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

By

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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 cultureindependent 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.

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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. Leifsonia. Pseudonocardia, Corynebacterium, Microbacterium, 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.

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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 Grampositive 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 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 (EI-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.

(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, 2008).

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 μ l of sterile distilled water, vortexed for 30 seconds and then macerated. 100 μ l of the solution was plated on chitin medium (Appendix 1) and incubated for 15 days at 25°C. Act inobacteria 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
<i>Dorymyrmex</i> 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 (37°) (Goodfellow and Williams, 2003; Maier and Gerba, 2009, Murphy and Iugo, 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.

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

Table 4. Actinobacteria associated with ants in Cambalache Forest.

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 Iugo, 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 (17° 57.222 N, 066° 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 (17° 57.060 N, 066° 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

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°C; co lonies were transferred and purified in Yeast Malt Extract Medium (YMEA) and incubated for several days at 25°C 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 37°C. DNA extraction was performed with the CTAB method, with a chloroform extraction step and followed by isopropanol (-20°C) 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 ddH₂O, 5X colorless *GoTaq*® Reaction Buffer (Promega Corp., Madison, WI), MgCl₂ 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 95°C for 3 minutes for an initial denaturalization step. thirty cycles consisted of 95°C for 45 seconds for denaturalization, 50°C for 45 minutes for annealing, 72°C for 1:30 seconds for polymerization. A final extension step of seven minutes at 72°C. 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 -20°C 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 resupended in 100 ul TE buffer 1/10X and heated at 95°C 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 18°C. 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_20 . 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 made (Bonferroni correction) were (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.

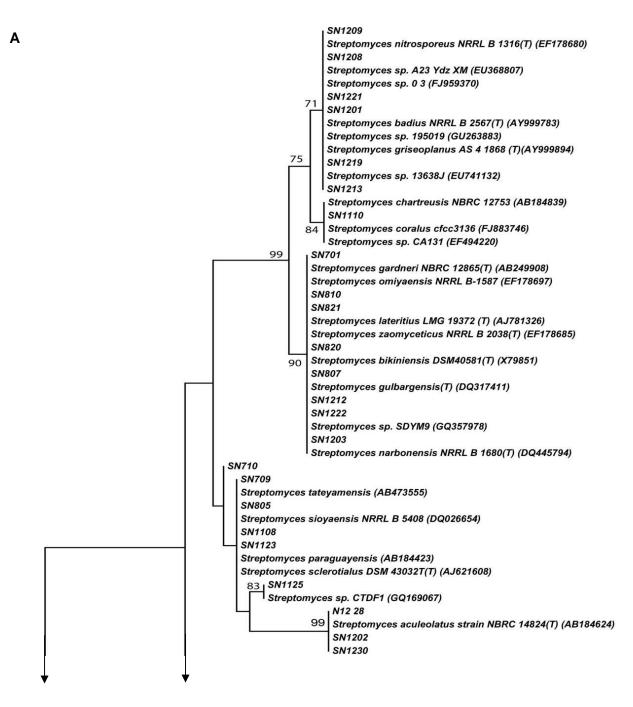


Figure 3. Neighbor-Joining tree based of 16S rRNA gene sequences (1000-1350pb) from cultured *Streptomyces* isolated from *Solenopsis* sp. ant and closely related species found in GenBank (accession number in parethesis). The numbers at the nodes indicate bootstrap support values (>50%) based on analysis 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.

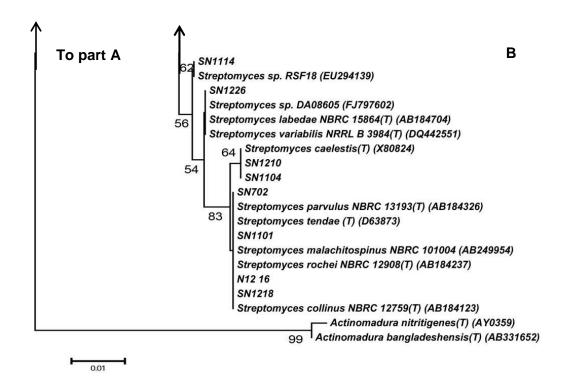


Figure 3. continued.

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.

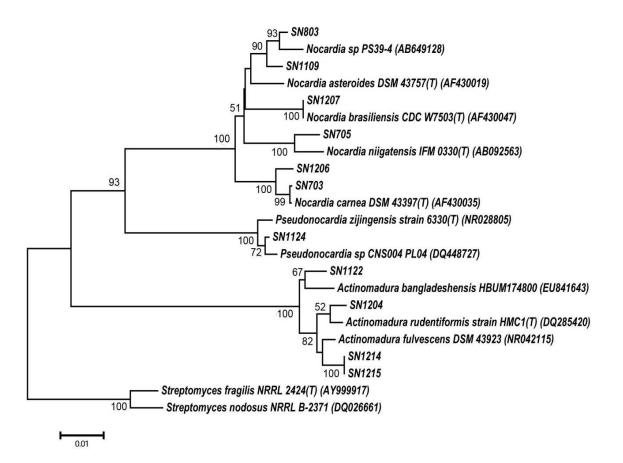


Figure 4. Neighbor-Joining tree based of 16S rRNA gene sequences (1000-1350pb) from cultured Actinobacteria isolated from *Solenopsis* sp. ant and closely related species found in GenBank (accession number in parethesis). The numbers at the nodes indicate bootstrap support values (>50%) based on analysis 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*,

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.

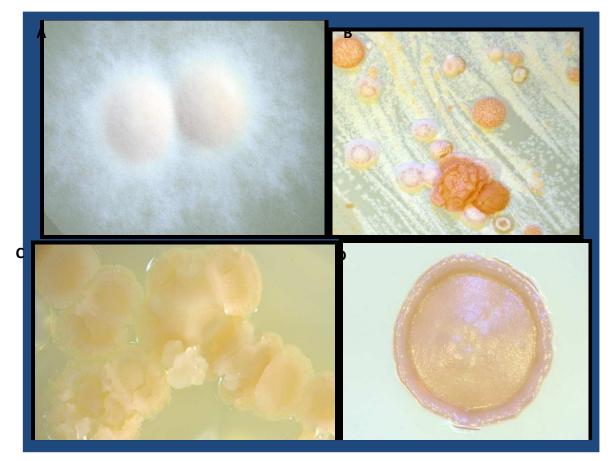
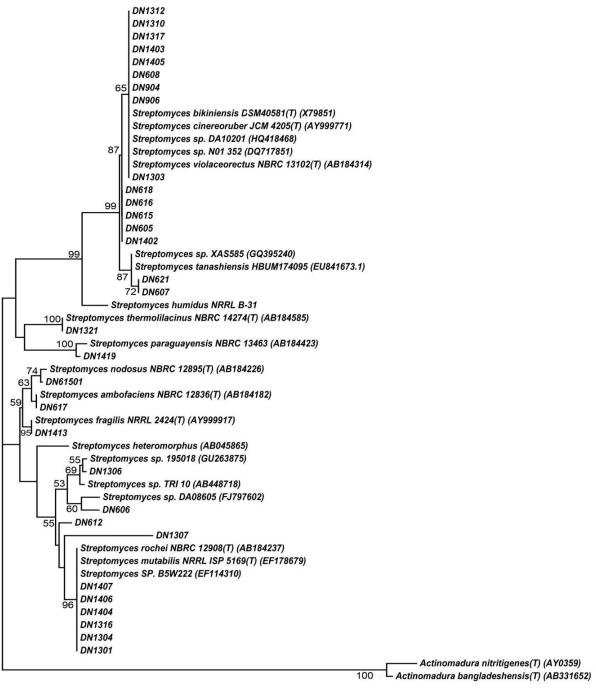


Figure 7. Colony morphology of the Actinobacteria isolated from *Solenopsis* sp. ants. A: *Nocardia* sp. strain SN1109, B: *Nocardia* sp. strain SN1206, C: *Actinomadura* sp. strain SN1204, D: *Actinomadura* sp. strain SN1214.

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



0.01

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).

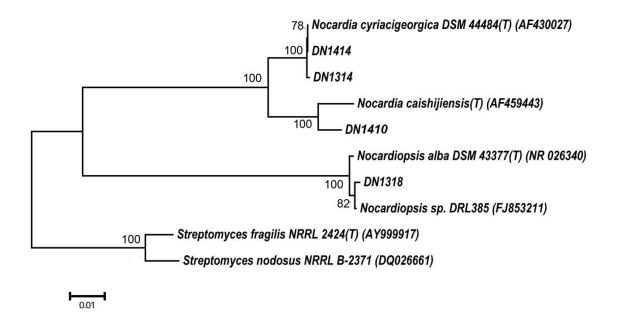


Figure 9. Neighbor-Joining tree based of 16S rRNA gene sequences (1000-1350pb) from cultured Actinobacteria isolated from *Dorymyrmex* sp. ants. in GenBank (accession number in parethesis). The numbers at the nodes indicate bootstrap support values (>50%) based on analysis of 1000 pseudoreplicates. The 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).

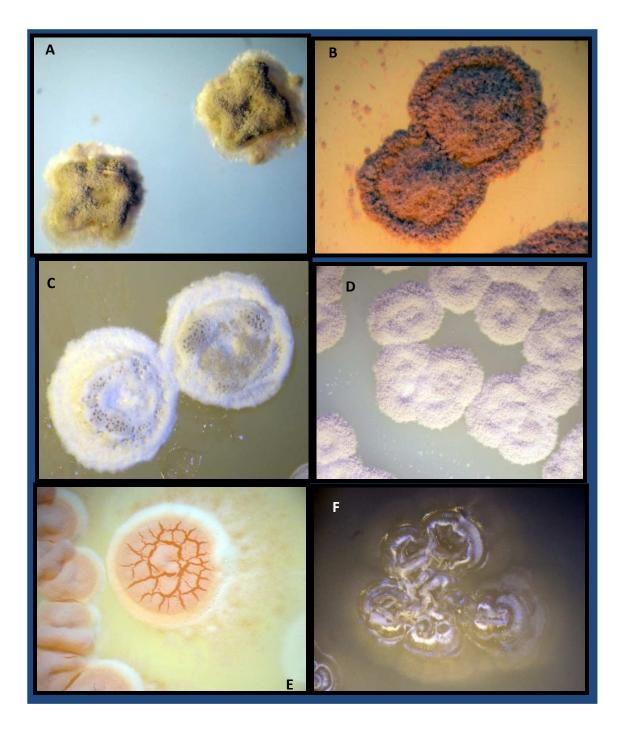


Figure 10. Colony morphology of Actinobacteria isolated from *Dorymyrmex* sp. ants. A: *Streptomyces* sp. strain DN1403, B: *Streptomyces* sp. strain DN1316, C: *Streptomyces* sp. strain DN1405, D: *Streptomyces* sp. strain DN1404, E: *Nocardia* sp. strain DN1410, F: *Streptomyces* sp. DN1410

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).

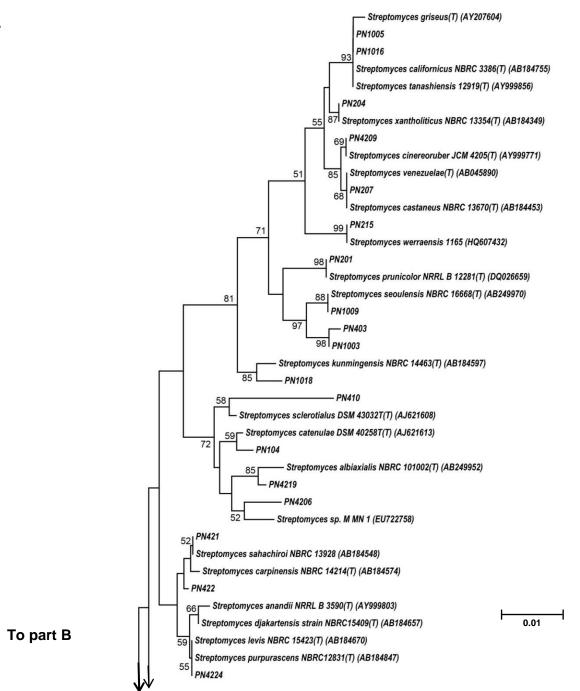


Figure 11. A. Neighbor-Joining tree based of 16S rRNA gene sequences (1000-1350pb) from cultured *Streptomyces* isolated from *Paratrechina* sp. ants and closely related species found in GenBank (accession number in parethesis). The numbers at the nodes indicate bootstrap support values (>50%) based 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.

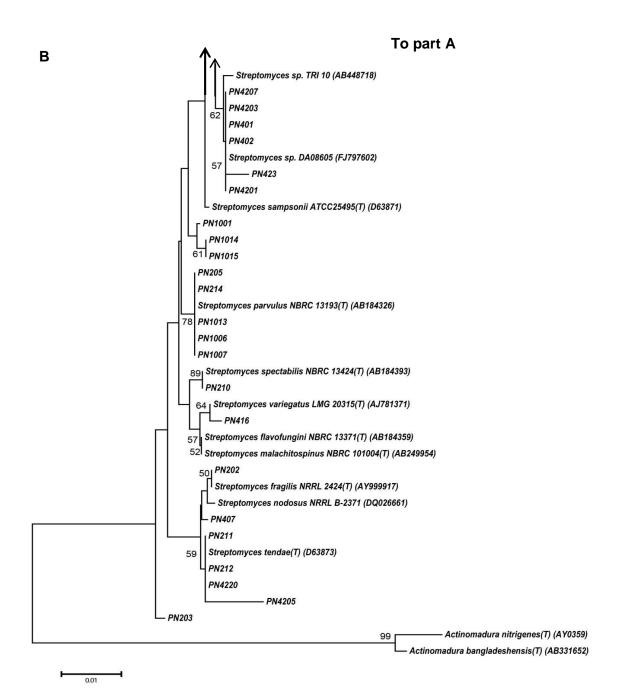


Figure 11 B. continued.

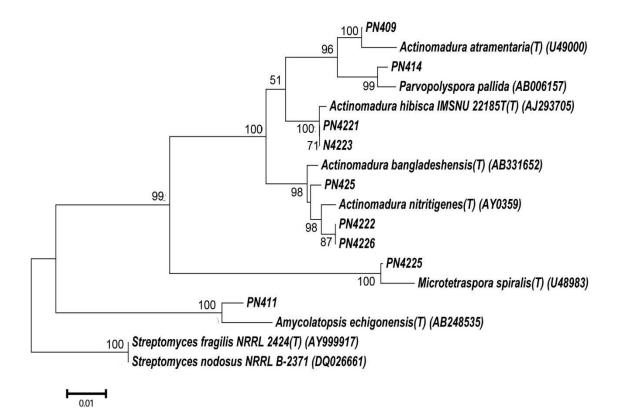


Figure 12. Neighbor-Joining tree based of 16S rRNA gene sequences (1000-1350pb) from cultured Actinobacteria isolated from *Paratrechina* sp. ants and closely related species found in GenBank (accession number in parethesis). The numbers at the nodes indicate bootstrap support values (>50%) based on 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.

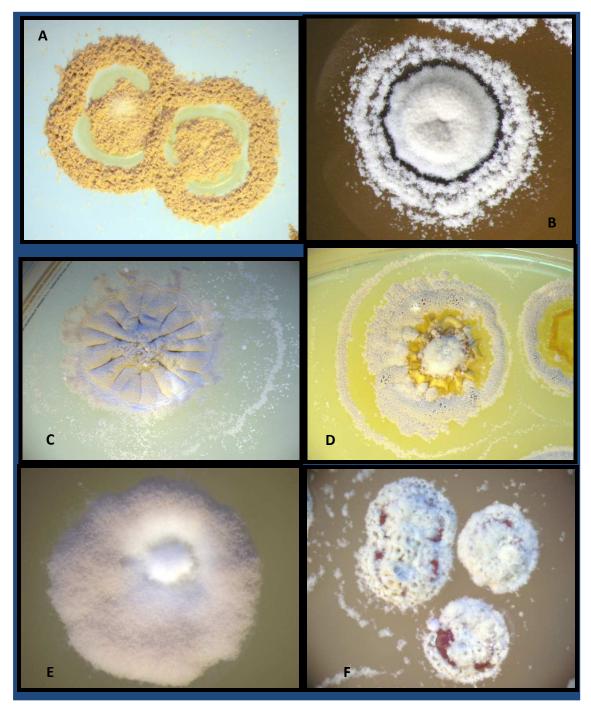


Figure 13. Colony morphology of the Actinobacteria isolated from *Paratrechina* sp. ants. A: *Streptomyces* sp. strain PN212, B: *Streptomyces* sp. strain PN4206, C: *Streptomyces* sp. strain PN1003, D: *Streptomyces* sp. strain PN1006, E: *Streptomyces* sp. strain PN1009, F: *Streptomyces* sp. strain PN1018

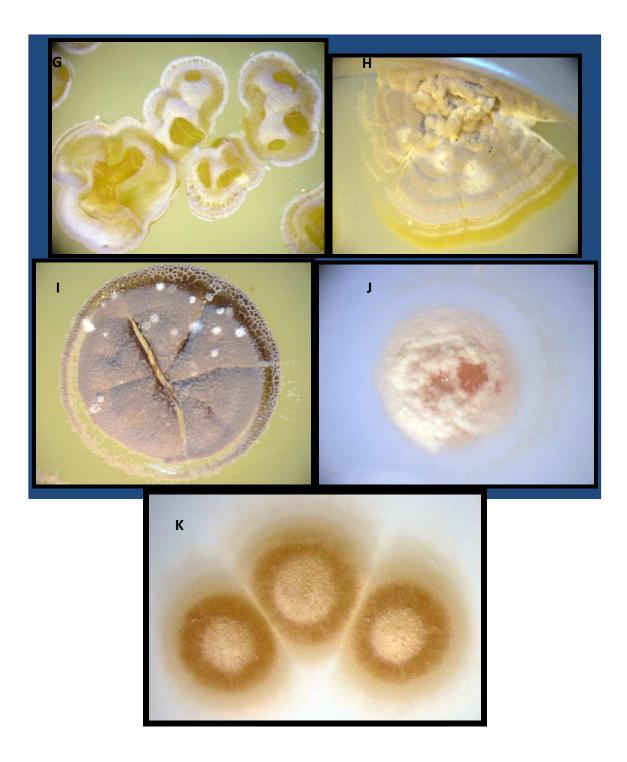


Figure 14. Colony Morphology of Actinobacteria isolated from *Paratrechina* sp. ants. G: *Streptomyces* sp. strain PN1004, H: *Streptomyces* sp. strain PN1007, I: *Streptomyces* sp. strain N1009, J: *Actinomadura* sp. strain PN4223, K: *Streptomyces* sp. strain PN4219.

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).

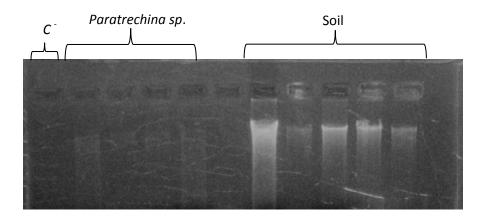


Figure 15. Genomic DNA from *Paratrechina* sp. ants of each sampled nest and its surrounding soil.

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).

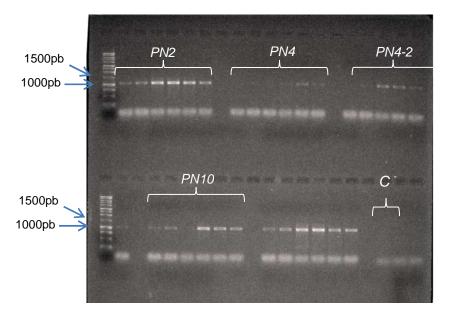


Figure 16. Amplification of 16S rDNA with the primers Act 283F and Act1369R of Actinobacteria associated with *Paratrechina* sp. in the four sampled nests.

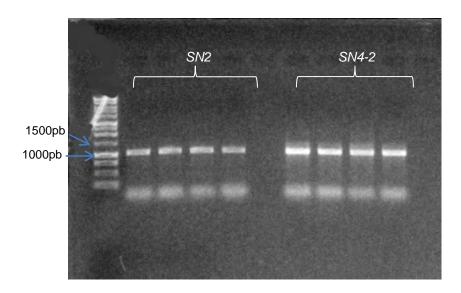


Figure 17. Amplification of 16S rDNA with the primers Act 283F and Act1369R of Actinobacteria in surrounding nest soil of *Paratrechina* sp.

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.

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

Table 5. Number of clones analyzed in each clone library

6.2.2 Restriction Fragment Length Polymorphism (RFLP)

Ants

A large number of enzyme restriction patterns were found in the DNA of the antassociated Actinobacteria in the four nests and the soils. We found 15 patterns for the enzyme Hinfl and 14 for the enzyme Haell. 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) (<u>http://rdp.cme.msu.edu/</u>). 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 HaelI. Fourteen restriction patterns were reported with HinfI and seven with the enzyme HaelI for nest 4 surrounding soil (SN4). Nine restriction patterns were generated with HinfI and six with HaelI in soil SN4-2. In the soil around nest N10, ten restriction patterns were reported with the enzyme HinfI and five with HaelI. Figure 20 and 21 shows some restriction patterns generated with the enzymes HinfI and HaelI in soils.

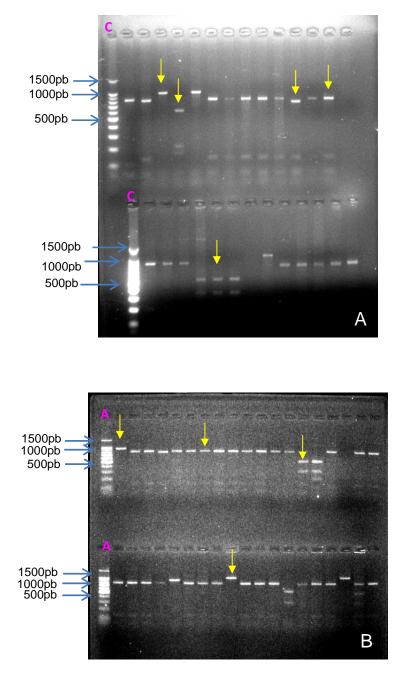


Figure 18. Arrows indicate restriction patterns of representative clones from *Paratrechina* sp. with Hinfl. A: Nest PN4-2. B: Nest PN10. C: molecular marker 100bp.

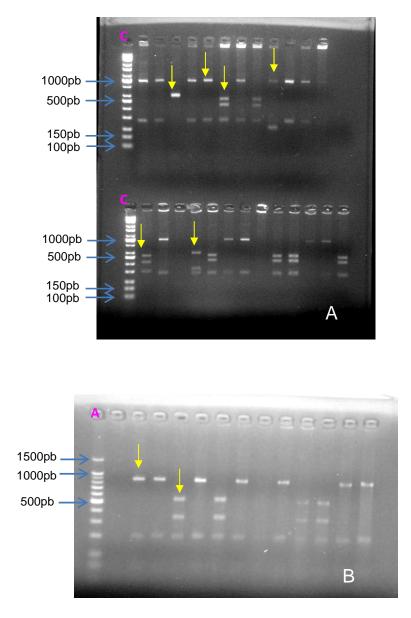


Figure 19. Arrows indicate restriction patterns of representative clones *Paratrechina* sp. with Haell. A: Nest PN4, B: Nest PN10. C: molecular marker 100bp.

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).

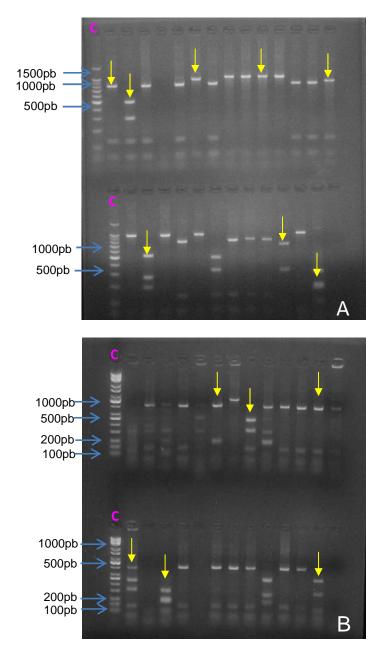


Figure 20. Arrows indicate restriction patterns of representative clones from soil with Hinfl. A: SN4, B: SN42. C: molecular marker 100bp.

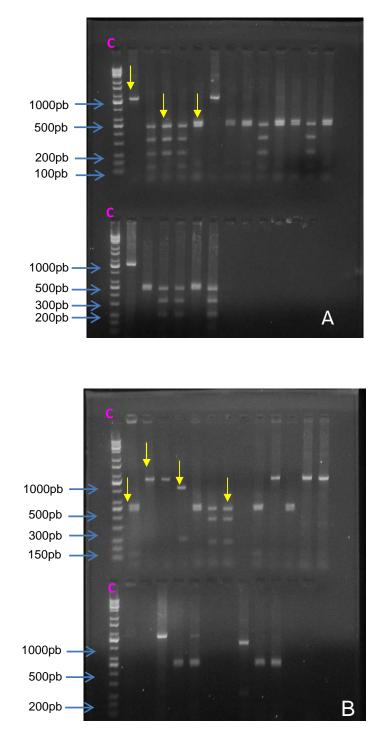


Figure 21. Arrows indicate restriction patterns of representative clones from soil with Haell. A: SN10, B: SN42. C: molecular marker 1 Kb

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).

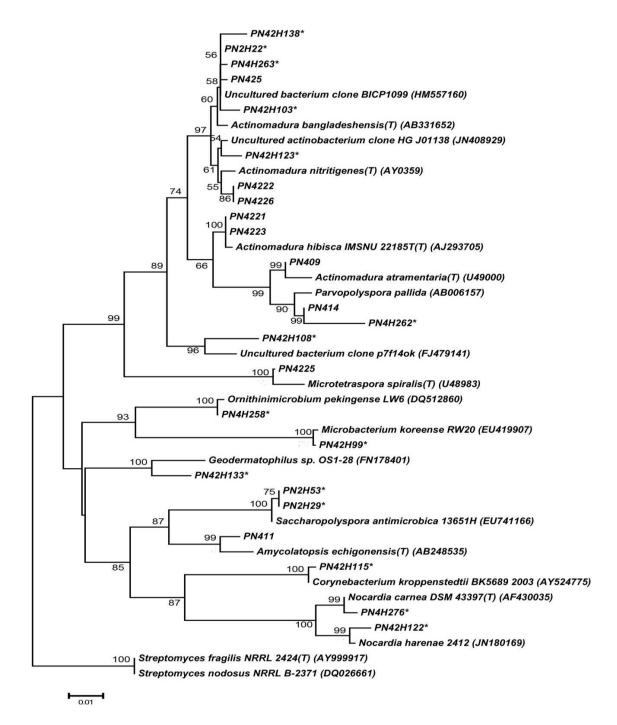


Figure 22. Neighbor-joining tree based of 16S rRNA gene sequences (1000-1350bp) from cultured *Streptomyces* isolated from *Paratrechina* sp. ants by culture independent and dependent methods and closely related species found in GenBank (accession number in parethesis) Asterisk indicates sequences obtained 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

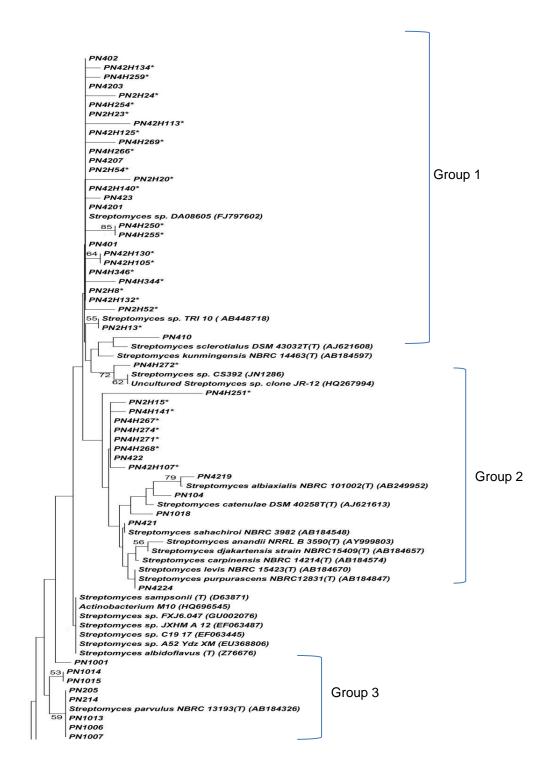


Figure 23. Neighbor-joining tree based of 16S rRNA gene sequences (1000-1350pb) from cultured Actinobacteria isolated from *Paratrechina* sp. ant ant and closely related species found in GenBank (accession number in parethesis). The numbers at the nodes indicate Bootstrap support values (>50%) based 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.

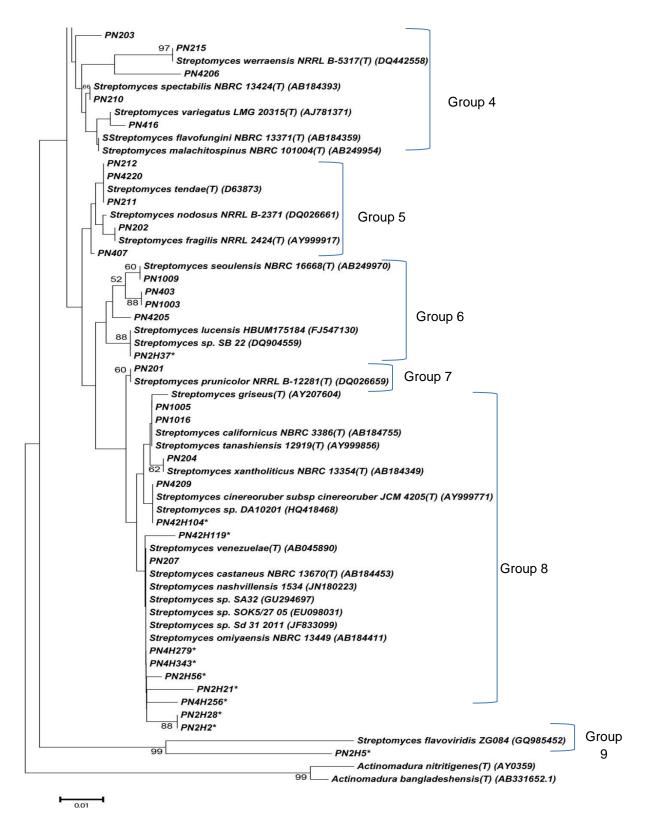


Figure 23. Continuation

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 associated 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%).

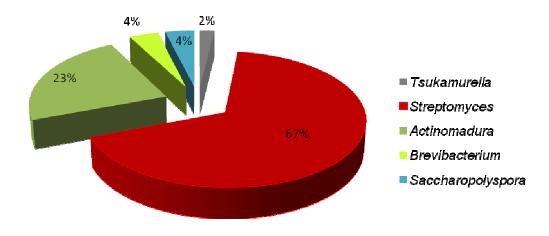


Figure 24. Frequency of the Actinobacteria genera found associated with *Paratrechina* sp. ants in nest PN2. Analysis based on 49 clones.

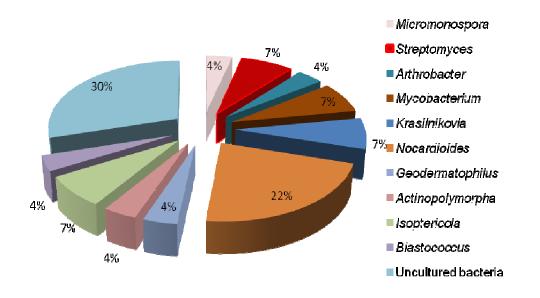


Figure 25. Frequency of Actinobacteria found in surrounding soil of nest 2 (SN2). Analysis based on 27 clones.

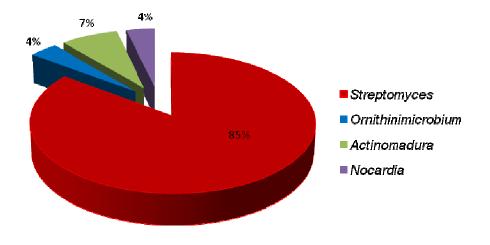


Figure 26. Frequency of the Actinobacteria genera found in *Paratrechina* sp. ants in nest PN4 at *Guayacan Centenario* in the wet season. Analysis based on 27 clones.

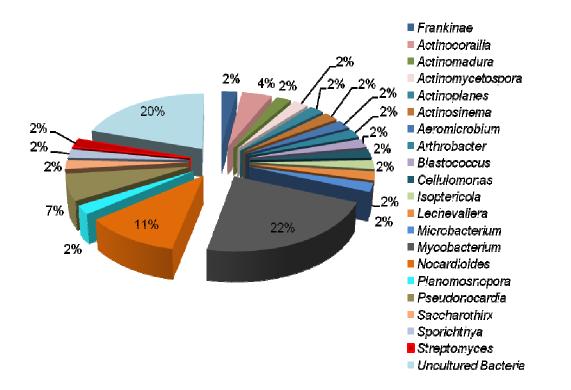


Figure 27. Frequency of the Actinobacteria genera found in the adjacent soil of *Guayacan Centenario* (SN4). Wet season. Analysis based on 44 clones.

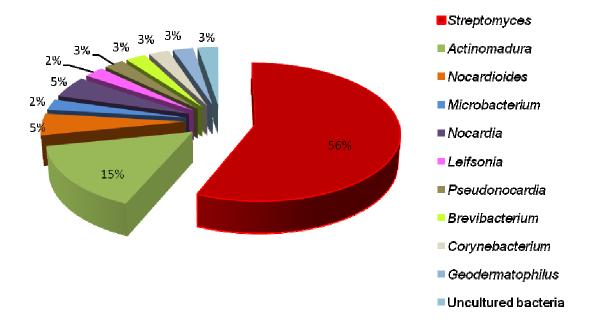


Figure 28. Frequency of the Actinobacteria genera found in *Paratrechina* sp. ants in nest PN4-2. Dry season. Analysis based on 39 clones.

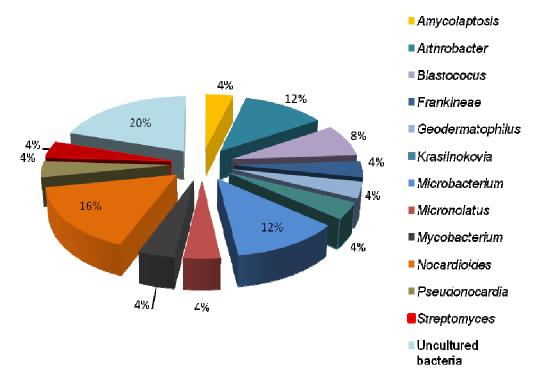


Figure 29. Frequency of the Actinobacteria genera found in the soil SN4-2 in dry season. Analysis based on 25 clones.

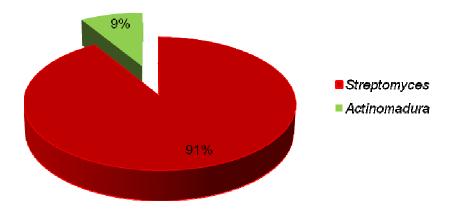


Figure 30. Frequency of the Actinobacteria genera found in *Paratrechina* sp. ants in nest PN10. Analysis based on 24 clones.

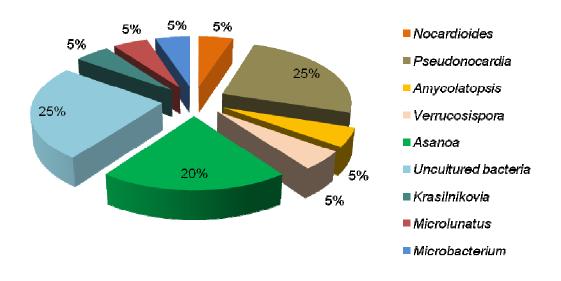
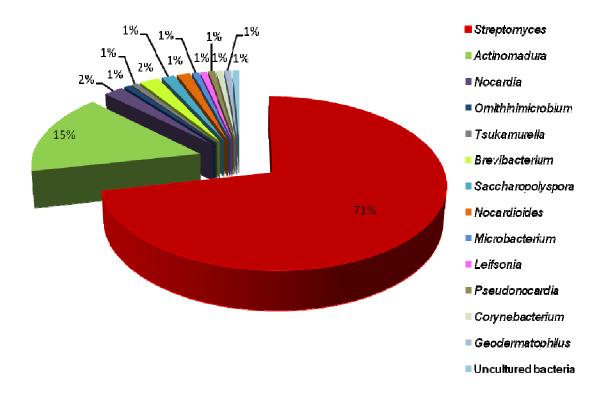
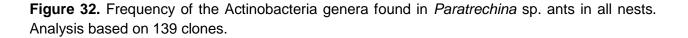


Figure 31. Frequency of the Actinobacteria genera found in the soil SN10. Analysis based on 21 clones.





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 dominatelf 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 \ge 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

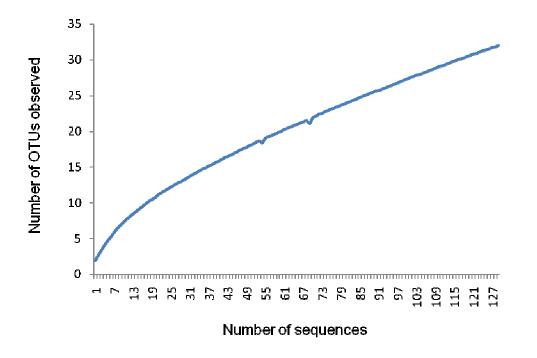


Figure 33. Rarefaction curve calculated on Actinobacteria associated with *Paratrechina* sp. ants in all nests sampled. OTUs were determined by a similarity \geq 97%.

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	<u>0.7200</u>	<=0.06
N2			<=0.06	<u>0.1800</u>
N4				1.0000
N4-2				

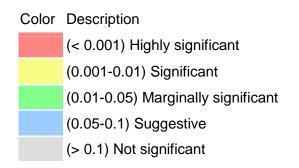


Table 8. Matrix showing Bonferroni corrected P-values comparing Actinobacteria communities between each *Paratrechina* sp. ant nest and its surrounding soil. Colors indicate the significant difference between each pair on a scale defined by Unifrac.

	Ants N2	Soil N2
Ants N2		<u><=0.01</u>
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		

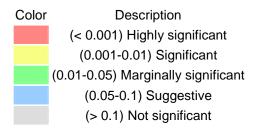
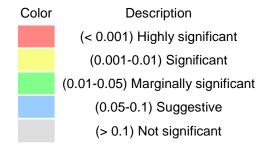


Table 9. Matrix showing Bonferroni corrected P-values comparing Actinobacteria communities between nest soils. Colors indicate the significant difference between each pair on a scale defined by Unifrac.

Soils	Soil N10	Soil N2	Soil N4	Soil N4-2
Soil N10		<=0.06	<=0.0 <u>6</u>	<u>0.1200</u>
Soil N2			<u>0.0600</u>	1.0000
Soil N4				1.0000
Soil N4-2				



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*.

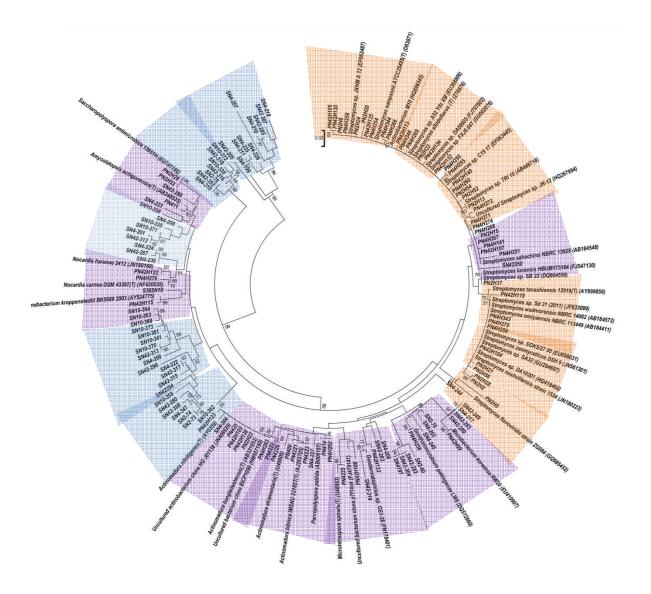


Figure 34. Neighbor-joining tree based of 16S rDNA gene sequences (1000-1350bp). Sequences isolated from *Paratrechina* sp. by culture independent and dependent methods, sequences isolated from soil around the nest and closely related species found in GenBank (accession number in parethesis). The numbers 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 streptomyces azaserine, an 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).

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, Saccharothirx and Sporichthya were exclusively associated with soil, while Actinomadura. Nocardia. Pseudonocardia. Microbacterium. Streptomyces, 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 fungusgrowing 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 ₂ HPO 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 ₂ O	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

Appsenditix22a. Coontinuation

N2	Rainy	PN222	Irregular	Yellow	Gray with with Purple spots	DDusity	⊞ifören	Y ello w
N4	Rainy	PN402	Irregular	Bedlaw	Brown with Dale gray White spots	Dusty	⊞ifören	Bediawy
N4	Rainy	PN403	Irregular	Bedlow	VG hatye	Dusty	⊞ifören	Bediawa
NN142	RDaingy	PN404	Irregular	Yetheyw	Gray	Dusty	⊞ifören	No
NN142	Rainyy	PN406	lCiegullar	Brown	R Grp je	Dusty	⊞ifören	Y ê\lio w
NN142	Rainyy	PN403	Irregular	Yetheyw	GMay	Glibuteting	⊞ifören	Y ê∿lo w
NN142	Rainyy	PN400	Irregular	DaCkegneen	GrayWa /hite white	Dusty	⊞ifören	GNeeen
NN142	Rainyy	PN409	Irregular	Darlelgræen	Vg/haite	Dusty	⊞ifören	Bi ldio vn
NN142	RDaingy	PN410	Irregular	Betalok v	VG/haitye	Dusty	Filiform	Y ê\lio w
NN142	Rainyy	PN412	lCiegullar	Darlelgræen	White	Dusty	⊞ifören	Y ê\lio w
NN142	RDaingy	PN419	lCiegullar	Bedlow	PàNkhitjeay	Dusty	Filiform	Y ê\lio w
NN142	Rainyy	PN426	Irregular	Palkeboown	N\&/ Idiada	Dusty	Filiform	Yellow
NN142	Rainyy	PN429	Irregular	Čeepuu	White	DDusity	Ufrikifolane	Bi Nio vn
N {4 42	Rafixy	PN428	Irregular	Ģ€#® ₩	Gray and White diff the edge	DRHHy	Undulate	Bre₩n
N4 ₄ 2	Dry Rainy	BN423	Irregular 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

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. Colony morphology of isolates from Solenopsis sp. ants.

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

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

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. Colony morphology of isolates from *Dorymyrmex* sp.

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

Appendix 2c. Continuation

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

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	<i>Burkholderia</i> 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 3a. Non-Actinobacteria cultures identified from *Solenopsis* sp. ants.

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

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

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

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	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.

