Govindarajan, M., Rajeswary, M., & Benelli, G. (2016). Chemical composition, toxicity and non-target effects of Pinus kesiya essential oil: An eco-friendly and novel larvicide against malaria, dengue and lymphatic filariasis mosquito vectors. *Ecotoxicology and Environmental Safety*, *129*, 85–90. https://doi.org/10.1016/j.ecoenv.2016.03.007

Groenhagen, U., Maczka, M., Dickschat, J. S., & Schulz, S. (2014). *Streptopyridines , volatile pyridine alkaloids produced by Streptomyces sp . FORM5*. 1421–1432. https://doi.org/10.3762/bjoc.10.146

Gu, Y., Mo, M., Zhou, J., Zou, C., & Zhang, K. (2007). Evaluation and identification of potential organic nematicidal volatiles from soil bacteria. *Soil Biology & Biochemistry*, *39*, 2567–2575. https://doi.org/10.1016/j.soilbio.2007.05.011

Guo, Y., Zheng, W., Rong, X., & Huang, Y. (2008). A multilocus phylogeny of the Streptomyces griseus 16S rRNA gene clade: Use of multilocus sequence analysis for streptomycete systematics. *International Journal of Systematic and Evolutionary Microbiology*, *58*(1), 149–159. https://doi.org/10.1099/ijs.0.65224-0

Gupta, S., Gupta, C., Garg, A. P., & Prakash, D. (2015). A biotechnological approach to microbial based perfumes and flavours. *Journal of Microbiology & Experimentation*, *2*(1), 11–18. https://doi.org/10.15406/jmen.2015.02.00034

Gust, B., Challis, G. L., Fowler, K., Kieser, T., & Chater, K. F. (2003). PCR-targeted Streptomyces Gene Replacement Identifies a Protein Domain Needed for Biosynthesis of the Sesquiterpene Soil Odor Geosmin. *PNAS*, *100*(4), 1541–1546.

Han, J. H., Cho, M. H., & Kim, S. B. (2012). Ribosomal and protein coding gene based multigene phylogeny on the family Streptomycetaceae. *Systematic and Applied Microbiology*, *35*(1), 1–6. https://doi.org/10.1016/j.syapm.2011.08.007

Hansen, M. C., Tolker-nielsen, T., Givskov, M., & Molin, S. (1998). Biased 16S rDNA PCR amplification caused by interference from DNA flanking the template region. *FEMS Microbiology Ecology*, *26*, 141–149.

Haocheng, L., An, K., Su, S., Yu, Y., Wu, J., Xiao, G., & Xu, Y. (2020). Aromatic Characterization of Mangoes (Mangifera indica L.) Using Solid Phase Extraction Coupled with Gas Chromatography–Mass Spectrometry and Olfactometry and Sensory Analyses. *Foods*, *9*(75), 1–20.

Heinsch, S. C., Hsu, S., Otto-hanson, L., Kinkel, L., & Smanski, M. J. (2019). Complete genome sequences of Streptomyces spp. isolated from disease-suppressive soils.

BMC Genomics, *20*.

Heringa, P. K. (1981). Soils of the Avalon Peninsula, Newfoundland. *Research Branch, Agriculture Canada*, *3*, 117.

Heul, H. U. van der, Bilyk, B. L., McDowall, kenneth J., Seipke, R. F., & Wezel, G. P. Van. (2018). Natural Product Reports Regulation of antibiotic production in Actinobacteria: new perspectives from the post-genomic era. *Natural Product Reports*, *35*, 575–604. https://doi.org/10.1039/c8np00012c

Ho, L. K., Daniel-Ivad, M., Jeedigunta, S. P., Li, J., Iliadi, K. G., Boulianne, G. L., Hurd, T. R., Smibert, C. A., & Nodwell, J. R. (2020). Chemical entrapment and killing of insects by bacteria. *Nature Communications*, *11*(1), 1–9. https://doi.org/10.1038/s41467-020-18462-0

Högnadóttir, Á., & Rouseff, R. L. (2003). Identification of aroma active compounds in orange essence oil using gas chromatography–olfactometry and gas chromatography– mass spectrometry. *Journal of Chromatography A*, *998*(1–2), 201–211. https://doi.org/10.1016/S0021-9673(03)00524-7

Holmes, D. E., Nevin, K. P., & Lovley, D. R. (2004). Comparison of 16S rRNA, nifD, recA, gyrB, rpoB and fusA genes within the family Geobacteraceae fam. nov. *International Journal of Systematic and Evolutionary Microbiology*, *54*, 1591–1599. https://doi.org/10.1099/ijs.0.02958-0

Hu, Y., Chou, W. K. W., Hopson, R., & Cane, D. E. (2011). Genome Mining in Streptomyces Clavuligerus: Expression and Biochemical Characterization of Two New Cryptic Sesquiterpene Synthases. *Cell Press*, *18*(1), 32–37. https://doi.org/10.1016/j.chembiol.2010.11.008

Hummadi, E. H., Dearden, A., Generalovic, T., Clunie, B., Harrott, A., Cetin, Y., Demirbek, M., Khoja, S., Eastwood, D., Dudley, E., Hazir, S., Touray, M., Ulug, D., Hazal Gulsen, S., Cimen, H., & Butt, T. (2020). Volatile organic compounds of Metarhizium brunneum influence the efficacy of entomopathogenic nematodes in insect control. *Biological Control*, *155*(December 2020), 104527. https://doi.org/10.1016/j.biocontrol.2020.104527

Ikawa, M., Sasner, J. J., & Haney, J. F. (2001). Activity of cyanobacterial and algal odor compounds found in lake waters on green alga Chlorella pyrenoidosa growth. *Hydrobiologia*, *443*, 19–22.

Ikeda, H., Kotaki, H., & Omura, S. (1987). Genetic studies of avermectin biosythesis in Streptomyces avermitilis. *Journal of Bacteriology*, *169*(12), 5615–5621. https://doi.org/10.1128/jb.169.12.5615-5621.1987

Inerney, J. O. M. C., Wilkinson, M., Patching, J. W., Embley, T. M., & Powell, R. (1995). Recovery and Phylogenetic Analysis of Novel Archaeal rRNA Sequences from a Deep-Sea Deposit Feeder. *Applied and Environmental Microbiology*, *61*(4), 1646–1648.

Insam, H., & Seewald, M. S. A. (2010). Volatile organic compounds (VOCs) in soils. *Biology and Fertility of Soil*, *46*, 199–213. https://doi.org/10.1007/s00374-010-0442-3

Jáchymová, J., Votruba, J., Víden, I., & Řezanka, T. (2002). Identification of Streptomyces odor spectrum. *Folia Microbiologica*, *47*(1), 37–41. https://doi.org/10.1007/BF02818563

Jain, P. K., & Jain, P. C. (2007). Isolation, characterization and antifungal activity of Streptomyces sampsonii GS 1322. *Indian Journal of Experimental Biology*, *45*(2), 203–206.

Jain, R., Jain, A., Rawat, N., Nair, M., & Gumashta, R. (2016). Feather hydrolysate from Streptomyces sampsonii GS 1322: A potential low cost soil amendment. *Journal of Bioscience and Bioengineering*, *121*(6), 672–677. https://doi.org/10.1016/j.jbiosc.2015.11.003

Jensen, S. E., Westlake, D. W. S., & Wolfe, S. (1983). Partial purification and characterization of isopenicillin N epimerase activity from Streptomyces clavuligerus. *Canadian Journal of Microbiology*, *29*(11), 1526–1531. https://doi.org/10.1139/m83-234

Jia, Q., Chen, X., Köllner, T. G., Rinkel, J., Fu, J., Labbé, J., Xiong, W., Dickschat, J. S., Gershenzon, J., & Chen, F. (2019). terpene synthase Genes originated from Bacteria through Horizontal Gene transfer Contribute to terpenoid Diversity in Fungi. *Scientific Reports*, *9*(January), 1–11. https://doi.org/10.1038/s41598-019-45532-1

Jiang, J., He, X., & Cane, D. E. (2007). Biosynthesis of the Earthy Odorant Geosmin by a Bifunctional Streptomyces Coelicolor Enzyme. *Nature Chemical Biology*, *3*(11), 711–715. https://doi.org/10.1038/jid.2014.371

Jirovetz, L., Buchbauer, G., Ngassoum, M. B., & Geissler, M. (2002). A roma compound analysis of Piper nigrum and Piper guineense essential oils from Cameroon using solid-phase microextraction–gas chromatography, solid-phase microextraction–gas chromatography– mass spectrometry and olfactometry. *Journal of Chromatography A*, *976*(1–2), 265–275. https://doi.org/10.1016/S0021-9673(02)00376-X

Johnson, E. G., Joshi, M. V., Gibson, D. M., & Loria, R. (2007). Cello-oligosaccharides released from host plants induce pathogenicity in scab-causing Streptomyces species. *Physiological and Molecular Plant Pathology*, *71*(1–3), 18–25. https://doi.org/10.1016/j.pmpp.2007.09.003

Johnson, J. S., Spakowicz, D. J., Hong, B., Petersen, L. M., Demkowicz, P., Chen, L., Leopold, S. R., Hanson, B. M., Agresta, H. O., Gerstein, M., Sodergren, E., & Weinstock, G. M. (2019). Evaluation of 16S rRNA gene sequencing for species and strain-level microbiome analysis. *Nature Communications*, *10*(5029), 1–11. https://doi.org/10.1038/s41467-019-13036-1

Jolley, K. A., Bray, J. E., & Maiden, M. C. J. (2018). Open-access bacterial population

genomics: BIGSdb software, the PubMLST.org website and their applications [version 1; peer review: 2 approved]. *Wellcome Open Research*, *3*(124), 1–20. https://doi.org/10.12688/wellcomeopenres.14826.1

Jolley, K. A., & Maiden, M. C. J. (2014). Using MLST to study bacterial variation: Prospects in the genomic era. *Future Microbiology*, *9*(5), 623–630. https://doi.org/10.2217/fmb.14.24

Jones, S. E., Ho, L., Rees, C. A., Hill, J. E., Nodwell, J. R., & Elliot, M. A. (2017). Streptomyces exploration is triggered by fungal interactions and volatile signals. *ELIFE*, *6*, 1–21. https://doi.org/10.7554/eLife.21738

Jones, S. E., Pham, C. A., Zambri, M. P., McKillip, J., Carlson, E. E., & Elliot, M. A. (2019). Streptomyces Volatile Compounds Influence Exploration and Microbial Community Dynamics by Altering Iron Availability. *MBio*, *10*(2), 1–18. https://doi.org/10.1128/mBio.00171-19

Joo, G. J. (2005). Production of an anti-fungal substance for biological control of Phytophthora capsici causing phytophthora blight in red-peppers by Streptomyces halstedii. *Biotechnology Letters*, *27*(3), 201–205. https://doi.org/10.1007/s10529-004-7879-0

Joycharat, N., Thammavong, S., Voravuthikunchai, S. P., Plodpai, P., Mitsuwan, W., Limsuwan, S., & Subhadhirasakul, S. (2014). Chemical constituents and antimicrobial properties of the essential oil and ethanol extract from the stem of Aglaia odorata Lour. *Natural Product Research*, *28*(23), 2169–2172. https://doi.org/10.1080/14786419.2014.924934

Kanchiswamy, C. N., Malnoy, M., & Maffei, M. E. (2015). Bioprospecting bacterial and fungal volatiles for sustainable agriculture. *Trends in Plant Science*, *20*(4), 206–211. https://doi.org/10.1016/j.tplants.2015.01.004

Kataoka, M., Ueda, K., Kudo, T., & Seki, T. (1997). Application of the variable region in 16S rDNA to create an index for rapid species identification in the genus Streptomyces. *FEMS Microbiology Letters*, *151*, 249–255.

