Diversity of Actinobacteria Associated with Common Ant Species in the Guánica Tropical Dry Forest, Puerto Rico.

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Abstract

The diversity of Actinobacteria associated with ants that do not grow fungi was determined in the Guánica subtropical dry forest. Actinobacteria produces secondary metabolites used as antibiotics antifungals and antivirals. A preliminary survey of the abundance and diversity of Actinobacteria in common ants from two different environments in Puerto Rico was conducted. Cambalache rain forest and Guánica dry forest were the locations selected for this purpose. The preliminary results indicated that Guánica Dry Forest had the largest number of morphospecies of Actinobacteria. The diversity of Actinobacteria associated with three dominant species of ants (*Dorymyrmex* sp., *Solenopsis* sp. and *Paratrechina* sp.) in the Guánica dry forest was assessed using culture-dependent methods. *Streptomyces, Actinomadura, Nocardia, Pseudonocardia* were associated with *Solenopsis* sp. ants, while *Streptomyces, Nocardia* and *Nocardiopsis* were found in association with *Dorymyrmex* sp. ants. The diversity of Actinobacteria associated with the ant *Paratrechina* sp. and its nest surrounding soil were determined using culture-independent methods. We integrated the results obtained with dependent and independent culture methods in *Paratrechina* sp. *Streptomyces, Actinomadura, Nocardia, Ornithiniimicrobium, Tsuamurella, Brevibacterium, Saccharopolyspora, Nocardioides, Microbacterium, Leifsonia, Pseudonocardia, Corynebacterium, Geodermatophilus, Amycolaptosis* and *Microtetraspora* were associated with this ant. *Streptomyces* and *Actinomadura* genera were the most abundant with both methodologies. We concluded that the diversity of Actinobacteria associated with ants that do not grow fungus (*Solenopsis* sp., *Dorymyrmex* sp. and *Paratrechina* sp.) in the subtropical Guánica Dry Forest was specific for each ant species. We compared the community of Actinobacteria associated with *Paratrechina* sp. ants and the soil. We established that the community associated to the ant is consistent and clearly different from the community found in the soil in which the ant lives.

Resumen

La diversidad de Actinobacterias asociadas a las hormigas que no cultivan hongos fue determinada en el Bosque Seco de Guánica. Las Actinobacterias producen metabolitos secundarios que son utilizados como antibioticos, antifúngicos y antivirales. Se llevó a cabo un estudio preliminar de la abundancia y la riqueza de Actinobacterias en hormigas comunes de dos ambientes diferentes en Puerto Rico. El bosque húmedo de Cambalache y el bosque seco de Guánica fueron los lugares elegidos para este propósito. Los resultados preliminaries indicaron que el Bosque Seco de Guánica tuvo el mayor número de morfoespecies de Actinobacterias. La diversidad de Actinobacterias asociada con tres especies comunes de hormigas (*Dorymyrmex* sp., *Solenopsis* sp. y *Paratrechina* sp.) en el bosque seco de Guánica se evaluó utilizando métodos dependiente de cultivo. Los géneros *Streptomyces, Actinomadura, Nocardia* y *Pseudonocardia* se encontraron asociados con *Solenopsis* sp., mientras que *Streptomyces, Nocardia* y *Nocardiopsis* se encontraron en *Dorymyrmex* sp. La diversidad de Actinobacterias asociadas a la hormiga *Paratrechina* sp. y a su suelo circundante se determinó utilizando métodos independientes de cultivo. *Streptomyces, Actinomadura, Nocardia, Ornithiniimicrobium, Tsuamurella, Brevibacterium, Saccharopolyspora, Nocardioides, Microbacterium, Leifsonia, Pseudonocardia, Corynebacterium, Geodermatophilus, Amycolaptosis* y *Microtetraspora* fueron los géneros asociados con *Paratrechina* sp. al integrar los resultados obtenidos con los métodos de cultivo dependientes e independientes. *Streptomyces* y *Actinomadura* fueron los generos más abundantes en ambas metodologías. En base a los resultados, se concluye que la diversidad de Actinobacterias asociados a las hormigas (*Solenopsis* sp., *Dorymyrmex* sp. y *Paratrechina* sp.) fue específica para cada especie. Se comparo la comunidad de Actinobacterias asociada con la hormiga *Paratrechina* sp. y el suelo. Se estableció que la comunidad asociada a la *Paratrechina* sp. es consistente y claramente diferente de la comunidad se encuentra en el suelo en el que la hormiga vive.

Dedication

This work is dedicated to all my family. I specially wish to thank my parents, Esperanza and Alfredo. They have always given me their love and encouragement along with their company, despite the distance. I also wish to thank my husband, Joseph K. Garrahan, who traveled from San Juan to Mayaguez many times and gave me all his love and unconditional support.

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1. Introduction

The Actinobacteria is a group of filamentous Gram-positive bacteria with high genotypic and phenotypic variability. They are characterized by a high content of guanine and cytosine (Stakebrandt, 1991; Stach et al. 2003). Most of these microorganisms are aerobic in nature, although some species are capable of fermenting organic compounds (McCarthy and Williams, 1990). These bacteria live in the sea, freshwater (Goofellow et al. 1990) and soil (Hayakawa et al. 2000), where they participate with other microorganisms in the decomposition of organic substances such as starch, cellulose, hemicellulose, lignin, pectin, keratin, chitin and humus. Products from the degradation of these compounds return to the soil (Vobis and Chai, 1998; Stakebrandt, 1991).

The Actinobacteria are ecologically important because they contribute to the flow of materials and energy for ecosystem conservation. They produce a wide variety of bioactive secondary metabolites that have applications in agriculture, medicine and industry. These bacteria produce enzymes such as proteases that are used in the detergent, food, pharmaceutical, diagnostics, and fine chemical industries (Kumara and Takagib, 1999), others like chitinases potents inhibitos de fungal growth in plants (Schlumbawn et al., 1986) and glucose isomerases that has the largest market in the food industry because of its application in the production of high-fructose corn syrup (HFCS) (Bhosales and Rao, 1996), as well as other compounds like polyenes and ciclohexamides (Tanaka and Omura, 1990). More than half of the antibiotics used by humans come from soil Actinobacteria, as well as anti-tumor agents and enzyme

inhibitors (Stach et al. 2003; Cundliffe, 2006). Some Actinobacteria are pathogens of plants, animals and humans (Trujillo and Goodfellow, 2003). Some species fix atmospheric nitrogen in association with non-leguminous plants (Tjepkema et al. 2002) while others are insect symbionts (Cafaro et al. 2011, Currie, 2001). Examples of such associations are the Pine beetle that uses a Actinobacteria (*Strepromyces* sp.) to protect its fungal food source from a competing fungus-(Scott et al. 2008) and, the beewolf larvae, which are protected from fungal infestation by another symbiotic Actinobacteria (Kaltenpoth et al., 2005). Recently Patil et al. (2010) reported the presence of an Actinobacteria of the genus *Nocardiopsis*, in the gut of the honey bee (*Apis mellifera*), which has inhibitor activity against *Bacillus* strains native to bees and some Gram-positive human pathogenic strains.

The most studied example is the fungus-growing ants (Attini) that form large colonies with a fungal monoculture. The ants have developed a symbiosis with Actinobacteria as a mean to control disease and protect their fungal crops (Fernández-Marín, 2006). These ants cut leaves, collect in their nest decomposing plant material or feces of insects, then chew and process them into 1 to 2 mm long pieces, which serve as substrate for the fungal cultivars, rich in lipids and carbohydrates and are the sole source of food for the ant larvae and the queen. In leaf-cutter ants, the cultivated fungus is a clone, which is vulnerable to the attack of pathogenic microorganisms (Currie, 2001). The transmission of the symbiotic Actinobacteria occurred by a lateral transfer between ant colonies and possibly by the recruitment and selection of strains from the environment (Cafaro et al., 2011).

The relationship between Actinobacteria and fungus-growing ants has been widely documented (Currie, 2001; Fernández-Marín, 2006; Poulsen et al., 2007; Little and Currie, 2008). However, there is little knowledge about the association between Actinobacteria and other groups of ants.

The only study about non fungus-growing ants was made by Kost et al. (2007), who isolated several Actinobacteria from two temperate ant species that do not grow fungi (*Lasius flavus* and *Myrmica rugulosa)*. The authors evaluated the inhibition effects of the bacterial isolates against the growth of the attine ant fungal parasite *Escovopsis* and found that more than 80% of these strains inhibited its growth, suggesting that Actinobacteria can be acquired from the environment. Under this scenario, an investigation was carried to determinate the diversity of Actinobacteria associated with ants that do not cultivate fungi in a subtropical area and their relationship to local soil microbial community.

2. Hypothesis

The Actinobacteria community associated with tropical ants is similar to the community found in the soil in which it lives.

Objetives

General Objective

To determine the diversity of Actinobacteria associated with the most common species of ants that do not cutivate fungi in Guánica tropical dry forest and to compare it with the surrounding soil.

Specific objectives

1. Characterize and identify Actinobacteria associated with the ants *Dorymyrmex* sp., *Solenopsis* sp. and *Paratrechina* sp. using culture-dependent methods.

2. Characterize and identify the Actinobacteria diversity associated with the ant *Paratrechina* sp. nest and its surrounding soil, using culture-independent methods.

3. Compare the community of Actinobacteria associated with *Paratrechina* sp. nest and its surrounding soil.

3. Literature review

3.1 The Actinobacteria

The Actinobacteria are Gram-positive bacteria characterized by their high content of guanine and cytosine <70% (Ventura et al., 2007). These bacteria form a phylum that is composed of 30 families. In the past, they were known as Actinobacteria because they form branching filaments resembling the hyphae of fungi (mycelium) at some stage of development (Raja and Prabakarana, 2011). Actinobacteria shapes include coccus (*Micrococcus*), rod-coccus (*Arthrobacter*), fragmenting hyphal forms (*Nocardia*) and in the genus *Streptomyces* a permanent and highly differentiated branched mycelium (Goodfellow and Williams, 1983). Most of the Actinobacteria form spores or propagules to withstand desiccation and heat. The shape of the spores varies and is a criterion used to separate taxonomic groups (Mardigan et al., 2009).

3.2 Ecology of the Actinobacteria

The Actinobacteria are distributed across various ecological habitats, including soil, the rhizosphere, plant material, ponds, lakes and in marine sediments and coastal environments including sand beaches (Suzuki et al., 1994, Okasaki, 2006, Nakashima et al., 2009, Hasegawa et al., 2006). Most of these bacteria are harmless commensals,

and saprophytes, but some are plant and animal pathogens while others are known to form symbiotic relationships with plants and insects (Mardigan et al., 2009).

The Actinobacteria are found in metabolically active and inactive states in their natural environments. For genera such as *Streptomyces*, these states can be easily distinguished by morphological differences between the hyphae and spores. Other groups such as nocardioforms have a transitory mycelium, while for *Arthrobacter* and *Rhodococcus* few to none cell shape changes are observed when they are in nutrient-poor environments (Goodfellow and Williams, 1983).

The Actinobacteria are involved in ecological processes such as decomposition of organic matter in soil (saprophytic) and also of high molecular weight compounds such as hydrocarbons in contaminated soil. They participate in soil environments by fixing nitrogen in association with plant roots by the production of various secondary metabolites (Suzuki et al., 1994).

Actinobacteria in soil

Actinobacteria grow extensively in soils (over 1 million cells per gram). They are a significant component of the microbial soil population (McCarthy and Williams,1992). The abundance of Actinobacteria is higher in soils containing rich organic matter (Nakashima et al., 2009). They colonize particulate organic substrates such as the fragments of roots and dead fungal hyphae on which their mycelium grows. The Actinobacteria produce spores that are carried by wind and rain, while the dispersion between soils occurs by arthropods and water movement. Hydrophobic spores of the

genus *Streptomyces* adhere easily to the cuticle of arthropods. The distribution of the Actinobacteria in soil depends on environmental factors such as nutrient availability, temperature and humidity, but the pH is the main factor controlling their distribution (pH 7.0-8.0.) Halophilic and halotolerans actinobacteria can grow a pH of 6.0 to 10 (Tang et al., 2002)

Some representatives of the genus *Streptomyces,* are good producers of cell wall degrading enzymes such as cellulases, hemicellulases, chitinases, amylases and glucanases. Other species produce enzymes that degrade lignin and cell wall materials of higher plants, making them major contributors to the materials and energy flow in soil (Hasegawa et al., 2006).

The major source of antibiotic and secondary metabolite-producing Actinobacteria is found in soil. Antibiotic production is highly variable between individuals of the same species in terms of quantity and quality. Similarly, the resistance to antibiotics is highly specific to individual microbial strains (Vining, 1990). The antibiotics produced by Actinobacteria inhibit the growth of soil borne microbes including both, Gram-positive and Gram-negative bacteria and many fungi (Davelos et al., 2004).

Actinobacteria in aquatic environments

The Actinobacteria are widely distributed in aquatic habitats. Many of the strains found in these environments have also been identified in surrounding terrestrial habitats, suggesting that they are transported from soil to the marine and fresh water environments. After being deposited in mud and/or sediments, spores or resting

propagules can survive for long periods of time. Some of the genera commonly reported in fresh water environments are *Micromonospora* and *Rhodococcus*. In the marine environment a greater number of genera have been identified such as *Streptomyces, Actinoplanes, Geodermatophilus, Mycobacterium, Nocardia, Streptoverticillum* and *Streptosporagium*. Marine Actinobacteria differ from their soilcounterparts in their capacity to grow under high salt concentrations (halotolerant) and at high hydrostatic pressures like those in the ocean bed (Goodfellow and Williams, 1983).

Actinobacteria as pathogens

Some Actinobacteria species are human pathogens. An example is *Mycobacterium tuberculosis*, a species responsible for Tuberculosis disease (Mardigan et al, 2009). Other common and highly studied diseases are caused by Actinobacteria, such as leprosy and diphtheria. *Nocardia* strains cause primary pulmonary diseases and infections in skin and soft tissues (Georghiou and Blacklock, 1992).

Some Actinobacteria also cause plant diseases. Potato scab is caused by *Streptomyces scabies*, and it is characterized by the disfigurement of potato tubers with shallow or deep lesions. This disease lowers the economic value of potatoes in USA (Woodruff, 1989). In other plants, *Corynebacterium* causes a variety of diseases such as toxin production, plant withering and decay, galls formation and, biosurfactants in the surface of leaves (Goodfellow and Williams, 1983).

Actinobacteria as symbionts in plants

The Actinobacteria in the genus *Frankia* are symbionts of non-leguminous plants (actinorhizal plants) that induce nitrogen fixation in root nodules (Clawson et al., 2004) Non leguminose plants are important for ecological succession, and in land reclamation and remediation. *Frankia* species live in the soil and they have nitrogenase-containing vesicles with multilaminated lipids forming an envelope (Berry et al., 1993). These vesicles are modified by the plant in the symbiosis to promote nitrogen fixation (Benson and Silvester, 1993). *Frankia* host plants are colonizers of nutrient-poor soils such as forests, bogs, sand dunes, arid soils and mine waste lands. The rate of nitrogen fixation in actinorhizal plants is similar to those of legumes. The total fixed nitrogen is released into the soil in a long term after the plant dies (Goodfellow and Williams, 1983).

Other groups of Actinobacteria as *Microbispora* and *Streptomyces* also grow as plant endophytes (Matsumoto et al., 1998). They obtain nutrition and protection from the host and in return, they produce bioactive metabolites that confer bacterial, fungal or herbivore resistance to the plant; hence increasing its fitness. Some species produce other compounds that behave as plant growth promoters that accelerate the formation of adventicious roots (Hasewaga et al., 2006).

Importance of Actinobacteria

The Actinobacteria produce secondary metabolites that have become drugs and commercial organic chemicals. In nature, these bacteria produce antibiotics to compete

with fungi and other bacteria for resources in the environment. *Streptomyces* species have been used to generate antifungals, antibacterial and chemotherapy drugs (cancer) (Raja and Prabakarana, 2011) and many other active products such as immunosuppressive compounds, animal health products, growth promoters and enzymes with academic and commercial value. The genus *Streptomyces* is one of the most important in industry due to its vast reservoir of secondary metabolites (Hashimoto, 2007).

The most bioactive compounds with a wide versatility and structural diversity in the structure have been identified from the Actinobacteria. Approximately 10,000 compounds have been isolated from these filamentous bacteria, of which 7600 are derived from *Streptomyces* and 2500 from so called rare-Actinobacteria. This represents 45% of total isolated microbial active metabolites. Some of the genera of rare-Actinobacteria (*Micromonospora, Actinomadura, Nocardia, Streptoverticillum, Actinoplanes, Streptosporagium* and *Saccharopolyspora*) have produced excellent antibacterial antibiotics with low toxicity (Raja and Prabakarana, 2011).

Typically, antifungals derived from *Streptomyces* species are macrolide polyenes (Miller, 1973) such as nystatin, which was the first antifungal compound used in human health and it was isolated from *S. noursei* (Lamped et al., 1959). Other important antifungals are amphotericin, which was obtained from *S. nodosus* from Venezuelan soil (Oroshnik and Mebane, 1963) and natamycin extracted from *S. natalensis* (Pedersen, 1992).

Species in the genus *Streptomyces* produce two thirds of the natural antibiotics used in medicine today such as neomycin and cloranphenicol (Kieser et al 2000). The

aminoglycoside antibiotics are also extracted mainly from this genus, some examples include streptomycin, neomycin and kanamycin isolated from *S. griseus*, *S. fradius* and *S. kanamyceticus,* respectively (Regna and Hansen et al., 2002 Murphy, 1950; Umezawa,1958) . Other notoriously important antibiotics are erithromycin obtained from *S. erythraea*, tetracycline extracted from *S. rimosus* and vancomycin produced by *S. orientalis* (Moellering 2006*).*

Menbers of the genus *Streptomyces* also produces antibiotics that are toxic to humans and continuously dividing cells such as those that cause cancer. These compounds have been reinvented as chemotherapeutic drugs. Compounds derived from *S. peuticeus* and *S. chartreusis* have been used as enzymatic inhibitors and antitumor agents (Sugiura et al., 2005). Staurosporine and rebeccamycin are natural antitumoral compounds produced by a rare Actinobacteria in the genus *Lechevaliera* (Onaka, 2006). Derivatives from *S. roseosporeus* and *S. higrocopicus* are used to treat inflammatory skin diseases (Fenton et al., 2004; Gupta and Chow, 2003).

 Some Actinobacteria species produce antivirals such as the fattiviracins, which are produced by *S. microflavus*. This particular species is known to produce at least 13 fattiviracin derivatives showing potent activity against enveloped DNA viruses belonging to Herpes and Influenza families (Uyeda, 2004).

The genus *Rhodococcus* has been used in practical applications in bioconversion and bioremediation due to its enzymatic diversity and tolerance to various organic solvents, their ability to metabolize recalcitrant organic compounds and to degrade xenobiotic pollutants (Hashimoto, 2007). Also, compounds used in agriculture against gram

positive pathogens such as ziracin, dalbavacin, spynosin derive from rare Actinobacteria as *Micromonospora* (Berdy, 2005).

Several investigations have described the use of Actinobacteria in agriculture as biocontrol agents and the production of disease resistant plants by inoculating endophytic Actinobacteria (Hasewaga et al., 2006). An example *Streptomyces hygroscopicus,* is known to control *Rhizoctonia* root rot of pea by production of geldanomycin, an antibioticactive against *Rhizoctonia solani*, and capable of reducing its saprophytic growth (Rothrock and Gottlieb, 1984). Other species of Actinobacteria such as *Actinoplanes philippinensis, Microbispora rosea, Micromonospora chalcea* and *Streptomyces griseoloalbus* are effective in controlling *Pythium aphanidermatum*, the disease agent in the cucumber rot (El-Tarabily, 2006).

Symbiosis in Insects

Insects are the most abundant animals on the planet; they have developed a wide variety of symbiotic relationships with various microorganisms (Chaves et al.,2009). These relationships generate different benefits for the host as (I) direct or indirect nutrition, (ii) protection against other organisms, and (iii) improvements in development, reproduction and communication. In return, the microorganisms obtain stable environmental conditions for growth, dispersion and protection. The microsymbionts of insects include fungi, bacteria, nematodes, mites and other micro arthropods. The type of symbiotic relationship developed can range from mutualism, commensalism, competition to parasitism (Klepzig et al. al., 2009). The development of symbiotic

relationships has allowed insects to colonize new and adverse environments (Chaves and Teneiro, 2009).

Symbiosis between bacteria and insects

Many insects have symbiotic relationships with bacteria that are maternally transmitted. Some associations have an ancient and obligated origin, while others are facultative (Ferrari ansd Vavre, 2011). The symbiosis between insects and intracellular bacteria is usually obligate and provides the host with essential nutritional factors that are absent in its environment. On the other hand, insects also have facultative bacterial symbionts which are also characterized by their ability to infect new hosts (Pontes and Dale, 2006).

Recent research shows that some symbionts that are vertically transmitted protect their hosts against pathogens or predators (Brownie and Johnson, 2009). They also protect their nutrition sources in a process called "symbiont-mediated protection" (Brownie and Johnson, 2009). In these cases, if the host does not survive long enough to reproduce, then the microbe will not survive to pass to the next generation either. This process has been investigated in plants, mice and insects (Brownlie and Johnson, 2009). An example in insects is the Drosophila CVD virus that causes mortality in larvae and pupae in *Drosophila melanogaster*. The virus is transmitted both, vertically and horizontally, and is found in laboratory as well as in natural populations. Laboratory experiments showed that fly populations without the endosymbiont *Wolbachia* accumulate the virus particles faster and have increased mortality, in comparison with

genetically identical flies that were infected with *Wolbachia.* The mechanism by which *Wolbachia* reduces mortality from CVD virus is unknown (Teixeira, 2008).

Another example is the endosymbiont bacteria *Regiella insecticola* that protects the pea aphids from the fungus *Pandora neoaphidis*, whose spores penetrate the cuticle of the aphid; killing it by producing spores in insect body (Scarborough et al. 2005). Aphids infected with *R. insecticola* are five times more resistant to the fungus and will produce 10 times fewer spores; hence protecting the entire aphid population. Apparently, the bacteria produce antifungal molecules, but the exact defense mechanism has not yet been determined (Brownlie and Johnson, 2009).

Symbiosis between Actinobacteria and insects

The Actinobacteria are involved in more than half of the cases in which an insect host or its food source are protected by a symbiotic bacterium from attack by other microorganisms, while their participation in nutritional symbiosis is scarce (Kaltenpoth, 2009). One insect that has an endosymbiotic relationship with Actinobacteria is the kissing bug *Triatoma infestans* (Hemiptera: Reduviidae). Durvasula et al. (2008) identified a *Corynebacter* species as endosymbiont of *T. infestans*, the main vector of Chagas disease in South America. This microorganism was isolated from an insectary colony of *T. infestans* as a monoculture and it is essential for the maturation of the triatomid bug.

Rhodnius prolixus (Hemiptera: Reduviidae) is a bug that has a symbiosis with a strain of the genus *Rhodococcus*. The symbiont has been shown to play a role in providing the host with essential B-complex vitamins (Hill et al., 1976). Recently, Kaltenpoth et al.

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(2009) determined that *Coriobacterium glomerans* is a symbiont of the fire bug *Pyrrhocoris apterus* (Hemiptera: Pyrrhocoridae). This bacterium was found in the intestine, the feces and hemolymph of adult individuals. The authors determined that the symbiont is vertically transmitted from the female to the egg surface. The function of this symbiont is still unknown.

Streptomyces species have also been isolated from the gut of honey bees; (Patil, et al., 2010). The antibiotic activity of *Streptomyces* isolates was tested against indigenous strains of *Bacillus* from the bees and *Escherichia coli*. The results indicate a defensive interaction rather than nutritional. The authors also studied the behavior of Actinobacteria populations in honey bees during the four seasons of the year and found that 70% of the bees had at least a CFU of Actinobacteria. Of the 401 Actinobacteria isolated colonies, 163 showed activity against *Bacillus marisflavus*, an indigenous strain of the bees. In addition, some strains showed activity against *B. subtilis* and human pathogens such as vancomycin-resistant *Enterococcus faecium* and *Staphylococcus aureus* (Patil, et al., 2010). Also, the authors found that a strain similar to *Nocardiopsis alba* was present in the gut of bees during the four seasons. This strain produces phenazine-like, redox-active molecules, which allow the bacteria to survive anoxic conditions as in the gut of bees (Patil et al., 2010).

Termites specialize in lignocellulose degradation as a primary source of nutrition. Some groups of termites have developed a symbiosis with multiple prokaryotes in the gut. However, the degree in which the host and the symbionts are involved in the degradation of plant polymers is still poorly understood (Scharf, 2001). Several studies confirm the presence of Actinobacteria as a minor part of the community of microorganisms in the termite gut. Different strains of this source have been cultivated and have the ability to degrade cellulose and other plant polymers such as xylan and starch (Hungate, 1946; Khucharoenphaisan et al., 2011; Pasti et al., 1999).

Some Actinobacteria families reported in the gut of termites are Propionibacteriaceae, Streptomycetaceae, Cellulomonodaceae, Corynebacteriaceae and Rubrobacteraceae (Lefebvre et al., 2009). All these studies suggest a role of Actinobacteria in the nutrition of termites. However, there is still no evidence showing a specific taxa symbiosis and termites. Apparently, Actinobacteria communities in termites depend more on geographical location than on a termite taxonomic affiliation (Kaltenpoth, 2009).

Another case of symbiosis between Actinobacteria and insects is the wolf wasp *Philantus triangulum* (Hymenoptera: Crabronidae), who builds its nests in soil. Females hunt honey bees and use them as food for their larvae. The latter develops inside a cocoon for nine months with the bee prey causing moisture conditions that favors infestation by fungi or bacteria. The wasp has developed an association with an Actinobacteria of the genus *Streptomyces*, which the female cultivates in the glands of the antennae. The bacteria are observed as a white substance, which spreads inside the walls of the cocoon before oviposition. The bacterium (*Streptomyces philanti)*

produces antibiotics; that protect the larva against attack by other microorganisms (Kaltenpoth et al., 2005).

Observations made by Kaltenpoth et al. (2005) show that the larva eats the white substance (bacteria), suggesting a transfer of bacteria from mother to daughter. Bioassays in which the bacteria were removed from inside the cocoon showed a high mortality rate in the larvae (94.3%) before emerging (Kaltenpoth et al., 2005). Furthermore, the Actinobacteria isolated from *Philantus triangulum* has been found in more than 30 species of the genus *Philantus* and the symbionts form a phylogenetic clade suggesting that this bacterium is an obligate symbiont of the wasp (Kaltenpoth et al., 2009).

The female wasps of the species *Trachypus boharti* and *T. denticollis* from South America have structures in their glands that contain bacteria very similar to those found in *Philanthus* spp. Molecular techniques confirmed the presence of strains related to *Streptomyces philanthi* in the two wasp species suggesting that transmission of the symbionts occurs horizontally and there are new acquisitions from the environment (Kaltenpoth et al., 2010). Thus, it is shown that Actinobacteria are symbionts of at least two closely related excavator wasps.

The pine beetle *Dendroctonus frontalis* (Curculionidae: Scolytinae) cultivates the fungus *Entomocorticium* sp., which is the larval food source. In return, the fungus is carried by the beetle in a specialized structure in the adult's body called mycangium. Once the beetle has excavated a hole in the pine tree, the fungus symbiont is deposited into it.

However, *Entomocorticium* sp. is attacked by *Ophiostoma minus* disrupting normal development of larvae (Scott et al, 2008). *Streptomyces mosacchari* produces a secondary metabolite called mycangymicin suppressing the growth of the antagonist fungus and has no inhibitory effect on mutualist fungus. The Actinobacteria is located at the mycangium and the galleries of the tree where the beetle symbiont fungus grows (Scott et al, 2008).

The herbivorous beetle *Dendroctonus rufipennis* uses different kinds of bacteria found in its oral secretions as a defense, which are dispersed in the galleries within the host tree. The beetle defends its cultivar against four species of antagonistic fungi: *Leptographium abietinum*, *Aspergillus fumigatus, A. nomius,* and *Trichoderma harzianum,* which invade the galleries and decrease reproduction and survival. *Micrococcus luteus* was isolated from the oral secretion of the beetle and presents inhibitory activity against three of the four antagonistic fungi (Cardoza et al., 2006).

Symbiosis between Actinobacteria and fungus-growing ants

The fungus-growing ants belong to the monophyletic group of the tribe Attinii, which is composed of 12 genera and approximately 210 species (Currie, 2001). These ants have an obligate symbiosis with a fungus (Agaricales: Lepiotaceae: Leucocoprineae and Pterulaceae), which serves as a source of food for the larvae and the queen. In return, the ants create the conditions for growth of the fungus, provide protection against competitors and become the way of dispersion. When the new queens leave the mother´s nest to form new colonies, they carry a piece of symbiont fungus in their mouth

structure, which is planted in the new nest. The new queen feces are used as fertilizer for the growth of fungus. Subsequently, the new soldiers are responsible for construction and maintenance of the nest, taking care of the new fungus and getting new substrates for its growth (Currie, 2001).

Some ants use as a substrate for their fungus cultivar, leaves and flowers, while others use decaying plant material, dead insects and feces. The colony size can vary from small, localized colonies under stones and leaves, to supercolonies of millions of workers such as in the genus *Atta* (Currie, 2001).

The transmission of the fungus occurs vertically, meaning that it is taken from the parent colony to the daughter colony. This suggests that the fungus spreads like an asexual clone, to avoid loss of productivity in the generation of reproductive structures and it is totally dependent on the survival of the ant (Zucchi et al., 2010). Ant species cultivate a specific fungal species, but in some genera, there is a fungus lateral transfer between colonies.

The success of the large colonies of Attini ants lies in their ability to maintain the fungus cultivar clean and healthy because new microorganisms are constantly entering the nest from the substrate used for cultivation (Currie, 2001). Fungi in the genus *Escovopsis* sp. (Ascomycota: anamorphic Hypocreales) parasitize the ants' cultivar and may cause the destruction of the colony (Reynolds and Currie, 2004). This fungus has developed parallel to the symbiosis between ants and their cultivar and has co-diversified between them (Currie et al., 2003). Attini ants have developed various defense mechanisms to

protect their crops against attack by pathogens such as grooming, weeding, metapleural gland secretions and Actinobacteria associations (Currie, 2001 and Cafaro et al., 2011).

Recent research shows that fungus-growing ants have developed a symbiosis with Actinobacteria as a strategy to defend their fungus cultivar. The most common genera isolated from the exoskeleton of ants are *Pseudonocardia* and *Streptomyces.* However, other genera like *Kitassatospora* and *Propionicimonas*, and *Microbacterium* have also been reported (Currie, 2001; Poulsen et al., 2002; Cafaro and Currie, 2005; Haede et al., 2009; Zucchi et al., 2010; Mueller et al., 2008; Cafaro et al., 2011). The Actinobacteria produce antibiotics that control the growth of the parasite *Escovopsis* and do not affect the mutualistic fungus. Symbiotic bacteria are located in the integument of the ant in specialized structures that facilitate their growth and maintenance and spread throughout the cultivar (Currie et al., 2006). In some genera, the bacteria are located on the front legs while in others, in the cervicolateral plates of the propleura (Currie et al., 1999). The symbiont Actinobacteria *Pseudonocardia* is vertically transmitted and can also be acquired from the environment such as soil, plants or exchange between colonies (Cafaro et al., 2010; Mueller et al., 2008, Shoenian et al., 2010).

Actinobacteria in ants that do not grow fungi

The only research about the Actinobacteria associated with ants that do not grow fungi was made by Kost et al., 2007. The authors were focused on determining if the Actinobacteria also exist in ants that do not grow fungi and if these strains are capable of inhibiting the growth of *Escovopsis weberi*, the parasite of fungus-growing ants. To

answer these questions, they collected individuals of *Myrmica rugulosa* and *Lasius flavus*, species of temperate climate, in a private garden at the University of Kaiserslautern, Germany.

They isolated mycelia-forming Actinobacteria from the cuticle of the ants, in six of the seven *M. rugulosa* individuals collected and two of the six *L. flavus* ants. Seventeen different strains from *M. rugulosa* and only two strains from *L. flavus* were isolated. Over 80% of the strains isolated from non fungus-growing ants inhibited the growth of *Escovopsis weberi* suggesting that Actinobacteria are also acquired from environments such as soil. However, the inhibition varied considerably between strains. The presence of fungicide-producing bacteria in non-fungus growing ants may be beneficial due to a high density of individuals in the nest, the interaction between them as the grooming and trophallaxis (transfer liquid mouth to mouth)(Richard and Errard, 2009), and their underground life style. These characteristics make them susceptible to entomopathogenic fungi (Schmid, 1998). However, few pathogens have been reported for fungus-growing ants (Hughes, 2004), possibly, the presence of antibiotics in the exocrine glands can help to maintain these ants healthy (Poulsen et al., 2002). It has been suggested that a community of Actinobacteria that produces fungicidal secondary metabolites may protect non fungus-growing ants from entomopathogenic fungal attacks.

Ecological characteristics of studied ants

Solenopsis: A genus in the subfamily Myrmicinae with worldwide distribution (Martins et al., 2012). These ants are omnivorous, feed on insects, animals and plant material. Nests are usually built on the ground, but are also found under rocks, logs or leaf litter (www.dpi.qld.gov.au).

Paratrechina: A genus in the subfamily Formicinae distributed in all continental areas of the world. The genus is more diverse in Australia and tropical Asia, but these ants were transported to the Americas by commercial boats. Typically, *Paratrechina* species live in dry areas and select hollow trees or palm litter for nesting. These ants prefer a high protein diet mainly composed of dead animals (Trager, 1984).

Dorymyrmex: A genus in the subfamily Dolichoderinae and it is distributed in the Neotropics. The genus has 90 described species although some are poorly defined. Typically, these ants live in dry and disturbed soils without vegetation. *Dorymyrmex* species present high endemicity and specialized habitats (Cuezzo and Guerrero, 2012).

4. Selection of sampling area and pre-sampling of Actinobacteria associated with ants.

The information about the presence and association of Actinobacteria in ants that do not grow fungus is limited to a single study conducted by Kost et al. (2007), which was developed in a temperate climate. We conducted a preliminary sampling was carried out to determine the abundance of Actinobacteria associated with non-growing-fungus ants in dry vs. wet environments in tropical areas of Puerto Rico. The Cambalache Forest was chosen as the wet environment. It is classified in the life zone of subtropical rainforest, and is located in the karst zone of northern Puerto Rico (Figure 1). The average annual rainfall is 60 inches and the average temperature is 25.5°C (DNRA, 2008). On the other hand, the Guánica Forest belongs to the subtropical dry life zone (Ewel and Whitmore, 1973), which is located on the southwest coast of Puerto Rico (Figure 1), in the driest part of the island, with annual rainfall of 30 inches, and temperature range between 26.6 and 37.7°C (DNRA, 2 008).

Field sampling

Two field trips to collect ants were performed to Cambalache and Guánica forests in July 2009. The ants found in these forests were identified by visual inspection in a 250 meters transect looking at ground litter, epiphytes, understory vegetation, decaying logs and twigs or dry and hollow standing trees (Armbrecht and Chacon de Ulloa, 1997). When possible, the nests were found by following the path of ants.

Figure 1. Location of Cambalache and Guánica Forests, PR

Ants were collected with sterile forceps and stored in sterile Falcon (50 ml) plastic tubes. Seven ant nests in Cambalache forest and five nests in Guánica Dry Forest were sampled. The location with the highest number of Actinobacteria isolated colonies was chosen as the sampling area for later studied.

Laboratory work

Five ants were transferred to a sterile tube with 500 µl of sterile distilled water, vortexed for 30 seconds and then macerated. 100 µl of the solution was plated on chitin medium (Appendix 1) and incubated for 15 days at 25℃. Actinobacteria colonies were transferred to YMEA (Appendix 1) medium and kept at room temperature until the growth of colonies was observed. The number of colonies was recorded for each nest as well as the number of Actinobacteria strains isolated from each sampling area. Some ants were stored in 70% ethanol for further identification.

For identification of Actinobacteria isolates, genomic DNA extraction and PCR amplification of 16S rRNA gene with primers 27F y 1492R (Lane, 1991) were performed. Sequencing was done at Nevada Genomic Center (Reno, NV). Sequences were edited in the program Sequencher (Genecodes, MI) and analyzed with the BLASTn algorithm (NCBI) (Altschul et al., 1990) to identify closely related species.

Results

The identification of the ant genus and the number of Actinobacteria isolated strains per nest from each of two sampling areas is presented in Tables 1 and 2.

The largest number of Actinobacteria isolated per nest was registered in the Guánica Dry forest, although the number of ant genera collected was lower. In this forest, 45 strains of Actinobacteria were isolated in total, from two ants morphospecies, while in the Cambalache forest, 19 Actinobacteria strains were isolated from six ant morphospecies. *Streptomyces* and *Nocardia* strains were isolated from the ants in the Guánica Dry forest, while only *Streptomyces* were identified in Cambalache forest. The identity of Actinobacteria associated with ants in these two environments is shown in Tables 3 and 4.

Table 1. Number of Actinobacteria strains isolated per nest in Guánica Dry Forest.

Nest	Ant genus	Actinobacteria isolates
Nest 1	*Solenopsis* sp.1	8
Nest 2	*Dorymyrmex* sp.1	16
Nest 3	*Dorymyrmex* sp.1	14
Nest 4	*Solenopsis* sp.1	5
Nest 5	*Solenopsis* sp.1	11

Table 2. Number of Actinobacteria strains isolated per nest in Cambalache wet Forest.

Nest	Ant genus	Actinobacteria isolates
Nest 1	*Paratrechina* sp.	2
Nest 2	*Pheidole* sp. 1	3
Nest 3	*Brachymyrmex* sp.	5
Nest 4	*Pheidole* sp. 2	2
Nest 5	Unidentified Attini	2
Nest 6	*Pheidole* sp. 2	4
Nest 7	*Paratrechina* sp.	6

Table 3. Actinobacteria associated with ants in Guánica Forest.

Ant	Gene bank code	Closely related species (BLASTn)	Maximum identity (%)	Source
Solenopsis sp.	JQ819728	*Streptomyces bikiniensis*	99	Beach sand
	EF017712	*Streptomyces venezuelae*	97	Wheat rhizosphere
		Streptomyces sp CNR881 PLO4	98	Marine sediment
Dorymyrmex sp.	GQ376163	*Nocardia caishijiensis*	99	Soil
	AB636656	*Nocardia nova*	98	Human pathogen
	AM999927	*Streptomyces roseoverticillatus*	98	
	GF608476	*Streptomyces* sp HBUM 171361	99	
		Streptomyces sp SHX-101	98	Potato scab infected tuber
	FJ461617	*Streptomyces corchorusii*	99	Sewage irrigation
	JQ819728	*Streptomyces bikiniensis*	99	Beach sand
	AB184597	*Streptomyces kunmingensis*	97	

Discussion

The genus *Streptomyces* represented 88% of the identified strains in Guánica Dry forest and 100% in Cambalache forest. These Actinobacteria are typically found in soil and decaying vegetation (Madigan and Martinko, 2005). They produce over two-thirds of the clinically useful antibiotics of natural origin and numerous antifungal compounds of medical importance (Watve et al., 2001). The genus *Pseudonocardia* and *Streptomyces* are associated with fungus-growing ants. They defend the ant-cultivated fungi against pathogenic microorganisms (Haedera et al., 2009; Currie, 2001).

The results indicate a higher number and diversity of Actinobacteria associated with ants in the Guánica Dry forest. They are important members of the soil community especially in condition of high pH, water stress (860 mm/yr) and high temperature (37º) (Goodfellow and Williams, 2003; Maier and Gerba, 2009, Murphy and lugo, 1986) such as the conditions found in the Guánica Dry forest. Therefore, this location was chosen as the sampling area for a larger project, consisting ooon the analysis of three species of ants using both, culture-dependent and independent methods, to establish whether Actinobacteria are acquired from the soil or are potential symbionts of the ants.

Table 4. Actinobacteria associated with ants in Cambalache Forest.

Ant	Gene Bank Code	Closely related species (BLASTn)	Maximum identity (%)	Source
Pheidole sp 1	FJ481059	*Streptomyces chartheusis*	99	Soil
	AJ781326	*Streptomyces lateritus*	99	
Pheidole sp 2	GQ924535	*Streptomyces sp ACT-0095*	97	Root
Pheidole sp 3	EUO54375	*Streptomyces sp 8-1*	99	Soil
Brachymyrmex sp.	AB184597	*Streptomyces kunmingensis*	97	Soil
	AJ399490	*Streptomyces luteogriseus*	100	Soil
Unidentified Attini	FJ054375	*Streptomyces sp 8-1*	100	Soil
Paratrechina sp.	FJ5792582	*Streptomyces virginiae*	97	
	AJ308573	*Streptomyces sp Nu40*	98	Soil
	FJ481059	*Streptomyces chartheusis*	99	Soil

5. Materials and Methods

5.1 Sampling area: Guánica Dry Forest

The Guánica Dry forest has an extension of 4000 ha and has been protected since 1930 (Murphy and Lugo, 1990). Currently, it is an International Biosphere Reserve. This forest is characterized by high evapotranspiration rates and low annual rainfall (860 mm/yr) (Ewel and Whitmore, 1978, Murphy and lugo, 1986), which is caused by the shadow effect of the rain in the Cordillera Central, a mountain range that runs east-west through Puerto Rico (Castilleja 1991). The climate is seasonal with a prolonged dry period from December to April and a shorter dry period between June and August (Murphy and Lugo, 1990).

The topography in the Guánica Dry forest is undulate with elevations ranging from sea level up to 228 m (Murphy, 1995). Most of the forest is on a limestone formation, which influences the formation of soils (Lugo et al., 1996). The latter are classified within the order Mollisol and they are characterized by a dark to grayish brown color, an alkaline pH (7.8) and high organic matter content (18-23%). The soils are rich in nutrients; however, the availability of phosphate and potassium is low (Murphy and Lugo, 1986). Soil depth varies depending on the proximity to the limestone base, which explains the great diversity of plants found in the area (Lugo et al., 1996). The vegetation in the Guánica Dry forest is characterized by different associations of plants, like scrub forest,

deciduous forest, deciduous and semi transition entre-evergreen forest and mahogany plantations (Lugo et al., 1978).

