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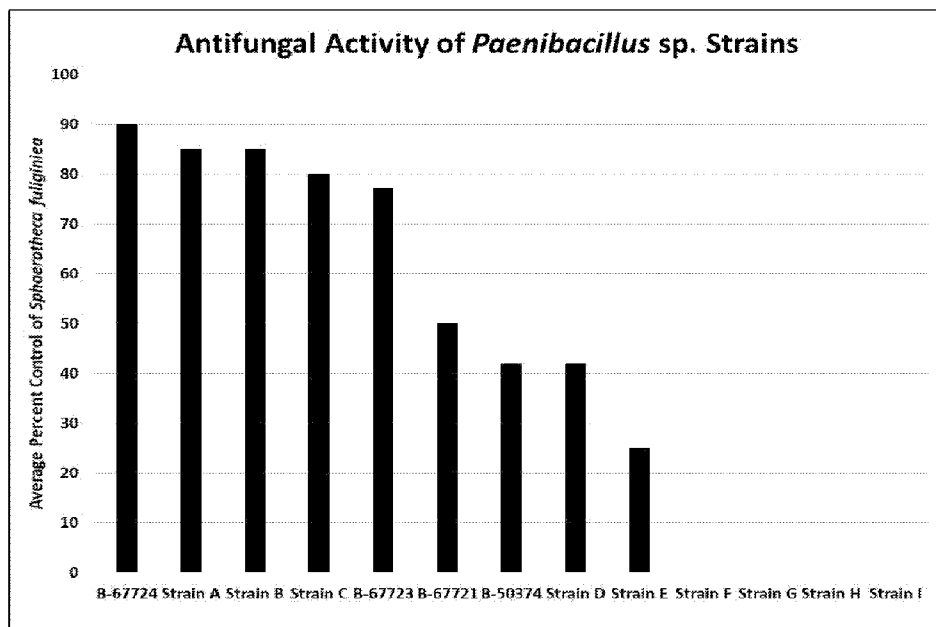
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(54) Title: PAENIBACILLUS STRAINS AND METHODS FOR THEIR USE

FIG. 1



(57) Abstract: The present invention provides a composition comprising a biologically pure culture of a *Paenibacillus* sp. strain or a cell-free preparation thereof comprising a fusaricidin and a tridecaptin; wherein the fusaricidin is produced with a fusaricidin synthetase gene of *fusA* encoded by a DNA sequence exhibiting at least 90.5% sequence identity to SEQ ID NO: 3; and the tridecaptin is produced with a nonribosomal peptide synthetase (NRPS) gene of *triE* encoded by a DNA sequence exhibiting at least 90.0% sequence identity to SEQ ID NO: 7. Also provided are methods of treating an agricultural plant to control a disease and methods of increasing the vigor and/or crop yield of an agricultural plant with the disclosed compositions.



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- *as to the applicant's entitlement to claim the priority of the earlier application (Rule 4.17(iii))*

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- *with sequence listing part of description (Rule 5.2(a))*

PAENIBACILLUS STRAINS AND METHODS FOR THEIR USE

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims priority to U.S. Provisional Patent Application No. 62/815,069, which was filed on March 7, 2019, the entire contents of which are incorporated herein by reference in its entirety.

TECHNICAL FIELD

[0002] The present invention relates to the field of bacterial strains and their ability to control plant diseases and to increase plant vigor and crop yield. In particular, the present invention is directed to *Paenibacillus* sp. strains producing fusaricidins and tridecaptins and their use to maintain plant health and improve plant growth.

REFERENCE TO SEQUENCE LISTING SUBMITTED ELECTRONICALLY

[0003] The official copy of the sequence listing is submitted electronically via EFS-Web as an ASCII-formatted sequence listing with a file named "BCS189006WO_ST25.txt" created on February 25, 2020, and having a size of 185 kilobytes, and is filed concurrently with the specification. The sequence listing contained in this ASCII-formatted document is part of the specification and is herein incorporated by reference in its entirety.

BACKGROUND

[0004] Fungicides have myriad uses, including for crop protection; as food, feed, and cosmetics preservatives; and as therapeutic agents for both human and veterinary applications. Crop yield reduction, foodborne diseases and fungal infections of both humans and animals are a problem in both developed and developing countries.

[0005] Synthetic insecticides or fungicides often are non-specific and therefore can act on organisms other than the target ones, including other naturally occurring beneficial organisms. Because of their chemical nature, they may also be toxic and non-biodegradable. Consumers worldwide are increasingly conscious of the potential environmental and health problems associated with the residuals of chemicals, particularly in food products. This has resulted in growing consumer pressure to reduce the use or at least the quantity of chemical (i.e., synthetic) pesticides. Thus, there is a need to manage food chain requirements while still allowing effective pest control.

[0006] A further problem arising with the use of synthetic insecticides or fungicides is that the repeated and exclusive application of an insecticide or fungicides often leads to selection of resistant pathogenic microorganisms. Normally, such strains are also cross-resistant against other active ingredients having the same mode of action. An effective control of the pathogens with said active compounds is then not possible any longer. However, active ingredients having new mechanisms of action are difficult and expensive to develop.

[0007] The risk of resistance development in pathogen populations as well as environmental and human health concerns have fostered interest in identifying alternatives to synthetic insecticides and fungicides for managing plant diseases. The use of biological control agents is one alternative.

[0008] *Paenibacillus* is a genus of low GC-content, endospore-forming, Gram-positive bacteria (*Firmicutes*). Bacteria belonging to this genus are prolific producers of industrially-relevant extracellular enzymes and antimicrobial substances, including non-ribosomal peptide classes. There is considerable variability between species and strains within the *Paenibacillus* genus with only certain strains showing efficacy in controlling plant pathogens and in promoting plant growth.

[0009] There is a need for *Paenibacillus* sp. strains with enhanced fungicidal activity and the ability to improve plant growth and vigor. Improvements to the efficacy of existing fungicides and the development of alternatives that are not susceptible to development of fungal resistance are highly desirable.

SUMMARY

[0010] The present invention is directed to a composition comprising a biologically pure culture of a *Paenibacillus* sp. strain or a cell-free preparation thereof comprising a fusaricidin and a tridecaptin; wherein the *Paenibacillus* sp. strain comprises a fusaricidin synthetase gene of *fusA* encoded by a DNA sequence exhibiting at least 90.5% sequence identity to SEQ ID NO: 3; and the *Paenibacillus* sp. strain comprises a nonribosomal peptide synthetase (NRPS) gene of *triE* encoded by a DNA sequence exhibiting at least 90.0% sequence identity to SEQ ID NO: 7.

[0011] In certain aspects, the fusaricidin synthetase gene of *fusA* is encoded by a DNA sequence comprising SEQ ID NO: 3 or a degenerate nucleotide sequence thereof encoding the same amino acid sequence. In other aspects, the NRPS gene of *triE* is encoded by a DNA sequence

comprising SEQ ID NO: 7 or a degenerate nucleotide sequence thereof encoding the same amino acid sequence.

[0012] In some embodiments, the composition comprises Fusaricidin A, Fusaricidin B, Fusaricidin C, Fusaricidin D, LiF05a, LiF05b, LiF06a, LiF06b, LiF07a, and/or LiF07b.

[0013] In other embodiments, the composition effectively controls a plant disease caused by a fungus selected from the group consisting of *Botrytis cinerea*, *Sphaerotheca fuliginea*, and *Puccinia triticina*.

[0014] In certain aspects, the *Paenibacillus* sp. strain is *Paenibacillus* sp. strain NRRL B-50374, *Paenibacillus* sp. strain NRRL B-67721, *Paenibacillus* sp. strain NRRL B-67723, *Paenibacillus* sp. strain NRRL B-67724, or a fungicidal mutant strain thereof.

[0015] In other aspects, the composition comprises a fermentation product of *Paenibacillus* sp. strain NRRL B-50374, *Paenibacillus* sp. strain NRRL B-67721, *Paenibacillus* sp. strain NRRL B-67723, *Paenibacillus* sp. strain NRRL B-67724, or a fungicidal mutant strain thereof.

[0016] In one aspect, the fungicidal mutant strain has a genomic sequence with greater than about 90% sequence identity to *Paenibacillus* sp. strain NRRL B-50374, *Paenibacillus* sp. strain NRRL B-67721, *Paenibacillus* sp. strain NRRL B-67723, or *Paenibacillus* sp. strain NRRL B-67724 and/or the fungicidal mutant strain has fungicidal activity and/or levels of a fusaricidin that are comparable to or better than that of *Paenibacillus* sp. strain NRRL B-50374, *Paenibacillus* sp. strain NRRL B-67721, *Paenibacillus* sp. strain NRRL B-67723, or *Paenibacillus* sp. strain NRRL B-67724.

[0017] In some embodiments, the *Paenibacillus* sp. strain further comprises a nitrogen fixation gene cluster; and the nitrogen fixation gene cluster comprises a nitrogen fixation gene of *nifB* encoded by a DNA sequence exhibiting at least 96.9% sequence identity to SEQ ID NO: 10.

[0018] In one embodiment, the nitrogen fixation gene cluster comprises a nitrogen fixation gene of *nifB* encoded by a DNA sequence comprising SEQ ID NO: 10 or a degenerate nucleotide sequence thereof encoding the same amino acid sequence.

[0019] In other embodiments, the expression of the nitrogen fixation gene cluster contributes to enhanced plant growth, plant vigor, and/or crop yield. In yet other embodiments, the *Paenibacillus* sp. strain comprises a fusaricidin synthetase gene of *fusA* encoded by a DNA sequence exhibiting at least 97.3% sequence identity to SEQ ID NO: 1 and the *Paenibacillus* sp.

strain comprises a NRPS gene of *triE* encoded by a DNA sequence exhibiting at least 97.5% sequence identity to SEQ ID NO: 5.

[0020] In one aspect, the fusaricidin synthetase gene of *fusA* is encoded by a DNA sequence comprising SEQ ID NO: 1 or a degenerate nucleotide sequence thereof encoding the same amino acid sequence. In another aspect, the NRPS gene of *triE* is encoded by a DNA sequence comprising SEQ ID NO: 5 or a degenerate nucleotide sequence thereof encoding the same amino acid sequence.

[0021] In certain aspects, the *Paenibacillus* sp. strain is *Paenibacillus* sp. strain NRRL B-50374, *Paenibacillus* sp. strain NRRL B-67721, *Paenibacillus* sp. strain NRRL B-67724, or a fungicidal mutant strain thereof.

[0022] In other aspects, the composition comprises a fermentation product of *Paenibacillus* sp. strain NRRL B-50374, *Paenibacillus* sp. strain NRRL B-67721, *Paenibacillus* sp. strain NRRL B-67724, or a fungicidal mutant strain thereof.

[0023] In some embodiments, the fungicidal mutant strain has a genomic sequence with greater than about 90% sequence identity to *Paenibacillus* sp. strain NRRL B-50374, *Paenibacillus* sp. strain NRRL B-67721, or *Paenibacillus* sp. strain NRRL B-67724 and/or the fungicidal mutant strain has fungicidal activity and/or levels of a fusaricidin that are comparable to or better than that of *Paenibacillus* sp. strain NRRL B-50374, *Paenibacillus* sp. strain NRRL B-67721, or *Paenibacillus* sp. strain NRRL B-67724.

[0024] In certain aspects, the present invention provides a method of treating an agricultural plant to control a disease, wherein the method comprises applying an effective amount of a composition disclosed herein to the plant, to a part of the plant and/or to a locus of the plant.

[0025] In one aspect, the method comprises applying the composition to foliar plant parts. In another aspect, the composition is applied at about 1×10^{10} to about 1×10^{12} colony forming units (CFU) of the *Paenibacillus* sp. strain per hectare or at about 0.5 kg to about 5 kg fermentation solids per hectare. In yet another aspect, the disease is a fungal disease or a bacterial disease.

[0026] In other embodiments, the present invention provides a method for increasing the vigor and/or crop yield of an agricultural plant, wherein the plant, the plant propagule, the seed of the plant and/or a locus where the plant is growing or is intended to grow is treated with an effective amount of a composition disclosed herein.

[0027] In one embodiment, the treatment is carried out as an in-furrow treatment, seed treatment, and/or foliar treatment.

[0028] In another embodiment, the agricultural plant is selected from the group consisting of soybean, corn, wheat, triticale, barley, oat, rye, rape, millet, rice, sunflower, cotton, sugar beet, pome fruit, stone fruit, citrus, banana, strawberry, blueberry, almond, grape, mango, papaya, peanut, potato, tomato, pepper, cucurbit, cucumber, melon, watermelon, garlic, onion, broccoli, carrot, cabbage, bean, dry bean, canola, pea, lentil, alfalfa, trefoil, clover, flax, elephant grass, grass, lettuce, sugarcane, tea, tobacco and coffee; each in its natural or genetically modified form.

[0029] In yet another embodiment, the present invention relates to a seed treated with a composition disclosed herein.

BRIEF DESCRIPTION OF THE DRAWINGS

[0030] **FIG. 1** depicts the control of *Sphaerotheca fuliginea* (PODOXA) achieved with *Paenibacillus* sp. strain NRRL B-50374, *Paenibacillus* sp. strain NRRL B-67721, *Paenibacillus* sp. strain NRRL B-67723, and *Paenibacillus* sp. strain NRRL B-67724 compared to several other *Paenibacillus* sp. strains.