Katz, L., & Baltz, R. H. (2016). Natural product discovery: past, present, and future. *Journal of Industrial Microbiology and Biotechnology*, *43*(2–3), 155–176. https://doi.org/10.1007/s10295-015-1723-5

Kelly, S. L., & Kelly, D. E. (2013). Microbial cytochromes P450: biodiversity and biotechnology. Where do cytochromes P450 come from, what do they do and what can they do for us? *Philosophical Transactions of the Royal Society B: Biological Sciences*, *368*(1612). https://doi.org/10.1098/rstb.2012.0476

Khamis, A., Raoult, D., & Scola, B. La. (2005). Comparison between rpoB and 16S rRNA Gene Sequencing for Molecular Identification of 168 Clinical Isolates of Corynebacterium. *Journal of Clinical Microbiology*, *43*(4), 1934–1936. https://doi.org/10.1128/JCM.43.4.1934

Khoja, S., Eltayef, K. M., Baxter, I., Myrta, A., Bull, J. C., & Butt, T. (2020). Volatiles of the entomopathogenic fungus, Metarhizium brunneum, attract and kill plant parasitic nematodes. *Biological Control*, *152*(September 2020), 104472. https://doi.org/10.1016/j.biocontrol.2020.104472

Kim, B. J., Kim, C. J., Chun, J., Koh, Y. H., Lee, S. H., Hyun, J. W., Cha, C. Y., & Kook, Y. H. (2004). Phylogenetic analysis of the genera Streptomyces and Kitasatospora based on partial RNA polymerase β-subunit gene (rpoB) sequences. *International Journal of Systematic and Evolutionary Microbiology*, *54*(2), 593–598. https://doi.org/10.1099/ijs.0.02941-0

Kim, D. R., Cho, G., Jeon, C. W., Weller, D. M., Thomashow, L. S., Paulitz, T. C., & Kwak, Y. S. (2019). A mutualistic interaction between Streptomyces bacteria, strawberry plants and pollinating bees. *Nature Communications*, *10*(4802). https://doi.org/10.1038/s41467-019-12785-3

Kirkpatrick, D. M., Leach, H. L., Xu, P., Dong, K., Isaacs, R., & Gut, L. J. (2018). Comparative Antennal and Behavioral Responses of Summer and Winter Morph Drosophila suzukii (Diptera: Drosophilidae) to Ecologically Relevant Volatiles. *Environmental Entomology*, *47*(3), 700–706. https://doi.org/10.1093/ee/nvy046

Klocke, J. A., Darlington, M. V., & Balandrin, M. F. (1987). 1,8-Cineole (Eucalyptol), a Mosquito Feeding and Ovipositional Repellent From Volatile Oil ofHemizonia Fitchii (Asteraceae). *Journal of Chemical Ecology*, *13*(12), 2131–2141. https://doi.org/10.1007/BF01012562

Kolter, R., Siegele, D. A., & Tormo, A. (1993). The stationary phase of the bacterial life cycle. *Annual Review of Microbiology*, *47*, 855–874. https://doi.org/10.1146/annurev.mi.47.100193.004231

Komaki, H. (2021). Reclassification of Streptomyces costaricanus and Streptomyces phaeogriseichromatogenes as later heterotypic synonyms of Streptomyces murinus. *International Journal of Systematic and Evolutionary Microbiology*, *71*(2), 1–6. https://doi.org/10.1099/ijsem.0.004638

Komatsu, M., Tsuda, M., Omura, S., Oikawa, H., & Ikeda, H. (2008). Identification and functional analysis of genes controlling biosynthesis of 2-methylisoborneol. *PNAS*, *105*(21), 7422–7427. https://doi.org/10.1073/pnas.0802312105

Korpi, A., Jarnberg, J., & Pasanen, A.-L. (2009). Microbial volatile organic compounds. *Critical Reviews in Toxicology*, *39*, 139–193. https://doi.org/10.1080/10408440802291497

Kroiss, J., Kaltenpoth, M., Schneider, B., Schwinger, M. G., Hertweck, C., Maddula, R. K., Strohm, E., & Svatos, A. (2010). Symbiotic streptomycetes provide antibiotic combination prophylaxis for wasp offspring. *Nature Chemical Biology*, *6*(4), 261–263. https://doi.org/10.1038/nchembio.331

Kumar, S., Stecher, G., Li, M., Knyaz, C., & Tamura, K. (2018). MEGA X: Molecular

evolutionary genetics analysis across computing platforms. *Molecular Biology and Evolution*, *35*(6), 1547–1549. https://doi.org/10.1093/molbev/msy096

Lehtinen, T., Efimova, E., Santala, S., & Santala, V. (2018). Improved fatty aldehyde and wax ester production by overexpression of fatty acyl-CoA reductases. *Microbial Cell Factories*, *17*(1), 1–10. https://doi.org/10.1186/s12934-018-0869-z

Li, R., Chou, W. K. W., Himmelberger, J. A., Litwin, K. M., Harris, G. G., Cane, D. E., & Christianson, D. W. (2014). Reprogramming the Chemodiversity of Terpenoid Cyclization by Remolding the Active Site Contour of epi-Isozizaene Synthase. *Biochemistry*, *53*, 1155–1168.

Li, X., Li, B., Cai, S., Zhang, Y., Xu, M., Zhang, C., Yuan, B., Xing, K., & Qin, S. (2020). Identification of rhizospheric actinomycete streptomyces lavendulae sps-33 and the inhibitory effect of its volatile organic compounds against ceratocystis fimbriata in postharvest sweet potato (Ipomoea batatas (L.) Lam.). *Microorganisms*, *8*(3). https://doi.org/10.3390/microorganisms8030319

Li, Y., Liu, J., Adekunle, D., Bown, L., Tahlan, K., & Bignell, D. R. D. (2019). TxtH is a key component of the thaxtomin biosynthetic machinery in the potato common scab pathogen Streptomyces scabies. *Molecular Plant Pathology*, *20*(10), 1379–1393. https://doi.org/10.1111/mpp.12843

Lian, Q., Zhang, J., Gan, L., Ma, Q., Zong, Z., & Wang, Y. (2017). The biocontrol efficacy of streptomyces pratensis LMM15 on botrytis cinerea in Tomato. *BioMed Research International*, *2017*. https://doi.org/10.1155/2017/9486794

Light, M., Shutler, D., Cutler, G. C., & Hillier, N. K. (2020). Varroa destructor mite electrophysiological responses to honey bee (Apis mellifera) colony volatiles. *Experimental and Applied Acarology*, *81*(4). https://doi.org/10.1007/s10493-020-00519-w

Lin, X., & Cane, D. E. (2009). Biosynthesis of the Sesquiterpene Antibiotic Albaflavenone in Streptomyces Coelicolor. Mechanism and Stereochemistry of the Enzymatic Formation of Epi-Isozizaene. *Journal of American Chemical Society*, *131*(18), 6332–6333. https://doi.org/10.1021/ja901313v.Biosynthesis

Links, M. G., Dumonceaux, T. J., Hemmingsen, S. M., & Hill, J. E. (2012). The Chaperonin-60 Universal Target Is a Barcode for Bacteria That Enables De Novo Assembly of Metagenomic Sequence Data. *PLoS ONE*, *7*(11). https://doi.org/10.1371/journal.pone.0049755

Linstrom, P. J., & Mallard, W. G. (2001). The NIST Chemistry WebBook: A chemical data resource on the Internet. *Journal of Chemical and Engineering Data*, *46*(5), 1059–1063. https://doi.org/10.1021/je000236i

Liu, K., Chen, Q., Liu, Y., Zhou, X., & Wang, X. (2012). Isolation and Biological Activities of Decanal, Linalool, Valencene, and Octanal From Sweet Orange Oil. *Journal of Food Science*, *77*(11). https://doi.org/10.1111/j.1750-3841.2012.02924.x

Liu, M., Jia, Y., Xie, Y., Zhang, C., Ma, J., Sun, C., & Ju, J. (2019). Identification of the actinomycin D biosynthetic pathway from marine-derived Streptomyces costaricanus SCSIO ZS0073. *Marine Drugs*, *17*(4), 1–13. https://doi.org/10.3390/md17040240

Lofstedt, C., & Bengtsson, M. (1988). Sex Pheromone Biosynthesis of (E,E)-8,10-dodecadienol in Codling mothCydia Pomonella involves E9 Desaturation. *Journal of Chemical Ecology*, *14*(3), 903–915.

Logrieco, A., Mulè, G., Moretti, A., & Bottalico, A. (2002). Toxigenic Fusarium species and mycotoxins associated with maize ear rot in Europe. *European Journal of Plant Pathology*, *108*(7), 597–609. https://doi.org/10.1023/A:1020679029993

Lücker, J., Bowen, P., & Bohlmann, J. (2004). Vitis vinifera terpenoid cyclases: functional identification of two sesquiterpene synthase cDNAs encoding (+)-valencene synthase and (?)-germacrene D synthase and expression of mono- and sesquiterpene synthases in grapevine flowers and berries. *Phytochemistry*, *65*(19), 2649–2659. https://doi.org/10.1016/j.phytochem.2004.08.017

Lyu, A., Yang, L., Wu, M., Zhang, J., & Li, G. (2020). High Efficacy of the Volatile Organic Compounds of Streptomyces yanglinensis 3-10 in Suppression of Aspergillus Contamination on Peanut Kernels. *Frontiers in Microbiology*, *11*, 1–17. https://doi.org/10.3389/fmicb.2020.00142

Madhyasth, M. S., & Bhat, R. V. (1984). Aspergillus parasiticus Growth and Aflatoxin Production on Black and White Pepper and the Inhibitory Action of Their Chemical Constituents. *Applied and Environmental Microbiology*, *48*(2), 376–379.

Maiden, M. C. J., Bygraves, J. A., Feil, E., Morelli, G., Russell, J., Urwin, R., Zhang, Q., Zhou, J., Zurth, K., Caugant, D. A., Feavers, I. M., Achtman, M., & Spratt, B. G. (1998). Multilocus sequence typing: A portable approach to the identification of clones within populations of pathogenic microorganisms. *Pnas*, *95*, 3140–3145.

Manter, D. K., Kelsey, R. G., & Karchesy, J. J. (2007). Antimicrobial Activity of Extractable Conifer Heartwood Compounds Toward Phytophthora ramorum. *Journal of Chemical Ecology*, *33*, 2133–2147. https://doi.org/10.1007/s10886-007-9368-0

Marchesi, J. R., Sato, T., Weightman, A. J., Martin, T. A., Fry, J. C., Hiom, S. J., & Wade, W. G. (1998). Design and Evaluation of Useful Bacterium-Specific PCR Primers That Amplify Genes Coding for Bacterial 16S rRNA. *Applied and Environmental Microbiology*, *64*(2), 795–799.

Martens, T., Brinkhoff, T., Simon, M., & Schulz, S. (2005). *Volatiles Released by a Streptomyces Species Isolated from the North Sea*. *2*.

Martín-Sánchez, L., Singh, K. S., Avalos, M., Van Wezel, G. P., Dickschat, J. S., & Garbeva, P. (2019). Phylogenomic analyses and distribution of terpene synthases among Streptomyces. *Beilstein Journal of Organic Chemistry*, *15*, 1181–1193.

https://doi.org/10.3762/bjoc.15.115

Mcmahon, C., Guerin, P. M., & Syed, Z. (2001). 1-Octen-3-ol isolated from bont ticks attracts Amblyomma variegatum. *Journal of Chemical Ecology*, *27*(3), 471–486. https://doi.org/10.1023/A:1010328720035

Mehling, A., Wehmeier, U. F., & Piepersberg, W. (1995). Nucleotide sequences of streptomycete 16S ribosomal DNA: Towards a specific identification system for streptomycetes using PCR. *Microbiology*, *141*(9), 2139–2147. https://doi.org/10.1099/13500872-141-9-2139

Meijerink, J., Braks, M. A. H., & Van Loon, J. J. . (2001). Olfactory receptors on the antennae of the malaria mosquito Anopheles gambiae are sensitive to ammonia and other sweat-borne components. *Journal of Insect Physiology*, *47*, 455–464.