The nest location and ant collection were performed in three different areas of the Guánica Dry forest. Ant workers from *Solenopsis* sp. and *Dorymyrmex* sp. were collected in Jaboncillo beach (17º 57.222 N, 066º 54.252 W). *Paratrechina* sp. ants were captured in the road to the Guayacan Centenario (17° 57.727 N, 066° 51.979 W) and in the forest near Tamarindo beach (17º 57.060 N, 066º 50.627 W).

5.2 Field sampling

Two samplings were performed in the Guánica Dry forest. The first sampling was conducted in October 2009 during the rainy season and the second sampling in March 2010 during the dry season. Several field trips were made before the first sampling to locate nests and optimize the best way to collect ants. Honey and tuna baits were used to locate nests. In each sampling, two nests from each ant species were collected (*Solenopsis* sp., *Paratrechina* sp., and *Dorymyrmex* sp.).

Dorymyrmex sp. nests were found near the sandy beach in an area covered by grasses in the first sampling. The two sampled nests were two meters away from each other. *Solenopsis* sp. nests were found on a hillside with forest cover and were separated by five meters.

A large nest of *Paratrechina* sp. was located right in the trunk of the Guayacan Centenario (Fig. 2) while the other nest was found several kilometers away, in the Tamarindo beach area under forest cover (Fig. 2). All nests were marked with flags and fluorescent tape with the aim of sampling again; however, the ants moved to other

31

location for the next sampling period, except for the *Paratrechina* sp. nest in the Guayacan Centenario tree.

We carried a field stereomicroscope and a collection of previously preserved ant specimens in 70% ethanol to the field in order to make correct identification of the sampled species. *Solenopsis* sp. and *Dorymyrmex* sp. nests were collected again in Jaboncillo beach, but the Tamarindo beach area under forest cover had recently been burned. The nearest nest was found 250 meters from the original location, under a *Coccoloba uvifera* tree.

Solenopsis sp. ants were captured with sterile forceps using tuna baits, which were placed a meter away from the nest entrance. When the ants left the nest, attracted by the smell of tuna, they were taken with sterile forceps. Also *Dorymyrmex sp.* and *Paratrechina sp.* ants carried dead animals, such as scorpions and geckos, to their nests, which were used as natural baits.

 Sixty to Seventy individual ants were collected from each sampled nest. After capturing the ants with heat-sterilized metal tweezers, they were stored alive in sterile plastic Falcon (50 ml) centrifuge tubes. At the same time, soil samples surrounding the nest were collected in sterile plastic Falcon (15 ml) tubes for culture-independent analyses.

Figure 2. (A) *Paratrechina* sp. nest near Tamarindo beach during second sampling. (B) *Solenopsis* sp. nest. (C) A view of Jaboncillo beach. (D) *Dorymyrmex* sp. nest. (E) *Paratrechina* sp. nest near Tamarindo beach during first sampling. (F) Nest in the Guayacan Centenario tree. The arrows indicate the entrance to the nests.

5.3 Culture-dependent techniques

Processing of samples

Ten ants were processed in the laboratory immediately after their capture; they were handled with heat-sterilized metal tweezers. Two individual ants were placed in a 1.5 ml tube with 500 ul of sterile distilled water, then vortexed for 30 seconds, and macerated with a plastic mortar. The suspension was spread in the middle of a plate containing chitin medium (Appendix 1) using a sterile triangular spreader. Actinobacteria growth on chitin plates was monitored for a month at 25℃; colonies were transferred and purified in Yeast Malt Extract Medium (YMEA) and incubated for several days at 25ºC or until they presented growth.

Pure colonies in YMEA were described macroscopically in terms of color of the substrate, color of the aerial hyphae, edge, shape, and diffusible pigmentation (Shirling and Gottli, 1969). Photographs of the morphology of the colony were taken for the record.

Molecular characterization of isolates

Extraction of genomic DNA

Different representative morphotype Actinobacteria strains were chosen for molecular identification. The extraction of genomic DNA was accomplished using the modified CTAB (hexadecyltrimethylammonium bromide) method (Cafaro et al., 2011). The aerial

part of the bacterial colonies in YMEA medium was scraped with a sterile lancet and macerated with a plastic mortar in EDTA solution (50uM) and digested with 120 µl of lysozyme (20mg/ml) at 37ºC. DNA extraction was performed with the CTAB method, with a chloroform extraction step and followed by isopropanol (-20ºC) precipitation. The pellet was washed with 70% ethanol. The DNA was re-suspended in buffer TE 1/10X (Tris-EDTA, pH 8). The presence and quality of DNA was assessed on 1% agarose gel stained with ethidium bromide.

Polymerase Chain Reaction (PCR) and gel electrophoresis.

For the molecular identification of the bacterial strains, the 16S rRNA gene was amplified with universal primers 27F (5′-AGAGTTTGATCCTGGCTCAG-3′) and 1492R (5′-GGTTACCTTGTTACGACTT-3′) (Lane, 1991). The PCR master mix consisted of ddH$_2$O, 5X colorless *GoTaq*® Reaction Buffer (Promega Corp., Madison, WI), MgCl$_2$ 3mM, dNTPs 1.2mM, primer forward and primer reverse 0.6uM and Taq polymerase 1ul/100ul reaction mix. The final reaction volume was 25ul. The cycling temperatures for the PCR reaction were 95ºC for 3 minutes for an initial denaturalization step. thirty cycles consisted of 95ºC for 45 seconds for denaturalization, 50ºC for 45 minutes for annealing, 72ºC for 1:30 seconds for polymerization. A final extension step of seven minutes at 72ºC. Amplification products were electrophored in 1% agarose gel stained with ethidium bromide. The PCR product was cleaned with Wizard SV Gel and PCR clean Up System kit (Promega Corp., Madison, WI), for removing the excess of nucleotide and primers.

DNA Sequencing

Clean PCR products were sent for sequencing at the HighThroughput Genomic Unit, University of Washington in Seattle. The samples were prepared according to the requirements of this institution. The primers used for sequencing were 27F (Lane, 1991) and U519F (5´-CAGCMGCCGCGGTAATWC-3´) (Baker et al., 2003).

Phylogenetic analysis

The sequences were edited to obtain high quality data in the program Sequencher (GeneCodes Corp., Ann Arbor, MI), then they were analyzed using the GenBank Public database and the BLASTn algorithm (Altschul et al., 1990) to identify closely related species. Afterwards, the obtained sequences and closely related strain sequences were aligned with the Clustal W program (multiple sequence alignment) (Thompson et al., 1994).

The phylogenetic trees were constructed using the Neighbor-Joining method (Saitou and Nei, 1987). Bootstrap test (1000 pseudoreplicates) was performed and support values were shown as the percentage of replicate trees in which taxa clustered together (Felsenstein, 1985). The tree was drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. Jukes-Cantor method was used for establishing the evolutionary distance (Jukes and Cantor 1969). The construction and the edition of the trees were made in the program Mega 5 (Tamura et al., 2011).

5.4 Culture-independent techniques

Processing of samples for total DNA extraction

Ants and soil samples were frozen at -20ºC upon collection until their processing in the laboratory. Only *Paratrechina* sp. samples were analyzed with these techniques.

Ants: The procedure used for extracting total DNA from Actinobacteria associated with ants followed the manufacturer's instructions of the Fast DNA Spin Kit for Soil (MP Biomedicals, Solon, OH); however, the protocol was modified in the step one to nine as follows. Ten ants were macerated in 300µl TE 1/10 buffer with a plastic sterile mortar in a 1.5 ml tube, then the content was transferred to MULTIMIX 2 Tissue Matrix Tube with 900µl Sodium Phosphate buffer and 122µl MT solution. The tubes were vortexed in Fastprep Instrument for five minutes at full speed and centrifuged at 10000x g for ten minutes. Six hundred µl of supernatant were transferred into a clean tube with 250µl Protein Precipitation Solution (PPS). The tube was mixed by hand ten times.

The tubes were centrifuged at 14000x g for 15 minutes. The supernatant transferred to a clean 15 ml tube with binding matrix suspension, then it was placed on the shaker at 120 rpm for ten minutes and let it stand in a rack for six more minutes. The DNA was re-supended in 100 ul TE buffer 1/10X and heated at 95ºC for 30 minutes to inactivate nucleases.

Soil: Ten soil sub-samples collected from around each nest of *Paratrechina* sp. were combined to form a single composite sample. 5 grams were placed in a petri dish in a

chemical hood for 10 hours to dry the sample in a temperature of 18ºC. Subsequently, the samples were macerated with a sterile syringe plunger to form a dust, with the aim to break the soil structure. Fast DNA Spin Kit for Soil was used for DNA soil extraction. The protocol was followed as described in the previous section. 800 mg of soil (dust) were added to a Multimix 2 Tissue Matrix Tube.

PCR amplification and gel electrophoresis

Actinobacteria specific primers Act283F (5'-GGGTAGCCGGCCUGAGAGGG-3') and ACT1360R (5'-CTGATCTGCGATTACTAGCGACTCC-3') (McVeigh, 1996) were used for amplification of the 16S rRNA gene in both ant and soil samples. The master mix and the conditions of the PCR reactions were the same as described before (see culture dependent techniques). PCR products were separated by electrophoresis in a 1% agarose gel and excised with a sterile scalpel. Then they were purified with Wizard SV Gel and PCR clean Up System kit (Promega Corp., Madison, WI).

Cloning of PCR products

The purified PCR products were linked into pGEM-T cloning vector and transformed in to *Escherichia coli* JM109 high efficiency competent cells recovered in SOC medium. Cells were plated in LB medium with ampicillin (100 µg/ml) with X-Gal (50mg/ml) and IPTG (100mM). The procedure was done according to pGEM®-T Easy Vector Systems kit instructions (Promega Corp., Madison, WI).

Separation and Purification of clones

Positive white colonies were separated and ordered in a new LB medium with ampicillin (concentration). The colonies were picked randomly with a sterile toothpick and suspended in 20 ul of ddH$_2$0. 5 μl of this solution were used as a template for colony-PCR. This technique was used to confirm the presence of inserts in clones.

Restriction Fragment Length Polymorphism (RFLP)

Positive colony-PCR products were characterized by digestion with restriction endonuclease Hinf I, and subsequently with Hae II. The RFLP technique was performed to find out how many different genotypes existed in our samples and to select which samples to sequence. Representatives of each restriction pattern for both enzymes were selected for amplification with universal primers T6 and SP7 and sequencing.

DNA Sequencing

Before sequencing selected PCR products, they were cleaned with Wizard SV Gel and PCR clean Up System kit (Promega Corp., Madison, WI). After product concentration assessment, they were sent for sequencing at the High Throughput Genomic Unit, University of Washington in Seattle.

Phylogenetic analysis

After *Paratrechina* sp. sequences were edited with Sequencher (GeneCodes Corp., Ann Arbor, MI), they were checked for chimeric sequences using Bellerophon (Huber, 2004) and seven were excluded from further analysis. Sequences were analyzed in BLASTn

and in the Ribosomal Data Base (Cole et al., 2009) to identify closely related species. Subsequently, all sequences were aligned using the Clustal W program (Thompson et al., 1994). The alignment was imported into Mega 5 (Tamura et al., 2011). Phylogenetic trees were constructed using the Neighbor Joining methods. The Jukes-Cantor method was used for establishing the evolutionary distance. The quality of the branching patterns of the trees was assessed by bootstrap resampling of the data sets with 1,000 pseudoreplications.

5.5 Diversity Index

A distance matrix with Jukes-Cantor correction was constructed with the DNADIST program (Felsentein, 1981). Richness estimator, diversity index and rarefaction curves were estimated with the Dotur program (Schloss and Handelsman, 2005) based on the number of operational taxonomic unit (OTUs) observed.

5.6 Comparison between ant OTUs and soil OTUs

To compare the OTUs isolated from *Paratrechina* sp. ant with the OTUs from their nest surrounding soil, The Unifrac program was used (Lozupone et al., 2006). This program compares microbial communities using phylogenetic trees and is based on sequence divergence before analysis (Lozupone et al., 2006). The P-test significance was used in this study and their values were corrected for multiple comparisons multiplying it by the number of comparisons that were made (Bonferroni correction) (http://bmf.colorado.edu/unifrac/help.psp#phylo_test). The program uses a phylogenetic tree of bacterial sequences as input file of at least two environments and determines whether there are significant differences between microbial communities.

6. Result

6.1 Results from culture-dependent methods

6.1.1 Results from *Solenopsis* sp.

Fourty-three Actinobacteria strains from *Solenopsis* sp. were identified using molecular methods. In the rainy season, we isolated six strains from nest 7 (SN7) and six other from nest 8 (SN8). Ten strains were isolated from nest 11 (SN11) and 21 from nest 12 (SN12) in the dry season. We found four genera of Actinobacteria in association with *Solenopsis* sp. (*Streptomyces, Nocardia, Pseudonocardia,* and *Actinomadura*). *Streptomyces* was the most abundant genus (74.42%). The number of strains identified by molecular methods per nest was generally low; therefore the diversity of Actinobacteria was not compared between dry and rainy seasons. The morphological characteristics of the identified strains are described in appendix 2b. The colony morphology and appearance of some representative strains are shown in figures 5,6 and 7.

Separate Neighbor-Joining trees were constructed for *Streptomyces* strains and for all other genera. The *Streptomyces* tree presents ten different clades (Figure 3). Strains SN1209, SN1208, SN1221, SN1201, SN1213 and SN1219 are related to *S. nitrosporeus*, *S. badius* and *S. griseoplanus*. The largest clade is composed of strains SN701, SN810, SN821, SN820, SN807, SN1212, SN1222 and SN1203 which are

associated with *S. zaomeyoticus*, *S. lateritus, S. bikiniensis, S. gulbarensis,* a strain isolated from soil and, *S. omiyaensis* isolated from sand. This clade is not resolved, presenting a polytomy because the 16S rDNA gene lacks enough phylogenetic signal to separate *Streptomyces* species (see Appendix 5). SN1110 strain forms an independent clade with *S. chartreusis* and *S. coralus*.

SN1125 is a close relative of *Streptomyces* sp. CTDF1, which was isolated from deepsea sediments and together with *Streptomyces aculeolatus* and strains SN1228, SN1202, SN1230, N12-28 form a monophyletic clade. SN1114 is associated with *Streptomyces* sp. RSF18 isolated from saline agriculture farm soil and forms a separate clade. SN1226 belongs to a group that contains *S. labedae, S. variabilis* and an unidentified *Streptomyces*. The latter clade is a relative sister group to a monophyletic clade containing *S. caelestis* plus isolates SN1210 and SN1204 in one branch and another unresolved group with strains SN702, SN1101, SN1216, SN1218 associated with *S. parvulus*, *S. tendae, S. malachitospinus, S. collinus* and *S. rochei*. Eight clades in this tree are associated with described species while two clades are associated only with undescribed *Streptomyces* species. One independent lineage is represented by the isolate SN710. We were unable to isolate a common strain in the four sampled nests.

A

SN1209
Streptomyces nitrosporeus NRRL B 1316(T) (EF178680)
SN1208
Streptomyces sp. A23 Ydz XM (EU368807)
Streptomyces sp. 0 3 (FJ959370)
SN1221
SN1201
Streptomyces badius NRRL B 2567(T) (AY999783)
Streptomyces sp. 195019 (GU263883)
Streptomyces griseoplanus AS 4 1868 (T)(AY999894)
SN1219
Streptomyces sp. 13638J (EU741132)
SN1213
Streptomyces chartreusis NBRC 12753 (AB184839)
SN1110
Streptomyces coralus cfcc3136 (FJ883746)
Streptomyces sp. CA131 (EF494220)
SN701
Streptomyces gardneri NBRC 12865(T) (AB249908)
Streptomyces omiyaensis NRRL B-1587 (EF178697)
SN810
SN821
Streptomyces lateritius LMG 19372 (T) (AJ781326)
Streptomyces zaomyceticus NRRL B 2038(T) (EF178685)
SN820
Streptomyces bikiniensis DSM40581(T) (X79851)
SN807
Streptomyces gulbargensis(T) (DQ317411)
SN1212
SN1222
Streptomyces sp. SDYM9 (GQ357978)
SN1203
Streptomyces narbonensis NRRL B 1680(T) (DQ445794)
SN710
SN709
Streptomyces tateyamensis (AB473555)
SN805
Streptomyces sioyaensis NRRL B 5408 (DQ026654)
SN1108
SN1123
Streptomyces paraguayensis (AB184423)
Streptomyces sclerotialus DSM 43032T(T) (AJ621608)
SN1125
Streptomyces sp. CTDF1 (GQ169067)
N12 28
Streptomyces aculeolatus strain NBRC 14824(T) (AB184624)
SN1202
SN1230

71
75
84
99
90
83
99

Figure 3. Neighbor-Joining tree based of 16S rRNA gene sequences (1000-1350pb) from cultured *Streptomyces* isolated from *Solenopsis* sp. ant and closely related species found in GenBank (accession number in parethesis). The numbers at the nodes indicate bootstrap support values (>50%) based on analysis of 1000 pseudoreplicates. Scale bar represents 0.01 substitutions per nucleotide. All positions containing gaps and missing data were eliminated. *Actinomadura* was used as outgroup.

44
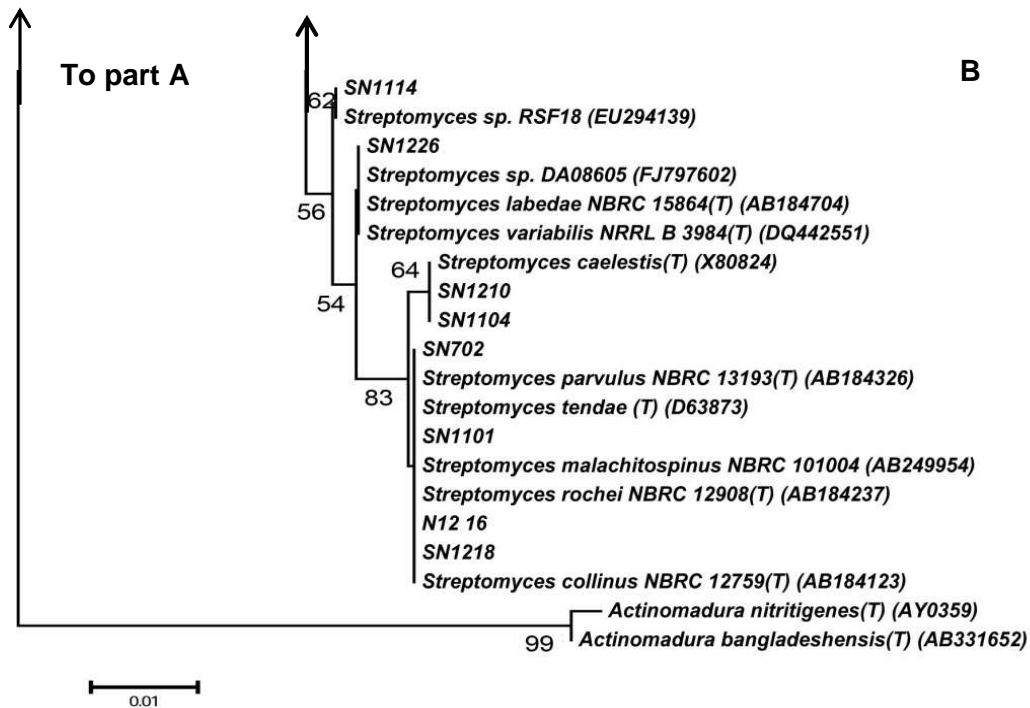
Figure 3. continued.

Nocardia was the second most abundant genus associated with *Solenopsis* sp. ants and was represented by six different isolates. SN803 strain was closely related to *Nocardia* sp. PS39-4 isolated from temperate peat swamp forest soil. SN1109 and SN1206 belong to the genus *Nocardia*, however they are not closely related to any described species. The isolates SN1207, SN705, SN703 were closely related to *N. brasiliensis*, *N. niigatensis* and *N. carnea,* respectively (Figure 4), including strains isolated from human lungs. *Nocardia* strains were isolated in all four sampled nests.
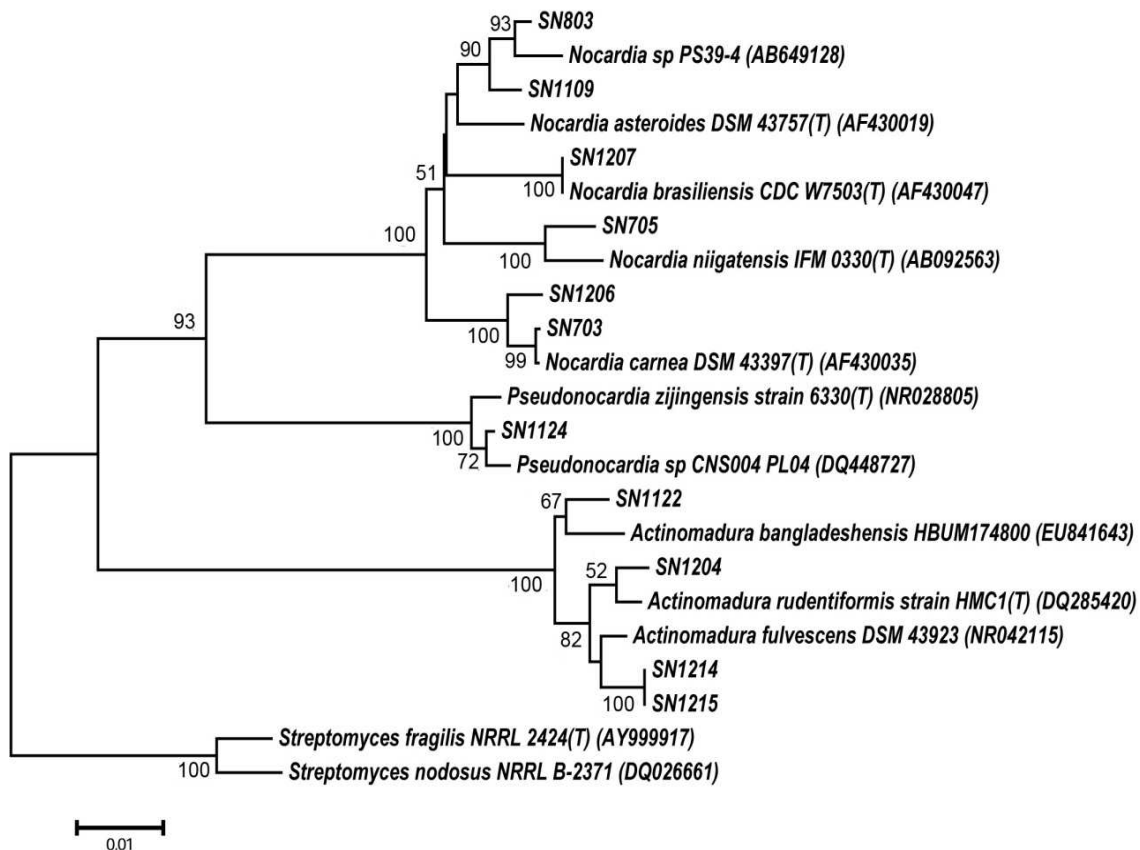
Figure 4. Neighbor-Joining tree based of 16S rRNA gene sequences (1000-1350pb) from cultured Actinobacteria isolated from *Solenopsis* sp. ant and closely related species found in GenBank (accession number in parethesis).The numbers at the nodes indicate bootstrap support values (>50%) based on analysis of 1000 replicates. The scale bar represents 0.01 substitutions per nucleotide. All positions containing gaps and missing data were eliminated. *Actinomadura* was used as outgroup.

The genus *Pseudonocardia* is represented in the tree by isolate SN1124. Other *Pseudonocardia* species have been isolated from attine ants (Cafaro et al 2011), but the closest relative to this isolate is found in marine sediments. In our isolates we also recovered representatives from the genus Actinomadura. SN1112 and SN1104 were associated with described species isolated from soil (*A. bangladensis* and *A. rudentiformis,* respectively), while SN1214 and SN1215 are affiliated with *A. fulvescens,*

46

which was also isolated from soil. Bacterial groups different to Actinobacteria were isolated and identified during this study, but not included in the results (see Appendix 3a).

6.1.2 Results from *Dorymyrmex* sp.

Thirty-five Actinobacteria strains from the ant *Dorymyrmex* sp. Eleven strains were isolated from nest 6 (DN6) and two strains from nest 9 (DN9), both sampled during the rainy season. Eigth strains were identified from nest 13 (DN13) and other fourteen from nest 14 (DN14) in the dry season. The genera of Actinobacteria present in association with *Dorymyrmex* sp. were *Streptomyces*, *Nocardia*, and *Nocardiopsis*. *Streptomyces* was the most abundant genus (88.57%). The number of strains identified in each nest was low; therefore the diversity of Actinobacteria is not compared between dry and rainy seasons. The morphological characteristics of the strains identified are described in Appendix 2c. The external appearance of some of the isolates is shown in Figure 10.
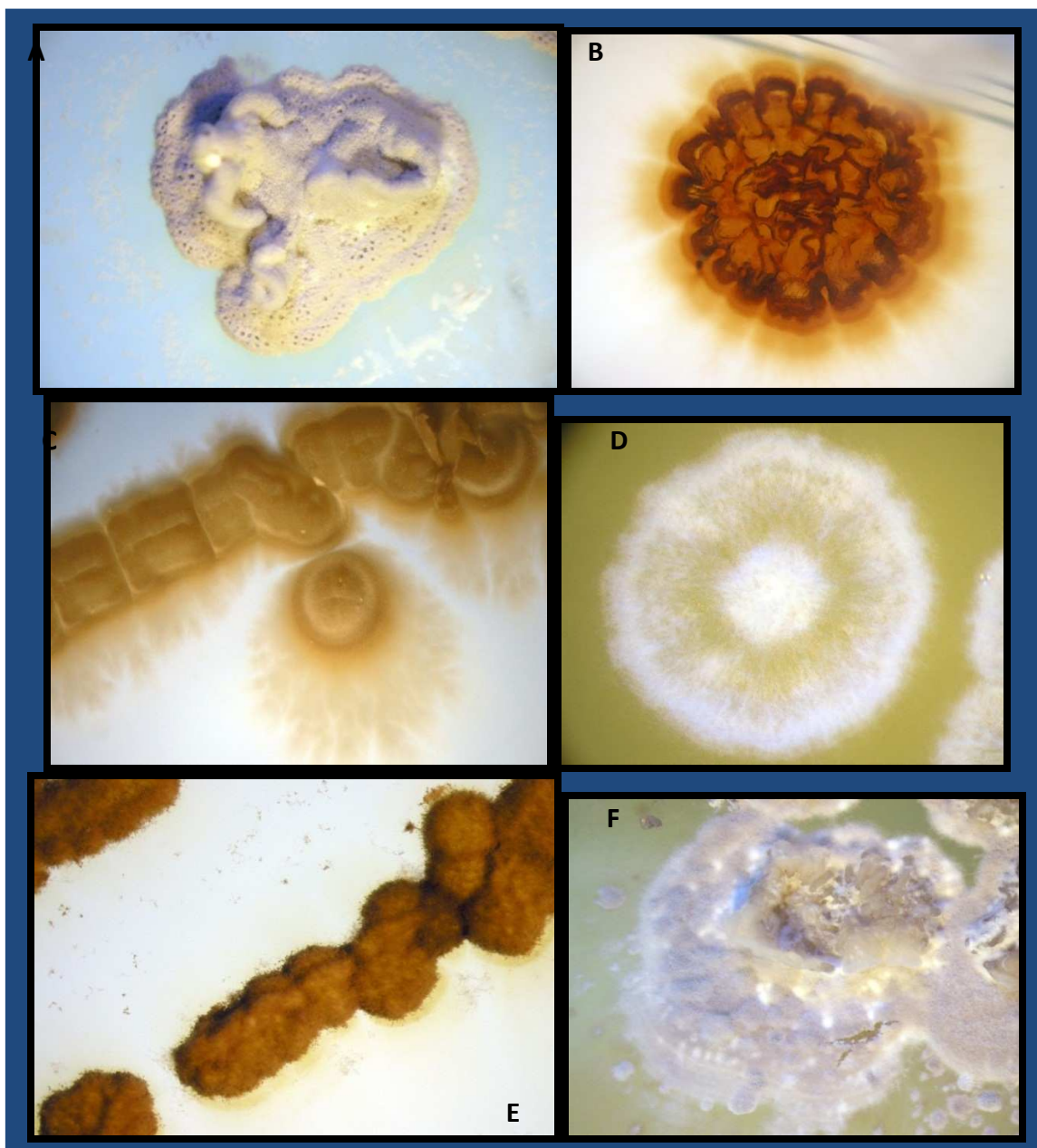
Figure 5. Colony morphology of *Streptomyces* bacteria isolated from *Solenopsis* sp. ants. A: Strain SN713, B: Strain SN1110, C: Strain SN1123, D: Strain SN1119, E: Strain SN1116, F: Strain SN1222.
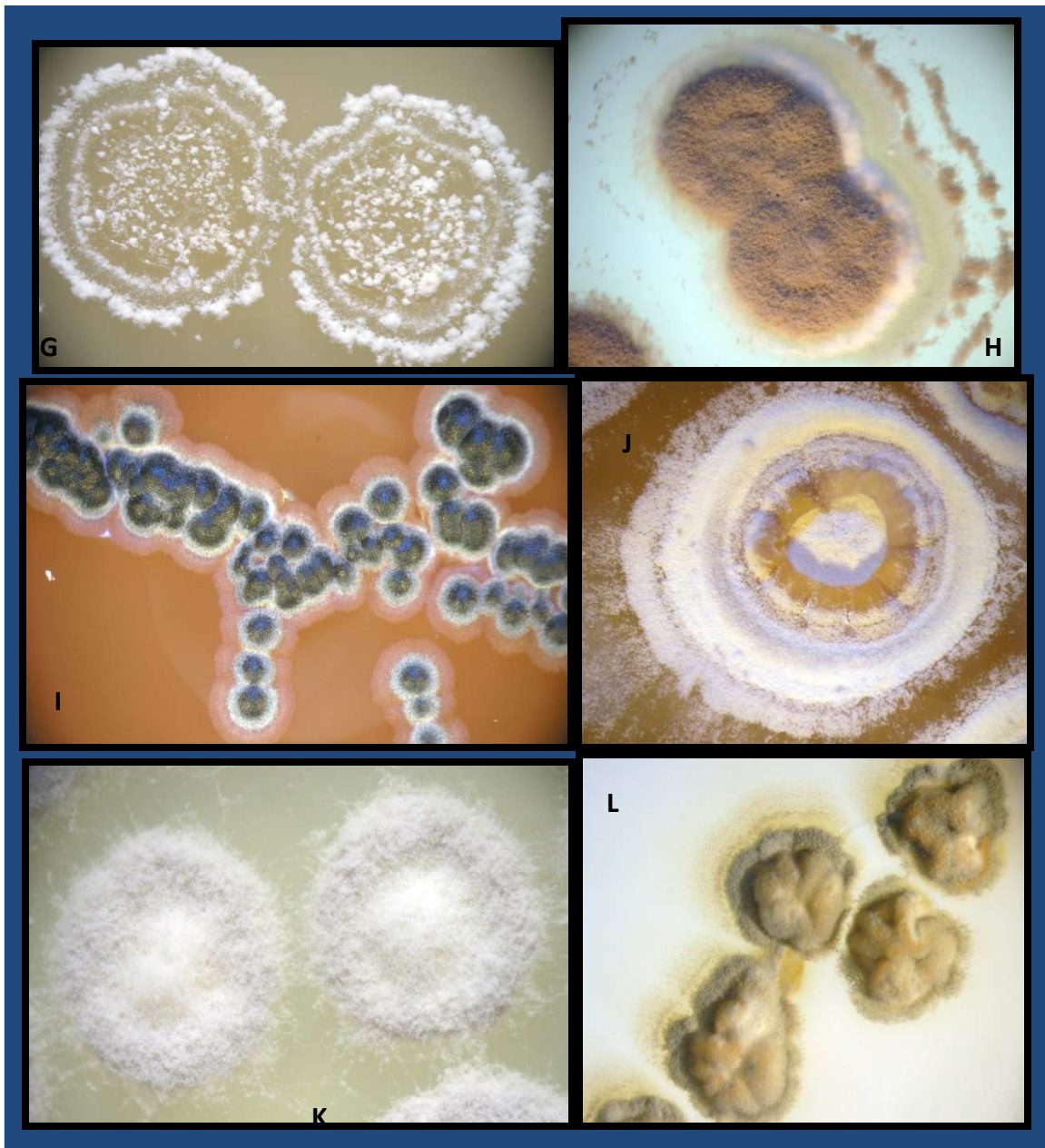
Figure 6. Colony morphology of *Streptomyces* bacteria isolated from *Solenopsis* sp. ants. G: Strain SN1201, H: Strain SN1226, I: Strain SN1202, J: Strain SN1219, K: Strain SN1216, L: Strain SN1114.
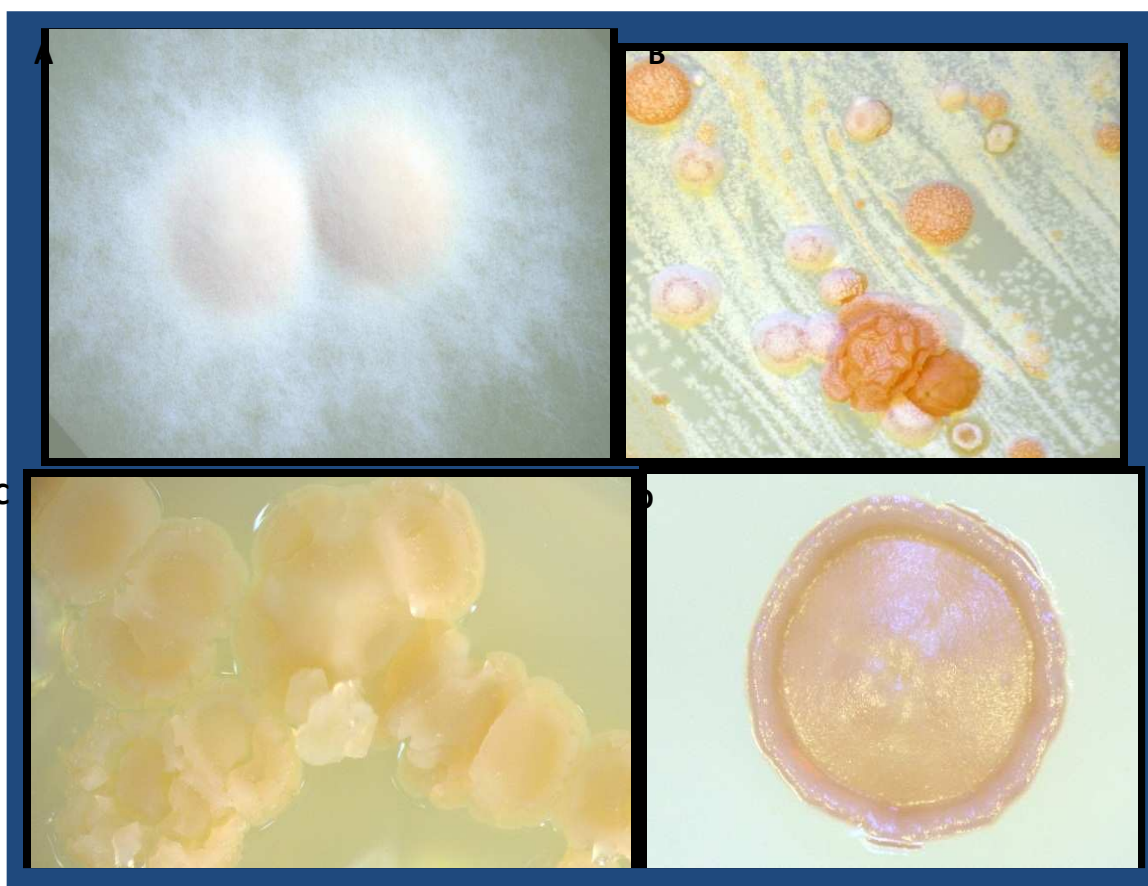
Figure 7. Colony morphology of the Actinobacteria isolated from *Solenopsis* sp. ants. A: *Nocardia* sp. strain SN1109, B: *Nocardia* sp. strain SN1206, C: *Actinomadura* sp. strain SN1204, D: *Actinomadura* sp. strain SN1214.

The phylogenetic relationships of these sequences were determined by constructing Neighbor-Joining tree from multiple sequence aligments. A separate phylogenetic tree was made for *Streptomyces* using *Actinomadura* as an outgroup and another tree for the other genera. Eleven different clades were recognized in the *Streptomyces* tree (Figure 8). The largest clade was comprised of nine strains DN1312, DN1310, DN1317, DN1403, DN1405, DN608, DN906, DN904, DN1303 which were related to *S. bikiniensis*, *S. cineoruber*, *S. violaceoerectus* and
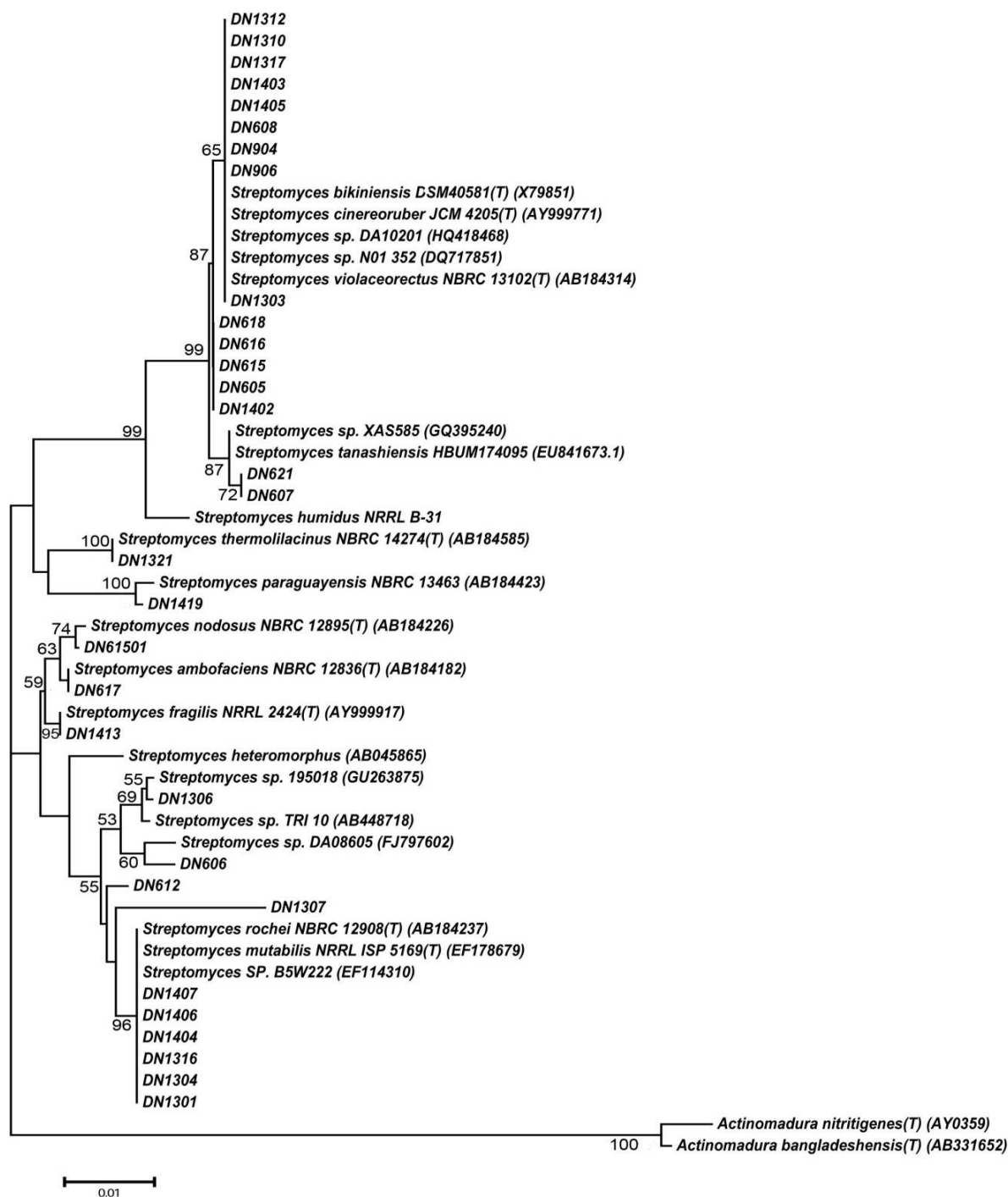
Figure 8. Neighbor-Joining tree based of 16S rRNA gene sequences (1000-1350pb) from cultured *Streptomyces* isolated from *Dorymyrmex* sp. ant and closely related species found in GenBank (accession number in parethesis).. The numbers at the nodes indicate bootstrap support values (>50%) based on 1000 pseudoreplicates. The scale bar represents 0.01 substitutions per nucleotide. All positions containing gaps and missing data were eliminated. *Actinomadura* was used as outgroup.

Streptomyces sp. DA10201 isolated from soil. This clade is not resolved, presenting a polytomy because the 16S rDNA gene lacks enough phylogenetic signal to separate *Streptomyces* species (see Appendix 5). Representative strains isolated from each of the four sampled nests were in this clade.

Strains DN618, DN616, DN615, DN605, DN1402, DN612 and DN1307 were not related to any described species or sequence deposited in GenBank. On the other hand, strains DN621 and DN607 were more closely related to *S. tanahiensis*. Strain DN1321 formed a well-supported clade (bootstrap value >70) with *S. termolilacinus* while DN1419 did the same with *S. paraguayensis*. In a weakly supported clade, DN61501, DN617 and DN1413 were each associated with *S. nodosus, S. ambofaciens* and *S. fragilis,* respectively. DN1306 and DN606 were associated with undescribed *Streptomyces* species. DN1306 was closely related to *Streptomyces* sp. 195018 isolated from a magnetite mine while DN606 was associated with *Streptomyces* sp. DA08605. The strains DN1407, DN1406, DN1404, DN1316, DN1304 and DN1301 belong to a clade containing *S. rochei* and *S.mutabilis*.