[0031] **FIG. 2** depicts the plant growth promotion in tomato plants resulting from drench treatments with whole broth cultures of *Paenibacillus* sp. strain NRRL B-50374, *Paenibacillus* sp. strain NRRL B-67721, *Paenibacillus* sp. strain NRRL B-67723, or *Paenibacillus* sp. strain NRRL B-67724.

DETAILED DESCRIPTION

[0032] The microorganisms and particular strains described herein, unless specifically noted otherwise, are all separated from nature and grown under artificial conditions such as in shake flask cultures or through scaled-up manufacturing processes, such as in bioreactors to maximize bioactive metabolite production, for example. Growth under such conditions leads to strain “domestication.” Generally, such a “domesticated” strain differs from its counterparts found in nature in that it is cultured as a homogenous population that is not subject to the selection pressures found in the natural environment but rather to artificial selection pressures.

[0033] As used herein, the verb “comprise” as is used in this description and in the claims and its conjugations are used in its non-limiting sense to mean that items following the word

are included, but items not specifically mentioned are not excluded. In addition, reference to an element by the indefinite article “a” or “an” does not exclude the possibility that more than one of the elements are present, unless the context clearly requires that there is one and only one of the elements. The indefinite article “a” or “an” thus usually means “at least one”.

[0034] In certain aspects, the *Paenibacillus* sp. strain of the present invention is selected from any one of the following: *P. terrae*, *P. brasilensis*, *P. polymyxa*, or *P. peoriae*. In one aspect, the *Paenibacillus* sp. strain of the present invention is *P. terrae*. In another aspect, the *Paenibacillus* sp. strain of the present invention is *P. brasilensis*. In another aspect, the *Paenibacillus* sp. strain of the present invention is *P. peoriae*. In another aspect, the *Paenibacillus* sp. strain of the present invention is *P. polymyxa*.

[0035] In one embodiment, a mutant strain of the *Paenibacillus* sp. strain is *Paenibacillus* sp. strain NRRL B-50374, *Paenibacillus* sp. strain NRRL B-67721, *Paenibacillus* sp. strain NRRL B-67723, or *Paenibacillus* sp. strain NRRL B-67724 is provided. The term “mutant” refers to a genetic variant derived from *Paenibacillus* sp. strain NRRL B-50374, *Paenibacillus* sp. strain NRRL B-67721, *Paenibacillus* sp. strain NRRL B-67723, or *Paenibacillus* sp. strain NRRL B-67724. In one embodiment, the mutant has one or more or all the identifying (functional) characteristics of *Paenibacillus* sp. strain NRRL B-50374, *Paenibacillus* sp. strain NRRL B-67721, *Paenibacillus* sp. strain NRRL B-67723, or *Paenibacillus* sp. strain NRRL B-67724. In a particular instance, the mutant or a fermentation product thereof controls (as an identifying functional characteristic) fungi, oomycetes and/or bacteria at least as well as the parent *Paenibacillus* sp. strain NRRL B-50374, *Paenibacillus* sp. strain NRRL B-67721, *Paenibacillus* sp. strain NRRL B-67723, or *Paenibacillus* sp. strain NRRL B-67724. Such mutants may be genetic variants having a genomic sequence that has greater than about 85%, greater than about 90%, greater than about 95%, greater than about 98%, or greater than about 99% sequence identity to *Paenibacillus* sp. strain NRRL B-50374, *Paenibacillus* sp. strain NRRL B-67721, *Paenibacillus* sp. strain NRRL B-67723, or *Paenibacillus* sp. strain NRRL B-67724. Mutants may be obtained by treating cells of *Paenibacillus* sp. strain NRRL B-50374, *Paenibacillus* sp. strain NRRL B-67721, *Paenibacillus* sp. strain NRRL B-67723, or *Paenibacillus* sp. strain NRRL B-67724 with chemicals or irradiation or by selecting spontaneous mutants from a population of *Paenibacillus* sp. strain NRRL B-50374, *Paenibacillus* sp. strain NRRL B-67721, *Paenibacillus* sp. strain NRRL B-67723, or *Paenibacillus* sp. strain NRRL B-67724 cells (such as phage resistant or antibiotic resistant mutants), by genome shuffling, as described below, or by other means well known to those practiced in the art.

[0036] Genome shuffling among *Paenibacillus* strains can be facilitated through the use of a process called protoplast fusion. The process begins with the formation of protoplasts from vegetative bacillary cells. The removal of peptidoglycan cell wall, typically using lysozyme and an osmotic stabilizer, results in the formation of a protoplast. This process is visible under a light microscope with the appearance of spherical cells. Addition of PEG, polyethylene glycol, then induces fusion among protoplasts, allowing genetic contents of two or more cells to come in contact facilitating recombination and genome shuffling. Fused cells then repartition and are recovered on a solid growth medium. During recovery, protoplasts rebuild peptidoglycan cell walls, transitioning back to bacillary shape. See Schaeffer, et. al., (1976) PNAS USA, vol. 73, 6:2151-2155).

[0037] In certain aspects, the present invention is directed to *Paenibacillus* sp. strains producing fusaricidins. The fusaricidins are a family of depsipeptides with a 15-guanidino-3-hydroxypentadecanoic acid (GHPD) tail, as well as their linear counterparts. The specific conserved characteristics of fusaricidins are this GHPD tail, as well as three of the six amino acids in the sequence: (1) Threonine, (4) Threonine, and (6) Alanine.

[0038] Originally discovered but not characterized by Nakajima *et al.* (*J. Antibiot.* **1972**, 25, 243–247) in the mid-70's, fusaricidins were described by Kurusu *et al.* (*J. Antibiot.*, **1987**, 40, 1506–1514) in the late 1980's. They were further studied by Kajimura *et al.* (*J. Antibiot.*, **1996**, 49, 129–135; *J. Antibiot.*, **1997** 50, 220–228), Kuroda *et al.* (*Heterocycles*, **2000**, 53, 1533–1549; *J. Mass Spectrom.*, **2001**, 36, 30–37), and Beatty *et al.* (*Can. J. Microbiol.*, **2002**, 48, 159–169) throughout the mid-1990's to the early 2000's. During this period of heavy investigation these compounds were renamed several times depending on the author (Fusaricidin A is also known as LiF04a, Gatavalin, or even KT-6291A). Though there are many publications on the topic, select compounds from the same group of 24 known fusaricidins is described each time.

[0039] After a somewhat quiet period on the topic, Vater *et al.* (*J. Am. Soc. Mass Spectrom.*, **2015**, 26, 1130-1141) described the structural elucidation of fusaricidins by mass spectrometry and described several analogs of the family. Vater *et al.* identified a new class of fusaricidin-like compounds with seven amino acids (i.e., an extra alanine connected to the (4) threonine residue in the peptide sequence). As used herein, the term “acyclic analog” refers to the compound that corresponds to the fusaricidin or fusaricidin-like compound but lacks the ester bond, resulting in a linear structure.

[0040] The amino acid chains of fusaricidins are linked together and modified by a non-ribosomal peptide synthetase (NRPS). The multi-domain NRPS consists of up to 15,000 amino

acids and is therefore considered among the longest proteins in nature (Schwarzer et al., (2003) Nonribosomal Peptides: From Genes to Products. Nat. Prod. Rep. 20, 275–287). NRPS incorporation is not limited to the 21 standard amino acids translated by the ribosome, and this promiscuity contributes to the great structural diversity and biological activity of non-ribosomal peptides (Li and Jensen, (2008). Nonribosomal biosynthesis of fusaricidins by *Paenibacillus polymyxa* PKB1 involves direct activation of a d-amino acid. Chem. Biol. 15, 118–127).

[0041] In *P. polymyxa* E68, the fusaricidin biosynthetic gene cluster (*fusGFEDCBA*) has been characterized, and the NRPS coding sequence, the largest coding DNA sequence (CDS) in the cluster, was observed to encode a six-module peptide (Choi et al., Identification and Functional Analysis of the Fusaricidin Biosynthetic Gene of *Paenibacillus polymyxa* E681. Biochem. Biophys. Res. Commun. 365, 89–95; Li and Jensen, Identification and Functional Analysis of the Fusaricidin Biosynthetic Gene of *Paenibacillus polymyxa* E681. Biochem. Biophys. Res. Commun. 365, 89–95; Li et al., (2013). Promoter Analysis and Transcription Regulation of fus Gene Cluster Responsible for Fusaricidin Synthesis of *Paenibacillus polymyxa* SQR-21. Appl. Microbiol. Biotechnol. 97, 9479–9489). The biosynthetic cluster includes other CDS responsible for biosynthesis of the lipid moiety but does not contain transporter genes (Li and Jensen, (2008). Nonribosomal biosynthesis of fusaricidins by *Paenibacillus polymyxa* PKB1 involves direct activation of a d-amino acid. Chem. Biol. 15, 118–127). In *P. polymyxa*, a promoter for the *fus* operon was identified and shown to be bound by a transcriptional repressor (AbrB) which previous studies implicated as a regulator of sporulation; this is of interest since fusaricidin was observed to be synthesized during sporulation, thus coordinating the microbe's secondary metabolism with its life cycle (Li et al., (2013). Promoter Analysis and Transcription Regulation of fus Gene Cluster Responsible for Fusaricidin Synthesis of *Paenibacillus polymyxa* SQR-21. Appl. Microbiol. Biotechnol. 97, 9479–9489).

[0042] In other aspects, the present invention is directed to *Paenibacillus* sp. strains producing tridecaptins. The tridecaptins are a group of linear cationic lipopeptides analogous to the polymyxins. The acyl tridecapeptides were first isolated in 1978 and display antimicrobial activity against Gram-positive and Gram-negative bacteria. Shoji, Junichi *et al.*, Journal of Antibiotics (1978), 31 (7), 646-51. More recently, tridecaptin A₁ has been characterized in a strain of *Paenibacillus terrae*. Lohans, Christopher T. *et al.*, ChemBioChem (2014), 15 (2), 243-249.

[0043] Allelic diversity is typically thought to be responsible for producing chemical diversity. However, an interesting feature of the *fus* cluster is that a diversity of fusaricidins, differing in their incorporated amino acids (Tyr, Val, Ile, allo-Ile, Phe), can be produced by a single

allele of *fusA*; the underlying mechanism is that the NRPS A-domain, responsible for recognition of amino acids, has relaxed substrate specificity (Han et al., (2012). Site-Directed Modification of the Adenylation Domain of the Fusaricidin Nonribosomal Peptide Synthetase for Enhanced Production of Fusaricidin Analogs. *Biotechnol. Lett.* 34, 1327–1334; Mousa et al., (2015) Biodiversity of Genes Encoding Anti-Microbial Traits within Plant Associated Microbes, *Front Plant Sci.* 2015; 6: 231).

[0044] In certain embodiments, the composition comprises a biologically pure culture of a *Paenibacillus* sp. strain comprising a fusaricidin synthetase gene of *fusA* encoded by a DNA sequence exhibiting at least 90.5% sequence identity to SEQ ID NO: 3 or SEQ ID NO: 1, a nonribosomal peptide synthetase (NRPS) gene of *triE* encoded by a DNA sequence exhibiting at least 90.0% sequence identity to SEQ ID NO: 7 or SEQ ID NO: 5, and/or a nitrogen fixation gene of *nifB* encoded by a DNA sequence exhibiting at least 96.9% sequence identity to SEQ ID NO: 10. In some aspects the sequence identity between the *fusA*, *triE*, or *nifB* of the *Paenibacillus* sp. strain and the respective sequence (i.e., SEQ ID NOs: 1 or 3 for *fusA*; SEQ ID NOs: 5 or 7 for *triE*; SEQ ID NO: 10 for *nifB*) is at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%. In other aspects, the sequence identity between the *fusA*, *triE*, or *nifB* of the *Paenibacillus* sp. strain and the respective sequence (i.e., SEQ ID NOs: 1 or 3 for *fusA*; SEQ ID NOs: 5 or 7 for *triE*; SEQ ID NO: 10 for *nifB*) is between about 80% and 100%, between about 85% and 100%, between about 90% and 100%, or between about 95% and 100%.

[0045] Due to the degeneracy of the genetic code, different nucleotide codons may be used to code for a particular amino acid. A host cell often displays a preferred pattern of codon usage. Structural nucleic acid sequences are preferably constructed to utilize the codon usage pattern of the particular host cell. This generally enhances the expression of the structural nucleic acid sequence in a transformed host cell. Any of the nucleic acid sequences disclosed herein may be modified to reflect the preferred codon usage of a host cell or organism in which they are contained.

[0046] Additional variations in the nucleic acid sequences described herein may encode proteins having equivalent or superior characteristics when compared to the proteins from which they are engineered. Mutations may include deletions, insertions, truncations, substitutions, fusions, shuffling of motif sequences, and the like.