Mekadim, C., Killer, J., Pechar, R., & Mrazek, J. (2018). Variable regions of the glyS, infB and rplB genes usable as novel genetic markers for identification and phylogenetic purposes of genera belonging to the family Propionibacteriaceae. *International Journal of Systematic and Evolutionary Microbiology*, *68*, 2697–2705. https://doi.org/10.1099/ijsem.0.002873

Minaeimoghadam, M., Askarianzadeh, A., Imani, S., Shojaei, M., Larijani, K., & Abbasipour, H. (2017). Identification of chemical compounds of the pheromone in different ages of female adults of the clearwing moth, Paranthrene diaphana Dalla Torre & Strand. *Archives of Phytopathology and Plant Protection*, *50*, 1019–1033. https://doi.org/10.1080/03235408.2017.1411174

Miñana-Galbis, D., Urbizu-Serrano, A., Farfán, M., Fusté, M. C., & Lorén, J. G. (2009). Phylogenetic analysis and identification of Aeromonas species based on sequencing of the cpn60 universal target. *International Journal of Systematic and Evolutionary Microbiology*, *59*(8), 1976–1983. https://doi.org/10.1099/ijs.0.005413-0

Monnin, T., Helft, F., Leroy, C., d'Ettorre, P., & Doums, C. (2018). Chemical Characterization of Young Virgin Queens and Mated Egg-Laying Queens in the Ant Cataglyphis cursor: Random Forest Classification Analysis for Multivariate Datasets. *Journal of Chemical Ecology*, *44*(2), 127–136. https://doi.org/10.1007/s10886-018-0923-7

Morrison III, W. R., Larson, N. L., Brabec, D., & Zhang, A. (2019). Methyl Benzoate as a Putative Alternative, Environmentally Friendly Fumigant for the Control of Stored Product Insects. *Journal of Economic Entomology*, *112*(5), 2458–2468. https://doi.org/10.1093/jee/toz179

Mostafiz, M. M., Jhan, P. K., Shim, J., & Lee, K.-Y. (2018). Methyl benzoate exhibits insecticidal and repellent activities against Bemisia tabaci (Gennadius) (Hemiptera: Aleyrodidae). *PLoS ONE*, 1–14.

Mowat, E., Rajendran, R., Williams, C., Mcculloch, E., Jones, B., Lang, S., & Ramage, G. (2010). Pseudomonasaeruginosaand their small di¡usible extracellular molecules

inhibitAspergillusfumigatus bio¢lmformation. *FEMS Microbiology Letters*, *313*, 96–102. https://doi.org/10.1111/j.1574-6968.2010.02130.x

Mukherjee, S., Stamatis, D., Bertsch, J., Ovchinnikova, G., Sundaramurthi, J. C., Lee, J., Kandimalla, M., Chen, I. M. A., Kyrpides, N. C., & Reddy, T. B. K. (2021). Genomes OnLine Database (GOLD) v.8: Overview and updates. *Nucleic Acids Research*, *49*(D1), D723–D733. https://doi.org/10.1093/nar/gkaa983

Mulyaningsih, S., Youns, M., El-Readi, M. Z., Ashour, M. L., Nibret, E., Sporer, F., Herrmann, F., Reichling, J., & Wink, M. (2010). Biological activity of the essential oil of Kadsura longipedunculata (Schisandraceae) and its major components. *Journal of Pharmacy and Pharmacology*, *62*(8), 1037–1044. https://doi.org/10.1111/j.2042-7158.2010.01119.x

Munita, J. M., & Arias, C. A. (2016). Mechanisms of antibiotic resistance. *American Society for Microbiology*, *6*, 1–24. https://doi.org/10.3389/fmicb.2015.00034

Na, S., Kim, Y. O., Yoon, S., Ha, S., Baek, I., & Chun, J. (2018). UBCG : Up-to-date bacterial core gene set and pipeline for phylogenomic tree reconstruction. *Journal of Microbiology*, *56*(4), 280–285. https://doi.org/10.1007/s12275-018-8014-6

Nagashima, K., Hisada, T., Sato, M., & Mochizuki, J. (2003). Application of new primer-enzyme combinations to terminal restriction fragment length polymorphism profiling of bacterial populations in human feces. *Applied and Environmental Microbiology*, *69*(2), 1251–1262. https://doi.org/10.1128/AEM.69.2.1251-1262.2003

Narayana, K. J. P., Prabhakar, P., Vijayalakshmi, M., Venkateswarlu, Y., & Krishna, P. S. J. (2008). Study on bioactive compounds from Streptomyces sp. ANU 6277. *Polish Journal of Microbiology*, *57*(1), 35–39.

Nei, M., & Kumar, S. (2000). Molecular Evolution and Phylogenetics. In *Genetical Research* (Issue 1). Oxford University Press. https://doi.org/10.1017/s0016672301219405

Ni, J., Robarge, W. P., Xiao, C., & Heber, A. J. (2012). Volatile organic compounds at swine facilities: A critical review. *Chemosphere*, *89*(7), 769–788. https://doi.org/10.1016/j.chemosphere.2012.04.061

Nie, Y., Chi, C., Fang, H., Liang, J., Lu, S., Lai, G., Tang, Y., & Wu, X. (2014). Diverse alkane hydroxylase genes in microorganisms and environments. *Scientific Reports*, *4*(4968), 1–11. https://doi.org/10.1038/srep04968

Ogunbinua, A. O., Flamini, G., Cioni, P. L., Adebayo, M. A., & Ogunwande, I. A. (2009). Constituents of Cajanus cajan (L.) Millsp., Moringa oleifera Lam., Heliotropium indicum L. and Bidens pilosa L. from Nigeria. *Natural Product Communications*, *4*(4), 573–578.

Olaide, O. Y., Tchouassi, D. P., Yusuf, A. A., Pirk, C. W. W., Masiga, D. K., Saini, R. K., & Torto, B. (2019). Zebra Skin Odor Repels the Savannah Tsetse Fly, Glossina

Pallidipes (Diptera: Glossinidae). *PLoS ONE*, 1–18.

Pan, R., Bai, X., Chen, J., Zhang, H., & Wang, H. (2019). Exploring structural diversity of microbe secondary metabolites using OSMAC strategy: A literature review. *Frontiers in Microbiology*, *10*(294), 1–20. https://doi.org/10.3389/fmicb.2019.00294

Paoli, M., Nam, A. M., Castola, V., Casanova, J., & Bighelli, A. (2011). Chemical variability of the wood essential oil of cedrus atlantica manetti from Corsica. *Chemistry and Biodiversity*, *8*(2), 344–351. https://doi.org/10.1002/cbdv.201000094

Parte, A. C., Carbasse, J. S., Meier-Kolthoff, J. P., Reimer, L. C., & Göker, M. (2020). List of prokaryotic names with standing in nomenclature (LPSN) moves to the DSMZ. *International Journal of Systematic and Evolutionary Microbiology*, *70*(11), 5607–5612. https://doi.org/10.1099/ijsem.0.004332

Peterson, E., & Kaur, P. (2018). Antibiotic resistance mechanisms in bacteria: Relationships between resistance determinants of antibiotic producers, environmental bacteria, and clinical pathogens. *Frontiers in Microbiology*, *9*(2928), 1–21. https://doi.org/10.3389/fmicb.2018.02928

Pierce, A. M., Pierce Jr., H. D., Oehlschlager, A. C., & Borden, J. H. (1990). 1-Octen-3-ol, attractive semiochemical for foreign grain beetle,Ahasverus advena (Waltl) (Coleoptera: Cucujidae). *Journal of Chemical Ecology*, *17*(3), 567–580.

Pinto-zevallos, D. M., Bezerra, R. H. S., Souza, S. R., & Ambrogi, B. G. (2018). Species- And Density-Dependent Induction of Volatile Organic Compounds by Three Mite Species in Cassava and Their Role in the Attraction of a Natural Enemy. *Experimental and Applied Acarology*, *74*(3), 261–274. https://doi.org/10.1007/s10493-018-0231-5

Pollak, F. C., & Berger, R. G. (1996). Geosmin and related volatiles in bioreactor-cultured Streptomyces citreus CBS 109.60. *Applied and Environmental Microbiology*, *62*(4), 1295–1299. https://doi.org/10.1128/aem.62.4.1295-1299.1996

Pollock, J., Laura, G., Trong, W., & Mick, W. (2018). The Madness of Microbiome : Attempting To Find Consensus. *Applied and Environmental Microbiology*, *84*(7), 1–12.

Pope, T. W., Campbell, C. A. M., Hardie, J., & Wadhams, L. J. (2004). Electroantennogram responses of the three migratory forms of the damson-hopaphid, Phorodon humuli, to aphid pheromones and plant volatiles. *Journal of Insect Physiology*, *50*(11), 1083–1092. https://doi.org/10.1016/j.jinsphys.2004.09.010

Posy, D. C., Mohamed, M. A., Coppel, H. C., & Jeanne, R. L. (1984). Identification of ant repellent allomone produced by social wasp Polistes fuscatus (Hymenoptera: Vespidae). *Journal of Chemical Ecology*, *10*(12), 1799–1807. https://doi.org/10.1007/BF00987362

Qin, Y., Polacek, N., Vesper, O., Staub, E., Einfeldt, E., Wilson, D. N., & Nierhaus, K. H.

(2006). The Highly Conserved LepA Is a Ribosomal Elongation Factor that Back-Translocates the Ribosome. *Cell*, *127*, 721–733. https://doi.org/10.1016/j.cell.2006.09.037

Quaderer, R., Omaru, S., Ikeda, H., & Cane, D. E. (2006). Pentalenolactone Biosynthesis. Molecular Cloning and Assignment of Biochemical Function to PtlI, a Cytochrome P450 of Streptomyces Avermitilis. *Journal of American Chemical Society*, *128*(40), 13036–13037. https://doi.org/10.1021/ja0639214.Pentalenolactone

Quast, C., Pruesse, E., Yilmaz, P., Gerken, J., Schweer, T., Yarza, P., Peplies, J., & Glöckner, F. O. (2013). The SILVA ribosomal RNA gene database project: improved data processing and web-based tools. *Nucleic Acids Research*, *41*(D1), 590–596. https://doi.org/10.1093/nar/gks1219

Rabe, P., Citron, C. A., & Dickschat, J. S. (2013). Volatile Terpenes from Actinomycetes: A Biosynthetic Study Correlating Chemical Analyses to Genome Data. *Chembiochem*, *14*, 2345–2354. https://doi.org/10.1002/cbic.201300329

Rasko, D. A., Altherr, M. R., Han, C. S., & Ravel, J. (2005). Genomics of the Bacillus cereus group of organisms. *FEMS Microbiology Reviews*, *29*, 303–329. https://doi.org/10.1016/j.femsre.2004.12.005

Raza, W., Ling, N., Liu, D., Wei, Z., Huang, Q., & Shen, Q. (2016). Volatile organic compounds produced by Pseudomonas fluorescens WR-1 restrict the growth and virulence traits of Ralstonia solanacearum. *Microbiological Research*, *192*, 103–113. https://doi.org/10.1016/j.micres.2016.05.014

Reller, L. B., Weinstein, M. P., & Petti, C. A. (2007). Detection and Identification of Microorganisms by Gene Amplification and Sequencing. *Clinical Infectious Diseases*, *44*(8), 1108–1114. https://doi.org/10.1086/512818

Reysenbach, A., Wickham, G. S., & Pace, N. R. (1994). Phylogenetic Analysis of the Hyperthermophilic Pink Filament Community in Octopus Spring , Yellowstone National Park. *Applied and Environmental Microbiology*, *60*(6), 2113–2119.