The genus *Nocardia* was the second most abundant associated with *Dorymyrmex* ants. DN1314 and DN1414 strains formed a close group with *N. cyriacigeorgica,* which was isolated from bronchial secretion. Meanwhile DN1410 is a close relative of *N. cahishijiensis* isolated from soil. DN1318 is the only strain belonging to the genus *Nocardiopsis* (Figure 9). Other bacterial groups were also isolated and identified during this process (Appendix 3b).
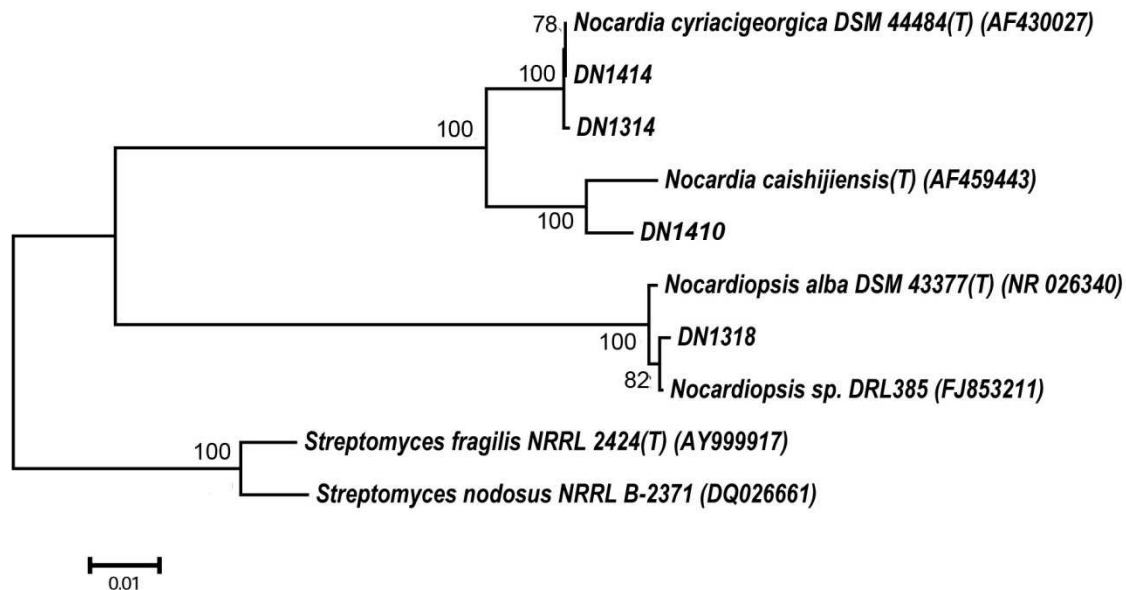
Figure 9. Neighbor-Joining tree based of 16S rRNA gene sequences (1000-1350pb) from cultured Actinobacteria isolated from *Dorymyrmex* sp. ants. in GenBank (accession number in parethesis).The numbers at the nodes indicate bootstrap support values (>50%) based on analysis of 1000 pseudoreplicates. The scale bar represents 0.01 substitutions per nucleotide. All positions containing gaps and missing data were eliminated. *Actinomadura* was used as outgroup.

6.1.3 Results from *Paratrechina* sp.

Fifty Actinobacteria strains were identified from *Paratrechina* sp. ants using molecular methods. Eleven strains were isolated from nest 2 (PN2) located in the forested area of Tamarindo Beach, thirteen strains were obtained from nest 4 (PN4) located in the *Guayacan Centenario.* Both nests were sampled in the rainy season. During the dry season, fourteen strains were also isolated from nest 4 (PN42) and twelve isolates were recovered from nest 10 (PN10) located on the Tamarindo beach under *Coccoloba uvifera*.

There were four genera isolated from *Paratrechina* sp. ants: *Streptomyces*, *Actinomadura*, *Amycolaptosis* and *Microtetraspora*. The genus *Streptomyces* was the most abundant (82%). The number of strains identified in each nest was low; therefore the diversity of Actinobacteria is not compared between dry and rainy seasons. The morphological characteristics of the isolated strains identified are described in Appendix 2a. Macromorphological characteristics of selected isolates are shown in Figure 13 and 14.

The phylogenetic relationships of isolates were determined by Neighbor-Joining analysis of 16S rDNA sequences. *Actinomadura*, *Amycolaptosis* and *Microtetraspora* isolates were analyzed together (Figure 12). A separate phylogenetic tree was made for most abundant genus *Streptomyces* (Figure 11).

Actinomadura was the second most abundant genus of Actinobacteria associated with *Paratrechina* sp. (14%). The strain PN409 was a close relative of *A. atramentaria*, like PN414 was with *Actinomadura pallida* (*Parvopollispora*) (Tamura and Kazunori, 1998). PN4221 and PN4223 are related to *A. hibisca* while PN422 and PN426 were close associated with *A. nitrigenes*. The strain PN425 belongs to the genus *Actinomadura,* but was not closely related to any described species. PN225 is the only representative of the genus *Microtetraspora spiralis*, PN411 was a close relative to *Amycolaptosis echigonensis,* which was isolated from soil. Other bacterial groups were isolated and identified during this study, but were not analyzed (Appendix 3c).
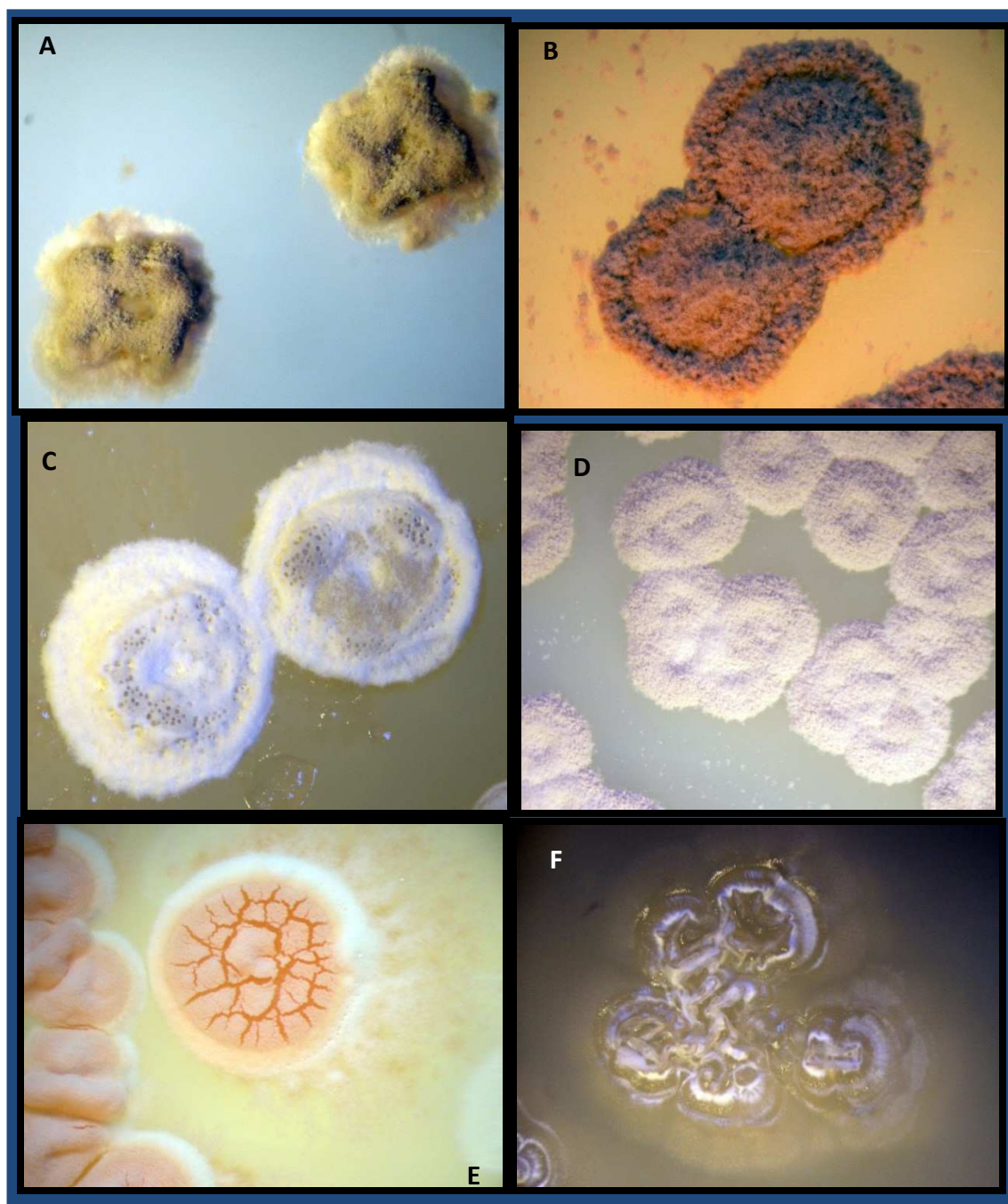
Figure 10. Colony morphology of Actinobacteria isolated from *Dorymyrmex* sp. ants. A: *Streptomyces* sp. strain DN1403, B: *Streptomyces* sp. strain DN1316, C: *Streptomyces* sp. strain DN1405, D: *Streptomyces* sp. strain DN1404, E: *Nocardia* sp. strain DN1410, F: *Streptomyces* sp. DN1410

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Twenty-tree different clades were identified in the *Streptomyces* tree (Figure 11a). All clades are associated with described species except for isolates grouping with *Streptomyces* sp. DA08605 and *Streptomyces* sp. M MN 1. PN203 isolate grouped as a separate lineage, while isolates PN1015, PN1014, PN1001 and PN1003, PN403 formed two different clades no related to any known species of *Streptomyces*.

The *Guayacan Centenario* nest (nest 4) was the only nest sampled during both dry and rainy seasons. Only one clade had strains from both season: PN4207, PN4203, PN401, PN402, PN423, PN4201 belong to *Streptomyces* sp. DA08605 branch figure 11 b, this strain was isolated from soil. Strains PN205, PN214, PN1013, PN1005, PN1007 were related to *S. parvulus*. PN210 was associated with *S. spectabilis* while PN416 formed a branch with *S. variegatus* in the same cluster. PN202 eas affiliated with *S. fragilis* and the strains PN211, PN212, PN4205 PN4220 were related to *S. tendae,* which was isolated from potatoes (Figure 11 b).

PN1005 and PN1016 strains belong to the clade formed by *S. griseus*, *S. tanahiensis* and *S. californicus* isolated from soil. PN201, PN204 and PN215 were close relatives of *S. prunicolor*, *S. xantholiticus* and *S. waerraensis,* respectively. PN2409 was related to *S. cinereoruber*, while PN207 belonged to the clade formed by *S. venezuelae* and *S. castaneus*. PN1009 is closely related to *S. seoulensis* and PN1018 to *S. kumimgensis*, which was isolated from soil. PN410 was associated with *S. escleroctiatus* while PN1004 is related to *S. catenulae* and PN219 was a close relative of *S. albiaxis*. PN421 and PN422 formed a branch with *S. sahachiroi* and *S. carpinensis*, both strains isolated from soil. PN4224 is associated with *S. levis* and *S. purpurascens* (Figure 11a).

A

Streptomyces griseus(T) (AY207604)
PN1005
PN1016
93
Streptomyces californicus NBRC 3386(T) (AB184755)
Streptomyces tanashiensis 12919(T) (AY999856)
PN204
55 87 Streptomyces xantholiticus NBRC 13354(T) (AB184349)
69 PN4209
Streptomyces cinereoruber JCM 4205(T) (AY999771)
51 85 Streptomyces venezuelae(T) (AB045890)
68 PN207
Streptomyces castaneus NBRC 13670(T) (AB184453)
99 PN215
Streptomyces werraensis 1165 (HQ607432)
98 PN201
Streptomyces prunicolor NRRL B 12281(T) (DQ026659)
88 Streptomyces seoulensis NBRC 16668(T) (AB249970)
PN1009
97 PN403
98 PN1003
Streptomyces kunmingensis NBRC 14463(T) (AB184597)
85 PN1018
58 PN410
Streptomyces sclerotialus DSM 43032T(T) (AJ621608)
59 Streptomyces catenulae DSM 40258T(T) (AJ621613)
PN104
85 Streptomyces albiaxialis NBRC 101002(T) (AB249952)
PN4219
PN4206
52 Streptomyces sp. M MN 1 (EU722758)
52 PN421
Streptomyces sahachiroi NBRC 13928 (AB184548)
Streptomyces carpinensis NBRC 14214(T) (AB184574)
PN422
66 Streptomyces anandii NRRL B 3590(T) (AY999803)
Streptomyces djakartensis strain NBRC15409(T) (AB184657)
59 Streptomyces levis NBRC 15423(T) (AB184670)
Streptomyces purpurascens NBRC12831(T) (AB184847)
55 PN4224

To part B

0.01

Figure 11. A. Neighbor-Joining tree based of 16S rRNA gene sequences (1000-1350pb) from cultured *Streptomyces* isolated from *Paratrechina* sp. ants and closely related species found in GenBank (accession number in parethesis). The numbers at the nodes indicate bootstrap support values (>50%) based on neighbor-joining analysis from 1000 pseudoreplicates. The scale bar represents 0.01 substitutions per nucleotide. All positions containing gaps and missing data were eliminated. *Actinomadura* was used as outgroup.

58

To part A

B
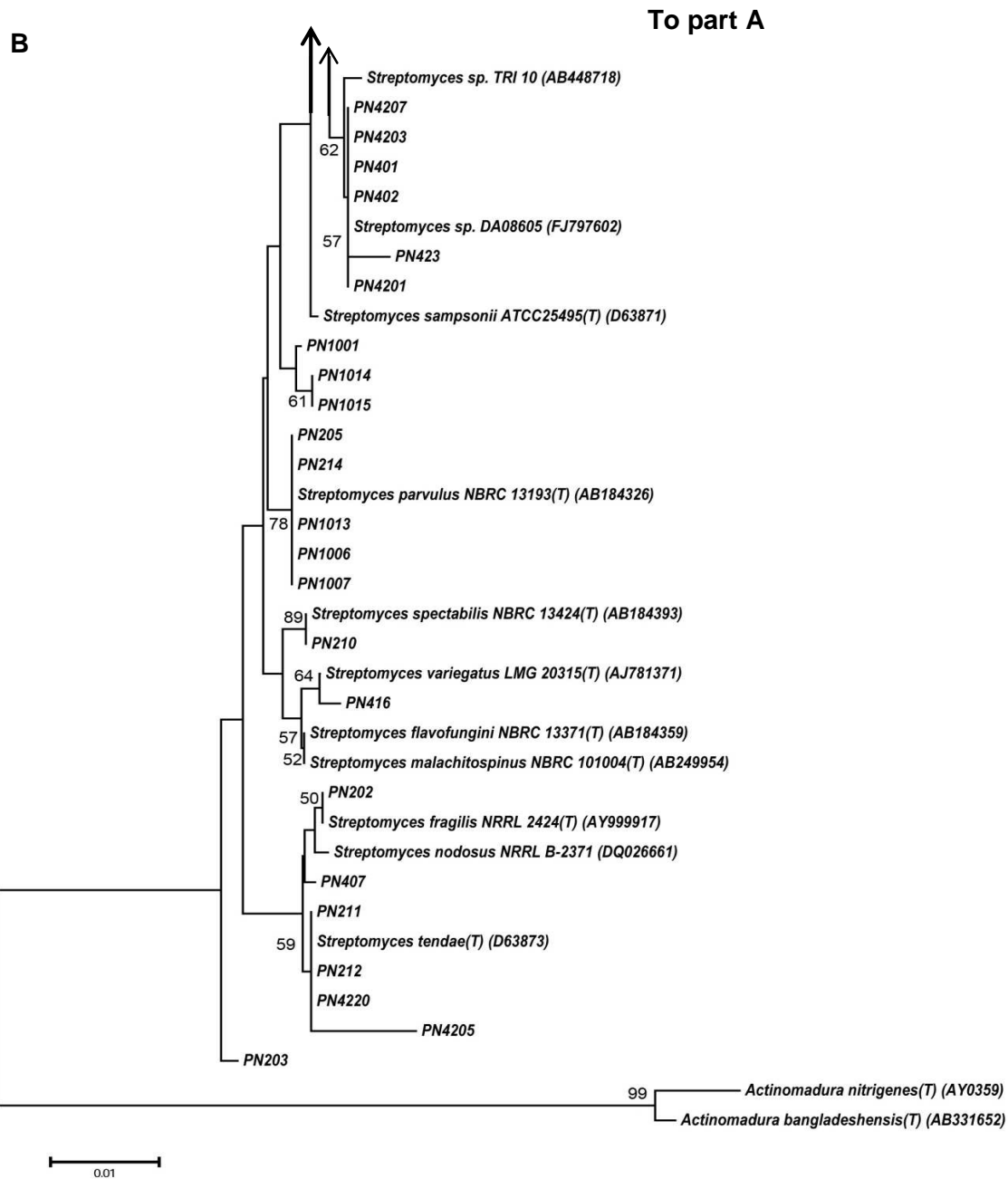
Figure 11 B. continued.

Figure 12. Neighbor-Joining tree based of 16S rRNA gene sequences (1000-1350pb) from cultured Actinobacteria isolated from *Paratrechina* sp. ants and closely related species found in GenBank (accession number in parethesis). The numbers at the nodes indicate bootstrap support values (>50%) based on neighbor-joining analysis from 1000 pseudoreplicates. The scale bar represents 0.01 substitutions per nucleotide. All positions containing gaps and missing data were eliminated. *Actinomadura* was used as outgroup.
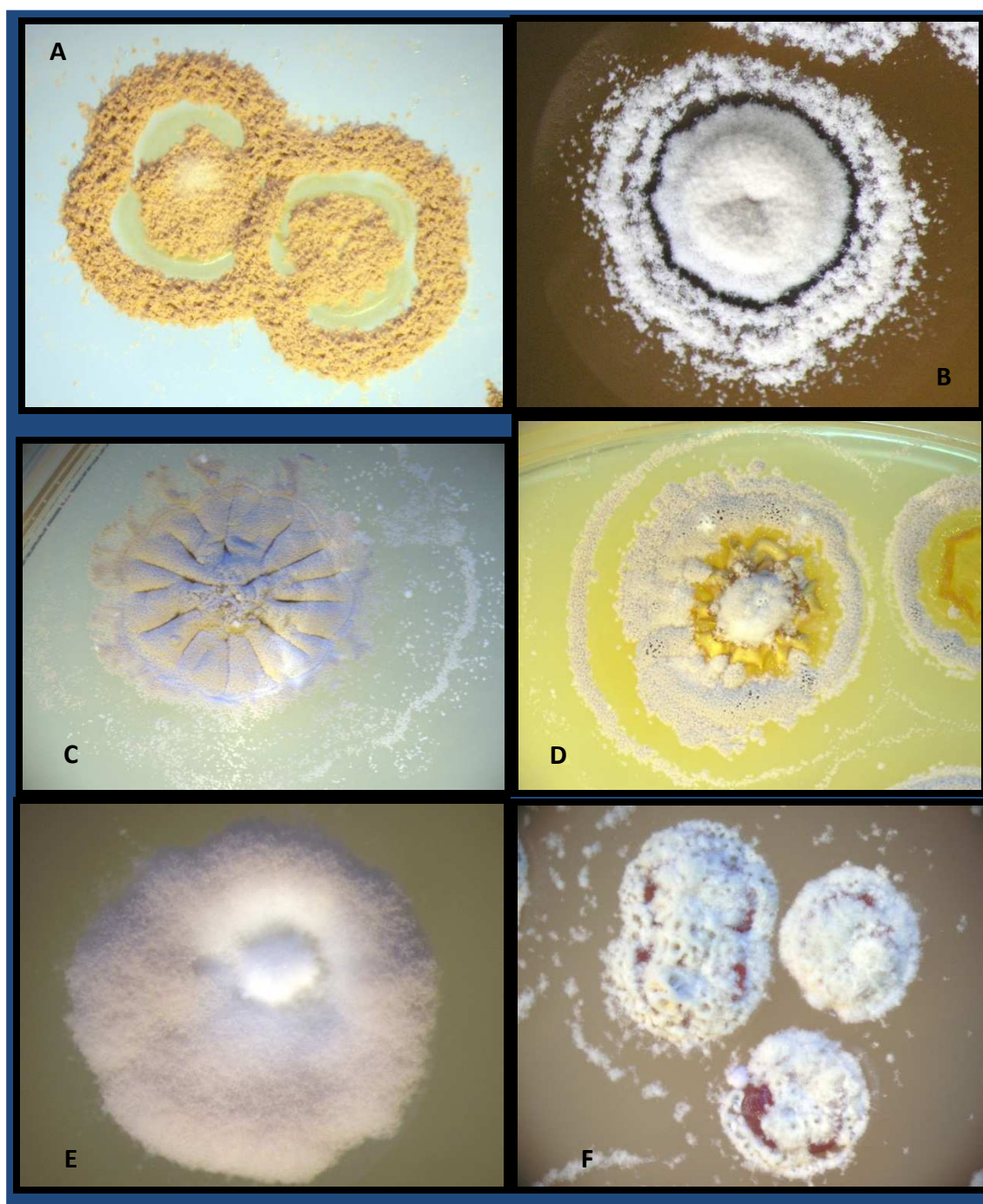
Figure 13. Colony morphology of the Actinobacteria isolated from *Paratrechina* sp. ants. A: *Streptomyces* sp. strain PN212, B: *Streptomyces* sp. strain PN4206, C: *Streptomyces* sp. strain PN1003, D: *Streptomyces* sp. strain PN1006, E: *Streptomyces* sp. strain PN1009, F: *Streptomyces* sp. strain PN1018

.
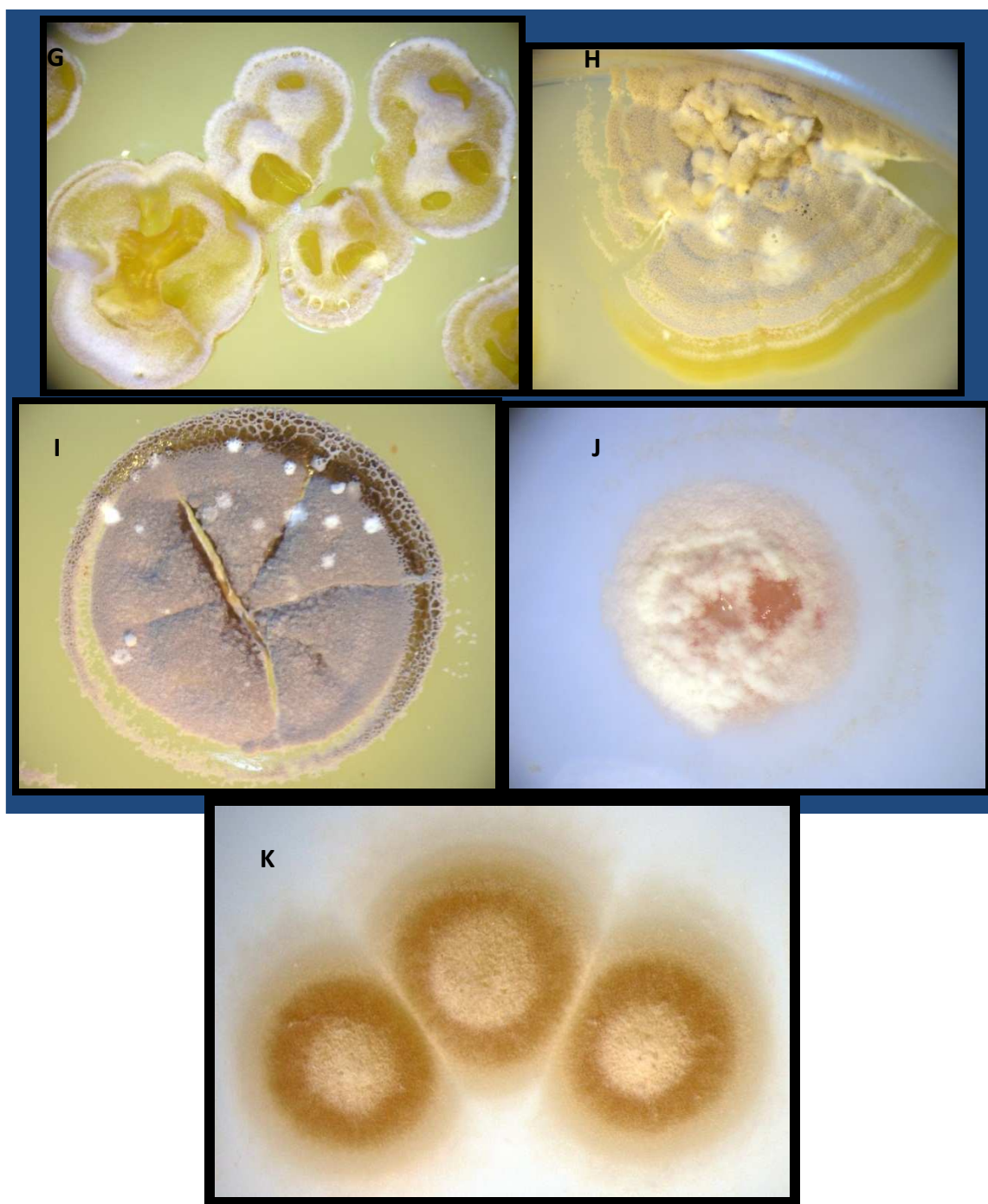
Figure 14. Colony Morphology of Actinobacteria isolated from *Paratrechina* sp. ants. G: *Streptomyces* sp. strain PN1004, H: *Streptomyces* sp. strain PN1007, I: *Streptomyces* sp. strain N1009, J: *Actinomadura* sp. strain PN4223, K: *Streptomyces* sp. strain PN4219.

6.2 Results from culture-independent methods

6.2.1 DNA extraction and PCR amplification

Soil and ant-associated actinobacteria genomic DNA were extracted with the Fast DNA Spin Kit for Soil (MP Biomedicals, Solon OH). The amount of DNA obtained for *Paratrechina* sp. ants was limited, in contrast to the large amount of DNA obtained for soil (Figure 15).
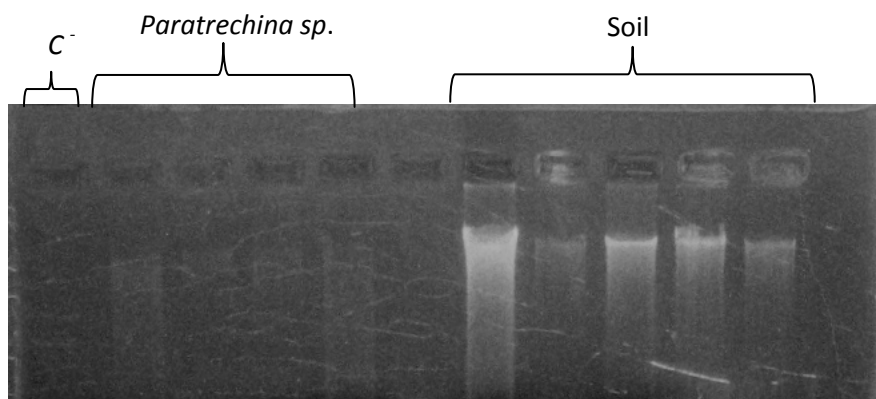
Figure 15. Genomic DNA from *Paratrechina* sp. ants of each sampled nest and its surrounding soil.

The 16s rDNA gene was amplified using actinobacteria-specific primers Act283F and Act1369R (McVeigh, 1996). We used 25ng DNA and dilution (1:5, 1:10, 1:20) for amplification (Figure 16). Moreover, genomic DNA from soil was purified with Elu Quik DNA Purification Kit® (Whatman, UK). The amplicon obtained was approximately 1100bp (Figure 17).
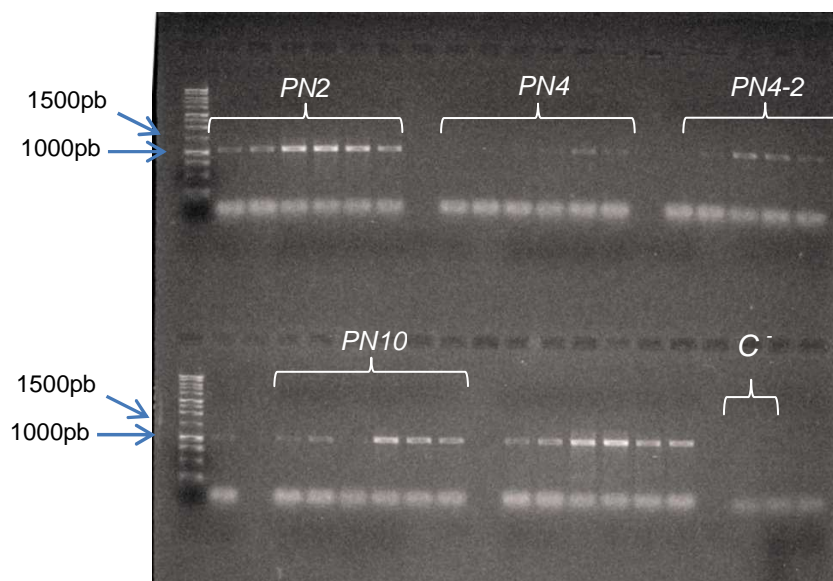
Figure 16. Amplification of 16S rDNA with the primers Act 283F and Act1369R of Actinobacteria associated with *Paratrechina* sp. in the four sampled nests.
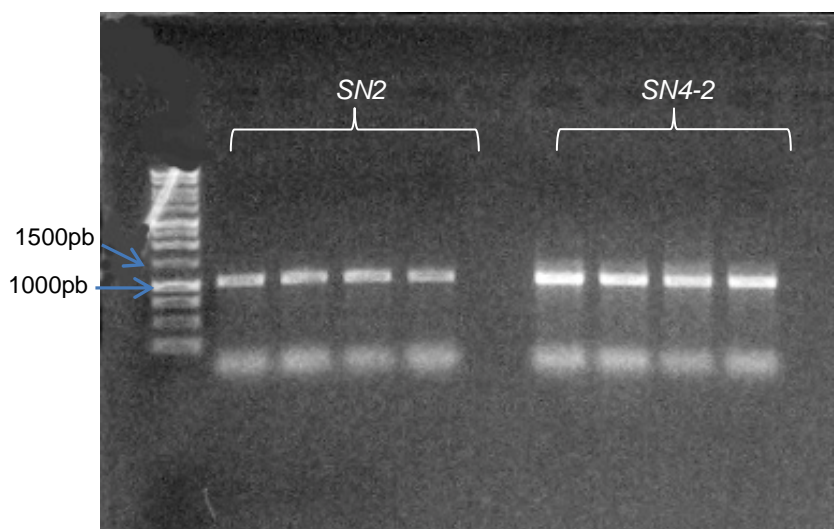
Figure 17. Amplification of 16S rDNA with the primers Act 283F and Act1369R of Actinobacteria in surrounding nest soil of *Paratrechina* sp.

Four ant-associated Actinobacteria clone libraries were created from each *Paratrechina* sp. nest (PN2, PN4, PN4-2 and PN10) and other four from the surrounding soil (SN2, SN4, SN4-2, and SN10). The presence of insert in the clones was verified by colony

PCR. Approximately 80% of the clones contained insert. 1631 clones were studied in this investigation. The number of clones analyzed for each library is shown in Table 5.

Table 5. Number of clones analyzed in each clone library

Source	Clone library	Clones Analyzed
Ant	PN2	241
Ant	PN4	201
Ant	PN4-2	220
Ant	PN10	158
Soil	SN2	229
Soil	SN4	231
Soil	SN4-2	181
Soil	SN10	170

6.2.2 Restriction Fragment Length Polymorphism (RFLP)

Ants

A large number of enzyme restriction patterns were found in the DNA of the ant-associated Actinobacteria in the four nests and the soils. We found 15 patterns for the enzyme HinfI and 14 for the enzyme HaeII. Several patterns were common to the four nests while some were specific to each nest. The nest PN4-2 had the highest number of different enzyme restriction patterns. Figure 18 and 19 shows some of the restriction patterns found for both enzymes.

Three clones were randomly chosen from each restriction pattern and were sequenced to verify their homogeneity. We found more than one genus present in some restriction patterns. We sequenced 144 clones with primers T7 to check identity. Of these, 57 were re-sequenced with reverse primer SP6. Close relatives of the 144 sequences were identified using GenBank and the DNA database Ribosomal Database Project II (RDP) (http://rdp.cme.msu.edu/). We were unable to obtain the complete sequence (1100bp) for all restriction patterns found in isolated from *Paratrechina* sp. Only 1100bp long sequences were used for phylogenetic analysis. Some of the sequenced clones belong to other bacterial phyla and were not analyzed (Appendix 4a).

Soils

Eight restriction patterns were found with the enzyme *Hinf*I for soil around nest 2 (SN2) and seven with HaeII. Fourteen restriction patterns were reported with HinfI and seven with the enzyme HaeII for nest 4 surrounding soil (SN4). Nine restriction patterns were generated with HinfI and six with HaeII in soil SN4-2. In the soil around nest N10, ten restriction patterns were reported with the enzyme HinfI and five with HaeII. Figure 20 and 21 shows some restriction patterns generated with the enzymes HinfI and HaeII in soils.
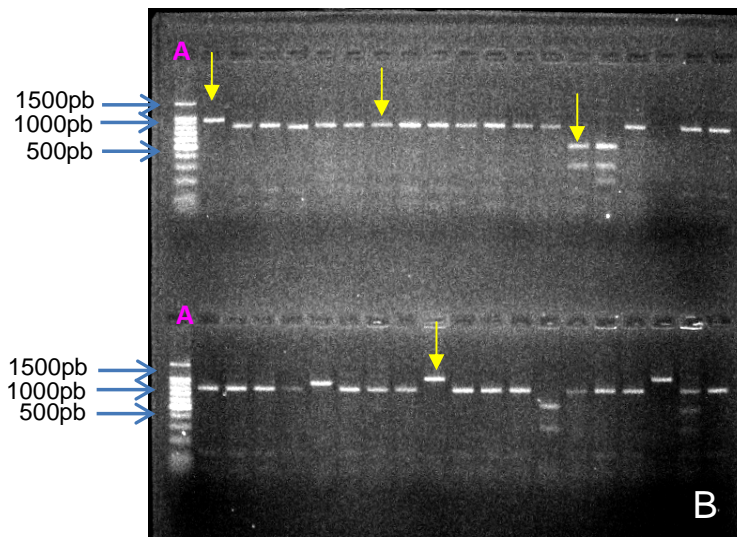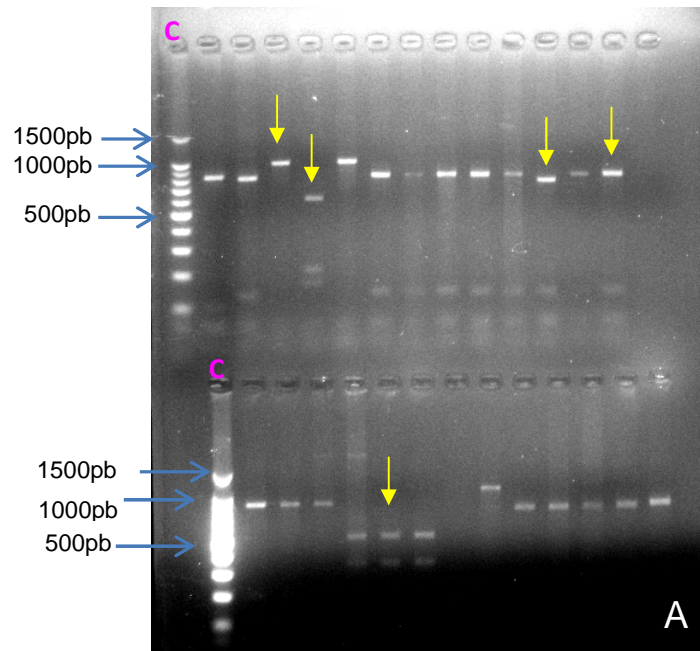
Figure 18. Arrows indicate restriction patterns of representative clones from *Paratrechina* sp. with HinfI. A: Nest PN4-2. B: Nest PN10. C: molecular marker 100bp.
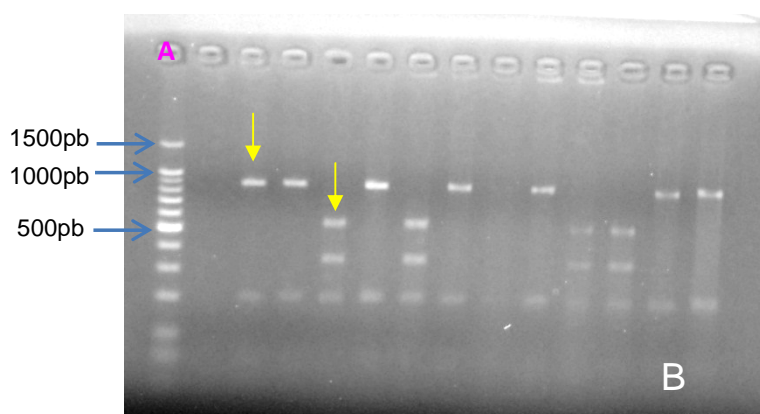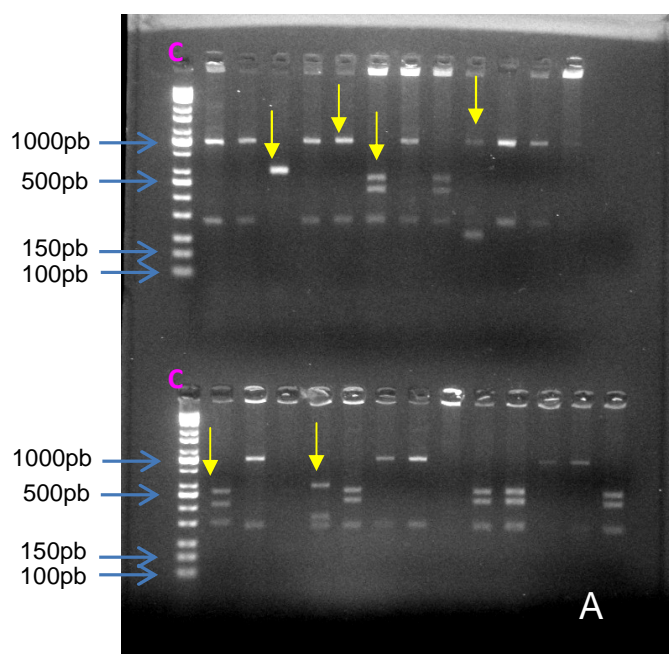
Figure 19. Arrows indicate restriction patterns of representative clones *Paratrechina* sp. with HaeII. A: Nest PN4, B: Nest PN10. C: molecular marker 100bp.

Three randomly chosen clones for each restriction pattern were sequenced to verify their homogeneity. This study found more than one genus present in some restriction patterns. We sequenced 147 clones with primer T7 and 79 with the reverse primer SP6. Close relatives of the 147 sequences were identified in GenBank and the DNA database Ribosomal Database Project II (RDP) (http://rdp.cme.msu.edu/). We were unable to

obtain the complete sequence (1100bp) for all restriction patterns present in surrounding nest soils. Some of the sequenced clones (29) belong to other bacterial phyla and were not included in the analysis (Appendix 4b).
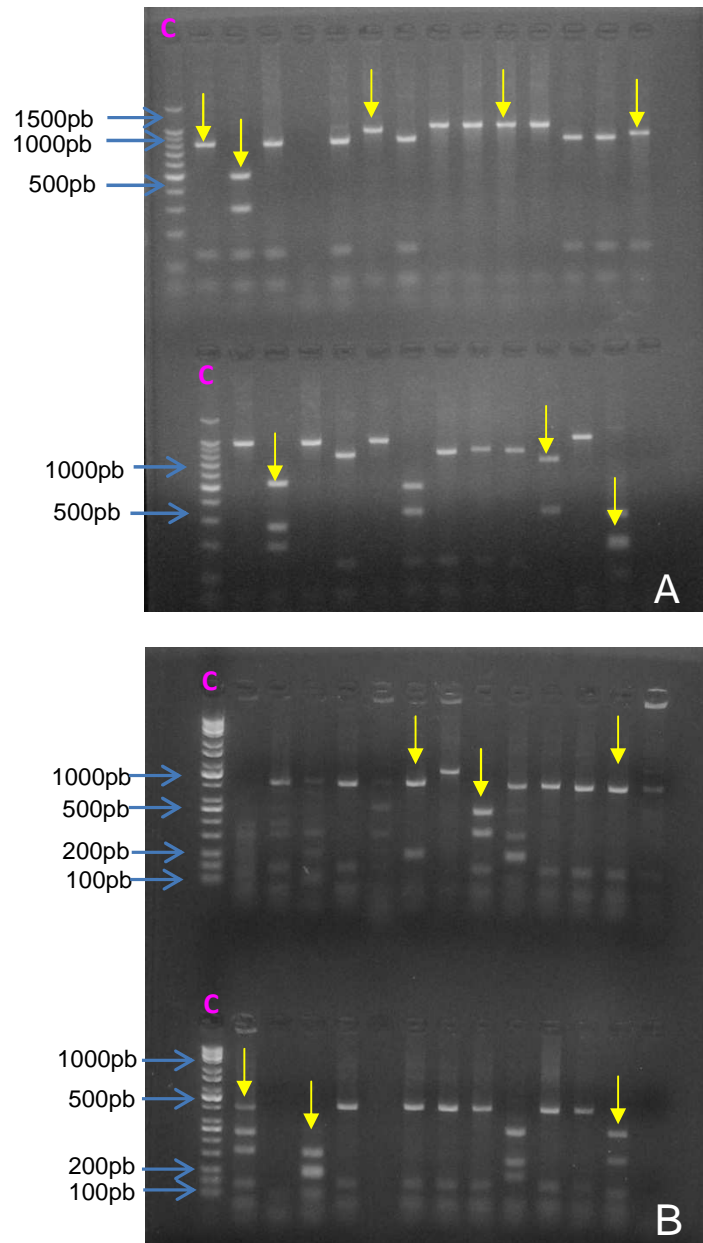
Figure 20. Arrows indicate restriction patterns of representative clones from soil with HinfI. A: SN4, B: SN42. C: molecular marker 100bp.
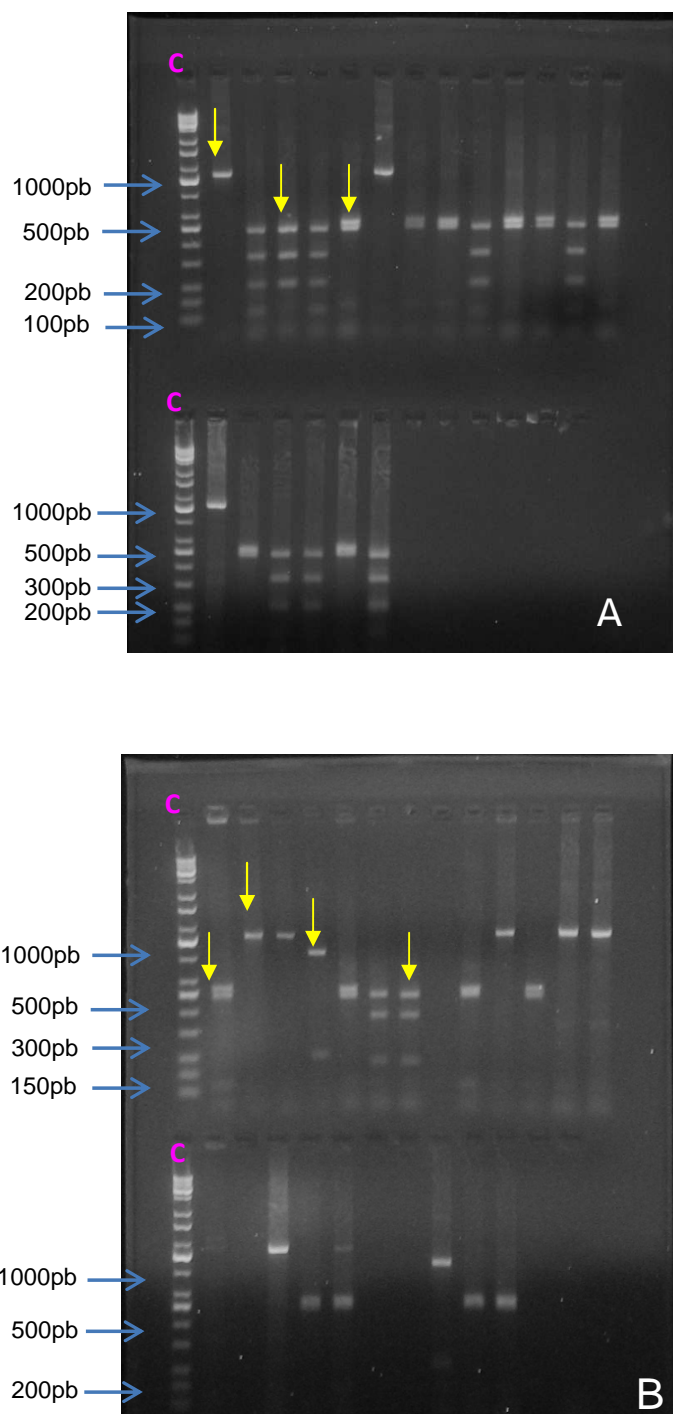
Figure 21. Arrows indicate restriction patterns of representative clones from soil with HaeII. A: SN10, B: SN42. C: molecular marker 1 Kb

6.2.3 Phylogenetic analysis of clones in *Paratrechina* sp.

We performed phylogenetic analysis on 57 partial 16S rDNA sequences of bacteria associated with *Paratrechina* sp. (approximately 1110bp). Sequences obtained by culture-independent methods were combined with those derived from cultures for an overall analysis. We combined 17 clones from ants from nest 2 (PN2H), 22 clones from nest 4 (PN4H) and 18 clones from nest 4-2 (PN42H). No clone from nest 10 was incorporated in the analysis because sequences were incomplete.