N605 1	
N615 1	AGCC
N618 1	
AY999771.1 Streptomyces ciner 1	TGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAAG
N616 1	
treptomyces violaceorectus NB 1	ACGARCGCTGGCGGCGTGCTTARCRCRTGCRAGTCGARCGATGARGCC
Q418468.1 Streptomyces DA1020 1	CGAACGATGAAGCCC
treptomyces bikiniensis DSM40 1	-AGAGETTGATCCTGGCTCAGGACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAAGCCC
94 1	CGAACGATGAAGCCC
96 1	
treptomyces tanashiensis HBUM 1	TGCTTACACATGCAAGTCGAACGATGAAG
N621 1	
N607 1	
treptomyces XAS585 1	TGCTTACCATGCAAGTCGAACGATGAAGCCC
N608 1	10011ACCA10CARD1CDARCOA10AR00CC
N606 1	GCGAGTCGAACGATGAA-CCACT
treptomyces DA08605 1	GGGCAAGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
N612 1	GTGCGAGTCGARCGATGAAGCCGCT
treptomyces TRI 10 AB448718 1	
N61501	ICCRRFICERCEATERABCC-CT
treptomyces nodosus NBRC 1289 1	ACGARCGCTGGCGGCGTGCTTARCRCRTGCRAGTCGARCGATGRAGCCCT
N617 1	RUGARUGUIGUGGUGIGUI ARUAUAI GUAAGTUGAAUGATGAAGUUUT
	GCTGGCGGCGTGCTTAACACATGCAAGCGAACGATGAACCACT
N1310 1 N1312 1	
	CTACCATGCAAGTCGACGATGAAGGCC
	TGCAGTCGACGATGAAGGCC
N1301 1	ATGCAGTCGACGATGAACCACCT
N1316 1	TGCAGTCGACGATGAACCAC
treptomyces rochei NBRC 12908 1	ACGARCGCTGGCGNCGTGCTTARCNCATGCRAGTCGARCGATGARCCRC
treptomyces B5W222 1	CACTTOGATCCTGGCTCAGGACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAACCACCT
treptomyces mutabilis NRRL IS 1	ACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAACCACCT
N1303 1	ATGCAGTCGACGATGAAGCCC
N1304 1	TGCAGTCGACGATGAACCAC
N1306 1	CTTACCATGCAGTCGAACGATGAAC <mark>C</mark> AC
treptomyces 195018 1	ACCATGCAGTCGAACGATGAACCAC
N1405 1	TGCAGTCGACGATGAAG <mark>C</mark> CC
N1402 1	TGCAGTCGAACGATG AAG <mark>C</mark> CC
N1403 1	CCAAAGTTGGCGGGGTCTACCATGCAGTCGACGATGAAG <mark>C</mark> CC
treptomyces N01 352 DQ717851 1	CCGGGGCGGGGGGGGCTTACCATGCAGTCGACGATGAAG <mark>C</mark> CC
N1404 1	<mark>TGCAGTCGACGATGAAC</mark> CAC
N1406 1	GCAGTCGACGATGAACCAC
N1407 1	TGCAGTCGACGATGAACC AC
N1321 1	TGCAGTCGAACGATGAACCCACT
treptomyces thermolilacinus N 1	TACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAACCCACT
treptomyces heteromorphus AB 1	<mark>ECTC</mark> AGGACGAACGCTGGCGGCGTGCTTAACACATGCAAG <mark>T</mark> CGAACGATGAAC <mark>C</mark> AC
N1413 1	ATGCAGTCGAACGATGAACCAC
treptomyces fragilis NRRL 242 1	AG <mark>RTTGATCCTG</mark> GCTC <mark>AGGACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAAC</mark> CAC
treptomyces humidus NRRL B-31 1	GATTCTGGCTCAGGACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAACCAC
N1307 1	ATGCAGTCGAACGATGAACCACCT
14 19 1	TGCAGTCGACGATGAACCCGCT
treptomyces paraguayensis NBR 1	GCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAACCCGCT
ctinomadura nitritigenes T 1	TTARCACATGCAAGTCGAGCGGAAAGGCCCCC

Diffi 12 BATTAGTERCHARGED TRADE TRADE OF CONTENTION CONTENTION OF CONTENT.				70	100	110	120	130	140	150
Diffi 15 SHITHGTERCHARGES FIGHTANGTERCHARGES FI				<u> </u> .	<u>. </u>		<u>. </u>			
Diffig 12 FATTABGEGGAAGGEGETHERTANGSGEGGAATCHECCTT RATCHEGGAARACCCTEGHAR CHEG Diffig SATTAGGEGAAGGEGTHERTANGSGEGGAATCHECCTT RATCHEGGAARACCCTEGHAR CHEG Diffig SATTAGGEGGAAGGEGTHERTANGSGEGGAATCHECCTT RATCHEGGAARACCCTEGHAR CHEG Diffig SATTAGGEGGAAGGEGTHERTANGSGEGGAATCHECCTT RATCHEGGAARACCCTEGHAR CHEG Diffig SATTAGGEGGAACGEGT HERTARCCGEGGCAATCHECCTT RATCHEGGAARACCCTEGHAR GGG Diffig SATTAGGEGGAACGEGT HERTARCCGEGGCAATCHECCTT RATCHEGGAARACCCTEGHAR GGG Streptomyces bikiniensis DSNG SATTAGGEGGAACGEGT HERTARCACGFGGCAATCHECCTT RATCHEGGAARAGCCTEGHAR GGG N 4 25 SATTAGGEGGAACGEGT THAGTARCACGFGGCAATCHECCTT RATCHEGGAARAGCCTEGHAR GGG N 5 10 SATTAGGEGCAACGEGT THAGTARCACGFGGCAATCHECCTT RATCHEGGAARAGCCTEGHAR GGG Streptomyces tanashiensis HBUH 25 SATTAGGEGCAACGEGT THAGTARCAGGGGCAAGTCHECCTT RATCHEGGAARAGCCTEGHAR GGG Diff01 14 SATTAGGEGCAACGEGT THAGTARCAGGGGCAAGTCHECCTT RATCHEGGAARAGCCTEGHAR GGG Diff01 12 SATTAGGEGCAAGGEGT THAGTARCAGGGGCAAGTCHECCTT RATCHEGGAARAGCCTEGHAR GGG Diff01 12 SATTAGGEGCAAGGEGT THAGTARCAGGGGCAAGTCHECCTT RATCHEGGAARAGCCTEGHAR										
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DN616 1 DN616 1 DN616 1 DN616 1 STUTMETEGGEALGEG TEAFTARTEGGEALGEG TEAFTARTEGGEALGEG TEAFTARTEGGEALGEG Streptomyces DALD20 25 SATTARTEGGEALGEG TEAFTARTEGGEALGEG TEAFTARTEGGEALGEG TEAFTARTEGGEALGEG Streptomyces tanashiensis HBH4 2 ATTARTEGGEALGEG TEAFTARTEGGEALGEG TEAFTARTEGGEALGEG TEAFTARTEGGEALGEG TEAFTARTEGGEALGEG TEAFTARTEGGEALGEG Streptomyces XAS585 11 STATTARTEGGEALGEG TEAFTARTEGGEALGEG Streptomyces DAU8605 51 Streptomyces DAU8605 54 Streptomyces DAU8605 54 Streptomyces DAU8605 54 <t< td=""><td>DN618</td><td>12</td><td>CATTIACTICC</td><td>CHARCECC</td><td>TGAGTIAACEC</td><td>GTGGGCAATC</td><td>TGCCCT<mark>T</mark>CA</td><td>TCTGGGACAR</td><td>GCCCTGGAAA</td><td>CEEGGI</td></t<>	DN618	12	CATTIACTICC	CHARCECC	TGAGTIAACEC	GTGGGCAATC	TGCCCT <mark>T</mark> CA	TCTGGGACAR	GCCCTGGAAA	CEEGGI
Streptomyces violaceorectus NB SHITAGIGCGAACGGE IGATIAGIGCGAACGGE IGATIAGIGCGAACGGE <thigatiagigcgaacgge< th=""> IGATIAGIGCGAACGGE<</thigatiagigcgaacgge<>	AY999771.1 Streptomyces ciner	51	GATTAGTGG	CGAACGGG	TGAGTAACAC	GTGGGCAATC	TGCCCT <mark>T</mark> CA	TCTGGGACAT	GCCCTGGAAA	CGGGG
Waliaks.I.Streptonyces DA1020 Zatraforschaktor Thaffaks.I.Streptonyces Da102 Zatraforschaktor Thaffaks.I.Streptonyces Da102 Zatraforschaktor Thaffaks.I.Streptonyces Da102 Zatraforschaktor Thaffaks.I.Streptonyces Da102 Zatraforschaktor Thaffaks.I.Streptonyces Thaffaks.I.Streptonyces Da102 Zatraforschaktor Thaffaks.I.Streptonyces Thaffaks.I.Strept	DN616	1								
Streptonyces bikiniensis DSM40 80 SATTAGTGECHARCGEG TEAGTAACAGTGECAATCTEC CTT CACTCTGEACAACCCCTGAALCCCCTGAALCCCCTGAALCCCCTGAALCCCCTGAALCCCCTGAALCCCCTGAALCCCCTGAALCCCCTGAALCCCCTGAALCCCCTGAALCCCCTGAALCCCCTGAALCCCCTGAALCCCCTGAALCCCCTGGAALCCCCCTGGAALCCCCTGGAACCCCCTGGAALCCCCTG	Streptomyces violaceorectus NB	59	CATTACTCC	CGAACCCC	TENETIMACAC	GTGGGCAATC	TGCCCT <mark>T</mark> CA	TCTGGGACAR	GCCCTGGAAA	CEEEGI
No.4 25 FATTAGTESCHARGES TEMET ANCAGETGESCHATCTSCCTT CATCTEGEAGAAGSCCTTERAIL CEGE ND.6 10 SATTAGTESCHARGES TEMET ANCAGETGESCHATCTSCCTT CATCTEGEAGAAGSCCTTERAIL CEGE ND.6 10 SATTAGTESCHARGES TEMET ANCAGETGESCHATCTSCCTT CATCTESCHARGESCTERAIL CEGE STETEDTOMYCES LABASHLENSIS HEMIT CEGE CATTAGTESCHARGESCT TEMET ANCAGETGESCHATCTSCCTT CATCTESCHARGESCT CEGE CATTAGTESCHARGESCT TEMET ANCAGETGESCHARCESCT CATCTESCHARGESCT CEGE CATTAGTESCHARGESCT TEMET ANCAGETGESCHARGESCT CEGE	HQ418468.1 Streptomyces DA1020	25	CATTACTCC	CERTACERE	TGAGTIAACAC	GTGGGCAATC	TGCCCT <mark>T</mark> CA	TCTGGGACAR	GCCCTGGAAA	CCCCCC
No. Straptonyces tanashiensis HBMI Straptonyces tanashiensis HBMI <td>Streptomyces bikiniensis DSM40</td> <td>80</td> <td>CATTACTEC</td> <td>CGAACGGG</td> <td>TCACTRACAC</td> <td>GTGGGCAATC</td> <td>TGCCCT<mark>T</mark>CA</td> <td>TCTGGGACAT</td> <td>GCCCTGGAAA</td> <td>CGGGG</td>	Streptomyces bikiniensis DSM40	80	CATTACTEC	CGAACGGG	TCACTRACAC	GTGGGCAATC	TGCCCT <mark>T</mark> CA	TCTGGGACAT	GCCCTGGAAA	CGGGG
Streptonyces tanashiensis HBUM 42 Shthafaroconacconacconacconacconacconacconacco	N9 4	25	CATTACTCC	CGAACGGG	TGAGTAACAC	GTGGGCAATC	TGCCCT <mark>T</mark> CA	TCTGGGACAL	GCCCTGGAAA	CECEC
DH621 DH731 CartagEscharger Train Analytic Geo Angene Control Science Train Theory of Science Control Science Contro Science Control Science Control Science Control Science Control	N9 6	10	CATTACTCC	CGAACGGG	TGAGTAACAC	GTGGGCAATC	TGCCCT <mark>T</mark> CA	TCTGGGACAL	GCCCTGGAAA	CECEC
DB607 14 GATTAGTGECHARGEGETIGETAGC_SETERECANTCTECCTT_ACTCTEGERARGECETIGENAL Streptomyces XR5585 41 GATTAGTGECHARGEGETIGETAGC_SETERECANTCTECCTT_ACTCTEGERARGECETIGENAL Shife 13 GATTAGTGECHARGEGETIGETAGC_SETERECANTCTECCTT_ACTCTEGERARGECETIGENAL Shife 13 GATTAGTGECHARGEGETIGETAGC_SETERECANTCTECCTT_CACTCTEGERARGECETIGENAL Shife 13 GATTAGTGECHARGEGETIGETAGCSETERGANCTEGECTT_CACTCTEGERARGECETIGENAL Shife 13 GATTAGTGECHARGEGETIGETAGCSETERGENATCTEGECANTCTECCTTCGACTETEGERARGECETIGENAL Shife 13 GATTAGTGECHARGEGETIGETAGCSETERGENATCTECCTT_CACTCTEGERARGECETIGENAL Shife 13 GATTAGTGECHARGEGETIGETARGCSETERGENATCTECCTT_CACTCTEGERARGECETIGENAL Shife 13 GATTAGTGECHARGEGETIGETARGACGTGEGENATCTECCTT_CACTCTEGERARGECETIGENAL Shife 13 GATTAGTGECHARGEGETIGETARGACGTGEGECANTCTECCTT_CACTCTEGERARGECETIGENAL Shife 13 GATTAGTGECHARGEGETIGETARGACGTGEGERANTCTECCTT_CACTCTEGERARGECETIGENAL Shife 13 GATTAGTGECHARGEGETIGETARGACGTGEGERANTCTECCTT_CACTCTEGERARGECETIGENAL Shife 13 GATTAGTGECHARGEGETIGETARGACGTGEGERANTCTECCTT_CACTCTEGERARGECETIGENAL Shife 14 GATTAGTGECHARGEGETIGETARGACGTGEGERANTCTECCTT_CACT	Streptomyces tanashiensis HBUM	42	GATTACTCC	CGAACGGG	TGAGTIAACAC	GTGGGCAATC	ТБСССТ <mark>Т</mark> СА	TCTGGGACAR	GCCCTGGAAA	CEEEG
Streptonyces XASS85 41 FATTAGTGCCHACGGG TEMETAACAGCHGGCAATCHGCCTT SACTGGGGAAGCCCTGGAA GGGG DM608 13 FATTAGTGCCHACGGG TEMETAACAGCHGGCAATCHGCCTT SACTGGGGAAGCCCTGGAA GGGCGGGGGGGGGGAATCHGCCTT SACTGGGGGAAGCCCTGGAA GGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	DN621	12	CATTACECC	CENTACERE	TGAGTHACAC	GTGGGCAA CC	TGCCCT <mark>T</mark> CA	TCTGGGACAR	GCCCTGGAAA	CECE
Streptonyces XASS85 41 FATTAGTGCCHACGGG TEMETAACAGCHGGCAATCHGCCTT SACTGGGGAAGCCCTGGAA GGGG DM608 13 FATTAGTGCCHACGGG TEMETAACAGCHGGCAATCHGCCTT SACTGGGGAAGCCCTGGAA GGGCGGGGGGGGGGAATCHGCCTT SACTGGGGGAAGCCCTGGAA GGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	DN607	14	CATTACTEC	CGAACGGG	телетнастс	GTGGGCAATC	TGCCCT <mark>T</mark> CA	TCTGGGACAR	GCCCTGGAAA	CHECC
DB668 13 GATTABGEGGAAGGEG TEAGETARCAGEGERAACGEG TEAGETARCAGEGAATCHECCTT CATCHEGGAAAGGEG TEAGETARCAGEGGAATCHECCTT CATCHEGGAAAGGEG TEAGETARCAGETGGGAATCHECCTT CATCHEGGAAAGGEG TEAGETARCAGETGGGGAATCHECCTT CATCHEGGAAAGGEGGGAAGGEGGGGAATCHECCCTT CATCHEGGAAAGGEGGAAGGEGGGGAATCHECCCTT CATCHEGGAAAGGEGGAAGGEGGGAAGGACCCEGGGAAATCHECCCTT CATCHEGGAAAGGEGGAAGGEGGGGAAGGACCHEGGAAATCHECCCTT CATCHEGGAAAGGEGGAAGGACCHEGGAAAGACCHEGGAAATCHECCCTT CATCHEGGAAAGGEGGAAGGACCHEGGAAAACGEGGAGAATCHECCCTT CATCHEGGAAAGGEGGAAGGACCHEGGAAATCHECCTT CATCHEGGAAAGGEGGAAGGACHEGGAAATCHECCTT CATCHEGGAAAGGEGGAAGGACHEGGAAATCHECCTT CATCHEGGAAAGGEGAAGGACHEGGAAATCHECCTT CATCHEGGAAAGGEGAAGGACHEGAAATCHEGGAAATCHECCTT CATCHEGGAAAGGACHEGAAGGAAGGAACHEGAAATCHECCTT CATCHEGGAAAGGACCHEGAAGGAAGGAACHEGAAATCHECCAAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA	Streptomyces XAS585	41								CHECC
DB666 31 FATTAGTOCCAACGOC TEAGTAACACGTOCCAACGOC TEAGTAACACGTOCCAACGOC CACC CACC <t< td=""><td></td><td>13</td><td>CATTACTCC</td><td>CRATACERE</td><td>тсактаасас</td><td>GTGGGCAATC</td><td>TGCCCT<mark>T</mark>CA</td><td>TCTGGGACAT</td><td>GCCCTGGAAA</td><td>CHERCE</td></t<>		13	CATTACTCC	CRATACERE	тсактаасас	GTGGGCAATC	TGCCCT <mark>T</mark> CA	TCTGGGACAT	GCCCTGGAAA	CHERCE
DH612 Streptonyces TRI 10 AB448718 Shiftsdi 16 Ab44	DN686	31	CATTACTCC	CRATACERE	тсактаасас	GTGGGCAATC	TRECET	TCTGGGACAT	GCCCTGGAAA	CEEEG
DM612 STEEPLONGCES TRI 10 RE448718 SATTRAFGEGARGEGE TEAGETARCREGFGGGARGEGECTT SATCTEGEGARARCCCTEGHAR SATTRAFGEGARGEGARGEG TEAGETARCREGFGGGARTCTECCCT SATTRAFGEGARGEGARGEGTGARTARCREGFGGGARTTECCCTCSCATCTEGEARAGEGCC	Streptomyces DA08605	54	GATTAGTGG	CEAACEE	TGAGTAACAC	GTGGGCAATC	TRECET	TCTGGGACAT	GCCCTGGAAA	CEREG
DN61501 16 GATTAGTGGCGANCGGG TGAGTANCACGTGGGCAAT TGCCCTGCACTCTGGGACAAGCCCTGGAAA-CGGG		35	GATTAGTGG	CEAACEE	TGAGTAACAC	GTGGGCAATC	TRECETTCA	TCTGGGACAT	GCCCTGGAAA	CEREG
DN6150116GATTAGTGGCGARCGGG-TGAGTARCACGTGGGCART_TGCCCTGCRCTCTGGGRCARGCCCTGGARA_CGGG	Streptomyces TRT 10 AB448718	32	GATTAGTGG	CEAACEE	TGAGTAACAC	GTGGGCAATC	TRECETTCA	TCTGGGACAT	GCCCTGGAAA	CCCCC
		16								CCCCC
	Streptomyces nodosus NBRC 1289	59							GCCCTGGAAA	CCCCC

		170 180 190 200 210 220 230
		<u></u>
DN605	110	ACCEENTACEACCTGEGAAEECANCTTCTCE-FETEBAAAECTCCEECEETEAAEEATEAECCCECEECCTATC
DN615	93	ACCEGATAC
DN618	91	RCCGGATAC
AY999771.1 Streptomyces ciner	129	RCCGGATACBACCTGCCGAEGCATCTCGGCE-FGTGBAAAGCTCCGGCGGTGAAGGATGAGCCCGCGGCCTATC
DN616	1	
Streptomyces violaceorectus NB	137	ACCEGATAC
HQ418468.1 Streptomyces DA1020	103	RCCGGATACGA <mark>CCTGGGAR</mark> GGCAT <mark>CTTCTC</mark> -GFTGBAAAGCTCCGGCGGTGB <mark>AGGATGAGCCCGCGGCCTATC</mark>
Streptomyces bikiniensis DSM40	158 103	RCCGGATRC GR <mark>CCCGGGRR</mark> GGCATCTTCCG-GGTGRARGCTCCGGCGGTGRAGGATGAGCCCGCGGCCTATC RCCGGATAC GRCCCGGGRRGGCATCTTCCG-GGTGRARGCTCCGGCGGTGRAGGATGAGCCCGCGGCCTATC
N9 4 N9 6	88	RCCGGATRC
Streptomyces tanashiensis HBUM	120	RCCGGATAC
DN621	90	RCC6GATAC - GAGTCTG6GAGGCTCTCCCGG-CCT6GAAAGCTCCGGCGGTGAAGGATGAGCCCGCGGCCTATC
DN607	93	RCCGGATAC
Streptomyces XAS585	119	ACCEGATACBA <mark>CTCTGGGAGGCATCTCCTGG-ACT</mark> GGAAAGCTCCGGCGGTGAAGGATGAGCCCGCGGCCTATC
DN608	91	RCCGGATAC
DN606	109	RCCGGATAC -ARCCACTGACCCCCATGGTCGGGT -GGTGGAAAGCTCCGGCGGTGCCGGTGCCGGCCGGCCGGCC
Streptomyces DA08605	132	ACCEGATAC - AACCACTGACCCCATGGTCGGGT - GGTGGAAAGCTCCGGCGGTGCAGGATGAGCCCGCGGCCTATC
DN612	113	ACCEGRATAC-GACACAGGACCCCATGGTCTCTC-TGTGGAAAGCTCCGGGGGGTGAAGGATGAGCCCGCGGGCCTATC
Streptomyces TRI 10 AB448718	110	ACCEGATAC-GACCACCEGCCCCATEGCCTEGT-EGTEGAAAGCTCCEGECEGTEAAGGATEAECCCECEECCTATC
DN61501	93	ACCEPATING-GAGCCGGGGGGGCTC-TCCCTC-ETTGEDAMMEGTCCEFCGETECMEEATEAFCCCCFCFCCTATC
Streptomyces nodosus NBRC 1289	137	ACCEGATAC-GAECCEGEGAECATC-TCCCTE-STIPSGAAAGCTCCEGECEGTECAEGATGAECCCECEGECCTATC
DN617	91	ACCEGATACTEATCCECCTEEECATC-CREECE-ETROGAAAGCTCCEECEETECAEEATEAECCCECEEECTATC
Streptomyces ambofaciens NBRC	131	ACCEGATACTGATCCECTTEGECATC-CAEGECE-ETTC GAANECTCCEECEGTECAEGATEAECCCECEECCTATC
DN1310	111	RCCGGATAC
DN1312	115	ACCEGATAC
DN1317	108	ACCEGATAC FA <mark>CCCGGGGAEGCAT</mark> CTCCTCE-EGT <mark>G</mark> EAAAGCTCCGGCGGTG <mark>A</mark> AGGATGAGCCCGCGGGCCTATC
DN1301	111	ACCEGATAC-TGATCCTCECAGECATCTECEACECTCEGAAAGCTCCEECEETECAGEAGCCCECECECECECECECECECECECECECECEC
DN1316	108	RCCGGATAC <mark>-T</mark> GA <mark>TCCTCGCR</mark> GGCAT <mark>CTGCGRG-ST</mark> TC <mark>GRAAGCTCCGGCGGTG</mark> CRGGATGRGCCCGCGGCCTATC
Streptomyces rochei NBRC 12908	137	ACCEENTAC <mark>TENTCCTCECR</mark> EECAT <mark>CTECERE</mark> - <mark>FT</mark> TCENARECTCCEECEETE <mark>C</mark> REENTERECCCECEECEECCTATC
Streptomyces B5W222	159	ACCEGATAC <mark>T</mark> FA <mark>TCCTCECR</mark> EECAT <mark>CTECER</mark> E <mark>TTC</mark> EARAECTCCEECEETE <mark>C</mark> AEEATEAECCCECECECETATC
Streptomyces mutabilis NRRL IS	139	RCCGGATAC <mark>-T</mark> GR <mark>CCCTCGCR</mark> GGCAT <mark>CTGCGR</mark> G- <mark>ST</mark> IC <mark>GRAAGCTCCGGCGGTG</mark> CRGGATGAGCCCGCGGCCTATC
DN1303	109	ACCEGATACGACCTGCCGAGECATCTCGGCG-GEGEGAAAGCTCCGECEGTGAAGGATGAGCCCGCGGCCTATC
DN1304	108	ACCEGATAC <mark>-T</mark> EA <mark>TCCTCECA</mark> EECAT <mark>CTECEA</mark> E- <mark>ST</mark> A <mark>C</mark> EAAAECTCCEECEETE <mark>C</mark> AEEATEAECCCECEECEECTATC
DN1306	116	ACCEGATAC <mark>T</mark> GA <mark>CCCECTTE</mark> EECAT <mark>CCAAECE</mark> E <mark>TAC</mark> EAAAECTCCEECEGTE <mark>C</mark> AEGATEAECCCECEEECTATC
Streptomyces 195018	113	ACCEENTRC-TERCCCECTTEEECATCCARECE-ETTCEANAGCTCCEECEETECAEEATEAECCCCECEECECTATC
DN1405	108	ACCEGATACEA <mark>CCCEGEAA</mark> EECAT <mark>CTTCTC</mark> E-EETEEAAAECTCCEECEETE <mark>A</mark> AEEATEAECCCECEEEECTATC
DN1402	109	ACCEGATAC GA <mark>CCTGCCGA</mark> EGCAT <mark>CTCGGC</mark> G-E <mark>GT</mark> GGAAAGCTCCGGCGETG <mark>A</mark> AGGATGAGCCCGCGGCCTATC
DN1403	130	ACCEENTACEACCTGCCGAEECATICTCGGCE-EGTGBAAAECTCC66CGGTGAAGGATGAGCCC6C66CCTATC
Streptomyces N01 352 DQ717851	128	ACCEENTING FACCCGCCGA FEONICTCGGCE-FEITGBAAAGCTCCGGCGGTGAAGGATGAGCCCGCGGGCCTATC
DN1404	108	ACCEGATAC <mark>-T5ATCCTCECA</mark> EECAT <mark>CTECEA</mark> E- <mark>FTTC</mark> EAAAECTCCEECEETE <mark>C</mark> AEGATEAECCCECEECCTATC
DN1406	107	ACCEGATIAC-TEATCCTCGCAEGCAIICTGCGAE-FTICEBAAAGCTCC66CGGTECAGGATGAGCCC6C66CCTATC
DN1407	108	ACCEPATAC-TSATCCTCECREECATCTECERE-STITCEAAAECTCCEECEETECREEATEAECCCECEECETATC
DN1321	111	ACCEGATAC
Streptomyces thermolilacinus N	136	ACCEGATACGA <mark>CCACTTCA</mark> GECAT <mark>CTGATEGT</mark> G T TGAAAGCTCCEGCEGTG <mark>C</mark> AEGATGAECCCECEGECCTATC
Streptomyces heteromorphus AB	144	ACCEGATA <mark>T</mark> GA <mark>GCTTCCACC</mark> GCAT <mark>GGTGGGG</mark> <mark>FC</mark> TG T AAAGCTCCGGCGGTG <mark>C</mark> AGGATGAGCCCGCGGCCTATC
DN1413	110	RCCGGATACGA <mark>CCTGCCAA</mark> GGCAT <mark>CTTGGCG-GG</mark> TGGAAAGCTCCGGCGGTG <mark>A</mark> AGGATGAGCCCGCGGCCTATC
Streptomyces fragilis NRRL 242	156	RCCGGATACGACCTGCCARGGCATCTTGGCC-GGTGGAAAGCTCCGGCGGTGRAGGATGAGCCCGCGGCCTATC

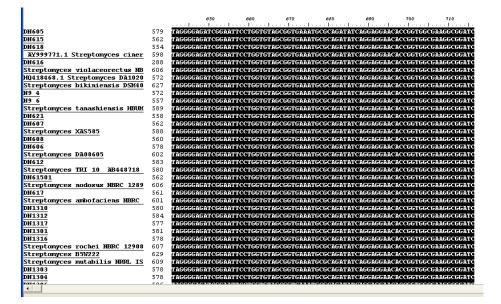
		250		60 270 280 290	300 320
DN605	187	TETTEETEGEETIN	THEC	raccaaggcgacgacgggtagccggcctgagag	
DN615	170	TGTTGGTGGGGTAA		TACCAAGGCGACGACGGGTAGCCGGCCTGAGAG	
DN618	168	TGTTGGTG <mark>G</mark> GGTAA		TACCAAGGCGACGACGGGTAGGCGGCCTGAGAG	
AY999771.1 Streptomyces ciner	206	TGTTGGTG <mark>G</mark> GGTAA		TACCAAGGCGACGACGGGTAGCCGGCCTGAGAG	
N616	1	ronnoonoodonaa	• <u> </u>		
Streptomyces violaceorectus NB	214	TGTTGGTG	TGGC	T ACCAAGGCGACGACGGGTAGCCGGCCTGAGAG	GCGACCGGCCACACTGGGACT
Q418468.1 Streptomyces DA1020	180	TGTTGGTGGGGTAA		TACCAAGGCGACGACGGGTAGCCGGCCTGAGAG	
Streptomyces bikiniensis DSM40	235	TGTTGGTGGGGTAA		CACCAAGGCGACGACGGGTAGCCGGCCTGAGAG	
19 4	180	TGTTGGTGGGGTAA		CACCAAGGCGACGACGGGTAGCCGGCCTGAGAG	
19 6	165	TGTTGGTGGGGTAA		CACCAAGGCGACGACGGGTAGCCGGCCTGAGAGG	
Streptomyces tanashiensis HBUM	197	TGTTGGTG <mark>G</mark> GGTAA	TGGC	TACCAAGGCGACGACGGGTAGCCGGCCTGAGAG	
N621	167	TGTTGGTG <mark>G</mark> GGTAA	TGGC	TACCAAGGCGACGACGGGTAGCCGGCCTGAGAG	
N607	170	TGTTGGTGGGGTAA	TGGC	TACCAAGGCGACGACGGGTAGGCGGCCTGAGAG	
Streptomyces XAS585	196	TGTTGGTGGGGTAA	TGGC	TACCAAGGCGACGACGGGTAGCCGGCCTGAGAG	
N608	168	TGTTGGTGGGGTAA	TGGC	TACCAAGGCGACGACGGGTAGCCGGCCTGAGAGG	
N606	187	TGTTGGTG <mark>A</mark> GGTAA	CECC	CACCAAGGCGACGACGGGTAGCCGGCCTGAGAG	
Streptomyces DA08605	210	TGTTGGTGAGGTAA	CGGC	CACCAAGGCGACGACGGGTAGCCGGCCTGAGAG	
N612	191	TGTTGGTG <mark>F</mark> GGT F A	TGGC	TACCAAGGCGACGACGGGTAGCCGGCCTGAGAG	
M612 Streptomyces TRI 10 AB448718	191	TGTTGGTG <mark>G</mark> GGTGA	TGGC	TACCARGECEACEACEGETAECCEECCTEAEAEA	
N61501	188	TGTTGGTGGGGTGA TGTTGGTG <mark>A</mark> GGTAA	CGGC	TACCAAGGCGACGACGGGTAGCCGGCCTGAGAG CACCAAGGCGACGACGGGTAGCCGGCCTGAGAG	
Streptomyces nodosus NBRC 1289	214	TGTTGGTG <mark>A</mark> GGTAA	CGGC	CACCAAGGCGACGACGGGTAGCCGGCCTGAGAG	
		TGTTGGTGAGGTAG			
N617	169		TGGC	CACCAAGGCGACGACGGGTAGCCGGCCTGAGAG	
Streptomyces ambofaciens NBRC	209	TGTTGGTG <mark>A</mark> GGTAG	TGGC	CACCAAGGCGACGACGGGTAGCCGGCCTGAGAG	
N1310	188	TGTTGGTG <mark>G</mark> GGTAA	CGGC	CACCAAGGCGACGACGGGTAGCCGGCCTGAGAG	
N1312	192	TGTTGGTG <mark>G</mark> GGTAA	IGGC	TACCAAGGCGACGACGGGTAGCCGGCCTGAGAG	
DN1317	185	TGTTGGTG <mark>G</mark> GGTAA		CACCAAGGCGACGACGGGTAGCCGGCCTGAGAGG	
DN1301	189	TGTTGGTG <mark>A</mark> GGTAA	T GGC	CACCAAGGCGACGACGGGTAGCCGGCCTGAGAGG	
DN1316	186	AGTTGGTG <mark>A</mark> GGTAA		CACCAAGGCGACGACGGGTAGCCGGCCTGAGAGG	
Streptomyces rochei NBRC 12908	215	A <mark>GTTGGTGA</mark> GGTAA	CGGC	CACCAAGGCGACGACGGGTAGCCGGCCTGAGAGG	
Streptomyces B5W222	237	TGTTGGTG <mark>A</mark> GGTAA	TGGC	CACCAAGGCGACGACGGGTAGCCGGCCTGAGAGG	
Streptomyces mutabilis NRRL IS	217	AGTTGGTGAGGTAA	TGGC	CACCAAGGCGACGACGGGTAGCCGGCCTGAGAGG	
<u>N1303</u>	186	TGTTGGTGGGGTAA	T GGC	raccaaggcgacgacgggtagccggcctgagag	
DN1304	186	A <mark>GTTGGTGA</mark> GGTAA	CGGC	CACCAAGGCGACGACGGGTAGCCGGCCTGAGAGG	
N1306	194	TGTTGGTG <mark>A</mark> GGTAA	TGGC	CRECAAGGCGACGACGGGTAGCCGGCCTGAGAGG	
Streptomyces 195018	191	TGTTGGTG <mark>A</mark> GGTAA		CACCAAGGCGACGACGGGTAGCCGGCCTGAGAGG	GGCGACCGGCCACACTGGGACT
DN1405	185	TGTTGGTG <mark>G</mark> GGTAA		CACCAAGGCGACGACGGGTAGCCGGCCTGAGAG	
DN1402	186	TGTTGGTG <mark>G</mark> GGTAA	TGGC	PACCAAGGCGACGACGGGTAGCCGGCCTGAGAG	56CGACC66CCACACT66GACT
DN1403	207	TGTTGGTG <mark>G</mark> GGTAA	TGGC	TACCAAGGCGACGACGGGTAGCCGGCCTGAGAGG	GGCGACCGGCCACACTGGGACT
Streptomyces N01 352 DQ717851	205	TGTTGGTG <mark>G</mark> GGTAA	TGGC	RACCAAGGCG CGACGGGTAGCCGGCCTGAGAGG	GGCGACCGGCCACACTGGGACT
DN1404	186	A GTTGGTG <mark>A</mark> GGTAA	CGGC	CACCAAGGCGACGACGGGTAGCCGGCCTGAGAG	FGCGACCGGCCACACTGGGACT
DN1406	185	AGTTGGTG <mark>A</mark> GGTAA	CGGC	CACCAAGGCGACGACGGGTAGCCGGCCTGAGAGG	GGCGACCGGCCACACTGGGACT
DN1407	186	A GTTEGTG A GGTAA	CGGC	CACCAAGGCGACGACGGGTAGCCGGCCTGAGAG	GGCGACCGGCCACACTGGGACT
DN1321	189	TGTTGGTG <mark>A</mark> GGTAA	CGGC	CACCAAGGCGACGACGGGTAGCCGGCCTGAGAGG	GCGACCGGCCACACTGGGACT
Streptomyces thermolilacinus N	214	TGTTGGTG <mark>A</mark> GGTAA	CGGC	CACCAAGGCGACGACGGGTAGCCGGCCTGAGAG	GGCGACCGGCCACACTGGGACT
Streptomyces heteromorphus AB	221	TGTTGGTG <mark>A</mark> GGTAA	CGGC	CACCAAGGCGACGACGGGTAGCCGGCCTGAGAG	
N1413	187	TGTTGGTG <mark>A</mark> GGTAA	CGGC	CACCAAGGCGACGACGGGTAGCCGGCCTGAGAGG	GGCGACCGGCCACACTG <u>GGACT</u>
treptomyces fragilis NRRL 242	233	TGTTGGTG <mark>A</mark> GGTAA	CGGC	CACCAAGGCGACGACGGGTAGCCGGCCTGAGAG	
Streptomyces humidus NRRL B-31	229	TGTTGGTG <mark>A</mark> GGTAA	TGGC	CACCAAGGCGACGACGGGTAGCCGGCCTGAGAGG	
N1307	189	TGTTGGTG <mark>A</mark> GGTAA	CGGC	ACCAAGGCGACCACGGGTAGCCGGCCTGAAAGG	
114 19	188	TGTTGGTG <mark>G</mark> GGT <mark>E</mark> A	TGGC	TACCAAGGCGACGACGGGTAGCCGGCCTGAGAG	
Streptomyces paraguayensis NBR	211	TGTTGGTGGGGTGA	TGGC	TACCAAGGCGACGACGGGGTAGCCGGCCTGAGAG	
Actinomadura nitritigenes T	197	TGTTGGTGGGGTGA	TGGC	TACCAAGGCGACGACGGGTAACCGGCCTGAGAG	
Actinomadura bangladeshensis T	218	TGTTGGTGGGGTGA	TGGC	TACCAAGGCGACGACGGGGTA <mark>A</mark> CCGGCCTGAGAGG	
Clustal Consensus	210		• UUV		

		490 · · · · · · · · · · · · · ·	500	510	520 · · · · · · ·	530	540	550 · · · · · · · ·
DN605	426	AACTACGTGCCAGCAI						GCGTATATAG
DN615	409	AACTACGTGCCAGCA	GCCGCGGTAA	TACGTAGGGCG	CAAGCGTTG	TCCGGAAT	TATTGO	GGCGTAAAGI
DN618	407	AACTACGTGCCAGCA	GCCGCGGTAA	TACGTAGGGCG	CGTITG	CGGAAT	TATTGO	GGCGTAAAG7
AY999771.1 Streptomyces ciner	445	AACTACGTGCCAGCAG	GCCGCGGTAA	TACGTAGGGCG	CAAGCGTTG	TCCGGAAT	TATTGO	GGCGTAAAG7
DN616	135	AACTACGTGCCAGCAG	GCCGCGGTAA	TACGTAGGGCG	CAAGCGTTG	TCCGGAAT		GGCGTAIAAGI
Streptomyces violaceorectus NB	453	AACTACGTGCCAGCA	GCCGCGGTAA	TACGTAGGGCG	CAAGCGTTG	TCCGGAAT		GGCGTAAAGI
Q418468.1 Streptomyces DA1020	419	AACTACGTGCCAGCA	GCCGCGGTAA	TACGTAGGGCG	CAAGCGTTG	TCCGGAAT		GGCGTAAAG
Streptomyces bikiniensis DSM40	474	AACTACGTGCCAGCA	GCCGCGGTAA	TACGTAGGGCG	CAAGCGTTG	TCCGGAAT		GGCGTAAAG
<u>194</u>	419	AACTACGTGCCAGCA	GCCGCGGTAA	TACGTAGGGCG	CAAGCGTTG	TCCGGAAT	TATITG?	GGCGTAAAG
F9 6	404	AACTACGTGCCAGCA	GCCGCGGTAA	TACGTAGGGCG	CAAGCGTTG	TCCGGAAT	TATTG	GGCGTAAAG
Streptomyces tanashiensis HBUM	436	AACTACGTGCCAGCA	GCCGCGGTAA	TACGTAGGGCG	CAAGCGTTG	TCCGGAAT	TATTGO	GGCGTAAAG
DN621	405	AACTACGTGCCAGCAI	GCCGCGGTAA	TACGTAGGGCG	CAAGCGTTG	TCCGGAAT	TATTG	GGCGTAAAG
DN607	409	AACTACGTGCCAGCAG					TATTGO	GGCGTAAAG
Streptomyces XAS585	435	AACTACGTGCCAGCA						GGCGTAAAG
01608	407	AACTACGTGCCAGCAI						GGCGTAAAG
DN606	426	AACTACGTGCCAGCAI						GGCGTAA <mark>-</mark> Ci
Streptomyces DA08605	449	AACTACGTGCCAGCAG						GGCGTAAAG
DN612	430	AACTACGTGCCAGCA						GGCGTAAAG
Streptomyces TRI 10 AB448718	427	AACTACGTGCCAGCAI						GGCGTAAAG
DN61501	409	AACTACGTGCCAGCA					TATTG	GGCGTAAAG
Streptomyces nodosus NBRC 1289	453	AACTACGTGCCAGCA	GCCGCGGTAA	TACGTAGGGCG	C <mark>G</mark> AGCGTTG	TCCGGAAT	TATTGO	GGCGTAAAG
DN617	408	AACTACGTGCCAGCAG	GCCGCGGTAA	TACGTAGGGCG	CAAGCGTTG	TCCGGAAT	TATTG	GGCGTAAAG
Streptomyces ambofaciens NBRC	448	AACTACGTGCCAGCA	GCCGCGGTAA	TACGTAGGGCG	CAAGCGTTG	TCCGGAAT	TATTG	GGCGTAAAG
DN1310	427	AACTACGTGCCAGCA	GCCGCGGTAA	TACGTAGGGCG	CAAGCGTTG	TCCGGAAT	TATTG	GGCGTAAAG
N1312	431	AACTACGTGCCAGCA	SCCGCGGTAA	TACGTAGGGCG	CAAGCGTTG	TCCGGAAT	TATITCE	GGCGTAAAG
DN1317	424	AACTACGTGCCAGCA	GCCGCGGTAA	TACGTAGGGCG	CAAGCGTTG	TCCGGAAT	TATITGS	GGCGTAAAG
DN1301	428	AACTACGTGCCAGCA	GCCGCGGTAA	TACGTAGGGCG	CAAGCGTTG	TCCGGAAT	TATTG	GGCGTAAAG
DN1316	425	AACTACGTGCCAGCA	GCCGCGGTAA	TACGTAGGGCG	CAAGCGTTG	TCCGGAAT	TATTG	GGCGTAAAG
Streptomyces rochei NBRC 12908	454	AACTACGTGCCAGCA	SCCGCGGTAA	TACGTAGGGCG	CAAGCGTTG	TCCGGAAT	TATTG(GGCGTAAAG
Streptomyces B5W222	476	AACTACGTGCCAGCA	GCCGCGGTAA	TACGTAGGGCG	CAAGCGTTG	TCCGGAAT	TATTG	GGCGTAAAG
Streptomyces mutabilis NRRL IS	456	AACTACGTGCCAGCA					TATITG?	GGCGTAAAG
DN1303	425	AACTACGTGCCAGCAI	GCCGCGGTAA	TACGTAGGGCG	CAAGCGTTG	TCCGGAAT	TATTCR	GGCGTAAAG
DN1304	425	AACTACGTGCCAGCA	GCCGCGGTAA	TACGTAGGGCG	CAAGCGTTG	TCCGGAAT	TATTG	GGCGTAAAG
DN1306	433	AACTACGTGCCAGCA	SCCGCGGTAA	TACGTAGGGCG	CGAGCGTTG	TCCGGAAT	TANTGO	GGCGTAAAG
Streptomyces 195018	430	AACTACGTGCCAGCA	GCCGCGGTAA	TACGTAGGGCG	C <mark>GAGCGTT</mark> G	TCCGGAAT		GGCGTAAAG
DN1405	424	AACTACGTGCCAGCA	GCCGCGGTAA	TACGTAGGGCG	CAAGCGTTG	TCCGGAAT		GGCGTAIAAGI
DN1402	425	AACTACGTGCCAGCAI	GCCGCGGTAA	TACGTAGGGCG	CAAGCGTTG	TCCGGAAT	manner	GGCGTAAAG
DN1403	446	AACTACGTGCCAGCA					CTGATATTG	GCGTAAAG
Streptomyces N01 352 DQ717851	443	AACTACGTGCCAGCA	GCCGCGGTAA	TACGTAGGGCG	CAAGCGTTG	TCCGGAAT	TATTG	GGCGTAAAG
DN1404	425	AACTACGTGCCAGCA	GCCGCGGTAA	TACGTAGGGCG	CAAGCGTTG	TCCGGAAT	TATTG	GGCGTAAAG
DN1406	424	AACTACGTGCCAGCA	GCCGCGGTAA	TACGTAGGGCG	CAAGCGTTG	TCCGGAAT	TATTG	GGCGTAAAG
DN1407	425	AACTACGTGCCAGCAI	GCCGCGGTAA	TACGTAGGGCG	CAAGCGTTG	TCCGGAAT	TATTG	GGCGTAAAG
N1321	428	AACTACGTGCCAGCAG	GCCGCGGTAA	TACGTAGGGCG	CAAGCGTTG	TCCGGAAT	TATTGO	GGCGTAAAG
Streptomyces thermolilacinus N	453	AACTACGTGCCAGCAG	GCCGCGGTAA	TACGTAGGGCG	CAAGCGTTG	TCCGGAAT	TATTG	GGCGTAAAG
Streptomyces heteromorphus AB	460	AACTACGTGCCAGCA						GGCGTAAAG
N1413	426	AACTACGTGCCAGCA					TATTG	GGCGTAAAG
Streptomyces fragilis NRRL 242	472	AACTACGTGCCAGCA	GCCGCGGTAA	TACGTAGGGCG	CAAGCGTTG	TCCGGAAT	TATTG	GGCGTAAAG
Streptomyces humidus NRRL B-31	469	AACTACGTGCCAGCAG						GGCGTAAAG
DN1307	428	AACTAC <mark>C</mark> TGCCAGCAG					TATTGO	GGCGTAAAG
114 19	427	AACTACGTGCCAGCAG AACTACGTGCCAGCAG	GCCGCGGTAA	TACGTAGGG <mark>T</mark> G	C <mark>G</mark> AGCGTTG	TCCGGAAT	TATTG	GGCGTAAAG
Streptomyces paraguayensis NBR	450	AACTACGTGCCAGCA	GCCGCGGTAA	TACGTAGGG <mark>T</mark> G	CGAGCGTTG	TCCGGAAT		GGCGTAAAG
Actinomadura nitritigenes T	436	AACTACGTGCCAGCAU	GCCGCGGTAA	TACGTAGGGCG	CAAGCGTTG	TCCGGAAT		GGCGTAAAG
Actinomadura bangladeshensis T	457	AACTACGTGCCAGCAG	GCCGCGGTAA	TACGTAGGGCG	CAAGCGTTG	TCCGGAAT	TATTGO	GGCGTAAAG
Clustal Consensus	120	****** *******	********	*** ** ** *	* ****	*****		******