Ribeiro, T. G., Novais, A., Branquinho, R., Machado, E., & Peixe, L. (2015). Phylogeny and Comparative Genomics Unveil Independent Diversification Trajectories of qnrB and Genetic Platforms within Particular Citrobacter Species. *American Society for Microbiology*, *59*(10), 5951–5958. https://doi.org/10.1128/AAC.00027-15

Riclea, R., Aigle, B., Leblond, P., Schoenian, I., Spiteller, D., & Dickschat, J. S. (2012). Volatile Lactones from Streptomycetes Arise via the Antimycin Biosynthetic Pathway. *ChemBioChem*, *13*, 1635–1645. https://doi.org/10.1002/cbic.201200260

Rinkel, J., Rabe, P., Zur Horst, L., & Dickschat, J. S. (2016). A detailed view on 1,8-cineol biosynthesis by Streptomyces clavuligerus. *Beilstein Journal of Organic Chemistry*, *12*, 2317–2324. https://doi.org/10.3762/bjoc.12.225

Rogall, T., Wolters, J., Flohr, T., & Bottger, E. C. (1990). Towards a Phylogeny and

Definition of Species at the Molecular Level within the Genus Mycobacterium. *International Journal of Systematic Bacteriology*, *40*(4), 323–330.

Santos, S. R., & Ochman, H. (2004). Identification and phylogenetic sorting of bacterial lineages with universally conserved genes and proteins. *Environmental Microbiology*, *6*(7), 754–759. https://doi.org/10.1111/j.1462-2920.2004.00617.x

Satyal, P., Hieu, H. V., Chuong, N. T. H., Hung, N. H., Sinh, L. H., Van The, P., Tai, T. A., Hien, V. T., & Setzer, W. N. (2019). Chemical composition, Aedes mosquito larvicidal activity, and repellent activity against Triatoma rubrofasciata of Severinia monophylla leaf essential oil. *Parasitology Research*, *118*(3), 733–742. https://doi.org/10.1007/s00436-019-06212-1

Scheller, U., Zimmer, T., Becher, D., Schauer, F., & Schunck, W. (1998). Oxygenation Cascade in Conversion of N-Alkanes to Alpha,omega-Dioic Acids Catalyzed by Cytochrome P450 52A3. *The Journal of Biological Chemistry*, *273*(49), 32528–32534.

Schirmer, A., Rude, M. A., Li, X., Popova, E., & del Cardayre, S. B. (2010). Microbial Biosynthesis of Alkanes. *Science*, *329*.

Schmidt, R., Cordovez, V., De Boer, W., Raaijmakers, J., & Garbeva, P. (2015). Volatile affairs in microbial interactions. *ISME Journal*, *9*(11), 2329–2335. https://doi.org/10.1038/ismej.2015.42

Schnurer, J., Olsson, J., & Borjesson, T. (1999). Fungal Volatiles as Indicators of Food and Feeds Spoilage. *Fungal Genetics and Biology*, *27*(2–3), 209–217.

Schöller, C. E. G., Gürtler, H., Pedersen, R., Molin, S., & Wilkins, K. (2002). Volatile metabolites from actinomycetes. *Journal of Agricultural and Food Chemistry*, *50*(9), 2615–2621. https://doi.org/10.1021/jf0116754

Schrader, K. K., Harries, M. D., & Page, P. N. (2015). Temperature effects on biomass, geosmin, and 2-methylisoborneol production and cellular activity by Nocardia spp. and Streptomyces spp. isolated from rainbow trout recirculating aquaculture systems. *Journal of Industrial Microbiology and Biotechnology*, *42*(5), 759–767. https://doi.org/10.1007/s10295-015-1600-2

Schulz-bohm, K., Geisen, S., Wubs, E. R. J., Song, C., Boer, W. De, & Garbeva, P. (2017). The prey's scent - volatile organic compound mediated interactions between soil bacteria and their protist predators. *ISME Journal*, *11*, 817–820. https://doi.org/10.1038/ismej.2016.144

Schulz, S., & Dickschat, J. S. (2007). Bacterial volatiles: The smell of small organisms. *Natural Product Reports*, *24*(4), 814–842. https://doi.org/10.1039/b507392h

Shi, W., Li, M., Wei, G., Tian, R., Li, C., Wang, B., Lin, R., Shi, C., Chi, X., Zhou, B., & Gao, Z. (2019). The occurrence of potato common scab correlates with the community composition and function of the geocaulosphere soil microbiome.

Microbiome, *7*(1), 1–18. https://doi.org/10.1186/s40168-019-0629-2

Shirasu, M., Ito, S., Itoigawa, A., Hayakawa, T., Kinoshita, K., Munechika, I., Imai, H., & Touhara, K. (2020). Key Male Glandular Odorants Attracting Female Ring-Tailed Lemurs. *Current Biology*, *30*, 1–8. https://doi.org/10.1016/j.cub.2020.03.037

Shirling, E. B., & Gottlieb, D. (1969). Cooperative description of type cultures of Streptomyces. IV. Species descriptions from the second, third and fourth studies. *International Journal of Systematic Bacteriology*, *19*(4), 391–512. https://doi.org/10.1099/00207713-19-4-391

Shirling, E. B., & Gottlieb, D. (1972). Cooperative Description of Type Strains of Streptomyces V. Additional Descriptions. *International Journal of Systematic Bacteriology*, *22*(4), 265–394. https://doi.org/10.1099/00207713-22-4-265

Siebenberg, S., Bapat, P. M., Lantz, A. E., Gust, B., & Heide, L. (2010). Reducing the variability of antibiotic production in Streptomyces by cultivation in 24-square deepwell plates. *Journal of Bioscience and Bioengineering*, *109*(3), 230–234. https://doi.org/10.1016/j.jbiosc.2009.08.479

Song, J., Lee, S. C., Kang, J. W., Baek, H. J., & Suh, J. W. (2004). Phylogenetic analysis of Streptomyces spp. isolated from potato scab lesions in Korea on the basis of 16S rRNA gene and 16S-23S rDNA internally transcribed spacer sequences. *International Journal of Systematic and Evolutionary Microbiology*, *54*(1), 203–209. https://doi.org/10.1099/ijs.0.02624-0

Soso, S. B., & Koziel, J. A. (2016). Analysis of Odorants in Marking Fluid of Siberian Tiger (Panthera tigris altaica) Using Simultaneous Sensory and Chemical Analysis with Headspace Solid-Phase Microextraction and Multidimensional Gas Chromatography-Mass Spectrometry-Olfactometry. *Molecules*, *21*(7), 1–22. https://doi.org/10.3390/molecules21070834

Stackebrandt, E., Koch, C., Gvozdiak, O., & Schumann, P. (1995). Taxonomic dissection of the genus Micrococcus: Kocuria gen. nov., Nesterenkonia gen. nov., Kytococcus gen. nov., Dermacoccus gen. nov., and Micrococcus cohn 1872 gen. emend. *International Journal of Systematic Bacteriology*, *45*(4), 682–692. https://doi.org/10.1099/00207713-45-4-682

Stensmyr, M. C., Dweck, H. K. M., Farhan, A., Ibba, I., Strutz, A., Mukunda, L., Linz, J., Grabe, V., Steck, K., Lavista-Llanos, S., Wicher, D., Sachse, S., Knaden, M., Becher, P. G., Seki, Y., & Hansson, B. S. (2012). A conserved dedicated olfactory circuit for detecting harmful microbes in drosophila. *Cell*, *151*(6), 1345–1357. https://doi.org/10.1016/j.cell.2012.09.046

Takamatsu, S., Lin, X., Nara, A., Komatsu, M., Cane, D. E., & Ikeda, H. (2011). Characterization of a silent sesquiterpenoid biosynthetic pathway in Streptomyces avermitilis controlling epi-isozizaene albaflavenone biosynthesis and isolation of a new oxidized epi-isozizaene metabolite. *Microbial Biotechnology*, *4*(2), 184–191.

https://doi.org/10.1111/j.1751-7915.2010.00209.x

Takamatsu, S., Xu, L., Fushinobu, S., Shoun, H., Komatsu, M., Cane, D. E., & Ikeda, H. (2011). Pentalenic acid is a shunt metabolite in the biosynthesis of the pentalenolactone family of metabolites: hydroxylation of 1-deoxypentalenic acid mediated by CYP105D7 (SAV_7469) of Streptomyces avermitilis. *The Journal of Antibiotics*, *64*, 65–71. https://doi.org/10.1038/ja.2010.135

Tang, Y., Ellis, N. M., Hopkins, M. K., Smith, D. H., Dodge, D. E., & Persing, D. H. (1998). Comparison of Phenotypic and Genotypic Techniques for Identification of Unusual Aerobic Pathogenic Gram-Negative Bacilli. *Journal of Clinical Microbiology*, *36*(12), 3674–3679.

Teske, A., Wawer, C., Muyzer, G., & Ramsing, N. B. (1996). Distribution of Sulfate-Reducing Bacteria in a Stratified Fjord (Mariager Fjord, Denmark) as Evaluated by Most-ProbableNumber Counts and Denaturing Gradient Gel Electrophoresis of PCR-Amplified Ribosomal DNA Fragments. *Applied and Environmental Microbiology*, *62*(4), 1405–1415.

Thangadurai, D., Anitha, S., Pullaiah, T., Reddy, P. N., & Ramachandraiah, O. S. (2002). Essential oil constituents and in vitro antimicrobial activity of Decalepis hamiltonii roots against foodborne pathogens. *Journal of Agricultural and Food Chemistry*, *50*(11), 3147–3149. https://doi.org/10.1021/jf011541q

Thomas, C. M., & Nielsen, K. M. (2005). Mechanisms of, and Barriers to, Horizontal Gene Transfer between Bacteria. *Nature Reviews Microbiology*, *3*, 711–722. https://doi.org/10.1038/nrmicro1234

Thompson, F. L., Gevers, D., Thompson, C. C., Dawyndt, P., Naser, S., Hoste, B., Munn, C. B., & Swings, J. (2005). Phylogeny and Molecular Identification of Vibrios on the Basis of Multilocus Sequence Analysis. *Applied and Environmental Microbiology*, *71*(9), 5107–5115. https://doi.org/10.1128/AEM.71.9.5107

Tian, X., Zhang, Z., Yang, T., Chen, M., Li, J., Chen, F., Yang, J., Li, W., Zhang, B., Zhang, Z., Wu, J., Zhang, C., Long, L., & Xiao, J. (2016). Comparative Genomics Analysis of Streptomyces Species Reveals Their Adaptation to the Marine Environment and Their Diversity at the Genomic Level. *Frontiers in Microbiology*, *7*, 1–16. https://doi.org/10.3389/fmicb.2016.00998

Toloza, A. C., Zygadlo, J., Cueto, G. M., Biurrun, F., Zerba, E., & Picollo, M. I. (2006). Fumigant and Repellent Properties of Essential Oils and Component Compounds Against Permethrin-Resistant Pediculus humanus capitis (Anoplura: Pediculidae) from Argentina. *Journal of Medical Entomology*, *43*(5), 889–895.