The phylogenetic relationships of sequences were determined by neighbor-joining analysis. Nine genera of Actinobacteria were found associated with *Paratrechina* sp. ants only with culture-independent methods. The most abundant genus was *Streptomyces* (74%); hence it was analyzed separately. Among the other genera recovered in the ants, Actinomadura was the second most abundant with 14 representatives. Sequences PN42H138, PN2H22, PN4H263 and PN42H103 clustered with an uncultured bacterium clone-BICP1099, which is associated with *Actinomadura blangladensis,* isolated from soil. Also, this clade has two sequences from nest 4, in the *Guayacan Centenario,* recovered in the two sampled seasons. PN24H123 is associated with an uncultured actinobacterium clone HGJO1138 isolated from rhizosphere of cucumber. PN4H262 is a close relative of clone PN414 and both are related to *Actinomadura (Parvopollispora) pallida* (figure 22).
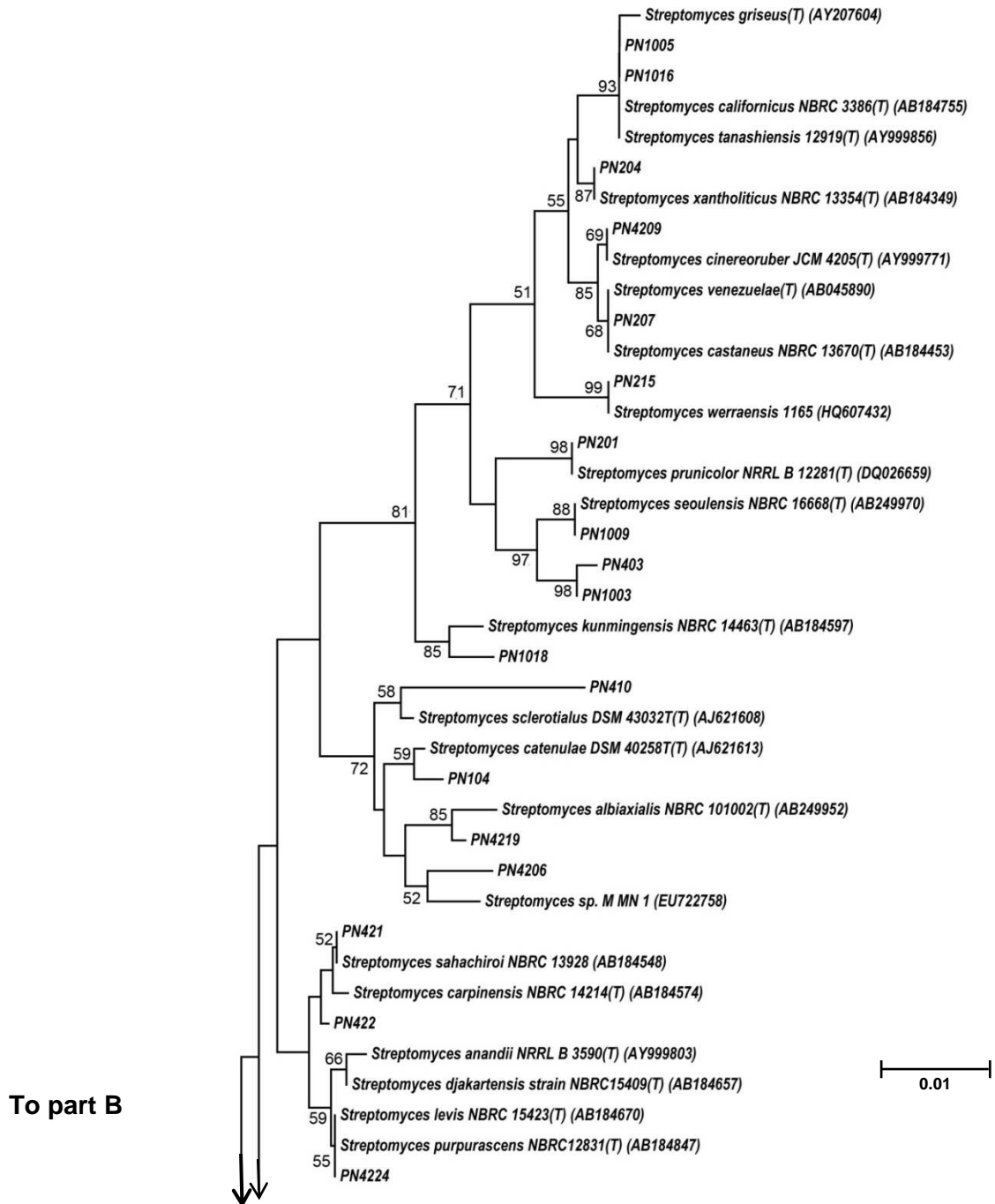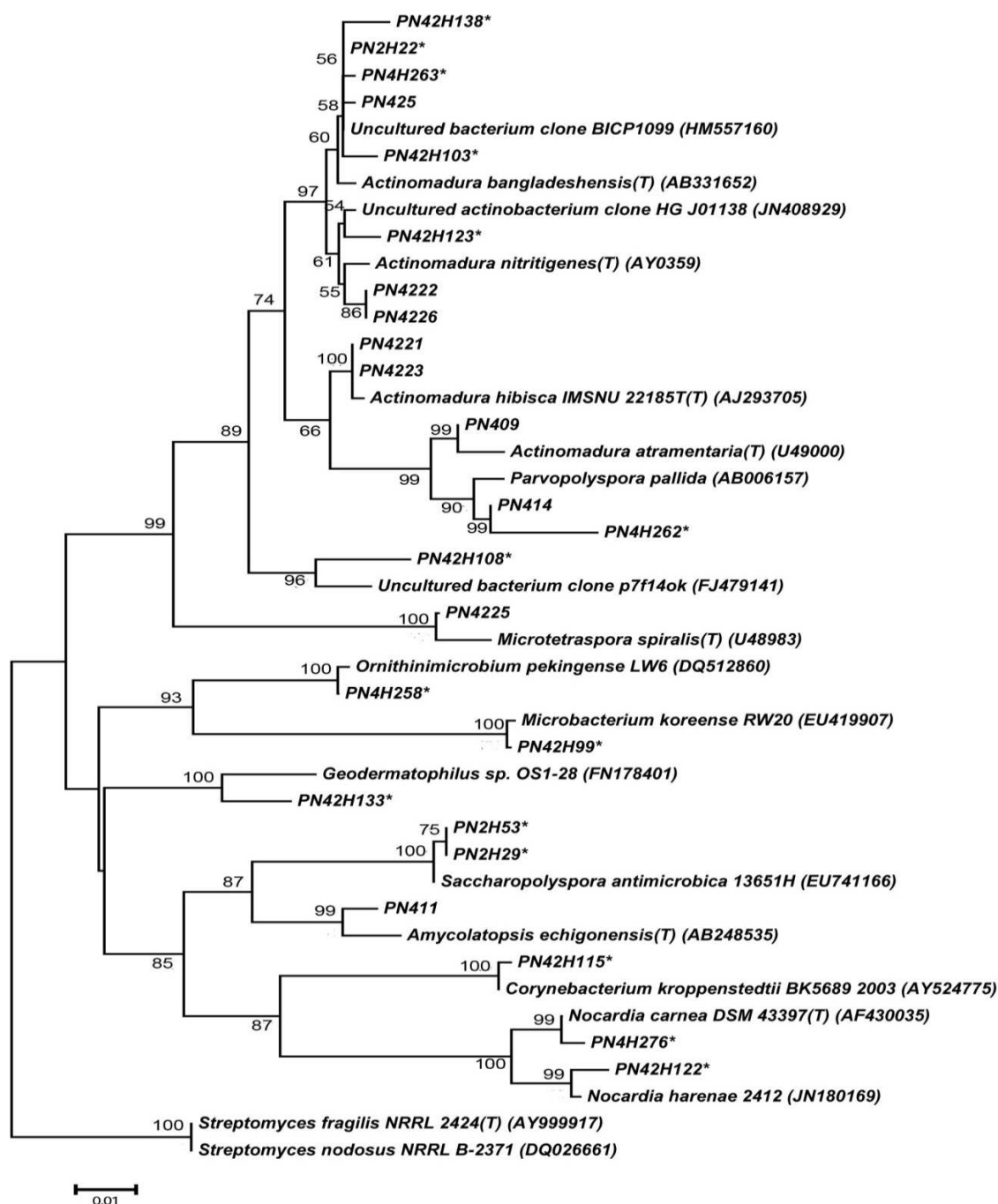
Figure 22. Neighbor-joining tree based of 16S rRNA gene sequences (1000-1350bp) from cultured *Streptomyces* isolated from *Paratrechina* sp. ants by culture independent and dependent methods and closely related species found in GenBank (accession number in parethesis) Asterisk indicates sequences obtained by culture-independent methods. The numbers at the nodes indicate bootstrap support values (>50%) based on Neighbor-joining analysis from 1000 pseudoreplicates. The scale bar represents 0.01 substitutions per nucleotide. All positions containing gaps and missing data were eliminated. *Streptomyces* was used as outgroup.

Clone PN42H108 was closely related with uncultured bacterium clone P7f140k isolated from undisturbed tall grass prairie (topsoil 5cm). Clone PN4H258 was associated with *Ornithinimicrobium pekinensis* isolated from activated sludge. Clone PN42H99 was a close relative of *Microbacterium koreense,* a strain isolated from a shrimp rearing tank. PN42H133 was phylogenetically close to *Geodermathophilus* sp. OSI-28, a strain isolated from cactus rhizosphere. PN2H29 and PN2H53 clones were associated with *Saccharopolyspora antimicrobica,* which was isolated from beach sand. PN42H110 a close relative of *Corynebacterium kroppenstedtii*, a strain isolated from blood culture. PN4H276 was associated with *Nocardia carnea,* while PN42H122 was a close relative of *N. harenae,* a strain isolated from soil (Figure 22).

The Streptomyces phylogenetic tree has nine monophyletic groups which were numbered according to figure 23. Nine clades had most of the recovered clones and isolated strain except two, PN1001 and PN203, which represent independent lineages. The groups 3, 4, 5 and 7 are formed by the isolate from culture dependent methods that were explained in a previous section. The group 1 has two subgroups, the first is composed of clone sequences that are related to *Streptomyces* sp DA08605 and in the second group, PN410 PN4H272 are associated with *Streptomyces sclerotialus* and *Streptomyces kunmingensis.*

We observed a clade composed by clones that are not closely related to any described species of Streptomyces in the group 2. The group 6 is comprised by clones PN2H15, PN4H141, PN4H267, PN4H274, PN4H271, PN4H268 PN4H2107 and isolated strain PN422 which are related with *Streptomyces seoulensis* and *Streptomyces lucensis*. The group 8 contains two subgroups, one is formed by clones that are associated with
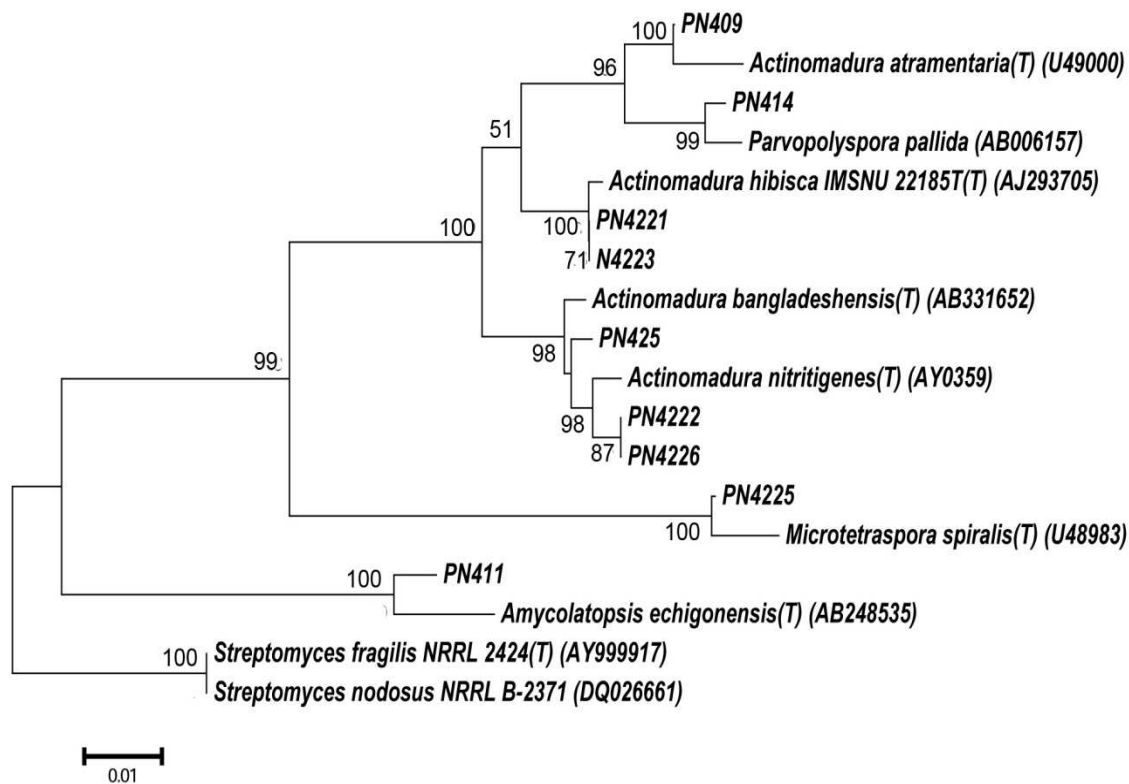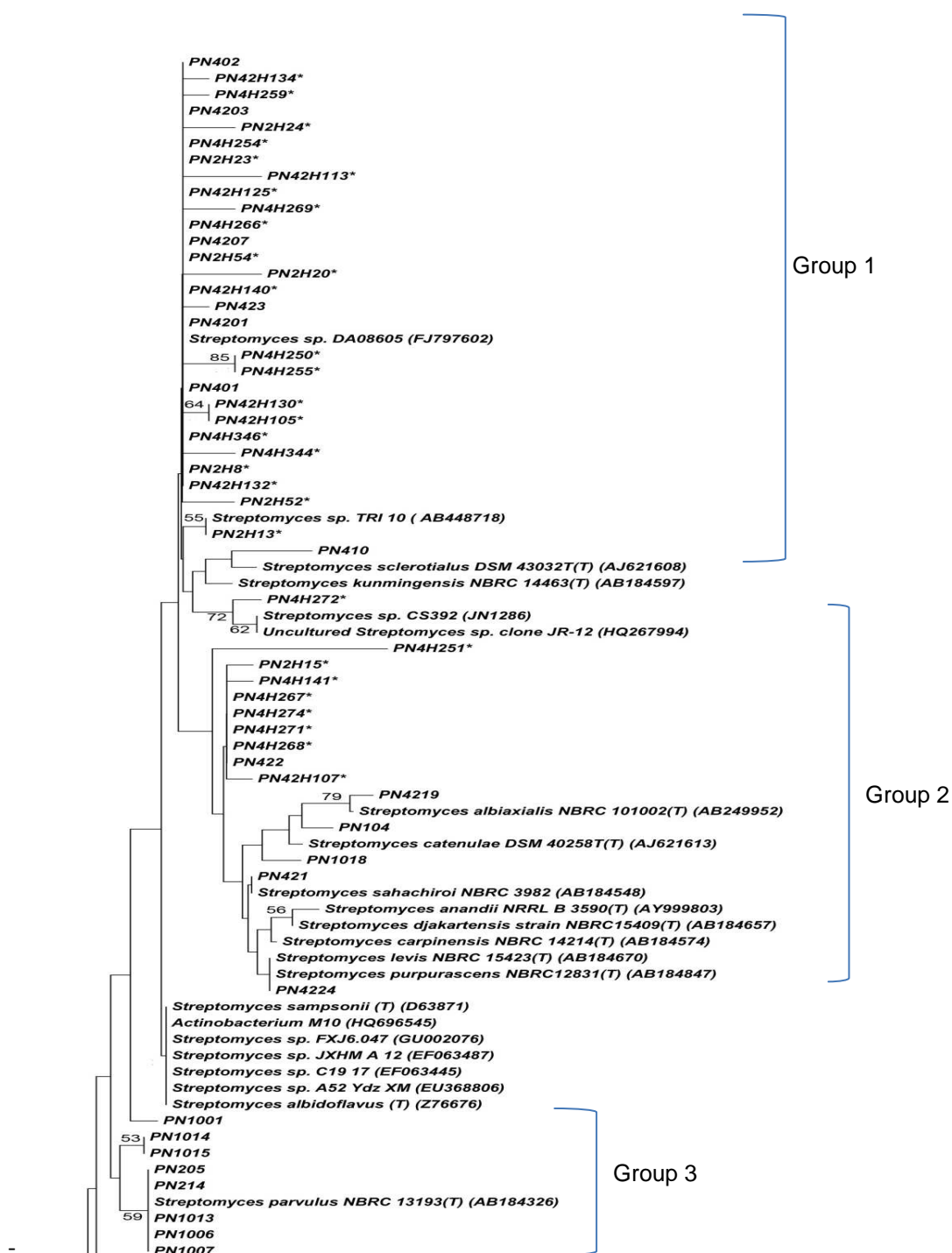
Figure 23. Neighbor-joining tree based of 16S rRNA gene sequences (1000-1350pb) from cultured Actinobacteria isolated from *Paratrechina* sp. ant ant and closely related species found in GenBank (accession number in parethesis). The numbers at the nodes indicate Bootstrap support values (>50%) based on Neighbor-joining analysis from 1000 replicates. The scale bar represents 0.01 substitutions per nucleotide. All positions containing gaps and missing data were eliminated.

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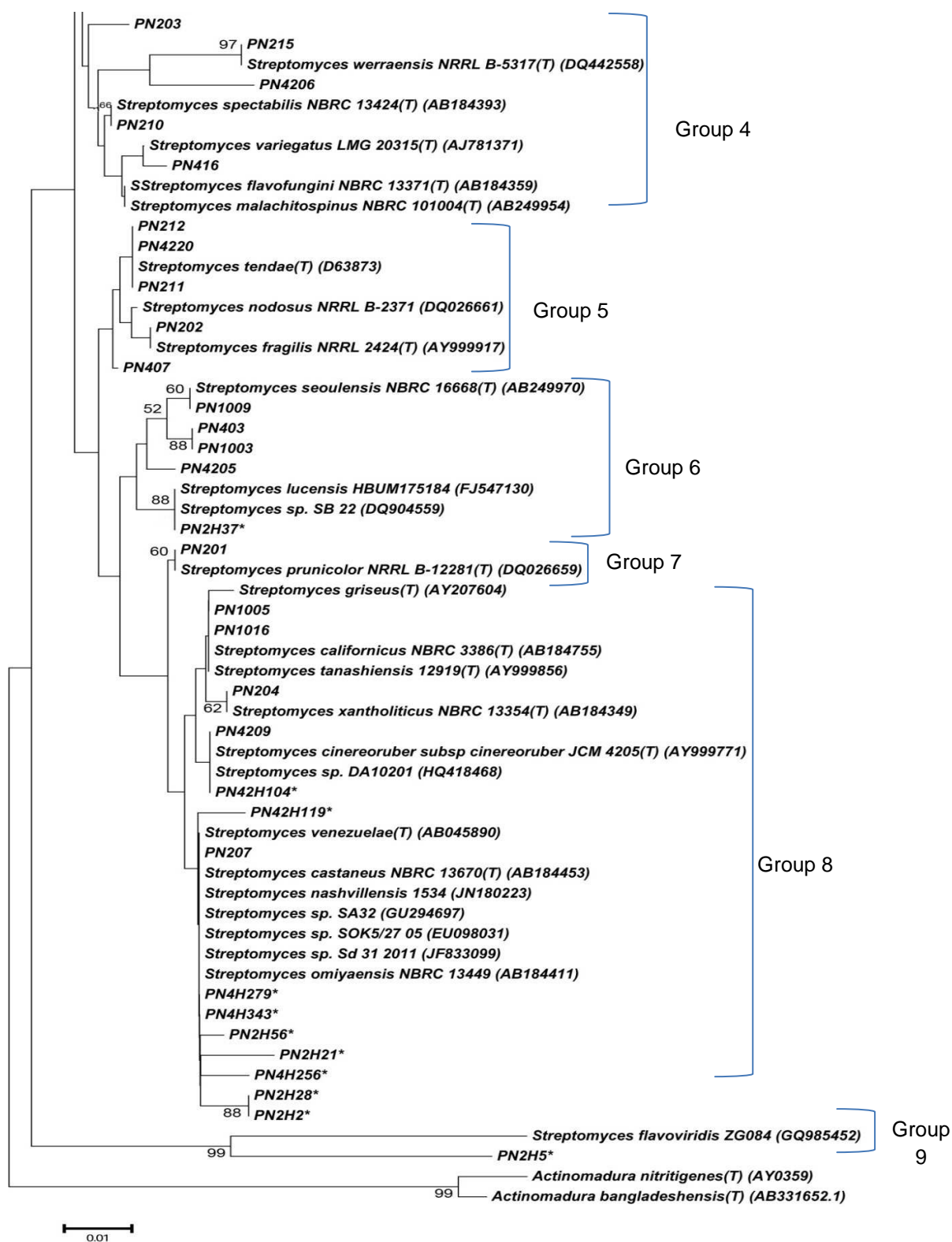
Figure 23. Continuation

Streptomyces venezuelae, *Streptomyces casteneus* and *Streptomyces omiyaensis.* The other group is composed by isolated strains on which their phylogenetic relationship was described previously, except for PN4209 and PN42H104 that are associated with *Streptomyces cinereoruber.* PN2H5 is a close relative of *Streptomyces flavoviridis* in group 9 (figure 23).

6.2.4 Actinobacteria genera found in each of the nests of *Paratrechina* sp. and their surrounding soil.

All clone data, sequenced with one (T7) or both primers (SP6 and T7), identified as Actinobacteria, were used to analyze Actinobacteria frequency and distribution in association with ant nests and their surrounding soil. We used 139 clones asssoiated with the ants and 118 clones from soil.

Actinobacteria associated to *Paratrechina* sp. ants in nest PN2 included five genera:*, Actinomadura, Brevibacterium, Saccharopolyspora, Streptomyces* and *Tsukamurella.* The most abundant genera were *Streptomyces* and *Actinomadura* (67% and 23%, respectively) (Figure 24). *Brevibacterium* and *Tsukamurella* were not included in the phylogenetic analysis because they were sequenced only with a single primer (T7). The genera of Actinobacteria found in the surrounding soil of nest PN2 were significantly different (Figure 25) with the genus *Nocardioides* as the most abundant (22%). *Streptomyces* represents only 7% of the clones while *Actinomadura* was not detected in the soil.

The genera of Actinobacteria associated with *Paratrechina* sp. ants in the *Guayacan Centenario* nest (PN4) during the rainy season were *Streptomyces, Ornithimicrobium, Actinomadura* and *Nocardia* (Figure 26). Again the genus *Streptomyces* was the most abundant (85%). More than 20 genera of Actinobacteria were found in the soil adjacent to the nest (Figure 27). *Mycobacterium* was the most abundant (22%) while *Streptomyces* and *Actinomadura* represent only 4% of the clones. *Nocardia* and *Ornithimicrobium* were not detected in the clones sampled for this soil.

During the dry season, the genera of Actinobacteria associated with the ants at the *Guayacan Centenario* nest (PN4-2) were more diverse including *Streptomyces Actinomadura, Brevibacterium, Corynebacterium, Geodematophilus, Leifsonia, Mycobacterium, Nocardia, Nocardioides* and *Pseudonocardia.* *Streptomyces* (56%) and *Actinomadura* (15%) were the most abundant genera. *Pseudonocardia* was not included in the phylogenetic analysis because its sequence was less than 900bp. We found 12 genera of actinobacteria in the soil adjacent to the *Guayacan Centenario* (PN4-2) (Figure 28). Uncultured actinobacteria was the most abundant category (20%). *Geodermatophilus*, *Microbacterium, Pseudonocardia, Streptomyces* and *Nocardiopsis* are common genera associated with ants and soil. *Streptomyces* represents only 2% of the clones identified in the soil (Figure 29).

Streptomyces and *Actinomadura* were the only genera of Actinobacteria associated with ants in nest PN10 (Figure 30). *Streptomyces* was the most abundant genus associated with the ants (91%). Eight genera of Actinobacteria were detected in the soil (SN10) (Figure 31). Uncultured actinobacteria was the most abundant category (25%).
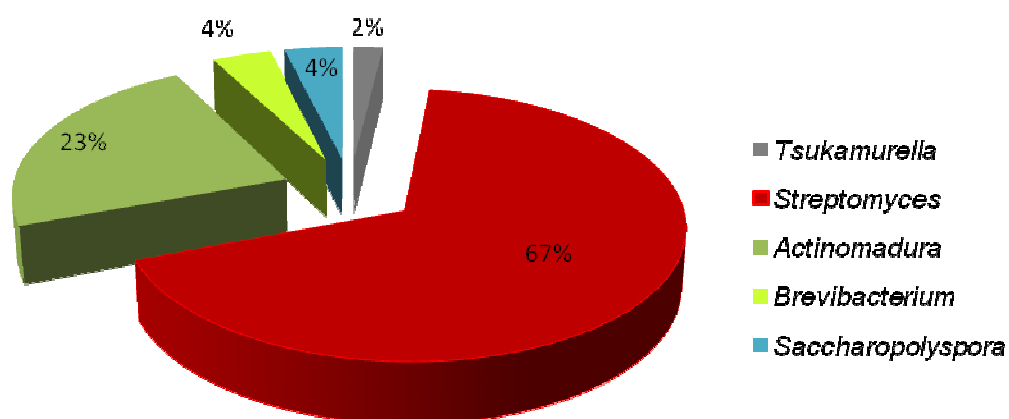
Figure 24. Frequency of the Actinobacteria genera found associated with *Paratrechina* sp. ants in nest PN2. Analysis based on 49 clones.
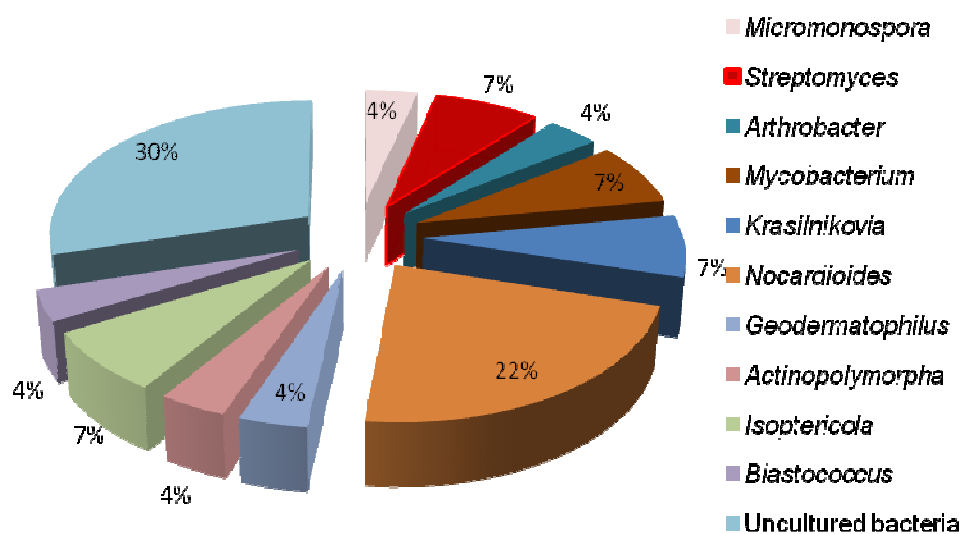
Figure 25. Frequency of Actinobacteria found in surrounding soil of nest 2 (SN2). Analysis based on 27 clones.
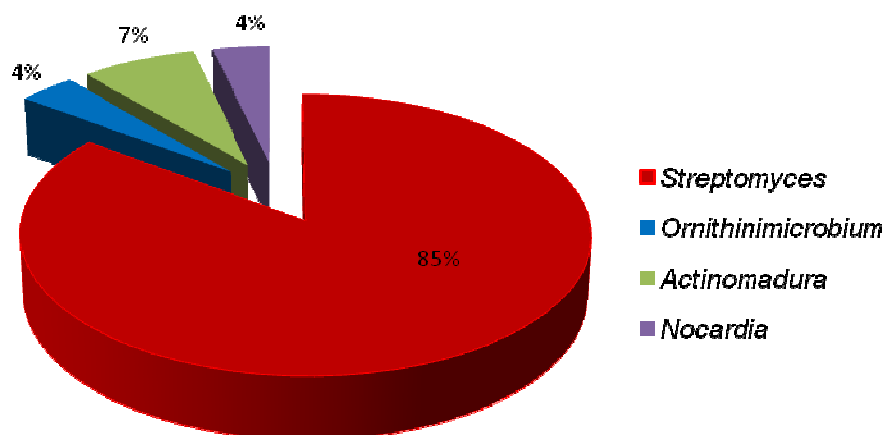
Figure 26. Frequency of the Actinobacteria genera found in *Paratrechina* sp. ants in nest PN4 at *Guayacan Centenario* in the wet season. Analysis based on 27 clones.
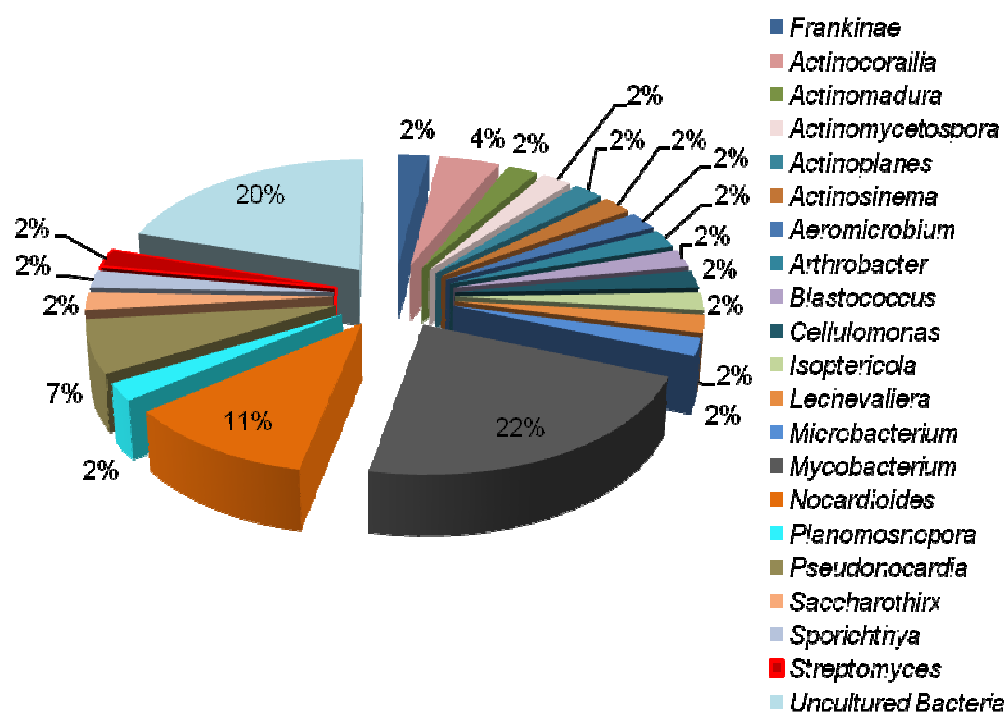
Figure 27. Frequency of the Actinobacteria genera found in the adjacent soil of *Guayacan Centenario* (SN4). Wet season. Analysis based on 44 clones.
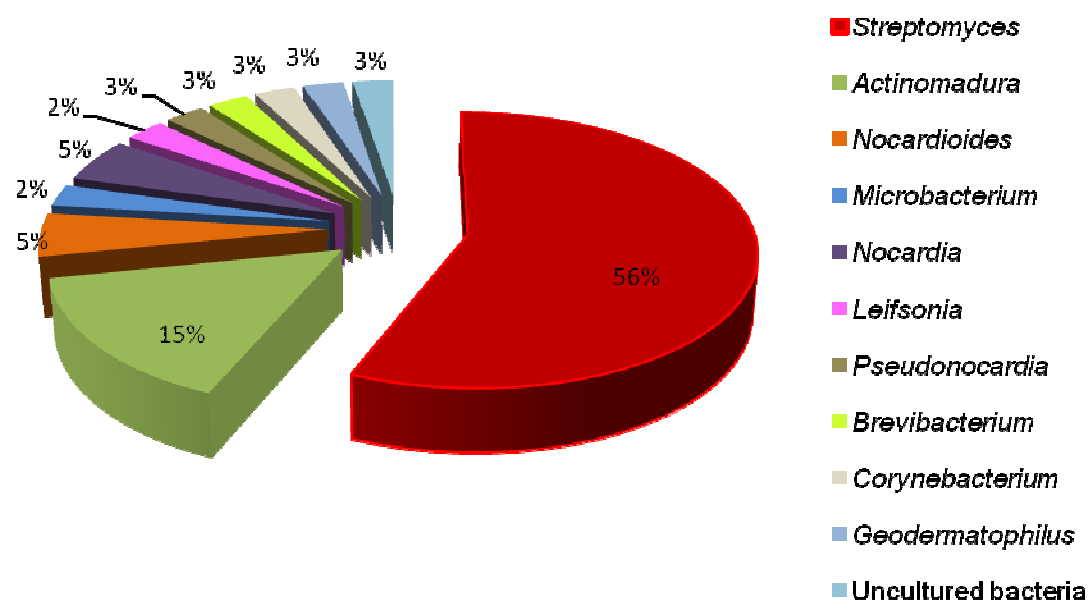
Figure 28. Frequency of the Actinobacteria genera found in *Paratrechina* sp. ants in nest PN4-2. Dry season. Analysis based on 39 clones.
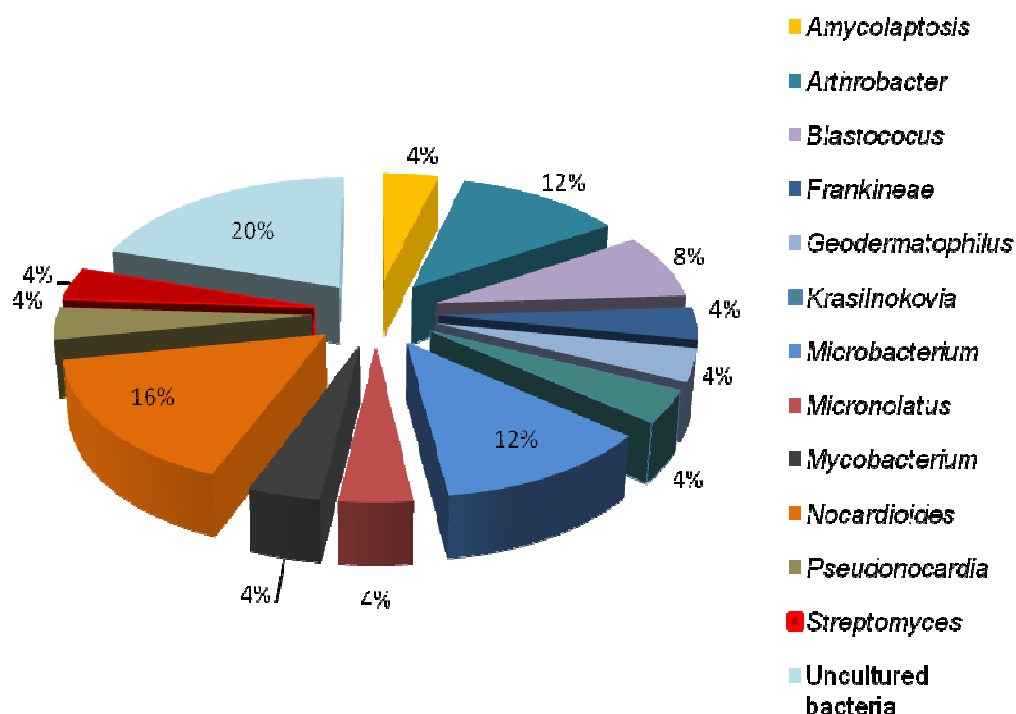
Figure 29. Frequency of the Actinobacteria genera found in the soil SN4-2 in dry season. . Analysis based on 25 clones.
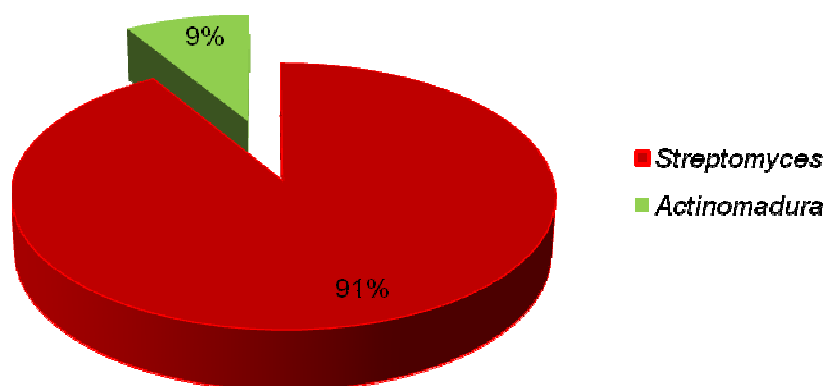
Figure 30. Frequency of the Actinobacteria genera found in *Paratrechina* sp. ants in nest PN10. Analysis based on 24 clones.
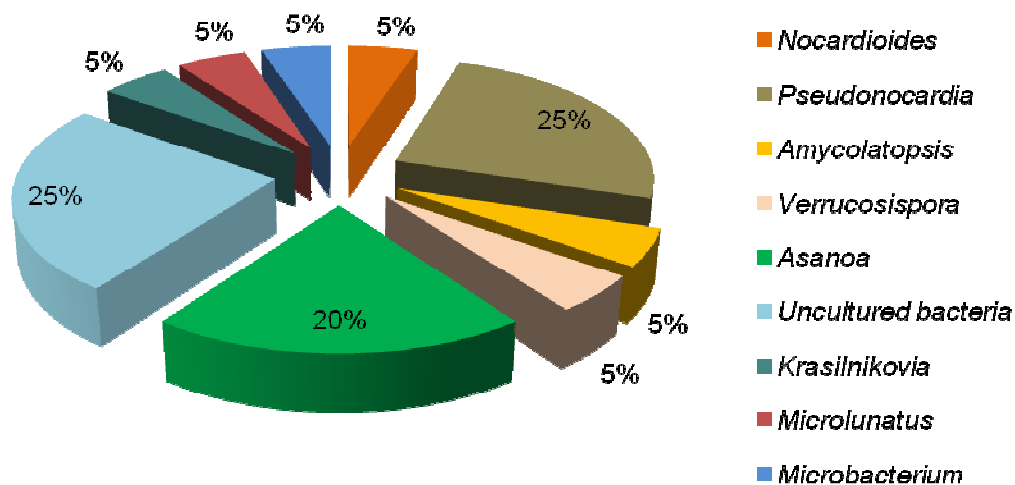
Figure 31. Frequency of the Actinobacteria genera found in the soil SN10. Analysis based on 21 clones.
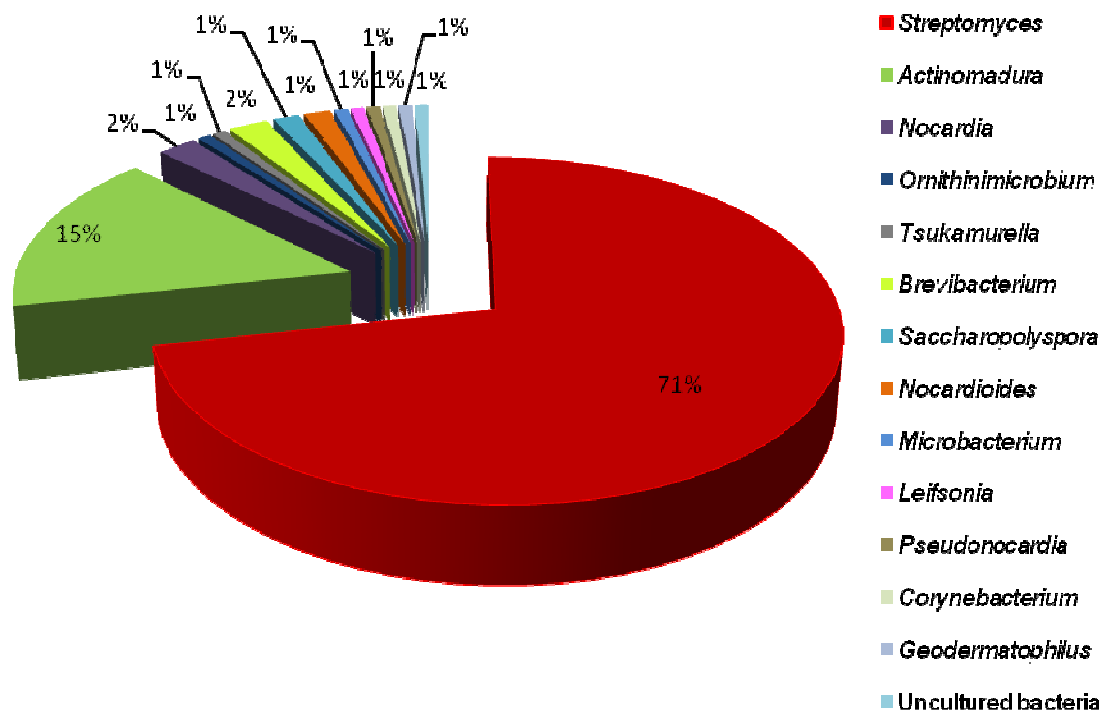
Figure 32. Frequency of the Actinobacteria genera found in *Paratrechina* sp. ants in all nests. Analysis based on 139 clones.