[0047] Mutations to a nucleic acid sequence may be introduced in either a specific or random manner, both of which are well known to those of skill in the art of molecular biology. A

myriad of site-directed mutagenesis techniques exist, typically using oligonucleotides to introduce mutations at specific locations in a nucleic acid sequence. Examples include single strand rescue (Kunkel et al., *Proc. Natl. Acad. Sci. U.S.A.*, 82: 488-492, 1985), unique site elimination (Deng and Nickloff, *Anal. Biochem.* 200:81, 1992), nick protection (Vandeyar, et al. *Gene* 65: 129-133, 1988), and PCR (Costa et al., *Methods Mol. Biol.* 57: 31-44, 1996). Random or non-specific mutations may be generated by chemical agents (for a general review, see Singer and Kusmierek, *Ann. Rev. Biochem.* 52: 655-693, 1982) such as nitrosoguanidine (Cerdeira-Olmedo et al., *J. Mol. Biol.* 33: 705-719, 1968; Guerola, et al. *Nature New Biol.* 230: 122-125, 1971) and 2-aminopurine (Rogan and Bessman, *J. Bacteriol.* 103: 622-633, 1970); or by biological methods such as passage through mutator strains (Greener, et al. *Mol. Biotechnol.* 7: 189-195, 1997).

[0048] The modifications may result in either conservative or non-conservative changes in the amino acid sequence. Conservative changes result from additions, deletions, substitutions, etc. in the structural nucleic acid sequence which do not alter the final amino acid sequence of the protein. In a preferred embodiment, the encoded protein has between 20 and 500 conservative changes, more preferably between 15 and 300 conservative changes, even more preferably between 10 and 150 conservative changes, and most preferably between 5 and 75 conservative changes.

[0049] Non-conservative changes include additions, deletions, and substitutions which result in an altered amino acid sequence. In a preferred embodiment, the encoded protein has between 10 and 250 non-conservative amino acid changes, more preferably between 5 and 100 non-conservative amino acid changes, even more preferably between 2 and 50 non-conservative amino acid changes, and most preferably between 1 and 30 non-conservative amino acid changes.

[0050] Additional methods of making the alterations described above are described by Ausubel et al., *Current Protocols in Molecular Biology*, John Wiley and Sons, Inc., 1995, Bauer et al., *Gene*, 37:73, 1985; Craik, *BioTechniques*, 3: 12-19, 1985; Frits Eckstein et al., *Nucleic Acids Research*, 10: 6487-6497, 1982; Sambrook, et al., *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989, Smith, et al, In: *Genetic Engineering: Principles and Methods*, Setlow et al., Eds., Plenum Press, N.Y., 1-32, 1981, and Osuna, et al., *Critical Reviews In Microbiology*, 20: 107-116, 1994.

[0051] Modifications may be made to the protein sequences of the present invention and the nucleic acid segments which encode them that maintain the desired properties of the molecule. The following is a discussion based upon changing the amino acid sequence of a protein to create an equivalent, or possibly an improved molecule.

[0052] Certain amino acids may be substituted for other amino acids in a protein sequence without appreciable loss of the desired activity.

[0053] It is thus contemplated that various changes may be made in the peptide sequences of the disclosed protein sequences, or their corresponding nucleic acid sequences without appreciable loss of the biological activity.

[0054] In making such changes, the hydropathic index of amino acids may be considered. The importance of the hydropathic amino acid index in conferring interactive biological function on a protein is generally understood in the art (Kyte and Doolittle, J. Mol. Biol., 157: 105-132, 1982). It is accepted that the relative hydropathic character of the amino acid contributes to the secondary structure of the resultant protein, which in turn defines the interaction of the protein with other molecules, for example, enzymes, substrates, receptors, DNA, antibodies, antigens, and the like.

[0055] Each amino acid has been assigned a hydropathic index on the basis of their hydrophobicity and charge characteristics. These are: isoleucine (+4.5); valine (+4.2); leucine (+3.8); phenylalanine (+2.8); cysteine/cysteine (+2.5); methionine (+1.9); alanine (+1.8); glycine (−0.4); threonine (−0.7); serine (−0.8); tryptophan (−0.9); tyrosine (−1.3); proline (−1.6); histidine (−3.2); glutamate/glutamine/aspartate/asparagine (−3.5); lysine (−3.9); and arginine (−4.5).

[0056] It is known in the art that certain amino acids may be substituted by other amino acids having a similar hydropathic index or score and still result in a protein with similar biological activity, i.e., still obtain a biologically functional protein. In making such changes, the substitution of amino acids whose hydropathic indices are within ± 2 is preferred, those within ± 1 are more preferred, and those within ± 0.5 are most preferred.

[0057] It is also understood in the art that the substitution of like amino acids may be made effectively on the basis of hydrophilicity. U.S. Patent No. 4,554,101 (Hopp) states that the greatest local average hydrophilicity of a protein, as governed by the hydrophilicity of its adjacent amino acids, correlates with a biological property of the protein. The following hydrophilicity values have been assigned to amino acids: arginine/lysine (+3.0); aspartate/glutamate (+3.0 $\pm$ 1); serine (+0.3); asparagine/glutamine (+0.2); glycine (0); threonine (−0.4); proline (−0.5 $\pm$ 1); alanine/histidine (−0.5); cysteine (−1.0); methionine (−1.3); valine (−1.5); leucine/isoleucine (−1.8); tyrosine (−2.3); phenylalanine (−2.5); and tryptophan (−3.4).

[0058] It is understood that an amino acid may be substituted by another amino acid having a similar hydrophilicity score and still result in a protein with similar biological activity, i.e.,

still obtain a biologically functional protein. In making such changes, the substitution of amino acids whose hydropathic indices are within ± 2 is preferred, those within ± 1 are more preferred, and those within ± 0.5 are most preferred.

[0059] As outlined above, amino acid substitutions are therefore based on the relative similarity of the amino acid side-chain substituents, for example, their hydrophobicity, hydrophilicity, charge, size, and the like. Exemplary substitutions which take various of the foregoing characteristics into consideration are well known to those of skill in the art and include: arginine and lysine; glutamate and aspartate; serine and threonine; glutamine and asparagine; and valine, leucine, and isoleucine.

[0060] The present invention also encompasses methods of treating a plant to control plant diseases by administering to a plant or a plant part, such as a leaf, stem, flowers, fruit, root, or seed or by applying to a locus on which plant or plant parts grow, such as soil, the disclosed *Paenibacillus* sp. strains or mutants thereof, or cell-free preparations thereof or metabolites thereof.

[0061] In a method according to the invention a composition containing a disclosed *Paenibacillus* sp. strain or a fungicidal mutant thereof can be applied to any plant or any part of any plant grown in any type of media used to grow plants (e.g., soil, vermiculite, shredded cardboard, and water) or applied to plants or the parts of plants grown aurally, such as orchids or staghorn ferns. The composition may for instance be applied by spraying, atomizing, vaporizing, scattering, dusting, watering, squirting, sprinkling, pouring or fumigating. As already indicated above, application may be carried out at any desired location where the plant of interest is positioned, such as agricultural, horticultural, forest, plantation, orchard, nursery, organically grown crops, turfgrass and urban environments.

[0062] Compositions of the present invention can be obtained by culturing the disclosed *Paenibacillus* sp. strains or a fungicidal mutant (strain) derived therefrom according to methods well known in the art, including by using the media and other methods described in the examples below. Conventional large-scale microbial culture processes include submerged fermentation, solid state fermentation, or liquid surface culture. Towards the end of fermentation, as nutrients are depleted, cells begin the transition from growth phase to sporulation phase, such that the final product of fermentation is largely spores, metabolites and residual fermentation medium. Sporulation is part of the natural life cycle of *Paenibacillus* and is generally initiated by the cell in response to nutrient limitation. Fermentation is configured to obtain high levels of colony forming units of and to promote sporulation. The bacterial cells, spores and metabolites in culture media

resulting from fermentation may be used directly or concentrated by conventional industrial methods, such as centrifugation, tangential-flow filtration, depth filtration, and evaporation.

[0063] Compositions of the present invention include fermentation products. In some embodiments, the concentrated fermentation broth is washed, for example, via a diafiltration process, to remove residual fermentation broth and metabolites. The term “broth concentrate,” as used herein, refers to whole broth (fermentation broth) that has been concentrated by conventional industrial methods, as described above, but remains in liquid form. The term “fermentation solid,” as used herein, refers to the solid material that remains after the fermentation broth is dried. The term “fermentation product,” as used herein, refers to whole broth, broth concentrate and/or fermentation solids. Compositions of the present invention include fermentation products.

[0064] The fermentation broth or broth concentrate can be dried with or without the addition of carriers using conventional drying processes or methods such as spray drying, freeze drying, tray drying, fluidized-bed drying, drum drying, or evaporation.

[0065] The resulting dry products may be further processed, such as by milling or granulation, to achieve a specific particle size or physical format. Carriers, described below, may also be added post-drying.

[0066] Cell-free preparations of fermentation broth of the strains of the present invention can be obtained by any means known in the art, such as extraction, centrifugation and/or filtration of fermentation broth. Those of skill in the art will appreciate that so-called cell-free preparations may not be devoid of cells but rather are largely cell-free or essentially cell-free, depending on the technique used (e.g., speed of centrifugation) to remove the cells. The resulting cell-free preparation may be dried and/or formulated with components that aid in its application to plants or to plant growth media. Concentration methods and drying techniques described above for fermentation broth are also applicable to cell-free preparations.

[0067] In one embodiment, the fermentation product comprises at least about 1×10^4 colony forming units (CFU) of the microorganism (e.g., *Paenibacillus* sp. strain NRRL B-50374, *Paenibacillus* sp. strain NRRL B-67721, *Paenibacillus* sp. strain NRRL B-67723, or *Paenibacillus* sp. strain NRRL B-67724 or a fungicidal mutant strain thereof)/mL broth. In another embodiment, the fermentation product comprises at least about 1×10^5 colony forming units (CFU) of the microorganism/mL broth. In another embodiment, the fermentation product comprises at least about 1×10^6 CFU of the microorganism/mL broth. In yet another embodiment, the fermentation product comprises at least about 1×10^7 CFU of the microorganism/mL broth. In another

embodiment, the fermentation product comprises at least about 1×10^8 CFU of the microorganism/mL broth. In another embodiment, the fermentation product comprises at least about 1×10^9 CFU of the microorganism/mL broth. In another embodiment, the fermentation product comprises at least about 1×10^{10} CFU of the microorganism/mL broth. In another embodiment, the fermentation product comprises at least about 1×10^{11} CFU of the microorganism/mL broth.

[0068] The inventive compositions can be used as such or, depending on their particular physical and/or chemical properties, in the form of their formulations or the use forms prepared therefrom, such as aerosols, capsule suspensions, cold-fogging concentrates, warm-fogging concentrates, encapsulated granules, fine granules, flowable concentrates for the treatment of seed, ready-to-use solutions, dustable powders, emulsifiable concentrates, oil-in-water emulsions, water-in-oil emulsions, macrogranules, microgranules, oil-dispersible powders, oil-miscible flowable concentrates, oil-miscible liquids, gas (under pressure), gas generating product, foams, pastes, pesticide coated seed, suspension concentrates, oil dispersion, suspo-emulsion concentrates, soluble concentrates, suspensions, wettable powders, soluble powders, dusts and granules, water-soluble and water-dispersible granules or tablets, water-soluble and water-dispersible powders for the treatment of seed, wettable powders, natural products and synthetic substances impregnated with active ingredient, and also microencapsulations in polymeric substances and in coating materials for seed, and also ULV cold-fogging and warm-fogging formulations.

[0069] In some embodiments, the inventive compositions are liquid formulations. Non-limiting examples of liquid formulations include suspension concentrations and oil dispersions. In other embodiments, the inventive compositions are solid formulations. Non-limiting examples of liquid formulations include freeze-dried powders and spray-dried powders.

[0070] All plants and plant parts can be treated in accordance with the invention. In the present context, plants are understood as meaning all plants and plant populations, such as desired and undesired wild plants or crop plants (including naturally occurring crop plants). Crop plants can be plants which can be obtained by traditional breeding and optimization methods or by biotechnological and recombinant methods, or combinations of these methods, including the transgenic plants and including the plant varieties capable or not of being protected by Plant Breeders' Rights. Plant parts are understood as meaning all aerial and subterranean parts and organs of the plants, such as shoot, leaf, flower and root, examples which may be mentioned being leaves, needles, stalks, stems, flowers, fruiting bodies, fruits and seeds, and also roots, tubers and rhizomes. The plant parts also include crop

material and vegetative and generative propagation material, for example cuttings, tubers, rhizomes, slips and seeds.

[0071] As has already been mentioned above, all plants and their parts may be treated in accordance with the invention. In a preferred embodiment, plant species and plant varieties, and their parts, which grow wild or which are obtained by traditional biological breeding methods such as hybridization or protoplast fusion are treated. In a further preferred embodiment, transgenic plants and plant varieties which have been obtained by recombinant methods, if appropriate in combination with traditional methods (genetically modified organisms), and their parts are treated. The term “parts” or “parts of plants” or “plant parts” has been explained hereinabove. Plants of the plant varieties which are in each case commercially available or in use are especially preferably treated in accordance with the invention. Plant varieties are understood as meaning plants with novel traits which have been bred both by traditional breeding, by mutagenesis or by recombinant DNA techniques. They may take the form of varieties, races, biotypes and genotypes.