Torres-romero, D., Munoz-Martınez, F., Jimenez, I. A., Castanys, S., Gamarro, F., & Bazzocchi, I. L. (2009). Novel dihydro-beta-agarofuran sesquiterpenes as potent modulators of human P-glycoprotein dependent multidrug resistance. *Organic and Biomolecular Chemistry*, *7*, 5166–5172. https://doi.org/10.1039/b915678j

Tsusaka, T., Makino, B., Ohsawa, R., & Ezura, H. (2020). Evaluation of heritability of β-eudesmol/ hinesol content ratio in Atractylodes lancea De Candolle. *BMC Hereditas*, *157*(1), 1–8. https://doi.org/10.1186/s41065-020-00123-3

Turner, S. L., Li, N., Guda, T., Githure, J., Carde, R. T., & Ray, A. (2011). Ultra-prolonged activation of CO2-sensing neurons disorients mosquitoes. *Nature*, *474*, 87–92. https://doi.org/10.1038/nature10081

Vale, G. A., Hall, D. R., Chamisa, A., & Torr, S. J. (2012). Towards an Early Warning System for Rhodesian Sleeping Sickness in Savannah Areas: Man-Like Traps for Tsetse Flies. *PLoS Neglected Tropical Diseases*, *6*(12). https://doi.org/10.1371/journal.pntd.0001978

Van Hoek, A. H. A. M., Mevius, D., Guerra, B., Mullany, P., Roberts, A. P., & Aarts, H. J. M. (2011). Acquired antibiotic resistance genes: An overview. *Frontiers in Microbiology*, *2*(September), 1–27. https://doi.org/10.3389/fmicb.2011.00203

VanderMolen, K. M., Raja, H. A., El-Elimat, T., & Oberlies, N. H. (2013). Evaluation of culture media for the production of secondary metabolites in a natural products screening program. *AMB Express*, *3*(71), 1–7.

Vernikos, G., Medini, D., Riley, D. R., & Tettlin, H. (2015). Ten years of pan-genome analyses. *Current Opinion in Microbiology*, *23*, 148–154. https://doi.org/10.1016/j.mib.2014.11.016

Vivaldo, G., Masi, E., Taiti, C., Caldarelli, G., & Mancuso, S. (2017). The network of plants volatile organic compounds. *Scientific Reports*, *7*, 1–18. https://doi.org/10.1038/s41598-017-10975-x

Vos, M., Quince, C., Pijl, A. S., de Hollander, M., & Kowalchuk, G. A. (2012). A comparison of rpoB and 16S rRNA as markers in pyrosequencing studies of bacterial diversity. *PLoS ONE*, *7*(2), 1–8. https://doi.org/10.1371/journal.pone.0030600

Wallingford, A. K., Cha, D. H., Linn, C. E., Wolfin, M. S., & Loeb, G. M. (2017). Robust manipulations of pest insect behavior using repellents and practical application for integrated pest management. *Environmental Entomology*, *46*(5), 1041–1050. https://doi.org/10.1093/ee/nvx125

Wang, Changlu, Wang, Z., Qiao, X., Li, Z., Li, F., Chen, M., Wang, Y., Huang, Y., & Cui, H. (2013). Antifungal activity of volatile organic compounds from Streptomyces alboflavus TD-1. *FEMS Microbiology Letters*, *341*(1), 45–51. https://doi.org/10.1111/1574-6968.12088

Wang, Chieh-mei, & Cane, D. E. (2008). Biochemistry and Molecular Genetics of the Biosynthesis of the Earthy Odorant Methylisoborneol in Streptomyces Coelicolor. *Journal of American Chemical Society*, *130*(28), 8908–8909. https://doi.org/10.1021/ja803639g.Biochemistry

Wang, L., Lee, F., Tai, C., Kasai, H., & Lee, F. (2007). Comparison of gyrB gene sequences , 16S rRNA gene sequences and DNA – DNA hybridization in the Bacillus subtilis group. *International Journal of Systematic and Evolutionary Microbiology*, 1846–1850. https://doi.org/10.1099/ijs.0.64685-0

Wang, Z., Wang, C., Li, F., Li, Z., Chen, M., Wang, Y., Qiao, X., & Zhang, H. (2013). Fumigant activity of volatiles from Streptomyces alboflavus TD-1 against Fusarium moniliforme Sheldon. *Journal of Microbiology*, *51*(4), 477–483. https://doi.org/10.1007/s12275-013-2586-y

Wu, D., Jospin, G., & Eisen, J. A. (2013). Systematic Identification of Gene Families for Use as '"Markers"' for Phylogenetic and Phylogeny-Driven Ecological Studies of Bacteria and Archaea and Their Major Subgroups. *PLoS ONE*, *8*(10). https://doi.org/10.1371/journal.pone.0077033

Xing, M., Zheng, L., Deng, Y., Xu, D., Xi, P., Li, M., Kong, G., & Jiang, Z. (2018). Antifungal activity of natural volatile organic compounds against litchi downy blight pathogen peronophythora litchii. *Molecules*, *23*(2), 1–15. https://doi.org/10.3390/molecules23020358

Xu, J., Wang, Y., Xie, S. J., Xu, J., Xiao, J., & Ruan, J. S. (2009). Streptomyces xiamenensis sp. nov., isolated from mangrove sediment. *International Journal of Systematic and Evolutionary Microbiology*, *59*(3), 472–476. https://doi.org/10.1099/ijs.0.000497-0

Xu, P., Ma, W., Han, H., Hou, B., & Jia, S. (2014). Characterization of Naphthalene Degradation by Streptomyces Sp. QWE-5 Isolated From Active Sludge. *Water Science & Technology*, *70*(6), 1129–1134. https://doi.org/10.2166/wst.2014.356

Yang, M., Lu, L., Pang, J., Hu, Y., Guo, Q., Li, Z., Wu, S., Liu, H., & Wang, C. (2019). Biocontrol activity of volatile organic compounds from Streptomyces alboflavus TD-1 against Aspergillus flavus growth and aflatoxin pro- duction. *Journal of Microbiology*, *57*(5), 396–404. https://doi.org/10.1007/s12275-019-8517-9

Zeigler, D. R. (2003). Gene sequences useful for predicting relatedness of whole genomes in bacteria. *International Journal of Systematic and Evolutionary Microbiology*, *53*, 1893–1900. https://doi.org/10.1099/ijs.0.02713-0

Zeng, F., Xu, P., & Leal, W. S. (2019). Odorant Receptors From Culex Quinquefasciatus and Aedes Aegypti Sensitive to Floral Compounds. *Insect Biochemistry and Molecular Biology*, *113*, 1–9. https://doi.org/10.1016/j.ibmb.2019.103213

Zhang, J., Chen, J., Hu, L., Jia, R., Ma, Q., Tang, J., & Wang, Y. (2020). Antagonistic action of Streptomyces pratensis S10 on Fusarium graminearum and its complete genome sequence. *Environmental Microbiology*, *23*(4), 1925–1940. https://doi.org/10.1111/1462-2920.15282

Zhang, K. mei, Shen, Y., Yang, J., Miu, X., Bhowmik, P. C., Zhou, X., Fang, Y. ming, & Xing, B. shan. (2019). The defense system for Bidens pilosa root exudate treatments

in Pteris multifida gametophyte. *Ecotoxicology and Environmental Safety*, *173*(February), 203–213. https://doi.org/10.1016/j.ecoenv.2019.01.097

Zhang, Q., Schlyter, F., Chen, G., & Wang, Y. (2007). Electrophysiological and Behavioral Responses of Ips Subelongatus to Semiochemicals From Its Hosts, Non-Hosts, and Conspecifics in China. *Journal of Chemical Ecology*, *33*, 391–404. https://doi.org/10.1007/s10886-006-9231-8

Zhao, B., Lin, X., Lei, L., Lamb, D. C., Kelly, S. L., Waterman, M. R., & Cane, D. E. (2008). Biosynthesis of the Sesquiterpene Antibiotic Albaflavenone in Streptomyces coelicolor A3 (2). *The Journal of Biological Chemistry*, *283*(13), 8183–8189. https://doi.org/10.1074/jbc.M710421200

Zhao, Y., Xiang, S., Dai, X., & Yang, K. (2013). A simplified diphenylamine colorimetric method for growth quantification. *Applied Microbiology and Biotechnology*, *97*(11), 5069–5077. https://doi.org/10.1007/s00253-013-4893-y

Zhu, X., Xu, B., Kader, A., Song, B., Zhang, Z., Li, F., & Yang, S. (2020). Behavioral Responses of Scolytus schevyrewi (Coleoptera: Curculionidae: Scolytinae) to Volatiles From Apricot Tree (Rosales: Rosaceae). *Environmental Entomology*, *49*(3), 586–592. https://doi.org/10.1093/ee/nvaa027

Appendices

A.2.1: Media preparations

SFM – 1 liter

Soy flour defatted	20 g
Mannitol	20 g
Agar (if making solid medium)	20g

Blend the soy flour for further refinement. If making solid agar, prepare agar and soy flour in one container and mannitol in another. Combine both after autoclave.

The synthetic medium – 1 liter

Glucose	30 g
$(NH_4)_2SO_4$	1 g
$CaCO_3$	2.5 g
NaCl	1 g
Agar (if making solid medium)	20 g

Make solutions of the following salts in dH_2O, then add specified volumes to the desire 1 L of medium being prepared.

Salts	solution volume	amount of solution to make 1 L medium
0.025 g $MgSO_4.7H_2O$	40 ml	2 ml
0.125 g K_2HPO_4	50 ml	12.5 ml
0.125 g $FeSO_4.7H_2O$	50 ml	12.5 ml
0.125 g ZnSO4.H_2O	50 ml	12.5 ml
0.125 g $MnSO_4.4H_2O$	50 ml	12.5 ml

Add all salt solutions before making up the final volume of 1 L. Adjust the pH to 7 with NaOH, then autoclave.

YMS – 1 liter

Yeast extract	4 g
Malt extract	10 g
Soluble starch	4 g

Agar (if making solid medium)	20 g

Adjust the pH to 7.4 with NaOH, then autoclave.

YPD – 1 liter

Yeast extract	10 g
Peptone	20 g
Dextrose	20 g
Agar	20 g

Combine the above ingredients and make up the volume to 1 L with dH_2O, then autoclave.

OBB- 1 liter

1. Weigh 20 g of oat bran (SKU6051S18, Bob's Red Mill Natural Foods, USA) in 500 ml of dH_2O and heat in a microwave until boiling.
2. Once boiling, reduce power to 1, and leave the mixture boil for 15-20 mins
3. Place the mixture on a stir plate to cool with stirring for 45-60 mins. Speeding up cooling may result in reduced and inconsistent thaxtomin production.
4. Filter the mixture through 4 single layers of cheesecloth in a Buchner funnel using a vacuum into a sidearm flask.
5. Scoop the remaining oatmeal into the funnel and rinse with 200-300 ml dH_2O
6. Apply a vacuum until most of the liquid is drained
7. Adjust the pH of the broth to 7.2 with 1M NaOH
8. Add 2 ml/L of trace solution (recipe below)
9. Add dH_2O to a volume of 1 liter
10. Dispense and autoclave for 20 mins

Trace elements for OBB (1 liter)

$ZnCl_2$	40 mg
$FeCl_3.6H_2O$	200 mg
$CuCl_2.2H_2O$	10 mg
$MnCl_2.4H_2O$	10 mg
$Na_2B_4O_7.10H_2O$	10 mg
$(NH_4)_6Mo_7O_{24}.4H_2O)$	10 mg

A.2.3.2.1: *Streptomyces* reference sequences used to make consensus sequence for *rpoB* primer design

The six *Streptomyces* sequences (NCBI accession provided) were used to create a consensus sequence which was then used to run against NCBI non-redundant nucleotide database specific for *Streptomyces*. The top 100 hits were used to create primers used in this study for *rpoB* gene sequencing of the isolates.

>*Streptomyces_coelicolor*_CP042324.1H

TCAGACCTCTTCGACGCTGCTCGGCTCGCGCCGCGACAGGTCGATGCCGAGCTCCTCCGCTGCGCGGAAGACGTCCTCGTCGGTGTCACGCATCTC
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>*Streptomyces_avermitilis*_AP019621.1

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>*Streptomyces_clavuligerus*_CP027858.1

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A.2.3.2.2: *Streptomyces* reference sequences for *rpoB* primer design

The *Streptomyces rpoB* sequences were used to create the primers used for *rpoB* sequencing in this study. The NCBI accession numbers are provided for the *Streptomyces* from the top 100 hits returned against a search with the consensus sequence (lcl|Query_40537) created using *Streptomyces rpoB* sequences in A.2.3.2.1.