Streptomyces and *Actinomadura* were not identified in the surrounding soil of nest 10 (SN10)(Figure 31). Figure 32 summarizes the frequency of 13 genera of Actinobacteria associated with *Paratrechina* sp. ants in all nests sampled. *Streptomyces* (71%) and *Actinomadura* (15%) were the most abundant genera in this study. Soils samples were different for all *Paratrechina* sp. nests and were not pulled together for analysis.

6.2.5 Diversity indices in *Paratrechina* sp.

We calculated diversity indices and rarefaction curves using 130 Actinobacteria sequences identified in the four nests of *Paratrechina* sp. Dotur program was used for these calculations (Schloss and Handelsman, 2005). A Jukes-Cantor distance matrix

was generated with the DNADIST program of PHYLIP (Felsenstein, 1981). The matrix was the DOTUR input file. The Dotur program distributes sequences in OTUs at different distances. The method used to allot sequences to an OTU was furthest neighbor. This methods assigns a sequence to a group of sequences only if this sequence is similar to all sequences in the group that is being formed (Schloss and Handelsman, 2005). We found 32 OTUs at 3% distance (or 97% similarity) in this study. Simpson and Shannon Diversity indices were calculated in Dotur. Nonparametric richness estimators including ACE (abundance-based coverage) (Chao, 1992), Chao1 (Chao, 1984, Chao et al., 1993) and Jacknife (Burnham and Overton 1979 and Smith, 1984) were also calculated. These indices and richness estimators compare the complexity of two or more communities and help estimate the completeness of sampling a community (Schloss and Handelsman, 2005).

The Simpson index or the concentration of dominance (S') is based on the probability of drawing a pair of individuals of the same species. Dominance values range from 0 to 1, where values close to 1 indicate few species dominateIf few species dominate (Brown and Bowman, 2001). The value of S' in this study was 0.098 indicating a high diversity of OTUs. The Shannon-Weaver index value H' varies from 0 for communities with a single OTU to high values for communities that have many OTUs (Brown and Bowman, 2001). The value of H' for this study was 2.68.

The estimated richness of ant-associated Actinobacteria in Guanica dry forest was extrapolated from the data using the models of Chao 1, Jacknife, and ACE. The values

are presented in Table 6. The rarefaction curve (Figure 33) indicates the need for more sampling effort.

Table 6. Richness estimators calculated on all sequences obtained from *Paratrechina* sp. ants in all four nest sampled. Number of sequences: 130. OTUs were determined by a similarity ≥ 97%.

Richness estimator	Average	95% Confidence Interval
ACE	86.4	51.1-187
Chao1	70	44.2-150
Jacknife	70.4	47.1-93.7
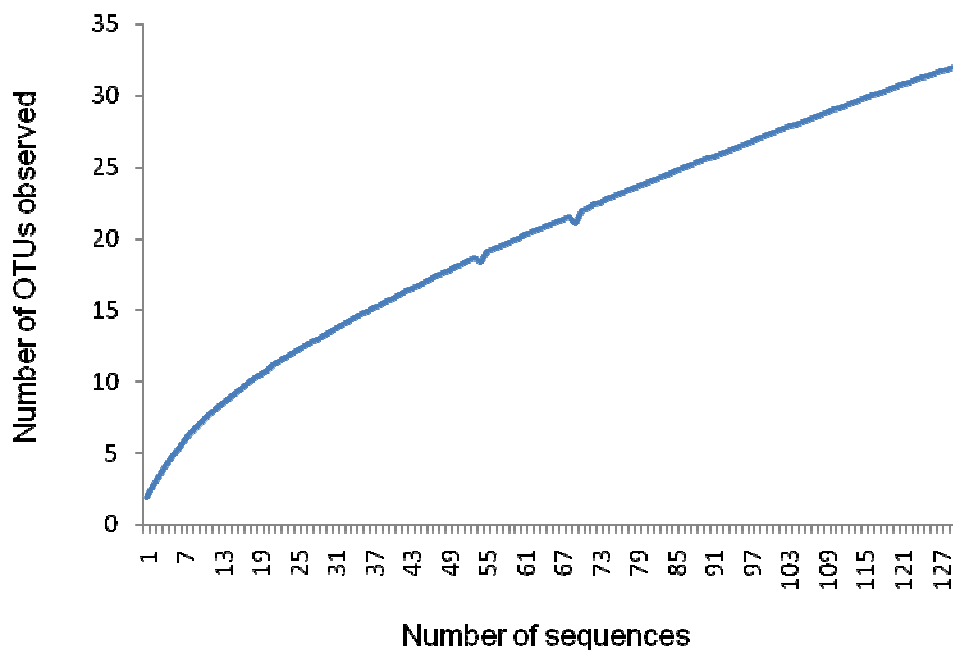
Figure 33. Rarefaction curve calculated on Actinobacteria associated with *Paratrechina* sp. ants in all nests sampled. OTUs were determined by a similarity ≥ 97%.

6.2.6 Comparison between ant-associated and soil Actinobacteria communities

Each *Paratrechina* sp. nest (PN2, PN4, PN4 and PN10-2) was considered as a different environment as well as their surrounding soils (SN2, SN4, SN4-2, and SN10). Actinobacteria communities were compared among the four ant nests. We found no significant differences (Table 7) indicating that the community of Actinobacteria is similar among *Paratrechina* sp. nests located in different parts of Guanica Dry forest and during different seasons. We also compared the Actinobacteria community associated with each ant nest versus each surrounding soil. The results indicate that there are significant differences (Table 8) between these two environments, in each of the four sampled nests. We also compared the Actinobacteria communities associated with soil among the four nests and no significant differences were found (Table 9).

Table 7. Matrix showing Bonferroni corrected P-values comparing Actinobacteria communities between *Paratrechina* sp. ant nests. Colors indicate the significant difference between each pair on a scale defined by Unifrac.

Ants	N10	N2	N4	N4-2
N10		<=0.06	0.7200	<=0.06
N2			<=0.06	0.1800
N4				1.0000
N4-2				

Color	Description
	(< 0.001) Highly significant
	(0.001-0.01) Significant
	(0.01-0.05) Marginally significant
	(0.05-0.1) Suggestive
	(> 0.1) Not significant

Table 8. Matrix showing Bonferroni corrected P-values comparing Actinobacteria communities between each *Paratrechina* sp. ant nest and its surrounding soil. Colors indicate the significant difference between each pair on a scale defined by Unifrac.

	Ants N2	Soil N2
Ants N2		<=0.01
Soil N2		

	Ants N4	Soil N4
Ants N4		<=0.01
Soil N4		

	Ants N4-2	Soil N4-2
Ants N4-2		<=0.01
Soil N4-2		

	Ants N10	Soil N10
Ants N10		<=0.01
Soil N10		

Color	Description
	(< 0.001) Highly significant
	(0.001-0.01) Significant
	(0.01-0.05) Marginally significant
	(0.05-0.1) Suggestive
	(> 0.1) Not significant

Table 9. Matrix showing Bonferroni corrected P-values comparing Actinobacteria communities between nest soils. Colors indicate the significant difference between each pair on a scale defined by Unifrac.

Soils	Soil N10	Soil N2	Soil N4	Soil N4-2
Soil N10		<=0.06	<=0.06	0.1200
Soil N2			0.0600	1.0000
Soil N4				1.0000
Soil N4-2				

Color	Description
	(< 0.001) Highly significant
	(0.001-0.01) Significant
	(0.01-0.05) Marginally significant
	(0.05-0.1) Suggestive
	(> 0.1) Not significant

We constructed a phylogenetic tree including all Actinobacteria sequences associated with the ant *Paretrechina* sp. and their nest soils plus close relatives identified by BLASTn . The results show that there are clades formed solely by sequences that belong to the ants and clades formed exclusively by sequences that are present in soils (Figure 34). Some clades are formed by sequences belonging to both, the ants and the soil. PN2H15, PN4H271, PN42H107, SN42350, PN4H268, PN4H274, PN4H141, PN4H267, PN4H251 are affiliated to *Streptomyces sahachiroi*. PN42H123, SN4204, PN425, PN42H103, PN42H138, PN2H122, PN4H263 belong to the clade of *Actinomadura nitrigenes* and *A. bangladensis*. PN42H133 and SN42314 are associated to *Geodermatophilus* sp. OSI-28. SN42289, SN42293, SN42349, SN4217 and PN42H199 are closely related to *Microbacterium koereense*. The sequences SN4224, SN42287, SN4230, PN42H122 and PN4H276 belong to the clade containing *Nocardia carnea* and *N. harenae*.
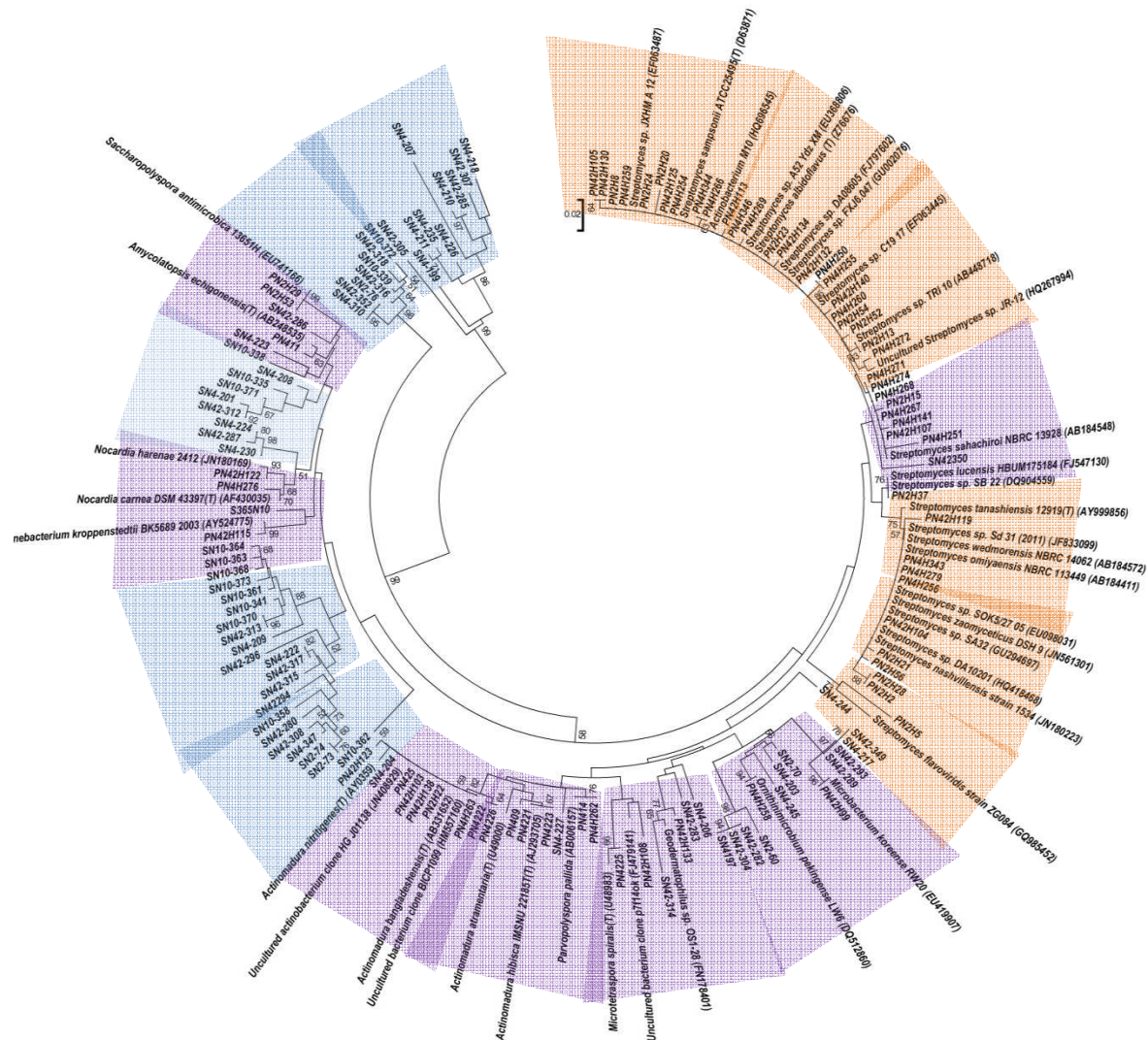
Figure 34. Neighbor-joining tree based of 16S rDNA gene sequences (1000-1350bp). Sequences isolated from *Paratrechina* sp. by culture independent and dependent methods, sequences isolated from soil around the nest and closely related species found in GenBank (accession number in parethesis). The numbers at the nodes indicate bootstrap support values (>50%) based on Neighbor-joining analysis from 1000 pseudoreplicates. The scale bar represents 0.01 substitutions per nucleotide. Orange color indicates Actinobacteria clades only associated to *Paratrechina* sp. ants, blue for Actinobacteria clades only associated with soil and purple for clades formed by sequences from both, soil and ants. All positions containing gaps and missing data were eliminated.

7. Discussion

This study describes the diversity of Actinobacteria associated with ants that do not grow fungi in a subtropical area with culture-dependent and independent methods. The Actinobacteria associated with *Solenopsis sp.*, *Paratrechina* sp., and *Dorymyrmex* sp. ants were studied with culture-dependent methods. Our results showed that the Actinobacteria community is specific for each ant species; however, some common trends were observed in all three species. *Streptomyces* was the most abundant Actinobacteria identified in all ant species.

Some strains isolated from different ant species are closely related to already described *Streptomyces* species in GenBank. For example, *S. rochei* and *S. bikiniensis* are associated with *Solenopsis* sp. and *Dorymyrmex* sp. ants. *Streptomyces tendae*, *S. parvulus*, and *S. sclerotialus* are associated with *Paratrechina* sp. and *Solenopsis* sp. ants, whereas *S. fragilis. S. cineoruber* and *S. nodosus* are present in *Paratrechina* sp. and *Dorymyrmex* sp. *Streptomyces bikiniensis,* a species isolated from soil, is characterized by the production of streptomycin, a potent antibiotic (Johnstones and Waksman, 1948). *Streptomyces fragilis* produces azaserine, an antibiotic that inhibits purine synthesis (Kaplan et al 1959). *Streptomyces tendae* generates a wide range of low molecular weight antibiotics and secondary metabolites, which have antitumor activity and inhibit chitin synthetases conferring fungicide, insecticide and acaricide activities (Bormann et al., 1999). *Streptomyces nodosus* produces amphotericin B, a potent antifungal with activity against fungi, some viruses and protists (Carey et al.,

2001). *Streptomyces cinereoruber* produces chitinases capable of degrading *Aspergillus niger* cell walls (Katsuichiro and Tagawa, 1991). The broad spectrum of secondary metabolites with antibacterials and antifungals properties found in these species suggest a defensive role of Actinobacteria associated with ants; hence some of the isolates in this study are potential candidates for inhibition assays against pathogenic microorganisms. Future work should establish if the role of these Actinobacteria is beneficial to the ants or they are mere transient associations.

Our research is a follow-up exploration on the results of Kost et al. (2007), who show that Actinobacteria associated with two species of temperate ants that do not grow fungi had an inhibitory effect on the growth of the fungus-growing ant specific parasite *Escovopsis weberi*. The same authors also determine that the identity of the isolated Actinobacteria associated to leaf-cutter ants (*Acromyrmex octopinosus*) belong to the genus *Streptomyces.* Other researches on fungus-growing ants showed *Streptomyces* as a member of the Actinobacteria community associated with fungus-growing ants. Zucchi et al. (2010) isolated 20 strains from the integument of *Ac. subterraneus* of which 17 were *Streptomyces*. Muller et al. (2008) isolated a single *Streptomyces* associated with another fungus-growing ant in the genus *Atta*. Haeder et al. (2009) also isolated *Streptomyces* strains from three fungus-growing ants species (*Ac. octospinosus*, *Ac. echinatior* and *Ac. volcanus*), which were very similar to *S. albidoflavus* and *S. griseus*. One strain of *Streptomyces* (Ao10) was present in all three ants and strongly inhibited the *Escovopsis* growth. The substance responsible for inhibiting the pathogen's growth was reported as candicidin (Haeder et al. 2009). We isolated two *Streptomyces* strains, PN1005 and PN1016, closely related to *S. griseus*, which is also a candicidin producer

(Gil and Campelo-Diaz, 2003). Thus, we believe that these strains associates with tropical ants might have unknown defensive roles against other microorganisms.

We cannot confirm the identity of our all isolates, since many of the *Streptomyces* clades in our study have low support to assign a species name. In this sense, Labeda et al. (2012) indicate the high similarity in the 16S rRNA gene sequence within *Streptomyces* favors the construction phylogenetic trees with weak statistical support. The authors specifically highlight the inability to determine an unknown strain to a described species with this gene. On the other hand, we also have several strains isolated in this study are not related to any described *Streptomyces* species indicating an increase in potential new species. Therefore it is necessary to conduct new phylogenetic analysis with other markers such as house keeping genes as atpD, syrB, recA rpoB, trpB (Rong and Huang, 2010) to further determine their identity.

The second most abundant cultures in two ant species were *Actinomadura* and *Nocardia* strains. The soil is the main source of microorganisms belonging to the genus *Actinomadura*. Some strains are pathogenic to humans causing actinomycetomas. The role of Actinomadura in nature is poorly known, but its widespread distribution suggests an important role in soil ecology (Quintana et al., 2003). Strains closely related to *A. rudentiformis* were isolated in this study, which exhibits antibiosis against *Entorococcus faecium* and some *Mycobacterium* pathogenic species (Le heroes and Meyer, 2007). Additionally, *Actinomadura hisbisca* produces polyenoles called pradamicin that have antifungal and antiviral activity (Park et al., 2011).

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The genus *Nocardia* is distributed in terrestrial habitats, especially in soils with high organic matter and decomposed plant material (Khan et al., 1997). Some species are pathogenic to humans. *Nocardia carnea*, *N. brasiliensis* and *N. niigatensis* and *N. ciryageorgica*, which are closely related to strains isolated in this study, cause pulmonary and systemic nocardiopsis in humans (Watanabe et al., 2006, Khan et al., 1997). Some *Nocardia* species use hydrocarbons as energy sources, while others are involved in the degradation of sandstone monuments (Palla et al., 2002). Based on the literature review the role of *Nocardia* associated with ants is unclear.

Only the Actinobacterial community associated with *Paratrechina* sp. was studied with culture-independent methods. We were able to identify thirteen genera of Actinobacteria and several uncultured clones in GenBank. The contrasting number against only four genera identified by culturing suggest that this technique allowed us to get a better understanding of the diversity of the community. The chitin medium used for isolation of Actinobacteria presents a bias that favored growth of *Actinomadura, Nocardia* and *Streptomyces* strains, especially the latter. Muller et al. (2008) mentioned a bias in the chitin medium favoring the genus *Pseudonocardia;* however only one *Pseudonocardia* strain was isolated in association with *Solenopsis* sp.

Our working hypothesis expected us to find high similarity between the Actinobacteria community in soil and the one associated with ants that do not grow fungi because these do not have a fungal culture to defend against pathogens. Furthermore, Actinobacteria isolated from the ants would represent transient and casual associations from soil dwellers. However, our results showed that each ant species has a specific

Actinobacteria community associated with it, which is different than the one from the surrounding soil. Although, four nests of *Paratrechina* sp. were sampled in different locations in the Guánica Dry forest and in different seasons, we found a consistent Actinobacteria community that is clearly different from the community associated with the soil. This assertion was tested statistically using the program UniFrac, which supported our findings. Additionally, no significant differences between ant-associated Actinobacteria communities among the four ant nests were found. The other hand, the value H', for the actinobacteria associated to *Paratrechina* sp ants in this study was 2.68. This value is low in comparison to other studies for the bacteria diversity in soils (H= 7.17, 6.612, 4.78) (Dunbar et al., 1999, Hayakawa et al, 2010, Srinivas et al, 2011). This indicate that the ants probably reclute Actinobacterias from soil or other enviroments.

Integrating the results with dependent and independent culture-methods, the Actinobacteria associated with *Paratrechina* sp. is composed of 15 different genera. *Streptomyces* and *Actinomadura* were most abundant in each nest. Although, *Streptomyces* was identified in the soil, it was never the most abundant genus. Similarly, *Actinomadura* was only detected in one soil sample, but this does not mean that it is not present in the other soils. More clones should be screened to determine its abundance.

Genera such as *Ornithinimicrobium, Tsuamurella*, *Brevibacterium, Saccharopolyspora*, *Leisfonia* and *Corynebacterium* were identified in some *Paratrechina* sp. nests at low frequencies, and could be considered as environmental contaminations. However, none

of these genera was identified in soils suggesting occasional or less consistent association with the ants and their role should be investigated in future works. Some clones in this study were closely related to *Saccharopolyspora antimicrobica,* which was isolated from soil and is characterized by microbial activity against *Staphylococcus aureus* and *Escherichia coli (*Yuang et al., 2008).

Genera such as *Arthrobacter*, *Micromonospora*, *Krasilnikovia, Actinopolymorpha*, *Isoptericola*, *Blastococcus*, *Actinocorallia, Actinomycetospora*, *Actinoplanes*, *Actinosinema*, *Aeromicrobium*, *Cellulomonas*, *Lechevaliera, Planomosnopora*, S*accharothirx* and *Sporichthya* were exclusively associated with soil, while *Streptomyces*, *Actinomadura*, *Nocardia, Pseudonocardia*, *Microbacterium,* *Nocardioides*, *Geodermatophilus* and *Amycolaptosis* were identified in association with ants and with soil. The presence of *Streptomyces*, *Actinomadura* and *Nocardia* was consistent throughout our sampling and this may be the result of adaptation of these genera to the ant microenvironment. *Microbacterium* and *Pseudonocardia* were found intermittently, although these genera have been previously associated with fungus-growing ants (Mueller et al., 2008, Cafaro and Currie 2005). *Pseudonocardia* is a symbiont that produces secondary metabolites that inhibit the growth of the parasite *Escovopsis* (Cafaro et al., 2011), while *Microbacterium* has been identified in cultivars of the *Atta* and other Attini ants species. *Microbacterium* could play a role as disease suppressor or its transient presence could due to degradation of plant material in the nest; however its real function is yet to be established (Muller et al., 2008). *Pseudonocardia* and *Microbacterium* are also found in environments such as in soil and plants (Lee et al., 2006, Muller et al., 2008, Madigan and Martinko, 2009).

Nocardioides is commonly found in soils (Prauser, 1976). *Amycolaptosis* produces vast numbers of antibiotics (Everest and Meyers, 2009) and *Geodermatophilus* is a genus mainly isolated from soils (Luedemman, 1968). The intermittent presence of these genera in ants may be due to environmental contamination or they are colonizing bacteria found in soil and have succeeded in establishing a habitat on the ants. Future research should clarify this question.

8. Conclusions

The Actinobacteria communities associated with ants that do not grow fungi in the subtropical Guánica Dry Forest are different between ant species and their environment. In the species *Solenopsis* sp., *Dorymyrmex* sp. and *Paratrechina* sp. each community is specific to the ants. *Solenopsis* sp. and *Dorymyrmex* sp. were studied only with culture dependent methods. We recovered four genera in culture for both, *Solenopsis* sp. and *Paratrechina* sp., while only three in *Dorymyrmex* sp. All ants have *Streptomyces* as the most abundant genus. *Actinomadura* was the next abundant recovered in association with the ants *Solenopsis* sp. and *Paratrechina* sp., but not with *Dorymyrmex* sp. *Nocardia* was present in *Dorymyrmex* sp. and *Solenopsis* sp. Each ant species have at least one unique genus to their community, *Pseudonocardia* (*Solenopsis* sp.)*, Nocardiopsis* (*Dorymyrmex* sp.) *Amycolaptosis* and *Microtetraspora* (*Paratrechina* sp.).

In order to obtain a broader view on the diversity of Actinobacteria associated to *Paratrechina* sp., we integrated the results obtained by independent and dependent culture methods. Fifteen genera of Actinobacteria were associated with this ant (*Streptomyces, Actinomadura, Nocardia, Ornithiniimicrobium, Tsuamurella, Brevibacterium, Saccharopolyspora, Nocardioides, Mycobacterium, Leifsonia, Pseudonocardia, Corynebacterium, Microtetraspora, Geodermatophilus* and *Amycolaptosis*). *Streptomyces* and *Actinomadura* were the most abundant genera with both methodologies.

We established that the community of Actinobacteria associated to *Paratrechina* sp. is

consistent and clearly different from the community found in the surrounding soil on the Guánica Dry forest. This is the first attempt to study of Actinobacteria diversity associated with ants that do not grow fungus in a subtropical area and to establish their relationship with the environment. Future research will explore the role of Actinobacteria in the ants.

9. Recommendations

To compare the diversity of Actinobacteria in ants species that inhabit both wet and dry forests and establish how the environment influence it. For example, by comparing the Cambalache rainforest with the Guánica Dry forest

To include other culture media for the Actinobacteria isolation to obtain a greater diversity of cultivated strains.

Perform inhibition assays between the most common Actinobacteria isolates from ants and their fungal pathogens to establish whether the Actinobacteria have a defensive and beneficial role for the ants.

To construct 16S rRNA clone libraries for *Solenopsis* sp. and *Dorymyrmex* sp. to expand the knowledge of the diversity of Actinobacteria associated with these ants.

Strains with antibiotic and antifungal properties must be tested against human pathogens and biological control for agriculture.

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11. Appendixes

Appendix 1. Media recipes

Chitin medium

Components	Amounts
Agar	15g
Chitin	3g
K_2HPO_4	0.575g
$MgSO_4$ X 7H20	0.375g
KH2PO$_4$	0.275g
$FeSO_4$ X 7H20	0.0075g
$MnCL_2$ X 4H20	0.00075g
$ZnSO_4$ X 7H20	0.00075g
$H_2$0	750 ml

Antifungals: Nystatin 20ml/L

Ciclohexamide: 0.05g/L

Both antifungals must be added just before pouring plate

YMEA medium (Yeast Malt Extract Agar)

Components	Amounts
Yeast extract	4g
Malt extract	10g
Dextrose	4g
Agar	20g
H_2O	1000ml

Antifungals: Nystatin 20ml/L

Ciclohexamide: 0.05g/L

Both antifungals must be added just before pouring plate

Appendix 2

Appendix 2a. Colony morphology of isolates from *Paratrechina* sp. ants.

Nest	Season	Code	form	Color of the substrate Hyphae	Color of the aerial hyphae	Surface	Margin	Diffusible Pigments
N2	Rainy	PN201	Irregular	translucent cream	White	Dusty	Entire	No
N2	Rainy	PN202	Irregular	Brown	White	Dull	Filiform	Brown
N2	Rainy	PN203	Irregular	yellow	No data	Dull	Undulate	No
N2	Rainy	PN204	Irregular	Yellow	Gray with white spots	Dusty	Entire	Yellow
N2	Rainy	PN205	Irregular	Yellow	White and gray	Dusty	Entire	Yellow
N2	Rainy	PN206	Irregular	Yellow	No data	Glistening	Undulate	No
N2	Rainy	PN207	Irregular	translucent yellow	White	Dull	Entire	Yellow
N2	Rainy	PN208	Irregular	Yellow	White	Dull	Entire	Yellow
N2	Rainy	PN209	Irregular	Yellow	White	Glistening	Entire	Yellow
N2	Rainy	PN210	Irregular	Yellow	White	Dull	Undulate	Yellow
N2	Rainy	PN211	Irregular	Yellow	White	Dusty	Undulate	Yellow
N2	Rainy	PN212	Irregular	Yellow	Purple	Dusty	Entire	No
N2	Rainy	PN213	Irregular	Yellow	White	Dusty	Entire	Yellow
N2	Rainy	PN214	Irregular	Yellow	White	Dusty	Filiform	No

N2	Rainy	PN222	Irregular	Yellow	Gray with purple spots	Dusty	Filiform	Yellow
N4	Rainy	PN402	Irregular	Brown	Brown with Pale gray White spots	Dusty	Filiform	Brown
N4	Rainy	PN405	Irregular	Brown	White	Dusty	Filiform	Brown
N42	Rainy	PN404	Irregular	Yellow	Gray	Dusty	Filiform	No
N42	Rainy	PN406	Irregular	Brown	Gray Purple	Dusty	Filiform	Yellow
N42	Rainy	PN403	Irregular	Yellow	Gray	Glistening Dusty	Filiform	Yellow
N42	Rainy	PN407	Irregular	Dark green	Gray White	Dusty	Filiform	Green
N42	Rainy	PN409	Irregular	Dark green Yellow	White	Dusty	Filiform	Brown No
N42	Rainy	PN410	Irregular	Yellow Black	White	Dusty	Filiform	Yellow
N42	Rainy	PN412	Irregular	Dark green Yellow	White	Dusty	Filiform	Yellow
N42	Rainy	PN419	Irregular	Brown	Pale gray White	Dusty	Filiform	Yellow
N42	Rainy	PN420	Irregular	Pale brown Yellow	White No data	Dusty	Filiform	Yellow
N42	Rainy	PN429	Irregular	Cream Yellow	White	Dusty Dull	Undulate Filiform	Brown No
N4-2	Dry Rainy	PN422 PN426	Irregular	Cream Yellow	Gray and White White on the edge	Dull Dusty	Undulate Filiform	Brown
N4-2 N4	Dry Rainy	PN423 PN421	Irregular	Red Yellow	White No data	Dusty Dull	Filiform	Brown Yellow
N4-2	Dry	PN424	Circular	Pale yellow	Gray and white	Dusty	Filiform	Yellow

Appendix 2a. Continuation

N4-2	Dry	PN425	Irregular	Dark Brown	No data	Dull	Filiform	Yellow
N4-2	Dry	PN426	Circular	Brown	White and gray	Dusty	Filiform	No
N10	Dry	PN1003	Irregular	Cream	Gray	Dusty	Filiform	No
N10	dry	PN1004	Irregular	Orange	White	Dusty	Undulate	Yellow
N10	Dry	PN1005	Irregular	Purple	Cream	Dusty	Undulate	No
N10	Dry	PN1006	Irregular	Dark yellow	Gray with White spot	Dusty	Undulate	Yellow
N10	Dry	PN1007	Irregular	Dark yellow	Gray with White spot	Dusty	Filiform	Yellow
N10	Dry	PN1009	Circular	Pale yellow	Dark gray	Dusty	Entire	Yellow
N10	Dry	PN1010	Irregular	Yellow	White	Dusty	Filiform	Yellow
N10	Dry	PN1012	Irregular	Translucent yellow	White	Dusty	Filiform	Yellow
N10	Dry	PN1014	Irregular	Yellow	White	Dusty	Filiform	No
N10	Dry	PN1015	Irregular	yellow	Gray	Dusty	Filiform	Yellow
N10	Dry	PN1016	Irregular	Purple	White	Dusty	Filiform	No
N10	Dry	PN1018	Irregular	Cream	Gray	Dusty	Filiform	No

Appendix 2b. Colony morphology of isolates *from Solenopsis* sp. ants.

Nest	Season	Code	form	Color of the substrate Hyphae	Color of the aerial hyphae	Surface	Margin	Diffusible Pigments
N7	Rainy	SN701	Irregular	Yellow	Gray and white	Dusty	Filiform	Yellow
N7	Rainy	SN702	Irregular	Yellow	Gray	Dusty	Filiform	No
N7	Rainy	SN703	Irregular	Pink	Gray	Dusty	Filiform	No
N7	Rainy	SN705	Irregular	Pink	Pale pink	Dusty	Filiform	No
N7	Rainy	SN707	Irregular	Yellow	No data	Glistering	Undulate	No
N7	Rainy	SN709	Irregular	Yellow	White	Dull	Undulate	No
N7	Rainy	SN712	Irregular	Irregular	Gray with White spot	Dusty	Filiform	No
N7	Rainy	SN713	Irregular	Irregular	white	Dull	Undulate	No
N8	Dry	SN801	Irregular	Yellow	Gray-Blue	Dusty	Filiform	No
N8	Dry	SN803	Irregular	Pink	Pink	Dusty	Filiform	No
N8	Dry	SN805	Irregular	Yellow	Gray and white	Dusty	Undulate	No

Appendix 2b. Continuation

N8	Dry	SN806	Irregular	Yellow	White with gray spot	Dusty	Filiform	No
N8	Dry	SN807	Irregular	Cream	No data	Dusty	Filiform	No
N8	Dry	SN808	Irregular	Yellow	White	Dusty	Filiform	No
N8	Dry	SN810	Irregular	Red	Pink	Dusty	Filiform	No
N8	Dry	SN811	Filiform	Brown	White	Dusty	Filiform	No
N8	Dry	SN815	Irregular	Yellow	White	Dusty	Undulate	No
N8	Dry	SN820	Irregular	Yellow	White	Dull	Undulate	No
N8	Dry	SN821	Irregular	Yellow	Gray and white	Dusty	Undulate	No
N11	Dry	SN1101	Irregular	Yellow	Gray	Dusty	Filiform	No
N11	Dry	SN1106	Irregular	Pale Gray	Gray	Dusty	Filiform	No
N11	Dry	SN1108	Circular	Black	White with dark points	Dusty	Irregular	No
N11	Dry	SN1109	Circular	Pink	Pink	Dull	Filiform	No
N11	Dry	SN1110	Irregular	Orange	White	Dull	Undulate	No

Appendix 2b. Continuation

N11	Dry	SN1112	Irregular	Pale yellow	Cream	Dusty	Filiform	No
N11	Dry	SN1114	Irregular	Dark yellow	Gray	Dusty	Undulate	Yellow
N11	Dry	SN1116	Circular	Yellow	Pink	Dusty	Entire	Yellow
N11	Dry	SN1122	Irregular	Red	No data	Glistening	Filiform	No
N11	Dry	SN1123	Circular	Brown	White	Dull	Filiform	No
N11	Dry	SN1124	Irregular	Yellow	No data	Wrinkled	Undulate	No
N11	Dry	SN1125	Irregular	White	Gray and white	Dusty	Filiform	No
N12	Dry	SN1201	Circular	Translucent	White	Dusty	Filiform	No
N12	Dry	SN1202	Circular	Black	White	Dull	Filiform	Dark brown
N12	Dry	SN1203	Irregular	Translucent	White	Dusty	Filiform	No
N12	Dry	SN1204	Irregular	Pale yellow	No data	Glistening	Lobate	No
N12	Dry	SN1206	Irregular	Red	Pink	Dusty	Undulate	No
N12	Dry	SN1207	Circular	Orange	Pink	Dusty	Filiform	No

N12	Dry	SN1208	Irregular	Pale yellow	Gray with white	Dusty	Filiform	No
N12	Dry	SN1209	Irregular	Transluscent	White	Dull	Undulate	No
N12	Dry	SN1211	Irregular	Transluscent	No data	Dusty	Undulate	Yellow
N12	Dry	SN1212	Irregular	Transluscent	Purple with White spots	Dusty	Undulate	No
N12	Dry	SN1213	Irregular	Pale yellow	White	Dusty	Filiform	No
N12	Dry	SN1214	Circular	Red	Pink	Dull	Entire	No
N12	Dry	SN1215	Irregular	Transluscent	No data	Dusty	Entire	Dark yellow
N12	Dry	SN1216	Irregular	White	No data	Dusty	Filiform	No
N12	Dry	SN1217	Irregular	Dark yellow	Purple	Dusty	Filiform	No
N12	Dry	SN1218	Circular	Pale pink	Pink	Dusty	Filiform	No
N12	Dry	SN1219	Irregular	White	White	Dusty	Filiform	Yellow
N12	Dry	SN1221	Irregular	Brown	White	Dusty	Filiform	Yellow
N12	Dry	SN1222	Irregular	Cream	Gray and white	Dusty	Filiform	Brown

Appendix 2b. Continuation

N12	Dry	SN1226	Circular	Brown	Gray with a White edge	Dusty	Filiform	No
N12	Dry	SN1228	Irregular	Dark brown	No data	Dull	Lobate	No

Appendix 2c. Colony morphology of isolates from *Dorymyrmex* sp.

Nest	Season	Code	form	Color of the substrate Hyphae	Color of the aerial hyphae	Surface	Margin	Pigments
N6	Rainy	DN601	Irregular	Grey	White	Dull	Undulate	Brown
N6	Rainy	DN602	Irregular	Yellow	White	Dull	Undulate	Yellow
N6	Rainy	DN603	Irregular	Yellow	White	Dusty	Filiform	Yellow
N6	Rainy	DN604	Irregular	Yellow	No data	Glistering	Undulate	Yellow
N6	Rainy	DN605	Irregular	Brown	White	Glistering	Filiform	Brown
N6	Rainy	DN607	Irregular	Yellow	White	Dusty	Undulate	Yellow
N6	Rainy	DN606	Irregular	Yellow	White	Dusty	Filiform	Yellow
N6	Rainy	DN608	Irregular	Brown	Gray with White edge	Dull	Filiform	No
N6	Rainy	DN610	Irregular	Yellow	White	Glistering	Filiform	Yellow
N6	Rainy	DN611	Irregular	Yellow	Gray	Dusty	Filiform	Yellow
N6	Rainy	DN612	Irregular	Yellow	White	Dusty	Filiform	Yellow
N6	Rainy	DN614	Irregular	Yellow	White	Glistering	Filiform	No
N6	Rainy	DN615	Irregular	Yellow	Gray	Dusty	Filiform	Yellow

Appendix 2c. Continuation

N6	Rainy	DN616	Irregular	Yellow	Gray with White spots	Dusty	Filiform	Brown
N6	Rainy	DN617	Irregular	Yellow	Gray-blue	Dusty	Filiform	Yellow
N6	Rainy	DN618	Irregular	Yellow	White	Dusty	Filiform	Brown
N6	Rainy	DN620	Irregular	Yellow	Dark gray	Dusty	Filiform	Yellow
N6	Rainy	DN621	Irregular	Yellow	White	Dusty	Filiform	Yellow
N6	Rainy	DN625	Irregular	Yellow	Purple	Dull	Filiform	Yellow
N6	Rainy	DN628	Irregular	Yellow	White	Dusty	Filiform	Brown
N6	Rainy	DN629	Irregular	Yellow	White with dark spots	Dusty	Filiform	Yellow
N9	Rainy	DN901	Irregular	Dark yellow	No data	Wrinkled	Entire	Brown
N9	Rainy	DN902	Irregular	Dark yellow	White	Dusty	Filiform	Brown
N9	Rainy	DN903	Irregular	Dark yellow	No data	Wrinkled	Filiform	Brown
N9	Rainy	DN904	Irregular	Dark yellow	No data	Wrinkled	Filiform	No
N9	Rainy	DN906	Irregular	Dark yellow	No data	Wrinkled	Filiform	Yellow
N9	Rainy	DN907	Irregular	Dark yellow	White	Wrinkled	Filiform	No
N13	Dry	DN1301	Irregular	Yellow	White	Dusty	Filiform	No
N13	Dry	DN1303	Irregular	Pink	White	Dusty	Filiform	No

N13	Dry	DN1304	Circular	Yellow	White and gray	Dusty	Filiform	No
N13	Dry	DN1306	Irregular	Yellow	Gray	Dusty	Filiform	No
N13	Dry	DN1307	Irregular	Yellow	Gray with White spot	Dusty	Filiform	No
N13	Dry	DN1309	Irregular	Translucent yellow	White	Dull	Filiform	No
N13	Dry	DN1310	Irregular	Translucent yellow	White and gray	Dusty	Filiform	No
N13	Dry	DN1312	Irregular	Orange	No data	Dusty	Undulate	No
N13	Dry	DN1314	Circular	Pink	Pink	Dusty	Filiform	No
N13	Dry	DN1316	Irregular	Yellow	Gray	Dusty	Filiform	No
N13	Dry	DN1317	Irregular	Yellow	No data	Dull	Undulate	Yellow
N13	Dry	DN1318	Circular	Cream	White	Dusty	Filiform	No
N13	Dry	DN1319	Irregular	Yellow	Pink	Dusty	Undulate	No
N13	Dry	DN1321	Irregular	Yellow	Pink	Dusty	Filiform	No
N14	Dry	DN1402	Irregular	Dark yellow	Gray	Dull	Filiform	No
N14	Dry	DN1403	Irregular	Pink	Gray	Dusty	Undulate	No
N14	Dry	DN1404	Irregular	Yellow	Gray	Dull	Undulate	No
N14	Dry	DN1405	Irregular	Yellow	Gray and white	Dusty	Undulate	No

N14	Dry	DN1406	Circular	Yellow	Gray	Dusty	Filiform	No
N14	Dry	DN1407	Irregular	Yellow	Gray	Dusty	Filiform	No
N14	Dry	DN1410	Circular	Pink	Gray	Dusty	Filiform	No
N14	Dry	DN1414	Circular	Pink	Pink	Dusty	Entire	No

Appendix 3

Appendix 3a. Non-Actinobacteria cultures identified from *Solenopsis* sp. ants.