		570	580	590	600	610	620	630
		<u></u>						
DN605	499	TAGGCGGCTTGTCA	CGTCGG	IGTGAAAGCCCGGG	GCTTAACCCC	CGGGTCTGCA <mark>T</mark>	CCGATACGGI	SCAGGCTAGAG'
DN615	482	TAGGCGGCTTGTC	CGTCGG	IGTGAAAGCCCGGG	GCTTAACCCC	GGGTCTGCA <mark>T</mark>	CCGATACCC	CAGGCTAGAG
DN618	474	TAGGCGGCTTGTC	CGTCGG	IGTGAAAGCCCGGG	GCTTAACCCC	GGGTCTGCAT	CCGATACCCG	CAGGCTAGAG
AY999771.1 Streptomyces ciner	518	TAGGCGGCTTGTC	CGTCGG	IGTGAAAGCCCGGG	GCTTAACCCC	GGGTCTGCAT	CGATACGG	GCAGGCTAGAG'
DN616	208	TAGGCGGCTTGTC	CGTCGG	IGTGAAAGCCCGGG	GCTTAACCCC	GGGTCTGCAT	CGATACGG	GCAGGCTAGAG'
Streptomyces violaceorectus NB	526	TAGGCGGCTTGTC	CGTCGGG	IGTGAAAGCCCGGG	GCTTAACCCC	GGGTCTGCA <mark>T</mark>	CCGATACCCG	SCAGGCTAGAG'
HQ418468.1 Streptomyces DA1020	492	TAGGCGGCTTGTC	CGTCGG	IGTGAAAGCCCGGG	GCTTAACCCC	GGGTCTGCAT	CCGATACGG	GCAGGCTAGAG
Streptomyces bikiniensis DSM40	547	TAGGCGGCTTGTC	CGTCGG	IGTGAAAGCCCGGG	GCTTAACCCC	GGGTCTGCAT	CGATACGG	GCAGGCTAGAG'
	40.0	The Paraverse and the Paraverse	aamaaaaa	Walt wak in in Paratatatatata		a a a a a a a a a a a a a a a a a a a		wak watawali ik wak wal

N9 6	477	TAGGCGGCTTGTC <mark>R</mark> CGTCGG <mark>C</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>TC</mark> CGATACGGGCAGGCTAGAG
Streptomyces tanashiensis HBUM	509	TAGGCGGCTTGTC <mark>R</mark> CGTCGG <mark>G</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>TC</mark> CGATACGGGCAGGCTAGAG
DN621	478	TAGGCGGCTTGTC <mark>R</mark> CGTCGG <mark>C</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>TC</mark> CGATACGGGCAGGCTAGAG
DN607	482	TAGGCGGCTTGTC <mark>A</mark> CGTCGG <mark>C</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>TC</mark> CGATACGGGCAGGCTAGAG
Streptomyces XAS585	508	TAGGCGGCTTGTC <mark>R</mark> CGTCGG <mark>C</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>TC</mark> CGATACGGGCAGGCTAGAG
DN608	480	TAGGCGGCTTGTC <mark>A</mark> CGTCGG <mark>C</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>TC</mark> CGATACGGGCAGGCTAGAB
DN606	498	TAGGCGGCTTGTC <mark>A</mark> CGTCGG <mark>T</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>GT</mark> CGATACGGGCAGGCTAGAG
Streptomyces DA08605	522	TAGGCGGCTTGTC <mark>a</mark> CGTCGG <mark>T</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>GT</mark> CGATACGGGCAGGCTAGAG
DN612	503	TAGGCGGCTTGTC <mark>G</mark> CGTCGG <mark>T</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>GT</mark> CGATACGGGCAGGCTAGAG
Streptomyces TRI 10 AB448718	500	TAGGCGGCTTGTC <mark>G</mark> CGTCGG <mark>T</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>GT</mark> CGATACGGGCAGGCTAGAG
DN61501	482	TAGGCGGCTTGTC <mark>a</mark> CGTCGG <mark>T</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>GT</mark> CGATACGGGCAGGCTAGAG
Streptomyces nodosus NBRC 1289	526	TAGGCGGCTTGTC <mark>G</mark> CGTCGG <mark>T</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>GT</mark> CGATACGGGCAGGCTAGAG
DN617	481	TAGGCGGCTTGTC <mark>A</mark> CGTCGG <mark>T</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>GT</mark> CGATACGGGCAGGCTAGAG
Streptomyces ambofaciens NBRC	521	TAGGCGGCTTGTC <mark>a</mark> CGTCGG <mark>T</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>GT</mark> CGATACGGGCAGGCTAGAG
DN1310	500	TAGGCGGCTTGTC <mark>A</mark> CGTCGG <mark>C</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>TC</mark> CGATACGGGCAGGCTAGAG
DN1312	504	TAGGCGGCTTGTC <mark>a</mark> CGTCGG <mark>G</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>TC</mark> CGATACGGGCAGGCTAGAG
DN1317	497	TAGGCGGCTTGTC <mark>a</mark> CGTCGG <mark>G</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>TC</mark> CGATACGGGCAGGCTAGAG
DN1301	501	TREECEGCTTETC <mark>a</mark> CETCEE <mark>T</mark> TETEAAAGCCCEEEGECTTAACCCCEEGTCTECA <mark>ET</mark> CEATACEEECAEECTAEAG
DN1316	498	TAGECCECTTGTC <mark>a</mark> CETCEE <mark>T</mark> TGTGAAAGCCCEEGEGCTTAACCCCEEGTCTGCA <mark>GT</mark> CEATACEGECAGECTAGAG
Streptomyces rochei NBRC 12908	527	TAGGCGGCTTGTC <mark>a</mark> CGTCGG <mark>T</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>GT</mark> CGATACGGGCAGGCTAGAG
Streptomyces B5W222	549	TAGGCGGCTTGTC <mark>a</mark> CGTCGG <mark>T</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>GT</mark> CGATACGGGCAGGCTAGAG
Streptomyces mutabilis NRRL IS	529	TNEECEECTTETC <mark>a</mark> Cetcee <mark>t</mark> tetgaangecceeegecttancecceeetcteca <mark>st</mark> ceataceeecaeectaeae
DN1303	498	TAGGCGGCTTGTC <mark>a</mark> CGTCGG <mark>G</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>TC</mark> CGATACGGGCAGGCTAGAG
DN1304	498	TAGGCGGCTTGTC <mark>a</mark> CGTCGG <mark>T</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>GT</mark> CGATACGGGCAGGCTAGAG
DN1306	506	TAGGCGGCTTGTC <mark>G</mark> CGTCGG <mark>T</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>GT</mark> CGATACGGGCAGGCTAGAG
Streptomyces 195018	503	TAGGCGGCTTGTC <mark>G</mark> CGTCGG <mark>T</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>GT</mark> CGATACGGGCAGGCTAGAG
DN1405	497	TAGGCGGCTTGTC <mark>A</mark> CGTCGG <mark>G</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>TC</mark> CGATACGGGCAGGCTAGAG
DN1402	498	TAGGCGGCTTGTC <mark>A</mark> CGTCGG <mark>E</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>TC</mark> CGATACGGGCAGGCTAGAG
DN1403	526	TAGGCGGCTTGTC <mark>a</mark> CGTCGG <mark>G</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>TC</mark> CGATACGGGCAGGCTAGAG
Streptomyces NO1 352 DQ717851	516	TAGGCGGCTTGTC <mark>A</mark> CGTCGG <mark>G</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>TC</mark> CGATACGGGCAGGCTAGAG
DN1404	498	TAGGCGGCTTGTC <mark>A</mark> CGTCGG <mark>T</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>GT</mark> CGATACGGGCAGGCTAGAG
DN1406	497	TAGGCGGCTTGTC <mark>A</mark> CGTCGG <mark>T</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>GT</mark> CGATACGGGCAGGCTAGAG
DN1407	498	TAGGCGGCTTGTC <mark>A</mark> CGTCGG <mark>T</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>GT</mark> CGATACGGGCAGGCTAGAG
DN1321	501	TAGGCGGCTTGTC <mark>5</mark> CGTCGGATGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>TT</mark> CGATACGGGCAGGCTAGAG
Streptomyces thermolilacinus N	526	TAGGCGGCTTGTCGCGTCGGATGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>TT</mark> CGATACGGGCAGGCTAGAG
Streptomyces heteromorphus AB	533	TAGGCGGCTTGTCGCGTCGG <mark>T</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>GT</mark> CGATACGGGCAGGCTAGAG
DN1413	499	TAGGCGGCTTGTC <mark>C</mark> CGTCGG <mark>T</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCR <mark>GT</mark> CGATACGGGCAGGCTAGAG
Streptomyces fragilis NRRL 242	545	TAGGCGGCTTGTC <mark>G</mark> CGTCGG <mark>T</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>GT</mark> CGATACGGGCAGGCTAGAG
Streptomyces humidus NRRL B-31	542	TAGGCGG <mark>TC</mark> TGTC ⁷ CGTCGG <mark>R</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>TT</mark> CGATACGGGCAG <mark>R</mark> CTAGAG
DN1307	501	TANGCGGCTTGTCCCGTCCGTGTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>GT</mark> CGATACGGGCAGGCTAGAG
<u>N14 19</u>	500	TAGGCGGC <mark>C</mark> TGTC ⁻ CGTCGG <mark>A</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>TT</mark> CGATACGGGCAGGCTAGAG
Streptomyces paraguayensis NBR	523	TAGGCGGCTTGTC ⁻ CGTCGGTTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>TT</mark> CGATACGGGCAGGCTAGAG
Actinomadura nitritigenes T	509	TAGGCGG <mark>T</mark> TTGTC ⁻ CGTC <mark>TCGTGTAAAGCCCCAC</mark> GGCTTAAC <mark>TGT</mark> GGGTCTGC <mark>GGTG</mark> GATACGGGCAG ^A CTAGAG
Actinomadura bangladeshensis T	530	TAGECCEGTITIGTCGCCTCTGTCGTCGAAMGCCCCACGECCTTANCCGTGGGTCGGGTGGATACCGGECAGACTAGAG
Clustal Consensus	181	** **** **** **** * ********* ******* ****

1306	506	lipboard slightly large. To show control panel, press the red arrow (upper left) INTERCEPTIVETOFOTOTOED INFORMATIC CONFERENCE IN MACCONFERENCE IN THE INFORMATIC CONFERENCE INFORMATICAL INFORMATIC CONFERENCE INFORMATICAL INFORMATIC
treptomyces 195018	503	TAGGCGGCTTGTCGCGTCGGTTGTGAAAGCCCCGGGGCTTAACCCCCGGGTCTGCA <mark>GT</mark> CGATACGGGCAGGCTAGAG
1405	497	TAGGCGGCTTGTCACGTCGGGTGTGAAAGCCCCGGGGCTTAACCCCCGGGTCTGCA <mark>TC</mark> CGATACGGGCAGGCTAGAG
1403	498	TAGGCGGCTTGTCACGTCGGCTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>TC</mark> CGATACGGGCAGGCTAGAG
11402	526	TAGGCGGCTTGTCACGTCGGCTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>TC</mark> CGATACGGGCAGGCTAGAG
reptomyces N01 352 D0717851	516	TABGCGGCTTGTC <mark>A</mark> CGTCGG <mark>G</mark> TGTGAANGCCCGGGGCTTAACCCCGGGTCTGCA <mark>TC</mark> CGATACGGGCAGGCTAGAG
1404	498	
11404	490	
		TAGGCGGCTTGTCRCGTCGG <mark>T</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>GT</mark> CGATACGGGCAGGCTAGAG
[1407	498	TAGGCGGCTTGTCACGTCGGTTGTGAAAGCCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAG
1321	501	TAGGCGGCTTGTC <mark>G</mark> CGTCGG <mark>A</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>TT</mark> CGATACGGGCAGGCTAGAG TAGGCGGCTTGTC <u>C</u> CGTCGG <mark>A</mark> TGTGAAAGCCCCGGGGCTTAACCCCGGGTCTGCA <mark>TT</mark> CGATACGGGCAGGCTAGAG
reptomyces thermolilacinus N reptomyces heteromorphus AB	526 533	
	533 499	
11413		
reptomyces fragilis NRRL 242	545	
reptomyces humidus NRRL B-31	542	TAGGCGG <mark>TCT</mark> GTCTCCGCGGGCGGGGCTTAACCCCCGGGTCTGCA <mark>TT</mark> CGATACGGGCAGGCTGGA
1307	501	TANGCGGCTTGTCCCGTCCGTTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>GT</mark> CGATACGGGCAGGCTAGAG
<u>14 19</u>	500	TAGGCGGCCTGTCGCGTCGGATGTGAAAGCCCCGGGCTTAACCCCCGGGTCTGCA <mark>TT</mark> CGATACGGGCAGGCTAGAG
reptomyces paraguayensis NBR	523	TREECEGE <mark>N</mark> TETC <mark>E</mark> CETCEE <mark>R</mark> TETEAAAGCCCEEGECTTAACCCCEEGTCTECA <mark>TT</mark> CEATACEEGECAEECTAEAG
tinomadura nitritigenes T	509	TAGGCGC <mark>T</mark> TTGTCCCGTCTCTCGTGAAAGCCCCACGGCTTAAC <mark>TGT</mark> GGGTCTGCGGTGGATACGGGCAGACTAGAG TAGGCGC <mark>T</mark> TTGTCCCGCTCTCTCGTGAAAGCCCCACGGCTTAACCGTGGGTCTGCGGTGGATACGGGCAGACTAGAG
ctinomadura bangladeshensis T	530	
lustal Consensus	181	** **** **** * ******** ******** ******
		650 660 670 680 690 700 710
KOF	6.20	TAEEEEABAYCEBAAWCCNEETEFIAACEETEFAAWCECECABAYAYCAEEAEEAACACCEETEECEAAE
1605	579	
1615 1410	562	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGAT
	554	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGGAAGGCGGAT
Y999771.1 Streptomyces ciner	598	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGAT
<u>1616</u>	288	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGAT
reptomyces violaceorectus NB	606	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGAT
418468.1 Streptomyces DA1020	572	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGAT
treptomyces bikiniensis DSM40	627	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGAT
9 4	572	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGAT
9 6	557	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGAT
treptomyces tanashiensis HBUM	589	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGAT
1621	558	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGAT
1607	562	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGAT
treptomyces XAS585	588	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGAT
1608	560	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGAT
1606	578	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGAT
reptomyces DA08605	602	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGAT
1612	583	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGAT
treptomyces TRI 10 AB448718	580	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGAT
161501	562	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGAT
reptomyces nodosus NBRC 1289	606	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGAT
1617	561	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGAT
reptomyces ambofaciens NBRC	601	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGA
1310	580	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGAT
1312	584	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGAT
1317	577	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCRGATATCAGGAGGAACACCGGTGGCGAAGGCGGAT
1301	581	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGAT
1316	578	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGAT
reptomyces rochei NBRC 12908	607	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGAT
reptomyces B5W222	629	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGAT
reptomyces mutabilis NRRL IS	609	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGAT
1303	578	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGAT
	0,0	
1304	578	TAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGAT



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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	TAGGGGAGA <mark>AT</mark> GGAATTCC <mark>C</mark> GGTGTAGCGGTGAAATGCGCAGATATC <mark>E</mark> GGAGGAACACCGGTGGCGAAGGCGG <mark>T</mark> TC
Actinomadura bangladeshensis T	610	TAGGGGAGA <mark>AT</mark> GGAATTCC <mark>C</mark> GGTGTAGCGGTGAAATGCGCAGATATC <mark>G</mark> GGAGGAACACCGGTGGCGAAGGCGG <mark>T</mark> TC
Clustal Consensus	241	*******

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		····· ···· ···· ···· ···· ···· ···· ····
DN605	659	GGCC <mark>AT</mark> TACTGACGCTGA <mark>-</mark> GGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAI
DN615	642	EGCC <mark>AT</mark> TACTGACGCTGAAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA
DN618	634	GGCC <mark>AT</mark> TACTGACGCTGA_GGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
AY999771.1 Streptomyces ciner	678	GGCC <mark>AT</mark> TACTGACGCTGA-GGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
DN616	368	GGCC <mark>AT</mark> TACTGACGCTGA-GGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
Streptomyces violaceorectus NB	686	GGCC <mark>AT</mark> TACTGACGCTGA <mark>-</mark> GGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
HQ418468.1 Streptomyces DA1020	652	EGCC <mark>AT</mark> TACTERCECTER <mark>-</mark> EGRECGARRECETEGEGRECGARCREGATTREATACCCTEETRETCCRCECCETARI
Streptomyces bikiniensis DSM40	707	GGCC <mark>AT</mark> TACTGACGCTGA-GGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAI
N9 4	652	GGCC <mark>AT</mark> TACTGACGCTGA <mark>-</mark> GGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAI
N9 6	637	GGCC <mark>AT</mark> TACTGACGCTGA-GGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAI
Streptomyces tanashiensis HBUM	669	GGCC <mark>AT</mark> TACTGACGCTGA-GGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAI
DN621	638	GGCC <mark>AT</mark> TACTGACGCTGA <mark>-</mark> GGAGCGAAAGCGTGGG <mark>-</mark> AGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAI
DN607	642	GGCC <mark>AT</mark> TACTGACGCTGA-GGAGCGAAAGCGTGGG G AGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAI
Streptomyces XAS585	668	GGCC <mark>AT</mark> TACTGACGCTGA <mark>-</mark> GGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAI
DN608	640	GGCC <mark>AT</mark> TACTGACGCTGA <mark>,</mark> GGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAI
DN 6 0 6	658	GGCC <mark>GA</mark> TACTGACGCTGA <mark>-</mark> GGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAI
Streptomyces DA08605	682	GGCC <mark>GA</mark> TACTGACGCTGA <mark>-</mark> GGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAI
DN612	663	GGCC <mark>GA</mark> TACTGACGCTGA-GGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAI
Streptomyces TRI 10 AB448718	660	GGCC <mark>GA</mark> TACTGACGCTGA-GGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAI
DN61501	642	EGCC <mark>GA</mark> TACTGACGCTGA <mark>,</mark> EGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAI
Streptomyces nodosus NBRC 1289	686	GGCC <mark>GA</mark> TACTGACGCTGA <mark>-</mark> GGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA
DN617	641	GGCC <mark>GA</mark> TACTGACGCTGA-GGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA
Streptomyces ambofaciens NBRC	681	GGCC <mark>GA</mark> TACTGACGCTGA-GGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA
DN1310	660	GGCC <mark>AT</mark> TACTGACGCTGA-GGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAJ
DN1312	664	GGCC <mark>AT</mark> TACTGACGCTGA-GGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA
DN1317	657	GGCC <mark>AT</mark> TACTGACGCTGA-GGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA
DN1301	661	EGCC <mark>GA</mark> TACTGACECTGA <mark>-</mark> EGAGCGAAAGCGTGEGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAI
DN1316	658	GGCC <mark>GA</mark> TACTGACGCTGA-GGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA
Streptomyces rochei NBRC 12908	687	GGCC <mark>GA</mark> TACTGACGCTGA <mark>-</mark> GGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA
Streptomyces B5W222	709	EGCC <mark>GA</mark> TACTGACECTGA <mark>_</mark> EGAGCGAAAGCGTGEGEAGCGAACAGGATTAGATACCCTEGTAGTCCACGCCGTAA
Streptomyces mutabilis NRRL IS	689	GGCC <mark>GA</mark> TACTGACGCTGA <mark>-</mark> GGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA
DN1303	658	GGCC <mark>AT</mark> TRCTGRCGCTGA <mark>-</mark> GGRGCGRARGCGTGGGGRGCGRRCRGGATTRGRTRCCCTGGTRGTCCRCGCCGTRA
DN1304	658	GGCC <mark>GA</mark> TACTGACGCTGA-GGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAJ
DN1306	666	GGCC <mark>GA</mark> TACTGACGCTGA <mark>-</mark> GGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAI
Streptomyces 195018	663	GGCC <mark>GA</mark> TACTGACGCTGA-GGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA
DN1405	657	GGCC <mark>AT</mark> TACTGACGCTGA-GGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA
DN1402	658	GGCC <mark>AT</mark> TACTGACGCTGA-GGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA
DN1403	686	EGCC <mark>AT</mark> TACTGACGCTGA <mark>,</mark> GGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA
Streptomyces N01 352 DQ717851	676	GGCC <mark>AT</mark> TACTGACGCTGA <mark>-</mark> GGAGCGAAAGCGTGGGGGGGGGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA
DN1404	658	EGCC <mark>GA</mark> TACTGACGCTGA <mark>-</mark> GGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA
DN1406	657	EGCC <mark>GA</mark> TACTGACGCTGA <mark>,</mark> EGAGCGAAAGCGTGEGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAI
DN1407	658	GGCC <mark>GA</mark> TACTGACGCTGA <mark>-</mark> GGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAI
DN1321	661	EGCC <mark>GA</mark> TACTGACECTGA <mark>_</mark> EGAGCGAAAGCGTGEGEAGCGAACAGGATTAGATACCCTEGTAGTCCACGCCGTAA
Streptomyces thermolilacinus N	686	GGCC <mark>GA</mark> TACTGACGCTGA-GGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA
	693	GGCC <mark>GA</mark> TACTGACGCTGA-GGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA
DN1413	659	GGCC <mark>GA</mark> TACTGACGCTGA-GGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA
	705	GGCC <mark>GA</mark> TACTGACGCTGA-GGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA
	702	GGCC <mark>AT</mark> TACTGACGCTGA_GGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA
M1307	661	GGCC <mark>GA</mark> TACTGACGCTGA-GGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA
114 19	660	GGCC <mark>GA</mark> TACTGACGCTGA_GGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA
	683	GGCC <mark>GA</mark> TACTGACGCTGA_GGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA
Actinomadura nitritigenes T	669	GGCC <mark>T</mark> GTACTGACGCTGA_GGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA
Actinomadura bangladeshensis T	690	GGCC <mark>T</mark> GTACTGACGCTGA-GGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA
	316	

		<i>690</i>	900 .	910	920	930 	940 · · · · · · · ·	950
N605	818	сааббстаааастсаааб				CEGRECATETE		
N615	802	CAAGGCTAAAACTCAAAG				CEGAECATETE		
N618 AY999771.1 Streptomyces ciner	793 837	GARGGCTARARCTCARAG GARGGCTARARCTCARAG				CGGAGCATGTG CGGAGCATGTG		
N616	527	CAAGGCTAAAACTCAAAG	GANTIGACO	GGGGCCCG	сасаавсав	CGGAGCATGTG	SCITANITCO	ACCCARCOCCI
treptomyces violaceorectus NB	845	CAAGGCTAAAACTCAAAG	GAATTGACG	GGGGCCCG	CACAAGC	CEGAECATETE	GCTTRATTCO	ACGCAACGCGT
Q418468.1 Streptomyces DA1020	811	CARGECTARAACTCARAG	GAATTGACG	GEEECCCE	CACAAGC <mark>A</mark> G	CEGRECATETE		
treptomyces bikiniensis DSM40	866	CAAGGCTAAAACTCAAAG				CEGACCATETE		
94	811	CARGECTAMAACTCARAG				CEGAECATETE		
96	796	CAAGGCTAAAACTCAAAG				CGGAGCATGTG		
treptomyces tanashiensis HBUM N621	828 796	CAAGGCTAAAACTCAAAG GAAGGCTAAAACTCAAAG				CGGAGCATGTG CGGAGCATGTG		
N607	801	CAAGGCTAAAACTCAAAG				CGGAGCATGTG		
treptomyces XAS585	827	CAAGGCTAAAACTCAAAG	GAATTGACG	GGGGCCCG	CACAAGCAG	CEGAECATETE	GCTTARTTCO	ACGCAACGCGI
N608	799	CAAGGCTAAAACTCAAAG	GAATTGACG	GEGECCCE	CACAAGCAG	CEGRECATETE		
N606	817	CAAGGCTAAAACTCAAAG				CEGAECATETE		
treptomyces DA08605	841	CARGECTARAACTCARAG				CEGRECATETE		
N612	822	CARGGETARAACTERAAG				CEGAECATETE		
treptomyces TRI 10 AB448718	819	CAAGGCTAAAACTCAAAG				CEGAECATETE		
N61501 treptomyces nodosus NBRC 1289	801 845	GARGGCTARARCTCARAG GARGGCTARARCTCARAG				CGGAGCATGTG CGGAGCATGTG		
N617	800	CAAGGCTAAAACTCAAAG	GANTIGACO	GGGGCCCG	Сасаавств	CGGAGCATGTG	SCITAMITCO	ACCCARCOCCI
treptomyces ambofaciens NBRC	840	CAAGGCTAAAACTCAAAG	GAATTGACG	GGGGCCCG	CACAAGCEG	CEGAECATETE	GCTTAATTCG	ACGCAACGCGT
N1310	819	СААББСТААААСТСАААБ				CEGRECATETE		
N1312	823	CAAGGCTAAAACTCAAAG	GAATTGACG	GGGGCCCG	CACAAGCAG	CEGAECATETE	GCTTAATTCG	ACGCAACGCGI
N1317	816	CARGECTARARCTCARAG	GRATTGACG	GGGGCCCG	CACAAGC <mark>A</mark> G	CEGRECATETE	GCTTAATTCG	ACCOMCCCC
4	820			*******	a Antonio a	MANAGA MANAGA	*****	******
Note: This is a print preview. It may copy	to the o	lipboard slightly large. To sl	how control pa	anel, press ti	ne red arrow I	upper left)		
N1316	81.1	СААББСТААААСТСАААБ	GAATTGACG	ыныссссь	CACARGED	CGGAGCATGIG	CITTATITCE	TREFERENCE
treptomyces rochei NBRC 12908	846	CAAGGCTAAAACTCAAAG	GAATTGACG	GGGGCCCG	CACAAGC	CGGAGCATGTG	GCTTAATTCG	ACGCAACGCGI
treptomyces B5W222	868	CARGECTARACTCARAG				CGGAGCATGTG		
treptomyces mutabilis NRRL IS	848	CAAGGCTAAAACTCAAAG				CEGRECATETE		
N1303	817 817	CARGGCTARAACTCARAG				CEGRECATETE	SCITIANTICG	ACGCAACGCGA
N1304 N1306	817	GARGECTARARCTCARRS GARGECTARARCTCARRS				CGGAGCATGTG CGGAGCATGTG		
	822	CARGECTARAACTCARAG	CANTIGACO	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CACARGOES	CGGRGCATGTG	SCITIZATICG CCTTAATTCC	ACCCANCECCI
treptomyces 195018 N1405	816	CARGECTARACTCARG				CEGRECATETE		
N1402	817	CARGECTARAACTCARAG				CEGRECATETE		
N1403	845	СААББСТААААСТСАААБ				CEGAECATETE	SCTTAATTCG	ACECAACECET
treptomyces N01 352 DQ717851	835	CARGECTARAACTCARAG				CEGAECATETE		
N1404	817	CAAGGCTAAAACTCAAAG			CACAAGC <mark>G</mark> G	CEGAECATETE	GCTTAATTCG	ACGCAACGCGI
N1406	816	CAAGGCTAAAACTCAAAG	GAATTGACG	GGGGCCCG	CACAAGC <mark>G</mark> G	CEGAECATETE	GCTTAATTCG	ACGCAACGCGA
N1407	817	CAAGGCTAAAACTCAAAG				CGGAGCATGTG		
N1321	820	CARGECTARAACTCARAG				CEGAECATETE		
treptomyces thermolilacinus N	845	CAAGGCTAAAACTCAAAG				CEGAECATETE		
treptomyces heteromorphus AB	852	CAAGGCTAAAACTCAAAG	GAATTGACG	GGGGCCCG	CACAAGCEG	CGGAGCATGTG	SCITAATICG	ACGCAACGCGI
N1413	818 864	CARGGCTAAAACTCAAAG CAAGGCTAAAACTCAAAG				CGGAGCATGTG CGGAGCATGTG		
treptomyces fragilis NRRL 242 treptomyces humidus NRRL B-31	861	CARGGETANAACTCARAG				CEGAECATETE		
N1307	820	CARGECTARACTCARG				CEGRECATETE		
14 19	819	CARGECTARACTCARAG	GAATTGACG	GGGGCCCG	CACAAGCEG	CEGAECATETE		
treptomyces paraguayensis NBR	842	CARGECTARAACTCAARG			CACAAGO	CEGRECATETE	SCITAATTCG	ACGCAACGCGA
ctinomadura nitritigenes T	827	CARGECTARAACTCARAG			FACAAGC	CGGAGCATGT <mark>T</mark>	GCTTAATTCG	ACGCAACGCGI
ctinomadura bangladeshensis T	848	CARGECTARACTCARAG	GAATTGACG	GEEECCCE	CACAAGC <mark>E</mark> G	CGGAGCATGT <mark>T</mark> CGGAGCATGT <mark>T</mark>	GCTTAATTCG	ACGCAACGCGI
lustal Consensus	455	*****	********	******	****** *	********	********	*********
		970	980	990	1000	1010	1020	1030
N605	898	CONTRACT TECONTENOS	an record	T.G.COT C	a enerro er	CCCCCTTET	CENTREMAN	CACCTECTECT
N615	882	CCTTACCAAGGCTTGACA				GCCCCCCTTGT		CAGGTGGTGCI
N618	873	CCTTACCAAGGCTTGACA			GAGATGET	GCCCCCTTGT		CAGGTGGTGCI
	917	CCTTACCARGGCTTGACA	TATACCGGA	m GCAT - C	GAGATGET	6 <mark>C</mark> CCCCCTTGT	EGTCGGT <mark>R</mark> TR	CAGGTGGTGCI
AY999771.1 Streptomyces ciner		CCTTRCCARGGCTTGRCZ	TATACCGGA	m GC <mark>AT - C</mark>	n GAGA <mark>T</mark> GCT	6 <mark>C</mark> CCCCCTTGT	EGTCCCT <mark>A</mark> TS	CAGGTGGTGCI
AY999771.1 Streptomyces ciner	607					Pagagamment		CAGGTGGTGCI
AY999771.1 Streptomyces ciner N616 treptomyces violaceorectus NB	925	CCTTRCCARGECTTGRCA						CAGGTGGTGCI
AY999771.1 Streptomyces ciner N616 treptomyces violaceorectus NB Q418468.1 Streptomyces DA1020	925 891	CCTTACCAAGGCTTGACA	ITA <mark>T</mark> ACCGGA	m GC <mark>AT - C</mark>	GAGATGCT	FCCCCCTTGT		
AY999771.1 Streptomyces ciner N616 treptomyces violaceorectus NB Q418468.1 Streptomyces DA1020 treptomyces bikiniensis DSM40	925 891 946	CCTTACCAAGGCTTGACA CCTTACCAAGGCTTGACA	ITA <mark>T</mark> ACCGGA ITA <mark>T</mark> ACCGGA	AAGC <mark>AT C</mark> AAGC <mark>AT C</mark>	AGAGA <mark>T</mark> GCT AGAGA <mark>T</mark> GCT	G <mark>C</mark> CCCCCTTGT G <mark>C</mark> CCCCCTTGT	EGTCGGT<mark>A</mark>TA	CAGGTGGTGCI
AY999771.1 Streptomyces ciner N616 treptomyces violaceorectus NB Q418468.1 Streptomyces DA1020 treptomyces bikiniensis DSN40 9 4	925 891 946 891	CCTTRCCRAGGCTTGRCR CCTTRCCRAGGCTTGRCR CCTTRCCRAGGCTTGRCR	ITA <mark>T</mark> ACCGGA ITA <mark>T</mark> ACCGGA ITA <mark>T</mark> ACCGGA	ANGCA <mark>T - C</mark> ANGCA T - C ANGCA T - C	AGAGA <mark>T</mark> GET AGAGA <mark>T</mark> GET AGAGA <mark>T</mark> GET	GCCCCCTTGT GCCCCCCTTGT GCCCCCCTTGT	egtocot <mark>a</mark> ta Egtocotata	CAGGTGGTGCZ
AY999771.1 Streptomyces ciner N616 treptomyces violaceorectus NB Q418468.1 Streptomyces DA1020 treptomyces bikiniensis DSN40 9 4 9 6	925 891 946 891 876	CCTTRCCARGGCTTGRCA CCTTRCCARGGCTTGRCA CCTTRCCARGGCTTGRCA CCTTRCCARGGCTTGRCA	ITA <mark>T</mark> ACCGGA ITA <mark>T</mark> ACCGGA ITA <mark>T</mark> ACCGGA ITA <mark>T</mark> ACCGGA	ANGCA <mark>T - C</mark> ANGCA <mark>T - C</mark> ANGCA <mark>T - C</mark> ANGCA <mark>T - C</mark>	AGAGA <mark>T</mark> GGT AGAGATGGT AGAGATGGT AGAGATGGT	FCCCCCCTTFT FCCCCCCCTTFT FCCCCCCCTTFT FCCCCCCCTTFT	EGTCGGT <mark>A</mark> TA EGTCGGTATA EGTCGGT <mark>A</mark> TA	CAGGTGGTGCI
XV999771.1 Streptomyces ciner N616 treptomyces violaceorectus NB Q418468.1 Streptomyces DA1820 treptomyces bikinensis DSH40 <u>9 4</u> 9 6 treptomyces tanashiensis HBUM	925 891 946 891 876 908	CCTTRCCRAGGCTTGRCR CCTTRCCRAGGCTTGRCR CCTTRCCRAGGCTTGRCR CCTTRCCRAGGCTTGRCR CCTTRCCRAGGCTTGRCR	YTA <mark>T</mark> ACCGGA YTATACCGGA YTATACCGGA YTATACCGGA YTATACCGGA	ANGCA <mark>T - C</mark> ANGCA T - C ANGCA T - C ANGCA T - C ANGCA T - C	AGAGATGGT AGAGATGGT AGAGATGGT AGAGATGGT AGAGATAGT	FCCCCCTTGT FCCCCCCTTGT FCCCCCCTTGT FCCCCCCTTGT FCCCCCCTTGT	GGTCGGT <mark>A</mark> TA GGTCGGT <mark>A</mark> TA GGTCGGT <mark>A</mark> TA GGTCGGT <mark>A</mark> TA	CAGGTGGTGC7 CAGGTGGTGC7 CAGGTGGTGC7
XV999771.1 Streptomyces ciner H616 Treptomyces violaceorectus NB 041468.1 Streptomyces DA1020 J teptomyces bikiniensis DSH40 9 4 9 6 treptomyces tanashiensis HBUM H621	925 891 946 891 876	CCTTACCAAGGCTTGACA CCTTACCAAGGCTTGACA CCTTACCAAGGCTTGACA CCTTACCAAGGCTTGACA CCTTACCAAGGCTTGACA CCTTACCAAGGCTTGACA	ATA <mark>T</mark> ACCGGA ATATACCGGA ATATACCGGA ATATACCGGA ATATACCGGA ATA <mark>T</mark> ACCGGA	AAGCA <mark>T - C</mark> AAGCA <mark>T - C</mark> AAGCA T - C AAGCA T - C AAGCA T - T AAGC <mark>AT - T</mark>	AGAGA <mark>T</mark> GGT AGAGATGGT AGAGATGGT AGAGATGGT	GCCCCCCTTGT GCCCCCCTTGT GCCCCCCTTGT GCCCCCCTTGT GCCCCCCTTGT GCCCCCCTTGT	EGTEEGT <mark>A</mark> TA EGTEEGTATA EGTEEGTATA EGTEEGTATA EGTEEGT <mark>A</mark> TA	CAGGTGGTGCI CAGGTGGTGCI CAGGTGGTGCI CAGGTGGTGCI
NY999771.1 Streptomyces ciner N616 Treptomyces violaceorectus NB Q418468.1 Streptomyces DA1020 9 4 9 6 treptomyces tanashiensis HBUM N621 N621	925 891 946 891 876 908 876	CCTTACCAAGGCTTGACA CCTTACCAAGGCTTGACA CCTTACCAAGGCTTGACA CCTTACCAAGGCTTGACA CCTTACCAAGGCTTGACA CCTTACCAAGGCTTGACA	ITA <mark>T</mark> ACCEEA ITA <mark>T</mark> ACCEEA ITATACCEEA ITATACCEEA ITATACCEEA ITATACCEEA ITATACCEEA	AAGCAT-C AAGCAT-C AAGCAT-C AAGCAT-C AAGCAT-T AAGCAT-T AAGCAT-T AAGCAT-T	AGAGATGGT AGAGATGGT AGAGATGGT AGAGATGGT AGAGATAGT AGAGATAGT AGAGATAGT	CCCCCTTGT CCCCCCTTGT CCCCCCTTGT CCCCCCTTGT CCCCCCTTGT CCCCCCTTGT CCCCCCTTGT CCCCCCTTGT	EGTCEGTAFA EGTCEGTAFA EGTCEGTAFA EGTCEGTAFA EGTCEGTAFA EGTCEGTAFA	CAGGTGGTGCI CAGGTGGTGCI CAGGTGGTGCI CAGGTGGTGCI CAGGTGGTGCI
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NX7997071.1 Streptomyces ciner NG16 VF16 treptomyces violaccorectum NB Q14864.3 Streptomyces DN1020 treptomyces bikinicnasis DS140 9 Teptomyces tanashiensis NUUM N600 Treptomyces XX5385 N600 N601 Treptomyces TRI 10 XB448718 N6190 N6190 Treptomyces nodosus NBRC 1289 N611 N611312	925 891 946 876 876 881 907 879 827 902 899 881 925 880 925 880 923		ITATACCGGA ITATACCGGA ITATACCGGA ITATACCGGA ITATACCGGA ITATACCGGA ITATACCGGA ITATACCGGA ITATACCGGA ITATACCGGA ITACACCGGA ITACACCGGA ITACACCGGA ITACACCGGA ITACACCGGA ITACACCGGA ITACACCGGA	An Geat - C an Seat - T an Seat - T an Seat - T an Seat - C an Seat - C an Seat - T an Seat - T an Seat - T an Seat - T an Seat - C	a Grights of A Grights of C Grights of C Grights of C Grights of C Grights of C Grights of A Grights of C Grights of A Grights of A Grights of C Grights of A Grights of A Grights of C G Grights of C G Grights of C G Grights of C G G G G G G G G G G G G G G G G G G G	5 CCCCTIGN 5 CCCCCTIGN 5 CCCCCTIGN	GGT CGGT ATA GGT CGGT GTA GGT CGGT GTA GGT CGGT GTA GGT CGGT GTA GGT CGGT GTA GGT CGGT ATA	CAGGTGGTGGT CAGGTGGTGGT CAGGTGGTGCT CAGGTGGTGCT CAGGTGGTGCT CAGGTGGTGCT CAGGTGGTGCT CAGGTGGTGCT CAGGTGGTGCT CAGGTGGTGCT CAGGTGGTGCT CAGGTGGTGCT CAGGTGGTGCT CAGGTGGTGCT CAGGTGGTGCT CAGGTGGTGCT
XV999711.1 Streptomyces ciner N616 treptomyces violaccorectus NB Val8468.3 Streptomyces Da1820 treptomyces bikiniensis DSN40 9 6 treptomyces tanashiensis HOUM M621 treptomyces XXS505 M600 treptomyces XXS505 M610 treptomyces TRI 10 AB448718 M61501 treptomyces nadosus NBRC 1289 M61501 treptomyces ambofaciens NBRC M1310 N1317	925 891 946 876 876 881 907 879 827 902 899 881 925 880 925 880 920 899 923 896		VI A TACCGGA VI A TA TACCGGA VI A TA ACCGGA VI A ACCGGA	An Seat C An Seat C An Seat C An Seat C An Seat C An Seat T An Seat C An Seat C An Seat C An Seat C	2 516716 51 2 516716 51 2 516716 51 2 516716 51 2 516717 51717 51 2 516717 517	5 CCCCTIGN 5 CCCCCTIGN 5 CCCCCTIGN	Gotego a ta Gotego a ta	CAGGTGGTGGT CAGGTGGTGGT CAGGTGGTGGT CAGGTGGTGGT CAGGTGGTGGT CAGGTGGTGGT CAGGTGGTGGT CAGGTGGTGGT CAGGTGGTGGT CAGGTGGTGGT CAGGTGGTGGT CAGGTGGTGGT CAGGTGGTGGT CAGGTGGTGGT CAGGTGGTGGT CAGGTGGTGGT CAGGTGGTGGT CAGGTGGTGCT
AT999711.1 Streptomyces ciner W616 treptomyces violaccorectus NB Q104604.1 Streptomyces DA1020 treptomyces tanashiensis HBUM M621 W609 W609 W609 treptomyces XAS505 W609 W619 treptomyces DA00509 W612 treptomyces TRI 10 #B448718 W61501	925 891 946 876 876 881 907 879 827 902 899 881 925 880 925 880 923			An Seat C An Seat C An Seat C An Seat C An Seat C An Seat T An Seat C An Seat C An Seat C An Seat C	a Grights of A Grights of C Grights of C Grights of C Grights of C Grights of C Grights of A Grights of C Grights of A Grights of A Grights of C Grights of A Grights of A Grights of C G Grights of C G Grights of C G Grights of C G G G G G G G G G G G G G G G G G G G	5 CCCCTIGN 5 CCCCCTIGN 5 CCCCCTIGN	Gotego a ta Gotego a ta	CAGGTGGTGGT CAGGTGGTGGT CAGGTGGTGCT CAGGTGGTGCT CAGGTGGTGCT CAGGTGGTGCT CAGGTGGTGCT CAGGTGGTGCT CAGGTGGTGCT CAGGTGGTGCT CAGGTGGTGCT CAGGTGGTGCT CAGGTGGTGCT CAGGTGGTGCT CAGGTGGTGCT CAGGTGGTGCT