>lcl|Query_40537

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A.2.3.3.1: NCBI reference *Streptomyces* and isolates *rpoB* sequences compiled

The *rpoB* sequences were used to create the phylogenetic tree comprising the *Streptomyces* reference sequences from NCBI (n= 211) and isolates sequences (n = 133). *M. tuberculosis* was used as an outgroup.

>NZ_CP023699.1_*S._kanamyceticus*

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>NZ_CP048882.1_*S._bathyalis*

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>AP018036.1_*M._tuberculosis*

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>JAC107

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>JAC103

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>JAC105

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>JAC108

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>JAC121

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>JAC126

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>JAC127

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>JAC42

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>JAC58

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>JAC61B

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>JAC71

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>JAC75

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>JAC81

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>JAC87

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>JAC83

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CGTCACCCACCGGCTGGCC

A.2.3.3.2: *Streptomyces* isolates *rpoB* sequences compiled

The *rpoB* sequences were used to create the phylogenetic tree comprising the *Streptomyces* isolates sequences (n = 133). *M. tuberculosis* was used as an outgroup.

>*M_tuberculosis*_AP018036.1

GCCGGGCTGGAGGTCCGCGACGTGCACCCGTCGCACTACGGCCGGATGTGCCCGATCGAAACCCCTGAGGGGCCCAACATCGGTCTGATCGGCTC
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>JAC62

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>JAC91

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>JAC106

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>JAC95

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>JAC44

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A.2.5.3.1a: Integration R-code for GC-MS before GC column cut

```
library(tidyverse)

library(stringr)

#write.csv(data2, "med-3-4-kovats.csv")

#getting the table of integrations into shape. Export as a text (tab delimited), put it in the working directory

intDF = read.table("med-3-4-int.txt", sep = "",skip = 2)

#here we read in the table of integrations

str(intDF) #check the structure

colnames(intDF)=c("RT","area","percent","SN","desc")#renaming the columns

intDF <- intDF %>% mutate("num" = 1:n())

head(intDF)

##########################################################################################################

#Now, we must read in another dataframe, that containing the chemical ID's, which we copied out of the

#Bruker method builder program

chemID=read.csv("med-3-4-ids.csv",head=F) #Read in the chem ID CSV corresponding to the integration dataframe from above

head(chemID)

str(chemID)

str(intDF)#check the structure, be sure column 1 contains RT's and col 3 contains ID's

chemID=data.frame(chemID$V1,chemID$V3,chemID$V8) #combine the only three parameters we want

colnames(chemID)=c("RT","ID","Ions") #rename the columns of the ID dataframe

str(chemID)

chemID$ID=as.character(chemID$ID) #make sure the ID column is character

chemID$RT=as.double(chemID$RT)

chemID$Ions=as.character(chemID$Ions)

chemID <- chemID %>% mutate("num" = 1:n())
```

```
##########################################################################
##############################################

#Now we will join the two dataframes

merged.df<-merge(x=intDF,y=chemID,by="num",all=TRUE)

str(merged.df)

tail(merged.df)

merged.df <- subset(merged.df, select = c("num", "SN","RT.y","area","ID","percent","Ions"))

names(merged.df)[names(merged.df) == "RT.y"] <- "RT"

##########################################################################
##############################################

#And now we will write this merged DF into a CSV

#write.csv(merged.df,"f18 hex_12-16-2019_mike standard apis db-5_liquid-final.csv")

#Be sure to give the final CSV an informative name!!! IE

#make sure the culture is stated, and that you indicate it is combined

#I preface this with a 1, so they will collect at the top of the folder

#1) load dplyr

library(dplyr)

#2) Load the txt file and set it to the container data

data=merged.df

#data<-read.csv("f18 hex_12-16-2019_mike standard apis db-5_liquid-final.csv")

head(data)

tail(data)

str(data)

#carbons=read.csv("carbons.csv")

#3) set the carbon standards

C08<-4.829

C09<-7.017

C10<-9.518
```

C11<-12.174

C12<-14.618

C13<-16.502

C14<-18.078

C15<-19.467

C16<-20.729

C17<-21.899

C18<-22.996

C19<-24.034

C20<-25.022

#C21<-25.902

#C22<-26.801

#C23<-27.712

#C24<-28.790

#C25<-30.201

#C26<-31.896

#C27<-34.067

#C28<-36.875

#C29<-40.524

#C30<-45.297

#C31<-51.49

#C32<-44.038

#C33<-47.437

#C34<-51.459

#C35<-56.635

#C36<-63.144

#C37<-71.263

#C38<-NA

```
#4) calculate the Kovats
# first separate by carbons
#(you will have to tailor this list to reflect how many hydrocarbons in the ladder you have)
part01<-data %>% filter(RT < C08)
part02<-data %>% filter(((RT > C08)&(RT < C09))|RT==C08)
part03<-data %>% filter(((RT > C09)&(RT < C10))|RT==C09)
part04<-data %>% filter(((RT > C10)&(RT < C11))|RT==C10)
part05<-data %>% filter(((RT > C11)&(RT < C12))|RT==C11)
part06<-data %>% filter(((RT > C12)&(RT < C13))|RT==C12)
part07<-data %>% filter(((RT > C13)&(RT < C14))|RT==C13)
part08<-data %>% filter(((RT > C14)&(RT < C15))|RT==C14)
part09<-data %>% filter(((RT > C15)&(RT < C16))|RT==C15)
part10<-data %>% filter(((RT > C16)&(RT < C17))|RT==C16)
part11<-data %>% filter(((RT > C17)&(RT < C18))|RT==C17)
part12<-data %>% filter(((RT > C18)&(RT < C19))|RT==C18)
part13<-data %>% filter(((RT > C19)&(RT < C20))|RT==C19)
part14<-data %>% filter(RT>=C20)
#part14<-data %>% filter(((RT > C20)&(RT < C21))|RT==C20)
#part15<-data %>% filter(((RT > C21)&(RT < C22))|RT==C21)
#part16<-data %>% filter(((RT > C22)&(RT < C23))|RT==C22)
#part17<-data %>% filter(((RT > C23)&(RT < C24))|RT==C23)
#part18<-data %>% filter(RT>=C24)
#part18<-data %>% filter(((RT > C24)&(RT < C25))|RT==C24)
#part19<-data %>% filter(((RT > C25)&(RT < C26))|RT==C25)
#part20<-data %>% filter(((RT > C26)&(RT < C27))|RT==C26)
#part21<-data %>% filter(((RT > C27)&(RT < C28))|RT==C27)
#part22<-data %>% filter(((RT > C28)&(RT < C29))|RT==C28)
#part23<-data %>% filter(((RT > C29)&(RT < C30))|RT==C29)
```

```
#part24<-data %>% filter(((RT > C30)&(RT < C31))|RT==C30)
#part25<-data %>% filter(((RT > C31)&(RT < C32))|RT==C31)
#part20<-data %>% filter(RT >= C31) #trimming off everything greater than C37
#part26<-data %>% filter(((RT > C32)&(RT < C33))|RT==C32)
#part27<-data %>% filter(((RT > C33)&(RT < C34))|RT==C33)
#part28<-data %>% filter(((RT > C34)&(RT < C35))|RT==C34)
#part29<-data %>% filter(((RT > C35)&(RT < C36))|RT==C35)
#part30<-data %>% filter(((RT > C36)&(RT < C37))|RT==C36)
#part31<-data %>% filter(((RT > C37)&(RT < C38))|RT==C36)
#part31<-data %>% filter(RT >= C37) #trimming off everything greater than C37
#part15<-data %>% filter(((RT > C21)&(RT < C22))|RT==C21)
#part16<-data %>% filter(((RT > C22)&(RT < C23))|RT==C22)
#part17<-data %>% filter(((RT > C23)&(RT < C24))|RT==C23)
#part18<-data %>% filter(((RT > C24)&(RT < C25))|RT==C24)
#part19<-data %>% filter(((RT > C25)&(RT < C26))|RT==C25)
#part20<-data %>% filter(((RT > C26)&(RT < C27))|RT==C26)
#part21<-data %>% filter(((RT > C27)&(RT < C28))|RT==C27)
#part22<-data %>% filter(((RT > C28)&(RT < C29))|RT==C28)
#part23<-data %>% filter(((RT > C29)&(RT < C30))|RT==C29)
#part24<-data %>% filter(((RT > C30)&(RT < C31))|RT==C30)
#part25<-data %>% filter(((RT > C31)&(RT < C32))|RT==C31)
#part26<-data %>% filter(((RT > C32)&(RT < C33))|RT==C32)
#part27<-data %>% filter(((RT > C33)&(RT < C34))|RT==C33)
#part23<-data %>% filter(RT > C29)
# second pull out just the retention times
head(data)
str(part01)
part01 <-part01$RT
```

```
part02 <-part02$RT
part03 <-part03$RT
part04 <-part04$RT
part05 <-part05$RT
part06 <-part06$RT
part07 <-part07$RT
part08 <-part08$RT
part09 <-part09$RT
part10 <-part10$RT
part11 <-part11$RT
part12 <-part12$RT
part13 <-part13$RT
part14 <-part14$RT
#part15 <-part15$RT
#part16 <-part16$RT
#part17 <-part17$RT
#part18 <-part18$RT
#part19 <-part19$RT
#part20 <-part20$RT
#part21 <-part21$RT
#part22 <-part22$RT
#part23 <-part23$RT
#part24 <-part24$RT
#part25 <-part25$RT
#part26 <-part26$RT
#part27 <-part27$RT
#part28 <-part28$RT
#part29<-part29$RT
```

```
#part30<-part30$RT
#part31<-part31$RT
# next calculate your Kovats
kov07<-700+(part01*0)
kov08 <-800+((part02-C08)/(C09-C08)*100)
kov09 <-900+((part03-C09)/(C10-C09)*100)
kov10<-1000+((part04-C10)/(C11-C10)*100)
kov11<-1100+((part05-C11)/(C12-C11)*100)
kov12<-1200+((part06-C12)/(C13-C12)*100)
kov13<-1300+((part07-C13)/(C14-C13)*100)
kov14<-1400+((part08-C14)/(C15-C14)*100)
kov15<-1500+((part09-C15)/(C16-C15)*100)
kov16<-1600+((part10-C16)/(C17-C16)*100)
kov17<-1700+((part11-C17)/(C18-C17)*100)
kov18<-1800+((part12-C18)/(C19-C18)*100)
kov19<-1900+((part13-C19)/(C20-C19)*100)
#kov20<-2000+((part14-C20)/(C21-C20)*100)
#kov21<-2100+((part15-C21)/(C22-C21)*100)
#kov22<-2200+((part16-C22)/(C23-C22)*100)
#kov23<-2300+((part17-C23)/(C24-C23)*100)
kov20<-NA
#kov25<-2500+((part19-C25)/(C26-C25)*100)
#kov26<-2600+((part20-C26)/(C27-C26)*100)
#kov27<-2700+((part21-C27)/(C28-C27)*100)
#kov28<-2800+((part22-C28)/(C29-C28)*100)
#kov29<-2900+((part23-C29)/(C30-C29)*100)
#kov30<-3000+((part24-C30)/(C31-C30)*100)
#kov31<-3100+((part25-C31)/(C32-C31)*100)
```

```
#kov32<-3200+((part26-C32)/(C33-C32)*100)

#kov33<-3300+((part27-C33/(C34-C33)*100))

#kov34<-3400+((part28-C34/(C35-C34)*100))

#kov35<-3500+((part29-C35/(C36-C35)*100))

#kov36<-3600+((part30-C36/(C37-C36)*100))

#kov37<-3700+((part31-C37/(10000000-C37)*100))

# Almagmate the data and put it back into the orginal

Kovats <-
c(kov07,kov08,kov09,kov10,kov11,kov12,kov13,kov14,kov15,kov16,kov17,kov18,kov1
9,kov20)#,

#kov21,kov22,kov23,kov24)#,kov24,kov25,kov26,kov27,kov28,kov29,kov30)#,kov31,k
ov31,kov33,kov34,#kov35,

#kov36,#kov37)#,kov33,kov34)we need to delete any parts we did not calculate

str(Kovats)

str(data)

Kovats=as.data.frame(Kovats)

Kovats <- Kovats %>% mutate("num" = 1:n())

data2 = full_join(data, Kovats,by="num")

data2$Kovats<-round(data2$Kovats,1)

head(data2)

tail(data2)

# save data2 (change the filename to reflect which files you processed)

write.csv(data2, "med-3-4-kovats.csv")
```