[0072] The treatment of the plants and plant parts with the compositions according to the invention is carried out directly or by acting on the environment, habitat or storage space using customary treatment methods, for example by dipping, spraying, atomizing, misting, evaporating, dusting, fogging, scattering, foaming, painting on, spreading, injecting, drenching, trickle irrigation and, in the case of propagation material, in particular in the case of seed, furthermore by the dry seed treatment method, the wet seed treatment method, the slurry treatment method, by encrusting, by coating with one or more coats and the like. It is furthermore possible to apply the active substances by the ultra-low volume method or to inject the active substance preparation or the active substance itself into the soil.

[0073] A preferred direct treatment of the plants is the leaf application treatment, i.e., compositions according to the invention are applied to the foliage, it being possible for the treatment frequency and the application rate to be matched to the infection pressure of the pathogen in question.

[0074] Preferred plants are those from the group of the useful plants, ornamentals, turfs, generally used trees which are employed as ornamentals in the public and domestic sectors, and forestry trees. Forestry trees comprise trees for the production of timber, cellulose, paper and products made from parts of the trees.

[0075] The term “agricultural plants” as used in the present context refers to crop plants which are employed as plants for obtaining foodstuffs, feedstuffs, fuels or for industrial purposes.

[0076] The terms “plant propagation material” and “plant propagule” are to be understood to denote all the generative parts of the plant such as seeds and vegetative plant material such as cuttings and tubers (e.g., potatoes), which can be used for the multiplication of the plant. This includes seeds, roots, fruits, tubers, bulbs, rhizomes, shoots, sprouts and other parts of plants. Seedlings and young plants, which are to be transplanted after germination or after emergence from soil, may also be mentioned. These young plants may also be treated totally or partially by immersion or pouring before transplantation.

[0077] The term “locus” is to be understood as any type of environment, soil, area or material where the plant is growing or intended to grow as well as the environmental conditions (such as temperature, water availability, radiation) that have an influence on the growth and development of the plant and/or its propagules. In addition, the term “locus” is to be understood as a plant, seed, soil, area, material or environment in which a pest is growing or may grow.

[0078] “Crop yield” is an indicator for the condition of the plant, whereas “crop” is to be understood as any plant or plant product which is further utilized after harvesting, e.g., fruits in the proper sense, vegetables, nuts, grains, seeds, wood (e.g., in the case of silviculture plants), flowers (e.g., in the case of gardening plants, ornamentals) etc., that is anything of economic value that is produced by the plant.

[0079] According to the present invention, “increased yield” of a plant, in particular of an agricultural, silvicultural and/or ornamental plant means that the yield of a product of the respective plant is increased by a measurable amount over the yield of the same product of the plant produced under the same conditions, but without the application of the composition of the invention.

[0080] The term “seed” embraces seeds and plant propagules of all kinds including but not limited to true seeds, seed pieces, suckers, corms, bulbs, fruit, tubers, grains, cuttings, cut shoots and the like and means in a preferred embodiment true seeds.

[0081] The term “seed treatment” comprises all suitable seed treatment techniques known in the art, such as seed dressing, seed coating, seed dusting, seed soaking, seed impregnation and seed pelleting.

[0082] The agricultural plants which can be treated and/or improved with the compositions and methods of the present invention include for example the following types of plants: turf, vines, cereals, for example wheat, barley, rye, oats, rice, maize and millet/sorghum; beet, for example sugar beet and fodder beet; fruits, for example pome fruit, stone fruit and soft fruit, for

example apples, pears, plums, peaches, almonds, cherries and berries, for example strawberries, raspberries, blackberries; legumes, for example beans, lentils, peas and soybeans; oil crops, for example oilseed rape, mustard, poppies, olives, sunflowers, coconuts, castor oil plants, cacao and peanuts; cucurbits, for example pumpkin/squash, cucumbers and melons; fibre plants, for example cotton, flax, hemp and jute; citrus fruit, for example oranges, lemons, grapefruit and tangerines; vegetables, for example spinach, lettuce, asparagus, cabbage species, carrots, onions, tomatoes, potatoes and bell peppers; Lauraceae, for example avocado, Cinnamomum, camphor, or else plants such as tobacco, nuts, coffee, aubergine, sugar cane, tea, pepper, grapevines, hops, bananas, latex plants and ornamentals, for example flowers, shrubs, deciduous trees and coniferous trees. This enumeration is no limitation.

[0083] The following plants are considered to be particularly suitable target crops for applying compositions and methods of the present invention: cotton, aubergine, turf, pome fruit, stone fruit, soft fruit, maize, wheat, barley, cucumber, tobacco, vines, rice, cereals, pear, beans, soybeans, oilseed rape, tomato, bell pepper, melons, cabbage, potato and apple.

[0084] Additional agricultural plants of particular interest include for example, cereals, for example wheat, rye, barley, triticale, oats or rice; beet, for example sugar beet or fodder beet; fruits, such as pomes, stone fruits or soft fruits, for example apples, pears, plums, peaches, almonds, cherries, strawberries, raspberries, blackberries or gooseberries; leguminous plants, such as lentils, peas, alfalfa or soybeans; oil plants, such as rape, mustard, olives, sunflowers, coconut, cocoa beans, castor oil plants, oil palms, ground nuts or soybeans; cucurbits, such as squashes, cucumber or melons; fiber plants, such as cotton, flax, hemp or jute; citrus fruit, such as oranges, lemons, grapefruits or mandarins; vegetables, such as broccoli, spinach, lettuce, asparagus, cabbages, carrots, onions, tomatoes, potatoes, cucurbits or paprika; lauraceous plants, such as avocados, cinnamon or camphor; energy and raw material plants, such as corn, soybean, rape, sugar cane or oil palm; corn; tobacco; nuts; coffee; tea; bananas; vines (table grapes and grape juice grape vines); hop; turf; natural rubber plants or ornamental and forestry plants, such as flowers, shrubs, broad-leaved trees or evergreens, for example conifers; and on the plant propagation material, such as seeds, and the crop material of these plants.

[0085] Examples of trees which can be improved in accordance with the method according to the invention are: *Abies* sp., *Eucalyptus* sp., *Picea* sp., *Pinus* sp., *Aesculus* sp., *Platanus* sp., *Tilia* sp., *Acer* sp., *Tsuga* sp., *Fraxinus* sp., *Sorbus* sp., *Betula* sp., *Crataegus* sp., *Ulmus* sp., *Quercus* sp., *Fagus* sp., *Salix* sp., *Populus* sp.

[0086] Preferred trees which can be improved in accordance with the method according to the invention are: from the tree species *Aesculus*: *A. hippocastanum*, *A. pariflora*, *A. carnea*; from the tree species *Platanus*: *P. aceriflora*, *P. occidentalis*, *P. racemosa*; from the tree species *Picea*: *P. abies*; from the tree species *Pinus*: *P. radiata*, *P. ponderosa*, *P. contorta*, *P. sylvestre*, *P. elliotii*, *P. montecola*, *P. albicaulis*, *P. resinosa*, *P. palustris*, *P. taeda*, *P. flexilis*, *P. jeffregi*, *P. baksiana*, *P. strobus*; from the tree species *Eucalyptus*: *E. grandis*, *E. globulus*, *E. camadensis*, *E. nitens*, *E. obliqua*, *E. regnans*, *E. pilularis*.

[0087] Especially preferred trees which can be improved in accordance with the method according to the invention are: from the tree species *Pinus*: *P. radiata*, *P. ponderosa*, *P. contorta*, *P. sylvestre*, *P. strobus*; from the tree species *Eucalyptus*: *E. grandis*, *E. globulus*, *E. camadensis*.

[0088] Very particularly preferred trees which can be improved in accordance with the method according to the invention are: horse chestnut, Platanaceae, linden tree, maple tree.

[0089] The present invention can also be applied to any turf grasses, including cool-season turf grasses and warm-season turf grasses. Examples of cold-season turf grasses are bluegrasses (*Poa* spp.), such as Kentucky bluegrass (*Poa pratensis* L.), rough bluegrass (*Poa trivialis* L.), Canada bluegrass (*Poa compressa* L.), annual bluegrass (*Poa annua* L.), upland bluegrass (*Poa glaucantha* Gaudin), wood bluegrass (*Poa nemoralis* L.) and bulbous bluegrass (*Poa bulbosa* L.); bentgrasses (*Agrostis* spp.) such as creeping bentgrass (*Agrostis palustris* Huds.), colonial bentgrass (*Agrostis tenuis* Sibth.), velvet bentgrass (*Agrostis canina* L.), South German mixed bentgrass (*Agrostis* spp. including *Agrostis tenuis* Sibth., *Agrostis canina* L., and *Agrostis palustris* Huds.), and redtop (*Agrostis alba* L.);

[0090] fescues (*Festuca* spp.), such as red fescue (*Festuca rubra* L. spp. *rubra*), creeping fescue (*Festuca rubra* L.), chewings fescue (*Festuca rubra commutata* Gaud.), sheep fescue (*Festuca ovina* L.), hard fescue (*Festuca longifolia* Thuill.), hair fescue (*Festuca capillata* Lam.), tall fescue (*Festuca arundinacea* Schreb.) and meadow fescue (*Festuca elanor* L.);

[0091] ryegrasses (*Lolium* spp.), such as annual ryegrass (*Lolium multiflorum* Lam.), perennial ryegrass (*Lolium perenne* L.) and Italian ryegrass (*Lolium multiflorum* Lam.);

[0092] and wheatgrasses (*Agropyron* spp.), such as fairway wheatgrass (*Agropyron cristatum* (L.) Gaertn.), crested wheatgrass (*Agropyron desertorum* (Fisch.) Schult.) and western wheatgrass (*Agropyron smithii* Rydb.)

[0093] Examples of further cool-season turf grasses are beachgrass (*Ammophila breviligulata* Fern.), smooth brome grass (*Bromus inermis* Leyss.), cattails such as timothy (*Phleum*

pratense L.), sand cattail (*Phleum subulatum* L.), orchardgrass (*Dactylis glomerata* L.), weeping alkaligrass (*Puccinellia distans* (L.) Parl.) and crested dog's-tail (*Cynosurus cristatus* L.)

[0094] Examples of warm-season turf grasses are Bermuda grass (*Cynodon spp.* L. C. Rich), zoysia grass (*Zoysia spp.* Willd.), St. Augustine grass (*Stenotaphrum secundatum* Walt Kuntze), centipede grass (*Eremochloa ophiuroides* Munro Hack.), carpetgrass (*Axonopus affinis* Chase), Bahia grass (*Paspalum notatum* Flugge), Kikuyu grass (*Pennisetum clandestinum* Hochst. ex Chiov.), buffalo grass (*Buchloe dactyloids* (Nutt.) Engelm.), blue grama (*Bouteloua gracilis* (H.B.K.) Lag. ex Griffiths), seashore paspalum (*Paspalum vaginatum* Swartz) and sideoats grama (*Bouteloua curtipendula* (Michx. Torr.) Cool-season turf grasses are generally preferred for the use according to the invention. Especially preferred are bluegrass, benchgrass and redtop, fescues and ryegrasses. Bentgrass is especially preferred.

[0095] The inventive compositions have potent microbicidal activity and can be used for control of unwanted microorganisms, such as fungi and bacteria, in crop protection and in the protection of materials.

[0096] The invention also relates to a method for controlling unwanted microorganisms, characterized in that the inventive compositions are applied to the phytopathogenic fungi, phytopathogenic bacteria and/or their habitat.

[0097] Fungicides can be used in crop protection for control of phytopathogenic fungi. They are characterized by an outstanding efficacy against a broad spectrum of phytopathogenic fungi, including soilborne pathogens, which are in particular members of the classes *Plasmodiophoromycetes*, *Peronosporomycetes* (Syn. *Oomycetes*), *Chytridiomycetes*, *Zygomycetes*, *Ascomycetes*, *Basidiomycetes* and *Deuteromycetes* (Syn. *Fungi imperfecti*). Some fungicides are systemically active and can be used in plant protection as foliar, seed dressing or soil fungicide. Furthermore, they are suitable for combating fungi, which inter alia infest wood or roots of plant.

[0098] Bactericides can be used in crop protection for control of *Pseudomonadaceae*, *Rhizobiaceae*, *Enterobacteriaceae*, *Corynebacteriaceae* and *Streptomycetaceae*.