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DNPT301	960 AFTERTERETERTEREFERENCESTERENTERETEREFEREFREGEREGEREGEREGEREGEREGEREGEREGE
Streptomyces nodosus NBRC 1289	1004 TETCETCASCTCETETCETEAGATETTEEETTAAETCCCECAACEAECECAACCCTTETCCC <mark>E</mark> TETTECCAECA <mark>E</mark> E
DN617	959 TGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCCGCAACGAGCGCAACCCTTGTCC <mark>C</mark> GTGTTGCCAGCA <mark>A</mark> G
Streptomyces ambofaciens NBRC	999 TETCETCAECTCETETCETEMEATETTEEETTAAETCCCECAACEAECCCTTETCCC <mark>C</mark> ETETTECCAECA <mark>A</mark> E
DN1310	978 TETCETCAECTCETETCETEMEATETTEEETTAAETCCCECAACGAECCCTTETCCC <mark>T</mark> ETETTECCAECA <mark>T</mark> E
DN1312	982 TGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCCGCAACGAGCGCAACCCTTGTCCT
DN1317	975 IGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCCGCAACGAGCGCAACCCTTGTCCTGTCGTGTGCCAGCATG
DN1301	979 TGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCCGCAACGAGCGCAACCCTTGTCCC <mark>C</mark> TGTTGCCAGCA <mark>G</mark> G
DN1316	976 TETCETCAECTCETETCETEAEATETTEEEFTTAAETCCCECAACEAECCCATCETCETCCC <mark>E</mark> FETTECCAECA <mark>E</mark> 5
Streptomyces rochei NBRC 12908	1005 TETCETCAECTCETETCETEAEATETTEEETTAAETCCCECAACEAECECAACCCTTETCC <mark>C</mark> ETETTECCAECA <mark>E</mark> 5
Streptomyces B5W222	1027 IGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCG <mark>C</mark> 5GGTGTTGCCAGCA <mark>G</mark> 5
Streptomyces mutabilis NRRL IS	1007 IGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCC <mark>C</mark> GTGTTGCCAGCA <mark>G</mark> G
DN1303	976 ГБТСБТСЯБСТСБТБТСБТБАБАТБТТБББТТАЛБТСССБСААСБАБСБСААСССТТБТСС <mark>Т</mark> БТБТТБССАБСА <mark>Т</mark> Б
DN1304	976 ТБТСБТСЯБСТСБТБТСБТБАБАТБТТБББТТААБТСССБСААСБАБСБСААСССТТБТСС <mark>С</mark> ТБТТБССАБСА <mark>Б</mark> 5
DN1306	984 TGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCCGCAACGAGCGCAACCCTTGTCG <mark>C</mark> 5TGTTGCCAGCA <mark>A</mark> G
Streptomyces 195018	981 TGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCCGCAACGAGCGCAACCCTTGTCG <mark>C</mark> 5TGTTGCCAGCA <mark>A</mark> G
DN1405	975 TGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCCGCAACGAGCGCAACCCTTGTCC <mark>T</mark> GTGTTGCCAGCA <mark>T</mark> G
DN1402	976 TGTCGTCRGCTCGTGTCGTGRGATGTTGGGTTARGTCCCGCARCGRGCGCRACCCTTGTCC <mark>T</mark> GTGTTGCCRGCR <mark>T</mark> G
DN1403	1004 ГБТСБТСЯБСТСБТБТСБТБАБАТБТТБББТТАЛБТСССБСААСБАБСБСААСССТТБТСС <mark>Т</mark> БТБТТБССАБСА <mark>Т</mark> Б
Streptomyces NO1 352 DQ717851	994 TETCETCAECTCETETCETEAEATETTEEETTAAETCCCECAACGAECECAACCCTTETCC <mark>T</mark> ETETTECCAECA <mark>T</mark> E
DN1404	976 TETCETCAECTCETETCETEAEATETTEEETTAAETCCCECAACEAECECAACCCTTETCC <mark>C</mark> ETETTECCAECA <mark>E</mark> E
DN1406	975 TGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCC <mark>C</mark> GTGTTGCCAGCA <mark>G</mark> G
DN1407	976 TETCETCAECTCETETCETEAGATETTEEETTAAETCCCECAACGAECECAACCCTTETCC <mark>C</mark> ETETTECCAECA <mark>E</mark> E
DN1321	979 TETCETCAECTCETETCETEREATETTEEETTAAETCCCECAACEAECECAACCCTTETCC <mark>C</mark> ETETTECCAECA <mark>E</mark> E
Streptomyces thermolilacinus N	1004 TETCETCAECTCETETCETEREATETTEEETTAAETCCCECAACEAECECAACCCTTETCC <mark>C</mark> ETETTECCAECA <mark>E</mark> E
Streptomyces heteromorphus AB	1011 IGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCC <mark>C</mark> GTGTTGCCAGCA <mark>G</mark> G
DN1413	977 IGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCC <mark>C</mark> GTGTTGCCAGCAGC
Streptomyces fragilis NRRL 242	1023 IGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCC <mark>C</mark> GTGTTGCCAGCAGC
Streptomyces humidus NRRL B-31	1020 TGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT <mark>TCT</mark> GTGTTGCCAGCA <mark>T</mark> G
DN1307	979 TGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCCCGTGTTGCCAGCAGG
N14 19	978 TGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCC <mark>T</mark> GTGTTGCCAGCA <mark>T</mark> G
Streptomyces paraguayensis NBR	1001 TGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTT <mark>A</mark> TCC <mark>T</mark> GTGTTGCCAGCACG
Actinomadura nitritigenes T	986 IGTCETCAGCTCETGTCETGAGATGTTGGETTAAGTCCCGCAACGAGCGCAACCCT <mark>C</mark> ET <mark>T</mark> CCATETTGCCAGCAC
Actinomadura bangladeshensis T	1007 IGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCT <mark>C</mark> GT <mark>T</mark> CCATGTTGCCAGCA
Clustal Consensus	586 ************************************

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NM617 Streptomyces ambofaciens NBRC NH1310 NH1317 NH1301 Streptomyces rochei NBRC 12908 Streptomyces B5W222 Streptomyces B5W222 Streptomyces M1303 NH1304 NH1306 Streptomyces 195018	1099 TCF-BEFET TREGERATICAC GEGREGACAACTOGEAGEAAGETGEGEACEACETCAAGTCATA 1079 TCF-BEFET TREGERATICAC BERGACCECCEGEGTCAACTCEGAGEAAGETGEGEACEACETCAAGTCATAC 1058 TCF-BEFETAFEGEGACTCACC BERGACCECCEGEGTCAACTCEGAGEAAGETGEGEACEACETCAAGTCATAC 1058 TCF-BEFETAFEGEGACTCACC BERGACCECCEGEGTCAACTCEGAGEAAGETGEGEACEACETCAAGTCATAC 1059 TCF-BEFETAFEGEGACTCACC BERGACCECCEGEGTCAACTCEGAGEAAGETGEGEACEACETCAAGTCATAC 1059 TCF-BEFETAFEGEGACTCACC BERGACCECCEGEGTCAACTCEGAGEAAGETGEGEACEACETCAAGTCATACA 1059 TCF-BEFETAFEGEGACTCACC BERGACCECCEGEGTCAACTCEGAGEAAGETGEGEACEACETCAAGTCATACA 1059 TCF-BEFETAFEGEGACTCACC BERGACCECCEGEGTCAACTCEGAGEAAGETGEGEACEACETCAAGTCATACA 1059 TCF-BEFETAFEGEGACTCACC BERGACCECCEGEGTCAACTCEGAGEAAGETGEGEACEACETCAAGTCATCA 1059 TCF-BEFETAFEGEGACTCACC BERGACCECCEGEGTCAACTCEGAGEAAGETGEGEACEACETCAAGTCATACA 1050 TCF-BEFETAFEGEGACTCACC BERGACCECCEGEGTCAACTCEGAGEAAGETGEGEACEACETCAAGTCATACA 1057 TCF-BEFETAFEGEGACTCACC BERGACCECCEGEGTCAACTCEGAGEAAGETGEGEACEACETCAAGTCATACA 1057 TCF-BEFETAFEGEGACTCACC BERGACCECCEGEGTCAACTCEGAGEAAGETGEGEACEACETCAAGTCATACA 1057 TCF-BEFETAFEGEGACTCACC BERGACCECCEGEGTCAACTCEGAGEAGAGETGEGEACEACETCAAGTCATACA 1057 TCF-BEFETAFEGEGACTCACC BERGACCECCEGEGTCAACTCEGAGEAGAGETGEGEACEACETCAAGTCATACA 1057 TCF-BEFETAFEGEGACTCACCBEGAGEACCECCEGEGTCAACTCEGAGEAGAAGETGEGEACCACCCTCAAGTCATACA 1056 TCF-BEFETAFEGEGACTCACCBEGAGEACCECCEGEGTCAACTCEGAGEAGAAGETGEGEACCACCCCCACGTCAAGTCATACA 1056 TCF-BEFETAFEGEGACTCACCBEGAGACCECCEGEGTCAACTCEGAGEAGAAGETGEGEACCACCCCCACGTCAAGTCATACA 1056 TCF-BEFETTAFEGEGACTCACCBEGAGACCECCEGEGTCAACTCEGAGEAAAGETGEGEACCACCCCCACGTCAAGTCATACA 1056 TCF-BEFETTAFEGEGACTCACCACCEGCEGAGTCAACTCEGAGAAGETGEGACCACCCCCACCTCAAGTCATACA 1056 TCF-BEFETTAFEGEGACTCACCBEGAGACGCCEGEGCTCAACTCEGAGAAGETGEGACCACCGCCACCTCAAGTCAACCECCEGAGTCAACTCEGAGAAGETGEGGACCACCCCCACCTCAAGTCAACCCCCACGTCAACTCEGAGAAGETGEGGACCACCCCCCACCTCAACTCEGAGAAGETGGAGCACCACCCCCACCTCACTCAACTCA
NT310 NT312 NT312 NT301 NT301 NT305 Streptonyces rochei NBRC 12908 Streptonyces B5W222 Streptonyces B5W222 NT304 NT304 NT304	1058 TCF-BETERTGEGEATCACCCCGEGETCAACTCGEAGEAGEGEGEGACEACGTCAAGTCGEA 1062 TCF-BETERTGEGEATCACCCACGEGEGCCAACTCGEAGEAGEAGEGACGACGTCAGTCAAGTCA
NT312 NT317 NT336 NT336 NT336 NT2eptonyces rochei NBRC 12908 treptonyces B5W222 treptonyces mutabilis NRRL IS NT304 NT304	1062 TCG-GGGB TGGGGACTCAC GGGAACCGCCGGGCAACTCGGAGGAGGTGGGGACGACGTCAAGTCATCA 1053 TCG-GGTGATGGGGACTCAC GGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAAGTCATCA 1059 TCG-GGTCG-GGGGACTCAC GGGGACCGCCGGGGTCAACTCGGAGGAAGGTGGGACGACGTCAAGTCATCA 1056 TCG-GGTCG-GGGGACTCAC GGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGACGACGTCAAGTCATCA 1058 TCG-GGTCGTGGGGACTCAC GGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGACCACGTCAAGTCATCA 1051 TCG-GGTCGTGGGGACTCAC GGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGACCACGTCAAGTCATCA 1051 TCG-GGTCGTGGGGACTCAC GGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACCACGTCAAGTCATCA 1051 TCG-GGTCGTGGGGACTCAC GGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACCACGTCAAGTCATCA 1053 TCG-GGTGGTGGGGACTCAC GGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACCACGTCAAGTCATCA 1054 TCG-GGTGGGGACTCAC GGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACCACGTCAAGTCATCA 1055 TCG-GGTGGGGGACTCAC GGGGACCACCCCGGGGTCAACTCGGAGGAAGGTGGGGACCACGTCAAGTCATCA 1055 TCG-GGTGGTGGGGACTCAC GGGGACCACCCCGGGGTCAACTCGGAGGAGGGTGGGACCACCGCAAGTCATCA 1056 TCG-GGTGGTGGGGACCCACGCCGGGGTCAACTCGGAGGAGGTGGGGACCACCGCCAAGTCATCA 1056 TCG-GGTGGGGACCCACGCGCGCGCGGGTCAACTCGGAGGAGGGGGACGACCGCCAGGTCAAGTCATCA 1056 TCG-GGTGGGGACCCACGCCGGGGTCAACTCGGAGGAGGTGGGGACCACCGCCAAGTCATCA 1056 TCG-GGTGGGGACCCACGCCGGGGTCAACTCGGAGGACGGTCGGACCACCGCCAAGTCATCA 1056 TCG-GGGGACCCACGCCGGGGTCAACTCGGAGGAGGACGGCCGCCGCGCGCG
NI317 NI301 NI306 treptomyces rochei NBRC 12908 treptomyces B5W222 treptomyces mutabilis NRRL IS NI304 NI304 NI304	1055 TOP GETER TOGERET CACE GEGREACCECCEGEGT CAACT CEGAGE MAGT CEGER CETCAMET CAT CA 1059 TOP GETE TOGERAT CACE DEGREACCECCEGEGT CAACT CEGAGE MAGT CEGER CETCAMET CAT CA 1056 TOP GEGREACT CACE DEGREACCECCEGEGT CAACT CEGAGE MEGT GEGER CETCAMET CAT CA 1058 TOP GETE CEGERAT CACE DEGREACCECCEGEGT CAACT CEGAGE MEGT GEGER CEACET CAMET CAT CA 1050 TOP GETE CEGERAT CACE DEGREACCECCEGEGT CAACT CEGAGE MEGT GEGER CEACET CAMET CAT CA 1067 TOP GETE CEGERAT CACE DEGREACCECCEGEGT CAACT CEGAGE MEGT GEGER CEACET CAMET CAT CA 1068 TOP GETE CEGERAT CACE DEGREACCECCEGEGT CAACT CEGAGE MEGT GEGER CEACET CAMET CAT CA 1068 TOP GETE CEGER CEACET CACE DEGREACCECCEGEGT CAACT CEGAGE MEGT GEGER CEACET CAMET CAT CA 1056 TOP GETE GEGER CT CACE DEGREACCECCEGEGT CAACT CEGAGE MEGT GEGER CEACET CAMET CAT CA 1056 TOP GETE TOP GEGER CT CACE DEGREACCECCEGEGT CAACT CEGAGE MEGT GEGER CEACET CAMET CAT CA 1056 TOP GETE TOP GEGER CT CACE DEGREACCECCEGEGT CAACT CEGAGE MEGT GEGER CEACET CAMET CAT CA 1056 TOP GETE TOP GEGER CT CACE DEGREACCECCEGEGT CAACT CEGAGE MEGT GEGER CEACET CAMET CAT CA
NT301 ATI316 Atreptomyces rochei NBRC 12908 Areptomyces B5W222 Atreptomyces mutabilis NRRL IS NT303 NT304 NT304	1059 1 PEGETECTOGERATICAC DEGRAFACCECCEGERTAACTCEGARGAGETGEGACCACGTAARTCATE 1056 1 PEGETECTOGERTCAC DEGRAFACCECCEGERTAACTCEGARGAGETGEGACCACGTAARTCATE 1058 1 PEGETECTOGERTCAC DEGRAFCCECCEGERTAACTCEGARGAGETGEGACGACGTCAARTCATE 1107 1 PEGETECTOGERACTCAC DEGRAFCCECCEGERTAACTCEGARGAGETGEGACGACGTCAARTCATE 1107 1 PEGETECTOGEGACTCAC DEGRAFCCECCEGERTAACTCEGARGAGETGEGACGACGTCAARTCATE 1087 1 PEGETECTOGEGACTCAC DEGRAFCCECCEGERTAACTCEGARGAAGETGEGACGACGTCAARTCATE 1087 1 PEGETECTOGEGARCTCAC DEGRAFCCECCEGERTAACTCEGARGAAGETGEGACCACGTCAARTCATE 1087 1 PEGETECTOGEGARCTCACDEGAGEACCECCEGERTAACTCEGARGAAGETGEGACCACGTCAARTCATE 1087 1 PEGETECTOGEGARCTCACDEGAGEACCECCEGERTAACTCEGARGAAGETGEGACCACGTCAARTCATE 1087 1 PEGETECTOGEGARCTCACDEGAGEACCECCEGERTAACTCEGARGAAGETGEGACCACGTCAARTCATE 1087 1 PEGETECTOGEGARCTCACDEGAGEACCECCEGERTAACTCEGARGAAGETGEGACCACGTCAARTCATE 1087 1 PEGETECTOGEGACTCACDEGAGEACCECCEGERTAACTCAACTCEGARGAAGETGEGACCACGTCAARTCATE 1087 1 PEGETECTOGEGARCTCACDEGAGEACCECCEGERTAACTCAACTCEGARGAAGETGEGACCACGTCAARTCATE 1087 1 PEGETECTOGEGACTCACDEGAGEACCECCEGERTAACTCAACTCAGTCAARCTGACGCACGTCAARTCATE 1087 1 PEGETECTOGEGACTCACDEGAGEACCECCEGERTAACTCAACTGAAGETGEGACCACCTCAARTCATE 1087 1 PEGETECTOGEGACTCACDEGAGEACCECCEGERTAACTGAACTGAAGETGEGACCACCECEGERTAACTGACTGACTGACTGACGTCAARTCACCECCEGERTAACTGACTGAACTGACGCACGCCACGTCAARTCACTGACTGACGCACGCTCACTCAACTGACGACGCCECEGERTAACTGACGCCEGERTAACTGACGCCEGERTAACTGACTGACGCACGCCACGCTCAACTGACTGACGCACGC
N1316 treptomyces rochei NBRC 12908 treptomyces B5W222 treptomyces mutabilis NRRL IS N1303 N1304 N1304	1055 n = 2 GGTECTRGGGACTCACCGEGGAGACCGECGGGGTCAACTCGGAGGAAGGTGGGACCACGTCAAGTCATCA 1085 n = 2 GGTECTGGGGACTCACGGGAGACCGCCGGGGTCAACTCGGAGGAGGTGGGACCACGTCAAGTCATCA 1010 n = 2 GGTECTGGGGACTCACGGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACCACGTCAAGTCATCA 1037 n = 2 GGTECTGGGGACTCACGGGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACCACGTCAAGTCATCA 1036 n = 2 GGTECTGGGGACTCACGGGGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACCACGTCAAGTCATCA 1056 n = 2 GGTECTGGGGACTCACGGGGAGCACCCCGGGGTCAACTCCGGAGGAAGGTGGGGACCACGTCAAGTCATCA 1056 n = 2 GGTECTGCGGGACTCACGGGGAGCACCCCGGGGTCAACTCCGGAGGAAGGTGGGGACCACCGTCAAGTCATCA
treptomyces rochei NBRC 12908 treptomyces B5W222 treptomyces mutabilis NRRL IS N1303 N1304 N1306	1085 1 PGGFDCTGGGGACTCACGFGAGACCGCCGGGGTCAACTCGGAGGAGGGGGGGACGACGTCAAGTCATA 1107 1 PGGFDCTGGGCAGGACTACGGGAGGACGACGGCGGGGAGGAGGAGGGACGACGGCGAAGTCATA 1087 1 PGGFDCTGGGGACTCACGGGGAGCCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAAGTCATA 1086 1 CGGGGGTGGGGGACTCACGGGGGGCCGCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAAGTCATA 1085 1 CGGGTGGGGGACTCACGGGGGGCCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAAGTCATAC
treptomyces rochei NBRC 12908 treptomyces B5W222 treptomyces mutabilis NRRL IS N1303 N1304 N1306	1085 1 PGGFDCTGGGGACTCACGFGAGACCGCCGGGGTCAACTCGGAGGAGGGGGGGACGACGTCAAGTCATA 1107 1 PGGFDCTGGGAGGACTACGGGAGGACGACCGCCGGGGTCAACTCGGAGGAGGGCGGGACGACGFCAAGTCATA 1087 1 PGGFTCTGGGGACTCACGGGGAGCCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGFCAAGTCATA 1086 1 CGGGTGGTGGGGACTCACGGGGGGCCGCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAAGTCATA 1085 1 CGGGTGGTGGGGACTCACGGGGGGCCGCGGGCTAACTCGGAGGAAGGTGGGGACGACGTCAAGTCATAC
treptomyces B5W222 treptomyces mutabilis NRRL IS N1303 N1304 N1306	1107 T BEGGTGETGGGGACTCACCGGGACACCCGGGGCAACTCGGAGGAGGTGGGGACGACGTCAAGTCATCA 1087 T BEGGTGCTGGGGACTCACCGGGACAACCGCCGGGCCAACTCGGAGGAAGGTGGGGACGACGTCAAGTCATCA 1056 TCGGGGGGTGGGGGCTCACCGGGAGACCGCCGGGGCGACCTCGGAGGAAGGTGGGGACGACGTCAAGTCATCA 1056 T BEGGTGGGGGACTCACGGGGACACCCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGCCAAGTCATCA
treptomyces mutabilis NRRL IS N1303 N1304 N1306	1987 п. <mark>2</mark> СБЯТЕ СБАБЛАСТСКСЕ СБАБЛАССКОССБАБЛАЛСТСБАКБЛАСЯТСБАКСКАСТСКАТС АТС 1956 гость Сарана Сарана Сарана Сососсвает салстоста сарана сарана сарана сарана сарана сарана сарана сарана с 1956 гость Сарана Сарана Сарана Сососсвает салстоста сарана сарана сарана сарана сарана сарана сарана сарана с
N1303 N1304 N1306	1056 TCG ² GGTG <mark>a</mark> TGGGGRCTCAC <mark>A</mark> GGAGCCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAAGTCATCA 1056 T <mark>gT</mark> GGTG <mark>2</mark> TGGGGRCTCAC <mark>G</mark> GGRCCCCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAAGTCATCA
N1304 N1306	1056 T <mark>BT</mark> EGTE <mark>C</mark> TEGEGRACTCRC <mark>E</mark> GERGRCCECCEGEGETCRRCTCEGERGRREGTEGEGERCERCETCRRETCRTCR
N1306	
treptomyces 195018	
	1061 TCGGGETG <mark>T</mark> TGGGGACTCAC <mark>G</mark> GGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAAGTCATCA
N1405	1055 TCGGGGTGATGGGGACTCACA GGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAAGTCATCA
N1402	1056 TCG <mark>E</mark> EGTG <mark>A</mark> TGGGGACTCAC <mark>A</mark> EGAGACCGCCGGGGTCAACTCGGAGGAGGTGGGGACGACGTCAAGTCATCA
N1403	1084 TCGEGGTEATGGGGACTCACAGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAAGTCATCA
treptomyces NO1 352 DQ717851	1074 TCGGEGTGATGGGGGACTCACAGGGGGACGGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAAGTCATCA
11404	1056 T-GTGGTGGGGGACTCACGGGGAGACCGCCGGGGTCAACTCGGAGGAGGTGGGGGACGACGTCAAGTCATCA
N1406	1055 T- <mark>FT</mark> GGTG <mark>C</mark> TGGGGRCTCRC <mark>G</mark> GGRGRCCGCCGGGGTCRRCTCGGRGGRGGRCGRCGRCGTCRRGTCRTCR
N1407	1056 T-GTGGTGCTGGGGACTCACCGGGGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAAGTCATCA
N1321	1059 T-G <mark>T</mark> EGTG <mark>C</mark> TGGGGACTCAC <mark>G</mark> GGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAAGTCATCA
treptomyces thermolilacinus N	1084 T-CTGGTECTGGGGACTCACGGGAGACCGCCGGGGTCAACTCGGAAGGTGGGGACGACGTCAAGTCATCA
treptomyces heteromorphus AB	1091 T-GTGGTGCTGGGGGACTCACCGGGGGGCCACCCGGGGGGGG
N1413	1057 T <mark>-CT</mark> GGTG <mark>C</mark> TGGGGACTCAC <mark>G</mark> GGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAAGTCATCA
treptomyces fragilis NRRL 242	
treptomyces humidus NRRL B-31	1100 TCGGGGTGATGGGGACTCACAGGAGAC <mark>T</mark> GCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAAGTCATCA
N1307	1059 T-STGETECTEGEGEACTCACCGEGEGECCACCCGEGETCAACTCGEAEGEAGEGEGEGACGACGECCAGETCATCA
14 19	1058 TCG <mark>E</mark> GG <mark>C</mark> GA <mark>TGGGGRCTCRC</mark> GGRGRC <mark>T</mark> GCCGGGGTCARCTCGGRGGRRGGTGGGGRCGRCGTCRRGTCRTCR
treptomyces paraguayensis NBR	
ctinomadura nitritigenes T	
	1081 TCG5-5GTG5-GGGGACTCAC5-5GAGACCCCCCCCCCCCCACGAGGAAGGTGGGGACGACGTCAAGTCATCA
	1060 C <mark>TAR</mark> TG <mark>GTGGGGRCTCA</mark> TG <mark>GGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGA</mark> TGACGTCAAGTCATCA
ctinomadura bangladeshensis T	1060 C <mark>TAR</mark> TG <mark>GTGGGGRCTCA</mark> TG <mark>GGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGA</mark> TGACGTCAAGTCATCA
ctinomadura bangladeshensis <u>T</u> lustal Consensus N60 <u>5</u>	1060
ctinomadura hangladeshensis T lustal Consensus N605 N615	1060 — Этальерсивсение сторенье в состояние солосто собласти собласти в состояние солостояние солостояние состояние сос
ctinomadura hangladeshensis T lustal Consensus N605 N615 N61 <u>8</u>	1060
ctinomadura hangladeshensis T lustal Consensus N605 N615 N61 <u>8</u>	1060 — Этальерсивсение сторенье в состояние солосто собласти собласти в состояние солостояние солостояние состояние сос
ctinomadura bangladeshensis T lustal Consensus N605 N615 N618 N618 N7999771.1 Streptomyces ciner	1060
ctinomadura bangladeshensis T lustal Consensus N605 N615 N618 RX999771.1 Streptomyces ciner N616	1060
ctinomadura bangladeshensis T lustal Consensus N605 N615 N618 N2999771.1 Streptomyces ciner N616 treptomyces violaceorectus NB	1060
ctinomadura bangladeshensis T lustal Consensus N605 N615 N615 N7999771.1 Streptonyces ciner 1616 treptonyces violaceorectus NB 0418466.1 Streptonyces DA1020	1060
ttinomadura bangladeshensis T lustal Consensus N605 N615 N616 N299771.1 Streptomyces ciner N616 Lireptomyces violaceorectus NB D418668.1 Streptomyces DA1020 treptomyces bikiniensis DSM40	1060
tinomadura bangladeshensis T lustal Consensus 1055 1051 1051 1051 1051 1051 1051 105	1060
ttinomadura bangladeshensis T lustal Consensus N605 N615 N618 RX999771.1 Streptomyces ciner N616 treptomyces violaceorectus NB V18466.1 Streptomyces DX1020 treptomyces bikiniensis DSN40 9 4	1060
ttinomadura bangladeshensis T lustal Consensus N605 N613 N2999771.1 Streptomyces ciner N616 Creptomyces violaceorectus NB D418468.1 Streptomyces DA1020 treptomyces bikiniensis DSN40 9 4 9 6 forptomyces tanashiensis HBUM	1060
ttinomadura bangladeshensis T lustal Consensus N605 N613 N2999771.1 Streptomyces ciner N616 Creptomyces violaceorectus NB D418468.1 Streptomyces DA1020 treptomyces bikiniensis DSN40 9 4 9 6 forptomyces tanashiensis HBUM	1060
ttinomadura bangladeshensis T lustal Consensus N605 N615 N618 N618 N618 N61999771.1 Streptomyces ciner N616 treptomyces violaceorectus NB J418466.1 Streptomyces DA1020 treptomyces bikiniensis DSM40 9 4 Creptomyces tanashiensis HBMM M621	1060
ttinomadura bangladeshensis T lustal Consensus N605 N615 N615 N616 Treptomyces violaceorectus NB D418468.1 Streptomyces Dā1020 Freptomyces bikiniensis DSN40 9 4 5 6 treptomyces tanashiensis HBUM M621 M601	1060
tinomadura bangladeshensis T lustal Consensus M605 M615 M618 M7999771.1 Streptomyces ciner M616 Creptomyces violaceorectus NB J418468.1 Streptomyces DA1020 treptomyces bikiniensis DSM40 9 4 9 5 0 5 100000000000000000000000000000000	1060
ttinomadura bangladeshensis T lustal Consensus N605 N615 N615 N616 AV999771.1 Streptomyces ciner N616 treptomyces violaceorectus NB V18466.1 Streptomyces DA1020 treptomyces bikiniensis DSM40 9 4 9 5 treptomyces tanashiensis HBUM N621 N621 Creptomyces XAS585 N608	1060
ctinonadura bangladeshensis T lustal Consensus N605 N615 N618 N618 N618 Okl3464.1 Streptonyces ciner N616 Creptonyces violaceorectus NB Okl3468.1 Streptonyces DA1020 Creptonyces bikiniensis DSN40 9 4 9 5 Creptonyces tanashiensis HBUM N621 N607 N606	1060
ttinomadura bangladeshensis T lustal Consensus N605 N615 N615 N616 RX999771.1 Streptomyces ciner N616 treptomyces violaceorectus NB J418464.1 Streptomyces DA1020 treptomyces bikiniensis DSN40 9 4 9 6 treptomyces tanashiensis HBUM N621 N607 Treptomyces X&S585 N608 N608 LTeptomyces D&08605	1060
tlinomadura bangladeshensis T lustal Consensus N605 N615 N615 N616 D418468,1 Streptomyces ciner N616 D418468,1 Streptomyces D41020 treptomyces bikiniensis D5N40 9 4 9 5 0 4 9 5 1 treptomyces tanashiensis HBUM N621 D40868 N607 Treptomyces X8585 N608 N606 N606 N606 N606 N606 N606 N606	1060
tlinomadura bangladeshensis T lustal Consensus N605 N615 N615 N616 D418468,1 Streptomyces ciner N616 D418468,1 Streptomyces D41020 treptomyces bikiniensis D5N40 9 4 9 5 0 4 9 5 1 treptomyces tanashiensis HBUM N621 D40868 N607 Treptomyces X8585 N608 N606 N606 N606 N606 N606 N606 N606	1060 TRATE FIGURE AT CATE GRADUE COCCEGATION ACT CARAGE GRADE THE GRAD THE CATE AT CATE
ctinomadura hangladeshensis T lustal Consensus N605 N615 N618 N618 Usyperstand Streptomyces ciner N616 Usyperstand Streptomyces Da1020 treptomyces bikiniensis DSN40 9 4 9 6 Usyperstand Streptomyces Da1020 treptomyces bikiniensis HBUM N621 Usyperstand Streptomyces Da08605 N608 N607 Usyperstand Streptomyces Da08605 N608 N606 N606 N606 N606 N606 N606 N606	1060
tinomadura bangladeshensis T lustal Consensus N605 N615 N615 N616 Eveptomyces violaceorectus NB D418468.1 Streptomyces DA1020 treptomyces bikiniensis DSM40 9 4 9 6 treptomyces tanashiensis HBUM N621 N621 Eveptomyces XAS585 N621 Eveptomyces XAS585 N605 Eveptomyces DA08605 N612 Ureptomyces TRI 10 AB448718 M61501	1060
Actinomadura bangladeshensis T Clustal Consensus DM605 DM615 DM615 DM616 Streptomyces violaceorectus NB H0418468.1 Streptomyces DA1020 Streptomyces bikiniensis DSM40 H9 4 H9 6 Streptomyces tanashiensis HBUM DM621	1060 TRATE THE GEGEN CETTE GEGENÉE COCCEGE OF CANCE COMEGNAGE TOGOGNE DE ACCECCAMET CATE 1083 TCC DE TEGEGON CENTE GENERACCECCEGE OF CANCE COMEGNAGE TOGOGNE DE ACCECCAMET CATE 1193 TATE CETTE GEGENCE CENTE DE ACATEGOCO GENERAL CECCEGAR GENERAL DE ACETECAMET CATE 1197 TATE CETTE GEGET CONTE DE ACATEGOCO GENERAL DE ACETECAMET CATE 1197 TATE CETTE GEGET GENERAL DE ACATEGOCO GENERAL DE ACETECAMET CATE 1197 TATE CETTE GEGET GENERAL DE ACATEGOCO GENERAL DE ACETECAMET CATE 1197 TATE CETTE GEGET GENERAL DE ACATEGOCO GENERAL DE ACETECAMET CONCERAL DE ACETECAMET 1197 TATE CETTE GEGET GENERAL DE ACATEGOCO GENERAL DE ACETECAMET CONCERAL DE ACETECAMET 1197 TATE CETTE GEGET GENERAL DE ACATEGOCO GENERAL DE ACETECAMET DE CONCERAL DE ACETECAMET DE CONCERAL DE ACETECAMET DE CONCERAL DE ACETECAMET 1197 TATE CETTE GEGET GENERAL DE ACATEGOCO GENERAL DE ACETECAMET DE CONCERAL DE CO
tinomadura bangladeshensis T lustal Consensus N605 N615 N615 N616 Treptonyces violaceorectus NB Q418468.1 Streptonyces DA1020 treptonyces bikiniensis DSN40 9 4 9 6 treptonyces tanashiensis HBUM	1060
tinonadura bangladeshensis T lustal Consensus 1005 1015 1015 1019 1019 1019 1019 1019	1060
tinonadura bangladeshensis T lustal Consensus 1605 1615 1618 187999771.1 Streptomyces ciner 1616 1616 1617 1799000000000000000000000000000000000	1060
tinonadura bangladeshensis T lustal Consensus 1605 1615 1615 1616 1619 1619 1619 1619 161	1060
tinonadura bangladeshensis T lustal Consensus 1605 1615 1615 1616 1619 1619 1619 1619 161	1060 TRATE FIGURE AT CATE FRANCESC CEGEDET CALCT CEGARGE MAGTEDEGENT TALET COMPETATOR 1083 TCF SPEEDEGER AT CATE FRANCESC CEGEDET CALCT CEGARGE MAGTEDEGENT FACET CAME TATT CALL 1083 TCF SPEEDEGER AT CATE FRANCESC CEGEDET CALCT CEGARGE MAGTEDEGENT FACET CAME TATT CALL 1083 TCF SPEEDEGER AT CATE FRANCESC CEGEDET CALCT CEGARGE MAGTEDEGENT FACET CALCET C
tinonadura bangladeshensis T lustal Consensus 4605 4615 4616 1618 W999771.1 Streptomyces ciner 4616 Greptomyces violaceorectus NB 1418464.1 Streptomyces DA1020 Greptomyces bikiniensis DS140 9 4 9 6 Greptomyces tanashiensis HBUM 4621 4607 Greptomyces XAS585 4608 Greptomyces DA08605 4612 Greptomyces DA08605 4612 Greptomyces TRI 10 AB448718	1060 TRATE FIGURE AT CATE GRADUE COCCEGATION ACT CARAGE GRADE THE GRAD THE CATE AT CATE
tlinonadura bangladeshensis T lustal Consensus N605 N615 N615 N616 N7999771.1 Streptomyces ciner N616 treptomyces violaceorectus NB J018468.1 Streptomyces DN1020 treptomyces bikiniensis DSN40 9 4 Streptomyces tanashiensis HBUM M621 N605 treptomyces X&S585 N606 treptomyces DA08605 N605 treptomyces DA08605 N612 treptomyces TRI 10 AB448718	1060

	1290		1310 1320		1340 1350
DN605	209	· · · · · · · · · · · · · · · · · · ·	· · · · · · · · · · · · · · · · · · ·		
DN615	191				
DN618	183				
AY999771.1 Streptomyces ciner	236 CEETCICAGIN	CGGATTGGGGTCTGCA	ACTEGACECCATGAAGT	GGAGT <mark>T</mark> GCTAGTA	ATCGCAGATCAGCATT
DN616			ACTCGACCCCATGAAGTC		ATCGCAGATCAGCATT
Streptomyces violaceorectus NB			ACTCGACCCCATGAAGTC		ATCGCAGATCAGCATT
HQ418468.1 Streptomyces DA1020	210 CHETCHCAGAN	CGGATTGGGGTCTGCA	ACTCGACCCCATGAAGTC	GGAGT <mark>T</mark> GCTAGTA	ATCGCAGATCAGCATT
Streptomyces bikiniensis DSM40	264 CHENCICARIAN	CGGATTGGGGTCTGCA	ACTCGACCCCATGAAGTC	GGAGT <mark>T</mark> GCTAGTA	ATCGCAGATCAGCATT
N9 4		CGGATTGGGGTCTGCA			
N9 6		CGGATTGGGGTCTGCA	ACT		
Streptomyces tanashiensis HBUM			ACTCGACCCCATGAAGTC	GGAGTTGCTAGTA	ATCGCAGATCAGCATT
DN621	195 CEETCICA				
DN607	179				
Streptomyces XAS585		CEGATTEEEETCTECA	ACTCGACCCCATGAAGTO	GGAGT <mark>T</mark> GCTAGTA	ATCGCAGATCAGCATT
DN608					
DN606	067				
Streptomyces DA08605		CREATTREECTCTCC	ACTCGACCCCATGAAGTO	CEACT C COTACTA	атексакатеаксатт
DN612		CGGATTGGGGTCT			
Streptomyces TRI 10 AB448718			ACTCGACCCCATGAAGTC	CENER <mark>C</mark> CONTREPT	ATCGCAGATCAGCATT
DN61501			ACTCGACCCCATGAAGTC		
Streptomyces nodosus NBRC 1289			ACTOGACCCCATGAAGTO		
DN617			NOTCO//COULTO//INDIA		
Streptomyces ambofaciens NBRC			ACTEGACCCCATGAAGTO	COMP. COMP.	atecacateaceatt
DN1310			Nonconcerent and the		
DN1312	210	<u>~~</u>			
DN1317	206				
DN1301	218 				
DN1316	202				
Streptomyces rochei NBRC 12908			ACTOGACCCCATGAAGTO	eenene eennenn	ATCGCAGATCAGCATT
Streptomyces B5W222			ACTOGACCCCATGAAGTO		ATCGCAGATCAGCATT
Streptomyces mutabilis NRRL IS			ACTCGACCCCATGAAGTC		ATCGCAGATCAGCATT
DN1303			RETEGRECCERTGRAGIE	венеговетнети	итсвсявитсявсятт
DN1304	218 CGGTCTCAGT				
DN 1304 DN 1306					
			ACTOGACCCCATGAAGTO		3000030300300300300
Streptomyces 195018 DN1405	221 189	CGGAIIGGGGGTCIGCA	RETEGREECCATGAAGT	GGRGI GGUTRGTR	ALCOCHGATCAGCATT
DN1405 DN1402	189 197				
DN 1402 DN 1403	197 220				
		ACC3MACCCCMARCA3	2000C3000030C73C74		700000000000000000000000000000000000000
Streptomyces N01 352 DQ717851 DN1404		CGGRIIIGGGGTCIGCA	ACTCGACCCCATGAAGTO	eestern eenstern	ALCOURDATURGUATT
DN 1404 DN 1406	202				
	194				
DN1407	201				
DN1321	206			CCTCM	7000070707070070
Streptomyces thermolilacinus N			ACTCGACCCCATGAAGTC		
Streptomyces heteromorphus AB		CHEATTHEEGETCTECA	ACTCGACCCCATGAAGTC	GGAGT <mark>O</mark> GCTAGTA	ATCGCAGATCAGCATT
DN1413	199				