A.2.5.3.1b: Integration R-Code for GC-MS after GC column cut

```
library(tidyverse)

library(stringr)

#write.csv(data2, "med-3-4-kovats.csv")

#getting the table of integrations into shape. Export as a text (tab delimited), put it in the working directory

intDF = read.table("med-3-4-int.txt", sep = "",skip = 2)

#here we read in the table of integrations

str(intDF) #check the structure

colnames(intDF)=c("RT","area","percent","SN","desc")#renaming the columns

intDF <- intDF %>% mutate("num" = 1:n())

head(intDF)

##########################################################################################################

#Now, we must read in another dataframe, that containing the chemical ID's, which we copied out of the

#Bruker method builder program

chemID=read.csv("med-3-4-ids.csv",head=F) #Read in the chem ID CSV corresponding to the integration dataframe from above

head(chemID)

str(chemID)

str(intDF)#check the structure, be sure column 1 contains RT's and col 3 contains ID's

chemID=data.frame(chemID$V1,chemID$V3,chemID$V8) #combine the only three parameters we want

colnames(chemID)=c("RT","ID","Ions") #rename the columns of the ID dataframe

str(chemID)

chemID$ID=as.character(chemID$ID) #make sure the ID column is character

chemID$RT=as.double(chemID$RT)

chemID$Ions=as.character(chemID$Ions)

chemID <- chemID %>% mutate("num" = 1:n())
```

```
##########################################################################
##############################################

#Now we will join the two dataframes

merged.df<-merge(x=intDF,y=chemID,by="num",all=TRUE)

str(merged.df)

tail(merged.df)

merged.df <- subset(merged.df, select = c("num", "SN","RT.y","area","ID","percent","Ions"))

names(merged.df)[names(merged.df) == "RT.y"] <- "RT"

##########################################################################
##############################################

#And now we will write this merged DF into a CSV

#write.csv(merged.df,"f18 hex_12-16-2019_mike standard apis db-5_liquid-final.csv")

#Be sure to give the final CSV an informative name!!! IE

#make sure the culture is stated, and that you indicate it is combined

#I preface this with a 1, so they will collect at the top of the folder

#1) load dplyr

library(dplyr)

#2) Load the txt file and set it to the container data

data=merged.df

#data<-read.csv("f18 hex_12-16-2019_mike standard apis db-5_liquid-final.csv")

head(data)

tail(data)

str(data)

#carbons=read.csv("carbons.csv")

#3) set the carbon standards

C08<-4.752

C09<-6.936

C10<-9.435
```

C11<-12.082

C12<-14.546

C13<-16.436

C14<-18.016

C15<-19.405

C16<-20.666

C17<-21.834

C18<-22.931

C19<-23.969

C20<-24.955

#C21<-25.902

#C22<-26.801

#C23<-27.712

#C24<-28.790

#C25<-30.201

#C26<-31.896

#C27<-34.067

#C28<-36.875

#C29<-40.524

#C30<-45.297

#C31<-51.49

#C32<-44.038

#C33<-47.437

#C34<-51.459

#C35<-56.635

#C36<-63.144

#C37<-71.263

#C38<-NA

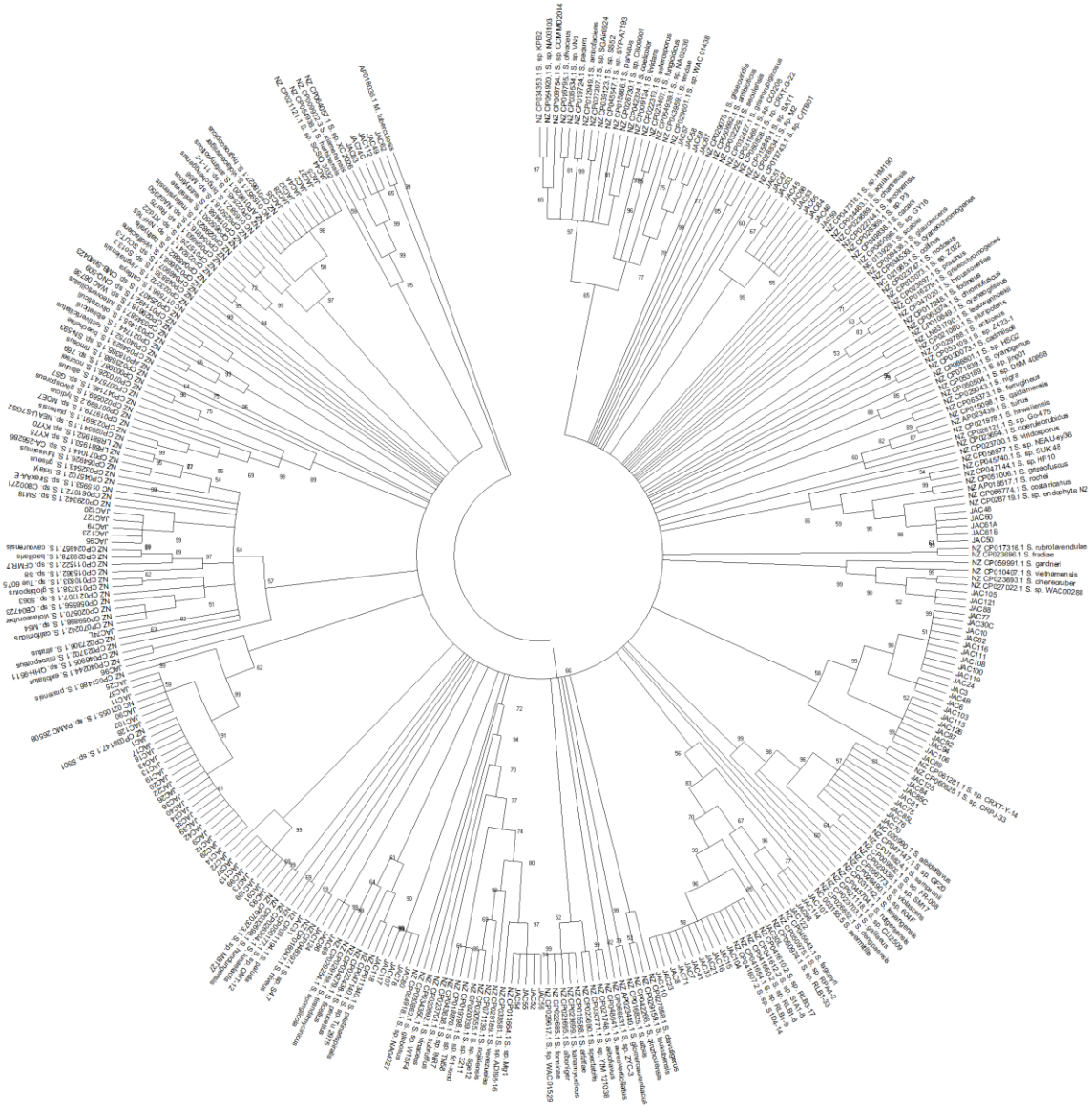
```
#4) calculate the Kovats
# first separate by carbons
#(you will have to tailor this list to reflect how many hydrocarbons in the ladder you have)
part01<-data %>% filter(RT < C08)
part02<-data %>% filter(((RT > C08)&(RT < C09))|RT==C08)
part03<-data %>% filter(((RT > C09)&(RT < C10))|RT==C09)
part04<-data %>% filter(((RT > C10)&(RT < C11))|RT==C10)
part05<-data %>% filter(((RT > C11)&(RT < C12))|RT==C11)
part06<-data %>% filter(((RT > C12)&(RT < C13))|RT==C12)
part07<-data %>% filter(((RT > C13)&(RT < C14))|RT==C13)
part08<-data %>% filter(((RT > C14)&(RT < C15))|RT==C14)
part09<-data %>% filter(((RT > C15)&(RT < C16))|RT==C15)
part10<-data %>% filter(((RT > C16)&(RT < C17))|RT==C16)
part11<-data %>% filter(((RT > C17)&(RT < C18))|RT==C17)
part12<-data %>% filter(((RT > C18)&(RT < C19))|RT==C18)
part13<-data %>% filter(((RT > C19)&(RT < C20))|RT==C19)
part14<-data %>% filter(RT>=C20)
#part14<-data %>% filter(((RT > C20)&(RT < C21))|RT==C20)
#part15<-data %>% filter(((RT > C21)&(RT < C22))|RT==C21)
#part16<-data %>% filter(((RT > C22)&(RT < C23))|RT==C22)
#part17<-data %>% filter(((RT > C23)&(RT < C24))|RT==C23)
#part18<-data %>% filter(RT>=C24)
#part18<-data %>% filter(((RT > C24)&(RT < C25))|RT==C24)
#part19<-data %>% filter(((RT > C25)&(RT < C26))|RT==C25)
#part20<-data %>% filter(((RT > C26)&(RT < C27))|RT==C26)
#part21<-data %>% filter(((RT > C27)&(RT < C28))|RT==C27)
```

```
#part22<-data %>% filter(((RT > C28)&(RT < C29))|RT==C28)
#part23<-data %>% filter(((RT > C29)&(RT < C30))|RT==C29)
#part24<-data %>% filter(((RT > C30)&(RT < C31))|RT==C30)
#part25<-data %>% filter(((RT > C31)&(RT < C32))|RT==C31)
#part20<-data %>% filter(RT >= C31) #trimming off everything greater than C37
#part26<-data %>% filter(((RT > C32)&(RT < C33))|RT==C32)
#part27<-data %>% filter(((RT > C33)&(RT < C34))|RT==C33)
#part28<-data %>% filter(((RT > C34)&(RT < C35))|RT==C34)
#part29<-data %>% filter(((RT > C35)&(RT < C36))|RT==C35)
#part30<-data %>% filter(((RT > C36)&(RT < C37))|RT==C36)
#part31<-data %>% filter(((RT > C37)&(RT < C38))|RT==C36)
#part31<-data %>% filter(RT >= C37) #trimming off everything greater than C37
#part15<-data %>% filter(((RT > C21)&(RT < C22))|RT==C21)
#part16<-data %>% filter(((RT > C22)&(RT < C23))|RT==C22)
#part17<-data %>% filter(((RT > C23)&(RT < C24))|RT==C23)
#part18<-data %>% filter(((RT > C24)&(RT < C25))|RT==C24)
#part19<-data %>% filter(((RT > C25)&(RT < C26))|RT==C25)
#part20<-data %>% filter(((RT > C26)&(RT < C27))|RT==C26)
#part21<-data %>% filter(((RT > C27)&(RT < C28))|RT==C27)
#part22<-data %>% filter(((RT > C28)&(RT < C29))|RT==C28)
#part23<-data %>% filter(((RT > C29)&(RT < C30))|RT==C29)
#part24<-data %>% filter(((RT > C30)&(RT < C31))|RT==C30)
#part25<-data %>% filter(((RT > C31)&(RT < C32))|RT==C31)
#part26<-data %>% filter(((RT > C32)&(RT < C33))|RT==C32)
#part27<-data %>% filter(((RT > C33)&(RT < C34))|RT==C33)
#part23<-data %>% filter(RT > C29)
# second pull out just the retention times
head(data)
```

```
str(part01)

part01 <-part01$RT
part02 <-part02$RT
part03 <-part03$RT
part04 <-part04$RT
part05 <-part05$RT
part06 <-part06$RT
part07 <-part07$RT
part08 <-part08$RT
part09 <-part09$RT
part10 <-part10$RT
part11 <-part11$RT
part12 <-part12$RT
part13 <-part13$RT
part14 <-part14$RT
#part15 <-part15$RT
#part16 <-part16$RT
#part17 <-part17$RT
#part18 <-part18$RT
#part19 <-part19$RT
#part20 <-part20$RT
#part21 <-part21$RT
#part22 <-part22$RT
#part23 <-part23$RT
#part24 <-part24$RT
#part25 <-part25$RT
#part26 <-part26$RT
```

```
#part27 <-part27$RT
#part28 <-part28$RT
#part29<-part29$RT
#part30<-part30$RT
#part31<-part31$RT
# next calculate your Kovats
kov07<-700+(part01*0)
kov08 <-800+((part02-C08)/(C09-C08)*100)
kov09 <-900+((part03-C09)/(C10-C09)*100)
kov10<-1000+((part04-C10)/(C11-C10)*100)
kov11<-1100+((part05-C11)/(C12-C11)*100)
kov12<-1200+((part06-C12)/(C13-C12)*100)
kov13<-1300+((part07-C13)/(C14-C13)*100)
kov14<-1400+((part08-C14)/(C15-C14)*100)
kov15<-1500+((part09-C15)/(C16-C15)*100)
kov16<-1600+((part10-C16)/(C17-C16)*100)
kov17<-1700+((part11-C17)/(C18-C17)*100)
kov18<-1800+((part12-C18)/(C19-C18)*100)
kov19<-1900+((part13-C19)/(C20-C19)*100)
#kov20<-2000+((part14-C20)/(C21-C20)*100)
#kov21<-2100+((part15-C21)/(C22-C21)*100)
#kov22<-2200+((part16-C22)/(C23-C22)*100)
#kov23<-2300+((part17-C23)/(C24-C23)*100)
kov20<-NA
#kov25<-2500+((part19-C25)/(C26-C25)*100)
#kov26<-2600+((part20-C26)/(C27-C26)*100)
#kov27<-2700+((part21-C27)/(C28-C27)*100)
#kov28<-2800+((part22-C28)/(C29-C28)*100)
```

```
#kov29<-2900+((part23-C29)/(C30-C29)*100)

#kov30<-3000+((part24-C30)/(C31-C30)*100)

#kov31<-3100+((part25-C31)/(C32-C31)*100)

#kov32<-3200+((part26-C32)/(C33-C32)*100)

#kov33<-3300+((part27-C33/(C34-C33)*100))

#kov34<-3400+((part28-C34/(C35-C34)*100))

#kov35<-3500+((part29-C35/(C36-C35)*100))

#kov36<-3600+((part30-C36/(C37-C36)*100))

#kov37<-3700+((part31-C37/(10000000-C37)*100))

# Almagmate the data and put it back into the orginal

Kovats <-
c(kov07,kov08,kov09,kov10,kov11,kov12,kov13,kov14,kov15,kov16,kov17,kov18,kov1
9,kov20)#,
#kov21,kov22,kov23,kov24)#,kov24,kov25,kov26,kov27,kov28,kov29,kov30)#,kov31,k
ov31,kov33,kov34,#kov35,

#kov36,#kov37)#,kov33,kov34)we need to delete any parts we did not calculate

str(Kovats)

str(data)

Kovats=as.data.frame(Kovats)

Kovats <- Kovats %>% mutate("num" = 1:n())

data2 = full_join(data, Kovats,by="num")

data2$Kovats<-round(data2$Kovats,1)

head(data2)

tail(data2)

# save data2 (change the filename to reflect which files you processed)

write.csv(data2, "med-3-4-kovats.csv")
```