[0099] Non-limiting examples of pathogens of fungal diseases which can be treated in accordance with the invention include:

[0100] diseases caused by powdery mildew pathogens, for example *Blumeria* species, for example *Blumeria graminis*; *Podosphaera* species, for example *Podosphaera leucotricha*; *Sphaerotheca* species, for example *Sphaerotheca fuliginea*; *Uncinula* species, for example *Uncinula necator*;

[0101] diseases caused by rust disease pathogens, for example *Gymnosporangium* species, for example *Gymnosporangium sabinae*; *Hemileia* species, for example *Hemileia vastatrix*; *Phakopsora* species, for example *Phakopsora pachyrhizi* and *Phakopsora meibomia*; *Puccinia* species, for example *Puccinia recondite*, *P. triticea*, *P. graminis* or *P. striiformis*; *Uromyces* species, for example *Uromyces appendiculatus*;

[0102] diseases caused by pathogens from the group of the *Oomycetes*, for example *Albugo* species, for example *Albugo candida*; *Bremia* species, for example *Bremia lactucae*; *Peronospora* species, for example *Peronospora pisi* or *P. brassicae*; *Phytophthora* species, for example *Phytophthora infestans*; *Plasmopara* species, for example *Plasmopara viticola*; *Pseudoperonospora* species, for example *Pseudoperonospora humuli* or *Pseudoperonospora cubensis*; *Pythium* species, for example *Pythium ultimum*;

[0103] leaf blotch diseases and leaf wilt diseases caused, for example, by *Alternaria* species, for example *Alternaria solani*; *Cercospora* species, for example *Cercospora beticola*; *Cladosporium* species, for example *Cladosporium cucumerinum*; *Cochliobolus* species, for example *Cochliobolus sativus* (conidia form: *Drechslera*, Syn: *Helminthosporium*), *Cochliobolus miyabeanus*; *Colletotrichum* species, for example *Colletotrichum lindemuthianum*; *Cycloconium* species, for example *Cycloconium oleaginum*; *Diaporthe* species, for example *Diaporthe citri*; *Elsinoe* species, for example *Elsinoe fawcettii*; *Gloeosporium* species, for example *Gloeosporium laeticolor*; *Glomerella* species, for example *Glomerella cingulata*; *Guignardia* species, for example *Guignardia bidwelli*; *Leptosphaeria* species, for example *Leptosphaeria maculans*, *Leptosphaeria nodorum*; *Magnaporthe* species, for example *Magnaporthe grisea*; *Marssonina* species, for example *Marssonina coronaria*; *Microdochium* species, for example *Microdochium nivale*; *Mycosphaerella* species, for example *Mycosphaerella graminicola*, *M. arachidicola* and *M. fijiensis*; *Phaeosphaeria* species, for example *Phaeosphaeria nodorum*; *Pyrenophora* species, for example *Pyrenophora teres*, *Pyrenophora tritici repentis*; *Ramularia* species, for example *Ramularia collo-cygni*, *Ramularia areola*; *Rhynchosporium* species, for example *Rhynchosporium secalis*; *Septoria* species, for example *Septoria apii*, *Septoria lycopersii*; *Typhula* species, for example *Typhula incarnata*; *Venturia* species, for example *Venturia inaequalis*;

[0104] root and stem diseases caused, for example, by *Corticium* species, for example *Corticium graminearum*; *Fusarium* species, for example *Fusarium oxysporum*; *Gaeumannomyces* species, for example *Gaeumannomyces graminis*; *Rhizoctonia* species, such as, for example *Rhizoctonia solani*; *Sarocladium* diseases caused for example by *Sarocladium oryzae*; *Sclerotium* diseases caused

for example by *Sclerotium oryzae*; *Tapesia* species, for example *Tapesia acuformis*; *Thielaviopsis* species, for example *Thielaviopsis basicola*;

[0105] ear and panicle diseases (including corn cobs) caused, for example, by *Alternaria* species, for example *Alternaria* spp.; *Aspergillus* species, for example *Aspergillus flavus*; *Cladosporium* species, for example *Cladosporium cladosporioides*; *Claviceps* species, for example *Claviceps purpurea*; *Fusarium* species, for example *Fusarium culmorum*; *Gibberella* species, for example *Gibberella zeae*; *Monographella* species, for example *Monographella nivalis*; *Septoria* species, for example *Septoria nodorum*;

[0106] diseases caused by smut fungi, for example *Sphacelotheca* species, for example *Sphacelotheca reiliana*; *Tilletia* species, for example *Tilletia caries*, *T. controversa*; *Urocystis* species, for example *Urocystis occulta*; *Ustilago* species, for example *Ustilago nuda*, *U. nuda tritici*;

[0107] fruit rot caused, for example, by *Aspergillus* species, for example *Aspergillus flavus*; *Botrytis* species, for example *Botrytis cinerea*; *Penicillium* species, for example *Penicillium expansum* and *P. purpurogenum*; *Sclerotinia* species, for example *Sclerotinia sclerotiorum*; *Verticilium* species, for example *Verticilium alboatrum*;

[0108] seed and soilborne decay, mould, wilt, rot and damping-off diseases caused, for example, by *Alternaria* species, caused for example by *Alternaria brassicicola*; *Aphanomyces* species, caused for example by *Aphanomyces euteiches*; *Ascochyta* species, caused for example by *Ascochyta lentis*; *Aspergillus* species, caused for example by *Aspergillus flavus*; *Cladosporium* species, caused for example by *Cladosporium herbarum*; *Cochliobolus* species, caused for example by *Cochliobolus sativus*; (conidia form: *Drechslera*, *Bipolaris* Syn: *Helminthosporium*); *Colletotrichum* species, caused for example by *Colletotrichum coccodes*; *Fusarium* species, caused for example by *Fusarium culmorum*; *Gibberella* species, caused for example by *Gibberella zeae*; *Macrophomina* species, caused for example by *Macrophomina phaseolina*; *Monographella* species, caused for example by *Monographella nivalis*; *Penicillium* species, caused for example by *Penicillium expansum*; *Phoma* species, caused for example by *Phoma lingam*; *Phomopsis* species, caused for example by *Phomopsis sojae*; *Phytophthora* species, caused for example by *Phytophthora cactorum*; *Pyrenophora* species, caused for example by *Pyrenophora graminea*; *Pyricularia* species, caused for example by *Pyricularia oryzae*; *Pythium* species, caused for example by *Pythium ultimum*; *Rhizoctonia* species, caused for example by *Rhizoctonia solani*; *Rhizopus* species, caused for example by *Rhizopus oryzae*; *Sclerotium* species, caused for example

by *Sclerotium rolfsii*; *Septoria* species, caused for example by *Septoria nodorum*; *Typhula* species, caused for example by *Typhula incarnata*; *Verticillium* species, caused for example by *Verticillium dahliae*;

[0109] cancers, galls and witches' broom caused, for example, by *Nectria* species, for example *Nectria galligena*;

[0110] wilt diseases caused, for example, by *Monilinia* species, for example *Monilinia laxa*;

[0111] leaf blister or leaf curl diseases caused, for example, by *Exobasidium* species, for example *Exobasidium vexans*;

[0112] *Taphrina* species, for example *Taphrina deformans*;

[0113] decline diseases of wooden plants caused, for example, by Esca disease, caused for example by *Phaemoniella clamydospora*, *Phaeoacremonium aleophilum* and *Fomitiporia mediterranea*; Eutypa dyebark, caused for example by *Eutypa lata*; Ganoderma diseases caused for example by *Ganoderma boninense*; Rigidoporus diseases caused for example by *Rigidoporus lignosus*;

[0114] diseases of flowers and seeds caused, for example, by *Botrytis* species, for example *Botrytis cinerea*;

[0115] diseases of plant tubers caused, for example, by *Rhizoctonia* species, for example *Rhizoctonia solani*; *Helminthosporium* species, for example *Helminthosporium solani*;

[0116] Club root caused, for example, by *Plasmodiophora* species, for example *Plasmodiophora brassicae*;

[0117] diseases caused by bacterial pathogens, for example *Xanthomonas* species, for example *Xanthomonas campestris* pv. *oryzae*; *Pseudomonas* species, for example *Pseudomonas syringae* pv. *lachrymans*; *Erwinia* species, for example *Erwinia amylovora*.

[0118] The following diseases of soya beans can be controlled with preference:

[0119] Fungal diseases on leaves, stems, pods and seeds caused, for example, by *Alternaria* leaf spot (*Alternaria* spec. *atrans tenuissima*), Anthracnose (*Colletotrichum gloeosporoides dematium* var. *truncatum*), brown spot (*Septoria glycines*), cercospora leaf spot and blight (*Cercospora kikuchii*), choanephora leaf blight (*Choanephora infundibulifera trispora* (Syn.)), dactuliophora leaf spot (*Dactuliophora glycines*), downy mildew (*Peronospora manshurica*), drechslera blight (*Drechslera glycini*), frog-eye leaf spot (*Cercospora sojae*), leptosphaerulina leaf spot (*Leptosphaerulina trifolii*), phyllosticta leaf spot (*Phyllosticta sojaecola*), pod and stem blight (*Phomopsis sojae*), powdery mildew (*Microsphaera diffusa*), pyrenochaeta leaf spot (*Pyrenochaeta glycines*), rhizoctonia aerial, foliage, and

web blight (*Rhizoctonia solani*), rust (*Phakopsora pachyrhizi*, *Phakopsora meibomia*), scab (*Sphaceloma glycines*), stemphylium leaf blight (*Stemphylium botryosum*), target spot (*Corynespora cassiicola*).

[0120] Fungal diseases on roots and the stem base caused, for example, by black root rot (*Calonectria crotalariae*), charcoal rot (*Macrophomina phaseolina*), fusarium blight or wilt, root rot, and pod and collar rot (*Fusarium oxysporum*, *Fusarium orthoceras*, *Fusarium semitectum*, *Fusarium equiseti*), mycoleptodiscus root rot (*Mycoleptodiscus terrestris*), neocosmospora (*Neocosmospora vasinfecta*), pod and stem blight (*Diaporthe phaseolorum*), stem canker (*Diaporthe phaseolorum* var. *caulivora*), phytophthora rot (*Phytophthora megasperma*), brown stem rot (*Phialophora gregata*), pythium rot (*Pythium aphanidermatum*, *Pythium irregulare*, *Pythium debaryanum*, *Pythium myriotylum*, *Pythium ultimum*), rhizoctonia root rot, stem decay, and damping-off (*Rhizoctonia solani*), sclerotinia stem decay (*Sclerotinia sclerotiorum*), sclerotinia southern blight (*Sclerotinia rolfii*), thielaviopsis root rot (*Thielaviopsis basicola*).

[0121] The inventive fungicidal compositions can be used for curative or protective/preventive control of phytopathogenic fungi. The invention therefore also relates to curative and protective methods for controlling phytopathogenic fungi by the use of the inventive compositions, which are applied to the seed, the plant or plant parts, the fruit or the soil in which the plants grow.

[0122] The fact that the compositions are well tolerated by plants at the concentrations required for controlling plant diseases allows the treatment of above-ground parts of plants, of propagation stock and seeds, and of the soil.

[0123] According to the invention all plants and plant parts can be treated including cultivars and plant varieties (whether or not protectable by plant variety or plant breeder's rights). Cultivars and plant varieties can be plants obtained by conventional propagation and breeding methods which can be assisted or supplemented by one or more biotechnological methods such as by use of double haploids, protoplast fusion, random and directed mutagenesis, molecular or genetic markers or by bioengineering and genetic engineering methods.

[0124] In some embodiments, the compositions disclosed herein are used to enhance plant growth, plant vigor, and/or crop yield. "Yield" is to be understood as any plant product of economic value that is produced by the plant such as grains, fruits in the proper sense, vegetables, nuts, grains, seeds, wood (e.g., in the case of silviculture plants) or even flowers (e.g., in the case of gardening plants, ornamentals). The plant products may in addition be further utilized and/or processed after harvesting.

[0125] According to the present invention, “increased yield” of a plant, in particular of an agricultural, silvicultural and/or ornamental plant means that the yield of a product of the respective plant is increased by a measurable amount over the yield of the same product of the plant produced under the same conditions, but without the application of the composition of the invention. Increased yield can be characterized, among others, by following improved properties of the plant:

- increased plant weight,
- increased plant height,
- increased biomass such as higher fresh and/or dry weight,
- higher grain yield,
- more tillers,
- larger leaves,
- increased shoot growth,
- increased protein content,
- increased oil content,
- increased starch content.
- increased pigment content

[0126] According to one embodiment of the present invention, the yield is increased by at least 5%. According to another embodiment of the present invention, the yield is increased by least 10%. According to another embodiment of the present invention, the yield is increased by least 15%. According to another embodiment of the present invention, the yield is increased by least 30%. According to another embodiment of the present invention, the yield is increased by least 40%.

[0127] Another indicator for the condition of the plant is the “plant vigor”. The plant vigor becomes manifest in several aspects such as the general visual appearance. Improved plant vigor can be characterized, among others, by following improved properties of the plant:

- improved vitality of the plant,
- improved plant growth,
- improved plant development,
- improved visual appearance,
- improved plant stand (less plant verse/lodging),
- improved emergence,

- enhanced root growth and/or more developed root system,
- enhanced nodulation, in particular rhizobial nodulation,
- bigger leaf blade,
- increased plant size,
- increased plant weight,
- increased plant height,
- increased tiller number,
- increased shoot growth,
- increased root growth (extensive root system),
- increased size of root mass (extensive root system),
- increased yield when grown on poor soils or unfavorable climate,
- enhanced photosynthetic activity,
- change of color (e.g., enhanced pigment content (e.g., Chlorophyll content),
- earlier flowering,
- earlier fruiting,
- earlier and improved germination,
- earlier (advanced) grain maturity,
- improved self-defence mechanisms,
- less non-productive tillers,
- less dead basal leaves,
- less input needed (such as fertilizers or water),
- greener leaves and increased green leaf area,
- complete maturation under shortened vegetation periods,
- less fertilizers needed,
- less seeds needed,
- easier harvesting,
- faster and more uniform ripening,
- longer shelf-life,
- longer panicles,
- delay of senescence,
- stronger and/or more productive tillers,

- better extractability of ingredients,
- improved quality of seeds (for being seeded in the following seasons for seed production),
- reduced production of ethylene and/or the inhibition of its reception by the plant,
- spindliness of leaves,
- increased number of ears/m².