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DN606	1067		
Streptomyces DA08605	1319	IGAATACGTTCCC-GGGCCTTGTAC	ACACCGCCCGTCACGTCACGAAAGTCGGTAACACCCCGAAGCCGGTGGC
DN612	1243		
Streptomyces TRI 10 AB448718	1297	IGAATACGTTCCC-GGGCCTTGTAC	ACACCGCCCGTCACGTCACGAAAGTCGGTAACACCCCGAAGCCGGTGGA
DN61501			ACACCECCETCACETCACEAAMETCEETAACAC
Streptomyces nodosus NBRC 1289			ACACCGCCCGTCACGTCACGAAAGTCGGTAACACCCCGAAGCCGGTGGC
DN617	1209		
Streptomyces ambofaciens NBRC		CANTACCTTCCC CCCCCTCTA	ACACCECCETCACETCACEAAAETCEETAACACCCEAAECCEETEEC
DN1310	1230		
DN1312	1210		
DN1317	1210		
DN1301	1200		
DN1316	1223		
Streptomyces rochei NBRC 12908			ACACCGCCCGTCACGTCACGAAAGTCGGTAACACCCCGAAGCCGGTGGC
Streptomyces B5W222	1346		ACACCGCCCGTCACGTCACGAAAGTCGGTAACACCCGAAGCCGGTGGC
Streptomyces mutabilis NRRL IS		IGAATACGITCCC-GGGCCTTGTAC	ACACCECCCETCACETCACEAAAETCEETAACACCCCEAAECCEETEEC
DN1303	1226		
DN1304	1227		
DN1306	1239		
Streptomyces 195018		IGAATACGTTCCC-GGGCCTTGTAC	ACACCGCCCGTCACGTCACGAAAGTCGGTAACACCCGAAGCCGGTGGC
DN1405	1189		
DN1402	1197		
DN1403	1220		
Streptomyces N01 352 DQ717851	1314	IGAATACGTTCCC_GGGCCTTGTAC	ACACCGCCCGTCACGTCACGAAAGTCGGTAACACCCCGAAGCCGGTGGC
DN1404	1202		
DN1406	1194		
DN1407	1201		
DN1321	1206		
Streptomyces thermolilacinus N		IGAATACGTTCCC-GGGCCTTGTAC	ACACCECCCETCACETCACEAAAETCEETAACACCCCEAAECCEETEEC
Streptomyces heteromorphus AB			ACACCECCETCACETCACEAAAETCEETAACACCCCEAAECCEETEEC
		IGARTRUGTICUC GEGUUTIETRU	ACACCECCETCACETCACEARAETCEETARCACCCEARECCEETEEC
DN1413	1199		
Streptomyces fragilis NRRL 242			ACACCECCETCACETCACEAAAETCEETAACACCCEAAECCEETEEC
Streptomyces humidus NRRL B-31	1340	IGAATACGTTCCC GGGCCTTGTAC	ACACCGCCCGTCACGTCACGAAAGTCGGTAACACCCGAAGCCGGTGGC
DN1307	1230		
N14 19	1252		
Streptomyces paraguayensis NBR			acacceccesteresteresarastessarcecesarsees
Actinomadura nitritigenes T			ACACCGCCCGTCACGTCACGAAAGTCGG <mark>C</mark> AACACCCCGAAGCC <mark>C</mark> GTGGC
Actinomadura bangladeshensis T	1319	IGAATACGTTCCCCGGGCCTTGTA	ACACCGCCCGTCACGTCACGAAAGTCGG <mark>C</mark> AACACCCCGAAGCC <mark>C</mark> GTGGC
Clustal Consensus			
		1450 1460	1470 1480 1490 1500 1510
DN605	1209		
DN615	1191		
DN618	1183		
AY999771.1 Streptomyces ciner	1395	TTGTGGGAGGGAGCTGTCGAAG	GTGGGAC
DN616	1071		
Streptomyces violaceorectus NB		TTGTGGGAGGGAGCTGTCGAAC	GTGGGAC <mark>T</mark> GGCGATTGGGACGAAGTCGTAACAAGGTAGCCGTACCGGA
HQ418468.1 Streptomyces DA1020	1369	CTTGTCGGAGGG	
Streptomyces bikiniensis DSM40			GTGGGAC <mark>T</mark> GGCGATTGGGACGAAGTCGTAACAAGGTAGCCGTACCGGA
N9 4	1239		
N9 6	1239		
		TTGT - GGGAGGGAGCTGTCGAA	GTGGGAC <mark>CA</mark> GCGATTGGGACGAAGTCGTAACAAG <mark>T</mark> AG
Streptomyces tanashiensis HBUM			IST GGGAC <mark>CH GUGAT I I GGGACGARGT CISTARCARG<mark>T</mark> AG</mark>
DN621	1202		
DN607	1179		
Streptomyces XAS585	1385	TTGTCGCAGGGAGCTGTCGAA	GTGGGAC <mark>CA</mark> GCGATTGGGACGAAGTCG <mark>AM</mark> CAA
DN608	1217		

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DN1403	1220
Streptomyces N01 352 DQ717851	1220 1314 STEANTROSTFCCC-SEECCTTETACACACCECCETCACETCACEANASTCESTAACACCCEEAASCCEFTESCCC
DN1404	
DN1404 DN1406	1194
DN1406 DN1407	1194
DN1321	1201
Streptomyces thermolilacinus N	1200 1323 FIGAATROGTTCCC-GGGCCTTGTACRCRCCGCCCGTCRCGTCRCGARAGTCGGTARCRCCCCGARGCCGGTGGCCC
Streptomyces heteromorphus AB	1323 9TOATTREBTTECC-GGCCTTBTRERCRECCCCCTCREDTERCOTERCOTERCOTERCEGTARCACCCCGARGCCGGTGGCCC
DN1413	1199
Streptomyces fragilis NRRL 242	1133 1342 GIGAATACGITCCC GGGCCTTGTACACCGCCCGTCACGTCACGAAAGTCGGTAACACCCCGAAGCCGGTGGCCC
Streptomyces humidus NRRL B-31	1342 JIOAANACOTTCCC BESCCTTGTACACCCCCCCCCCCCCCCCCAABACCCCCGAABCCCCGABCCCCCGABCCCCCGABCCCCCGABCCCCCGABCCCCGABCCCCGABCCCCGABCCCCGABCCCCGABCCCCGABCCCCGABCCCCGABCCCCGABCCCCGABCCCCGABCCCCGABCCCCGABCCCCGABCCCCGABCCCCCGABCCCCCGABCCCCCGABCCCCCGABCCCCGABCCCCCGABCCCCCGABCCCCCGABCCCCCGABCCCCCCGABCCCCCCGABCCCCCGABCCCCCCCC
DN1307	1230
N14 19	1252
Streptomyces paraguayensis NBR	1321 FIGANTACETTCCC EGGCCTTGTACACCCCCCCCCCCCCCCCCCCCCCCCCCCC
Actinomadura nitritigenes T	1299 STEANTACETTCCC SEGCCTTETACACCCCCCCCCCCCCCCCCCGAAGCCCCCGAAGCCCCCGAAGCCCCCC
Actinomadura bangladeshensis T	1319 STGAATACGTTCCCCGGGCCTTGTACACCCCCCGTCACGTCACGAAAGTCGGCAACCCCCGAAGCCCCGTGGCCC
Clustal Consensus	
	1450 1460 1470 1480 1490 1500 1510
	2450 2460 2470 2480 2490 2500 1510
DN605	1209
DN615	1191
DN618	1183
AY999771.1 Streptomyces ciner	1395 CCTTGT GGGAGGGGGGCTGTCGAAGGTGGGAC
DN616	1071
Streptomyces violaceorectus NB	1403 CCTTGTGEGAGGOAGCTGTCGAAGGTGGGACTGGCGATTGGGACGAAGTCGTAACAAGGTAGCCGTACCGGAAG
HQ418468.1 Streptomyces DA1020	1369 CCTTGT GGGAGGG
Streptomyces bikiniensis DSM40	1423 CCTTGTGGGAGGGAGCTGTCGAAGGTGGGACTGGGACGAAGTCGTAACAAGGTAGCCGTACCGGAAG
N9 4	1239
N9 6	1224
Streptomyces tanashiensis HBUM	1386 CCTTGTGEGAGGGAGCTGTCGAAGGTGGGACCAGCGATGGGACGAAGTCGTAACAAGTAG
DN621	1202
DN607	1179
Streptomyces XAS585	1385 CCTTGTGGGAGGGAGCTGTCGAAGGTGGGACCAECGATTGGGACGAAGTCG <mark>A</mark> ACAA
DN608	1217
DN606	1067
Streptomyces DA08605	1398 CCTTGTGGGAGGGAGCTTAGAAGG <mark>T</mark> GG <mark>ATCGC</mark> GG <mark>T</mark> C
DN612	1243
Streptomyces TRI 10 AB448718	1376 CCTTGTGGGRGGGRGCTGTCGRAGGTGGGRCTGGCGRTTGGGRCG
DN61501	1337
Streptomyces nodosus NBRC 1289	1402 CCTTGTGGGRGGGRGCTGTCGARGGTGGGRCTGGGRCGARGTCGTARCRAGGTRGCCGTRCCGGRR
DN617	1209
Streptomyces ambofaciens NBRC	1398 CCTTGTGGGAGGGAGCTGTCGAAGGTGGGAC <mark>T</mark> GGCGATTGGGACGAAGTCGTAACAAGGTAGCCGTA
DN1310	1230
DN1312	1210
DN1317	1206
DN1301	1223
DN1316	
Streptomyces rochei NBRC 12908	1403 CCTTGTGGRGGGGGGGGCTGTCGGRGGGGGGGGGGGG
Streptomyces B5W222	1425 CCTTGTGGGAGGGAGCTGTCGAAGGTGGGACTGGCGATTGGGACGAAGTCGTAACAAGGTAGCCGTACCGGAA
Streptomyces mutabilis NRRL IS	1405 CCTTET GEGAGEGAGCTETCGAAGETGEGACT 1936
DN1303	1226
DN1304 DN1306	1227
	1239 1380 Cetviet – Egenegementergenneetigener Elegentigeacgangt (gaachg
Streptomyces 195018 DN1405	1380 CONTEN - CEBAGEBARGIENEGEMEENGEBAGI <mark>ERGEAUTEB</mark> ACGAAG <mark>I</mark> CGAACAG
DN1403 DN1402	1189
	1177
4	

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Streptomyces N01 352 DQ717851	1393 CCTTGTGGGAGGGAGCTGTCGAAGGTGGGAC <mark>T</mark> G
DN1404	1202
DN1406	1194
DN1407	1201
DN1321	1206
Streptomyces thermolilacinus N	1402 CCTTG <mark>C</mark> GGGAGGGAGCTGTCGAAGGTGGGAC <mark>T</mark> G
Streptomyces heteromorphus AB	1409 CONTETGEGAGEGAECTETCEAAGETEGEAC <mark>T</mark> E
DN1413	1199
Streptomyces fragilis NRRL 242	1421 CCTTGTGGGAGGGAGCTGTCGAAGGTGGGAC <mark>T</mark> G
Streptomyces humidus NRRL B-31	1419 CCIVIGTGEGAGEGAECIGICGAAGGIGEGAC <mark>T</mark> I
DN1307	1230
N14 19	1252
Streptomyces paraguayensis NBR	1400 CC <mark>C</mark> T <mark>TGTGGGGAGGGA<mark>AT</mark>CGTCGAAGGTGGGAC<mark>T</mark>3</mark>
Actinomadura nitritigenes T	1378 CTTGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
Actinomadura bangladeshensis T	1399 ACCTTGTGTGTGGGGGGGGGGGGGGGGGGGGGGGGGGGG
Clustal Consensus	

		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	GGCTGGA <mark>TCAC</mark> C <mark>TCCT</mark> T	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 DN1317	1210		1210
DN1317 DN1301	1205		1205
DN1301 DN1316	1223		1223
Streptomyces rochei NBRC 12908	1472		1472
Streptomyces B5W222	1503	GGCTGGA <mark>TCAC</mark> C <mark>TCAATA</mark> TTC	
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

		1530 1540	
DN605	1200		1200
N605 N615	1191		1209
DN618			1183
AY999771.1 Streptomyces ciner	1425		1425
N616	1071		
Streptomyces violaceorectus NB	1477		1477
Q418468.1 Streptomyces DA1020	1381		1381
Streptomyces bikiniensis DSM40	1501	GGCTGGA <mark>TCAC</mark> C <mark>TCCT</mark> T	
19 4	1239		1239
19 6	1224		
Streptomyces tanashiensis HBUM	1446		1446
N621	1202		1202
DN607	1179		1179
Streptomyces XAS585	1440		1440
N608	1217		1217
DN606	1067		1067
Streptomyces DA08605	1433		
DN612	1243		
Streptomyces TRI 10 AB448718	1420		
N61501	1337		1337
Streptomyces nodosus NBRC 1289	1476		1476
DN617	1209		1209
Streptomyces ambofaciens NBRC	1464		1464
N1310	1230		1230
DN1312	1210		1210
DN1317	1206		1206
DN1301	1223		1223
DN1316	1202		1202
Streptomyces rochei NBRC 12908	1472		1472
Streptomyces B5W222	1503	GGCTGGA <mark>TCAC</mark> C <mark>TCAA</mark> TA <mark>T</mark> TC	1523
Streptomyces mutabilis NRRL IS	1483	GG	1484
N1303	1226		1226
DN1304	1227		1227
DN1306	1239		1239
Streptomyces 195018	1434		1434
DN1405	1189		
DN1402	1197		1197
DN1403	1220		1220
Streptomyces N01 352 DQ717851			1461
DN1404	1202		
DN1406	1194		
DN1407	1201		1201
DN1321	1206		1206
Streptomyces thermolilacinus N	1476		1476
Streptomyces heteromorphus AB	1483		1483
DN1413	1199		
Streptomyces fragilis NRRL 242	1499	<u> EC</u>	1500
Streptomyces humidus NRRL B-31	1495		
DN1307	1230		
<u>114 19</u>	1252		
Streptomyces paraguayensis NBR	1468		1468
Actinomadura nitritigenes T	1454	GGCTGGA <mark>TCAC</mark> C <mark>TCCT</mark>	
Actinomadura bangladeshensis T	1478	GGCTGGA <mark>ATCAC</mark> CTCCTAAT-	1497
Clustal Consensus			

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

		10	20	30	40	50	60
SN701 1				•••••			
Streptomyces gardneri NBRC 128 1				GACGAA	CRCTRRCRRC	G <mark>T GC</mark> TT <mark>D</mark> A CA	TATECAAG
Streptomyces omiyaensis NRRL B 1						GTGCTTAACA	
SN810 1							
SN821 1							
Streptomyces lateritius LMG 19 1				GACGAA	cec <mark>r</mark> ee <mark>c</mark> eec	GTGCTTDACA	GATGCAAGT
Streptomyces zaomyceticus NRRL 1			60	TCAGGACGAA			
SN820 1							GCA G
Streptomyces bikiniensis DSM40 1		GAGTT	TGATCCTGGC	TCAGGACGAA	cec <mark>r</mark> ee <mark>c</mark> eec	G <mark>TGC</mark> TT <mark>D</mark> ACA	CAT GCAAG
SN807 1							
Streptomyces gulbargensis T 1				CGAACG	CTGGCCGGCCT	G <mark>CTTAAC</mark> ACA	TGCAAGTCI
Streptomyces chartreusis NBRC 1				ACGAA	CGC <mark>T</mark> GG <mark>C</mark> GGC	G <mark>T GC</mark> TT <mark>A</mark> ACA	CAT GCAAG
SN709 1							
Streptomyces tateyamensis AB4 1			CTGGCT	AGGACGAACG	C <mark>TGGC</mark> CGCCT	G <mark>CTTAAC</mark> ACA	TGCAAGTC(
SN710 1							
SN805 1							
Streptomyces sioyaensis NRRL 1			T	AGGACGAACG	C <mark>TGGC</mark> GG <mark>C</mark> CT	G <mark>CTTAA C</mark> ACA	TGCAAGTC
SN702 1							
Streptomyces parvulus NBRC 131 1						G <mark>TGC</mark> TT <mark>B</mark> ACA	
Streptomyces tendae T D6387 1	CAT <mark>T</mark> C <mark>AC</mark> G	G <mark>A</mark> GAGTT	TGAT <mark>C</mark> CTGGC	TCAGGACGAA	CGC <mark>T</mark> GG <mark>C</mark> GGC	G <mark>TGC</mark> TT <mark>A</mark> ACA	CATGCAAG
SN1101 1							А
Streptomyces malachitospinus N 1				GACGAA	CGC <mark>T</mark> GG <mark>CG</mark> GC	G <mark>TGC</mark> TT <mark>A</mark> ACA	CATGCAAG
SN1104 1							- <mark>CCAT</mark> GCAG
SN1108 1						CTTAC	CATGCAGT
SN1123 1							
Streptomyces paraguayensis 1					-GC <mark>T</mark> GG <mark>C</mark> GGC	G <mark>T GC</mark> TT <mark>A</mark> ACA	
SN1212 1							TGCA
Streptomyces rochei NBRC 12908 1				ACGAA	CEC <mark>T</mark> EE <mark>CEN</mark> C	G <mark>T GC</mark> T T <mark>A</mark> AC <mark>I</mark>	ICAT GCAAG
Streptomyces caelestis T X8 1		- <mark>A</mark> GAGTT	TGAT <mark>C</mark> CTGGC	TCAGGACGAA	CGC <mark>T</mark> GG <mark>C</mark> GGC	G <mark>T GC</mark> TT <mark>A</mark> ACA	.CATGCAAG
SN1210 1							
N12 16 1							T G CA G
SN1218 1							<mark>T</mark> G <mark>C</mark> AG
SN1222 1							TGCAG
Streptomyces 1						<u>-</u>	AC <mark>ATGCA</mark> -G
SN1203 1							TGCAG
Streptomyces narbonensis NRRL 1	CCTTT			TCAGGACGAA			
Streptomyces variabilis NRRL B 1			TGAT <mark>T</mark> CTGGC	TCAGGACGAA			
Streptomyces labedae NBRC 1586 1						G <mark>TGC</mark> TT <mark>A</mark> ACA	
Streptomyces collinus NBRC 127 1					GG <mark>C</mark> GGC	G <mark>TGC</mark> TT <mark>B</mark> ACA	
SN1125 1							ATGCAAG
Streptomyces CTDF1 GQ169067 1							AG
Streptomyces sclerotialus DSM 1					CECTEECEEC	G <mark>T GC</mark> T T <mark>B</mark> A CA	
SN1213 1							TGCAG
Streptomyces 13638J EU741132 1			TGG0	TCAGGACGAA	CEC <mark>TEE</mark> CEEC	GIR CITERATOR	
SN1219 1							TGCA
Streptomyces griseoplanus AS 4 1							AC <mark>ATGCAA</mark> G
Streptomyces 195019 GU263883 1 Streptomyces badius NRRL B 256 1			07004	TCAGGACGAA			ACCATGCA
			CTGGC	ТСАББАСБАА	CECTERCERC	GT GCD 100 1001	CATECAAE
SN1201 1 SN1221 1							
						ACTTTTCAT(AC <mark>CAT</mark> GCAG
Streptomyces 0 3 FJ959370 1 Streptomyces A23 Ydz XM EU368 1					GQ	- GT GCT TACA	ACCATECA

Streptomyces 0 3 FJ959370	1	GCACTTTTEATCACCATECAET
Streptomyces A23 Ydz XM EU368	1	GTGCTTACACATGCAAGTC
SN1208	1	TGCAGTC
SN1209	1	TGCAGT
Streptomyces nitrosporeus NRRL	1	GGACGAACGC <mark>T</mark> GG <mark>CGGCGTGCTTP</mark> ACAC <mark>AT</mark> GCAAGTC
SN1110	1	GCTTACCATGCAGTC
Streptomyces coralus cfcc3136	1	CGGGCGAATCGCGCGTGCTT ACACATGCAAGTC
Streptomyces CA131	1	TACCATGCAAGTC
SN1114	1	GCTTACCATGCAGTC
Streptomyces RSF18 EU294139	1	GCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
SN1226	1	TTACCATGCAGTC
Streptomyces DA08605	1	GEGCAAGCEGEGAGCT <mark>TACAC</mark> ATGCAAGTC
N12 28	1	TGCAGT
Streptomyces aculeolatus strai	1	CTGGCGTGCTTAACACATGCAAGTC
SN1202	1	TGCAGTC
SN1230	1	
Actinomadura nitritigenes T	1	TTBACACATGCAAGTC
Actinomadura bangladeshensis T	1	GACGAACGC <mark>TGGCGTGC</mark> TTPACAC <mark>ATGCAAGTC</mark>
Clustal Consensus		

▲ Note: This is a print preview. It may copy to the	clipbo	ard slightly large. To show control panel, press the red arrow (upper left)
Streptomyces gardneri NBRC 128	50	CTTCGGGGTGGATTAGTGGCGAACGGGTG AGTAACACGTGGGCAATCTGCCCTTCACTCTGGG
Streptomyces omiyaensis NRRL B	51	CTTCGGGGTGGATTAGTGGCGAACGGGTG AGTAACACGTGGGCAATCTGCCCTTCACTCTGGG
SN810	1	G <mark>gggt</mark> ggattagtggcgaacgggtg <mark>agtaacg</mark> cgtgggcaatctgccct <mark>t</mark> cactctggg
SN821	1	G <mark>gg</mark> g <mark>t</mark> ggattagtggcgaacgggtg-agtaac <mark>g</mark> cgtgggcaatctgccct <mark>t</mark> cactctggg
Streptomyces lateritius LMG 19	50	CTTCEGESTGGATTAGTGGCGAACGGGTG AGTAACACGTGGGCAATCTGCCCT <mark>T</mark> CACTCTGGG
Streptomyces zaomyceticus NRRL	56	CTTCGGGGTGGATTAGTGGCGAACGGGTG AGTAACACGTGGGCAATCTGCCCTTCACTCTGGG
SN820	20	CT <mark>TC</mark> GGGG <mark>T</mark> GGATTAGTGGCGAACGGGTG <mark>-</mark> AGTAACACGTGGGCAATCTGCCCT <mark>T</mark> CACTCTGGG.
Streptomyces bikiniensis DSM40	70	CTTCEGEETGEATTAGTEGCEAACGEGTE AGTAACACGTEGECAATCTECCCTTCACTCTEGE
SN807	1	GTAACACGTGGGCAATCTGCCCT <mark>T</mark> CACTCTGGG
Streptomyces gulbargensis T	50	TTCGGGAGGGGATTAGTGGCGAACGGGTG AGTAACACGTGGGCAATCTGCCCTTCACTCTGGG
Streptomyces chartreusis NBRC	49	CTTCGGTGGGGATTAGTGGCGAACGGGTG AGTAACACGTGGGCAATCTGCCCTTCACTCTGGG
SN709	6	T <mark>tCg</mark> g <mark>ga</mark> gggattagtggcgaacgggtg <mark>-</mark> agtaacacgtgggcaatctgccct <mark>g</mark> cactctggg
Streptomyces tateyamensis AB4	61	T <mark>TCG</mark> G <mark>GR</mark> GGGATTAGTGGCGAACGGGTG <mark>-</mark> AGTAACACGTGGGCAATCTGCCCT <mark>G</mark> CACTCTGGG
SN710	1	-T <mark>CE</mark> CE-E <mark>T</mark> GEATTAGTEGCEAACEGETE <mark>-</mark> AGTAACACETEGECAATCTECCCT <mark>E</mark> CACTCTEEG
SN805	4	T <mark>TCG</mark> G <mark>CC</mark> G <mark>GGATTAGTGGCGAACGGGTG-</mark> AGTAACACGTGGGCAATCTGCCCT <mark>T</mark> CACTCTGGG
Streptomyces sioyaensis NRRL	56	T <mark>TCGEGA</mark> GGGATTAGTGGCGAACGGGTG <mark>AGTAACACGTGGGCAATCTGCCCT</mark> CACTCTGGG
SN702	1	T <mark>gg</mark> ggattagtggcgaacgggtg <mark>agtaacacgtgggcaatctgccctg</mark> cactctggg
Streptomyces parvulus NBRC 131	49	CT <mark>TCEGT</mark> EGEGATTAGTGGCGAACGGGTG-AGTAACACGTGGGCAATCTGCCCT <mark>G</mark> CACTCTGGG
Streptomyces tendae T D6387	79	CTTCE <mark>GTE</mark> GGEATTAGTGGCGAACGGGTG <mark>-AGTAACACGTGGGCAATCTGCCCT</mark> GCACTCTGGG
SN1101	17	CTTCGGTGGGGATTAGTGGCGAACGGGTG AGTAACACGTGGGCAATCTGCCCTGCACTCTGGG
Streptomyces malachitospinus N	50	C <mark>TTC</mark> G <mark>GT</mark> G <mark>GGATTAGTGGCGAACGGGTG-</mark> AGTAACACGTGGGCAATCTGCCCT <mark>G</mark> CACTCTGGG
SN1104	24	CTTC <mark>GGT</mark> E <mark>GGEATTAGTGGCGAACGGGTG</mark> AGTAACACGTGGGCAATCTGCCCT <mark>G</mark> CACTCTGGG
SN1108	29	T <mark>TCGEGAGE</mark> GEATTAGTGGCGAACGGGTG <mark>-</mark> AGTAACACGTGGGCAATCTGCCCT <mark>G</mark> CACTCTGGG
SN1123	10	T <mark>CC</mark> G <mark>TG</mark> GGATTAGTGGCGAACGGGTG <mark>-</mark> AGTAACACGTGGGCAATCTGCCCT <mark>G</mark> CACTCTGGG
Streptomyces paraguayensis	45	TTCGETGGGGGATTAGTGGCGAACGGGTG AGTAACACGTGGGCAATCTGCCCTGCACTCTGGG
SN1212	20	CTTCGGGGTGGATTAGTGGCGAACGGGTG AGTAACACGTGGGCAATCTGCCCTTCACTCTGGG
Streptomyces rochei NBRC 12908	49	CT <mark>TC</mark> E <mark>GT</mark> E <mark>GGGATTAGTGGCGAACGGGTG</mark> -AGTAACACGTGGGCAATCTGCCCT <mark>G</mark> CACTCTGGG
Streptomyces caelestis T X8	70	C <mark>TTC</mark> GGT <mark>GG</mark> GGATTAGTGGCGAACGGGTG-AGTAACACGTGGGCAATCTGCCCT <mark>G</mark> CACTCTGGG
SN1210	1	
N12 16	21	CT <mark>TC</mark> G <mark>GT</mark> GGGATTAGTGGCGAACGGGTG <mark>AGTAACACGTGGGCAATCTGCCCTG</mark> CACTCTGGG
SN1218	21	CT <mark>TC</mark> G <mark>GT</mark> GGGATTAGTGGCGAACGGGTG AGTAACACGTGGGCAATCTGCCCTGCACTCTGGG
SN1222	21	CT <mark>TCEGGET</mark> GGATTAGTGGCGAACGGGTG <mark>-</mark> AGTAACACGTGGGCAATCTGCCCT <mark>T</mark> CACTCTGGG
Streptomyces	26	CTTCPGGETGGATTAGTGGCGAACGGGTG-AGTAACACGTGGGCAATCTGCCCT <mark>T</mark> CACTCTGGG.
SN1203	21	CT <mark>TC</mark> GGGG <mark>T</mark> GGATTAGTGGCGAACGGGTG-AGTAACACGTGGGCAATCTGCCCT <mark>T</mark> CACTCTGGG
Streptomyces narbonensis NRRL	76	CT <mark>TC6666T</mark> 66ATTA6T66C6AAC666T6-AGTAACAC6T666CAATCT6CCCT <mark>T</mark> CACTCT666
Streptomyces variabilis NRRL B	66	TTCGGGAGGGGATTAGTGGCGAACGGGTG AGTAACACGTGGGCAATCTGCCCTGCACTCTGGG
Streptomyces labedae NBRC 1586	37	TTCGEGAEGGGATTAGTGGCGAACGGGTG-AGTAACACGTGGGCAATCTGCCCT <mark>C</mark> CACTCTGGG.
Streptomyces collinus NBRC 127	40	CT <mark>TCEGT</mark> EGGGATTAGTGGCGAACGGGTG-AGTAACACGTGGGCAATCTGCCCT <mark>G</mark> CACTCTGGG
SN1125	25	TTCGGTGGTGGTGGATTAGTGGCGAACGGGTG-AGTAACACGTGGGCAATCTGCCCTGCACTCTGGG
Streptomyces CTDF1 GQ169067	20 48	TT <mark>CGGTGGT</mark> GGATTAGTGGCGAACGGGTG <mark>-</mark> AGTAACACGTGGGCAATCTGCCCT <mark>G</mark> CACTCTGGG.
Streptomyces sclerotialus DSM SN1213	48	TTCGGTGGTGGTGGATTAGTGGCGAACGGGTG-AGTAACACGTGGGCAATCTGCCCTGCACTCTGGG TTCGGTGGTGGATTAGTGGCGAACGGGTG-AGTAACACGTGGGCAATCTGCCCTTCACTCTGGG
Streptomyces 13638J EU741132	60	TT <mark>CGGTEGT</mark> GGATTAGTGGCGAACGGGTG <mark>AGTAACACGTGGGCAATCTGCCCTT</mark> CACTCTGGG TT <mark>CGGTEGT</mark> GGATTAGTGGCGAACGGGTG <mark>AGTAACACGTGGGCAATCTGCCCTT</mark> CACTCTGGG
SN1219	21 32	TICGGTEGTGGATTAGTGGCGAACGGGTG GTTCGGEGTGGATTAGTGGCGAACGGGTG-AGTAACACGTGGGCAATCTGCCCTTCACTCTGGG GTTCGGEGTGGATTAGTGGCGAACGGGTG-AGTAACACGTGGGCAATCTGCCCTTCACTCTGGG
Streptomyces griseoplanus AS 4 Streptomyces 195019 GU263883	34 29	TTCGGTGGTGGATTAGTGGCGAACGGGTG-AGTAACACGTGGGCAATCTGCCCTTCACTCTGGG
Streptomyces badius NRRL B 256	61	TTCGGTGGTGGATTAGTGGCGAACGGGTG-AGTAACACGTGGGCAATCTGCCCTTCACTCTGGG TTCGGTGGTGGATTAGTGGCGAACGGGTG-AGTAACACGTGGGCAATCTGCCCTTCACTCTGGG
Streptomyces badius NRRL B 256 SN1201	21	TTCGGTGGTGGATTAGTGGCGAACGGGTG-AGTAACACGTGGGCAATCTGCCCTTCACTCTGGG TTCGGTGGATTAGTGGCGAACGGGTG-AGTAACACGTGGGCAATCTGCCCTTCACTCTGGG
SN1201 SN1221	21	
	38	TT <mark>CGGTGGT</mark> GGATTAGTGGCGAACGGGTG ⁻ AGTAACACGTGGGCAATCTGCCCT <mark>T</mark> CACTCTGGG TT <mark>CGGTGGT</mark> GGATTAGTGGCGAACGGGTG ⁻ AGTAACACGTGGGCAATCTGCCCT <mark>T</mark> CACTCTGGG
Streptomyces 0 3 FJ959370 Streptomyces A23 Ydz XM EU368	38	TTCCCTCGTGGTGGATTAGTGGCGAACGGGTG-AGTAACACGTGGGCAATCTGCCCTTCACTCTGGG TTCCGTGGTGGATTAGTGGCGAACGGGTG-AGTAACACGTGGGCAATCTGCCCTTCACTCTGGG
Streptomyces A23 Ydz XM E0368 SN1208	22	TTCCGTGCTGGATTAGTGGCGAACGGGTG-AGTAACACGTGGGCAATCTGCCCTTCACTCTGGG TTCCGTGCTGGATTAGTGGCGAACGGGTG-AGTAACACGTGGGCAATCTGCCCTT
SN1208 SN1209	20	TTCGCFGGFGGATTAGTGGCGAACGGGTG AGTAACACGTGGGCAATCTGCCCTFCACTCTGGG CTTCGGGGTGGATTAGTGGCGAACGGGTG AGTAACACGTGGGCAATCTGCCCTTCACTCTGGG
SN1209 Streptomyces nitrosporeus NRRL	20	CTTCGGGGTGGATTAGTGGCGAACGGGTG-AGTAACACGTGGGCAATCTGCCCTTCACTCTGGG CTTCGGGGTGGATTAGTGGCGAACGGGTG-AGTAACACGTGGGCAATCTGCCCTTCACTCTGGG
Streptomyces hitrosporeus NKKL	31	CHICCORDULITING AND ALL AND AL

Streptomyces nitrosporeus NRRL	51	C <mark>TTCGGGGGT</mark> GGATTAGTGGCGAACGGGTG <mark>-</mark> AGTAACACGTGGGCAATCTGCCCT <mark>T</mark> CACTCTGGGA
SN1110	29	C <mark>TTC</mark> GG <mark>T</mark> GGGATTAGTGGCGAACGGGTG <mark>-</mark> AGTAACACGTGGGCAATCTGCCCT <mark>T</mark> CACTCTGGGA
Streptomyces coralus cfcc3136	47	C <mark>TTC</mark> G <mark>GT</mark> GGGATTAGTGGCGAACGGGTG <mark>-</mark> AGTAACACGTGGGCAATCTGCCCT <mark>T</mark> CACTCTGGGA
Streptomyces CA131	27	C <mark>TTC</mark> G <mark>GT</mark> GGGATTAGTGGCGAACGGGTG <mark>-</mark> AGTAACACGTGGGCAATCTGCCCT <mark>T</mark> CACTCTGGGA
SN1114	31	T <mark>TCG</mark> G <mark>GA</mark> GGGATTAGTGGCGAACGGGTG <mark>-</mark> AGTAACACGTGGGCAATCTGCCCT <mark>G</mark> CACTCTGGGA
Streptomyces RSF18 EU294139	45	T <mark>t c</mark> gg <mark>ga</mark> gggattagtggcgaacgggtg <mark>agtaacacgtgggcaatctgccctg</mark> cactctggga
SN1226	27	CT <mark>TC</mark> GG <mark>T</mark> GGGATTAGTGGCGAACGGGTG <mark>AGTAACACGTGGGCAATCTGCCCT</mark> GCACTCTGGGA
Streptomyces DA08605	44	C <mark>TTC</mark> G <mark>GT</mark> GGGATTAGTGGCGAACGGGTG <mark>-</mark> AGTAACACGTGGGCAATCTGCCCT <mark>G</mark> CACTCTGGGA
N12 28	22	T <mark>TCG</mark> G <mark>CC</mark> GGGATTAGTGGCGAACGGGTG <mark>-</mark> AGTAACACGTGGGCAATCTGCCCT <mark>G</mark> CACTCTGGGA
Streptomyces aculeolatus strai	44	T <mark>CC</mark> GC <mark>CC</mark> GGATTAGTGGCGAACGGGTG <mark>-</mark> AGTAACACGTGGGCAATCTGCCCT <mark>G</mark> CACTCTGGGA
SN1202	23	T <mark>CCGCCC</mark> GGGATTAGTGGCGAACGGGTG <mark>AGTAACACGTGGGCAATCTGCCCT</mark> GCACTCTGGGA
SN1230	23	T <mark>TCG</mark> G <mark>CC</mark> GGGATTAGTGGCGAACGGGTG <mark>-</mark> AGTAACACGTGGGCAATCTGCCCT <mark>G</mark> CACTCTGGGA
Actinomadura nitritigenes T	32	T <mark>TCG</mark> GGG <mark>GTACTCG</mark> AG <mark>C</mark> GGCGAACGGGTG <mark>-AGTAACACGTG</mark> AGCAA <mark>C</mark> CTGCCC <mark>CT</mark> GACTCTGGGA
Actinomadura bangladeshensis T	52	T <mark>CCGCGCGTACTCC</mark> ACCGGCCGAACGGGTGGAGTAACACGTC <mark>A</mark> GCAA <mark>C</mark> CTGCCC <mark>CT</mark> GACTCTGGGA
Clustal Consensus		
4		