A.3.1.1: Phylogenetic comparison of *Streptomyces* isolates to *Streptomyces* reference sequences. The phylogenetic tree consists of 345 sequences, 211 Streptomyces and 133 isolates rpoB sequences. M. tuberculosis served as an outgroup

A.3.5.1: AntiSMASH predicted BGCs in the genome of *S. griseofuscus*.

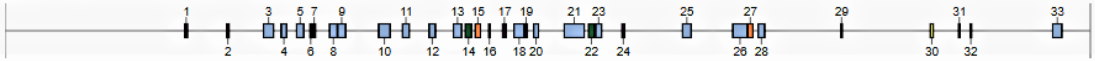
NZ_CP051006.1 (Streptomyces griseofuscus)

Region	Type	From	To	Most similar known cluster		Similarity
Region 1	T1PKS, NRPS, NRPS-like	112,034	176,874	nosiheptide	RiPP	8%
Region 2	NAPAA	315,216	347,707			
Region 3	siderophore	371,242	381,585	natamycin	Polyketide	9%
Region 4	other, lanthipeptide-class-iv	392,231	431,617	A-503083 A / A-503083 B / A-503083 E / A-503083 F	NRP	7%
Region 5	terpene	472,998	492,936	ebelactone	Polyketide	5%
Region 6	NRPS-like, NRPS, T1PKS	493,026	576,592	conglobatin	NRP	10%
Region 7	RiPP-like	748,506	756,410	informatipeptin	RiPP:Lanthipeptide	28%
Region 8	T1PKS	783,802	825,096	versipelostatin	Polyketide	5%
Region 9	lanthipeptide-class-i, lanthipeptide-class-ii, NRPS	896,103	956,839			
Region 10	T1PKS, NRPS-like, transAT-PKS-like	1,071,986	1,121,491	cinnabaramide A	NRP + Polyketide:Modular type I	18%
Region 11	thiopeptide, LAP, terpene	1,283,460	1,335,655	hopene	Terpene	92%
Region 12	NRPS, NRPS-like, betalactone	1,421,074	1,508,569	kirromycin	NRP + Polyketide:Modular type I + Polyketide:Trans-AT type I	16%
Region 13	lanthipeptide-class-i	1,676,556	1,701,597			
Region 14	NRPS-like	1,808,287	1,851,978			

Region 15	NRPS, siderophore	1,916,492	1,978,624	friulimicin A / friulimicin B / friulimicin C / friulimicin D	NRP	21%
Region 16	RRE-containing, NRPS, T1PKS	1,981,322	2,042,654	meilingmycin	Polyketide	2%
Region 17	terpene	2,150,766	2,171,477	geosmin	Terpene	100%
Region 18	RiPP-like	2,183,111	2,194,436			
Region 19	PKS-like, T1PKS, other	2,320,695	2,378,251	meilingmycin	Polyketide	5%
Region 20	siderophore, NRPS	2,550,673	2,598,163			
Region 21	terpene	3,159,315	3,179,207	julichrome Q3-3 / julichrome Q3-5	Polyketide	22%
Region 22	butyrolactone	4,004,072	4,015,004	thioviridamide	RiPP	10%
Region 23	T2PKS	4,642,100	4,714,611	spore pigment	Polyketide	83%
Region 24	siderophore	5,480,347	5,492,116	desferrioxamin B / desferrioxamine E	Other	83%
Region 25	melanin	5,564,462	5,575,058	melanin	Other	60%
Region 26	NRPS-like	5,828,286	5,871,217	SCO-2138	RiPP	64%
Region 27	ectoine	6,446,392	6,456,481	ectoine	Other	100%
Region 28	hglE-KS, T1PKS	7,049,867	7,101,670	cinnamycin	RiPP:Lanthipeptide	14%
Region 29	T3PKS	7,167,442	7,208,506	herboxidiene	Polyketide	7%
Region 30	NRPS, NAPAA, ectoine	7,212,385	7,324,494	stenothricin	NRP:Cyclic depsipeptide	27%
Region 31	T1PKS	7,342,702	7,389,296			
Region 32	NRPS, T1PKS	8,241,290	8,397,648	pentamycin	Polyketide	100%
Region 33	terpene	8,603,150	8,628,841	carotenoid	Terpene	63%

A.3.5.2: AntiSMASH predicted BGCs in the genome of *S. murinus*.

NZ_CP066774.1 (Streptomyces murinus)



Region	Type	From	To	Most similar known cluster		Similarity
Region 1	terpene	1,415,244	1,435,309	julichrome Q3-3 / julichrome Q3-5	Polyketide	25%
Region 2	terpene	1,743,048	1,762,753			
Region 3	NRPS, T1PKS, siderophore	2,033,372	2,112,355	kinamycin	Polyketide	22%
Region 4	PKS-like, NRPS-like, terpene	2,172,479	2,215,397	phenalinolactone A	Terpene + Saccharide:Hybrid/tailoring	94%
Region 5	other, T1PKS, PKS-like	2,293,820	2,350,506	meilingmycin	Polyketide	5%
Region 6	RiPP-like	2,399,516	2,410,341			
Region 7	terpene	2,420,993	2,442,439	geosmin	Terpene	100%
Region 8	T1PKS, NRPS, RRE-containing	2,553,201	2,613,349	meilingmycin	Polyketide	2%
Region 9	siderophore, NRPS	2,617,364	2,679,661	friulimicin A / friulimicin B / friulimicin C / friulimicin D	NRP	21%
Region 10	NRPS, NRPS-like, betalactone	2,939,557	3,029,950	kirromycin	NRP + Polyketide:Modular type I + Polyketide:Trans-AT type I	16%
Region 11	terpene, thiopeptide, LAP	3,127,522	3,180,293	hopene	Terpene	92%
Region 12	transAT-PKS-like, NRPS-like, T1PKS	3,336,566	3,386,364	cinnabaramide A	NRP + Polyketide:Modular type I	18%
Region 13	NRPS, lanthipeptide-class-i, lanthipeptide-class-ii	3,527,781	3,592,060	bleomycin	NRP:Glycopeptide + Polyketide:Modular type I + Saccharide:Hybrid/tailoring	12%
Region 14	NRPS	3,621,606	3,671,116	mirubactin	NRP	78%

Region 15	T1PKS	3,699,365	3,740,844	versipelostatin	Polyketide	5%
Region 16	RiPP-like	3,805,892	3,816,107	informatipeptin	RiPP:Lanthipeptide	28%
Region 17	betalactone	3,914,206	3,943,661	fusaricidin B	Polyketide + NRP:Lipopeptide	25%
Region 18	NRPS , T1PKS , NRPS-like	4,004,151	4,086,302	conglobatin	NRP	10%
Region 19	terpene	4,089,318	4,110,045	ebelactone	Polyketide	5%
Region 20	other , lanthipeptide-class-iv	4,159,254	4,197,035	A-503083 A / A-503083 B / A-503083 E / A-503083 F	NRP	7%
Region 21	T1PKS , NRPS	4,399,957	4,557,322	pentamycin	Polyketide	100%
Region 22	NRPS	4,591,579	4,634,440	diisonitrile antibiotic SF2768	NRP	66%
Region 23	T1PKS , NRPS-like	4,646,766	4,693,709	borrelidin	Polyketide:Modular type I	9%
Region 24	terpene	4,854,234	4,875,922			
Region 25	other , NRPS	5,330,762	5,398,215	actinomycin D	NRP	89%
Region 26	ectoine , NRPS , NAPAA	5,726,015	5,839,731	stenothricin	NRP:Cyclic depsipeptide	27%
Region 27	T3PKS	5,843,100	5,884,164	herboxidiene	Polyketide	7%
Region 28	T1PKS , hglE-KS	5,925,431	5,976,996	cinnamycin	RiPP:Lanthipeptide	14%
Region 29	ectoine	6,576,827	6,587,237	ectoine	Other	100%
Region 30	lanthipeptide-class-iii	7,280,477	7,303,167			
Region 31	melanin	7,502,940	7,513,536	melanin	Other	60%
Region 32	siderophore	7,593,123	7,604,892	desferrioxamin B / desferrioxamine E	Other	83%
Region 33	T2PKS , T1PKS	8,242,983	8,315,594	spore pigment	Polyketide	83%