[0128] The improvement of the plant vigor according to the present invention particularly means that the improvement of any one or several or all of the above mentioned plant characteristics are improved independently of the pesticidal action of the composition or active ingredients. An increased vigor may for example result in a higher percentage of plants that can be transplanted to the field or an increased number of marketable plants (such as tomatoes).

[0129] In certain aspects, the compositions of the present invention are applied at about 1×10^4 to about 1×10^{14} colony forming units (CFU) per hectare, at about 1×10^4 to about 1×10^{12} colony forming units (CFU) per hectare, at about 1×10^4 to about 1×10^{10} colony forming units (CFU) per hectare, at about 1×10^4 to about 1×10^8 colony forming units (CFU) per hectare, at about 1×10^6 to about 1×10^{14} colony forming units (CFU) per hectare, at about 1×10^6 to about 1×10^{12} colony forming units (CFU) per hectare, at about 1×10^6 to about 1×10^{10} colony forming units (CFU) per hectare, at about 1×10^6 to about 1×10^8 colony forming units (CFU) per hectare, at about 1×10^8 to about 1×10^{14} colony forming units (CFU) per hectare, at about 1×10^8 to about 1×10^{12} colony forming units (CFU) per hectare, or at about 1×10^8 to about 1×10^{10} colony forming units (CFU) per hectare.

[0130] In other aspects, the compositions of the present invention are applied at about 1×10^6 to about 1×10^{14} colony forming units (CFU) per hectare, at about 1×10^6 to about 1×10^{12} colony forming units (CFU) per hectare, at about 1×10^6 to about 1×10^{10} colony forming units (CFU) per hectare, at about 1×10^6 to about 1×10^8 colony forming units (CFU) per hectare. In yet other aspects, the compositions of the present invention are applied at about 1×10^9 to about 1×10^{13} colony forming units (CFU) per hectare. In one aspect, the compositions of the present invention are applied at about 1×10^{10} to about 1×10^{12} colony forming units (CFU) per hectare.

[0131] In certain embodiments, the compositions of the present invention are applied at about 0.1 kg to about 20 kg fermentation solids per hectare. In some embodiments, the compositions of the present invention are applied at about 0.1 kg to about 10 kg fermentation solids per hectare. In other embodiments, the compositions of the present invention are applied at about 0.25 kg to about 7.5 kg fermentation solids per hectare. In yet other embodiments, the

compositions of the present invention are applied at about 0.5 kg to about 5 kg fermentation solids per hectare. The compositions of the present invention may also be applied at about 1 kg or about 2 kg fermentation solids per hectare.

[0132] The inventive compositions, when they are well tolerated by plants, have favorable homeotherm toxicity and are well tolerated by the environment, are suitable for protecting plants and plant organs, for enhancing harvest yields, for improving the quality of the harvested material. They can preferably be used as crop protection compositions. They are active against normally sensitive and resistant species and against all or some stages of development.

[0133] Plants which can be treated in accordance with the invention include the following main crop plants: maize, soya bean, alfalfa, cotton, sunflower, *Brassica* oil seeds such as *Brassica napus* (e.g., canola, rapeseed), *Brassica rapa*, *B. juncea* (e.g., (field) mustard) and *Brassica carinata*, *Arecaceae* sp. (e.g., oilpalm, coconut), rice, wheat, sugar beet, sugar cane, oats, rye, barley, millet and sorghum, triticale, flax, nuts, grapes and vine and various fruit and vegetables from various botanic taxa, e.g., *Rosaceae* sp. (e.g., pome fruits such as apples and pears, but also stone fruits such as apricots, cherries, almonds, plums and peaches, and berry fruits such as strawberries, raspberries, red and black currant and gooseberry), *Ribesiodae* sp., *Juglandaceae* sp., *Betulaceae* sp., *Anacardiaceae* sp., *Fagaceae* sp., *Moraceae* sp., *Oleaceae* sp. (e.g. olive tree), *Actinidaceae* sp., *Lauraceae* sp. (e.g., avocado, cinnamon, camphor), *Musaceae* sp. (e.g., banana trees and plantations), *Rubiaceae* sp. (e.g., coffee), *Theaceae* sp. (e.g., tea), *Sterculiaceae* sp., *Rutaceae* sp. (e.g., lemons, oranges, mandarins and grapefruit); *Solanaceae* sp. (e.g., tomatoes, potatoes, peppers, capsicum, aubergines, tobacco), *Liliaceae* sp., *Compositae* sp. (e.g., lettuce, artichokes and chicory – including root chicory, endive or common chicory), *Umbelliferae* sp. (e.g., carrots, parsley, celery and celeriac), *Cucurbitaceae* sp. (e.g., cucumbers – including gherkins, pumpkins, watermelons, calabashes and melons), *Alliaceae* sp. (e.g., leeks and onions), *Cruciferae* sp. (e.g., white cabbage, red cabbage, broccoli, cauliflower, Brussels sprouts, pak choi, kohlrabi, radishes, horseradish, cress and chinese cabbage), *Leguminosae* sp. (e.g., peanuts, peas, lentils and beans – e.g., common beans and broad beans), *Chenopodiaceae* sp. (e.g. Swiss chard, fodder beet, spinach, beetroot), *Linaceae* sp. (e.g., hemp), *Cannabeacea* sp. (e.g., cannabis), *Malvaceae* sp. (e.g., okra, cocoa), *Papaveraceae* (e.g., poppy), *Asparagaceae* (e.g., asparagus); useful plants and ornamental plants in the garden and woods including turf, lawn, grass and *Stevia rebaudiana*; and in each case genetically modified types of these plants.

[0134] In certain aspects, the fermentation product further comprises a formulation ingredient. The formulation ingredient may be a wetting agent, extender, solvent, spontaneity

promoter, emulsifier, dispersant, frost protectant, thickener, and/or an adjuvant. In one embodiment, the formulation ingredient is a wetting agent. In other aspects, the fermentation product is a freeze-dried powder or a spray-dried powder.

[0135] Compositions of the present invention may include formulation ingredients added to compositions of the present invention to improve recovery, efficacy, or physical properties and/or to aid in processing, packaging and administration. Such formulation ingredients may be added individually or in combination.

[0136] The formulation ingredients may be added to compositions comprising cells, cell-free preparations, isolated compounds, and/or metabolites to improve efficacy, stability, and physical properties, usability and/or to facilitate processing, packaging and end-use application. Such formulation ingredients may include agriculturally acceptable carriers, inerts, stabilization agents, preservatives, nutrients, or physical property modifying agents, which may be added individually or in combination. In some embodiments, the carriers may include liquid materials such as water, oil, and other organic or inorganic solvents and solid materials such as minerals, polymers, or polymer complexes derived biologically or by chemical synthesis. In some embodiments, the formulation ingredient is a binder, adjuvant, or adhesive that facilitates adherence of the composition to a plant part, such as leaves, seeds, or roots. See, for example, Taylor, A.G., et al., "Concepts and Technologies of Selected Seed Treatments," *Annu. Rev. Phytopathol.*, 28: 321-339 (1990). The stabilization agents may include anti-caking agents, anti-oxidation agents, anti-settling agents, antifoaming agents, desiccants, protectants or preservatives. The nutrients may include carbon, nitrogen, and phosphorus sources such as sugars, polysaccharides, oil, proteins, amino acids, fatty acids and phosphates. The physical property modifiers may include bulking agents, wetting agents, thickeners, pH modifiers, rheology modifiers, dispersants, adjuvants, surfactants, film-formers, hydrotropes, builders, antifreeze agents or colorants. In some embodiments, the composition comprising cells, cell-free preparation and/or metabolites produced by fermentation can be used directly with or without water as the diluent without any other formulation preparation. In a particular embodiment, a wetting agent, or a dispersant, is added to a fermentation solid, such as a freeze-dried or spray-dried powder. In some embodiments, the formulation inerts are added after concentrating fermentation broth and/or during and/or after drying. A wetting agent increases the spreading and penetrating properties, or a dispersant increases the dispersability and solubility of the active ingredient (once diluted) when it is applied to surfaces. Exemplary wetting agents are known to those of skill in the art and include

sulfosuccinates and derivatives, such as MULTIWET™ MO-70R (Croda Inc., Edison, NJ); siloxanes such as BREAK-THRU® (Evonik, Germany); nonionic compounds, such as ATLOX™ 4894 (Croda Inc., Edison, NJ); alkyl polyglucosides, such as TERWET® 3001 (Huntsman International LLC, The Woodlands, Texas); C12-C14 alcohol ethoxylate, such as TERGITOL® 15-S-15 (The Dow Chemical Company, Midland, Michigan); phosphate esters, such as RHODAFAC® BG-510 (Rhodia, Inc.); and alkyl ether carboxylates, such as EMULSOGEN™ LS (Clariant Corporation, North Carolina).

DEPOSIT INFORMATION

[0137] Samples of the *Paenibacillus* sp. strains of the invention have been deposited with the Agricultural Research Service Culture Collection located at the National Center for Agricultural Utilization Research, Agricultural Research Service, U.S. Department of Agriculture (NRRL), 1815 North University Street, Peoria, IL 61604, U.S.A., under the Budapest Treaty. *Paenibacillus* sp. NRRL B-67721, *Paenibacillus* sp. NRRL B-67723, and *Paenibacillus* sp. NRRL B-67724 were each deposited on December 4, 2018. *Paenibacillus* sp. NRRL B-50374 was deposited on May 18, 2010.

[0138] The *Paenibacillus* sp. strains have been deposited under conditions that assure that access to the culture will be available during the pendency of this patent application to one determined by the Commissioner of Patents and Trademarks to be entitled thereto under 37 C.F.R. § 1.14 and 35 U.S.C. §122. However, it should be understood that the availability of a deposit does not constitute a license to practice the subject invention in derogation of patent rights granted by governmental action.

[0139] The following examples are given for purely illustrative and non-limiting purposes of the present invention.

EXAMPLES

Example 1. Antifungal Activity against *Sphaerotheca fuliginea* of *Paenibacillus* sp. Strains NRRL B-50374, NRRL B-67721, NRRL B-67723, and NRRL B-67724

[0140] *Paenibacillus* sp. strain NRRL B-50374, *Paenibacillus* sp. strain NRRL B-67721, *Paenibacillus* sp. strain NRRL B-67723, and *Paenibacillus* sp. strain NRRL B-67724 were cultured in a soy-based medium to produce whole broths along with several other *Paenibacillus* sp. strains. The whole broths were diluted in a mixture of water and organic solvent to a concentration

of 20%. The diluted whole broths were applied to young plants which were subsequently exposed to an inoculum of *Sphaerotheca fuliginea* (PODOXA) also known as Cucumber Powdery Mildew.

[0141] Several days after exposure to the inoculum of plant pathogen, each plant was scored for percent control of the pathogen relative to the untreated control plants. Each treatment was evaluated with three replicates and the average percent control was reported.

[0142] All of the strains had previously been evaluated for antifungal activity in several initial rounds of screening and outperformed other *Paenibacillus* sp. strains. The present analysis represented a subsequent round of screening to further narrow the list of candidate strains with superior antifungal activity. *Paenibacillus* sp. strain NRRL B-50374, *Paenibacillus* sp. strain NRRL B-67721, *Paenibacillus* sp. strain NRRL B-67723, and *Paenibacillus* sp. strain NRRL B-67724 were among the *Paenibacillus* strains with the greatest antifungal activity in this subsequent analysis (see **FIG. 1**).

Example 2. Antifungal Activity against *Botrytis cinerea* of *Paenibacillus* sp. Strains NRRL B-50374, NRRL B-67721, NRRL B-67723, and NRRL B-67724

[0143] *Paenibacillus* sp. strain NRRL B-50374, *Paenibacillus* sp. strain NRRL B-67721, *Paenibacillus* sp. strain NRRL B-67723, and *Paenibacillus* sp. strain NRRL B-67724 were cultured in a soy-based medium to produce whole broths that were diluted in a mixture of water and organic solvent to concentrations of 20% and 5%. The diluted whole broths were applied to young plants which were subsequently exposed to an inoculum of *Botrytis cinerea* (BOTRCI) also known as Gray Mold.

[0144] Several days after exposure to the inoculum of plant pathogen, each plant was scored for percent control of the pathogen relative to the untreated control plants. Each treatment was evaluated with three replicates and the average percent control was reported. This assay was repeated several times and representative results are shown in **Table 1**. *Paenibacillus* sp. strain NRRL B-50374, *Paenibacillus* sp. strain NRRL B-67721, *Paenibacillus* sp. strain NRRL B-67723, and *Paenibacillus* sp. strain NRRL B-67724 demonstrated consistently high antifungal activity against *Botrytis cinerea* (BOTRCI).

Table 1. Control of *Botrytis cinerea* (BOTRCI) achieved with *Paenibacillus* sp. strain NRRL B-50374, *Paenibacillus* sp. strain NRRL B-67721, *Paenibacillus* sp. strain NRRL B-67723, and *Paenibacillus* sp. strain NRRL B-67724 at dilution rates of 20% and 5%.