38701	82	170 180 190 200 210 220 BEETGYMYNACCEEDYMA CACCECCTCCECMGGAGGCTE ETGAMAGCTCCEECECETCAM
<u>18701</u> Streptomyces gardneri NBRC 128 Strentomyces omivaensis NBBI R	82 129 130	ВБЕТСТИАТАССЕВАТАА. САССВОСТССВОАТВОАВСТВ. БТЕВААВСТССВОССБТВАА ОБОТСТААТАССЕВАТАА. САССВОСТССВОАТВОАВСТВ. БТЕВААВСТССВОССВТВАА ВЛИГИАТАССЕВАТАА. САССВОСТССВОАТВОВОВСТВ. БТЕВААВСТССВОЕВСВОТВАА ПЛИГИАТАССВОАТАА. САССВОСТССВОАТВОВОВСТВ. БТЕВААВСТССВОЕВСВОТВАА
Note: This is a print preview. It may copy to the	clipboard	slightly large. To show control panel, press the red arrow (upper left)
N821	76	GEGTCTAATACCEEATAA - CACCEGCTTCCCCCATEGAAGCTC-BTTGAAAGCTCCEECEETEBAA
treptomyces lateritius LMG 19	129	GGGTCTAATACCGGATAA GACCGGCTTCCGCATGGGAAGCTG GTTGAAAGCTCCGGCGGTGAA GGGTCTAATACCGGATAA GACCGGCTTCCGCATGGGAAGCTG GTTGAAAGCTCCGGCGGTGAA
treptomyces zaomyceticus NRRL	135	GGGTCTAATACCGGATA <mark>A-C</mark> AC <mark>CGGCTTCC</mark> GCAT <mark>GGGAGCT</mark> G- <mark>GT</mark> GAAAGCTCCGGCGGTG <mark>A</mark> AG
SN820	99	BEETCTAATACCEEATAC-BACCTGGGAAGECATCTTCTCGG-BTGGAAAGCTCCGECGETGAA
treptomyces bikiniensis DSM40	149	GEGTCTAATACCEGATAC-EACCEBEGAAEECATCTTCTCEE-ETEEAAAECTCCEECEGTE <u>9</u> AU
SN807	50 129	
treptomyces gulbargensis T	129	GGGTCTAATACCGGATA <mark>C-GA</mark> GTTCGGGAG <mark>GCAT</mark> CTCCTGGA-CT <mark>G</mark> GAAAGCTCCGGCGGTG <mark>8</mark> AG GGGTCTAATACCGGATA <mark>A-CAC</mark> TCCTGTCCTCCTGGACGGGG-GTT <mark>2</mark> AAAGCTCCGGCGGTG <mark>8</mark> AG
treptomyces chartreusis NBRC	85	GGGTCTAATACCGGATA <mark>T GACCTCCTGCCATCGCGTGGTGG</mark> -GT <mark>GGAAAGCTCCGGCGGTGAA</mark>
treptomyces tateyamensis AB4	140	GGGTCTAATACCGGATA <mark>TT</mark> GAC <mark>CTGCCATC</mark> GCAT <mark>GGTGGTG</mark> G-GT <mark>G</mark> GAAAGCTCCGGCGGTGGAG
N710	78	GGGT CTAATACCGGATAT-GACGGGAT CGCATGGT CT CCGTGTGGAAAGCT CCGGCGGT GCAG
1805	83	GGGTCTAATACCGGATA <mark>T-GACACGACC</mark> GCAT <mark>GGTCTGT</mark> GT <mark>G</mark> GAAAGCTCCGGCGGTG <mark>A</mark> AG
treptomyces sioyaensis NRRL	135	GGGTCTAATACCGGATA <mark>C-GACACGACC</mark> GCAT <mark>GGTCTGTGT</mark> GTGGAAAGCTCCGGCGGTG <mark>A</mark> AG
N702	74	GGGTCTAATACCGGATA <mark>T</mark> TEAC <mark>CGTCACAG</mark> GCAT <mark>CTGTGAC</mark> G-GT <mark>G</mark> GAAAGCTCCGGCGGTG <mark>C</mark> AG
treptomyces parvulus NBRC 131	128	GGGTCTAATACCGGATA <mark>C</mark> T <mark>S</mark> AC <mark>CTTCACGG</mark> GCAT <mark>CTGTGAA</mark> G-GT <mark>C</mark> GAAAGCTCCGGCGGTG <mark>C</mark> AG
treptomyces tendae T D6387	158	REPT CTARTACCERR TACTER C CTCECA RECATCTECER RE-TUCRARA BCTCCERCERTERA
N1101	96	GGGTCTAATACCGGATA <mark>C</mark> T <mark>GA<mark>ACCTTGCAG</mark>GCAT<mark>CTGTGAG</mark>G<mark>-</mark>GT<mark>C</mark>GAAAGCTCCGGCGGTG<mark>C</mark>AG</mark>
treptomyces malachitospinus N	129	GGGTCTAATACCGGATACTGAACCTTGCAGGCATCTGTGAGG-GTCGAAAGCTCCGGCGGTGCAA
N1104	103	GEGTCTAATACCEGATA <mark>CTEAACCTTECAG</mark> ECAT <mark>CTGT</mark> GAG <mark>E-STC</mark> GAAAGCTCCEGCEGTE <mark>C</mark> AG
N1108	108	GGGTCTAATACCGGATATIGACCTIGCAGGCATGIGTGGGGGGGGGG
N1123	89	GGGTCTAATACCGGATAC-DACATCCTCCCGCATGGGAAGGGTCTGGAAGGTCCGGCGGTGGA
treptomyces paraguayensis	124	GGGTCTAATACCGGATA <mark>N-G</mark> AC <mark>ATCCTCCC</mark> GCAT <mark>GGGAAGGG</mark> TGT <mark>G</mark> GAAAGCTCCGGCGGTG <mark>C</mark> AG
N1212	99	GGGTCTAATACCGGATA <mark>A - C</mark> AC <mark>CGGCTTCC</mark> GCAT <mark>GGGGGCT</mark> G-GT <mark>T</mark> GAAAGCTCCGGCGGTGAA
treptomyces rochei NBRC 12908	128	GGGTCTAATACCGGATA <mark>CT</mark> GA <mark>TCCTCGCAG</mark> GCAT <mark>CTGCGAG</mark> G <mark>-T</mark> T <mark>C</mark> GAAAGCTCCGGCGGTG <mark>C</mark> AG
treptomyces caelestis T X8	149	GGGTCTAATACCGGATAC <mark>T</mark> GAG <mark>CATCTT</mark> GGGCAT <mark>CCAAGGT</mark> G <mark>TTC</mark> GAAAGCTCCGGCGGTG <mark>C</mark> AG
<u>N1210</u>	1	
112 16	100	GGGTCTAATACCGGATA <mark>C</mark> TGA <mark>TCCTCGCAG</mark> GCAT <mark>CTGCGGGG</mark> G <mark>-T</mark> T <mark>C</mark> GAAAGCTCCGGCGGTG <mark>C</mark> AG
N1218 N1222	100 100	GGETCTAATACCEGATA <mark>CTEGA</mark> TCCTCECAEGCAT <mark>CTGCGGEG-T</mark> TCEAAAGCTCCGGCGGCGGAG GEGTCTAATACCEGATA <mark>A-OACCEGCTTCC</mark> GCAT <mark>6GAGGCT</mark> G-GT <mark>T</mark> GAAAGCTCCGGCGGTGAA
<u>W1222</u>	105	GGGTCTAATACCGGATAA OACCGGCTTCCGCATGGAGGCTG GTTGAAAGCTCCGGCGGGGAA GGGTCTAATACCGGATAA OAC <mark>CGGCTTCC</mark> GCATGGAAGCTG GTTGAAAGCTCCGGCGGGGAA
n1203	105	GGGTCTAATACCGGATAA-OACCGGCTTCCGCATGGGGGCTG-GTTGAAAGCTCCGGCGGTGAA GGGTCTAATACCGGATA <mark>A-C</mark> ACCGGCTTCCGCATGGGGGGCTG-GTTGAAAGCTCCGGCGGTGAA
Streptomyces narbonensis NRRL	155	GGGTCTAATACCGGATA <mark>A-OACCGGCTTCCGCATGGGGGGCTG</mark> -GTTGAAAGCTCCGGCGGTG <mark>A</mark> AG GGGTCTAATACCGGATA <mark>A-OACCGGCTTCCGCAT</mark> GGGGGGCT <mark>G</mark> -GT <mark>T</mark> GAAAGCTCCGGCGGTG <mark>A</mark> AG
treptomyces variabilis NRRL B	145	GGGTCTAATACCGGATA <mark>CTG</mark> AC <mark>CCGCTTGG</mark> GCAT <mark>CCAAGCG</mark> G <mark>-T</mark> TCGAAAGCTCCGGCGGTG <mark>C</mark> AA
treptomyces labedae NBRC 1586	116	GGGT CTAATACCGGATACTGACCCGCTTGGGCATCCAAGCGG-TTCGAAAGCTCCGGCGGTGCAG
treptomyces collinus NBRC 127	119	GGGTCTAATACCGGATA <mark>CTGA<mark>TCCGTCT</mark>GGGCAT<mark>CCAGAT</mark>GG-<mark>T</mark>TCGAAAGCTCCGGCGGTGCAG</mark>
N1125	104	GGGTCTAATACCGGATA <mark>T</mark> TGAC <mark>ACGAGGGG</mark> GCAT <mark>CTTCTCGT</mark> -GTGGAAAGCTCCGGCGGTG <mark>C</mark> AG
Streptomyces CTDF1 GQ169067	99	GGGTCTAATACCGGATA <mark>T-GACACGGGGGGGGGGCAT<mark>CTTCTTC</mark>GTGTGGAAAGCTCCGGCGGTG<mark>C</mark>AG</mark>
treptomyces sclerotialus DSM	127	GGGTCTAATACCGGATA <mark>C-GACACGGGATC</mark> GCAT <mark>GGTCTCC</mark> GTGTGGAAAGCTCCGGCGGTG <mark>C</mark> AG
N1213	101	GGGTCTAATACCGGATA <mark>A-C</mark> AC <mark>TCTGTCCC</mark> GCAT <mark>GGGACGGG</mark> -GT <mark>T</mark> GAAAGCTCCGGCGGTG <mark>A</mark> AG
treptomyces 13638J EU741132	139	GGGTCTAATACCGGATA <mark>A - C</mark> AC <mark>TCTGTCCC</mark> GCATGGGACGGC - GTTGAAAGCTCCGGCGGTG <mark>2</mark> AG GGGTCTAATACCGGATA <mark>A - C</mark> AC <mark>TCTGTCCC</mark> GCAT <mark>GGGACGG</mark> C-GT <mark>T</mark> GAAAGCTCCGGCGGTG <mark>2</mark> AG
N1219	100	GGGTCTAATACCGGATA <mark>A-C</mark> AC <mark>TCTGTCCC</mark> GCAT <mark>GGGACGGG</mark> -GT <mark>T</mark> GAAAGCTCCGGCGGTG <mark>A</mark> AG
treptomyces griseoplanus AS 4	111	GGGTCTAATACCGGATA <mark>A-O</mark> AC <mark>TCTGTCCC</mark> GCAT <mark>GGGACGG</mark> G-GT <mark>TA</mark> AAAGCTCCGGCGGTG <mark>A</mark> AG
treptomyces 195019 GU263883	108	GGGTCTAATACCGGATA <mark>A - C</mark> AC <mark>TCTGTCCC</mark> GCAT <mark>GGGACGGG-</mark> GT <mark>TA</mark> AAAGCTCCGGCGGTG <mark>A</mark> AG
treptomyces badius NRRL B 256	140	GEGTETAATACCEGATA <mark>A – C</mark> AC <mark>TCTGTCCC</mark> GCAT <mark>GEGACEE</mark> G – GT <mark>T</mark> GAAAGCTCCEGCEGTE <mark>A</mark> AC
N1201	100	GGGTCTAATACCGGATA <mark>A - C</mark> AC <mark>TCTGTCCC</mark> GCAT <mark>GGGACGGG</mark> -GT <mark>T</mark> GAAAGCTCCGGCGGTG <mark>A</mark> AG
N1221	108	GGGTCTAATACCGGATA <mark>A - C</mark> AC <mark>TCTGTCCC</mark> GCAT <mark>GGGACGG</mark> G-GT <mark>T</mark> GAAAGCTCCGGCGGTG <mark>A</mark> AG
treptomyces 0 3 FJ959370	117	GGGTCTAATACCGGATA <mark>A - C</mark> AC <mark>TCTGTCCC</mark> GCAT <mark>GGGACGGG</mark> -GT <mark>T</mark> GAAAGCTCCGGCGGTG <mark>A</mark> AG
treptomyces A23 Ydz XM EU368	114 101	GGGTCTAATACCGGATAA-CAC <mark>TCTGTCCC</mark> GCAT <mark>GGGACGG</mark> -GT <mark>T</mark> GAAAGCTCCGGCGGTG <mark>A</mark> AG GGGTCTAATACCGGATAA-CAC <mark>TCTGTCCC</mark> GCATGGGACGGG-GT <mark>T</mark> GAAAGCTCCGGCGGTG <mark>A</mark> AG
N1208 N1209	101 99	
	130	GGGTCTAATACCGGATAA <mark>-T</mark> AC <mark>TCTGTTCC</mark> GCAT <mark>GGGACGGG</mark> -GT <mark>T</mark> GAAAGCTCCGGCGGTG <mark>A</mark> AG GGGTCTAATACCGGATAA <mark>-T</mark> AC <mark>TCTGTCCC</mark> GCAT <mark>GGGACGG</mark> G-GT <mark>T</mark> GAAAGCTCCGGCGGTG <mark>A</mark> AG
treptomyces nitrosporeus NRRL N1110	130	GGGTCTAATACCGGATAA-TAGTCTGTCCGGCATGGGACGGG-GTTGAAAGCTCCGGCGGTGAA GGGTCTAATACCGGATAT-CAG <mark>CTCCTCAGG</mark> GCAT <mark>CTTGGGGG</mark> -GT <mark>T</mark> GAAAGCTCCGGCGGTG <mark>T</mark> AB
treptomyces coralus cfcc3136	126	GGGTCTAATACCGGATA <mark>T - OACTCCTCAGGGCATCTTGGGGG</mark> -GTTGAAAGCTCCGGCGGTGAA GGGTCTAATACCGGATA <mark>T - O</mark> AC <mark>TCCTCAAGGCATCTTGGGGG</mark> -GT <mark>T</mark> GAAAGCTCCGGCGGTG <mark>A</mark> AG
treptomyces CA131	106	GGGTCTAATACCGGATA <mark>T - CactcCtCaa</mark> gCat <mark>CttGGGGG</mark> - G <mark>tt</mark> GAAAGCtCCGGCGGTG <mark>A</mark> A GGGTCTAATACCGGATA <mark>T - CactcCtCagGCCAtCttGGGGG</mark> - GttGAAAGCtCCGGCGGTG <mark>A</mark> AG
	100	
treptomyces CA131	106	GGGT CTAATA C CGGATA <mark>T – C</mark> A C <mark>T C C T CA GG</mark> G C AT <mark>C T T</mark> GGG G G <mark>T</mark> GAAAG C T C C G G C G G T C <mark>P</mark> AG
W1114	110	GEGTCTAATACCEEATAC-EACCACTEAGECATCCTCEETE-ETECAAAGCTCCEECEETE
treptomyces RSF18 EU294139	124	GGGTCTAATACCGGATA <mark>C - GACCACTGAGG</mark> GCAT <mark>CCTCGGTG</mark> - GTGGAAAGCTCCGGCGGTGGA GGGTCTAATACCGGATA <mark>C - G</mark> AC <mark>CACTGAGG</mark> GCAT <mark>CCTCGGT</mark> G- GTGGAAAGCTCCGGCGGTGGA
N1226	106	GGGT CTAATACCGGATAC-AACCACT GACCGCATGGT CGGGT GGT GGAAAGCT CCGGCGGT GCAG
treptomyces DA08605	123	GGGT CTAATACCGGATAC-AACCACT GACCGCAT GGT CGGGT GGT GGAAAGCT CCGGCGGT GCAG
112 28	101	GGGTCTAATACCGGATA <mark>G-T</mark> AC <mark>CTTCGGGC</mark> GCAT <mark>GCCTGTT</mark> G-GT <mark>G</mark> GAAAGCTCCGGCGGTG <mark>C</mark> AG
treptomyces aculeolatus strai	123	
N1202	102	_GGGTCTAATACCGGATA <mark>G_T</mark> AC <mark>CTTCGGGC</mark> GCAT <mark>GCCTGTT</mark> G <mark>_</mark> GT <mark>G</mark> GAAAGCTCCGGCGGTG <mark>C</mark> AB
N1230	102	GGGTCTAATACCGGATAG-TACCTTCGGGCGCATGCCTGTTC-GTGGAAAGCTCCGGCGGTGAA
ctinomadura nitritigenes T	111	GGGTCTAATACCGGATA <mark>T - GACCACGGGTC</mark> GCAT <mark>GGCCTTGTG</mark> GGAAAGT <mark>TTTT - CGGT</mark> GGG GGGTCTAATACCGGATA <mark>T - GACCACGCTCC</mark> GCAT <mark>GGTGTGTG</mark> GT <mark>G</mark> GAAAGT <mark>TTTT - CGGT</mark> GGG
otinomadura bangladeshensis T	132	GGGTCTAATACCGGATA <mark>T-GACCAGCCTCC</mark> GCAT <mark>GGTGTGTTG</mark> GTG <mark>GAAAG</mark> TTTT-CGGT <mark>TGG</mark>

	4.00		
<u>SN701</u> Streptomyces gardneri NBRC 128	160 207	TATCAGCTTGTTGGTGGGGTAATGGC TATCAGCTTGTTGGTGGGGTAATGGC	CCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA CTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
Streptomyces omiyaensis NRRL B	207	TATCAGCTTGTTGGTG <mark>G</mark> GGT <mark>A</mark> ATGGC	
SN810	154	TATCAGCTTGTTGGTG <mark>G</mark> GGT <mark>a</mark> ATGGC	
SN821	154	TATCAGCTTGTTGGTG <mark>G</mark> GGT <mark>A</mark> ATGGC	
Streptomyces lateritius LMG 19	207	TATCAGCTTGTTGGTGGGGTAATGGC	CCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
4			
🛃 Note: This is a print preview. It may copy to the	clipboar	d slightly large. To show control panel, press t	he red arrow (upper left)
SN820	177	TAT CAGCTT GTT GET GET GAAT GEC TAT CAGCTT GTT GGT GGG GAAT GEC TAT CAGCTT GTT GGT GGG GAAC GEC TAT CAGCTT GTT GGT GGG GGAAC GEC TAT CAGCTT GTT GGT GGG GGAAC GGC	CT <mark>ACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGGCGA</mark>
Streptomyces bikiniensis DSM40 SN807	227 128	TATCAGCTTGTTGGTGGGGT <mark>aac</mark> ggc	CCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA CCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
<u>snov/</u> Streptomyces gulbargensis T	207	TATCAGCTTGTTGGTGGGGTGACGGC	COACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGGCGA
Streptomyces chartreusis NBRC	206	TAT CAGCTTGTTGGTG <mark>A</mark> GGT <mark>A</mark> ATGGC	TCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGGCGA
SN709	164	TATCAGCTTGTTGGTG <mark>G</mark> GGT <mark>G</mark> ATGGC	CT <mark>ACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGGCGA</mark>
Streptomyces tateyamensis AB4 SN710	219 157	TATCAGCTTGTTGGTG <mark>G</mark> GGT <mark>G</mark> ATGGC TATCAGCTTGTTGGTG <mark>G</mark> GGT <mark>G</mark> ATGGC	
SN805	162	TATCAGCTTGTTGGTGGGGGGGATGGC	
Streptomyces sioyaensis NRRL	214	TATCAGCTTGTTGGTG <mark>G</mark> GGT <mark>C</mark> ATGGC	CT <mark>ACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA</mark>
SN702	153	TATCAGCTTGTTGGTGAGGT <mark>a</mark> ATGGC	
Streptomyces parvulus NBRC 131	207 237	TATCAGCTTGTTGGTG <mark>A</mark> GGT <mark>A</mark> ATGGC TATCAGCTTGTTGGTG <mark>A</mark> GGT <mark>A</mark> ATGGC	
Streptomyces tendae T D6387 SN1101	175	TATCASCTIGTTGGTGAGGTATGGC	TCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA TCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
Streptomyces malachitospinus N	208	TAT CAGCTAGT TGGT GAGGTAAT GGC TAT CAGCTAGT TGGT GAGGTAAT GGC TAT CAGCTAGT TGGT GAGGTAAT GGC TAT CAGCT TGT TGGT G <mark>G</mark> GGT <mark>G</mark> AT GGC	TCACCAAGGCGACGACGGGGTAGCCGGCCTGAGAGGGGCGA
SN1104	182	TATCAGCT <mark>A</mark> GTTGGTG <mark>A</mark> GGT <mark>a</mark> ATGGC	TCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGGCGA
SN1108	187	TATCAGCTTGTTGGTG <mark>G</mark> GGT <mark>G</mark> ATGGC	CTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGGCGA
<u>SN1123</u> Streptomyces paraguayensis	168 203	TATCAGCTTGTTGGTG <mark>G</mark> GGT <mark>G</mark> ATGGC TATCAGCTTGTTGGTG <mark>G</mark> GGT <mark>G</mark> ATGGC	CTA COMMERCENCENCERETA ROCERCOTEN EN RERORD
Streptomyces paraguayensis SN1212	177	TATCAGCTTGTTGGTCGGGTAATGGC	CTACCAAGGCGACGACGGGGTAGCCGGCCTGAGAGGGGCGA CT <mark>ACCAAGGCGACGACGGGGTAGCCGGCCTGAGAGGGGCG</mark> A
Streptomyces rochei NBRC 12908	207	TAT CAGCTTGTTGGTGGGGTATGGC TAT CAGCTAGTTGGTG <mark>A</mark> GGT <mark>AAC</mark> GGC	TCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGGCGA
Streptomyces caelestis T X8	228	TATCAGCTTGTTGGTG <mark>A</mark> GGT <mark>A</mark> ATGGC	TCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
SN1210 N12 16	1 179	TATCA COTA CTTCCTCA COTA A COC	TCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGGCGA
SN1218	179	TAT CAGCT <mark>A</mark> GTTGGTG <mark>A</mark> GGT <mark>AAC</mark> GGO TAT CAGCT <mark>A</mark> GTTGGTG <mark>A</mark> GGT <mark>AA</mark> CGGO	TOACCAAGGCGACGACGGGGTAGCCGGCCTGAGAGGGGCGA TCACCAAGGCGACGACGGGGTAGCCGGCCTGAGAGGGGCGA
SN1222	178	TATCAGCTTGTTGGTG <mark>G</mark> GGT <mark>B</mark> ATGGC	CCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
Streptomyces	183	TATCAGCTTGTTGGTGGGGT <mark>B</mark> ATGGC	CCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGGCGA
<u>SN1203</u> Streptomyces narbonensis NRRL	178 233	TATCAGCTTGTTGGTG <mark>G</mark> GGT <mark>A</mark> ATGGC TATCAGCTTGTTGGTG <mark>G</mark> GGT <mark>A</mark> ATGGC	
Streptomyces variabilis NRRL B	224	TATCAGCTTGTTGGTG <mark>A</mark> GGT <mark>A</mark> ATGGC	
Streptomyces labedae NBRC 1586	195	TATCAGCTTGTTGGTG <mark>A</mark> GGT <mark>A</mark> ATGGC	
Streptomyces collinus NBRC 127	198	TATCAGCTTGTTGGTGAGGTAGTGGC	TCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
SN1125 Streptomyces CTDF1 GQ169067	183 178	TATCAGCTTGTTGGTG <mark>G</mark> GGT <mark>G</mark> ATGGC TATCAGCTTGTTGGTG <mark>G</mark> GGT <mark>A</mark> ATGGC	
Streptomyces sclerotialus DSM	206	TATCASCITIGTIGGTGGGGT <mark>A</mark> ATGGC	
SN1213	179	TATCAGCTTGTTGGTG <mark>G</mark> GGT <mark>a</mark> ATGGC	CT <mark>ACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGGCGA</mark>
Streptomyces 13638J EU741132	217	TATCAGCTTGTTGGTG <mark>G</mark> GGT <mark>B</mark> ATGGC	CTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGGCGA
<u>SN1219</u> Streptomyces griseoplanus AS 4	178 189	TATCAGCTTGTTGGTG <mark>G</mark> GGT <mark>A</mark> ATGGC TATCAGCTTGTTGGTG <mark>G</mark> GGT <mark>A</mark> ATGGC	
Streptomyces griseopianus AS 4 Streptomyces 195019 GU263883	189	TATCAGCTTGTTGGTGGGGGGADATGGC TATCAGCTTGTTGGTGGGGGGADATGGC	
Streptomyces badius NRRL B 256	218	TATCAGCTTGTTGGTG <mark>G</mark> GGT <mark>a</mark> ATGGC	CT <mark>ACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA</mark>
SN1201	178	TATCAGCTTGTTGGTG <mark>G</mark> GGT <mark>A</mark> ATGGC	
SN1221 Streptomyces 0 3 FJ959370	186 195	TATCAGCTTGTTGGTG <mark>G</mark> GGT <mark>A</mark> ATGGC TATCAGCTTGTTGGTG <mark>G</mark> GGT <mark>A</mark> ATGGC	
Streptomyces A23 Ydz XM EU368	195	TATCAGCTTGTTGGTGGGGGTATGGC TATCAGCTTGTTGGTGGGGGTAATGGC	
SN1208	179	TATCAGCTTGTTGGTG <mark>G</mark> GGT <mark>a</mark> ATGGC	CT <mark>ACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGGCGA</mark>
SN1209	177	TATCAGCTTGTTGGTG <mark>G</mark> GGT <mark>G</mark> ATGGC	
Streptomyces nitrosporeus NRRL SN1110	208 186	TATCAGCTTGTTGGTG <mark>G</mark> GGT <mark>G</mark> ATGGC TATCAGCTTGTTGGTG <mark>A</mark> GGT <mark>AAC</mark> GGC	
SNIIIU Streptomyces coralus cfcc3136	204	TATCAGCTTGTTGGTGAGGTGAGGTGAGGG TATCAGCTTGTTGGTGAGGTAATGGC	
Streptomyces CA131	184	TATCAGCTTGTTGGTG <mark>a</mark> GGT <mark>a</mark> ATGGC TATCAGCTTGTTGGTG <mark>a</mark> GGT <mark>a</mark> ATGGC	
SN1114	188	TATCAGCTTGTTGGTG <mark>G</mark> GGT <mark>G</mark> ATGGC	
Streptomyces RSF18 EU294139 SN1226	202 185	TATCAGCTTGTTGGTG <mark>G</mark> GGT <mark>G</mark> ATGGC TATCAGCTTGTTGGTG <mark>A</mark> GGT <mark>A</mark> ATGGC	
4	100	THE REAL PROPERTY OF THE PROPE	***************************************
SN1226	185	TATCAGCTTGTTGGTGAGGTAATGGC	TCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGGCGA
Streptomyces DA08605	202	TAT CAGCTTGTTGGTG <mark>AGGT</mark> ATGGC TAT CAGCTTGTTGGTG <mark>AGGTAAG</mark> GGC TAT CAGCTTGTTGGTG <mark>G</mark> GGT <mark>C</mark> ATGGC	TCACCAAGGCGACGACGGGGTAGCCGGCCTGAGAGGGGCGA
N12 28	179	TATCAGCTTGTTGGTG <mark>G</mark> GGT <mark>G</mark> ATGGC	CT <mark>ACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA</mark>
Streptomyces aculeolatus strai	201 180	TATCAGCTTGTTGGTG <mark>G</mark> GGT <mark>G</mark> ATGGC TATCAGCTTGTTGGTG <mark>G</mark> GGT <mark>G</mark> ATGGC	CT <mark>ACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA</mark>
SN1202 SN1230	180 180	TATCARCTTRTTRRTCRCRCCT	CTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGA
Actinomadura nitritigenes T	189	TATCAGCTTGTTGGTG <mark>G</mark> GGT <mark>C</mark> ATGGC	CTACCAAGGCGACGACGGGTA <mark>A</mark> CCGGCCTGAGAGGGCGA
Actinomadura bangladeshensis T	210	TATCAGCTTGTTGGTG <mark>G</mark> GGT <mark>G</mark> ATGGC	CTACCAAGGCGACGACGGGTA <mark>A</mark> CCGGCCTGAGAGGGCGA
Clustal Consensus			

			330		340		350		360		370		4	880
											.			1
SN701	240	CTGAGAC	ACGECCO	94094C	TCCTA	CCCC	IGECA	GCAGT	CCCC/	ататт	ECAU	ААТ	GGGCG	
Streptomyces gardneri NBRC 128	287	CTGAGAC	ACGGCCC	CAGAC	TCCTA	CCCC	AGGCA	GCAGT	GGGGA	ATATT	GCAG	AAT	GGGCG	AAAG
Streptomyces omiyaensis NRRL B	288	CTGAGAC	ACGGCCC	CAGAC	TCCTA	CGGG	AGGCA	GCAGT	GGGGA	ATATT	GCAG	AAT	GGGCG	AAG
SN810	234	CTGAGAC	ACGGCCC	CAGAC	TCCTA	CGGG	LGGCA	GCAGT	GGGGA	ATATT	GCAG	AAT	GGGCC	AAAG
SN821	234	CTGAGAC	ACGGCCC	CAGAC	TCCTA	CGGG	IGGCA	GCAGT	GGGGA	ATATT	GCAG	AAT	GGGCG	B AAG
Streptomyces lateritius LMG 19	287	CTGAGAC	ACGGCCC	CAGAC	TCCTA	CGGG	LGGCA	GCAGT	GGGGA	ATATT	GCAG	AAT	GGGCC	AAAG
Streptomyces zaomyceticus NRRL	293	CTGAGAC	ACGGCCC	CAGAC	TCCTA	CGGG	AGGCA	GCAGT	GGGGA	ATATT	GCAG	AAT	GGGCG	AAG
SN820	257	CTGAGAC	ACGGCCC	CAGAC	TCCTA	CGGG	IGGCA	GCAGT	GGGGA	ATATT	GCAG	AAT	GGGCC	CAAG
Streptomyces bikiniensis DSM40	307	CTGAGAC	ACGGCCC	CAGAC	TCCTA	CGGG	IGGCA	GCAGT	GGGGA	ATATT	GCAG	AAT	GGGCG	CAAG
51907	200	CTCACAC	accecco	a ca c	TOCTA	cece	CCCA	COACT	cecer		CON		CCCC	

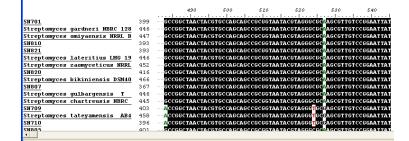
Note: This is a print preview. It may copy to the Streptomyces gulbargensis T	287	CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCG ^D AM
Streptomyces chartreusis NBRC	286	CT GAGA CA CGGC C CAGA CT C CTA CGGGA GGCA GCA GT GGGGA A TA TT GCA CAA TG GGC G <mark>a</mark> aa
58709	244	CTEAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCG <mark>A</mark> AA
Streptomyces tateyamensis AB4	299	CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCG
5N710	237	CTEAGACACEGCCCAEACTCCTACEGEGAEGCAECAETEEEGGAATATTECACAATEEGCE <mark>C</mark> AA
50805	242	CT GAGA CA C G G C C CA G A C T C C T A C G G G A G G C A G T G G G G G A A T T G C A C A A T G G G C G A A G G
Streptomyces sioyaensis NRRL	294	CT GAGA CA C G G C C CAGA CT C C TA C G G G A G G C A G T G G G G A A T A T T G C A C A A T G G G C G A A
50702	233	CT GA GA CA C G G C C CA GA C T C C TA C G G G A G G C A G T G G G G A A T T G C A CA A T G G G C G A A
Streptomyces parvulus NBRC 131	287	CTGAGA CA CGGCCCAGA CT C CTA CGGGAGGCAGCAGTGGGGAATATTGCA CAATGGGCGAA
Streptomyces tendae T D6387	317	CTGAGA CA CGGC CCAGA CT C CTA CGGGA GGCAG CA GTGGGGGA ATA TTGCA CA A TGGG CGAA
SN1101	255	CTEAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGGAATATTGCACAATGGGCG ⁰ AA
Streptomyces malachitospinus N	288	CT GAGA CA COCCCAGA CT C CTA COGGA GO CAGTAGO CAGTAGO CA ATT FOCA CAA TO SO COM
SN1104	262	CT5A5ACAC655CCCA5ACTCCTAC555A55CA5T55555AATAT15CACAAT555C55AA
SN1104 SN1108	262	CTGAGACACGGCCCCAGACTCCTACGGGAGGCAGCAGTGGGGGAATATTGCACAATGGGCGGAA
	248	
W1123		
treptomyces paraguayensis	283	CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGWAA
W1212	257	CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCG ⁹ AF
treptomyces rochei NBRC 12908	287	CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCG <mark>P</mark> AA
treptomyces caelestis T X8	308	CT6AGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCG <mark>4</mark> AA
W1210	1	
112 16	259	CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCG <mark>P</mark> AA
N1218	259	CTEAGACACGECCCAEACTCCTACEEEAGECAECAETEEEGAATATTECACAATEGECE <mark>P</mark> AP
N1222	258	CTEAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCG <mark>P</mark> AA
treptomyces	263	CT GAGA CACGGC C CAGACT C CTACGGGAGGCAGCAGT GGGGAAT ATT G CACAAT GGGC G <mark>A</mark> AA
N1203	258	CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCG <mark>A</mark> AA
treptomyces narbonensis NRRL	313	CTEAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGG <mark>A</mark> G <mark>G</mark> AA
treptomyces variabilis NRRL B	304	CTEAGACACEGCCCAEACTCCTACEGEAEGCAECAETEEEGAATATTECACAATEEECE <mark>8</mark> AA
treptomyces labedae NBRC 1586	275	CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCG <mark>8</mark> A/
treptomyces collinus NBRC 127	278	CTEAGACACEGCCCAGACTCCTACEGEAGECAGCAGTEGEEAATATTECACAATEGECE <mark>B</mark> AI
N1125	263	CT GAGA CA CGGC C CAGA CT C CTA CGGGA GGCA GCA GT GGGGA A TA TT GCA CAA TGGG CG <mark>C</mark> AI
Streptomyces CTDF1 GQ169067	258	CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCG <mark>C</mark> AP
Streptomyces sclerotialus DSM	286	CT GAGA CACGGC C CAGACT C C TACGGGAGG CAGCAGT GGGGAATATT G CACAAT GGGC G <mark>C</mark> AA
N1213	259	CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCG <mark>A</mark> AA
Streptomyces 13638J EU741132	297	CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCG <mark>A</mark> AA
SN1219	258	CT GAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCG <mark>a</mark> AA
Streptomyces griseoplanus AS 4	269	CTEAGA CACEGC CCAEACT C CTACEGEGAE GCAECAETE E GEGAATATTE CACAATE E GEGA
Streptomyces 195019 GU263883	266	CTEAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCG <mark>9</mark> AA
Streptomyces badius NRRL B 256	298	CTEAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCG <mark>D</mark> AA
5N1201	2.58	CTEAGACACEGCCCAGACTCCTACEGEAGECAGCAGTEEGEAATATTECACAATEGECE
SN1221	266	CT GAGA CA CGGC C CA GA CT C CTA CGGG A GGC A GC A
Streptomyces 0 3 FJ959370	275	CT GAGA CA C G G C C C A G A C T C C T A C G G G A G G C A G T G G G G A T A T T G C A C A A T G G G C G A A
Streptomyces A23 Ydz XM EU368	272	CT GAGA CA C G G C C CA G A C T C C TA C G G G A G G C A G T G G G G G A A T T G C A C A A T G G G C G A A
5N1208	2.59	CTGAGA CA CGGCCCAGA CT C CTA CGGGAGGCAGCAGTGGGGAATATTGCA CAATGGGCGAA
5N1209	257	CT GAGA CA C G G C C CA G A C T C C T A C G G G A G G C A G T G G G G G A A T T G C A C A A T G G G C G A A G G
Streptomyces nitrosporeus NRRL	288	CT GAGA CA C G G C C CAGA C T C C TA C G G G A G G C A G T G G G G G A T A T T G C A CAA T G G G C G A A
SN1110	266	CT GAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCG <mark>A</mark> AA
Streptomyces coralus cfcc3136	284	CT5A5ACAC655CCCA5ACTCCTAC555A55CA5T55555AATAT15CACAAT555C55AA
Streptomyces Coralus crcc3136	264	CTGAGACACGGCCCCAGACTCCTACGGGAGGCAGCAGTGGGGGAATATTGCACAATGGGCGGAA
Willia CA131		CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAA CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGGAATATTGCACAATGGGCGTAA
	268	
Streptomyces RSF18 EU294139	282	CTEAGACACEECCCAEACTCCTACEEEAGECAECAETEEGEEAATATTECACAATEEGECEEAA
SN1226	265	CTGAGACACGGCCCA <mark>P</mark> ACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCG <mark>P</mark> AP
treptomyces DA08605	282	CTGAGACACGGCCCA <mark>a</mark> aCTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCG <mark>a</mark> aa
112 28	259	CT6A6ACAC66CCCA6ACTCCTAC666A66CA6C666666ATATT6CACAAT666C6 <mark>C</mark> A
Streptomyces aculeolatus strai	281	CTEAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCG <mark>C</mark> AA

treptomyces aculeolatus strai	281	CTEAGACACEGCCCAEACTCCTACEGEGAEGCAECAETEEGEGAATATTECACAATEEGECE
W1202	260	CT GAGA CA C G G C C A GA C T C C T A C G G G A G G C A G T G G G G A A T A T T G C A C A A T G G G C G <mark>C</mark> A A G C
W1230	260	CT GAGA CA C G G C C A GA C T C C T A C G G G A G G C A G T G G G G A A T T T G C A C A A T G G G C G <mark>C</mark> A A G C
ctinomadura nitritigenes T	269	CT GAGA CA C G G C C A GA C T C C TA C G G G A G G C A G T G G G G A A T A T T G C G C A A T G G G C G <mark>G</mark> A A G C
ctinomadura bangladeshensis T	290	CT GAGA CA C G G C C A GA C T C C TA C G G G A G G C A G T G G G G A A T T G G G C G <mark>G</mark> A A G C
lustal Consensus		

		410	420	430	440	450	460
		<u> </u>					
SN701	320	GCGTGAGGGATGACG	GCCTTCGGG	TGTAAACCTC	ITTCAGCAGG	GAAGAAGCGA	LAAGTGACGGI
Streptomyces gardneri NBRC 128	367	GCGTGAGGGATGACG					
Streptomyces omiyaensis NRRL B	368	GCGTGAGGGATGACG	GCCTTCGGG	TGTAAACCTC:	ITTCAG <mark>C</mark> AGG	GAAGAAGCGA	GAGTGACGG
SN810	314	GCGTGAGGGA <mark>C</mark> GACG	GCCTTCGGG	TGTAAACCTC	ITTCAGCAGG	GAAGAAGCGA	AAGTGACGG
SN821	314	GCGTGAGGGA <mark>C</mark> GACG	GCCTTCGGG	TGTAAACCTC	ITTCAGCAGG	GAAGAAGCGA	AAGTGACGG
Streptomyces lateritius LMG 19	367	GCGTGAGGGATGACG	GCCTTCGGG	TGTAAACCTC	ITTCAGCAGG	GAAGAAGCGA	AAGTGACGG
Streptomyces zaomyceticus NRRL	373	GCGTGAGGGATGACG	GCCTTCGGG	TGTAAACCTC	ITTCAGCAGG	GAAGAAGCGA	AAGTGACGG
SN820	337	GCGTGAGGGATGACG	GCCTTCGGG	TGTAAACCTC	ITTCAGCAGG	GAAGAAGCG	AAGTGACGG
Streptomyces bikiniensis DSM40	387	GCGTGAGGGATGACG	GCCTTCGGG	TGTAAACCTC	ITTCAGCAGG	GAAGAAGCG	AAGTGACGG
SN807	288	GCGTGAGGGATGACG	GCCTTCGGG	TGTAAACCTC	ITTCAGCAGG	GAAGAAGCGA	AAGTGACGG
Streptomyces gulbargensis T	367	GCGTGAGGGATGACG	GCCTTCGGG	TGTAAACCTC	ITTCAGCAGG	GAAGAAGCGA	AAGTGACGGT
Streptomyces chartreusis NBRC	366	GCGTGAGGGATGACG	GCCTTCGGG	TGTAAACCTC	ITTCAGCAGG	GAAGAAGCGA	AAGTGACGG
CHIJUO	324	COLTON COCO TON CO	CCCTTCCCC	TOTABACCTC	PTTCACCACC	<u></u>	TA A REA A REAL

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SN710	317	GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCG <mark>C</mark> AAGTGACGGT
SN805	322	GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGA <mark>G</mark> AGTGACGGT
Streptomyces sioyaensis NRRL	374	GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGA <mark>G</mark> AGTGACGGT
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	GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCG <mark>C</mark> AAGTGACGGT
SN1123	328	GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
Streptomyces paraguayensis	363	GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCG <mark>C</mark> AAGTGACGGT
SN1212	337	GCGTGAGGGA <mark>C</mark> GACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
Streptomyces rochei NBRC 12908	367	GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
Streptomyces caelestis T X8	388	GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
SN1210	1	
N12 16	339	GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
SN1218	339	GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
SN1222	338	GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
Streptomyces	343	GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
SN1203	338	GCGTGAGGGA <mark>C</mark> GACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGT
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	GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCG <mark>C</mark> AAGTGACGGT
Streptomyces CTDF1 GQ169067	338	GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCG <mark>C</mark> AAGTGACGGT
Streptomyces sclerotialus DSM	366	GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCG <mark>C</mark> AAGTGACGGT
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 0 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	GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGA <mark>G</mark> AGTGACGGT
Streptomyces DA08605	362	GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGA <mark>G</mark> AGTGACGGT
N12 28	339	GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGA <mark>G</mark> AGTGACGGT
Streptomyces aculeolatus strai	361	GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGA <mark>G</mark> AGTGACGGT
SN1202	340	GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGA <mark>g</mark> agtgaCggt
SN1230	340	GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGA <mark>G</mark> AGTGACGGT
Actinomadura nitritigenes T	349	GCGTG <mark>E</mark> GGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGA <mark>C</mark> GAAGC <mark>T</mark> AA <mark>C</mark> GTGACGGT



▲ Note: This is a print preview. It may copy to the	clipboar	d slightly large. To show control panel, press the red arrow (upper left)
Streptomyces sloyaensis NRRL	453	COBRETATOTACITACITECCARCARCORDITATACITARISECUCOARCETTETCCCRAATTAT
SN702	392	GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGC <mark>G</mark> AGCGTTGTCCGGAATTAT
Streptomyces parvulus NBRC 131	446	GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGC <mark>A</mark> AGCGTTGTCCGGAATTAT
Streptomyces tendae T D6387	476	GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGC <mark>A</mark> AGCGTTGTCCGGAATTAT
SN1101	414	GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCGAGCGTTGTCCGGAATTAT
Streptomyces malachitospinus N	447	GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCG <mark>A</mark> AGCGTTGTCCGGAATTAT
SN1104	421	
SN1108	426	
SN1123	407	ACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCGAGCGTTGTCCGGAATTAT ACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCGAGCGTTGTCCGGAATTAT
Streptomyces paraguayensis	442	ACCEGECTAACTACETECCAECAECEEEEETAATACETAEGE <mark>T</mark> EEEAECETTETCCEEAATTAT ECCEGECTAACTACETECCAECAECEEEETAATACETAEGEEEECE <mark>A</mark> AECETTETCCEGAATTAT
SN1212	416 446	GCCGGCTAACTACGTGCCAGCAGCCGCGGGTAATACGTAGGGCGC@AGCGTTGTCCGGAATTAT GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGC@AGCGTTGTCCGGAATTAT
Streptomyces rochei NBRC 12908		
Streptomyces caelestis T X8 SN1210	467 1	GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGC <mark>G</mark> AGCGTTGTCCGGAATTAT
N12 16	418	GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCGAGCGTTGTCCGGAATTAT
N12 16 SN1218	418	- GCCGGCTAACTACGTGCCAGCAGCCGCGGGTAATACGTAGGGCGCGAGCGTTGTCCGGAATTAT
SN1218 SN1222	418	- GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCGAGCGTTGTCCGGAATTAT
SN1222 Streptomyces	417	GCCGGCTAACTACGTGCCAGCAGCCGCGGGTAATACGTAGGGCGCGAGCGTTGTCCGGAATTAT GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCGAGCGTTGTCCGGAATTAT
SN1203	417	GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAGCGTTGTCCGGAATTAT
Streptomyces narbonensis NRRL	473	TTEAAGGETAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCGAGCGTTGTCCGGAATTAT
Streptomyces variabilis NRRL B	463	GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCGCAGCGTTGTCCGGAATTAT
Streptomyces labedae NBRC 1586	434	- SCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCGCGAGCGTTGTCCGGAATTAT
Streptomyces collinus NBRC 127	437	GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCGCGAGCGTTGTCCGGAATTAT
SN1125	422	- ACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCGAGCGTTGTCCGGAATTAT
Streptomyces CTDF1 GQ169067	417	ACCEGCTAACTACGTGCCAGCCGCGGGGTAATACGTAGGGTGCGAGCGTTGTCCGGAATTAT
Streptomyces sclerotialus DSM	445	- GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCGAGCGTTGTCCGGAATTAT
SN1213	418	- GCCGGCTAACTACGTGCCAGCCGCGGGGGAATACGTAGGGCGCC
Streptomyces 13638J EU741132	456	
SN1219	417	- GCCGGCTAACTACGTGCCAGCCGCGGGGGAATACGTAGGGCGCC
Streptomyces griseoplanus AS 4	428	
Streptomyces 195019 GU263883	425	
Streptomyces badius NRRL B 256	457	GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCCAGCGTTGTCCGGAATTAT
SW1201	417	
SN1221	425	GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCCAGCGTTGTCCGGAATTAT
Streptomyces 0 3 FJ959370	434	GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCGCAGCGTTGTCCGGAATTAT
Streptomyces A23 Ydz XM EU368	431	
SW1208	418	GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCGAGCGTTGTCCGGAATTAT
SN1209	416	
Streptomyces nitrosporeus NRRL	447	
SN1110	425	GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGC <mark>P</mark> AGCGTTGTCCGGAATTAT
Streptomyces coralus cfcc3136	443	
Streptomyces CA131	423	GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGC <mark>D</mark> AGCGTTGTCCGGAATTAT
SN1114	427	GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCG <mark>G</mark> AGCGTTGTCCGGAATTAT
Streptomyces RSF18 EU294139	441	GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCC
SN1226	424	GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCG <mark>B</mark> AGCGTTGTCCGGAATTAT
Streptomyces DA08605	441	GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCC <mark>B</mark> AGCGTTGTCCGGAATTAT
N12 28	418	GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGC <mark>B</mark> AGCGTTGTCCGGAATTAT
Streptomyces aculeolatus strai	440	
SN1202	419	GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGC <mark>B</mark> AGCGTTGTCCGGAATTAT
SN1230	419	
Actinomadura nitritigenes T	428	GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGC <mark>B</mark> AGCGTTGTCCGGAATTAT
Actinomadura bangladeshensis T	449	
Clustel Conserve		