Code	Gene Bank number	Closely related species	Percentage of identity	Source	Phylum
SN1211	GU323365.1	Bacillus pumilus strain HS3	100		Firmicutes
SN1112	AB586071.1	*Burkholderia* sp. JCM 20553	99		Proteobacteria
SN1106	GU144371.1	*Burkholderia fungorum* strain UFLA04-219	97	Old second forest soil	Proteobacteria
SN815	DQ520809.1	Bradyrhizobiaceae bacterium NR111	97	Soil	Proteobacteria
SN802	GQ249215.1	*Burkholderia* sp. lxb-5	99	Coking plant soil with hihg concentration of PAHs	Proteobacteria
SN712	AY691400.1	*Rhizobium* sp. tpud22.2	99	Host of *Mimosa pudica*	Proteobacteria

Appendix 3b. Non-Actinobacteria cultures identified from *Dorymyrmex* sp. ants.

Code	Gene Bank number	Closely related species	Percentage of identity	Source	Phylum
DN603	HM113360.1	*Burkholderia fungorum* strain DBT1	99	Oil refinery wastewater treatment plant	Proteobacteria
DN901	AJ549086.1	*Devosia riboflavina*	99	Endosimbiont of marine ciliate	Proteobacteria
DN902	GU144371.1	*Burkholderia fungorum* strain UFLA04-219	100	Old second forest soil	Proteobacteria
DN903	GU144371.1	*Burkholderia fungorum* strain UFLA04-219	99	Old second forest soil	Proteobacteria
DN907	DQ530647.1	*Cupriavidus* sp. cmp2	99	Host of *Mimosa asperata*	Proteobacteria
DN1319	FJ763645.1	*Bacillus pumilus* strain X22	99	Wastewater of silk industry	Firmicutes
DN1412	FJ763645.1	*Bacillus pumilus* strain X22	99	Wastewater of silk industry	Firmicutes

Appendix 3c. Non-Actinobacteria cultures identified from *Paratrechina* sp. ants.

Code	Gene Bank number	Closely related species	Percentage of identity	Source	Phylum
PN206	AF514702.1	*Bradyrhizobium* sp. La5-8	99	Host of *Lonchocarpus atropurpureus*	Proteobacteria
PN4212	FJ763645.1	*Bacillus pumilus* strain X22	99	Wastewater of silk industry	Firmicutes

Appendix 4

Appendix 4a. Non-Actinobacteria sequences identified from *Paratrechina* sp. ants by culture-independent methods.

Nest	Clone code	Gene Bank number	Closely related species	Percentage of identity	Source	Phylum
N4-2	H100	JF947351.1	*Enterococcus canis* strain 2104	97	Dorsal patch	Firmicutes
N4-2	H106	HM059721.1	*Geobacillus* sp.	99	Compost	Firmicutes
N4-2	H129	JF135243.1	Uncultured bacterium clone ncd1556d09c1	96	Skin, volar forearm	unknown classification
N4-2	H143	HM241101.1	Uncultured bacterium clone LIM33	96	Limestone rock	Acidobacteria
N10	H152	JF825503.1	Uncultured Geobacillus sp. clone ASC135	89	Asparagus straw compost	Firmicutes

Appendix 4b. Non-Actinobacteria sequences identified from soil by culture-independent methods.

Nest	Clone code	Gene Bank number	Closely related species	Percentage of identity	Source	Phylum
N4-2	S284	EU132454.1	Uncultured bacterium clone FFCH9382	95	Soil	Acidobacteria
N4-2	s285	EU132325.1	Uncultured bacterium clone FFCH10450	97	Soil	Acidobacteria
N4-2	S305	GQ287576.1	Uncultured bacterium clone P1s-141	98	Soil	Acidobacteria
N4-2	S307	JF718677.1	Uncultured bacterium clone CK2	97	Soil	Acidobacteria
N10	S336	AY493926.1	Uncultured soil bacterium clone 539	96	Soil	Acidobacteria
N10	S354	EU276448.1	Uncultured Acidobacteriales bacterium clone Plot03-2D01	97	Agricultural soil	Acidobacteria
N4	S188	HM062484.1	Uncultured Acidobacteria	99	Soil	Acidobacteria
N4	S191	HM062484.1	Uncultured Acidobacteria	99	Soil	Acidobacteria
N4	S194	HM062397.1	Uncultured Acidobacteria bacterium clone KBS_T1_R4_149264	96	Soil	Acidobacteria
N4	S218	HQ864092.1	Uncultured bacterium clone TP-SL-B-33	97	Soil samples from	Acidobacteria

Appendix 2b. Continuation

						permafrost	
N4	S221	EU202822.1	Uncultured Acidobacteriales bacterium	97	Agricultural soil	Acidobacteria
N4	S226	AM935718.1	Uncultured Acidobacteriaceae	95	Hydrocarbon-contaminated soil	Acidobacteria
N4	S228	AM935718.1	Uncultured Acidobacteria bacterium	99	Limestone rock	Acidobacteria
N4	S242	FJ889253.1	Uncultured Acidobacteriales bacterium	99	Agricultural soil	Acidobacteria
N4	S199	EU132283.1	Uncultured bacterium clone FFCH3185	93	Soil from an undisturbed mixed grass	Acidobacteria
N4S	S196	FJ478812.1	Uncultured bacterium clone p9e17ok	95	Agricultural soil	Acidobacteria
N4S	S225	FJ479574.1	Uncultured bacterium clone p5i06ok	97	Undisturbed tall grass prairie	Acidobacteria
N4S	S207	FM873930.1	Uncultured bacterium partial clone MB03E09	95	Mattress dust	Acidobacteria
N4S	S210	EU132325.1	Uncultured bacterium clone FFCH10450	97	Soil from an undisturbed mixed grass	Acidobacteria
N4S	S200	JF718677.1	Uncultured bacterium clone CK2	97	Soil	Acidobacteria
N4S	S214	EU132325.1	Uncultured bacterium clone FFCH10450	97	Soil from an undisturbed mixed grass	Acidobacteria
N4S	S235	HM131976.1	Uncultured soil bacterium clone D1B28	98	Banana wilt farm soil	Acidobacteria
N4S	S211	HQ397556.1	Uncultured bacterium clone BSS62	98	Coastal saline soil	Acidobacteria
N4S	S192	JF809791.1	Uncultured bacterium clone 2M1S-B100	92	Medea hypersaline basin, Mediterranean	Acidobacteria
N2S	S92	AM935448.1	Uncultured Acidobacteria bacterium	99	Pilot-scale bioremediati-on	Acidobacteria
N2S	S91	JF718677.1	Uncultured bacterium clone CK2	99	Soil microbe in exogenous rare Earths	Acidobacteria
N2S	S63	GQ214125.1	Uncultured bacterium clone P958	95	Loess	Acidobacteria
N2S	S72	HQ397556.1	Uncultured bacterium clone BSS62	99	Agricultural soil	Acidobacteria
N2S	S85	AY921944.1	Uncultured Acidobacteria bacterium	97	Farm soil adjacent to a silage storage	Acidobacteria

Appendix 5. Multiple sequence aligment of *Streptomyces* strain isolated from *Dorymyrmex* sp. and related closely species found in Genbank.

First alignment block (positions ~90–150):

Label	Num
DN605	32
DN615	15
DN618	12
AY999771.1 Streptomyces ciner	51
DN616	1
Streptomyces violaceorectus NB	59
HQ418468.1 Streptomyces DA1020	25
Streptomyces bikiniensis DSM40	80
N9 4	25
N9 6	10
Streptomyces tanashiensis HBUM	42
DN621	12
DN607	14
Streptomyces XAS585	41
DN608	13
DN606	31
Streptomyces DA08605	54
DN612	35
Streptomyces TRI 10 AB448718	32
DN61501	16
Streptomyces nodosus NBRC 1289	59

Second alignment block (positions ~170–230):

Label	Num
DN605	110
DN615	93
DN618	91
AY999771.1 Streptomyces ciner	129
DN616	1
Streptomyces violaceorectus NB	137
HQ418468.1 Streptomyces DA1020	103
Streptomyces bikiniensis DSM40	158
N9 4	103
N9 6	88
Streptomyces tanashiensis HBUM	120
DN621	90
DN607	93
Streptomyces XAS585	119
DN608	91
DN606	109
Streptomyces DA08605	132
DN612	113
Streptomyces TRI 10 AB448718	110
DN61501	93
Streptomyces nodosus NBRC 1289	137
DN617	91
Streptomyces ambofaciens NBRC	131
DN1310	111
DN1312	115
DN1317	108
DN1301	111
DN1316	108
Streptomyces rochei NBRC 12908	137
Streptomyces B5W222	159
Streptomyces mutabilis NRRL IS	139
DN1303	109
DN1304	108
DN1306	116
Streptomyces 195018	113
DN1405	108
DN1402	109
DN1403	130
Streptomyces N01 352 DQ717851	128
DN1404	108
DN1406	107
DN1407	108
DN1321	111
Streptomyces thermolilacinus N	136
Streptomyces heteromorphus AB	144
DN1413	110
Streptomyces fragilis NRRL 242	156

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                                          250       260       270       280       290       300       310
                                     ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
DN605                            187 TGTTGGTGGGGTAATGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
DN615                            170 TGTTGGTGGGGTAATGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
DN618                            168 TGTTGGTGGGGTAATGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
 AY999771.1 Streptomyces ciner   206 TGTTGGTGGGGTAATGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
DN616                            1
Streptomyces violaceorectus NB   214 TGTTGGTGGGGTAATGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
HQ418468.1 Streptomyces DA1020   180 TGTTGGTGGGGTAATGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
Streptomyces bikiniensis DSM40   235 TGTTGGTGGGGTAACGGCCCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
N9 4                             180 TGTTGGTGGGGTAACGGCCCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
N9 6                             165 TGTTGGTGGGGTAACGGCCCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
Streptomyces tanashiensis HBUM   197 TGTTGGTGGGGTAATGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
DN621                            167 TGTTGGTGGGGTAATGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
DN607                            170 TGTTGGTGGGGTAATGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
Streptomyces XAS585              196 TGTTGGTGGGGTAATGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
DN608                            168 TGTTGGTGGGGTAATGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
DN606                            187 TGTTGGTGAGGTAACGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
Streptomyces DA08605             210 TGTTGGTGAGGTAACGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
DN612                            191 TGTTGGTGGGGTGATGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
Streptomyces TRI 10  AB448718    188 TGTTGGTGGGGTGATGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
DN61501                          170 TGTTGGTGAGGTAACGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
Streptomyces nodosus NBRC 1289   214 TGTTGGTGAGGTAACGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
DN617                            169 TGTTGGTGAGGTAGTGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
Streptomyces ambofaciens NBRC    209 TGTTGGTGAGGTAGTGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
DN1310                           188 TGTTGGTGGGGTAACGGCCCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
DN1312                           192 TGTTGGTGGGGTAATGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
DN1317                           185 TGTTGGTGGGGTAACGGCCCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
DN1301                           189 TGTTGGTGAGGTAATGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
DN1316                           186 AGTTGGTGAGGTAACGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
Streptomyces rochei NBRC 12908   215 AGTTGGTGAGGTAACGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
Streptomyces B5W222              237 TGTTGGTGAGGTAATGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
Streptomyces mutabilis NRRL IS   217 AGTTGGTGAGGTAATGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
DN1303                           186 TGTTGGTGGGGTAATGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
DN1304                           186 AGTTGGTGAGGTAACGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
DN1306                           194 TGTTGGTGAGGTAATGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
Streptomyces 195018              191 TGTTGGTGAGGTAATGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
DN1405                           185 TGTTGGTGGGGTAACGGCCCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
DN1402                           186 TGTTGGTGGGGTAATGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
DN1403                           207 TGTTGGTGGGGTAATGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
Streptomyces N01 352  DQ717851   205 TGTTGGTGGGGTAATGGCCTACCAAGGCG CGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
DN1404                           186 AGTTGGTGAGGTAACGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
DN1406                           185 AGTTGGTGAGGTAACGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
DN1407                           186 AGTTGGTGAGGTAACGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
DN1321                           189 TGTTGGTGAGGTAACGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
Streptomyces thermolilacinus N   214 TGTTGGTGAGGTAACGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
Streptomyces heteromorphus   AB  221 TGTTGGTGAGGTAACGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
DN1413                           187 TGTTGGTGAGGTAACGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
Streptomyces fragilis NRRL 242   233 TGTTGGTGAGGTAACGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
Streptomyces humidus NRRL B-31   229 TGTTGGTGAGGTAATGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
DN1307                           189 TGTTGGTGAGGTAACGGCTCACCAAGGCGACGACGGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
N14 19                           188 TGTTGGTGGGGTAATGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
Streptomyces paraguayensis NBR   211 TGTTGGTGGGGTGATGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGA
Actinomadura nitritigenes T      197 TGTTGGTGGGGTGATGGCCTACCAAGGCGACGACGGGTAACCGGCCTGAGAGGGCGACCGGTCACACTGGGACTGA
Actinomadura bangladeshensis T   218 TGTTGGTGGGGTGATGGCCTACCAAGGCGACGACGGGTAACCGGCCTGAGAGGGCGACCGGTCACACTGGGACTGA
Clustal Consensus
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Sequence alignment (partial 16S rRNA gene region, positions ~490–550).

Label	Position
DN605	426
DN615	409
DN618	407
AY999771.1 Streptomyces ciner	445
DN616	135
Streptomyces violaceorectus NB	453
HQ418468.1 Streptomyces DA1020	419
Streptomyces bikiniensis DSM40	474
N9 4	419
N9 6	404
Streptomyces tanashiensis HBUM	436
DN621	405
DN607	409
Streptomyces XAS585	435
DN608	407
DN606	426
Streptomyces DA08605	449
DN612	430
Streptomyces TRI 10 AB448718	427
DN61501	409
Streptomyces nodosus NBRC 1289	453
DN617	408
Streptomyces ambofaciens NBRC	448
DN1310	427
DN1312	431
DN1317	424
DN1301	428
DN1316	425
Streptomyces rochei NBRC 12908	454
Streptomyces B5W222	476
Streptomyces mutabilis NRRL IS	456
DN1303	425
DN1304	425
DN1306	433
Streptomyces 195018	430
DN1405	424
DN1402	425
DN1403	446
Streptomyces N01 352 DQ717851	443
DN1404	425
DN1406	424
DN1407	425
DN1321	428
Streptomyces thermolilacinus N	453
Streptomyces heteromorphus AB	460
DN1413	426
Streptomyces fragilis NRRL 242	472
Streptomyces humidus NRRL B-31	469
DN1307	428
N14 19	427
Streptomyces paraguayensis NBR	450
Actinomadura nitritigenes T	436
Actinomadura bangladeshensis T	457
Clustal Consensus	120

Representative aligned sequence (most rows):
AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAAT --------- TATTGGGCGTAAAGAG

Clustal Consensus:
****** ******************** ** ** ** **** *****   ************ ***

DN605 499 TAGGCGGCTTGTCACGTCGG-TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCATCCGATACGGGCAGGCTAGAGT
DN615 482 TAGGCGGCTTGTCACGTCGG-TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCATCCGATACGGGCAGGCTAGAGT
DN618 474 TAGGCGGCTTGTCACGTCGG-TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCATCCGATACGGGCAGGCTAGAGT
AY999771.1 Streptomyces ciner 518 TAGGCGGCTTGTCACGTCGG-TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCATCCGATACGGGCAGGCTAGAGT
DN616 208 TAGGCGGCTTGTCACGTCGG-TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCATCCGATACGGGCAGGCTAGAGT
Streptomyces violaceorectus NB 526 TAGGCGGCTTGTCACGTCGG-TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCATCCGATACGGGCAGGCTAGAGT
HQ418468.1 Streptomyces DA1020 492 TAGGCGGCTTGTCACGTCGG-TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCATCCGATACGGGCAGGCTAGAGT
Streptomyces bikiniensis DSM40 547 TAGGCGGCTTGTCACGTCGG-TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCATCCGATACGGGCAGGCTAGAGT

N9 6 477 TAGGCGGCTTGTCACGTCGG-TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCATCCGATACGGGCAGGCTAGAGT
Streptomyces tanashiensis HBUM 509 TAGGCGGCTTGTCACGTCGG-TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCATCCGATACGGGCAGGCTAGAGT
DN621 478 TAGGCGGCTTGTCACGTCGG-TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCATCCGATACGGGCAGGCTAGAGT
DN607 482 TAGGCGGCTTGTCACGTCGG-TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCATCCGATACGGGCAGGCTAGAGT
Streptomyces XAS585 508 TAGGCGGCTTGTCACGTCGG-TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCATCCGATACGGGCAGGCTAGAGT
DN608 480 TAGGCGGCTTGTCACGTCGG-TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCATCCGATACGGGCAGGCTAGAGT
DN606 498 TAGGCGGCTTGTCACGTCGGTTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGT
Streptomyces DA08605 522 TAGGCGGCTTGTCACGTCGGTTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGT
DN612 503 TAGGCGGCTTGTCGCGTCGGTTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGT
Streptomyces TRI 10 AB448718 500 TAGGCGGCTTGTCGCGTCGGTTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGT
DN61501 482 TAGGCGGCTTGTCACGTCGGTTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGT
Streptomyces nodosus NBRC 1289 526 TAGGCGGCTTGTCGCGTCGGTTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGT
DN617 481 TAGGCGGCTTGTCACGTCGGTTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGT
Streptomyces ambofaciens NBRC 521 TAGGCGGCTTGTCACGTCGGTTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGT
DN1310 500 TAGGCGGCTTGTCACGTCGG-TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCATCCGATACGGGCAGGCTAGAGT
DN1312 504 TAGGCGGCTTGTCACGTCGG-TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCATCCGATACGGGCAGGCTAGAGT
DN1317 497 TAGGCGGCTTGTCACGTCGG-TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCATCCGATACGGGCAGGCTAGAGT
DN1301 501 TAGGCGGCTTGTCACGTCGGTTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGT
DN1316 498 TAGGCGGCTTGTCACGTCGGTTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGT
Streptomyces rochei NBRC 12908 527 TAGGCGGCTTGTCACGTCGGTTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGT
Streptomyces B5W222 549 TAGGCGGCTTGTCACGTCGGTTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGT
Streptomyces mutabilis NRRL IS 529 TAGGCGGCTTGTCACGTCGGTTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGT
DN1303 498 TAGGCGGCTTGTCACGTCGG-TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCATCCGATACGGGCAGGCTAGAGT
DN1304 498 TAGGCGGCTTGTCACGTCGGTTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGT
DN1306 506 TAGGCGGCTTGTCGCGTCGGTTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGT
Streptomyces 195018 503 TAGGCGGCTTGTCGCGTCGGTTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGT
DN1405 497 TAGGCGGCTTGTCACGTCGG-TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCATCCGATACGGGCAGGCTAGAGT
DN1402 498 TAGGCGGCTTGTCACGTCGG-TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCATCCGATACGGGCAGGCTAGAGT
DN1403 526 TAGGCGGCTTGTCACGTCGG-TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCATCCGATACGGGCAGGCTAGAGT
Streptomyces N01 352 DQ717851 516 TAGGCGGCTTGTCACGTCGG-TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCATCCGATACGGGCAGGCTAGAGT
DN1404 498 TAGGCGGCTTGTCACGTCGGTTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGT
DN1406 497 TAGGCGGCTTGTCACGTCGGTTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGT
DN1407 498 TAGGCGGCTTGTCACGTCGGTTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGT
DN1321 501 TAGGCGGCTTGTCGCGTCGGATGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCATTCGATACGGGCAGGCTAGAGT
Streptomyces thermolilacinus N 526 TAGGCGGCTTGTCGCGTCGGATGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCATTCGATACGGGCAGGCTAGAGT
Streptomyces heteromorphus AB 533 TAGGCGGCTTGTCGCGTCGGTTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGT
DN1413 499 TAGGCGGCTTGTCGCGTCGGTTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGT
Streptomyces fragilis NRRL 242 545 TAGGCGGCTTGTCGCGTCGGTTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGT
Streptomyces humidus NRRL B-31 542 TAGGCGGTCTGTCGCGTCGGATGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCATTCGATACGGGCAGATAGAGT
DN1307 501 TAAGCGGCTTGTCGCGTCCGTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGT
N14 19 500 TAGGCGGCCTGTCGCGTCGGATGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCATTCGATACGGGCAGGCTAGAGT
Streptomyces paraguayensis NBR 523 TAGGCGGCNTGTCGCGTCGGATGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCATTCGATACGGGCAGGCTAGAGT
Actinomadura nitritigenes T 509 TAGGCGGTTTGTCGCGTCTCGTGAAAGCCCACGGCTTAACTGTGGGTCTGCGTGGATACGGGCAGAGCTAGAGG
Actinomadura bangladeshensis T 530 TAGGCGGTTTGTCGCGTCTCGTGAAAGCCCACGGCTTAACCGTGGGTCTGCGTGGATACGGGCAGAACTAGAGG
Clustal Consensus 181 ** **** **** **** * ********** ******* ******* ********** ******

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DN1306                          506  TAGGCGGCTTGTCGCCGTCGGTTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGT
Streptomyces 195018             503  TAGGCGGCTTGTCGCCGTCGGTTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGT
DN1405                          497  TAGGCGGCTTGTCACGTCGGGTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCATCCGATACGGGCAGGCTAGAGT
DN1402                          498  TAGGCGGCTTGTCACGTCGGGTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCATCCGATACGGGCAGGCTAGAGT
DN1403                          526  TAGGCGGCTTGTCACGTCGGGTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCATCCGATACGGGCAGGCTAGAGT
Streptomyces N01 352  DQ717851  516  TAGGCGGCTTGTCACGTCGGGTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCATCCGATACGGGCAGGCTAGAGT
DN1404                          498  TAGGCGGCTTGTCACGTCGGTTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGT
DN1406                          497  TAGGCGGCTTGTCACGTCGGTTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGT
DN1407                          498  TAGGCGGCTTGTCACGTCGGTTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGT
DN1321                          501  TAGGCGGCTTGTCGCCGTCGGATGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCATTCGATACGGGCAGGCTAGAGT
Streptomyces thermolilacinus N  526  TAGGCGGCTTGTCGCCGTCGGATGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCATTCGATACGGGCAGGCTAGAGT
Streptomyces heteromorphus  AB  533  TAGGCGGCTTGTCGCGTCGGTTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGT
DN1413                          499  TAGGCGGCTTGTCGCGTCGGTTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGT
Streptomyces fragilis NRRL 242  545  TAGGCGGCTTGTCGCCGTCGGTTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGT
Streptomyces humidus NRRL B-31  542  TAGGCCGGTCGTCGCGTCGGATGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCATTCGATACGGCAGACTAGAGT
DN1307                          501  TAAGCGGCTTGTCGCCGTCGTTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGT
N14 19                          500  TAGGCGGCCTGTCGCCGTCGGATGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCATTCGATACGGGCAGGCTAGAGT
Streptomyces paraguayensis NBR  523  TAGGCGGCNTGTCGCCGTCGGATGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCATTCGATACGGGCAGGCTAGAGT
Actinomadura nitritigenes T     509  TAGGCGGTTTGTCGCGTCTTGTCGTGAAAGCCCACGGCTTAACCTGTGGGTCTGCGGTGGATACGGGCAGACTAGAGG
Actinomadura bangladeshensis T  530  TAGGCGGTTTGTCGCCGTCTTGTCGTGAAAGCCCACGGCTTAACCGTGGGTCTGCGGTGGATACGGGCAGACTAGAGG
Clustal Consensus               181  ** ****  **** **** *  ***********  ********   ********    *********** ******
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                                          650       660       670       680       690       700       710
                                     ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|.

DN605                           579  TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
DN615                           562  TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
DN618                           554  TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
 AY999771.1 Streptomyces ciner  598  TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
DN616                           288  TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
Streptomyces violaceorectus NB  606  TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
HQ418468.1 Streptomyces DA1020  572  TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
Streptomyces bikiniensis DSM40  627  TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
N9 4                            572  TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
N9 6                            557  TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
Streptomyces tanashiensis HBUM  589  TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
DN621                           558  TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
DN607                           562  TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
Streptomyces XAS585             588  TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
DN608                           560  TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
DN606                           578  TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
Streptomyces DA08605            602  TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
DN612                           583  TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
Streptomyces TRI 10  AB448718   580  TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
DN61501                         562  TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
Streptomyces nodosus NBRC 1289  606  TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
DN617                           561  TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
Streptomyces ambofaciens NBRC   601  TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
DN1310                          580  TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
DN1312                          584  TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
DN1317                          577  TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
DN1301                          581  TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
DN1316                          578  TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
Streptomyces rochei NBRC 12908  607  TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
Streptomyces B5W222             629  TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
Streptomyces mutabilis NRRL IS  609  TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
DN1303                          578  TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
DN1304                          578  TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
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Top panel:

Label	Pos	Sequence
DN605	579	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
DN615	562	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
DN618	554	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
AY999771.1 Streptomyces ciner	598	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
DN616	288	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
Streptomyces violaceorectus NB	606	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
HQ418468.1 Streptomyces DA1020	572	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
Streptomyces bikiniensis DSM40	627	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
N9 4	572	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
N9 6	557	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
Streptomyces tanashiensis HBUM	589	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
DN621	558	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
DN607	562	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
Streptomyces XAS585	588	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
DN608	560	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
DN606	578	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
Streptomyces DA08605	602	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
DN612	583	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
Streptomyces TRI 10 AB448718	580	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
DN61501	562	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
Streptomyces nodosus NBRC 1289	606	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
DN617	561	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
Streptomyces ambofaciens NBRC	601	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
DN1310	580	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
DN1312	584	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
DN1317	577	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
DN1301	581	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
DN1316	578	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
Streptomyces rochei NBRC 12908	607	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
Streptomyces B5W222	629	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
Streptomyces mutabilis NRRL IS	609	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
DN1303	578	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
DN1304	578	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC

Bottom panel:

Note: This is a print preview. It may copy to the clipboard slightly large. To show control panel, press the red arrow (upper left)

Label	Pos	Sequence
Streptomyces 195018	583	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
DN1405	577	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
DN1402	578	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
DN1403	606	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
Streptomyces N01 352 DQ717851	596	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
DN1404	578	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
DN1406	577	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
DN1407	578	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
DN1321	581	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
Streptomyces thermolilacinus N	606	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
Streptomyces heteromorphus AB	613	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
DN1413	579	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
Streptomyces fragilis NRRL 242	625	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
Streptomyces humidus NRRL B-31	622	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
DN1307	581	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
N14 19	580	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
Streptomyces paraguayensis NBR	603	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC
Actinomadura nitritigenes T	589	TAGGGGAGATGGAATTCCGGTGTAGCGGTGAAATGCGCAGATATCGGGAGGAACACCGGTGGCGAAGGCGGTTC
Actinomadura bangladeshensis T	610	TAGGGGAGATGGAATTCCGGTGTAGCGGTGAAATGCGCAGATATCGGGAGGAACACCGGTGGCGAAGGCGGTTC
Clustal Consensus	241	********* ******* ************************* *********************** **

| | | 730 | 740 | 750 | 760 | 770 | 780 | 790 |

Name	Pos	Sequence
DN605	659	GGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
DN615	642	GGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
DN618	634	GGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
AY999771.1 Streptomyces ciner	678	GGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
DN616	368	GGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
Streptomyces violaceorectus NB	686	GGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
HQ418468.1 Streptomyces DA1020	652	GGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
Streptomyces bikiniensis DSM40	707	GGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
N9 4	652	GGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
N9 6	637	GGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
Streptomyces tanashiensis HBUM	669	GGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
DN621	638	GGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
DN607	642	GGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
Streptomyces XAS585	668	GGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
DN608	640	GGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
DN606	658	GGCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
Streptomyces DA08605	682	GGCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
DN612	663	GGCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
Streptomyces TRI 10 AB448718	660	GGCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
DN61501	642	GGCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
Streptomyces nodosus NBRC 1289	686	GGCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
DN617	641	GGCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
Streptomyces ambofaciens NBRC	681	GGCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
DN1310	660	GGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
DN1312	664	GGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
DN1317	657	GGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
DN1301	661	GGCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
DN1316	658	GGCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
Streptomyces rochei NBRC 12908	687	GGCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
Streptomyces B5W222	709	GGCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
Streptomyces mutabilis NRRL IS	689	GGCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
DN1303	658	GGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
DN1304	658	GGCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
DN1306	666	GGCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
Streptomyces 195018	663	GGCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
DN1405	657	GGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
DN1402	658	GGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
DN1403	686	GGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
Streptomyces N01 352 DQ717851	676	GGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
DN1404	658	GGCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
DN1406	657	GGCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
DN1407	658	GGCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
DN1321	661	GGCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
Streptomyces thermolilacinus N	686	GGCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
Streptomyces heteromorphus AB	693	GGCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
DN1413	659	GGCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
Streptomyces fragilis NRRL 242	705	GGCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
Streptomyces humidus NRRL B-31	702	GGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
DN1307	661	GGCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
N14 19	660	GGCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
Streptomyces paraguayensis NBR	683	GGCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
Actinomadura nitritigenes T	669	GGCCTGTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
Actinomadura bangladeshensis T	690	GGCCTGTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
Clustal Consensus	316	**** ************ ****************** **************************************

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Label	Position
DN61501	960
Streptomyces nodosus NBRC 1289	1004
DN617	959
Streptomyces ambofaciens NBRC	999
DN1310	978
DN1312	982
DN1317	975
DN1301	979
DN1316	976
Streptomyces rochei NBRC 12908	1005
Streptomyces B5W222	1027
Streptomyces mutabilis NRRL IS	1007
DN1303	976
DN1304	976
DN1306	984
Streptomyces 195018	981
DN1405	975
DN1402	976
DN1403	1004
Streptomyces N01 352 DQ717851	994
DN1404	976
DN1406	975
DN1407	976
DN1321	979
Streptomyces thermolilacinus N	1004
Streptomyces heteromorphus AB	1011
DN1413	977
Streptomyces fragilis NRRL 242	1023
Streptomyces humidus NRRL B-31	1020
DN1307	979
N14 19	978
Streptomyces paraguayensis NBR	1001
Actinomadura nitritigenes T	986
Actinomadura bangladeshensis T	1007
Clustal Consensus	586

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Streptomyces nodosus NBRC 1269   1084
DN617   1039
Streptomyces ambofaciens NBRC   1079
DN1310   1058
DN1312   1062
DN1317   1055
DN1301   1059
DN1316   1056
Streptomyces rochei NBRC 12908   1085
Streptomyces B5W222   1107
Streptomyces mutabilis NRRL IS   1087
DN1303   1056
DN1304   1056
DN1306   1064
Streptomyces 195018   1061
DN1405   1055
DN1402   1056
DN1403   1084
Streptomyces N01 352 DQ717851   1074
DN1404   1056
DN1406   1055
DN1407   1056
DN1321   1059
Streptomyces thermolilacinus N   1084
Streptomyces heteromorphus AB   1091
DN1413   1057
Streptomyces fragilis NRRL 242   1103
Streptomyces humidus NRRL B-31   1100
DN1307   1059
N14 19   1058
Streptomyces paraguayensis NBR   1081
Actinomadura nitritigenes T   1060
Actinomadura bangladeshensis T   1083
Clustal Consensus

                                 1210   1220   1230   1240   1250   1260   1270

DN605   1137
DN615   1121
DN618   1112
  AY999771.1 Streptomyces ciner 1156
DN616   846
Streptomyces violaceorectus NB   1164
HQ418468.1 Streptomyces DA1020   1130
Streptomyces bikiniensis DSM40   1184
N9 4   1130
N9 6   1115
Streptomyces tanashiensis HBUM   1147
DN621   1115
DN607   1120
Streptomyces XAS585   1146
DN608   1118
DN606   1067
Streptomyces DA08605   1159
DN612   1140
Streptomyces TRI 10 AB448718   1137
DN61501   1119
Streptomyces nodosus NBRC 1289   1163

Streptomyces fragilis NRRL 242   1182
Streptomyces humidus NRRL B-31   1180
DN1307   1138
N14 19   1138
Streptomyces paraguayensis NBR   1161
Actinomadura nitritigenes T   1139
Actinomadura bangladeshensis T   1159
Clustal Consensus

| | | 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 |

Name	Pos	Sequence
DN605	1209	--
DN615	1191	--
DN618	1183	--
AY999771.1 Streptomyces ciner	1236	CGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTCGGAGTTGCTAGTAATCGCAGATCAGCATTGC
DN616	926	CGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTCGGAGTTGCTAGTAATCGCAGATCAGCATTGC
Streptomyces violaceorectus NB	1244	CGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTCGGAGTTGCTAGTAATCGCAGATCAGCATTGC
HQ418468.1 Streptomyces DA1020	1210	CGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTCGGAGTTGCTAGTAATCGCAGATCAGCATTGC
Streptomyces bikiniensis DSM40	1264	CGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTCGGAGTTGCTAGTAATCGCAGATCAGCATTGC
N9 4	1210	CGGTCTCAGTTCGGATTGGGGTCTGCAACT
N9 6	1195	CGGTCTCAGTTCGGATTGGGGTCTGCAACT
Streptomyces tanashiensis HBUM	1227	CGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTCGGAGTTGCTAGTAATCGCAGATCAGCATTGC
DN621	1195	CGGTCTCA
DN607	1179	--
Streptomyces XAS585	1226	CGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTCGGAGTTGCTAGTAATCGCAGATCAGCATTGC
DN608	1198	CGGTCTCAGTTCGGATTGGG
DN606	1067	--
Streptomyces DA08605	1239	CGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTCGGAGTCGCTAGTAATCGCAGATCAGCATTGC
DN612	1220	CGGTCTCAGTTCGGATTGGGGTCT
Streptomyces TRI 10 AB448718	1217	CGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTCGGAGTCGCTAGTAATCGCAGATCAGCATTGC
DN61501	1199	CGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTCGGAGTCGCTAGTAATCGCAGATCAGCATTGC
Streptomyces nodosus NBRC 1289	1243	CGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTCGGAGTCGCTAGTAATCGCAGATCAGCATTGC
DN617	1199	CGGTCTCAGTT
Streptomyces ambofaciens NBRC	1239	CGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTCGGAGTCGCTAGTAATCGCAGATCAGCATTGC
DN1310	1218	CGGTCTCAGTTCG
DN1312	1210	--
DN1317	1206	--
DN1301	1218	CGGTCT
DN1316	1202	--
Streptomyces rochei NBRC 12908	1244	CGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTCGGAGTCGCTAGTAATCGCAGATCAGCATTGC
Streptomyces B5W222	1266	CGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTCGGAGTCGCTAGTAATCGCAGATCAGCATTGC
Streptomyces mutabilis NRRL IS	1246	CGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTCGGAGTCGCTAGTAATCGCAGATCAGCATTGC
DN1303	1216	CGGTCTCAGTT
DN1304	1215	CGGTCTCAGTTCG
DN1306	1224	CGGTCTCAGTTCGGAT
Streptomyces 195018	1221	CGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTCGGAGTCGCTAGTAATCGCAGATCAGCATTGC
DN1405	1189	--
DN1402	1197	--
DN1403	1220	--
Streptomyces N01 352 DQ717851	1234	CGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTCGGAGTTGCTAGTAATCGCAGATCAGCATTGC
DN1404	1202	--
DN1406	1194	--
DN1407	1201	--
DN1321	1206	--
Streptomyces thermolilacinus N	1243	CGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTCGGAGTCGCTAGTAATCGCAGATCAGCATTGC
Streptomyces heteromorphus AB	1250	CGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTCGGAGTCGCTAGTAATCGCAGATCAGCATTGC
DN1413	1199	--