Treatment	Application Rate	Average Percent Control
<i>Paenibacillus</i> sp. strain NRRL B-50374	20%	98
	5%	85
<i>Paenibacillus</i> sp. strain NRRL B-67721	20%	88
	5%	0
<i>Paenibacillus</i> sp. strain NRRL B-67723	20%	98
	5%	68
<i>Paenibacillus</i> sp. strain NRRL B-67724	20%	60
	5%	50

Example 3. Antifungal Activity against *Puccinia triticina* of *Paenibacillus* sp. Strains NRRL B-50374, NRRL B-67721, NRRL B-67723, and NRRL B-67724

[0145] *Paenibacillus* sp. strain NRRL B-50374, *Paenibacillus* sp. strain NRRL B-67721, *Paenibacillus* sp. strain NRRL B-67723, and *Paenibacillus* sp. strain NRRL B-67724 were cultured in a soy-based medium to produce whole broths that were diluted in a mixture of water and organic solvent to concentrations of 20% and 5%. The diluted whole broths were applied to young plants which were subsequently exposed to an inoculum of *Puccinia triticina* (PUCCRT) also known as Wheat Leaf Rust.

[0146] Several days after exposure to the inoculum of plant pathogen, each plant was scored for percent control of the pathogen relative to the untreated control plants. Each treatment was evaluated with three replicates and the average percent control was reported. This assay was repeated several times and representative results are shown in **Table 2**. *Paenibacillus* sp. strain NRRL B-50374, *Paenibacillus* sp. strain NRRL B-67721, *Paenibacillus* sp. strain NRRL B-67723, and *Paenibacillus* sp. strain NRRL B-67724 demonstrated consistently high antifungal activity against *Botrytis cinerea* (BOTRCI).

Table 2. Control of *Puccinia triticina* (PUCCRT) achieved with *Paenibacillus* sp. strain NRRL B-50374, *Paenibacillus* sp. strain NRRL B-67721, *Paenibacillus* sp. strain NRRL B-67723, and *Paenibacillus* sp. strain NRRL B-67724 at dilution rates of 20% and 5%.

Treatment	Application Rate	Average Percent Control
<i>Paenibacillus</i> sp. strain NRRL B-50374	20%	77
	5%	17
<i>Paenibacillus</i> sp. strain NRRL B-67721	20%	80
	5%	17
<i>Paenibacillus</i> sp. strain NRRL B-67723	20%	65
	5%	25
<i>Paenibacillus</i> sp. strain NRRL B-67724	20%	80
	5%	50

Example 4. Analysis of Fusaricidin and Tridecaptin Biosynthetic Gene Clusters in

***Paenibacillus* sp. strains NRRL B-50374, NRRL B-67721, NRRL B-67723, and NRRL B-67724**

[0147] The genomes of *Paenibacillus* sp. strains NRRL B-50374, NRRL B-67721, NRRL B-67723, and NRRL B-67724 were sequenced and analyzed for the presence of known gene clusters encoding proteins responsible for the biosynthesis of antimicrobial compounds. This analysis revealed that each of the four strains has a fusaricidin synthetase (*fusA*) with at least 90.5% sequence identity to that found in the other strains (see **Table 3**). In addition, all four strains possess a tridecaptin gene cluster. Identification of a tridecaptin gene cluster in a laboratory strain of *Paenibacillus terrae* had previously been reported. Lohans CT, van Belkum MJ, Cochrane SA, Huang Z, Sit CS, McMullen LM, and Vederas JC. (2014) Biochemical, Structural, and Genetic Characterization of Tridecaptin A1, an Antagonist of *Campylobacter jejuni*. ChemBioChem 15:243-249. The tridecaptin biosynthetic gene cluster contains *triA*, *triB*, *triC*, *triD*, and *triE*. In each of the four strains, the gene encoding the nonribosomal peptide synthetase (NRPS) TriE exhibited at least 90.0% sequence identity to that found in the other strains (see **Table 4**). The nucleotide sequences for the *fusA* and the *triE* genes from the four strains are presented in **Table 5**

and **Table 6**, respectively. Without wishing to be bound to any theory, the expression of fusaricidins and tridecaptin in these strains may contribute to their capacity to effectively colonize plants and prevent plant disease.

Table 3. Percent identity matrix created with Multiple Alignment using Fast Fourier Transform (MAFFT) for the *fusA* genes from *Paenibacillus* sp. strains NRRL B-50374, NRRL B-67721, NRRL B-67723, and NRRL B-67724.

	Percent Sequence Identity			
Strain	NRRL B-67724	NRRL B-50374	NRRL B-67721	NRRL B-67723
NRRL B-67724	100.00	97.34	97.80	90.51
NRRL B-50374	97.34	100.00	98.18	90.71
NRRL B-67721	97.80	98.18	100.00	90.67
NRRL B-67723	90.51	90.71	90.67	100.00

Table 4. Percent identity matrix created with MAFFT for the *triE* genes from *Paenibacillus* sp. strains NRRL B-50374, NRRL B-67721, NRRL B-67723, and NRRL B-67724.

	Percent Sequence Identity			
Strain	NRRL B-67724	NRRL B-50374	NRRL B-67721	NRRL B-67723
NRRL B-67724	100.00	97.58	97.65	90.06
NRRL B-50374	97.58	100.00	98.48	90.28
NRRL B-67721	97.65	98.48	100.00	90.09
NRRL B-67723	90.06	90.28	90.09	100.00

Table 5. Nucleotide sequences of genes encoding the fusaricidin synthetase (*fusA*) in *Paenibacillus* sp. strains NRRL B-50374, NRRL B-67721, NRRL B-67723, and NRRL B-67724.

Strain	SEQ ID NO:	Sequence
NRRL B-50374	1	ATGAATGACATGCAGTTATATGATTTAAACAAATGCGCAGAAAGCGTATATGGTATACCGAATTAATCTCTACCCAGATACG TCAGTGTCAACAGCTTCCGGTACAGCTAAGATGAAGGGGCATATCAATATGCTGCCCTTTATGCAAGTCCATTAATTTG ATTATCAACACAGTATGATGCTCCGATCCGTATTACCTCAGTGGATGGAGTGCCTCAGCAGTACGTCGTTCCCTTAT GAAGAGAGACAGCTGGAGTGCCTGGATCTTAGCCACTATGAAGTGTATCTGAGGTGGAAGCCCTTACTTGAGCAACA CAAAAGCAACCTTTGCCCTGCTGGATTCTGAGCTCTTCCAGTTTAAATGTGAAGATTAGCGAGGAAGAGTATTG GATTAAATCAAGATGCACCATAATTATTCTGACGGAATATCAATGGTGTCTATGGCAATCAGCTGACAAACATTTTA CATGGAGTTAAATCAAGGAATGAACCGAAGCTGGCGACGATTGCTCGTATATTCAATATATTGCAGATGAGAAATG CATACGAACCTTCTGACAGATACCAAAAGGATAAAGGCTTACTGGCTGGATAAAATTTTCTGATTTGCTGAGCTTACGG GTTGGAAGTCATATAATCCGTTATCTTTAAGCACCCACGCCGTTCCGGAGCATTTTACCGTACCAGAAAGTCTATATC ACGAGCTGCAAGCATTTTGCCAAACAGACAGGATTTCTTTGTTCCAGTTCTTCAATGGTGCGATGTATATCTACATAC ACAAATGACGAATCAGCCGATGTGGTATTGGCACTTCGTTCCGTAACCGGGGGAACAAAGAGAGAAAGCAAAA GATAGGTATGTTTGTCAACACCGCTGCTGCCAGAACATACGTCAAAAGGATATGGATGTGTGAGCTTCCCTGCAGG ATGTAGCCAGAGATCAGATGTCAAGTCTCGCGCATCAGAAAGTATCCGTACAAATCAGTTAATTCAGGATCTTAGAGAA ATGCATGGTAAACAGGATATTCAGCGGCTTTTGGCGTTTCAATGGAATATCGTCTTATCAATGGGTTGATTTGGAT GATGTCCGCTTTTGACGGATTATGATTTCTGCGGGGACGAAGTGAACGATTTCTGCTTCATATCGTGGAGATCCTG GATGAAGCGGAACCTGTAATGATGTCGATTATCGGACGGAGCTGTTTGAACGCAGTGAAAGTTAAGGACATGGTTTC CCAGTTGCTTACGATCGCCGAGCAGATCATTCACCTCAGCTTCTATCGCAGAGGTAACTTATTGGGTGAACC AGAAAGCAGTCCAATTTTGGCTCTTTCGGAAGCGCTGCAGTGCATTAATCCACGTGAGAGACCATCCATGGCTTATT CGAGGAACAAGCCGAGCGCACGCCAGATCACGTAGCCGTTTCAGATGGACGAACAGAGCATTAACATACCTAGCTCTAA ACGAGCAGGCTAACAGCTTGCAGATATTTCGCTCCGAGGAGTAGTTGCAGATACGCTCGTAGGGATTATGGCT GACCGTTCTTGGAGATGGTCAATGGGATGTTGGCCATTTTGAAGCAGGTGGTGCCTATGTACCGATTGACCCCGAT TATCCCGAGGAACGTATCCATTATATGCTGGAGGATTCAGGGGTCCTGTGTGCTCACCCAAAGTCACTATAGGGAG AGCACCACTTTTGAACGGAAGCTTGTGAGTTGGACGAAGCTACAACGTATACAGGAGATGCTTCCAAATCTGGAGAG TATTTGGGACCAAGCCATCTAGCCATATGTTATCTACACGTGCGGTACGACCGCAAGCCGAAGGGCACGCTGATTG AACACAAATAATGTGTTGCTGCTCTTTAACGATAAAATCTATTGATTTACGCTCTCAGGATACGTGGACGCTAT TCCATTCGTTCTGCTTCGATTTCTCCGTTGGAGATGTACGGAGCGCTTCTTACGGAGGGAATTTGGTGTGTTCC ATCTCTCACAGCCAAGAGCCCGACGCTTCTTCCGAGTTGTTGAAAGACAAACCAAGTCAACCAATTTTAAATCAGACGCC

Strain	SEQ ID NO:	Sequence
		GACGTATTTTATCAGGTGCTACAGGAAGAGTTAACGCACCTCTTCGACAGAGCTTGGCCCTTAGAAAAATCATTTTGG TGGAGAGGCCCTTAAGTCCATCTCTCTGAGAAACTGGCGGGTCAAGTATCCTGATGTGCAGCTGATTAATATGTACGG AATTACGGAAACAACGGTCCATGTCAACCTACAGGAAATCACGGAACATGAGATTGAAGCGGGAAGCAATATT GGCAGAACGATCCCCACACTTAGCGCTTATAATCTCGATGAGCAAGACGGCTGCAGCTGTGGGTTCCGGGAGA GCTATACATTGACAGGGACGGTCTTGCCCGTGGTAATTTGAATCGGCCGGAATTTGACGTCTGAGAAAATTCGTTGAGCA TCCGTATCGGGGGAGAGCGGCTGTACCGAACTGGGATCTTGCTCGTTGGTTGCCCTGATGGCAATATTGAATATT GGACGGATCGACCATCAGGTCAAAATTCGCGGCTACCGAATTGAGCTTGGCGAGGTAGAACGCCCAATTCACAAGG CTCCGAACGTACGAGAAACGATTGCTCCGACGGGATGACGAACAGGGCCAAAATTTGCTGTGGCCCTACTATGTA GCCTCCAGTATCTTTCCCGGGGAAATTGCGGTCTCAGCTGGCAGCGGAATCTCCCGCTTACATGATTCCTTCTTATT TTGTCCGGCTGGAGCAAAATGCCGCTTACGCCAAATGGCAAACTGGATCGCCGTGCTGCCGCTCCGAAAGCAGC GTACAAATCCGGCGAGGCTTAATTTGGCTCCGAGAACTGCTGTGGAAGCTCAGATGGTACTCATCTGGCAAGATATCTTG GGATTGCCCGCGTGGTGCAGAGATAATTTCTTTGAAATTTGGTGGTCACTCTTTGGGGCAACAGTGTCTGTTTCA CGGATTCACAAAGAAATTTGGGATGTAGCATTTTCGTGGTGAGGTGTTTCAGTCCCTACCGTCTGAAATCCTTGGCGCAA CTTGTGAAATAACACATTCGACCTGTACGAATCCATCCACAGGCAACGGAAGCGAAAGCTTACCCAGTGTCTC AGCGCAAAAGCGGTTATACGTGCTGAGACAGATGGATGGGGAGAGCTTAGCTACAAATATGCCAGGGGCTTCACA GTGGATGGACCGTTGGATCGCACGCGGCTGGAGTCCGCTTCCAGGACTGATCCAGCGTCAATGAATCCCTAAGAAC CGGCTTTTATATGCAGGATGGAGAGCTTGTTCAGCGTGTGCATAGGAATGTGCCGTTCCGTTGAACATACAGAGGC TTCGGTGGAGGACGGATACGCTCATTCACAACTTTATTCGTGCCCTTTGATCTGAGCCAGGCTCCATTACTGCGTGT AGCTTGGTGAAGCTCCAGGAGCGTCTCTGTGCTGTTGATATGCATCACAATTCATTCAGATGGGTTTCTATTCTC AAATATTGATACAGGAACCTTACTCATTTGTATCAAGGAGAACAGCTACCAAGACTGCACATCCAAATACAAGGATTAT GCCGTATGGCAACGAGAACAGTCAGAGAACCAATGGCAAGATCTTGAGAAATATTGGCTGCAATCCTTTTGAAGGAGA GTTGCCGGTATTGGATTGCTACAGACTTCCAAACGACCTTCAAGTTCGGAGCTTCGAGGGTAGCCGAATTGATTTTAC ATTGGATGAGTCTGGAAATAAGGCGATACAGAGCTTGATCCCGTACAGGTACTACACTGTATATGGTATTGCTGGC CGCTTATTCGGTACTACTGCACAAATATACAGGACAGGAGGACATCGTCGTAGTTCTCCAGTAGCCGGAAGACCCG AGGCTGAGCTTGAGGCAATCATCGGAATGTTGTCAACACACTGGCTTGGCAGCTACCCGCGCAGGAGATAAAACC TTTCAGGATTATCTTCTGAAATCAAGGAACGGCGCTCAAGCGGTTTGAGCATCAGGATTACCCCTTTTGAAAAATTG GTCGAAAAGCTGGCGTAGGACGTGATGTACGCCGAATCCGCTCTTTTGACACCTTATTGGTATTACAAAATACCCGAG CAGGAAGAGCAGGATATGGACGGAGTGCACTTTACTCCTTACTTGATGGACACCGTACAGCCAAATTTGACCTGTCC CTCAATGTAGAGGAGAGGATCAAAATTAGCCTTTGGCCTCGAGTATAGTACGGCTTTATATCGGCGTGAAGTGT AGAGCGACTTGCAACGCACCTTGCTCCGGGTTCTGCAATGCAGTCTCGGCCAATCCTCAGTTGCAACTGGCCGAGATTGA