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Clustal	Conse	ensus

		57	0	580		590		00	61	0		620
SN701	478	बस्यरतनवननव				AARCCO		TTAA CO			TCO	1
Streptomyces gardneri NBRC 128	525	CGTAGGCGGC										
Streptomyces omiyaensis NRRL B	526	CGTAGGCGGC	TTGTC	CGTCGG	GTGTGA	AAGCCO	GGGGGC	TTAAC	CCGGG	TCTGC	TC	GATA
SN810	472	CGTAGGCGGC	TTGTC <mark>A</mark>	CGTCGG	GTGTGA	AAGCCO	GGGGGC	TTAAC	CCCGGG	TCTGC	TC	GATA
5N821	472	CGTAGGCGGC	TTGTC <mark>A</mark>	CGTCGG	GTGTGA	AAGCCO	GGGGGC	TTAAC	CCCGGG	TCTGC	TC	GATA
Streptomyces lateritius LMG 19	525	CGTAGGCGGC	ттбтса	сбтсбб	GTGTGA	AAGCCO	GGGGGC	TTAACO	CCCGGG	TCTGC	TC	GATA
Streptomyces zaomyceticus NRRL	531	CGTAGGCGGC	ТТБТС<mark>а</mark>	CGTCGG	GTGTGA	AAGCCO	GGGGGC	TTAACO	CCGGGG	TCTGC	TC	GATA
5N820	495	CGTAGGCGGC	TTGTC <mark>a</mark>	CGTCGG	GTGTGA	AAGCCO	Geeec	TTAAC	CCGGG	TCTGC	TC C	GATA
Streptomyces bikiniensis DSM40	545	CGTAGGCGGC	TTGTC <mark>a</mark>	CGTCGG	GTGTGA	AAGCCO	Geeec	TTAAC	CCGGG	TCTGC	a <mark>T C</mark> C	GATA
5N807	446	CGTAGGCGGC	TTGTC <mark>a</mark>	CGTCGG	GTGTGA	AAGCCO	GGGGGC	TTAAC	CCGGGG	TCTGC	TCC	GATA
Streptomyces gulbargensis T	525	CGTAGGCGGC	TTGTC <mark>a</mark>	CGTCGG	GTGTGA	AAGCCO	GGGGGC	TTAAC	CCGGG	TCTGC	a <mark>T C</mark> C	GATA
Streptomyces chartreusis NBRC	524	CGTAGGCGGC	TTGTC <mark>a</mark>	CGTCGG	GTGTGA	AAGCCO	GGGGGC	TTAACO	CCGGG	TCTGC	TT C	GATA
5N709	482	CGTAGGCGGC	TTGTC <mark></mark> G	CGTCGG	ATGTGA	AAGCCO	GGGGGC	TTAACO	CCCGGG	TCTGC	TT	GATA
Streptomyces tateyamensis AB4	537	CGTAGGCGGC										
SN710	475	CGTAGGCGGC	CTGTCA	CGTCGG	ATGTGA	AAGCCO	GGGGGC	TTAACO	CCCGGG	TCTGC	TT	GATA
SN805	480	CGTAGGCGGC	TTGTC6	CGTCGG	A TGTGA	AAGCCO	Geeec	TTAACO	CCCGGG	TCTGC	TT	GATA
Streptomyces sioyaensis NRRL	532	CGTAGGCGGC										
SN702	471	CGTAGGCGGC	TTGTC <mark>a</mark>	CGTCGG	TGTGA	AAGCCO	Geeec	TTAAC	CCCCCC	TCTGC	a G T C	GATA
Streptomyces parvulus NBRC 131	52.5	CETABLICORE	TTGTCA	CRTCRC	TETEA	AAGCCO	HERERO	TTAACO	Color Minis	TOTAC	IG T K	BATA

streptomyces tendae i D5387	555	CBTAGSUBBUTTETCAUETCEETTETEAAAGCCCCBBBBCTTAACCCCBBBTCTECAETCEA
SN1101	493	CGTAGGCGGCTTGTC <mark>a</mark> CGTCGG <mark>T</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>GT</mark> CGA
Streptomyces malachitospinus N	526	CGTAGGCGGCTTGTC <mark>A</mark> CGTCGG <mark>T</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>GT</mark> CGA
SN1104	500	CGTAGGCGGCTTGTC <mark>G</mark> CGTCGG <mark>T</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>GT</mark> CGA
SN1108	505	CGTAGGCGGCTTGTC <mark>C</mark> CGTCGG <mark>A</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>TT</mark> CGA
5N1123	486	CGTAGGCGGC <mark>C</mark> TGTC <mark>G</mark> CGTCGG <mark>A</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>TT</mark> CGA
Streptomyces paraguayensis	521	CGTAGGCGGC <mark>N</mark> TGTC <mark>G</mark> CGTCGG <mark>A</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>TT</mark> CGA
5N1212	495	CGTAGGCGGCTTGTC <mark>A</mark> CGTCGG <mark>G</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>TC</mark> CGA
Streptomyces rochei NBRC 12908	525	CGTAGGCGGCTTGTC <mark>A</mark> CGTCGG <mark>T</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>GT</mark> CGA
Streptomyces caelestis T X8	546	CGTAGGCGGCTTGTC <mark>G</mark> CGTCGG <mark>T</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>GT</mark> CGA
5N1210	15	CGTAGGCGGCTTGTC <mark>G</mark> CGTCGG <mark>T</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>GT</mark> CGA
112 16	497	CGTAGGCGGCTTGTC <mark>A</mark> CGTCGG <mark>T</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>GT</mark> CGA
SN1218	497	CGTAGGCGGCTTGTC <mark>A</mark> CGTCGG <mark>T</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>GT</mark> CGA
SN1222	496	CGTAGGCGGCTTGTC <mark>R</mark> CGTCGG <mark>G</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>TC</mark> CGA
Streptomyces	501	CGTAGGCGGCTTGTC <mark>B</mark> CGTCGG <mark>G</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>TC</mark> CGA
SN1203	496	CGTAGGCGGCTTGTC <mark>a</mark> CGTCGG <mark>g</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>TC</mark> CGA
treptomyces narbonensis NRRL	553	CGTAGGCGGCTTGTC <mark>A</mark> CGTCGG <mark>G</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>TC</mark> CGA
Streptomyces variabilis NRRL B	542	CGTAGGCGGCTTGTC <mark>A</mark> CGTCGG <mark>T</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>GT</mark> CGA
Streptomyces labedae NBRC 1586	513	CGTAGGCGGCTTGTC <mark>A</mark> CGTCGG <mark>T</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>GT</mark> CGA
Streptomyces collinus NBRC 127	516	CGTAGGCGGCTTGTC <mark>A</mark> CGTCGG <mark>T</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>GT</mark> CGA
SN1125	501	CGTAGGCGGCTTGTC <mark>G</mark> CGTCGG <mark>A</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>TT</mark> CGA
Streptomyces CTDF1 G0169067	496	CGTAGGCGGCTTGTCGCGTCGG3TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>TT</mark> CGA
Streptomyces sclerotialus DSM	524	CGTAGGCGGCTTGTC <mark>E</mark> CGTCGG <mark>A</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>TT</mark> CGA
SN1213	497	CGTAGGCGGCTTGTC <mark>A</mark> CGTCGG <mark>A</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>TT</mark> CGA
Streptomyces 13638J EU741132	535	CETAGECEECTTETCACETCEEATETEAAAECCCEEEECTTAACCCCEEETCTECATTCEA
SN1219	496	CGTAGGCGGCTTGTCACGTCGGATGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>TT</mark> CGA
Streptomyces griseoplanus AS 4	507	CGTAGGCGGCTTGTC <mark>A</mark> CGTCGG <mark>A</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>TT</mark> CGA
Streptomyces 195019 GU263883	504	CGTAGGCGGCTTGTCACGTCGGATGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>TT</mark> CGA
Streptomyces badius NRRL B 256	536	CGTAGGCGGCTTGTCACGTCGGATGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCATTCGA
SN1201	496	CGTAGGCGGCTTGTCACGTCGGATGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCATTCGA
581201	504	CGTAGGCGGCTTGTCACGTCGGATGTGAAAGCCCGGGGCTTAACCCCCGGGTCTGCATTCGA
	513	CGTAGGCGGCTTGTCACGTCGGATGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCATTCGA CGTAGGCGGCTTGTCACGTCGGATGTGAAAGCCCCGGGGCTTAACCCCGGGTCTGCATTCGA
Streptomyces 0 3 FJ959370		CGTAGGCGGCTTGTCGCGTCGGGTGTGTGAAAGCCCGGGGCTTAACCCCCGGGTCTGCATTCGA
Streptomyces A23 Ydz XM EU368 SN1208	510 497	
511209	495	CGTAGGCGGCTTGTC <mark>A</mark> CGTCGG <mark>A</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>TT</mark> CGA
Streptomyces nitrosporeus NRRL	526	CGTAGGCGGCTTGTC <mark>A</mark> CGTCGG <mark>B</mark> TGTGAAAGCCCGGGGCTTAACCCCCGGGTCTGCA <mark>TT</mark> CGA
SN1110	504	CGTAGGCGGCTTGTC <mark>A</mark> CGTCGG <mark>G</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>TT</mark> CGA
Streptomyces coralus cfcc3136	522	CGTAGGCGGCTTGTC <mark>A</mark> CGTCGG <mark>G</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>TT</mark> CGA
Streptomyces CA131	502	CGTAGGCGGCTTGTC <mark>A</mark> CGTCGG <mark>G</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>TT</mark> CGA
SN1114	506	CGTAGGCGGCTTGTC <mark>A</mark> CGTCGG <mark>T</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>GT</mark> CGA
treptomyces RSF18 EU294139	520	CGTAGGCGGCTTGTC <mark>A</mark> CGTCGG <mark>T</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>GT</mark> CGA
SN1226	503	CGTAGGCGGCTTGTC <mark>a</mark> CGTCGG <mark>T</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>GT</mark> CGA
treptomyces DA08605	520	CGTAGGCGGCTTGTC <mark>A</mark> CGTCGG <mark>T</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>GT</mark> CGA
112 28	497	CGTAGGCGGCTTGTC <mark>C</mark> CGTCGG <mark>A</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>TT</mark> CGA
Streptomyces aculeolatus strai	519	CGTAGGCGGCTTGTC <mark>G</mark> CGTCGG <mark>A</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>TT</mark> CGA
SN1202	498	CGTAGGCGGCTTGTC <mark>G</mark> CGTCGG <mark>a</mark> tgtgaaagcccggggcttaaccccgggtctgca <mark>tt</mark> cga
SN1230	498	CGTAGGCGGCTTGTC <mark>G</mark> CGTCGG <mark>a</mark> TGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCA <mark>TT</mark> CGA
Actinomadura nitritigenes T	507	CGTAGGCGG <mark>T</mark> TTGTC <mark>G</mark> CGTC <mark>TG</mark> TGAAAGCCC <mark>AC</mark> GGCTTAAC <mark>TGT</mark> GGGTCTGC <mark>GGTG</mark> GA
Actinomadura bangladeshensis T	528	CGTAGGCGG <mark>T</mark> TTGTC <mark>GCGTC</mark> TG <mark>TC</mark> GTGAAAGCCC <mark>AC</mark> GGCTTAACC <mark>GT</mark> GGGTCTGC <mark>GGTG</mark> GA
Clustal Consensus	15	

N701	558	GGTAGGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCGGAGATATCAGGAGGAACACCCGGT
<u></u>	550	001A0000A0A11000A1110100101A000010AAA1000A0A1A10A00A0
A Note: This is a print preview. It may copy to the	olinhoav	d slightly large. To show control panel, press the red arrow (upper left)
Mote: This is a plink preview. It may copy to the	SOU	of the second se
SN1108	585	GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC
SN1123	566	GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC
Streptomyces paraguayensis	601	GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC
SN1212	575	GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC-GGT
Streptomyces rochei NBRC 12908	605	GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC
Streptomyces caelestis T X8	626	GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC-GGT
SN1210	95	GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC-GGT
N12 16	577	GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC
SN1218	577	GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC
SN1222	576	GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC-GGT
Streptomyces	581	GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC
SN1203	576	G G TA G G G G A T C G G A A T C C T G G T G T A G C G G T G A A T G C G C A G A T A T C A G G A G G A A C A C C
Streptomyces narbonensis NRRL	633	GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC-GGT
Streptomyces variabilis NRRL B	622	GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC
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	GGTAGGGGAGAT CGGAAT T C C T GGT G T AG C G G T GAAAT G C G C AGAT AT C A G G A G A C A C C G G T
Streptomyces 195019 GU263883	584	GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC-GGT
Streptomyces badius NRRL B 256	616	GETAGEGEAGATCGEAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC-GGT
SN1201	576	GGTAGGGGGAGAT CGGAAT T C C T GGT G T AG C G G T GAAAT G C G C AGAT AT C AG G A G A C A C C - G G T
SN1221	584	GGTAGGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC-GGT
Streptomyces 0 3 FJ959370	593	GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC-GGT
Streptomyces A23 Ydz XM EU368	590	GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC-GGT
SN1208	577	GGTAGGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC-GGT
5N1209	575	GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC GGT
Streptomyces nitrosporeus NRRL	606	GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC GGT
SN1110	584	GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC GGT
Streptomyces coralus cfcc3136	602	GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC GGT
	582	GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC GGT
Streptomyces CA131 SN1114	586	
Streptomyces RSF18 EU294139	600	GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC-GGT
511226	583	GGTAGGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC-GGT
Streptomyces DA08605	600	GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC GGT
12 28	577	GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTG <mark>G</mark> AATGCGCAGATATCAGGAGGAACACC-GGT
Streptomyces aculeolatus strai	599	GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTG <mark>G</mark> AATGCGCAGATATCAGGAGGAACACC GGT
SN1202	578	GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTG <mark>G</mark> AATGCGCAGATATCAGGAGGAACACC-GGT
SN1230	578	GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTG <mark>G</mark> AATGCGCAGATATCAGGAGGAACACC-GGT
Actinomadura nitritigenes T	587	GGTAGGGGAGA <mark>at</mark> ggaattcc <mark>c</mark> ggtgtagcggtgaaatgcgcagatatc <mark>g</mark> ggaggaacacc-ggt
Actinomadura bangladeshensis T Clustal Consensus	608 73	GGTAGGGGAGA <mark>rt</mark> ggaattcc <mark>c</mark> ggtgtagcggtgaaatgcgcagatatc <mark>g</mark> gdaggaacacc-ggt



SCIENCOMVCED DALAUGAVENDID	000	DEDITION OF A DEDITIONO OF A
SN1212	654	CTGGGCC <mark>AT</mark> TACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGT.
Streptomyces rochei NBRC 12908	684	CTGGGCC <mark>GA</mark> TACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGT.
Streptomyces caelestis T X8	705	CTGGGCC <mark>GA</mark> TACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGT.
SN1210	174	CTGGGCC <mark>GR</mark> TACTGACGCTGAGGAGCGAAAGCGTGGGGGAGCGAACAGGATTAGATACCCTGGT.
N12 16	656	CTGGGCC <mark>GA</mark> TACTGACGCTGAGGAGCGAAAGCGTGGGGGGGGGAGCGAACAGGATTAGATACCCTGGT
SN1218	656	CTGGGCC <mark>GR</mark> TACTGACGCTGAGGAGCGAAAGCGTGGGGGAGCGAACAGGATTAGATACCCTGGT.
SN1222	655	CTGGGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGGAGCGAACAGGATTAGATACCCTGGT.
Streptomyces	660	CTGGGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGGGGG
SN1203	655	CTGGGCC <mark>AT</mark> TACTGACGCTGAGGAGCGAAAGCGTGGGGGAGCGAACAGGATTAGATACCCTGGT.
Streptomyces narbonensis NRRL	712	CTGGGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGGGGG
Streptomyces variabilis NRRL B	701	CTGGGCC <mark>GR</mark> TACTGACGCTGAGGAGCGAAAGCGTGGGGGAGCGAACAGGATTAGATACCCTGGT
Streptomyces labedae NBRC 1586	672	CTGGGCC <mark>GA</mark> TACTGACGCTGAGGAGCGAAAGCGTGGGGGGGGGAGCGAACAGGATTAGATACCCTGGT
Streptomyces collinus NBRC 127	675	CTGGGCC <mark>GR</mark> TACTGACGCTGAGGAGCGAAAGCGTGGGGGAGCGAACAGGATTAGATACCCTGGT
SN1125	660	CTGGGCC <mark>GA</mark> TACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGT.
Streptomyces CTDF1 GQ169067	655	CTGGGCC <mark>GR</mark> TACTGACGCTGAGGAGCGAAAGCGTGGGGGAGCGAACAGGATTAGATACCCTGGT
Streptomyces sclerotialus DSM	683	CTGGGCC <mark>GA</mark> TACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGT
SN1213	656	CTGGGCC <mark>AT</mark> TACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGT.
Streptomyces 13638J EU741132	694	CTGGGCC <mark>AT</mark> TACTGACGCTGAGGAGCGAAAGCGTGGGGGAGCGAACAGGATTAGATACCCTGGT
SN1219	655	CTGGGCC <mark>AT</mark> TACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGT
Streptomyces griseoplanus AS 4	666	CTGGGCC <mark>AT</mark> TACTGACGCTGAGGAGCGAAAGCGTGGGGGAGCGAACAGGATTAGATACCCTGGT
Streptomyces 195019 GU263883	663	CTGGGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGT
Streptomyces badius NRRL B 256	695	CTGGGCC <mark>AT</mark> TACTGACGCTGAGGAGCGAAAGCGTGGGGGAGCGAACAGGATTAGATACCCTGGT
SN1201	655	CTGGGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGT
SN1221	663	CTGGGCC <mark>AT</mark> TACTGACGCTGAGGAGCGAAAGCGTGGGGGAGCGAACAGGATTAGATACCCTGGT
Streptomyces 0 3 FJ959370	672	CTGGGCC <mark>AT</mark> TACTGACGCTGAGGAGCGAAAGCGTGGGGGAGCGAACAGGATTAGATACCCTGGT
Streptomyces A23 Ydz XM EU368	669	CTGGGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGGAGCGAACAGGATTAGATACCCTGGT
SN1208	656	CTGGGCC <mark>AT</mark> TACTGACGCTGAGGAGCGAAAGCGTGGGGGAGCGAACAGGATTAGATACCCTGGT
SN1209	654	CTGGGCC <mark>AT</mark> TACTGACGCTGAGGAGCGAAAGCGTGGGGGAGCGAACAGGATTAGATACCCTGGT
Streptomyces nitrosporeus NRRL	685	CTGGGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGT
SN1110	663	CTGGGCC <mark>AT</mark> TACTGACGCTGAGGAGCGAAAGCGTGGGGGAGCGAACAGGATTAGATACCCTGGT
Streptomyces coralus cfcc3136	681	CTGGGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGT
Streptomyces CA131	661	CTGGGCC <mark>AT</mark> TACTGACGCTGAGGAGCGAAAGCGTGGGGGAGCGAACAGGATTAGATACCCTGGT
SN1114	665	CTGGGCC <mark>GA</mark> TACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGT
Streptomyces RSF18 EU294139	679	CT 6 6 6 C GATA CT 6 A C 6 C T 6 A 6 G A 6 C 6 A A 6 C 6 T 6 G 6 G A C A 6 G A T A 6 A T A 6 A T A C C C T 6 G
SN1226	662	CTGGGCC <mark>GA</mark> TACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGT
Streptomyces DA08605	679	CT 6 6 6 C GA TA CT 6 A C 6 C T 6 A 6 G A 6 C 6 A A 6 C 6 T 6 G 6 G A C A 6 G A T A 6 A T A 6 A T A C C C T 6 G
N12 28	656	CTGGGCC <mark>GA</mark> TACTGACGCTGAGGAGCGAAAGCGTGGGGAGC <mark>D</mark> AACAGGATTAGATACCCTGGT
Streptomyces aculeolatus strai	678	CTEGECCEGATACTEACECTEAEEAECEAAAECETEEEEAECAACAEEATTAEATACCCTEET
SN1202	657	CTGGGCC <mark>GA</mark> TACTGACGCTGAGGAGCGAAAGCGTGGGGAGC <mark>A</mark> AACAGGATTAGATACCCTGGT
SN1230	657	CTGGGCC <mark>GA</mark> TACTGACGCTGAGGAGCGAAAGCGTGGGGGGGC <mark>A</mark> AACAGGATTAGATACCCTGGT
Actinomadura nitritigenes T	666	CTEGECCTETACTEACECTEAGEAECEAAAECETEEGEGAECEAACAGEATTAEATACCCTGET
Actinomadura bangladeshensis T	687	CTEGECC <mark>T</mark> GTACTEACECTEAGEAGCEAAAGCETEGEGAGCEAACAGEATTAEATACCCTEGT
Clustal Consensus	146	******

		810 820 830 840 850 860
SN701	718	TTGGGACTAGGTGTTGGCGACATTCCACGTCGGTGCCGCAGCTAACGCATTAAGTTC
Streptomyces gardneri NBRC 128	764	TIGGG <mark>a</mark> actaggtgt <mark>t</mark> ggcgacattccacgt <mark>c</mark> gtg <mark>g</mark> gtgccgcagctaacgcattaagt <mark>t</mark> c
Streptomyces omiyaensis NRRL B	765	TTGGGAACTAGGTGTTGGCGACATTCCACGTCGTGGGGGCCGCAGCTAACGCATTAAGTTC
SN810	711	TTGGG <mark>8</mark> ACTAGGTGT <mark>T</mark> GGCGACATTCCACGT <mark>C</mark> GTC <mark>G</mark> GTGCCGCAGCTAACGCATTAAGT <mark>T</mark> C
SN821	711	TreesActagetetTegeceacattccacetCetegeceacetaacecattaaetTc
Streptomyces lateritius LMG 19	764	TTGGGAACTAGGTGTTGGCGACATTCCACGTCGTGGTGCCGCAGCTAACGCATTAAGTTC
Streptomyces zaomyceticus NRRL	770	TTEEE <mark>P</mark> ACTAGETET <mark>T</mark> EECEACATTCCACET <mark>C</mark> ETE <mark>E</mark> GTECCECAECTAACECATTAAET <mark>T</mark> C
Streptomyces caelestis T X8	785	GTGGG <mark>CACTAGGTGT</mark> GGGC <mark>ACATTCCACGT</mark> GTG <mark>C</mark> GTGCCGCAGCTAACGCATTAAGTGC
SN1210	254	GTEEE <mark>C</mark> ACTAEETETEEEEE <mark>BACATTCCACET</mark> ETE <mark>C</mark> ETECCECAECTAACECATTAAET <mark>E</mark> C
N12 16	736	GTEEE <mark>C</mark> ACTAEETETEEEEE <mark>AACATTCCACET</mark> ETE <mark>C</mark> ETECCECAECTAACECATTAAET <mark>E</mark> C
SN1218	736	GTGGG <mark>C</mark> ACTAGGTGT <mark>G</mark> GGC <mark>P</mark> ACATTCCACGT <mark>T</mark> GTC <mark>C</mark> GTGCCGCAGCTAACGCATTAAGT <mark>G</mark> C
SN1222	735	TEGENACTAGETETEGECEACATTCCACETCECECECECAECTAACECATTAAET
Streptomyces	740	TTGGGPACTAGGTGTTGGCGACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTC
SN1203	735	TTGGGAACTAGGTGTTGGCGACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTC
Streptomyces narbonensis NRRL	792	TTGGGPACTAGGTGTTGGCGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTTC
Streptomyces variabilis NRRL B	781	GTGGG <mark>C</mark> ACTAGGTGT <mark>G</mark> GGCGACATTCCACGT <mark>C</mark> GTGCCGCAGCTAACGCATTAAGTGC
Streptomyces Labedae NBRC 1586	752	GTGGG <mark>C</mark> ACTAGGTGT <mark>G</mark> GGCGACATTCCACGT <mark>C</mark> GTGCCGCAGCTAACGCATTAAGTGC
Streptomyces collinus NBRC 127	755	GTGGG <mark>C</mark> ACTAGGTGT <mark>G</mark> GGC <mark>B</mark> ACATTCCACGT <mark>T</mark> GTC <mark>C</mark> GTGCCGCAGCTAACGCATTAAGTGC
SN1125	740	TTGGGAACTAGGTGTGGGTGGCATTCCACGTCATCCGCGCGCG
Streptomyces CTDF1 GQ169067	735	TTGGGAACTAGGTGTGGGTGGCATTCCACGTCATCCGTGCCGCAGCTAACGCATTAAGTTC
Streptomyces sclerotialus DSM	763	TTGGGPACTAGGTGT <mark>G</mark> GGCGACATTCCACGTCGTCGCGCGCGCGCGCAGCTAACGCATTAGGTC
SN1213	736	TTGGGPACTAGGTGT <mark>T</mark> GGCGACATTCCACGTCGTGGTGCCGCAGCTAACGCATTAAGTTC
	774	TTGGGACTAGGTGTTGGCGACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTC
	735	
SN1219		
Streptomyces griseoplanus AS 4	746	
Streptomyces 195019 GU263883	743	TTGGG®ACTAGGTGTTGGCGACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTC
Streptomyces badius NRRL B 256	775	TTGGGACTAGGTGTTGGCGACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTC
SN1201	735	TTGGGACTAGGTGTTGGCGACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTC
SN1221	743	TGGGAACTAGGTGTTGGCGACATTCCACGTCGGTGCCGCAGCTAACGCATTAAGTTC
Streptomyces 0 3 FJ959370	752	TGGGAACTAGGTGT <mark>T</mark> GGCGACATTCCACGTCGGTGCCGCAGCTAACGCATTAAGT <mark>T</mark> C
Streptomyces A23 Ydz XM EU368	749	TTGGGAACTAGGTGTTGGGCGACATTCCACGTCGTGGGGGGGG
SN1208	736	TIGGENACTAGGTGTTGGGCGACATTCCACGTCGTGGGGGGGGGG
SN1209	734	T <mark>TGGGR</mark> ACTAGGTGT <mark>T</mark> GGCGACATTCCACGT <mark>C</mark> GTC <mark>G</mark> GTGCCGCA
Streptomyces nitrosporeus NRRL	765	TGGGRACTAGGTGTTGGCGACATTCCACGTCGTGGTGCCGCAGCTAACGCATTAAGTTC
SN1110	743	GTGGGRACTAGGTGT <mark>T</mark> GGCGACATTCCACGT <mark>C</mark> GTC <mark>G</mark> GTGCCGCAGCTAACGCATTAAGT <mark>T</mark> C
Streptomyces coralus cfcc3136	761	G <mark>TGGGB</mark> ACTAGGTGT <mark>T</mark> GGCGACATTCCACGT <mark>C</mark> GTC <mark>G</mark> GTGCCGCAGCTAACGCATTAAGT <mark>T</mark> C
Streptomyces CA131	741	G <mark>TGGG</mark> ACTAGGTGT <mark>T</mark> GGCGACATTCCACGT <mark>C</mark> GTGCCGCAGCTAACGCATTAAGT <mark>T</mark> C
SN1114	745	TTGGG <mark>C</mark> ACTAGGTGT <mark>G</mark> GGCGACATTCCACGT <mark>C</mark> GTGCCGCAGCTAACGCATTAAGT <mark>G</mark> C
Streptomyces RSF18 EU294139	759	TTGGG <mark>C</mark> ACTAGGTGT <mark>G</mark> GGCGACATTCCACGT <mark>C</mark> GTGCCGCAGCTAACGCATTAAGT <mark>C</mark> C
SN1226	742	G <mark>TGGG<mark>C</mark>ACTAGGTGT<mark>G</mark>GGCGACATTCCACGT<mark>C</mark>GTGCCGCAGCTAACGCATTAAGT<mark>G</mark>C</mark>
Streptomyces DA08605	759	GTGGG <mark>C</mark> ACTAGGTGT <mark>G</mark> GGCGACATTCCACGT <mark>C</mark> GTGCCGCAGCTAACGCATTAAGT <mark>G</mark> C
N12 28	736	GTGGG <mark>C</mark> ACTAGGTGT <mark>G</mark> GGCG <mark>E</mark> CATTCCACGT <mark>C</mark> GTGCCG <mark>T</mark> AGCTAACGCATTAAGT <mark>G</mark> C
Streptomyces aculeolatus strai	758	CTGGGCACTAGGTGTCGGGCGCCATTCCACGTCGTCCGTGCCGTAGCTAACGCATTAAGTCC
SN1202	737	GTGGG <mark>C</mark> ACTAGGTGT <mark>G</mark> GGCG <mark>G</mark> CATTCCACGT <mark>C</mark> GTCC <mark>G</mark> TGCCG <mark>T</mark> AGCTAACGCATTAAGT <u>G</u> C
SN1230	737	GTGGG <mark>C</mark> ACTAGGTGTGGGGCGGCATTCCACGTCGTCCGTGCCG <mark>T</mark> AGCTAACGCATTAAGT <u>C</u> C
Actinomadura nitritigenes T	746	TTGGGCCCTAGGTGTGGGG-GTTCTTCCACGGATTCCGCGCCCGTAGCTAACGCATTAAGCGC
Actinomadura bangladeshensis T	767	TTGGGCGCTAGGTGTGGGGGCGTTCTTCCACGGATTCCGCGCCCGTAGCTAACGCATTAAGCGC
Clustal Consensus	107	

Clustal Consensus

			890	2	900	9	10	2	920	93	0		940
SN701	798	GER ANTE	GCTAAAAC		GGAAT	TGACG			CAAGC		GCAT	etterer	
Streptomyces gardneri NBRC 128	844		GCTAAAAC										
Streptomyces omiyaensis NRRL B	845	CGCAAG	GCTAAAAAC	TCAAA	GGAAT	TGACG	GGGGCC	CGCA	CAAGO	GCGGA	GCAT	JTGG	ттаа
SN810	791	CGCAAG	GCTAAAAA	TCAAA	GGAAT	TGACG	GEGEC	CGCA	CAAGC	GCGGA	GCAT	STGG	ттаа
SN821	791	CGCAAG	GCTAAAAC	TCAAA	GGAAT	TGACG	GEGEC	CGCA	CAAGC	GCGGA	GCAT	GTGG	ттаа
Streptomyces lateritius LMG 19	844	CGCAAG	GCTAAAAC	TCAAA	GGAAT	TGACG	GGGGC(CGCA	CAAGC	GCGGA	GCAT	GTGG	TTAA
Streptomyces zaomyceticus NRRL	850	CGCAAG	GCTAAAAA	TCAAA	GGAAT	TGACG	GGGGCC	CGCA	CAAGO	GCGGA	GCAT	STGG	ттаа
SN820	814	CGCAAG	GCTAAAAA	TCAAA	GGAAT	TGACG	GGGGCC	CGCA	CAAGC	GCGGA	GCAT	JTGG	ттаа
Streptomyces bikiniensis DSM40	864	CGCAAG	GCTAAAAC	TCAAA	GGAAT	TGACG	GGGGCC	CGCA	CAAGC	GCGGA	GCAT	STGG	TTAA
SN807	765	CRCAAR	GCTAAAAC	тсаал	GGAAT	TRACG	66660	CGCA	CAAGC	ARCEGA	GCAT	TGG	TTAA

SN1218	816	CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGGCCCGCACAAGC <mark>g</mark> GCGGAGCATGTGGCTTAA
SN1222	815	CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGC <mark>A</mark> GCGGAGCATGTGGCTTAA
Streptomyces	820	CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGC <mark>A</mark> GCGGAGCATGTGGCTTAA
SN1203	815	CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGC <mark>A</mark> GCGGAGCATGTGGCTTAA
Streptomyces narbonensis NRRL	872	CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGC <mark>A</mark> GCGGAGCATGTGGCTTAA
Streptomyces variabilis NRRL B	861	CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGC <mark>G</mark> GCGGAGCATGTGGCTTAA
Streptomyces Labedae NBRC 1586	832	CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGC <mark>G</mark> GCGGAGCATGTGGCTTAA
Streptomyces collinus NBRC 127	835	CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGC <mark>G</mark> GCGGAGCATGTGGCTTAA
SN1125	820	CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGC <mark>G</mark> GCGGAGCATGTGGCTTAA
Streptomyces CTDF1 GQ169067	815	CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGGCCCGCACAAGC <mark>G</mark> GCGGAGCATGTGGCTTAA
Streptomyces sclerotialus DSM	843	CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGC <mark>G</mark> GCGGAGCATGTGGCTTAA
SN1213	816	CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGC <mark>A</mark> GCGGAGCATGTGGCTTAA
Streptomyces 13638J EU741132	854	CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGC <mark>A</mark> GCGGAGCATGTGGCTTAA
SN1219	815	CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGC <mark>A</mark> GCGGAGCATGTGGCTTAA
Streptomyces griseoplanus AS 4	826	C G C A A G G C TA A A A C T C A A A G G A A T T G A C G G G G G C C C G C A A G C <mark>A</mark> G C G G A G C A T G T G G C T T A A
Streptomyces 195019 GU263883	823	CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGC <mark>A</mark> GCGGAGCATGTGGCTTAA
Streptomyces badius NRRL B 256	855	CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGC <mark>A</mark> GCGGAGCATGTGGCTTAA
SN1201	815	C G CAAGG C TAAAA C T CAAAGGAATT GA C G G G G G C C G C A CAAG C <mark>A</mark> G C G G AG C AT G T G G C T T AA
SN1221	823	CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGC <mark>A</mark> GCGGAGCATGTGGCTTAA
Streptomyces 0 3 FJ959370	832	C G C A A G G C T A A A A G G A A T T G A C G G G G G C C C G C A A G C <mark>A</mark> G C G G A G C A T G T G G C T T A A
Streptomyces A23 Ydz XM EU368	829	CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGC <mark>A</mark> GCGGAGCATGTGGCTTAA
SN1208	816	CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGC <mark>A</mark> GCGGAGCATGTGGCTTAA
SN1209	777	
Streptomyces nitrosporeus NRRL	845	CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGC <mark>A</mark> GCGGAGCATGTGGCTTAA
SN1110	823	C G CAAGG C TAAAA C T CAAAGGAAT T GA C G G G G G C C C G C A AG C <mark>A</mark> G C G G AG C AT G T G G C T T AA
Streptomyces coralus cfcc3136	841	CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGC <mark>A</mark> GCGGAGCATGTGGCTTAA
Streptomyces CA131	821	C G C A A G G C TA A A A C T C A A A G G A A T T G A C G G G G G C C C G C A A G C <mark>A</mark> G C G G A G C A T G T G G C T T A A
SN1114	825	C G CAAGG C TAAAA C T CAAAGGAA T T GA C G G G G G C C G C A C A G C <mark>G</mark> G C G G A G C A T G T G G C T T A S
Streptomyces RSF18 EU294139	839	CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGG <mark>G</mark> GCGGGAGCATGTGGCTTAA
SN1226	822	C G CAAGG C TAAAA C T CAAAGGAA T T GA C G G G G G C C G C A CAAG C <mark>G</mark> G C G G AG C A T G T G G C T T AA
Streptomyces DA08605	839	CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGC <mark>G</mark> GCGGAGCATGTGGCTTAA
N12 28	816	C G CAAGG C TAAAA C T CAAAGGAAT T GA C G G G G G C C C G C A AG C <mark>G</mark> G C G G A G C AT G T G G C T T AA
Streptomyces aculeolatus strai	838	CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGC <mark>G</mark> GCGGAGCATGTGGCTTAA
SN1202	817	C G CAAGG C TAAAA C T CAAAGGAATT GA C G G G G G C C G C A C A G G <mark>G</mark> G C G G A G C A T G T G G C T T A S
SN1230	817	CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGC <mark>G</mark> GCGGAGCATGTGGCTTAA
Actinomadura nitritigenes T	825	CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCC <mark>CG</mark> ACAAGC <mark>G</mark> GCGGAGCATGT <mark>T</mark> GCTTAA
Actinomadura bangladeshensis T	846	CGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGC <mark>G</mark> GCGGAGCATGT <mark>T</mark> GCTTAA

		970	380	990	2000	2020	1020
SN701	878	MARGANINAGEMARE					
Streptomyces gardneri NBRC 128	924	AACCTTACCAAGGCTT					
Streptomyces omiyaensis NRRL B	925	AACCTTACCAAGGCTT					
SN810	871	AACCTTACCAAGGTTT					
SN821	871	AACCTTACCAAGGCTT					
Streptomyces lateritius LMG 19	924	AACCTTACCAAGGCTT	GACATA	ACCEGAAA CCAT	TAGAGA TAG	GCCCCCTT	STEGTCEGT <mark>a</mark>
Streptomyces zaomyceticus NRRL	930	AACCTTACCAAGGCTT	GACATAT	ACCGGAAA <mark>GCAT</mark>	TAGAGATAG	GCCCCCTT	GTGGTCGGT <mark>A</mark>
SN820	894	AACCTTACCAAGGCTT	GACATA	ACCEGAAA CCAT	CAGAGATCC	GCCCCCTT	GTGGTCGGT <mark>A</mark>
Streptomyces bikiniensis DSM40	944	AACCTTACCAAGGCTT	GACATA	ACCEGAAA CCAT	-CAGAGATCC	GCCCCCTT	GTGGTCGGT <mark>a</mark>
SN807	845	AACCTTACCAAGGCTT	GACATA	ACCEGAAA GCAT	TAGAGA TAG	GCCCCCTT	FTGGTCGGT
Streptomyces gulbargensis T	924	AACCTTACCAAGGCTT	GACATAT	ACCEGAAA GCAT	TAGAGA TAG	GCCCCCTT	GT G G T C G G T A
Streptomyces chartreusis NBRC	923	AACCTTACCAAGGCTT				GCCCCCTT	GTGGTCGGT <mark>G</mark>
SN709	881	AACCTTACAAGGCTT	GACATA	ACCEGANAACCC	TGC		

SN12U3	895	AACCITTACCAACHCITTBACATATACCEBBAAAGCAT TABABATABTBCCCCCCCTTETEBTCB
Streptomyces narbonensis NRRL	952	AACCTTACCAAGGCTTGACATA <mark>T</mark> ACCGGAAA <mark>GCAT - CA</mark> GAGA <mark>TG</mark> CCCCCCTTGTGGTCGG
Streptomyces variabilis NRRL B	941	AACCTTACCAAGGCTTGACATA <mark>C</mark> ACCGGAAA <mark>GCAT-CA</mark> GAGA <mark>TG</mark> G <mark>T</mark> GCCCCCCTTGTGGTCGG
Streptomyces labedae NBRC 1586	912	AACCTTACCAAGGCTTGACATACACCGGAAA <mark>GCAT-CA</mark> GAGA <mark>TG</mark> GTGCCCCCCTTGTGGTCGG AACCTTACCAAGGCTTGACATACACCGGAAA <mark>GCAT-TA</mark> GAGA <mark>TA</mark> G <mark>TGC</mark> CCCCCTTGTGGTCGG
Streptomyces collinus NBRC 127	915	AACCTTACCAAGGCTTGACATA <mark>C</mark> ACCGGAAA <mark>GCAT-TA</mark> GAGA <mark>TA</mark> G <mark>TGC</mark> CCCCCTTGTGGTCGG
SN1125	900	AACCTTACCAAGGCTTGACATA <mark>C</mark> ACCGGAAA <mark>ACTC-TG</mark> GAGA <mark>CA</mark> GG <mark>GT</mark> CCCCCTTGTGGTCGG
Streptomyces CTDF1 GQ169067	895	AACCTTACCAAGGCTTGACATA <mark>C</mark> ACCGGAAA <mark>CATC-CA</mark> GAGA <mark>TGG</mark> GTGCCCCCTTGTGGTCGG
Streptomyces sclerotialus DSM	923	AACCTTACCAAGGCTTGACATA <mark>C</mark> ACCGGAAA <mark>CGTC-TG</mark> GAGA <mark>CA</mark> G <mark>GCG</mark> CCCCCTTGTGGTCGG
SN1213	896	AACCTTACCAAGGCTTGACATA <mark>T</mark> ACCGGAAA <mark>GCAT-CA</mark> GAGA <mark>TGG</mark> TGCCCCCCTTGTGGTCGG
Streptomyces 13638J EU741132	934	AACCTTACCAAGGCTTGACATA <mark>T</mark> ACCGGAAA <mark>GCAT-CA</mark> GAGA <mark>TGGT</mark> G <mark>C</mark> CCCCCTTGTGGTCGU
SN1219	895	AACCTTACCAAGGCTTGACATA <mark>T</mark> ACCGGAAA <mark>GCAT-CA</mark> GAGA <mark>TGG</mark> CCCCCTTGTGGTCGG
Streptomyces griseoplanus AS 4	906	AACCTTACCAAGGCTTGACATA <mark>T</mark> ACCGGAAA <mark>GCAT-CA</mark> GAGA <mark>TGGT</mark> G <mark>C</mark> CCCCCTTGTGGTCGG
Streptomyces 195019 GU263883	903	AACCTTACCAAGGCTTGACATA <mark>T</mark> ACCGGAAA <mark>GCAT-CA</mark> GAGA <mark>TGG</mark> CCCCCCTTGTGGTCGG
Streptomyces badius NRRL B 256	935	AACCTTACCAAGGCTTGACATA <mark>T</mark> ACCGGAAA <mark>GCAT-CA</mark> GAGA <mark>TGG</mark> CCCCCCTTGTGGTCGG
SN1201	895	AACCTTACCAAGGCTTGACATA <mark>T</mark> ACCGGAAA <mark>GCAT - CA</mark> GAGA <mark>TG</mark> G <mark>TGC</mark> CCCCCTTGTGGTCGG
SN1221	903	AACCTTACCAAGGCTTGACATA <mark>T</mark> ACCGGAAA <mark>GCAT - CA</mark> GAGA <mark>TGG</mark> TGCCCCCCTTGTGGTCGG
Streptomyces 0 3 FJ959370	912	AACCTTACCAAGGCTTGACATA <mark>T</mark> ACCGGAAA <mark>GCAT-CA</mark> GAGA <mark>TG</mark> G <mark>T</mark> GCCCCCCTTGTGGTCG
Streptomyces A23 Ydz XM EU368	909	AACCTTACCAAGGCTTGACATA <mark>T</mark> ACCGGAAA <mark>GCAT – CA</mark> GAGA <mark>TGG</mark> TGCCCCCCTTGTGGTCGI
5N1208	896	AACCTTACCAAGGCTTGACATA <mark>T</mark> ACCGGAAA <mark>GCAT - CA</mark> GAGA <mark>TGG</mark> TGCCCCCTTGTGGTCGC
SN1209	777	
Streptomyces nitrosporeus NRRL	925	AACCTTACCAAGGCTTGACATA <mark>T</mark> ACCGGAAA <mark>GCGC-CA</mark> GAGA <mark>TGGTGC</mark> CCCCCTTGTGGTCGI
SN1110	903	AACCTTACCAAGGCTTGACATA <mark>C</mark> ACCGGAAA <mark>CGGC-CA</mark> BAGA <mark>TGG</mark> TCGCCCCCTTGTGGTCG
Streptomyces coralus cfcc3136	921	AACCTTACCAAGGCTTGACATA <mark>C</mark> ACCGGAAA <mark>CGGC-CA</mark> GAGA <mark>TGGTCG</mark> CCCCCTTGTGGTCG
Streptomyces CA131	901	AACCTTACCAAGGCTTGACATA <mark>C</mark> ACCGGAAA <mark>CGGC-CA</mark> GAGA <mark>TGC</mark> TCGCCCCCTTGTGGTCGI
SN1114	905	AACCTTACCAAGGCTTGACATA <mark>C</mark> ACCGGAAA <mark>GCAT-CA</mark> GAGA <mark>TG</mark> G <mark>TGC</mark> CCCCCTTGTGGTCGG
Streptomyces RSF18 EU294139	919	AACCTTACCAAGGCTTGACATA <mark>C</mark> ACCGGAAA <mark>GCAT-CA</mark> GAGA <mark>TGGTGC</mark> CCCCCTTGTGGTCGG
SN1226	902	AACCTTACCAAGGCTTGACATA <mark>C</mark> ACCGGAAA <mark>CGTC-TG</mark> BAGA <mark>CA</mark> GGCGCCCCCTTGTGGTCGI
Streptomyces DA08605	919	AACCTTACCAAGGCTTGACATA <mark>C</mark> ACCGGGAAA <mark>CGTC-TG</mark> GAGA <mark>CA</mark> G <mark>GCG</mark> CCCCCTTGTGGTCGG
112 28	896	AACCTTACCAAGGCTTGACATA <mark>C</mark> ACCGGAAA <mark>ACCG-TG</mark> GAGA <mark>CACGGT</mark> CCCCCTTGTGGTCGU
Streptomyces aculeolatus strai	918	AACCTTACCAAGGCTTGACATA <mark>C</mark> ACCGGAAA <mark>ACCG-TG</mark> GAGA <mark>CACG</mark> G <mark>T</mark> CCCCCTTGTGGTCGI
5N1202	897	AACCTTACCAAGGCTTGACATA <mark>C</mark> ACCGGAAA <mark>CCCC-TG</mark> GAGA <mark>CA</mark> G <mark>G</mark> GCCCCCTTGTGGTCGI
5N1230	897	AACCTTACCAAGGCTTGACATA <mark>C</mark> ACCGGAAA <mark>CCCC-TG</mark> GAGA <mark>CA</mark> GGGGCCCCCTTGTGGTCGI
Actinomadura nitritigenes T	905	AACCTTACCAAGGCTTGACAT-CGCCGGAAA <mark>ACTCGCA</mark> GAGA <mark>TGCGGGGTCCT</mark> TT <mark>T</mark> TGGGGC
Actinomadura bangladeshensis T Clustal Consensus	926	AACCTTACCAAGGCTTGACAT <mark>-CG</mark> CCGGAAA <mark>TCCCG</mark> CAGAGA <mark>TGCGGGGT</mark> CC <mark>T</mark> TT <mark>T</mark> TGG <mark>GC</mark> C

		1050 1060 1070 1080 1090 1100
SN701	957	
Streptomyces gardneri NBRC 128	1003	GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT <mark>C</mark>
Streptomyces omiyaensis NRRL B	1004	GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT <mark>C</mark>
SN810	950	GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT <mark>C</mark>
SN821	950	GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT <mark>C</mark>
Streptomyces lateritius LMG 19	1003	GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT <mark>C</mark>
Streptomyces zaomyceticus NRRL	1009	GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT <mark>C</mark>
SN820	973	GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT <mark>C</mark>
Streptomyces bikiniensis DSM40	1023	GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT <mark>C</mark>
SN807	924	GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT <mark>C</mark>
Streptomyces gulbargensis T	1003	GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT <mark>C</mark>
Streptomyces chartreusis NBRC	1002	GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT <mark>T</mark>
SN709	919	
Streptomyces tateyamensis AB4	1015	GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT <mark>T</mark>
SN710	953	GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT <mark>T</mark>
SN805	958	GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT <mark>T</mark>