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DN606                            1067  --------------------------------------------------------------
Streptomyces DA08605             1319  GTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACACCCGAAGCCGGTGGCCC
DN612                            1243  --------------------------------------------------------------
Streptomyces TRI 10  AB448718    1297  GTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACACCCGAAGCCGGTGGTCC
DN61501                          1279  GTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACAC
Streptomyces nodosus NBRC 1289   1323  GTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACACCCGAAGCCGGTGGCCC
DN617                            1209  --------------------------------------------------------------
Streptomyces ambofaciens NBRC    1319  GTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACACCCGAAGCCGGTGGCCC
DN1310                           1230  --------------------------------------------------------------
DN1312                           1210  --------------------------------------------------------------
DN1317                           1206  --------------------------------------------------------------
DN1301                           1223  --------------------------------------------------------------
DN1316                           1202  --------------------------------------------------------------
Streptomyces rochei NBRC 12908   1324  GTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACACCCGAAGCCGGTGGCCC
Streptomyces B5W222              1346  GTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACACCCGAAGCCGGTGGCCC
Streptomyces mutabilis NRRL IS   1326  GTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACACCCGAAGCCGGTGGCCC
DN1303                           1226  --------------------------------------------------------------
DN1304                           1227  --------------------------------------------------------------
DN1306                           1239  --------------------------------------------------------------
Streptomyces 195018              1301  GTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACACCCGAAGCCGGTGGCCC
DN1405                           1189  --------------------------------------------------------------
DN1402                           1197  --------------------------------------------------------------
DN1403                           1220  --------------------------------------------------------------
Streptomyces N01 352  DQ717851   1314  GTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACACCCGAAGCCGGTGGCCC
DN1404                           1202  --------------------------------------------------------------
DN1406                           1194  --------------------------------------------------------------
DN1407                           1201  --------------------------------------------------------------
DN1321                           1206  --------------------------------------------------------------
Streptomyces thermolilacinus N   1323  GTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACACCCGAAGCCGGTGGCCC
Streptomyces heteromorphus  AB   1330  GTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACACCCGAAGCCGGTGGCCC
DN1413                           1199  --------------------------------------------------------------
Streptomyces fragilis NRRL 242   1342  GTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACACCCGAAGCCGGTGGCCC
Streptomyces humidus NRRL B-31   1340  GTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACACCCGAAGCCGGTGGCCC
DN1307                           1230  --------------------------------------------------------------
N14 19                           1252  --------------------------------------------------------------
Streptomyces paraguayensis NBR   1321  GTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACACCCGAAGCCGGTGGCCC
Actinomadura nitritigenes T      1299  GTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGCGAACACCCGAAGCCGGTGGCCC
Actinomadura bangladeshensis T   1319  GTGAATACGTTCCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGCGAACACCCGAAGCCGGTGGCCC
Clustal Consensus
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                                           1450      1460      1470      1480      1490      1500      1510
                                      ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|-.
DN605                            1209  --------------------------------------------------------------
DN615                            1191  --------------------------------------------------------------
DN618                            1183  --------------------------------------------------------------
 AY999771.1 Streptomyces ciner   1395  CCTTGT GGGAGGGAGCTGTCGAAGGTGGGAC
DN616                            1071  --------------------------------------------------------------
Streptomyces violaceorectus NB   1403  CCTTGT GGGAGGGAGCTGTCGAAGGTGGGACTGGCGATTGGGACGAAGTCGTAACAAGGTAGCCGTACCGGAAG
HQ418468.1 Streptomyces DA1020   1369  CCTTGT GGGAGGG
Streptomyces bikiniensis DSM40   1423  CCTTGT GGGAGGGGAGCTGTCGAAGGTGGGACTGGCGATTGGGACGAAGTCGTAACAAGGTAGCCGTACCGGAAG
N9 4                             1239  --------------------------------------------------------------
N9 6                             1224  --------------------------------------------------------------
Streptomyces tanashiensis HBUM   1386  CCTTGT GGGAGGGAGCTGTCGAAGGTGGGACCAGCGATTGGGACGAAGTCGTAACAAGTAG
DN621                            1202  --------------------------------------------------------------
DN607                            1179  --------------------------------------------------------------
Streptomyces XAS585              1385  CCTTGT GGGAGGGAGCTGTCGAAGGTGGGACCAGCGATTGGGACGAAGTCGAACAA
DN608                            1217  --------------------------------------------------------------
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DN1403                          1220 --------------------------------------------------------------
Streptomyces N01 352  DQ717851  1314 GTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACACCCGAAGCCGGTGGCCC
DN1404                          1202 --------------------------------------------------------------
DN1406                          1194 --------------------------------------------------------------
DN1407                          1201 --------------------------------------------------------------
DN1321                          1206 --------------------------------------------------------------
Streptomyces thermolilacinus N  1323 GTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACACCCGAAGCCGGTGGCCC
Streptomyces heteromorphus  AB  1330 GTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACACCCGAAGCCGGTGGCCC
DN1413                          1199 --------------------------------------------------------------
Streptomyces fragilis NRRL 242  1342 GTGAATACGTTCCC GGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACACCCGAAGCCGGTGGCCC
Streptomyces humidus NRRL B-31  1340 GTGAATACGTTCCC GGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACACCCGAAGCCGGTGGCCC
DN1307                          1230 --------------------------------------------------------------
N14 19                          1252 --------------------------------------------------------------
Streptomyces paraguayensis NBR  1321 GTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACACCCGAAGCCGGTGGCCC
Actinomadura nitritigenes T     1299 GTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGCGAACACCCGAAGCCGTGGCCC
Actinomadura bangladeshensis T  1319 GTGAATACGTTCCCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGCGAACACCCGAAGCCGTGGCCC
Clustal Consensus
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                                        1450      1460      1470      1480      1490      1500      1510
                                     ····|····|····|····|····|····|····|····|····|····|····|····|····|····|····|····|·
DN605                           1209 --------------------------------------------------------------
DN615                           1191 --------------------------------------------------------------
DN618                           1183 --------------------------------------------------------------
 AY999771.1 Streptomyces ciner  1395 CCTTGT GGGAGGGAGCTGTCGAAGGTGGGAC
DN616                           1071 --------------------------------------------------------------
Streptomyces violaceorectus NB  1403 CCTTGT GGGAGGGAGCTGTCGAAGGTGGGACTTGGCGATTGGGACGAAGTCGTAACAAGGTAGCCGTACCGGAAG
HQ418468.1 Streptomyces DA1020  1369 CCTTGT GGGAGGG
Streptomyces bikiniensis DSM40  1423 CCTTGT GGGAGGGAGCTGTCGAAGGTGGGACTTGGCGATTGGGACGAAGTCGTAACAAGGTAGCCGTACCGGAAG
N9 4                            1239 --------------------------------------------------------------
N9 6                            1224 --------------------------------------------------------------
Streptomyces tanashiensis HBUM  1386 CCTTGT GGGAGGGAGCTGTCGAAGGTGGGACCAGCGATTGGGACGAAGTCGTAACAAGTAG
DN621                           1202 --------------------------------------------------------------
DN607                           1179 --------------------------------------------------------------
Streptomyces XAS585            1385 CCTTGT GGGAGGGAGCTGTCGAAGGTGGGACCAGCGATTGGGACGAAGTCGACAA
DN608                           1217 --------------------------------------------------------------
DN606                           1067 --------------------------------------------------------------
Streptomyces DA08605           1398 CCTTGT GGGAGGGAGCTTAGAAGCTGCATCGCGGTC
DN612                           1243 --------------------------------------------------------------
Streptomyces TRI 10  AB448718  1376 CCTTGT GGGAGGGAGCTGTCGAAGGTGGGACTTGGCGATTGGGACG
DN61501                         1337 --------------------------------------------------------------
Streptomyces nodosus NBRC 1289  1402 CCTTGT GGGAGGGAGCTGTCGAAGGTGGGACTTGGCGATTGGGACGAAGTCGTAACAAGGTAGCCGTACCGGAAG
DN617                           1209 --------------------------------------------------------------
Streptomyces ambofaciens NBRC  1398 CCTTGT GGGAGGGAGCTGTCGAAGGTGGGACTTGGCGATTGGGACGAAGTCGTAACAAGGTAGCCGTA
DN1310                          1230 --------------------------------------------------------------
DN1312                          1210 --------------------------------------------------------------
DN1317                          1206 --------------------------------------------------------------
DN1301                          1223 --------------------------------------------------------------
DN1316                          1202 --------------------------------------------------------------
Streptomyces rochei NBRC 12908  1403 CCTTGT GGGAGGGAGCTGTCGAAGGTGGGACTTGGCGATTGGGACGAAGTCGTAACAAGGTAGCCGTACCG
Streptomyces B5W222            1425 CCTTGT GGGAGGGAGCTGTCGAAGGTGGGACTTGGCGATTGGGACGAAGTCGTAACAAGGTAGCCGTACCGGAAG
Streptomyces mutabilis NRRL IS  1405 CCTTGT GGGAGGGAGCTGTCGAAGGTGGGACTTGGCGATTGGGACGAAGTCGTAACAAGGTAGCCGTACCGGAAG
DN1303                          1226 --------------------------------------------------------------
DN1304                          1227 --------------------------------------------------------------
DN1306                          1239 --------------------------------------------------------------
Streptomyces 195018            1380 CCTTGT GGGAGGGAGCTGTCGAAGGTGGGACTTGGCGATTGGACGAAGTCGAACAG
DN1405                          1189 --------------------------------------------------------------
DN1402                          1197 --------------------------------------------------------------
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Streptomyces NO1 352  DQ717851   1393  CCTTGT--GGGAGGGAGCTGTCGAAGGTGGGACT
DN1404                           1202  -------------------------------------
DN1406                           1194  -------------------------------------
DN1407                           1201  -------------------------------------
DN1321                           1206  -------------------------------------
Streptomyces thermolilacinus N   1402  CCTTGC--GGGAGGGAGCTGTCGAAGGTGGGACT
Streptomyces heteromorphus   AB  1409  CCTTGT--GGGAGGGAGCTGTCGAAGGTGGGACT
DN1413                           1199  -------------------------------------
Streptomyces fragilis NRRL 242   1421  CCTTGT--GGGAGGGAGCTGTCGAAGGTGGGACT
Streptomyces humidus NRRL B-31   1419  CCTTGT--GGGAGGGAGCTGTCGAAGGTGGGACT
DN1307                           1230  -------------------------------------
N14 19                           1252  -------------------------------------
Streptomyces paraguayensis NBR   1400  CCCTTGTGGGGAGGGATCGTCGAAGGTGGGACT
Actinomadura nitritigenes T      1378  CTGGTG----GGGGGAGCCGTCGAAGGTGGGCCC
Actinomadura bangladeshensis T   1399  ACCTTGTGTGGCGGGAGCCGTCGAAGGTGGGCCC
Clustal Consensus
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                                                  1530      1540
                                          ....|....|....|....|.
DN605                            1209  -------------------- 1209
DN615                            1191  -------------------- 1191
DN618                            1183  -------------------- 1183
 AY999771.1 Streptomyces ciner   1425  -------------------- 1425
DN616                            1071  -------------------- 1071
Streptomyces violaceorectus NB   1477  -------------------- 1477
HQ418468.1 Streptomyces DA1020   1381  -------------------- 1381
Streptomyces bikiniensis DSM40   1501  GGCTGGATCACCTCCTT---- 1517
N9 4                             1239  -------------------- 1239
N9 6                             1224  -------------------- 1224
Streptomyces tanashiensis HBUM   1446  -------------------- 1446
DN621                            1202  -------------------- 1202
DN607                            1179  -------------------- 1179
Streptomyces XAS585              1440  -------------------- 1440
DN608                            1217  -------------------- 1217
DN606                            1067  -------------------- 1067
Streptomyces DA08605             1433  -------------------- 1433
DN612                            1243  -------------------- 1243
Streptomyces TRI 10  AB448718    1420  -------------------- 1420
DN61501                          1337  -------------------- 1337
Streptomyces nodosus NBRC 1289   1476  -------------------- 1476
DN617                            1209  -------------------- 1209
Streptomyces ambofaciens NBRC    1464  -------------------- 1464
DN1310                           1230  -------------------- 1230
DN1312                           1210  -------------------- 1210
DN1317                           1206  -------------------- 1206
DN1301                           1223  -------------------- 1223
DN1316                           1202  -------------------- 1202
Streptomyces rochei NBRC 12908   1472  -------------------- 1472
Streptomyces B5W222              1503  GGCTGGATCACCTCAATATTC 1523
Streptomyces mutabilis NRRL IS   1483  GG------------------ 1484
DN1303                           1226  -------------------- 1226
DN1304                           1227  -------------------- 1227
DN1306                           1239  -------------------- 1239
Streptomyces 195018              1434  -------------------- 1434
DN1405                           1189  -------------------- 1189
DN1402                           1197  -------------------- 1197
DN1403                           1220  -------------------- 1220
```

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```
                                      1530        1540
                              . . . . | . . . . | . . . . | . . . . | . .
DN605                    1209  ------------------  1209
DN615                    1191  ------------------  1191
DN618                    1183  ------------------  1183
 AY999771.1 Streptomyces ciner  1425  ------------------  1425
DN616                    1071  ------------------  1071
Streptomyces violaceorectus NB  1477  ------------------  1477
HQ418468.1 Streptomyces DA1020  1381  ------------------  1381
Streptomyces bikiniensis DSM40  1501  GGCTGGATCACCTCCTT  1517
N9 4                     1239  ------------------  1239
N9 6                     1224  ------------------  1224
Streptomyces tanashiensis HBUM  1446  ------------------  1446
DN621                    1202  ------------------  1202
DN607                    1179  ------------------  1179
Streptomyces XAS585      1440  ------------------  1440
DN608                    1217  ------------------  1217
DN606                    1067  ------------------  1067
Streptomyces DA08605     1433  ------------------  1433
DN612                    1243  ------------------  1243
Streptomyces TRI 10  AB448718  1420  ------------------  1420
DN61501                  1337  ------------------  1337
Streptomyces nodosus NBRC 1289  1476  ------------------  1476
DN617                    1209  ------------------  1209
Streptomyces ambofaciens NBRC  1464  ------------------  1464
DN1310                   1230  ------------------  1230
DN1312                   1210  ------------------  1210
DN1317                   1206  ------------------  1206
DN1301                   1223  ------------------  1223
DN1316                   1202  ------------------  1202
Streptomyces rochei NBRC 12908  1472  ------------------  1472
Streptomyces B5W222      1503  GGCTGGATCACCTCAATATTC  1523
Streptomyces mutabilis NRRL IS  1483  GG----------------  1484
DN1303                   1226  ------------------  1226
DN1304                   1227  ------------------  1227
DN1306                   1239  ------------------  1239
Streptomyces 195018      1434  ------------------  1434
DN1405                   1189  ------------------  1189
DN1402                   1197  ------------------  1197
DN1403                   1220  ------------------  1220
Streptomyces N01 352  DQ717851  1461  ------------------  1461
DN1404                   1202  ------------------  1202
DN1406                   1194  ------------------  1194
DN1407                   1201  ------------------  1201
DN1321                   1206  ------------------  1206
Streptomyces thermolilacinus N  1476  ------------------  1476
Streptomyces heteromorphus  AB  1483  ------------------  1483
DN1413                   1199  ------------------  1199
Streptomyces fragilis NRRL 242  1499  GG----------------  1500
Streptomyces humidus NRRL B-31  1495  ------------------  1495
DN1307                   1230  ------------------  1230
N14 19                   1252  ------------------  1252
Streptomyces paraguayensis NBR  1468  ------------------  1468
Actinomadura nitritigenes T    1454  GGCTGGATCACCTCCT----  1469
Actinomadura bangladeshensis T  1478  GGCTGGAATCACCTCCTTAT  1497
Clustal Consensus
```

Appendix 5. Multiple sequence aligment of *Streptomyces* strain isolated from *Solenopsis* sp. and related closely species found in Genbank.

Streptomyces 0 3 FJ959370 1
Streptomyces A23 Ydz XM EU368 1
SN1208 1
SN1209 1
Streptomyces nitrosporeus NRRL 1
SN1110 1
Streptomyces coralus cfcc3136 1
Streptomyces CA131 1
SN1114 1
Streptomyces RSF18 EU294139 1
SN1226 1
Streptomyces DA08605 1
N12 28 1
Streptomyces aculeolatus strai 1
SN1202 1
SN1230 1
Actinomadura nitritigenes T 1
Actinomadura bangladeshensis T 1
Clustal Consensus

Note: This is a print preview. It may copy to the clipboard slightly large. To show control panel, press the red arrow (upper left)

Streptomyces gardneri NBRC 128 50
Streptomyces omiyaensis NRRL B 51
SN810 1
SN821 1
Streptomyces lateritius LMG 19 50
Streptomyces zaomyceticus NRRL 56
SN820 20
Streptomyces bikiniensis DSM40 70
SN807 1
Streptomyces gulbargensis T 50
Streptomyces chartreusis NBRC 49
SN709 6
Streptomyces tateyamensis AB4 61
SN710 1
SN805 4
Streptomyces sioyaensis NRRL 56
SN702 1
Streptomyces parvulus NBRC 131 49
Streptomyces tendae T D6387 79
SN1101 17
Streptomyces malachitospinus N 50
SN1104 24
SN1108 29
SN1123 10
Streptomyces paraguayensis 45
SN1212 20
Streptomyces rochei NBRC 12908 49
Streptomyces caelestis T X8 70
SN1210 1
N12 16 21
SN1218 21
SN1222 21
Streptomyces 26
SN1203 21
Streptomyces narbonensis NRRL 76
Streptomyces variabilis NRRL B 66
Streptomyces labedae NBRC 1586 37
Streptomyces collinus NBRC 127 40
SN1125 25
Streptomyces CTDF1 GQ169067 20
Streptomyces sclerotialus DSM 48
SN1213 22
Streptomyces 13638J EU741132 60
SN1219 21
Streptomyces griseoplanus AS 4 32
Streptomyces 195019 GU263883 29
Streptomyces badius NRRL B 256 61
SN1201 21
SN1221 29
Streptomyces 0 3 FJ959370 38
Streptomyces A23 Ydz XM EU368 35
SN1208 22
SN1209 20
Streptomyces nitrosporeus NRRL 51

```
Streptomyces nitrosporeus NRRL     51  CTTCGGGTGGATTAGTGGCGAACGGGTG AGTAACACGTGGGCAATCTGCCCTTCACTCTGGGA
SN1110                             29  CTTCGGTGGGGATTAGTGGCGAACGGGTG AGTAACACGTGGGCAATCTGCCCTTCACTCTGGGA
Streptomyces coralus cfcc3136     47  CTTCGGTGGGGATTAGTGGCGAACGGGTG AGTAACACGTGGGCAATCTGCCCTTCACTCTGGGA
Streptomyces CA131                27  CTTCGGTGGGGATTAGTGGCGAACGGGTG AGTAACACGTGGGCAATCTGCCCTTCACTCTGGGA
SN1114                            31  TTCCGGGAGGGGATTAGTGGCGAACGGGTG AGTAACACGTGGGCAATCTGCCCTGCACTCTGGGA
Streptomyces RSF18  EU294139      45  TTCCGGGAGGGGATTAGTGGCGAACGGGTG AGTAACACGTGGGCAATCTGCCCTGCACTCTGGGA
SN1226                            27  CTTCGGTGGGGATTAGTGGCGAACGGGTG AGTAACACGTGGGCAATCTGCCCTGCACTCTGGGA
Streptomyces DA08605              44  CTTCGGTGGGGATTAGTGGCGAACGGGTG AGTAACACGTGGGCAATCTGCCCTGCACTCTGGGA
N12 28                           22  TTCCGCCGGGGATTAGTGGCGAACGGGTG AGTAACACGTGGGCAATCTGCCCTGCACTCTGGGA
Streptomyces aculeolatus strai    44  TTCCGCCGGGGATTAGTGGCGAACGGGTG AGTAACACGTGGGCAATCTGCCCTGCACTCTGGGA
SN1202                           23  TTCCGCCGGGGATTAGTGGCGAACGGGTG AGTAACACGTGGGCAATCTGCCCTGCACTCTGGGA
SN1230                           23  TTCCGCCGGGGATTAGTGGCGAACGGGTG AGTAACACGTGGGCAATCTGCCCTGCACTCTGGGA
Actinomadura nitritigenes T       32  TTCGGGGTACTCGAGCGGCGAACGGGTG AGTAACACGTGAGCAACCTGCCCTGCACTCTGGGA
Actinomadura bangladeshensis T    52  TTCGGGGTACTCGAGCGGCGAACGGGTGGAGTAACACGTGAGCAACCTGCCCTGACTCTGGGA
Clustal Consensus
```

150

SN701   82
Streptomyces gardneri NBRC 128   129
Streptomyces omixaensis NRRL B   130

Note: This is a print preview. It may copy to the clipboard slightly large. To show control panel, press the red arrow (upper left)

SN821   76
Streptomyces lateritius LMG 19   129
Streptomyces zaomyceticus NRRL   135
SN820   99
Streptomyces bikiniensis DSM40   149
SN807   50
Streptomyces gulbargensis T   129
Streptomyces chartreusis NBRC   128
SN709   85
Streptomyces tateyamensis AB4   140
SN710   78
SN805   83
Streptomyces sioyaensis NRRL   135
SN702   74
Streptomyces parvulus NBRC 131   128
Streptomyces tendae T   D6387   158
SN1101   96
Streptomyces malachitospinus N   129
SN1104   103
SN1108   108
SN1123   89
Streptomyces paraguayensis   124
SN1212   99
Streptomyces rochei NBRC 12908   128
Streptomyces caelestis T   X8   149
SN1210   1
N12 16   100
SN1218   100
SN1222   100
Streptomyces   105
SN1203   100
Streptomyces narbonensis NRRL   155
Streptomyces variabilis NRRL B   145
Streptomyces labedae NBRC 1586   116
Streptomyces collinus NBRC 127   119
SN1125   104
Streptomyces CTDF1 GQ169067   99
Streptomyces sclerotialus DSM   127
SN1213   101
Streptomyces 13638J EU741132   139
SN1219   100
Streptomyces griseoplanus AS 4   111
Streptomyces 195019 GU263883   108
Streptomyces badius NRRL B 256   140
SN1201   100
SN1221   108
Streptomyces O 3 FJ959370   117
Streptomyces A23 Ydz XM EU368   114
SN1208   101
SN1209   99
Streptomyces nitrosporeus NRRL   130
SN1110   108
Streptomyces coralus cfcc3136   126
Streptomyces CA131   106

Streptomyces CA131   106
SN1114   110
Streptomyces RSF18 EU294139   124
SN1226   106
Streptomyces DA08605   123
N12 28   101
Streptomyces aculeolatus strai   123
SN1202   102
SN1230   102
Actinomadura nitritigenes T   111
Actinomadura bangladeshensis T   132
Clustal Consensus

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                                       250      260      270      280      290      300
                              |....|....|....|....|....|....|....|....|....|....|....|....|
SN701                                   160  TATCAGCTTGTTGGTGGGGTAATGGCCCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
Streptomyces gardneri NBRC 128          207  TATCAGCTTGTTGGTGGGGTAATGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
Streptomyces omiyaensis NRRL B          208  TATCAGCTTGTTGGTGGGGTAATGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
SN810                                   154  TATCAGCTTGTTGGTGGGGTAATGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
SN821                                   154  TATCAGCTTGTTGGTGGGGTAATGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
Streptomyces lateritius LMG 19          207  TATCAGCTTGTTGGTGGGGTAATGGCCCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
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Note: This is a print preview. It may copy to the clipboard slightly large. To show control panel, press the red arrow (upper left)

```
SN820                                   177  TATCAGCTTGTTGGTGGGGTAATGGCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
Streptomyces bikiniensis DSM40          227  TATCAGCTTGTTGGTGGGGTAAGGGCCGACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
SN807                                   128  TATCAGCTTGTTGGTGGGGTAAGGGCCGACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
Streptomyces gulbargensis  T            207  TATCAGCTTGTTGGTGGGGTAAGGGCCGACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
Streptomyces chartreusis NBRC           206  TATCAGCTTGTTGGTGAGGGTAATGGCTGACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
SN709                                   164  TATCAGCTTGTTGGTGGGGTGATGGCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
Streptomyces tateyamensis  AB4          219  TATCAGCTTGTTGGTGGGGTGATGGCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
SN710                                   157  TATCAGCTTGTTGGTGGGGTGATGGCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
SN805                                   162  TATCAGCTTGTTGGTGGGGTAATGGCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
Streptomyces sioyaensis NRRL            214  TATCAGCTTGTTGGTGGGGTGATGGCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
SN702                                   153  TATCAGCTTGTTGGTGAGGGTGATGGCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
Streptomyces parvulus NBRC 131          207  TATCAGCTTGTTGGTGAGGTGATGGCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
Streptomyces tendae  T   D6387          237  TATCAGCTTGTTGGTGAGGTAATGGCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
SN1101                                  175  TATCAGCTAGTTGGTGAGGTAATGGCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
Streptomyces malachitospinus N          208  TATCAGCTAGTTGGTGAGGTAATGGCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
SN1104                                  182  TATCAGCTAGTTGGTGAGGTAATGGCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
SN1108                                  187  TATCAGCTTGTTGGTGGGGTGATGGCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
SN1123                                  168  TATCAGCTTGTTGGTGGGGTGATGGCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
Streptomyces paraguayensis              203  TATCAGCTTGTTGGTGGGGTGATGGCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
SN1212                                  177  TATCAGCTTGTTGGTGGGGTCATGGCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
Streptomyces rochei NBRC 12908          207  TATCAGCTAGTTGGTGAGGTAACGGGCTGACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
Streptomyces caelestis  T   X8          228  TATCAGCTTGTTGGTGAGGTAATGGCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
SN1210                                  1
N12 16                                  179  TATCAGCTAGTTGGTGAGGTAACGGGCTGACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
SN1218                                  179  TATCAGCTAGTTGGTGAGGTAAGGGCTGACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
SN1222                                  178  TATCAGCTTGTTGGTGGGGTAATGGCCGACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
Streptomyces                            183  TATCAGCTTGTTGGTGGGGTAATGGCCGACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
SN1203                                  178  TATCAGCTTGTTGGTGGGGTAATGGCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
Streptomyces narbonensis NRRL           233  TATCAGCTTGTTGGTGGGGTAATGGCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
Streptomyces variabilis NRRL B          224  TATCAGCTTGTTGGTGAGGTAATGGCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
Streptomyces labedae NBRC 1586          195  TATCAGCTTGTTGGTGAGGTAATGGCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
Streptomyces collinus NBRC 127          198  TATCAGCTTGTTGGTGAGGTAGTGGCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
SN1125                                  183  TATCAGCTTGTTGGTGGGGTGATGGCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
Streptomyces CTDF1  GQ169067            178  TATCAGCTTGTTGGTGGGGTAATGGCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
Streptomyces sclerotialus DSM           206  TATCAGCTTGTTGGTGGGGTAATGGCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
SN1213                                  179  TATCAGCTTGTTGGTGGGGTAATGGCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
Streptomyces 13638J  EU741132           217  TATCAGCTTGTTGGTGGGGTAATGGCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
SN1219                                  178  TATCAGCTTGTTGGTGGGGTAATGGCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
Streptomyces griseoplanus AS 4          189  TATCAGCTTGTTGGTGGGGTAATGGCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
Streptomyces 195019  GU263883           186  TATCAGCTTGTTGGTGGGGTAATGGCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
Streptomyces badius NRRL B 256          218  TATCAGCTTGTTGGTGGGGTAATGGCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
SN1201                                  178  TATCAGCTTGTTGGTGGGGTAATGGCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
SN1221                                  186  TATCAGCTTGTTGGTGGGGTAATGGCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
Streptomyces O 3  FJ959370              195  TATCAGCTTGTTGGTGGGGTAATGGCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
Streptomyces A23 Ydz XM  EU368          192  TATCAGCTTGTTGGTGGGGTAATGGCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
SN1208                                  179  TATCAGCTTGTTGGTGGGGTAATGGCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
SN1209                                  177  TATCAGCTTGTTGGTGGGGTCATGGCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
Streptomyces nitrosporeus NRRL          208  TATCAGCTTGTTGGTGGGGTCATGGCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
SN1110                                  186  TATCAGCTTGTTGGTGAGGTAACGGGCTGACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
Streptomyces coralus cfcc3136           204  TATCAGCTTGTTGGTGAGGTAATGGCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
Streptomyces CA131                      184  TATCAGCTTGTTGGTGAGGTAATGGCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
SN1114                                  188  TATCAGCTTGTTGGTGGGGTCATGGCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
Streptomyces RSF18  EU294139            202  TATCAGCTTGTTGGTGGGGTGATGGCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
SN1226                                  185  TATCAGCTTGTTGGTGAGGTAATGGCTGACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
```

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SN1226                                  185  TATCAGCTTGTTGGTGAGGTAATGGCTGACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
Streptomyces DA08605                    202  TATCAGCTTGTTGGTGAGGTAACGGGCTGACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
N12 28                                  179  TATCAGCTTGTTGGTGGGGTGATGGCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
Streptomyces aculeolatus strai          201  TATCAGCTTGTTGGTGGGGTGATGGCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
SN1202                                  180  TATCAGCTTGTTGGTGGGGTCATGGCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
SN1230                                  180  TATCAGCTTGTTGGTGGGGTCATGGCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
Actinomadura nitritigenes  T            189  TATCAGCTTGTTGGTGGGGTGATGGCTACCAAGGCGACGACGGGTAACCGGCCTGAGAGGGCGA
Actinomadura bangladeshensis T          210  TATCAGCTTGTTGGTGGGGTGATGGCTACCAAGGCGACGACGGGTAACCGGCCTGAGAGGGCGA
Clustal Consensus
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                              330       340       350       360       370       380
                              |....|....|....|....|....|....|....|....|....|....|....|....|
SN701                     240 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
Streptomyces gardneri NBRC 128 287 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
Streptomyces omiyaensis NRRL B 288 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
SN810                     234 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
SN821                     234 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
Streptomyces lateritius LMG 19 287 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
Streptomyces zaomyceticus NRRL 293 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
SN820                     257 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGGAAGCC
Streptomyces bikiniensis DSM40 307 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGGAAGCC
```

Note: This is a print preview. It may copy to the clipboard slightly large. To show control panel, press the red arrow (upper left)

```
Streptomyces gulbargensis  T  287 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
Streptomyces chartreusis NBRC 286 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
SN709                     244 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
Streptomyces tateyamensis  AB4 299 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
SN710                     237 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
SN805                     242 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
Streptomyces sioyaensis NRRL   294 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
SN702                     233 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
Streptomyces parvulus NBRC 131 287 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
Streptomyces tendae  T   D6387 317 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
SN1101                    255 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
Streptomyces malachitospinus N 288 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
SN1104                    262 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
SN1108                    267 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
SN1123                    248 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
Streptomyces paraguayensis     283 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGTAAGCC
SN1212                    257 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
Streptomyces rochei NBRC 12908 287 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
Streptomyces caelestis  T   X8 308 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
SN1210                      1  -----------------------------------------------------------------
N12 16                    259 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
SN1218                    259 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
SN1222                    258 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
Streptomyces                   263 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
SN1203                    258 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
Streptomyces narbonensis NRRL  313 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAGAAGCC
Streptomyces variabilis NRRL B 304 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
Streptomyces labedae NBRC 1586 275 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
Streptomyces collinus NBRC 127 278 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
SN1125                    263 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
Streptomyces CTDF1  GQ169067  258 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
Streptomyces sclerotialus DSM  286 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
SN1213                    259 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
Streptomyces 13638J  EU741132  297 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
SN1219                    258 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
Streptomyces griseoplanus AS 4 269 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
Streptomyces 195019  GU263883  266 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
Streptomyces badius NRRL B 256 298 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
SN1201                    258 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
SN1221                    266 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
Streptomyces 0 3  FJ959370     275 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
Streptomyces A23 Ydz XM  EU368 272 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
SN1208                    259 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
SN1209                    257 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
Streptomyces nitrosporeus NRRL 288 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
SN1110                    266 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
Streptomyces coralus cfcc3136  284 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
Streptomyces CA131             264 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
SN1114                    268 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
Streptomyces RSF18  EU294139   282 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
SN1226                    265 CTGAGACACGGCCCAAACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
Streptomyces DA08605           282 CTGAGACACGGCCCAAACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
N12 28                    259 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
Streptomyces aculeolatus strai 281 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
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Streptomyces aculeolatus strai 281 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
SN1202                    260 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
SN1230                    260 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCC
Actinomadura nitritigenes T    269 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCCAATGGGCGAAAGCC
Actinomadura bangladeshensis T 290 CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCCAATGGGCGAAAGCC
Clustal Consensus
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                              410       420       430       440       450       460
                         ....|....|....|....|....|....|....|....|....|....|....|....|
SN701                    320 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
Streptomyces gardneri NBRC 128    367 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
Streptomyces omiyaensis NRRL B    368 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAGAGTGACGGT
SN810                    314 GCGTGAGGGACGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
SN821                    314 GCGTGAGGGACGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
Streptomyces lateritius LMG 19    367 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
Streptomyces zaomyceticus NRRL    373 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
SN820                    337 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
Streptomyces bikiniensis DSM40    387 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
SN807                    288 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
Streptomyces gulbargensis  T    367 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
Streptomyces chartreusis NBRC    366 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
SN702                    324 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
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SN710                    317 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGGAAGTGACGGT
SN805                    322 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAGAGTGACGGT
Streptomyces sioyaensis NRRL    374 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAGAGTGACGGT
SN702                    313 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
Streptomyces parvulus NBRC 131    367 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
Streptomyces tendae  T   D6387    397 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
SN1101                   335 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
Streptomyces malachitospinus N    368 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
SN1104                   342 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
SN1108                   347 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGGAAGTGACGGT
SN1123                   328 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
Streptomyces paraguayensis    363 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGGAAGTGACGGT
SN1212                   337 GCGTGAGGGACGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
Streptomyces rochei NBRC 12908    367 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
Streptomyces caelestis  T   X8    388 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
SN1210                   1
M12 16                   339 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
SN1218                   339 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
SN1222                   338 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
Streptomyces             343 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
SN1203                   338 GCGTGAGGGACGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
Streptomyces narbonensis NRRL    393 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
Streptomyces variabilis NRRL B    384 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
Streptomyces labedae NBRC 1586    355 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
Streptomyces collinus NBRC 127    358 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
SN1125                   343 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGGAAGTGACGGT
Streptomyces CTDF1  GQ169067    338 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGGAAGTGACGGT
Streptomyces sclerotialus DSM    366 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGGAAGTGACGGT
SN1213                   339 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
Streptomyces 13638J  EU741132    377 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
SN1219                   338 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
Streptomyces griseoplanus AS 4    349 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
Streptomyces 195019  GU263883    346 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
Streptomyces badius NRRL B 256    378 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
SN1201                   338 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
SN1221                   346 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
Streptomyces O 3  FJ959370    355 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
Streptomyces A23 Ydz XM  EU368    352 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
SN1208                   339 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
SN1209                   337 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
Streptomyces nitrosporeus NRRL    368 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
SN1110                   346 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
Streptomyces coralus cfcc3136    364 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
Streptomyces CA131       344 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
SN1114                   348 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
Streptomyces RSF18  EU294139    362 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
SN1226                   345 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAGAGTGACGGT
Streptomyces DA08605     362 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAGAGTGACGGT
M12 28                   339 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAGAGTGACGGT
Streptomyces aculeolatus strai    361 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAGAGTGACGGT
SN1202                   340 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAGAGTGACGGT
SN1230                   340 GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAGAGTGACGGT
Actinomadura nitritigenes T    349 GCGTGCGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGACGAAGCTAACGTGACGGT
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154

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                              490      500      510      520      530      540
                         ...|....|....|....|....|....|....|....|....|....|....|
SN701                          399 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
Streptomyces gardneri NBRC 128 446 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
Streptomyces omiyaensis NRRL B 447 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
SN810                          393 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
SN821                          393 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
Streptomyces lateritius LMG 19 446 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
Streptomyces zaomyceticus NRRL 452 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
SN820                          416 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
Streptomyces bikiniensis DSM40 466 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
SN807                          367 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
Streptomyces gulbargensis  T   446 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
Streptomyces chartreusis NBRC  445 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
SN709                          403 — ACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAGCGTTGTCCGGAATTAT
Streptomyces tateyamensis  AB4 458 — ACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAGCGTTGTCCGGAATTAT
SN710                          396 — ACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAGCGTTGTCCGGAATTAT
SN805                          401 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAGCGTTGTCCGGAATTAT

Streptomyces sioyaensis NRRL   453 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
SN702                          392 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
Streptomyces parvulus NBRC 131 446 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
Streptomyces tendae  T   D6387 476 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
SN1101                         414 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
Streptomyces malachitospinus N 447 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
SN1104                         421 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
SN1108                         426 — ACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAGCGTTGTCCGGAATTAT
SN1123                         407 — ACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAGCGTTGTCCGGAATTAT
Streptomyces paraguayensis     442 — ACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAGCGTTGTCCGGAATTAT
SN1212                         416 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
Streptomyces rochei NBRC 12908 446 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
Streptomyces caelestis  T   X8 467 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAGCGTTGTCCGGAATTAT
SN1210                         1   —
M12 16                         418 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
SN1218                         418 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
SN1222                         417 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
Streptomyces                   422 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
SN1203                         417 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
Streptomyces narbonensis NRRL  473 — TTAAAGGGTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
Streptomyces variabilis NRRL B 463 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
Streptomyces labedae NBRC 1586 434 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAGCGTTGTCCGGAATTAT
Streptomyces collinus NBRC 127 437 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAGCGTTGTCCGGAATTAT
SN1125                         422 — ACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAGCGTTGTCCGGAATTAT
Streptomyces CTDF1  GQ169067   417 — ACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAGCGTTGTCCGGAATTAT
Streptomyces sclerotialus DSM  445 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
SN1213                         418 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
Streptomyces 13638J  EU741132  456 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
SN1219                         417 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
Streptomyces griseoplanus AS 4 428 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
Streptomyces 195019  GU263883  425 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
Streptomyces badius NRRL B 256 457 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
SN1201                         417 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
SN1221                         425 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
Streptomyces 0 3  FJ959370     434 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
Streptomyces A23 Ydz XM  EU368 431 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
SN1208                         418 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
SN1209                         416 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
Streptomyces nitrosporeus NRRL 447 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
SN1110                         425 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
Streptomyces coralus cfcc3136  443 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
Streptomyces CA131             423 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
SN1114                         427 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
Streptomyces RSF18  EU294139   441 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
SN1226                         424 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAGCGTTGTCCGGAATTAT
Streptomyces DA08605           441 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAGCGTTGTCCGGAATTAT
M12 28                         418 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAGCGTTGTCCGGAATTAT
Streptomyces aculeolatus strai 440 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
SN1202                         419 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
SN1230                         419 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
Actinomadura nitritigenes T    428 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
Actinomadura bangladeshensis T 449 — GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTAT
Clustal Consensus
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Note: This is a print preview. It may copy to the clipboard slightly large. To show control panel, press the red arrow (upper left)

SN701 478
Streptomyces gardneri NBRC 128 525
Streptomyces omiyaensis NRRL B 526
SN810 472
SN821 472
Streptomyces lateritius LMG 19 525
Streptomyces zaomyceticus NRRL 531
SN820 495
Streptomyces bikiniensis DSM40 545
SN807 446
Streptomyces gulbargensis T 525
Streptomyces chartreusis NBRC 524
SN709 482
Streptomyces tateyamensis AB4 537
SN710 475
SN805 480
Streptomyces sioyaensis NRRL 532
SN702 471
Streptomyces parvulus NBRC 131 525

Streptomyces tendae T D6387 555
SN1101 493
Streptomyces malachitospinus N 526
SN1104 500
SN1108 505
SN1123 486
Streptomyces paraguayensis 521
SN1212 495
Streptomyces rochei NBRC 12908 525
Streptomyces caelestis T   X8 546
SN1210 15
N12 16 497
SN1218 497
SN1222 496
Streptomyces 501
SN1203 496
Streptomyces narbonensis NRRL 553
Streptomyces variabilis NRRL B 542
Streptomyces labedae NBRC 1586 513
Streptomyces collinus NBRC 127 516
SN1125 501
Streptomyces CTDF1 GQ169067 496
Streptomyces sclerotialus DSM 524
SN1213 497
Streptomyces 13638J EU741132 535
SN1219 496
Streptomyces griseoplanus AS 4 507
Streptomyces 195019 GU263883 504
Streptomyces badius NRRL B 256 536
SN1201 496
SN1221 504
Streptomyces 0 3 FJ959370 513
Streptomyces A23 Ydz XM EU368 510
SN1208 497
SN1209 495
Streptomyces nitrosporeus NRRL 526
SN1110 504
Streptomyces coralus cfcc3136 522
Streptomyces CA131 502
SN1114 506
Streptomyces RSF18 EU294139 520
SN1226 503
Streptomyces DA08605 520
N12 28 497
Streptomyces aculeolatus strai 519
SN1202 498
SN1230 498
Actinomadura nitritigenes T 507
Actinomadura bangladeshensis T 528
Clustal Consensus 15

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                              650       660       670       680       690       700
                         ....|....|....|....|....|....|....|....|....|....|....|....|
SN701                558  GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCCGGT
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SN1104               580  GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC GGT
SN1108               585  GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC GGT
SN1123               566  GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC GGT
Streptomyces paraguayensis   601  GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC GGT
SN1212               575  GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC GGT
Streptomyces rochei NBRC 12908   605  GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC GGT
Streptomyces caelestis  T   X8   626  GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC GGT
SN1210               95   GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC GGT
N12_16               577  GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC GGT
SN1218               577  GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC GGT
SN1222               576  GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC GGT
Streptomyces         581  GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC GGT
SN1203               576  GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC GGT
Streptomyces narbonensis NRRL   633  GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC GGT
Streptomyces variabilis NRRL B   622  GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC GGT
Streptomyces labedae NBRC 1586   593  GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC GGT
Streptomyces collinus NBRC 127   596  GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC GGT
SN1125               581  GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC GGT
Streptomyces CTDF1  GQ169067   576  GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC GGT
Streptomyces sclerotialus DSM   604  GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC GGT
SN1213               577  GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC GGT
Streptomyces 13638J  EU741132   615  GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC GGT
SN1219               576  GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC GGT
Streptomyces griseoplanus AS 4   587  GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC GGT
Streptomyces 195019  GU263883   584  GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC GGT
Streptomyces badius NRRL B 256   616  GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC GGT
SN1201               576  GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC GGT
SN1221               584  GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC GGT
Streptomyces 0_3  FJ959370   593  GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC GGT
Streptomyces A23 Ydz XM  EU368   590  GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC GGT
SN1208               577  GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC GGT
SN1209               575  GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC GGT
Streptomyces nitrosporeus NRRL   606  GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC GGT
SN1110               584  GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC GGT
Streptomyces coralus cfcc3136   602  GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC GGT
Streptomyces CA131   582  GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC GGT
SN1114               586  GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC GGT
Streptomyces RSF18  EU294139   600  GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC GGT
SN1226               583  GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC GGT
Streptomyces DA08605   600  GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC GGT
N12_28               577  GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAATGCGCAGATATCAGGAGGAACACC GGT
Streptomyces aculeolatus strai   599  GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAATGCGCAGATATCAGGAGGAACACC GGT
SN1202               578  GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAATGCGCAGATATCAGGAGGAACACC GGT
SN1230               578  GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAATGCGCAGATATCAGGAGGAACACC GGT
Actinomadura nitritigenes T   587  GGTAGGGGAGAATGGAATTCCGGGTGTAGCGGTGAAATGCGCAGATCGGGAGGAACACC GGT
Actinomadura bangladeshensis T   608  GGTAGGGGAGAATGGAATTCCGGGTGTAGCGGTGAAATGCGCAGATCGGGAGGAACACC GGT
Clustal Consensus    73   ***********  *******  ***********  **************  *********** ***
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                              730       740       750       760       770       780
                         ....|....|....|....|....|....|....|....|....|....|....|....|
SN701                638  CTGGGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAG
Streptomyces gardneri NBRC 128   684  CTGGGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAG
Streptomyces omiyaensis NRRL B   685  CTGGGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAG
SN810                631  CTGGGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAG
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Streptomyces paraguayensis     660   CTGGGCCGATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTA
SM1212                         654   CTGGGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAG
Streptomyces rochei NBRC 12908 684   CTGGGCCGATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAG
Streptomyces caelestis  T   X8 705   CTGGGCCGATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAG
SM1210                         174   CTGGGCCGATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAG
N12 16                         656   CTGGGCCGATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAG
SM1218                         656   CTGGGCCGATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAG
SM1222                         655   CTGGGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAG
Streptomyces                   660   CTGGGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAG
SM1203                         655   CTGGGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAG
Streptomyces narbonensis NRRL  712   CTGGGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAG
Streptomyces variabilis NRRL B 701   CTGGGCCGATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAG
Streptomyces labedae NBRC 1586 672   CTGGGCCGATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAG
Streptomyces collinus NBRC 127 675   CTGGGCCGATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAG
SM1125                         660   CTGGGCCGATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAG
Streptomyces CTDF1  GQ169067   655   CTGGGCCGATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAG
Streptomyces sclerotialus DSM  683   CTGGGCCGATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAG
SM1213                         656   CTGGGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAG
Streptomyces 13638J  EU741132  694   CTGGGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAG
SM1219                         655   CTGGGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAG
Streptomyces griseoplanus AS 4 666   CTGGGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAG
Streptomyces 195019  GU263883  663   CTGGGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAG
Streptomyces badius NRRL B 256 695   CTGGGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAG
SM1201                         655   CTGGGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAG
SM1221                         663   CTGGGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAG
Streptomyces 0 3  FJ959370     672   CTGGGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAG
Streptomyces A23 Ydz XM  EU368 669   CTGGGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAG
SM1208                         656   CTGGGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAG
SM1209                         654   CTGGGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAG
Streptomyces nitrosporeus NRRL 685   CTGGGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAG
SM1110                         663   CTGGGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAG
Streptomyces coralus cfcc3136  681   CTGGGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAG
Streptomyces CA131             661   CTGGGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAG
SM1114                         665   CTGGGCCGATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAG
Streptomyces RSF18  EU294139   679   CTGGGCCGATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAG
SM1226                         662   CTGGGCCGATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAG
Streptomyces DA08605           679   CTGGGCCGATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAG
N12 20                         656   CTGGGCCGATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCAACAGGATTAGATACCCTGGTAG
Streptomyces aculeolatus strai 678   CTGGGCCGATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCAACAGGATTAGATACCCTGGTAG
SM1202                         657   CTGGGCCGATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCAACAGGATTAGATACCCTGGTAG
SM1230                         657   CTGGGCCGATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCAACAGGATTAGATACCCTGGTAG
Actinomadura nitritigenes T    666   CTGGGCCTGTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAG
Actinomadura bangladeshensis T 687   CTGGGCCTGTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAG
Clustal Consensus              146   *******  ****************************** *************************
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SN701	718	TGGGAACTAGGTGTGGGCGACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTGCCCCG
Streptomyces gardneri NBRC 128	764	TGGGAACTAGGTGTGGGCGACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTGCCCCG
Streptomyces omiyaensis NRRL B	765	TGGGAACTAGGTGTGGGCGACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTGCCCCG
SN810	711	TGGGAACTAGGTGTGGGCGACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTGCCCCG
SN821	711	TGGGAACTAGGTGTGGGCGACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTGCCCCG
Streptomyces lateritius LMG 19	764	TGGGAACTAGGTGTGGGCGACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTGCCCCG
Streptomyces zaomyceticus NRRL	770	TGGGAACTAGGTGTGGGCGACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTGCCCCG

Streptomyces caelestis T X8	785	GTGGGCACTAGGTGTGGGCGACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG
SN1210	254	GTGGGCACTAGGTGTGGGCGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG
N12 16	736	GTGGGCACTAGGTGTGGGCGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG
SN1218	736	GTGGGCACTAGGTGTGGGCGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG
SN1222	735	TGGGGAACTAGGTGTGGGCGACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTGCCCCG
Streptomyces	740	TGGGGAACTAGGTGTGGGCGACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTGCCCCG
SN1203	735	TGGGGAACTAGGTGTGGGCGACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTGCCCCG
Streptomyces narbonensis NRRL	792	TGGGGAACTAGGTGTGGGCGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG
Streptomyces variabilis NRRL B	781	GTGGGCACTAGGTGTGGGCGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG
Streptomyces labedae NBRC 1586	752	GTGGGCACTAGGTGTGGGCGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG
Streptomyces collinus NBRC 127	755	GTGGGCACTAGGTGTGGGCGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG
SN1125	740	TGGGGAACTAGGTGTGGGTGGCATTCCACGTCATCGTGCCGCAGCTAACGCATTAAGTGCCCCG
Streptomyces CTDF1 GQ169067	735	TGGGGAACTAGGTGTGGGTGGCATTCCACGTCATCGTGCCGCAGCTAACGCATTAAGTGCCCCG
Streptomyces sclerotialus DSM	763	TGGGGAACTAGGTGTGGGCGACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTGCCCCG
SN1213	736	TGGGGAACTAGGTGTGGGCGACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTGCCCCG
Streptomyces 13638J EU741132	774	TGGGGAACTAGGTGTGGGCGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG
SN1219	735	TGGGGAACTAGGTGTGGGCGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG
Streptomyces griseoplanus AS 4	746	TGGGGAACTAGGTGTGGGCGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG
Streptomyces 195019 GU263883	743	TGGGGAACTAGGTGTGGGCGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG
Streptomyces badius NRRL B 256	775	TGGGGAACTAGGTGTGGGCGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG
SN1201	735	TGGGGAACTAGGTGTGGGCGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG
SN1221	743	TGGGGAACTAGGTGTGGGCGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG
Streptomyces 0 3 FJ959370	752	TGGGGAACTAGGTGTGGGCGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG
Streptomyces A23 Ydz XM EU368	749	TGGGGAACTAGGTGTGGGCGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG
SN1208	736	TGGGGAACTAGGTGTGGGCGACATTCCACGTCGTCCGTGCCGCA
SN1209	734	TGGGGAACTAGGTGTGGGCGACATTCCACGTCGTCCGTGCCGCA
Streptomyces nitrosporeus NRRL	765	TGGGGAACTAGGTGTGGGCGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG
SN1110	743	GTGGGCACTAGGTGTGGGCGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG
Streptomyces coralus cfcc3136	761	GTGGGCACTAGGTGTGGGCGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG
Streptomyces CA131	741	GTGGGCACTAGGTGTGGGCGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG
SN1114	745	TGGGGCACTAGGTGTGGGCGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG
Streptomyces RSF18 EU294139	759	TGGGGCACTAGGTGTGGGCGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG
SN1226	742	GTGGGCACTAGGTGTGGGCGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG
Streptomyces DA08605	759	GTGGGCACTAGGTGTGGGCGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG
N12 28	736	GTGGGCACTAGGTGTGGGCGGCATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG
Streptomyces aculeolatus strai	758	GTGGGCACTAGGTGTGGGCGGCATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG
SN1202	737	GTGGGCACTAGGTGTGGGCGGCATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG
SN1230	737	GTGGGCACTAGGTGTGGGCGGCATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG
Actinomadura nitritigenes T	746	TGGGCCGCTAGGTGTGGGCGTTCTTCCACGCATCCGCGCCGAGCTAACGCATTAAGCGCCCCG
Actinomadura bangladeshensis T	767	TGGGCCGCTAGGTGTGGGCGTTCTTCCACGCATCCGCGCCGAGCTAACGCATTAAGCGCCCCG
Clustal Consensus		**** ******** ** ******* ** * ***** *

Clustal Consensus   ····· ········· ·· ········ ·· · ···· ·

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                              890    900    910    920    930    940
                              |····|····|····|····|····|····|····|····|····|····|
SN701                    798  CGCAAGGCTAAAACTCACAGGAATTGACGGGGGCCCGCACAAGCAGCGGAGCATGTGGCTTAATT
Streptomyces gardneri NBRC 128  844  CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCAGCGGAGCATGTGGCTTAATT
Streptomyces omiyaensis NRRL B  845  CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCAGCGGAGCATGTGGCTTAATT
SN810                    791  CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCAGCGGAGCATGTGGCTTAATT
SN821                    791  CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCAGCGGAGCATGTGGCTTAATT
Streptomyces lateritius LMG 19  844  CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCAGCGGAGCATGTGGCTTAATT
Streptomyces zaomyceticus NRRL  850  CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCAGCGGAGCATGTGGCTTAATT
SN820                    814  CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCAGCGGAGCATGTGGCTTAATT
Streptomyces bikiniensis DSM40  864  CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCAGCGGAGCATGTGGCTTAATT
SN807                    765  CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCAGCGGAGCATGTGGCTTAATT
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SN1218                      816  CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATT
SN1222                      815  CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCAGCGGAGCATGTGGCTTAATT
Streptomyces                820  CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCAGCGGAGCATGTGGCTTAATT
SN1203                      815  CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCAGCGGAGCATGTGGCTTAATT
Streptomyces narbonensis NRRL   872  CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCAGCGGAGCATGTGGCTTAATT
Streptomyces variabilis NRRL B  861  CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATT
Streptomyces labedae NBRC 1586  832  CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATT
Streptomyces collinus NBRC 127  835  CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATT
SN1125                      820  CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATT
Streptomyces CTDF1  GQ169067   815  CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATT
Streptomyces sclerotialus DSM   843  CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCAGCGGAGCATGTGGCTTAATT
SN1213                      816  CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCAGCGGAGCATGTGGCTTAATT
Streptomyces 13638J  EU741132  854  CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCAGCGGAGCATGTGGCTTAATT
SN1219                      815  CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCAGCGGAGCATGTGGCTTAATT
Streptomyces griseoplanus AS 4  826  CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCAGCGGAGCATGTGGCTTAATT
Streptomyces 195019  GU263883  823  CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCAGCGGAGCATGTGGCTTAATT
Streptomyces badius NRRL B 256  855  CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCAGCGGAGCATGTGGCTTAATT
SN1201                      815  CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCAGCGGAGCATGTGGCTTAATT
SN1221                      823  CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCAGCGGAGCATGTGGCTTAATT
Streptomyces 0 3  FJ959370    832  CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCAGCGGAGCATGTGGCTTAATT
Streptomyces A23 Ydz XM  EU368  829  CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCAGCGGAGCATGTGGCTTAATT
SN1208                      816  CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCAGCGGAGCATGTGGCTTAATT
SN1209                      777
Streptomyces nitrosporeus NRRL  845  CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCAGCGGAGCATGTGGCTTAATT
SN1110                      823  CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCAGCGGAGCATGTGGCTTAATT
Streptomyces coralus cfcc3136   841  CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCAGCGGAGCATGTGGCTTAATT
Streptomyces CA131           821  CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCAGCGGAGCATGTGGCTTAATT
SN1114                      825  CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATT
Streptomyces RSF18  EU294139   839  CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATT
SN1226                      822  CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATT
Streptomyces DA08605         839  CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATT
N12 28                      816  CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCAGCGGAGCATGTGGCTTAATT
Streptomyces aculeolatus strai  838  CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATT
SN1202                      817  CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATT
SN1230                      817  CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATT
Actinomadura nitritigenes T    825  CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATT
Actinomadura bangladeshensis T  846  CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATT
Clustal Consensus
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160

970 980 990 1000 1010 1020

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SN701 878 AACCTTACCAAGGCTTGACATAACCGGAAAGCAT TAGAGATAGGGCCCCCCTTGTGGTCGGTA
Streptomyces gardneri NBRC 128 924 AACCTTACCAAGGCTTGACATAACCGGAAAGCAT TAGAGATAGGGCCCCCCTTGTGGTCGGTA
Streptomyces omiyaensis NRRL B 925 AACCTTACCAAGGCTTGACATAACCGGAAAGCAT TAGAGATAGGGCCCCCCTTGTGGTCGGTA
SN810 871 AACCTTACCAAGGCTTGACATAACCGGAAAGCAT TAGAGATAGGGCCCCCCTTGTGGTCGGTA
SN821 871 AACCTTACCAAGGCTTGACATAACCGGAAAGAT TAGAGATAGGGCCCCCCTTGTGGTCGGTA
Streptomyces lateritius LMG 19 924 AACCTTACCAAGGCTTGACATAACCGGAAAGCAT TAGAGATAGGGCCCCCCTTGTGGTCGGTA
Streptomyces zaomyceticus NRRL 930 AACCTTACCAAGGCTTGACATAACCGGAAAGCAT TAGAGATAGGGCCCCCCTTGTGGTCGGTA
SN820 894 AACCTTACCAAGGCTTGACATAACCGGAAAGCAT CAGAGATGGGGCCCCCCTTGTGGTCGGTA
Streptomyces bikiniensis DSM40 944 AACCTTACCAAGGCTTGACATAACCGGAAAGCAT CAGAGATGGGGCCCCCCTTGTGGTCGGTA
SN807 845 AACCTTACCAAGGCTTGACATAACCGGAAAGCAT TAGAGATAGGGCCCCCCTTGTGGTCGGTA
Streptomyces gulbargensis T 924 AACCTTACCAAGGCTTGACATAACCGGAAAGCAT TAGAGATAGGGCCCCCCTTGTGGTCGGTA
Streptomyces chartreusis NBRC 923 AACCTTACCAAGGCTTGACATAACCGGAAAGCAT TAGAGATAGGGCCCCCCTTGTGGTCGGTA
SN709 881 AACCTTACCAAGGCTTGACATAACCGGAAACCC TGGA

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SN1203 895 AACCTTACCAAGGCTTGACATAACCGGAAAGCAT TAGAGATAGTGCCCCCCTTGTGGTCGGTA
Streptomyces narbonensis NRRL 952 AACCTTACCAAGGCTTGACATAACCGGAAAGCAT CAGAGATGGGGCCCCCTTGTGGTCGGTG
Streptomyces variabilis NRRL B 941 AACCTTACCAAGGCTTGACATAGACCGGAAAGCAT CAGAGATGGGGCCCCCTTGTGGTCGGTG
Streptomyces labedae NBRC 1586 912 AACCTTACCAAGGCTTGACATAGACCGGAAAGCAT CAGAGATGGGGCCCCCTTGTGGTCGGTG
Streptomyces collinus NBRC 127 915 AACCTTACCAAGGCTTGACATAGACCGGAAAGCAT-TAGAGATAGTGCCCCCCTTGTGGTCGGTG
SN1125 900 AACCTTACCAAGGCTTGACATAGACCGGAAAACTC-TGGAGACAGGGTCCCCCTTGTGGTCGGTG
Streptomyces CTDF1 GQ169067 895 AACCTTACCAAGGCTTGACATAGACCGGAAACATC CAGAGATGGGTGCCCCCTTGTGGTCGGTG
Streptomyces sclerotialus DSM 923 AACCTTACCAAGGCTTGACATAGACCGGAAACGTC TGGAGACAGGCGCCCCCTTGTGGTCGGTG
SN1213 896 AACCTTACCAAGGCTTGACATAACCGGAAAGCAT CAGAGATGGGGCCCCCTTGTGGTCGGTA
Streptomyces 13638J EU741132 934 AACCTTACCAAGGCTTGACATAACCGGAAAGCAT CAGAGATGGGGCCCCCTTGTGGTCGGTA
SN1219 895 AACCTTACCAAGGCTTGACATAACCGGAAAGCAT CAGAGATGGGGCCCCCTTGTGGTCGGTA
Streptomyces griseoplanus AS 4 906 AACCTTACCAAGGCTTGACATAACCGGAAAGCAT CAGAGATGGGGCCCCCTTGTGGTCGGTA
Streptomyces 195019 GU263883 903 AACCTTACCAAGGCTTGACATAACCGGAAAGCAT CAGAGATGGGGCCCCCTTGTGGTCGGTA
Streptomyces badius NRRL B 256 935 AACCTTACCAAGGCTTGACATAACCGGAAAGCAT CAGAGATGGGGCCCCCTTGTGGTCGGTA
SN1201 895 AACCTTACCAAGGCTTGACATAACCGGAAAGCAT CAGAGATGGGGCCCCCTTGTGGTCGGTA
SN1221 903 AACCTTACCAAGGCTTGACATAACCGGAAAGCAT CAGAGATGGGGCCCCCTTGTGGTCGGTA
Streptomyces O 3 FJ959370 912 AACCTTACCAAGGCTTGACATAACCGGAAAGCAT CAGAGATGGGGCCCCCTTGTGGTCGGTA
Streptomyces A23 Ydz XM EU368 909 AACCTTACCAAGGCTTGACATAACCGGAAAGCAT CAGAGATGGGGCCCCCTTGTGGTCGGTA
SN1208 896 AACCTTACCAAGGCTTGACATAACCGGAAAGCAT CAGAGATGGGGCCCCCTTGTGGTCGGTA
SN1209 777
Streptomyces nitrosporeus NRRL 925 AACCTTACCAAGGCTTGACATAACCGGAAAGCGC CAGAGATGGGGCCCCCTTGTGGTCGGTG
SN1110 903 AACCTTACCAAGGCTTGACATAGACCGGAAACGGC CAGAGATGGCTGCCCCCTTGTGGTCGGTG
Streptomyces coralus cfcc3136 921 AACCTTACCAAGGCTTGACATAGACCGGAAACGGC CAGAGATGGCTGCCCCCTTGTGGTCGGTG
Streptomyces CA131 901 AACCTTACCAAGGCTTGACATAGACCGGAAACGGC CAGAGATGGCTGCCCCCTTGTGGTCGGTG
SN1114 905 AACCTTACCAAGGCTTGACATAGACCGGAAAGCAT CAGAGATGGGGCCCCCTTGTGGTCGGTG
Streptomyces RSF18 EU294139 919 AACCTTACCAAGGCTTGACATAGACCGGAAAGCAT CAGAGATGGGGCCCCCTTGTGGTCGGTG
SN1226 902 AACCTTACCAAGGCTTGACATAGACCGGAAACGTC TGGAGACAGGCGCCCCCTTGTGGTCGGTG
Streptomyces DA08G05 919 AACCTTACCAAGGCTTGACATAGACCGGAAACGTC TGGAGACAGGCGCCCCCTTGTGGTCGGTG
N12 28 896 AACCTTACCAAGGCTTGACATAGACCGGAAAACCG TGGAGACACGGTCCCCCTTGTGGTCGGTG
Streptomyces aculeolatus strai 918 AACCTTACCAAGGCTTGACATAGACCGGAAAACCG TGGAGACACGGTCCCCCTTGTGGTCGGTG
SN1202 897 AACCTTACCAAGGCTTGACATAGACCGGAAACCCC TGGAGACAGGGGCCCCCTTGTGGTCGGTG
SN1230 897 AACCTTACCAAGGCTTGACATAGACCGGAAACCCC TGGAGACAGGGGCCCCCTTGTGGTCGGTG
Actinomadura nitritigenes T 905 AACCTTACCAAGGCTTGACAT CGCCGGAAAACTCGCAGAGATGCGGGTCCTTTTGGGCCGGT
Actinomadura bangladeshensis T 926 AACCTTACCAAGGCTTGACAT CGCCGGAAATCCCGCAGAGATGCGGGTCCTTTTGGGCCGGT
Clustal Consensus

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                              1050      1060      1070      1080      1090      1100
                         ....|....|....|....|....|....|....|....|....|....|....|....|
SN701                     957 GGT
Streptomyces gardneri NBRC 128   1003 GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCCTG
Streptomyces omiyaensis NRRL B   1004 GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCCTG
SN810                     950 GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCTTG
SN821                     950 GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCTTG
Streptomyces lateritius LMG 19   1003 GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCTTG
Streptomyces zaomyceticus NRRL   1009 GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCTTG
SN820                     973 GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCTTG
Streptomyces bikiniensis DSM40   1023 GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCTTG
SN807                     924 GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCTTG
Streptomyces gulbargensis   T    1003 GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCTTG
Streptomyces chartreusis NBRC    1002 GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCTTG
SN709                     919
Streptomyces tateyamensis  AB4   1015 GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCTTG
SN710                     953 GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCTTG
SN805                     958 GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCTTG
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Note: This is a print preview. It may copy to the clipboard slightly large. To show control panel, press the red arrow (upper left)

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Streptomyces labedae NBRC 1586   991 GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCCGG
Streptomyces collinus NBRC 127   994 GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCCTG
SN1125                    979 GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCTTG
Streptomyces CTDF1  GQ169067     974 GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCTTG
Streptomyces sclerotialus DSM    1002 GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCTTG
SN1213                    975 GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCTTG
Streptomyces 13638J  EU741132    1013 GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCTTG
SN1219                    974 GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCTTG
Streptomyces griseoplanus AS 4   985 GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCTTG
Streptomyces 195019  GU263883    982 GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCTTG
Streptomyces badius NRRL B 256   1014 GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCTTG
SN1201                    974 GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCTTG
SN1221                    982 GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCTTG
Streptomyces O 3  FJ959370       991 GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCTTG
Streptomyces A23 Ydz XM  EU368   988 GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCTTG
SN1208                    975 GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCTTG
SN1209                    777
Streptomyces nitrosporeus NRRL   1004 GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCTTG
SN1110                    982 GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCTTG
Streptomyces coralus cfcc3136    1000 GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCTTG
Streptomyces CA131               980 GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCTTG
SN1114                    984 GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTGTCTTG
Streptomyces RSF18  EU294139     998 GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCGCTGTCTTG
SN1226                    981 GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCCGG
Streptomyces DA08605             998 GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCCGG
N12 28                    975 GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCTTG
Streptomyces aculeolatus strai   997 GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCTTG
SN1202                    976 GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCTTG
SN1230                    976 GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCTTG
Actinomadura nitritigenes T      984 GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTCCA
Actinomadura bangladeshensis T   1005 GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTCCA
Clustal Consensus
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Sequence alignment (positions ~1130–1180)

Taxon	Position
SN701	959
Streptomyces gardneri NBRC 128	1083
Streptomyces omiyaensis NRRL B	1084
SN810	1030
SN821	1030
Streptomyces lateritius LMG 19	1083
Streptomyces zaomyceticus NRRL	1089
SN820	1053
Streptomyces bikiniensis DSM40	1102
SN807	1004
Streptomyces gulbargensis T	1083
Streptomyces chartreusis NBRC	1082
SN709	919
Streptomyces tateyamensis AB4	1095
SN710	1033
SN805	1038
Streptomyces sioyaensis NRRL	1090
SN702	1029
Streptomyces parvulus NBRC 131	1083

Note: This is a print preview. It may copy to the clipboard slightly large. To show control panel, press the red arrow (upper left)

Taxon	Position
Streptomyces CTDF1 GQ169067	1054
Streptomyces sclerotialus DSM	1082
SN1213	1055
Streptomyces 13638J EU741132	1093
SN1219	1054
Streptomyces griseoplanus AS 4	1065
Streptomyces 195019 GU263883	1062
Streptomyces badius NRRL B 256	1094
SN1201	1054
SN1221	1062
Streptomyces O 3 FJ959370	1071
Streptomyces A23 Ydz XM EU368	1068
SN1208	1055
SN1209	777
Streptomyces nitrosporeus NRRL	1084
SN1110	1062
Streptomyces coralus cfcc3136	1080
Streptomyces CA131	1060
SN1114	1063
Streptomyces RSF18 EU294139	1077
SN1226	1061
Streptomyces DA08605	1078
N12 28	1055
Streptomyces aculeolatus strai	1077
SN1202	1056
SN1230	1056
Actinomadura nitritigenes T	1062
Actinomadura bangladeshensis T	1084

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SN1202                          1134 CCCTTATGTCTTGGGCTGCACACGTGCTACAATGGCCGGTACAATGAGCTGCGATACCGCAAGGT
SN1230                          1134 CCCTTATGTCTTGGGCTGCACACGTGCTACAATGGCCGGTACAATGAGCTGCGATACCGCAAGGT
Actinomadura nitritigenes T     1135 CCCTTATGTCTTGGGCTGCAAACATGCTACAATGGCCGGTACAGAGGGCTGCGATACCGTAAGGT
Actinomadura bangladeshensis T  1155 CCCTTATGTCTTGGGCTGCAAACATGCTACAATGGCCGGTACAGAGGGCTGCGATACCGTGAGGT
Clustal Consensus
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                                        1290      1300      1310      1320      1330      1340
                                     ....|....|....|....|....|....|....|....|....|....|....|....|....|
SN701                            959 ---------------------------------------------------------------
Streptomyces gardneri NBRC 128  1241 AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCATGAAGTCGGAGTTGCTAGTAAT
Streptomyces omiyaensis NRRL B  1242 AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCATGAAGTCGGAGTTGCTAGTAAT
SN810                           1049 ---------------------------------------------------------------
SN821                           1087 ---------------------------------------------------------------
Streptomyces lateritius LMG 19  1241 AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCATGAAGTCGGAGTTGCTAGTAAT
Streptomyces zaomyceticus NRRL  1247 AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCATGAAGTCGGAGTTGCTAGTAAT
SN820                           1207 ---------------------------------------------------------------
Streptomyces bikiniensis DSM40  1260 AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCATGAAGTCGGAGTGGCTAGTAAT
SN807                           1162 AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCATGAA
Streptomyces gulbargensis   T   1241 AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCATGAAGTCGGAGTTGCTAGTAAT
Streptomyces chartreusis NBRC   1240 AAGCCTTGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCATGAAGTCGGAGTTGCTAGTAAT
SN709                           919 AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCATGAAGTCGGAGTCGCTAGTAAT
Streptomyces tateyamensis  AB4 1253 AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCATGAAGTCGGAGTCGCTAGTAAT
SN710                           1190 ---------------------------------------------------------------
SN805                           1196 AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCATGAAGTCGGA
Streptomyces sioyaensis NRRL   1248 AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCATGAAGTCGGAGTTGCTAGTAAT
SN702                           1186 AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTC
Streptomyces parvulus NBRC 131 1240 AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCATGAAGTCGGAGTCGCTAGTAAT
Streptomyces tendae   T   D6387 1270 AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCATGAAGTCGGAGTCGCTAGTAAT
SN1101                          1208 AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCATGAAGTCGGAG
Streptomyces malachitospinus N 1241 AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCATGAAGTCGGAGTCGCTAGTAAT
SN1104                          1215 AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCATGAAGTCGGAGTCGCTAGTA
SN1108                          1221 AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCATGAAGTCGGAGT
SN1123                          1202 AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCATGAAGTC
Streptomyces paraguayensis     1237 AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCATGAAGTCGGAGTCGCTAGTAAT
SN1212                          1211 AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCC
Streptomyces rochei NBRC 12908 1240 AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCATGAAGTCGGAGTCGCTAGTAAT
Streptomyces caelestis   T   X8 1261 AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCATGAAGTCGGAGTCGCTAGTAAT
SN1210                          729 AAGTCGGTCTCAGTTCGGATTGGGG TCTGC
N12 16                          1212 AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAA
SN1218                          1212 AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAA
SN1222                          1212 AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACT
Streptomyces                    1217 AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCATGAAGTCGGAGTTGCTAGTAAT
SN1203                          1212 AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGACC
Streptomyces narbonensis NRRL  1269 AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCATGAAGTCGGAGTTGCTAGTAAT
Streptomyces variabilis NRRL B 1257 AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCATGAAGTCGGAGTCGCTAGTAA
Streptomyces labedae NBRC 1586 1228 AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCATGAAGTCGGAGTCGCTAGTAA
Streptomyces collinus NBRC 127 1231 AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCATGAAGTCGGAGTCGCTAGTAA
SN1125                          1217 AAGCCGGTCTCAGTTCGGATTGGGG TCTGC
Streptomyces CTDF1  GQ169067   1212 AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCATGAAGTCGGAGTCGCTAGTAAT
Streptomyces sclerotialus DSM  1240 AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCATGAAGTCGGAGTCGCTAGTAAT
SN1213                          1213 AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGAC
Streptomyces 13638J  EU741132  1251 AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCATGAAGTCGGAGTTGCTAGTAAT
SN1219                          1212 AAGCCGGTCTCAGTTCGGATTGGGG TCT
Streptomyces griseoplanus AS 4 1223 AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCATGAAGTCGGAGTTGCTAGTAAT
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Streptomyces 195019 GU263883	1220	AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCATGAAGTCGGAGTTGCTAGTAAT
Streptomyces badius NRRL B 256	1252	AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCATGAAGTCGGAGTTGCTAGTAAT
SN1201	1212	AAGCCGGTCTCAGTTCGGATTGGGG TCT
SN1221	1220	AAGCCGGTCTCAGTTCGGAT
Streptomyces 0 3 FJ959370	1229	AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCATGAAGTCGGAGTTGCTAGTAAT
Streptomyces A23 Ydz XM EU368	1226	AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCATGAAGTCGGAGTTGCTAGTAAT
SN1208	1213	AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCAT
SN1209	777	
Streptomyces nitrosporeus NRRL	1242	AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCATGAAGTCGGAGTTGCTAGTAAT
SN1110	1220	AAGCCTGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCA
Streptomyces coralus cfcc3136	1238	AAGCCTGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCATGAAGTCGGAGTTGCTAGTAAT
Streptomyces CA131	1218	AAGCCTGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCATGAAGTCGGAGTTGCTAGTAAT
SN1114	1215	AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCATGAAGTCGGAGTCGGCTA
Streptomyces RSF18 EU294139	1229	AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCATGAAGTCGGAGTCGGCTAGTAAT
SN1226	1218	AAGCCGGTCTCAGTTCGGATTGGGG TCTG
Streptomyces DA08605	1235	AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCATGAAGTCGGAGTCGGCTAGTAAT
N12 28	1215	AAGCCGGTCTCAGTTCGGAT
Streptomyces aculeolatus strai	1237	AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCATGAAGTCGGAGTCGGCTAGTAAT
SN1202	1214	AAGCCGGTCTCAGTTCGGATTGGGGGTCTGCAACTCGA
SN1230	1214	AAGCCGGTCTCAGTTCGGATTGGGGGTCTGCAACTCGA
Actinomadura nitritigenes T	1215	AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCATGAAGTCGGAGTCGGCTAGTAAT
Actinomadura bangladeshensis T	1235	AAGCCGGTCTCAGTTCGGATCGAAG TCTGCAACTCGACTTCGGTGAAGTCGGAGTCGGCTAGTAAT
Clustal Consensus		

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                              1370      1380      1390      1400      1410      1420
                         ....|....|....|....|....|....|....|....|....|....|....|....|
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SN701	959	
Streptomyces gardneri NBRC 128	1320	CTGCGGTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACAC
Streptomyces omiyaensis NRRL B	1321	CTGCGGTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACAC
SN810	1049	
SN821	1087	
Streptomyces lateritius LMG 19	1320	CTGCGGTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACAC
Streptomyces zaomyceticus NRRL	1326	CTGCGGTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACAC
SN820	1207	
Streptomyces bikiniensis DSM40	1339	CTGCGGTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACAC
SN807	1207	
Streptomyces gulbargensis T	1320	CTGCGGTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACAC
Streptomyces chartreusis NBRC	1319	CTGCGGTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACAC
SN709	919	
Streptomyces tateyamensis AB4	1332	CTGCGGTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACAC
SN710	1190	
SN805	1247	
Streptomyces sioyaensis NRRL	1327	CTGCGGTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACAC
SN702	1220	
Streptomyces parvulus NBRC 131	1319	CTGCGGTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACAC
Streptomyces tendae T D6387	1349	CTGCGGTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACAC
SN1101	1260	
Streptomyces malachitospinus N	1320	CTGCGGTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACAC
SN1104	1276	
SN1108	1274	
SN1123	1250	
Streptomyces paraguayensis	1316	CTGCGGTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACAC
SN1212	1251	
Streptomyces rochei NBRC 12908	1319	CTGCGGTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACAC
Streptomyces caelestis T X8	1340	CTGCGGTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACAC
SN1210	758	
N12 16	1243	
SN1218	1243	
SN1222	1245	
Streptomyces	1296	CTGCGGTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACAC
SN1203	1250	
Streptomyces narbonensis NRRL	1348	CTGCGGTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACAC
Streptomyces variabilis NRRL B	1336	CTGCGGTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACAC
Streptomyces labedae NBRC 1586	1307	CTGCGGTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACAC
Streptomyces collinus NBRC 127	1310	CTGCGGTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACAC
SN1125	1246	
Streptomyces CTDF1 GQ169067	1291	CTGCGGTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACAC
Streptomyces sclerotialus DSM	1319	CTGCGGTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACAC
SN1213	1250	
Streptomyces 13638J EU741132	1330	CTGCGGTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACAC
SN1219	1239	
Streptomyces griseoplanus AS 4	1302	CTGCGGTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACAC
Streptomyces 195019 GU263883	1299	CTGCGGTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACAC
Streptomyces badius NRRL B 256	1331	CTGCGGTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACAC
SN1201	1239	

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SN1221                            1239
Streptomyces 0 3  FJ959370        1308 CTGCGGTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACAC
Streptomyces A23 Ydz XM  EU368    1305 CTGCGGTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACAC
SN1208                            1255
SN1209                             777
Streptomyces nitrosporeus NRRL   1321 CTGCGGTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACAC
SN1110                            1261
Streptomyces coralus cfcc3136    1317 CTGCGGTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACAC
Streptomyces CA131                1297 CTGCGGTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACAC
SN1114                            1273
Streptomyces RSF18  EU294139     1308 CTGCGGTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACAC
SN1226                            1246
Streptomyces DA08605             1314 CTGCGGTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACAC
N12 28                            1234
Streptomyces aculeolatus strai   1316 CTGCGGTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACAC
SN1202                            1251
SN1230                            1251
Actinomadura nitritigenes T      1294 CTGCGGTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGGAACAC
Actinomadura bangladeshensis T   1314 CTGCGGTGAATACGTTCCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGGAACAC
Clustal Consensus
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                                         1450      1460      1470      1480      1490      1500
                                      ...|....|....|....|....|....|....|....|....|....|....|....|....|
SN701                             959
Streptomyces gardneri NBRC 128   1399 CAACCCCTTGT  GGGAGGGAGCTGTCGAAGGTGGGACTGGCGATTGGGACGAAG
Streptomyces omiyaensis NRRL B   1400 CAACCCCTTGT  GGGAGGGAGCTGTCGAAGGTGGGACCAGCGATTGGGACGAAGTCGTAACAA
SN810                            1049
SN821                            1087
Streptomyces lateritius LMG 19   1399 CAACCCCTTGT  GGGAGGGAGCTGTCGAAGGTGGGACTGGCGATTGGGACGAAGTCGTAACAA
Streptomyces zaomyceticus NRRL   1405 CAACCCCTTGT  GGGAGGGAACTGTCGAAGGTGGGACTGGCGATTGGGACGAAGTCGTAACAA
SN820                            1207
Streptomyces bikiniensis DSM40   1418 CAACCCCTTGT  GGGAGGGAGCTGTCGAAGGTGGGACTGGCGATTGGGACGAAGTCGTAACAA
SN807                            1207
Streptomyces gulbargensis  T     1399 CAACCCCTTGT  GGGAGGGAGCTGTCGAAGGTGGGACTGGCGATTGGGACGAAGTCGTAACAA
Streptomyces chartreusis NBRC    1398 CAACCCCTTGT  GGGAGGGAGCTGTCGAAGGTGGGACTGGCGATTGGGACGAAGTCGTAACAA
SN709                             919
Streptomyces tateyamensis  AB4   1411 CAACCCTTGTG  GGGCGAACCGTCGAAGGTGGGACTGGCGATTGGGACGAAGTCGT
SN710                            1190
SN805                            1247
Streptomyces sioyaensis NRRL     1406 CAACCCCTTGT  GGGAGGGAATCGTCGAAGGTGGGACTGGCGATTGGGACGAAGTCGTAACAA
SN702                            1220
Streptomyces parvulus NBRC 131   1398 CAACCCCTTGT  GGGAGGGAGCTGTCGAAGGTGGGACTGGCGATTGGGACGAAGTCGTAACAA
Streptomyces tendae  T   D6387   1428 CAACCCCTTGT  GGGAGGGAGCTGTCGAAGGTGGGACTGGCGATTGGGACGAAGTCGTAACAA
SN1101                           1260
Streptomyces malachitospinus N   1399 CAACCCCTTGT  GGGAGGGAGCTGTCGAAGGTGGGACTGGCGATTGGGACGAAGTC  TAACAA
SN1104                           1276
SN1108                           1274
SN1123                           1250
Streptomyces paraguayensis       1395 CAACCCGCTTGT GGGGAGGGAATCGTCGAAGGTGGGACTGGCGATTGGGACGAAGTCGTAACAA
SN1212                           1251
Streptomyces rochei NBRC 12908   1398 CAACCCCTTGT  GGGAGGGAGCTGTCGAAGGTGGGACTGGCGATTGGGACGAAGTCGTAACAA
Streptomyces caelestis  T   X8   1419 CAACCCCTTGT  GGGAGGGAGCTGTCGAAGGTGGGACTGGCGATTGGGACGAAGTCGTAACAA
SN1210                            758
N12 16                           1243
SN1218                           1243
SN1222                           1245
Streptomyces                     1375 CAACCCCTTGTG GCAGCCAT
SN1203                           1250
Streptomyces narbonensis NRRL    1427 CAACCCCTTGT  GGGAGGGAGCTGTCGAAGGTGGGACTGGCGATTGGGACGAAGTCGTAACAA
Streptomyces variabilis NRRL B   1415 CAACCCCTTGT  GGGAGGGAGCTGTCGAAGGTGGGACTGGCGATTGGGACGAAGTCGTAACAA
Streptomyces labedae NBRC 1586   1386 CAACCCCTTGT  GGGAGGGAGCTGTCGAAGGTGGGACTGGCGATTGGGACGAAGTCGTAACAA
Streptomyces collinus NBRC 127   1389 CAACCCCTTGT  GGGAGGGAGCTGTCGAAGGTGGGACTGGCGATTGGGACGAAGTCGTAACAA
SN1125                           1246
Streptomyces CTDF1  GQ169067     1370 TAACCCGCTTGTGGGGAGGGAATCGTCGAAGGTGGACGC
Streptomyces sclerotialus DSM    1398 CAACCCCTTGT  GGGAGGGAATCGTCGAAGGTGGGACTGGCGATTGGGACGAAGTCGTAACAA
SN1213                           1250
Streptomyces 13638J  EU741132    1409 CAACCCCTTGT  GGGAGGGAGCTGTCGAAGGTGGGACTGGCGATTGGGACGAAGTCGTAACAA
SN1219                           1239
Streptomyces griseoplanus AS 4   1381 CAACCCCTTGT  GGGAGGGAGC
Streptomyces 195019  GU263883    1378 CAACCCCTTGT  GGGAGGGAGCTGTCGAAGGTGGGACTGGCGATTGGGACGAAGTCGAACAG
Streptomyces badius NRRL B 256   1410 CAACCCCTTGT  GGGAGGGAGCTGTCGAAGGTGGGACTGGCGATTGGGACGAAGTCGTAACAA
SN1201                           1239
SN1221                           1239
Streptomyces 0 3  FJ959370       1387 CAACCCCTGTGGGAGGAGCCTCACGAGAGAAGAAA
Streptomyces A23 Ydz XM  EU368   1384 CAACCCCTTGT  GGGAGGGAGCTGTCGAAGGTGGGACTGGCGATTGGGACGAAGTCGTAACAA
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SN1208                        1255  -----------------------------------------
SN1209                        777   -----------------------------------------
Streptomyces nitrosporeus NRRL 1400  CAACCCCTTGT---GGGAGGGAGCTGTCGAAGGTGGGACTGGCGATTGGGACGAAGTCGTAACAA
SN1110                        1261  -----------------------------------------
Streptomyces coralus cfcc3136 1396  CAACCCCGTTGT-GGGGAGGGAGCTGTCGAAGGTGGGACTGGCGATTGG-ACGAAGTCG-AACAA
Streptomyces CA131            1376  CAACCCCGTTGT-GGGGAGGGAGCGTGTCGAAGGTGGGACTGGCGATTGGGACGAAGTCGACAGGC
SN1114                        1273  -----------------------------------------
Streptomyces RSF18  EU294139  1387  CAACCGTGGGAGGAGCCTCGAAGGGGAGCCCT---------------------------------
SN1226                        1246  -----------------------------------------
Streptomyces DA08605          1393  CAACCCCTTGT---GGGAGGGAGCTTAGAAGCTGGATCGCGGTC---------------------
N12 28                        1234  -----------------------------------------
Streptomyces aculeolatus strai 1395  CAACCGTTGT----GGAGGGAGCGTCGAAGGTGGGACTGGCGATTGGGACGAAGTCGTAACAA
SN1202                        1251  -----------------------------------------
SN1230                        1251  -----------------------------------------
Actinomadura nitritigenes T   1373  CAACCGTTGT----GGCGGGAGCGTCGAAGGTGGGCCGGCGATTGGGACGAAGTCGTAACAA
Actinomadura bangladeshensis T 1394  CAACCAGCTTGT-GTGGCGGGAGCGTCGAAGGTGGGCCGGCGATTGGGACGAAGTC TAACAA
Clustal Consensus
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                                              1530      1540
                                      ....|....|....|....|....|.
SN701                         959                                      959
Streptomyces gardneri NBRC 128 1451                                    1451
Streptomyces omiyaensis NRRL B 1477  AGGTGC-----------------------    1482
SN810                         1049                                    1049
SN821                         1087                                    1087
Streptomyces lateritius LMG 19 1476  AGG--------------------------    1478
Streptomyces zaomyceticus NRRL 1482  AGGTGC-----------------------    1487
SN820                         1207                                    1207
Streptomyces bikiniensis DSM40 1495  AGGTGCGGCTGGATCACCTCCTT------    1517
SN807                         1207                                    1207
Streptomyces gulbargensis  T  1476  AG---------------------------    1477
Streptomyces chartreusis NBRC 1475  AGG--------------------------    1477
SN709                         919                                      919
Streptomyces tateyamensis  AB4 1465                                    1465
SN710                         1190                                    1190
SN805                         1247                                    1247
Streptomyces sioyaensis NRRL  1470                                    1470
SN702                         1220                                    1220
Streptomyces parvulus NBRC 131 1475  NC---------------------------    1476
Streptomyces tendae  T   D6387 1505  AGGTGCGGCTGGATCACCTCCTTTGT---    1530
SN1101                        1260                                    1260
Streptomyces malachitospinus N 1468                                    1468
SN1104                        1276                                    1276
SN1108                        1274                                    1274
SN1123                        1250                                    1250
Streptomyces paraguayensis    1468                                    1468
SN1212                        1251                                    1251
Streptomyces rochei NBRC 12908 1472                                    1472
Streptomyces caelestis  T   X8 1496  AGGTGCGGCTGGATCACCTCCTT------    1518
SN1210                        758                                      758
N12 16                        1243                                    1243
SN1218                        1243                                    1243
SN1222                        1245                                    1245
Streptomyces                  1394                                    1394
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SN1218                        1243 ----------------------------------- 1243
SN1222                        1245 ----------------------------------- 1245
Streptomyces                  1394 ----------------------------------- 1394
SN1203                        1250 ----------------------------------- 1250
Streptomyces narbonensis NRRL 1504 AGGTGCG---------------------------- 1510
Streptomyces variabilis NRRL B 1492 AGGTGCGG--------------------------- 1499
Streptomyces labedae NBRC 1586 1454 ----------------------------------- 1454
Streptomyces collinus NBRC 127 1459 ----------------------------------- 1459
SN1125                        1246 ----------------------------------- 1246
Streptomyces CTDF1  GQ169067  1409 ----------------------------------- 1409
Streptomyces sclerotialus DSM 1475 AGGTGCGGCTGGATCACCTCCTTT-- 1498
SN1213                        1250 ----------------------------------- 1250
Streptomyces 13638J  EU741132 1486 AGTGCGGC-------------------------- 1493
SN1219                        1239 ----------------------------------- 1239
Streptomyces griseoplanus AS 4 1401 ----------------------------------- 1401
Streptomyces 195019  GU263883 1438 ----------------------------------- 1438
Streptomyces badius NRRL B 256 1487 AGGTGCGGCT------------------------ 1496
SN1201                        1239 ----------------------------------- 1239
SN1221                        1239 ----------------------------------- 1239
Streptomyces 0 3  FJ959370    1421 ----------------------------------- 1421
Streptomyces A23 Ydz XM  EU368 1452 ----------------------------------- 1452
SN1208                        1255 ----------------------------------- 1255
SN1209                        777  ----------------------------------- 777
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Note: This is a print preview. It may copy to the clipboard slightly large. To show control panel, press the red arrow (upper left)

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SN1110                        1261 ----------------------------------- 1261
Streptomyces coralus cfcc3136 1473 G--------------------------------- 1473
Streptomyces CA131            1441 ----------------------------------- 1441
SN1114                        1273 ----------------------------------- 1273
Streptomyces RSF18  EU294139  1418 ----------------------------------- 1418
SN1226                        1246 ----------------------------------- 1246
Streptomyces DA08605          1433 ----------------------------------- 1433
N12 28                        1234 ----------------------------------- 1234
Streptomyces aculeolatus strai 1455 ----------------------------------- 1455
SN1202                        1251 ----------------------------------- 1251
SN1230                        1251 ----------------------------------- 1251
Actinomadura nitritigenes T   1448 AGGTGCGGCTGGATCACCTCCT 1469
Actinomadura bangladeshensis T 1472 AGGTGCGGCTGGAATCACCTCCTAAT 1497
Clustal Consensus
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