Streptomyces Labedae NBRC 1586	991	GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT <mark>C</mark> C
Streptomyces collinus NBRC 127	994	GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT <mark>C</mark> G
SN1125	979	GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT <mark>T</mark> C
Streptomyces CTDF1 GQ169067	974	GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT <mark>T</mark> C
Streptomyces sclerotialus DSM	1002	GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT <mark>T</mark> C
SN1213	975	GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT <mark>T</mark> C
Streptomyces 13638J EU741132	1013	GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT <mark>T</mark> C
SN1219	974	GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT <mark>T</mark> C
Streptomyces griseoplanus AS 4	985	GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT <mark>T</mark> C
Streptomyces 195019 GU263883	982	GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT <mark>T</mark> C
Streptomyces badius NRRL B 256	1014	GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT <mark>T</mark> C
SN1201	974	GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT <mark>T</mark> C
SN1221	982	GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT <mark>T</mark> C
treptomyces 0 3 FJ959370	991	GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT <mark>T</mark> C
treptomyces A23 Ydz XM EU368	988	GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT <mark>T</mark> C
N1208	975	GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT <mark>T</mark> C
N1209	777	
treptomyces nitrosporeus NRRL	1004	GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT <mark>T</mark> C
SN1110	982	GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT <mark>T</mark> C
treptomyces coralus cfcc3136	1000	GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT <mark>T</mark> C
Streptomyces CA131	980	GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT <mark>T</mark> C
SN1114	984	GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCC <mark>C</mark> TGT <mark>G</mark> C
Streptomyces RSF18 EU294139	998	GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCC <mark>C</mark> TGT <mark>C</mark> C
SN1226	981	GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT <mark>C</mark> G
Streptomyces DA08605	998	GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT <mark>C</mark> C
12 28	975	GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT <mark>C</mark> C
Streptomyces aculeolatus strai	997	GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT <mark>C</mark> C
N1202	976	GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT <mark>C</mark> C
SN1230	976	GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT <mark>C</mark> C
Actinomadura nitritigenes T	984	GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCT <mark>C</mark> GT <mark>T</mark> C
Actinomadura bangladeshensis T	1005	GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCT <mark>C</mark> GT <mark>T</mark> G

			1130	1140		1160			
SN701	959								
Streptomyces gardneri NBRC 128	1083	CTTC	CGGGTGA	FGGGGACTCA	CAGGAGAC	GCCGGGGTC	AACTCGGAGG	AAGGTGGGG	ACGA
Streptomyces omiyaensis NRRL B	1084	CTTC	GGGTGA	IGGGGACTCA	GAGAGAC	GCCGGGGTC	AACTCGGAGG	AAGGTGGGG	ACGA
SN810	1030	CTTC	GGGTGA	IGGGGACTC					
SN821	1030	CTTC	GGGTGA	FEGEGACTCA	GAGAGAC	GCCGGGGTC	AACTCGGAGG	AAGGTGGGG	
Streptomyces lateritius LMG 19	1083	CTTC	GGGGTGA	FGGGGGACTCA	C <mark>A</mark> GGAGAC	GCCGGGGTC	AACTCGGAGG	AAGGTGGGG	ACGA
Streptomyces zaomyceticus NRRL	1089	CTTC	GGGTGA	IGGGGACTCA	CAGGAGAC	GCCGGGGTC	AACTCGGAGG	AAGGTGGGG	ACGA
SN820	1053	CTTC	GGGTGA	IGGGGACTCA	GAGAGAC	GCCGGGGTC	AACTCGGAGG	AAGGTGGGG	ACGA
Streptomyces bikiniensis DSM40	1102	CTTC	GGGTGA	IGGGGACTCA	C <mark>A</mark> GGAGAC (GCCGGGGTC	AACTCGGAGG	AAGGTGGGG	ACGA
SN807	1004	CTTC	GGGGTGA	FGGGGGACTCA	GAGAGAC	GCCGGGGTC	AACTCGGAGG	AAGGTGGGG	ACGA
Streptomyces gulbargensis T	1083	CTTC	GGGGTGA	FGGGGGACTCA	C <mark>A</mark> GGAGAC	GCCGGGGTC	AACTCGGAGG	AAGGTGGGG	ACGA
Streptomyces chartreusis NBRC	1082	CTTC	GGGGTGA	IGGGGACTCA	CAGGAGAC	GCCGGGGTC	AACTCGGAGG	AAGGTGGGG	ACGA
SN709	919								
Streptomyces tateyamensis AB4	1095	TTC	GGGTGA	GGGGGACTCA	GAGAGAC	GCCGGGGTC	AACTCGGAGG	AAGGTGGGG	ACGA
SN710	1033	CTTC	CGCCCCC	FGGGGGACTCA	GAGAGAC	GCCGGGGGTC	AACTCGGAGG	AAGGTGGGG	ACGA
SN805	1038	CTTC	GGGGTGA	FGGGGGACTCA	C <mark>A</mark> GGAGAC <mark>1</mark>	GCCGGGGTC	AACTCGGAGG	AAGGTGGGG	ACGA
Streptomyces sioyaensis NRRL	1090	CTTC	GGGGTGA	IGGGGACTCA	CAGGAGAC	GCCGGGGTC	AACTCGGAGG	AAGGTGGGG	ACGA
SN702	1029	CTT	-G <mark>T</mark> GGTG <mark>C</mark>	IGGGGACTCA	CGGGAGAC C	GCCGGGGTC	AACTCGGAGG	AAGGTGGGG	ACGA
Streptomyces parvulus NBRC 131	1083	стт	-CTECTCC	IGGGGACTCA	GEBAGAC	GCCGGGGTC	AACTCGGAG	AAGGTGGGG	ACGA

Streptomyces CTDF1 GQ169067	1054	C <mark>C</mark> TC	C——G <mark>e</mark> ggtg <mark>a</mark> tggggactcac <mark>a</mark> ggagac <mark>t</mark> gccggggtcaactcggaggaaggtggggacga
Streptomyces sclerotialus DSM	1082	СТТС	C——G <mark>e</mark> ggtg <mark>a</mark> tggggactcac <mark>a</mark> ggagac <mark>t</mark> gccggggtcaactcggaggaaggtggggacga
SN1213	1055	СТТС	
Streptomyces 13638J EU741132	1093	сттс	
5N1219	1054	СТТС	
Streptomyces griseoplanus AS 4	1065	СТТС	C——G <mark>e</mark> ggtg <mark>a</mark> tggggactcac <mark>a</mark> ggagac <mark>t</mark> gccggggtcaactcggaggaaggtggggacga
Streptomyces 195019 GU263883	1062	сттс	
Streptomyces badius NRRL B 256	1094	CTTC	C——G <mark>e</mark> ggtg <mark>a</mark> tggggactcac <mark>a</mark> ggagac <mark>t</mark> gccggggtcaactcggaggaaggtggggacga
5N1201	1054	сттс	
SN1221	1062	CTTC	
Streptomyces 0 3 FJ959370	1071	сттс	
Streptomyces A23 Ydz XM EU368	1068	СТТС	C——
SN1208	1055	СТТС	C——G <mark>e</mark> ggtg <mark>a</mark> tggggactcac <mark>a</mark> ggagac <mark>t</mark> gccggggtcaactcggaggaaggtggggacga
5N1209	777		
Streptomyces nitrosporeus NRRL	1084	CTTC	C——G <mark>e</mark> ggtg <mark>a</mark> tggggactcac <mark>a</mark> ggagac <mark>t</mark> gccggggtcaactcggaggaaggtggggacga
5N1110	1062	сттс	
Streptomyces coralus cfcc3136	1080	СТТС	
Streptomyces CA131	1060	СТТС	C——G <mark>e</mark> ggtg <mark>a</mark> tggggactcac <mark>a</mark> ggagac <mark>c</mark> gccggggtcaactcggaggaaggtggggacga
SN1114	1063		<mark>a</mark> te <mark>cc</mark> eeggactcac <mark>a</mark> ggagac <mark>c</mark> gccggggtcaactcggagggaggtggggacga
Streptomyces RSF18 EU294139	1077		<mark>A</mark> TG <mark>CC</mark> GGGGACTCAC <mark>A</mark> GGAGAC <mark>C</mark> GCCGGGGTCAACTCGGAGGAAGGTGGGGACGA
5N1226	1061	СТТ	<mark>6</mark> TGGTG <mark>C</mark> TGGGGACTCAC <mark>G</mark> GGAGAC <mark>C</mark> GCCGGGGTCAACTCGGAGGAAGGTGGGGACGA
Streptomyces DA08605	1078	CTT-	<mark>GT</mark> GGTG <mark>C</mark> TGGGGACTCAC <mark>G</mark> GGAGAC <mark>C</mark> GCCGGGGTCAACTCGGAGGAAGGTGGGGACGA
N12 28	1055		<mark>T</mark> CGG <mark>G</mark> GGTG <mark>G</mark> TGGGGACTCAC <mark>G</mark> GGAGAC <mark>T</mark> GCCGGGGTCAACTCGGAGGAAGGTGGGGACGA
Streptomyces aculeolatus strai	1077	C <mark>C</mark> T T	<mark>T C G G G G G G G G G G G C T C A C G</mark> G G A G A C <mark>T</mark> G C C G G G G T C A C T C G G A G G T G G G G A C G A
5N1202	1056	TTTC	
5N1230	1056	TTTC	
Actinomadura nitritigenes T	1062		<mark>AA</mark> TE <mark>G</mark> TGGGGACTCA <mark>T</mark> GGGAGAC <mark>C</mark> GCCGGGGTCAACTCGGAGGAAGGTGGGGA <mark>T</mark> GA
Actinomadura bangladeshensis T	1084		<mark>e</mark> g <mark>e</mark> tggggactca <mark>te</mark> ggagac <mark>c</mark> gccggggtcaactcggaggaaggtgggga <mark>t</mark> ga

		1210	1220	1230	1240	1250	1260
5N701	959			• • • • • • • •			
Streptomyces gardneri NBRC 128	1161	CCCTTATGTCTTG	GCTGCACACG	TGCTACAATGG	CCGGTACAA	GAGCTGCGAT	GCCCCGAG
Streptomyces omiyaensis NRRL B	1162	CCCTTATGTCTTG	GCTGCACACG	IGCTACAATGO	CCGGTACAA	GAGCTGCGAT	GCCG <mark>C</mark> GAG
5N810	1049						
5N821	1087						
Streptomyces lateritius LMG 19	1161	CCCTTATGTCTTG	GCTGCACACG	TGCTACAATGG	CCGGTACAA	GAGCTGCGAT	GCCGTGAG
treptomyces zaomyceticus NRRL	1167	CCCTTATGTCTTG	GCTGCACACG	TGCTACAATGG	CCGGTACAA	GAGCTGCGAT	GCCG <mark>C</mark> GAG
5N820	1131	CCCTTATGTCTTG	GCTGCACACG	TGCTACAATGG	CCGGTACAA	GAGCTGCGAT	GCCG <mark>C</mark> GAG
Streptomyces bikiniensis DSM40	1180	CCCTTATGTCTTG	GCTGCACACG	TGCTACAATGG	CCGGTACAA	GAGCTGCGAT	GCCG <mark>C</mark> GAG
N807	1082	CCCTTATGTCTTG	GCTGCACACG	TGCTACAATGG	CCGGTACAA	GAGCTGCGAT	GCCG <mark>T</mark> GAG
Streptomyces gulbargensis T	1161	CCCTTATGTCTTG	GCTGCACACG	TGCTACAATGG	CCGGTACAA	GAGCTGCGAT	GCCG <mark>T</mark> GAG
Streptomyces chartreusis NBRC	1160	CCCTTATGTCTTG	GCTGCACACG	TGCTACAATGG	C <mark>A</mark> GGTACAA <mark>T</mark>	GAGCTGCGAT	ACC6 <mark>T</mark> GAG
N709	919						
treptomyces tateyamensis AB4	1173	CCCTTATGTCTTG	GCTGCACACG	TGCTACAATGG	CCGGTACAA	GAGCTGCGAT	
N710	1111	CCCTTATGTCTTG	GCTGCACACG	TGCTACAATGG	CCGGTACAA	GAGCTGCGAT	GCCG <mark>T</mark> GAG
N805	1116	CCCTTATGTCTTG	GCTGCACACG	TGCTACAATGG	CCGGTACAA	GAGCTGCGAT	ACC6 <mark>C</mark> 6A6
treptomyces sioyaensis NRRL	1168	CCCTTATGTCTTG	GCTGCACACG	TGCTACAATGG	CCGGTACAA	GAGCTGCGAT	ACCG <mark>C</mark> GAG
N702	1106	CCCTTATGTCTTG	GCTGCACACG	TGCTACAATGG	CCGGTACAA	GAGCTGCGAT	ACCG <mark>C</mark> GAG
treptomyces parvulus NBRC 131	1160	CCCTTATGTCTTG	GCTGCACACG	TGCTACAATGG	CCGGTACAA	GAGCTGCGAT	
treptomyces tendae T D6387	1190	CCCTTATGTCTTG	GCTGCACACG	TGCTACAATGG	CCGGTACAA	GAGCTGCGAT	
N1101	1128	CCCTTATGTCTTG	GCTGCACACG	TGCTACAATGG	CCGGTACAA	GAGCTGCGAT	
treptomyces malachitospinus N	1161	CCCTTATGTCTTG	GCTGCACACG	TGCTACAATGG	CCGGTACAA	GAGCTGCGAT	
SN1104	1135	CCCTTATGTCTTG	GCTGCACACG	TGCTACAATGG	CCGGTACAA	GAGCTGCGAT	
N1108	1141	CCCTTATGTCTTG	GCTGCACACG	TGCTACAATGG	CCGGTACAA	GAGCTGCGAT	
SN1123	1122	CCCTTATGTCTTG	GCTGCACACG	TGCTACAATGG	CCGGTACAA	GAGCTGCGAT	
Streptomyces paraguayensis	1157	CCCTTATGTCTTG	GCTGCACACG	TGCTACAATGG	CCGGTACAA	GAGCTGCGAT	
N1212	1131	CCCTTATGTCTTG				GAGCTGCGAT	
treptomyces rochei NBRC 12908	1160	CCCTTATGTCTTG				GAGCTGCGAT	
treptomyces caelestis T X8	1181	CCCTTATGTCTTG				GAGCTGCGAT	
N1210	649	CCCTTATGTCTTG				GAGCTGCGAT	
112 16	1132	CCCTTATGTCTTG				GAGCTGCGAT	
N1218	1132	CCCTTATGTCTTG				GAGCTGCGAT	
SN1222	1132	CCCTTATGTCTTG				GAGCTGCGAT	
Streptomyces	1137	CCCTTATGTCTTG				GAGCTGCGAT	
N1203	1132	CCCTTATGTCTTG				GAGCTGCGAT	
Streptomyces narbonensis NRRL	1189	CCCTTATGTCTTG				GAGCTGCGAT	
treptomyces variabilis NRRL B	1177	CCCTTATGTCTTG				GAGCTGCGAT	
treptomyces labedae NBRC 1586	1148	CCCTTATGTCTTG				GAGCTGCGAT	
Streptomyces collinus NBRC 127	1151	CCCTTATGTCTTG				GAGCTGCGAT	
SN1125	1137	CCCTTATGTCTTG				GAG <mark>T</mark> TGCGAT	
treptomyces CTDF1 GQ169067	1132	CCCTTATGTCTTG				GAG <mark>T</mark> TGCGAT	
Streptomyces sclerotialus DSM	1160	CCCTTATGTCTTG	GCTGCACACG	TGCTACAATGG	CCGGTACAA	GAGCTGCGAT	ACCG <mark>C</mark> GAG

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 13638J EU741132	1171	CCCTTATGTCTTGGGCTGCACACGTGCTACAATGGCCGGTACAA <mark>T</mark> GAGCTGCGAT <mark>g</mark> CCG <mark>C</mark> GAGG <mark>C</mark>
SN1219	1132	CCCTTATGTCTTGGGCTGCACACGTGCTACAATGGCCGGTACAA <mark>T</mark> GAGCTGCGAT <mark>G</mark> CCG <mark>C</mark> GAGG <mark>C</mark>
Streptomyces griseoplanus AS 4		CCCTTATGTCTTGGGCTGCACACGTGCTACAATGGCCGGTACAA <mark>T</mark> GAGCTGCGAT <mark>G</mark> CCG <mark>C</mark> GAGG <mark>C</mark>
Streptomyces 195019 GU263883	1140	CCCTTATGTCTTGGGCTGCACACGTGCTACAATGGCCGGTACAA <mark>T</mark> GAGCTGCGAT <mark>G</mark> CCG <mark>C</mark> GAGG <mark>C</mark>
Streptomyces badius NRRL B 256	1172	CCCTTATGTCTTGGGCTGCACACGTGCTACAATGGCCGGTACAA <mark>T</mark> GAGCTGCGAT <mark>G</mark> CCG <mark>C</mark> GAGG <mark>C</mark>
SN1201		CCCTTATGTCTTGGGCTGCACACGTGCTACAATGGCCGGTACAA <mark>T</mark> GAGCTGCGAT <mark>G</mark> CCG <mark>C</mark> GAGG <mark>C</mark>
SN1221		CCCTTATGTCTTGGGCTGCACACGTGCTACAATGGCCGGTACAA <mark>T</mark> GAGCTGCGAT <mark>G</mark> CCG <mark>C</mark> GAGG <mark>C</mark>
Streptomyces 0 3 FJ959370		CCCTTATGTCTTGGGCTGCACACGTGCTACAATGGCCGGTACAA <mark>T</mark> GAGCTGCGAT <mark>G</mark> CCG <mark>C</mark> GAGG <mark>C</mark>
Streptomyces A23 Ydz XM EU368		CCCTTATGTCTTGGGCTGCACACGTGCTACAATGGCCGGTACAA <mark>T</mark> GAGCTGCGAT <mark>G</mark> CCG <mark>C</mark> GAGG <mark>C</mark>
SN1208	1133	CCCTTATGTCTTGGGCTGCACACGTGCTACAATGGCCGGTACAA <mark>T</mark> GAGCTGCGAT <mark>G</mark> CCG <mark>C</mark> GAGG <mark>C</mark>
SN1209	777	
Streptomyces nitrosporeus NRRL		CCCTTATGTCTTGGGCTGCACACGTGCTACAATGGCCGGTACAA <mark>T</mark> GAGCTGCGA <mark>AGT</mark> CG <mark>T</mark> GAGG <mark>C</mark>
SN1110		CCCTTATETCTTEEECTECACACETECTACAATEEC <mark>A</mark> EETACAA <mark>T</mark> EAECTECEAT <mark>A</mark> CCE <mark>T</mark> EAECT
Streptomyces coralus cfcc3136	1158	CCCTTATGTCTTGGGCTGCACACGTGCTACAATGGG <mark>A</mark> GGTACAA <mark>T</mark> GAGCTGCGAT <mark>A</mark> CCG <mark>T</mark> GAGG <mark>T</mark>
Streptomyces CA131		CCCTTATETCTTEEECTECACACETECTACAATEEC <mark>A</mark> GETACAA <mark>T</mark> EAECTECEAT <mark>A</mark> CCE <mark>T</mark> EAEE <mark>T</mark>
SN1114		CCCTTATGTCTTGGGCTGCACACGTGCTACAATGGCCGGTACAA <mark>T</mark> GAGCTGCGATACCG <mark>C</mark> GAGG <mark>T</mark>
Streptomyces RSF18 EU294139	1149	CCCTTATGTCTTGGGCTGCACACGTGCTACAATGGCCGGTACAA <mark>T</mark> GAGCTGCGATA <mark>CCGC</mark> GAGG <mark>T</mark>
SN1226		CCCTTATGTCTTGGGCTGCACACGTGCTACAATGGCCGGTACAA <mark>T</mark> GAGCTGCGAT <mark>A</mark> CCG <mark>T</mark> GAGG <mark>T</mark>
Streptomyces DA08605		CCCTTATGTCTTGGGCTGCACACGTGCTACAATGGCCGGTACAA <mark>T</mark> GAGCTGCGAT <mark>A</mark> CCG <mark>T</mark> GAGG <mark>T</mark>
N12 28		CCCTTATGTCTTGGGCTGCACACGTGCTACAATGGCCGGTACAA <mark>T</mark> GAGCTGCGAT <mark>A</mark> CCG <mark>CA</mark> AGG <mark>T</mark>
Streptomyces aculeolatus strai		CCCTTATGTCTTGGGCTGCACACGTGCTACAATGGCCGGTACAA <mark>T</mark> GAGCTGCGATA <mark>CCGCA</mark> AGG <mark>T</mark>
SN1202		CCCTTATETCTTEEECTECACACETECTACAATEECCEEETACAA <mark>T</mark> EAECTECEATA <mark>CCE</mark> CAAEE <mark>T</mark>
SN1230		CCCTTATGTCTTGGGCTGCACACGTGCTACAATGGCCGGTACAA <mark>T</mark> GAGCTGCGATA <mark>CCGCA</mark> AGG <mark>T</mark>
Actinomadura nitritigenes T		CCCTTATGTCTTGGGCTGCAPACATGCTACAATGGCCGGTACAGAGGGCTGCGATACCC <mark>TA</mark> AGG <mark>T</mark>
Actinomadura bangladeshensis T	1155	CCCTTATGTCTTGGGCTGCA <mark>P</mark> AC <mark>A</mark> TGCTACAATGGCCGGTACA <mark>GA</mark> GGCTGCGAT <mark>A</mark> CCE <mark>T</mark> GAGG <mark>T</mark>

Clustal Consensus

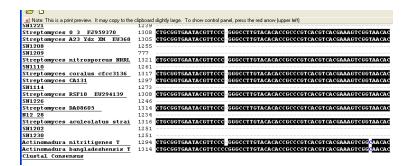
SN1230	1134	CCCTTATGTCTTGGGCTGCACACGT	GCTACAATGGCCGGTACAA <mark>T</mark> GAGCTGCGAT	ACCG <mark>CA</mark> AGG
Actinomadura nitritigenes T	1135	CCCTTATGTCTTGGGCTGCAAACAT	GCTA CAAT GGCCGGTA CA <mark>GA</mark> GGCT GC GAT	CCG <mark>TA</mark> AGG
Actinomadura bangladeshensis T	1155	CCCTTATGTCTTGGGCTGCA <mark>B</mark> AC <mark>A</mark> T	GCTACAATGGCCGGTACA <mark>GA</mark> G <mark>G</mark> GCTGCGAT	CCGTGAGG
Clustal Consensus				
		1290 1300	1310 1320 1330	1340
			•••••••••••••••••••••••••••••••••••••••	
5N701	959 1241	AAGCCGGTCTCAGTTCGGATTGGGG	TCTGCAACTCGACCCCATGAAGTCGGAGT	
Streptomyces gardneri NBRC 128 Streptomyces omiyaensis NRRL B	1241	AAGCCGGTCTCAGTTCGGATTGGGG	TCTGCAACTCGACCCCATGAAGTCGGAGT	
SN810	1049	ARGCCGGICICAGIICGGAIIGGGG	ICIGCARCICGACCCCATGARGICGGAGI	, GCTAGTAA
5821	1049			
Streptomyces lateritius LMG 19	1241	AAGCCGGTCTCAGTTCGGATTGGGG	TCTGCAACTCGACCCCATGAAGTCGGAGT	CCTOCTO
Streptomyces zaomyceticus NRRL	1247	AAGCCGGTCTCAGTTCGGATTGGGG	TCTGCAACTCGACCCCATGAAGTCGGAGT	
N820	1207		renounce concectarion of cook of	
treptomyces bikiniensis DSM40	12.60	AAGCCGGTCTCAGTTCGGATTGGGG	TCTGCAACTCGACCCCATGAAGTCGGAGT	GCTAGTAA
N807	1162	AAGCCGGTCTCAGTTCGGATTGGGG	TCTGCAACTCGACCCCATGAA	
Streptomyces gulbargensis T	1241		TCTGCAACTCGACCCCATGAAGTCGGAGT	GCTAGTAA
Streptomyces chartreusis NBRC	1240		TCTGCAACTCGACCCCATGAAGTCGGAGT	
SN709	919			
Streptomyces tateyamensis AB4	1253	AAGCCGGTCTCAGTTCGGATTGGGG	TCTGCAACTCGACCCCATGAAGTCGGAGT	GCTAGTAA
SN710	1190			
SN805	1196	AAGCCGGTCTCAGTTCGGATTGGGG	TCTGCAACTCGACCCCATGAAGTCGGA	
treptomyces sioyaensis NRRL	1248	AAGCCGGTCTCAGTTCGGATTGGGG	TCTGCAACTCGACCCCATGAAGTCGGAGT	GCTAGTAA
N702	1186	AAGCCGGTCTCAGTTCGGATTGGGG	TCTGCAACTC	
Streptomyces parvulus NBRC 131	1240		TCTGCAACTCGACCCCATGAAGTCGGAGT	GCTAGTAA
Streptomyces tendae T D6387	1270	AAGCCGGTCTCAGTTCGGATTGGGG	TCTGCAACTCGACCCCATGAAGTCGGAGT	GCTAGTAA
SN1101	1208	AAGCCGGTCTCAGTTCGGATTGGGG	TCTGCAACTCGACCCCATGAAGTCGGAG	
Streptomyces malachitospinus N	1241		TCTGCAACTCGACCCCATGAAGTCGGAGT	
N1104	1215		TCTGCAACTCGACCCCATGAAGTCGGAGT	GCTAGTA-
N1108		AAGCCGGTCTCAGTTCGGATTGGGG	TCTGCAACTCGACCCCATGAAGTCGGAGT	
SN1123		AAGCCGGTCTCAGTTCGGATTGGGG	TCTGCAACTCGACCCCATGAAGTC	
Streptomyces paraguayensis	1237		TCTGCAACTCGACCCCATGAAGTCGGAGT	GCTAGTAA
SN1212		AAGCCGGTCTCAGTTCGGATTGGGG	TCTGCAACTCGACCCC	
Streptomyces rochei NBRC 12908		AAGCCGGTCTCAGTTCGGATTGGGG	TCTGCAACTCGACCCCATGAAGTCGGAGT	
treptomyces caelestis T X8	1261		TCTGCAACTCGACCCCATGAAGTCGGAGT	GCTAGTAA
N1210	729	AAG <mark>T</mark> CGGTCTCAGTTCGGATTGGGG	тстве	
12 16		AAGCCGGTCTCAGTTCGGATTGGGG	ТСТБСАА	
N1218		AAGCCGGTCTCAGTTCGGATTGGGG	ТСТБСАА	
N1222	1212		TCTGCAACT	
Streptomyces		AAGCCGGTCTCAGTTCGGATTGGGG	TCTGCAACTCGACCCCATGAAGTCGGAGT	CICCIVA COTVAVA
SN1203	1212 1269		TCTGCAACTCGACC	
Streptomyces narbonensis NRRL Streptomyces variabilis NRRL B	12.69		TCTGCAACTCGACCCCATGAAGTCGGAGT TCTGCAACTCGACCCCATGAAGTCGGAGT	
treptomyces labedae NBRC 1586		AAGCCGGTCTCAGTTCGGATTGGGG	TCTGCAACTCGACCCCATGAAGTCGGAGTC	
treptomyces collinus NBRC 127		AAGCCGGTCTCAGTTCGGATTGGGG	TCTGCAACTCGACCCCATGAAGTCGGAGT	
W1125	1231		TCTGCAACTCGACCCCATGAAGTCGGAGTC	
treptomyces CTDF1 GQ169067		AAGCCGGTCTCAGTTCGGATTGGGG	TCTGCAACTCGACCCCATGAAGTCGGAGT	GCTAGTAR
Streptomyces sclerotialus DSM		AAGCCGGTCTCAGTTCGGATTGGGG	TCTGCAACTCGACCCCATGAAGTCGGAGT	
SN1213	1213		TCTGCAACTCGAC	
Streptomyces 13638J EU741132	1251		TCTGCAACTCGACCCCATGAAGTCGGAGT	GCTAGTAA
SN1219	1212		тст	
Streptomyces griseoplanus AS 4		AAGCCGGTCTCAGTTCGGATTGGGG	TCTGCAACTCGACCCCATGAAGTCGGAGT	GCTAGTAA

. Note: This is a print preview. It may copy to the	clipboard slightly large. To show control panel, press the red arrow (upper left)
SCLEDENWAGES TAJOTA POSOJOOD	1220 AASCCGGTCTCAGTTGG5ATTG555 TCTGCAACTCGACCCCATGAAGTC55AGTTGCTAGTAAT
Streptomyces badius NRRL B 256	1252 AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCATGAAGTCGGAGTTGCTAGTAAT
SN1201	1212 AAGCCGGTCTCAGTTCGGATTGGGG TCT
SN1221	1220 AAGCCGGTCTCAGTTCGGAT
Streptomyces 0 3 FJ959370	1229 AAGCCGGTCTCAGTTCGGATTGGGG-TCTGCAACTCGACCCCATGAAGTCGGAGT <mark>T</mark> GCTAGTAAT
Streptomyces A23 Ydz XM EU368	1226 AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCATGAAGTCGGAGT <mark>T</mark> GCTAGTAAT
SN1208	1213 AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCAT
SN1209	777
Streptomyces nitrosporeus NRRL	1242 AAGCCGGTCTCAGTTCGGATTGGGG <mark>-</mark> TCTGCAACTCGACCCCATGAAGTCGGAGT <mark>T</mark> GCTAGTAAT
SN1110	1220 AAGCC <mark>T</mark> GTCTCAGTTCGGATTGGGG-TCTGCAACTCGACCCCA
Streptomyces coralus cfcc3136	1238 AAGCCTGTCTCAGTTCGGATTGGGG-TCTGCAACTCGACCCCATGAAGTCGGAGTTGCTAGTAAT
Streptomyces CA131	1218 AAGCCTGTCTCAGTTCGGATTGGGG-TCTGCAACTCGACCCCATGAAGTCGGAGTTGCTAGTAAT
SN1114	1215 AAGCCGGTCTCAGTTCGGATTGGGG TCTGCAACTCGACCCCATGAAGTCGGAGTC
Streptomyces RSF18 EU294139	1229 AAGCCGGTCTCAGTTCGGATTGGGG-TCTGCAACTCGACCCCATGAAGTCGGAGT <mark>C</mark> GCTAGTAAT
SN1226	1218 AAGCCGGTCTCAGTTCGGATTGGGG TCTG
Streptomyces DA08605	1235 AAGCCGGTCTCAGTTCGGATTGGGG-TCTGCAACTCGACCCCATGAAGTCGGAGT <mark>C</mark> GCTAGTAAT
N12 28	1215 AAGCCGGTCTCAGTTCGGAT
Streptomyces aculeolatus strai	1237 AAGCCGGTCTCAGTTCGGATTGGGG-TCTGCAACTCGACCCCATGAAGTCGGAGT <mark>C</mark> GCTAGTAAT
SN1202	1214 AAGCCGGTCTCAGTTCGGATTGGGGGTCTGCAACTCGA
SN1230	1214 AAGCCGGTCTCAGTTCGGATTGGGGGGTCTGCAACTCGA
Actinomadura nitritigenes T	1215 AAGCCGGTCTCAGTTCGGATTGGGG [_] TCTGCAACTCGACCCCATGAAGTCGGAGT <mark>C</mark> GCTAGTAAT
Actinomadura bangladeshensis T	1235 AAGCCGGTCTCAGTTCGGAT <mark>C</mark> GAAG-TCTGCAACTCGAC <mark>TT</mark> CGTGAAGTCGGAGT <mark>C</mark> GCTAGTAAT
Clustal Consensus	

SN701 959 1049 SN810 SN821 1087 1320 CT6C66T6AATAC6TTCCC-666CCTT6TACACACC6CCC6TCAC6GTCAC6AAAGTC66TAACA 1326 CT6C66T6AATAC6TTCCC-666CCTT6TACACACC6CCC6TCAC6AC6AC6AC6GTCAC6A Streptomyces lateritius LMG 19 Streptomyces zaomyceticus NRRL SN820 1207 Streptomyces bikiniensis DSM40 SN807 1207 1320 CT6CG6T6AATACGTTCCC-G6GCCTT6TACACACCGCCCGTCACGTCACGAAAGTC6GTAACA 1319 CT6CG6T6AATACGTTCCC-G6GCCTT6TACACACCGCCCGTCACGTCACGAAAGTC6GTAACA Streptomyces gulbargensis T Streptomyces chartreusis NBRC 919 SN709 Streptomyces tateyamensis AB4 SN710 1190 1247 SN805 Streptomyces sioyaensis NRRL 1220 SN702 Streptomyces parvulus NBRC 131 Streptomyces tendae T D6387 1260 SN1101 Streptomyces malachitospinus N SN1104 1276 SN1108 1274 1250 SN1123 Streptomyces paraguayensis 1251 SN1212 1319 CTBCGETGAATACGTTCCC-GGGCCTTETACACACCGCCCGTCACGTCACGAAAGTCGGTAACA 1340 CTBCGETGAATACGTTCCC-GGGCCTTETACACACCGCCCGTCACGTCACGAAAGTCGGTAACA Streptomyces rochei NBRC 12908 Streptomyces caelestis T X8 SN1210 758 N12 16 1243 SN1218 1243 1245 SN1222 Streptomyces 1250 SN1203 1348 CTGCGGTGAATACGTTCCC Streptomyces narbonensis NRRL GGCCTTGTACACCGCCCGTCACGTCACGAAAGTCGGTAACA 1336 CT6CG6TGAATACGTTCCC GGGCCTT6TACACCCCCCCCTCACGTCACGAAAGTCGGTAACA 1307 CT6CG6TGAATACGTTCCC GGGCCTT6TACACCCCCCCCGTCACGTCACGAAAGTCGGTAACAC Streptomyces variabilis NRRL B Streptomyces labedae NBRC 1586 treptomyces collinus NBRC 127 SN1125 1246 Streptomyces CTDF1 GQ169067 Streptomyces sclerotialus DSM SN1213 1250 Streptomyces 13638J EU741132 SN1219 1239
 Shriptomyces griseoplanus AS 4
 1302
 CTGCGGFGAATACGTTCCC
 DGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACA

 Streptomyces 195019
 GU263883
 1299
 CTGCGGFGAATACGTTCCC
 GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACA

 Streptomyces badius NRRL B 256
 1331
 CTGCGGFGAATACGTCCC
 GGGCCTTGTACAACACCGCCCGCGTCACGTCACGAAAGTCGGTAACAA
 SN1201 1239



		1450	1460	1470	1480	1490	1500
SN701	959						
Streptomyces gardneri NBRC 128	1399	CAACCCCTT	GEGAGEGAGC	GTCGAAGGTG	GACTORCOA	TTEEGACEAA	
Streptomyces omiyaensis NRRL B		CAACCCCTTGT		GTCGAAGGTG			
SN810	1049						
SN821	1087						
Streptomyces lateritius LMG 19		CAACCCCTTGT	GEGAGEGAGC	GTCGAAGGTG	GACTERCEA	TTGGGACGAA	TCGTAACA
Streptomyces zaomyceticus NRRL		CAACCCCTTGT	GGGAGGGA				
SN820	1207		000000000000000000000000000000000000000	orconnooro		Trocomconin	
Streptomyces bikiniensis DSM40		CAACCCCTTGT	CCCC CCCC CC	GTCGAAGGTG	CACTOCCCA	TTEECOCCOD	TCGTAACA
SN807	1207						
Streptomyces gulbargensis T		CAACCCCTTGT	RECORDER	GTCGAAGGTG	CACTOCCCA	TTRECACCAA	TCGTABCB
Streptomyces chartreusis NBRC		CAACCCCTTGT	GGGAGGGAGC	GTCGAAGGTG			
SN709	919	on the other of the	or of the second second	onconnoono			
Streptomyces tateyamensis AB4		CAACCCTTGTG	THE CONTRACTOR	CGAAGGTEGE	CTCCC TATT	CCDA CCAA CT	CT
SN710	1190	CAACCC 11010	Consolance o	COMMONTEOD	ACTOOC ATT	OULACOMACI (.01
5805	1247						
				GTCGAAGGTG			
Streptomyces sioyaensis NRRL SN702		CAACCCCTT <mark>GT</mark>	GEGAGEGA	GICGAAGGIG	JEACTEECEA	TIGGGACGAA	этсвтааса
	1220						
Streptomyces parvulus NBRC 131		CAACCCCTTGT		GTCGAAGGTG			
Streptomyces tendae T D6387		CAACCCCTT <mark>GT</mark>	GGGAGGGAGC	GTCGAAGGTG	GACTGGCGA	TTGGGACGAA	TCGTAACA
SN1101	1260						
Streptomyces malachitospinus N		CAACCCCTT <mark>GT</mark>	GGGAGGGAGC	GTCGAAGGTG	GGACTGGCGA	TTGGGACGAA	FTC TAACA
5N1104	1276						
SN1108	1274						
SN1123	1250						
Streptomyces paraguayensis	1395	CAACCCC <mark>C</mark> TGT-G	GGGAGGGA <mark>AT</mark>	GTCGAAGGTG	GGACTGGCGA	TTGGGACGAA	STCGTAACA
SN1212	1251						
Streptomyces rochei NBRC 12908		CAACCCCTTGT	GGGAGGGAGC	GTCGAAGGTG			
Streptomyces caelestis T X8	1419	CAACCCCTTGT	GGGAGGGAGC	GTCGAAGGTG	GGACTGGCGA	TTGGGACGAA	TCGTAACA
SN1210	758						
N12 16	1243						
SN1218	1243						
SN1222	1245						
Streptomyces	1375	CAACCCCTTGTG-G	EAEGEAT				
SN1203	1250						
Streptomyces narbonensis NRRL	1427	CAACCCCTTGT	GEGAGEGAGC	GTCGAAGGTG	GACTGGCGA	TTGGGACGAA	TCGTAACA
Streptomyces variabilis NRRL B	1415	CAACCCCTTGT	GGGAGGGAGC			TTGGGACGAA	
Streptomyces labedae NBRC 1586		CAACCCCTTGT		GTCGAAGGTG			
Streptomyces collinus NBRC 127		CAACCCCTTGT		GTCGAAGGTG			
SN1125	1246						
Streptomyces CTDF1 60169067		TAACCCCCTTTGT	STARGER AND STARGER	GTCGAAGGTG	acec		
Streptomyces sclerotialus DSM		CAACCCCTTGT		GTCGAAGGTG		TTRESCACEAA	тсатааса
SN1213	1250						
Streptomyces 13638J EU741132		CAACCCCTTGT	CCCACCCACC	GTCGAAGGTG	CACTCCCCA	TTOCCACCAA	TCCTDDCD
SN1219	1239	anneeden of	and an and a state of the state	0.100/140/016			
Streptomyces griseoplanus AS 4		CAACCCCTTGT	CECACCEACC				
Streptomyces griseopianus AS 4 Streptomyces 195019 GU263883		CAACCCCTTGT	GGGAGGGAGC	GTCGAAGGTG	CACTOCACT	TTCCCACCA	
		CAACCCCTTGT	GGGAGGGAGC	GTCGAAGGTG			
Streptomyces badius NRRL B 256		Garace Color Might	GGGAGGGAGC	GICGAAGGTG	GAUTGGUGA	THEEGACEAA	THEFTAACA
5N1201	1239						
5N1221	1239						
Streptomyces 0 3 FJ959370	1387	CAACCCCT GT G G G A		CAGAGAAGAAA			

SN1208 SN1209	1255 777		
			GTCGAAGGTGGGACTGGCGATTGGGACGAAGTCGTAACA
Streptomyces nitrosporeus NRRL SN1110	1261	CAACCCCTTGTGGGAGGGAGCT	GTUGAAGGTGGGAUTGGUGATTGGGAUGAAGTUGTAAU
Streptomyces coralus cfcc3136			GTCGAAGGTGGGACTGGCGATTGG ACGAAGTCG AACA
Streptomyces CA131			GTCGAAGGTGGGACTGGCGATTGGGACGAAGTCG <mark>AC</mark> AG
SN1114	1273	CAACCCCC1101-0000A000A0C1	OTCOAGO TOBOACTOOCOATTOOOACOAGO COAGO
Streptomyces RSF18 EU294139		CAACCCTGGGAGGAGCCTCGAAGGG	PARCCCT
SN1226	1246		
Streptomyces DA08605		CAACCCCTTGTGGGAGGGAGCT	TA GANGET GEAT COCCEPTC
N12 28	1234		
Streptomyces aculeolatus strai	1395	CAACCCTTGTGGAGGGAGC	GTCGAAGGTGGGACTGGCGATTGGGACGAAGTCGTAAC.
SN1202	1251		
SN1230	1251		
Actinomadura nitritigenes T		CAACCCTTGTGECGEGAGOC	GTCGAAGGTGGG <mark>C</mark> GGCGATTGGGACGAAGTCGTAAC
Actinomadura bangladeshensis T	1394	CAACCACCTTGT-GTGGGGGGGGGGGGGGGGGGGGGGGGG	GTCGAAGGTGGG <mark>GC</mark> GGCGATTGGGACGAAGTC <mark>-</mark> TAAC
Clustal Consensus			
		1530 1540	
SN701	959		959
Streptomyces gardneri NBRC 128			
Streptomyces omiyaensis NRRL B		AGGTGC	
SN810	1049		
SN821	1087		
Streptomyces lateritius LMG 19	1476	AGG	- 1478
Streptomyces zaomyceticus NRRL		AGGTGC	
SN820			- 1207
Streptomyces bikiniensis DSM40		AGGTGCGGCTGGATCACCTCCTT	
SN807	1207		1207
Streptomyces gulbargensis T	1476		
Streptomyces chartreusis NBRC	1475		
SN709			
Streptomyces tateyamensis AB4			
SN710			
SN805			
Streptomyces sioyaensis NRRL			
SN702			
Streptomyces parvulus NBRC 131		NG	
Streptomyces tendae T D6387		AGGTGCGGCTGGATCACCTCCTT <mark>TC</mark>	
<u>SN1101</u>			
Streptomyces malachitospinus N			
SN1104			
SN1108			
SN1123			
Streptomyces paraguayensis			
SN1212			
Streptomyces rochei NBRC 12908		AGGTGCGGCTGGATCACCTCCTT	
Streptomyces caelestis T X8		AGGTGCGGCTGGATCACCTCCTT	
SN1210			
N12 16			
SN1218			
SN1222			
Streptomvces	1394		- 1394

SN1218		1243
SN1222		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 AGGTGCGGCTGGATCACCTCCTT T	1498
SN1213	1250	1250
Streptomyces 13638J EU741132	1486 AGTGCCCC	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
	1100 00000000	4400

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SN1110	1261 1261
Streptomyces coralus cfcc3136	1473 6 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 AGGTGCGGCTGGA <mark>ATCACCT</mark> CCTAAT 1497
Clustal Consensus	