Strain	SEQ ID NO:	Sequence
		AATGATCACACCGGAGGAGAAAGTACAGATCGTTGAAGTATTTAACGCGACATCGGCCCTTATCCAAAGGACAAGA CCATTTCATGATCTGTCGCGGAACAAGTCAAGCGTACACCGGAGCAGACGGCGCTGTATTTCGGCGATGTCCAGCTA ACGTACCTTGAAATTGGAAGACAAGGAGCCGACTGGCCCAACAACACTGCGTCGTTTGGGAACGTTGAGGGAGCAGCC TGTGCCGTGATGGCGGACGAAGCAATTGAGATGGTCAATTGGTATGCTCGCGGTGCTTCAGGCAGGTGAGCCTATG TGCCGATTGATCCTGATTACCCGGAAGATCGGGTTCGTTATATGCTTGATGATTCGACGCCAAGCTATTATTGGTGC AAAAGGCGAGCTTATAAGTGTAGACTACGGTATACCGATTGTCGATCTTAGCAGTGAAGAGGCTTATGCTGCTGAG CCTGCCACCGGAGACGGCTCAGGGATCGCAGGGCTTGCTTATGTCATCTATACATCGGGTACGACGGGTAGACC GAAGGGCTTATGGTTGAACACCGGAACGTTGGTCCGTGGTCAAGAGACCAACTATGTGGAGCTGAATGAATCCA CAGGAATTTGCAAACAGGAGCCGTGGCTTTGATGCTTCTACATTTGAGATATGGGAGCGTTGCTTAACGGTGGGC AGCTCTATTTGTAGAGAAATGACGACATCTCTGATTGCTGATAGGCTCAAAGCGGCTATTGCCAAGTACGGGATTACAA CATTGTGGCTTACTCACCCCTTTTCAATCAGCTTCTCTGCAAGGATGATACCTGTTTCAGAGGGCTAAAGCATTTGTT AGTCGGCGGTGACGTACTGCTCTATCTCATATGAATCGTGAATCGAGGCTAATCCTGATCTTGTCCTCATCAATTGC TATGGTCCGACAGAGAATACGACCTTCTCCACCCTCAAGATTCAGGTTGTGCCGAAGGGGGTGTGCCGATTGGT CGCCCAATTAGTAATTCGACCGCTTATGTGGTCAATGGATCGCTGCAATTACAGCTATTGGTGTCTGGGTGAATC ATTGTCGGCGGTGAAGGTGTAGCAGCGGATATCTCAAATCGTCTGATCTCACAGCAGAGAAATTGTTCCTAGTCT GTGAAGGACGGAGAACCTGTCTACCGAACTGGGATTTGGTACGCTGGCTTCCAGATGGGAATTTGGAGTTTAAAGG AAGAAATTGATGAGCAGGTCAAATAACGTGTTACCGCATCGAACTCCCTGAATCGAGGCCCAACTGGCCAAAGGTGG AGTCGGTAATCGACCGCGTAGTGTCTGTCGCGGACGAGCTTGGCGAGAAAGCAGCTTTGCGCTTATTATGTGGCG GATCGTACGCTACGGCAGCGGAAGTACGCTTCTCCCTATCGCAGGTACTTCCAGGCTATATGATTCCTACTTTA TCCAGATGGATCGTATGCCATTAAACATCAAACGGAAAGGTGGACCGCAGGTCTCTGCCGGCTCCTCAAGTAGGCGCG CATACAGGACGGAAATACAGCTCCTCGTACACCGGCTGAGGAAGCTTTGGCATCTGTCTGGCAAAGGGGTGCTGGG TGCCGAACAGGTGGGTATCCATGATAATTTCTTTGAATTGGGTGGAGACTCCATAAAAGCTATCCAGGTGTCGTACAG GTTACTACAGCGCGCTATCGGTTAGAGATGAAGCAGCTGTTCAAATCGCCAACTTGGCGAGCTAGGAGCGGAA TACAAACGGCTGTGCATATGGCTGAACAGGGAGTTGTGCGTGGAGCGACTCGCTTGACTCCAGTCCAAACAGTGGTCT TTGGACGGAAGCAGGACGCTCATCACTTCAATCAAGCGGTTATGCTGTATCGTGAACAGGGAATTTGAGGAAAAAG GCCTTGCTCAGGTGCTAAGAAAACCTCGCTGAGCATCATGACGCCCTTCGCAATGGTTTCCGTCAGACAGAGCATGGT TACGAAGCTTGAATCGTATCTTGAAGAAGGAGAGCTTTATAGCCTGTTTCAACCGCTGATTTACGGAAATGAATCCGAT CCGGCTGCAGCCATTACATCGCTGTCGGATGACATTCAGCGCAGTATCAATCTGGCAGAGGCCCGCTGCTGAAGTTA GGACTTTTCCATTGTCAGGATGGAGACCCTTCTGATCGTATCCACCAATTTGGTGGTGGACGGAGTATCCTGGCGG ATTTTGTTCGAGGATATTGCAGCAGGCTATGAGCAGGTGATTCAAGGACAAGCGCTGACATTCCCCGCAGAAAGACGAA

Strain	SEQ ID NO:	Sequence
		TTCCTCCGTGACTGGGAGACGCCCTTGCTCGTTATTCGGAAAGGTCCTGAAATGGAGACTCATCGGGCGTATTGGAG GGAGCTGGAGAATCAGCCACTCGAAGAGTTGCCGAAGGATGAGGCTGTGGAAGAGCCCTCTTTTACAGGATAGCAAAG TAATAACAGCAAAATGGACTATAGAAAGAACCGACCAATTTGTGAGAAAGCCCATCGTGTCTTATCAACAGAGACG AATGATCTGCTATTGACTGCTCTGGGCAATGGCGTATCCAAATGCTGTGCAATCGGAAAGGTTGCTGTGAATCTGGAA GGACACGGTCTGTGAGCCGATTATACCGAATATCGACATACCCGTACCCGTGCTGGCTGTTTACAAGTCAATACCCGGTG ATTTAGACTTGGGGATGACCCAGAAAGTGGCTCCTTGATCAAGTCTGTGAAGAAGAGGCTGCGCCGAATTCGAA CAAAGGTATTGGCTACGGTTGCTTAAACGATGGCAAGTCAGTTGGATGAAGACAGCTTCAGCTTGCAGCCCTGAGA TTTCTTTTAACTATTGGGGCAATTTGATCAGGATTTGCAAGGAGCTGTTGCAGATTTCCTCTATCCGACCCGGAAG CGCCAAAGCTTGTGGAGGAACAGCCTATACGCTAGATATCAATGGCATGGTGACGGACGGAGCCCTGACTCTGA CGATTACTTATAACGGGAAAACAGTATAAGTTATCTACGATGGAAACAGCTCGCTGGATATATTGAAGAAAAGCCTGCGA GAGCTTCTCAGCATTCGTAACCCAAAGAAAACCCGTATTGACACCAAGCGACGTGCTTGCGAAGGGTCTAAGCAT TGCCGATCTGGAGAGCTTCTAAGCAGATCAGCCACATAGGCGATATTGAGAATGTATATAGTCTGACGCCGATGC AGAAGGCATGCTGTTCCATGATATGTTGAGCCGATACAGGTGCTTATTTGAGCAGGCTGCCCTTGTACTTTAAGG GTAGCTTTGATCCGACTGCAATTCGACACAGCTGCTGGATGCCGTGGAGGCTATGCCATCCTGCGCACGAACCTTT ACAGCGGATGGGACGAGCCTTTCAGGTTGTATTTCGACACAGAGCGCTAAATTTGGTGTACGAAGACCTGCGT GAGATGAATGCATCGCAGCGGAAGCTTACCTGAAGACATTTGGTGCTAAGGACAAAGCACAGGGCTTCAACCTAGC TGAAGACGAGCTTCTCCGTGATCAATTTACAAACAGATGAAGAGAGCTTCCGACTCTTATGGAGCTTTCACCCACAT CGTCATGGATGGTGTGTTCCGTTAATACGCAGGAGGTATTGAACACTATTTTGCCCTCCTGTGAAAGGAAGA GCCGAGCTGGCAGAGGTCCATCCGTACAGTCGATATATCGAATGGCTGGAACAGCAGGATGAAGCATGTCGTCCA ACTATTGGAGCCGATATCTGGCCGGTTACGAGCAGCAGCCTTTTACCTCAAGTGGTGGAGCAAGTAAGGGAGAA GGCTATGTAGCAGAAAGCTGAATTAATCCTCTCAGCAGGGAATTTGACTGAGCGCTTGAAAAGGTGGCCAGGGATGC TCATGTCAGATGAATATATTGCTGAGTCCCTCTGGGGCATTTGCGCTTCAACGCTACAACGGTAGCCGGGATGTCGT GTACGGAAAGTATCAGGCCGACAGCAGAAATTCGGGCAATGACCGGATGATCGGTTTGTTCATCAATACGA TTCCCGTTCTGTGAAGACAGAGGAGAAATCTCCCTTTCACCGTTCTGATGAAGCAGCAGCAGGAACAATATATGGCTT CTCAATGTATGACACCTACCCGTTGTTGAGATTCAGGCTCAGACGGATCAGAACGAGGATCTAATCTCCCATATTA TGGTGTGTTGAGAACTATCCTGTGGAGGAGGAGGTAGAGCGTCTGGGTGGTGGCGAGGCTGCTTGTGAGATTGAGGAA GCGGAGCTTCTTGAGCAAAACGAATTATGATTTTAAATTTAATGTCTCCCTCCCTGGCGAAGAGATGAGATTGCTGTTCAG TACAATGCACTGTTTATGACCAAGTGACAAATGGGCAATCAAGGGCCATCTGTTTACCTTATGGAACAATATGTA GAGAACCTGCTATTTCGTTGATCTAGAAATTAGTACGCCGACGAGAGAGAACAGATTCTGAACGTATGGG AAATATGAAGGCAATTCAGAGCACTGTAAACAGTTCCACGGCTATTGGAGGAACAGGGGACGAACGCCGGAT

Strain	SEQ ID NO:	Sequence
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Strain	SEQ ID NO:	Sequence
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Strain	SEQ ID NO:	Sequence
		ATCTGGGTGACTCCATCAAGGCGATCCAAGTGTCTCTCGAGATTGTTCCAAAGCTGGATATAAATTAGAGATGAAG GATCTCTTCAAATATCCGACAATTGCCGAGCTAAGCCCGTATCTTCAGGCAGCTGGACGTATAGCGGAACACAGGGTGA AATTAAAGGTGACAGAGTTAATGCCAATTACAGCGTTGGTTCTTTTGAACGCCATACAGCGGAGCCGACCATATA ATCATGCCGTCTATGCTCTATCGGAAAGACGGCTTTGATGAGGCTGCACTCCGTTGACAAATGACCAAAATTGCGATCC ATCATGACGCGCTGCGCATGTTTTCGGCCCTACAGAAAGCTGGATACGCAGCTTGGAAATCGGGGAACGGACGAAGGC GAGCTCTACACATTGGACATTGCCGATATGCCGAGGCGGAAGACAGACAGCTGCGGTTACAGGCCCAAGCCGATGC CATTACGGCAAGCTTTGACTTGGAAAGGTGGCCCACTGTTCAAGCTAGCCCTGTTCCATTGTGACGATGGCGATCATTT GTTGATTGTCATTACACCTCTTGGTTGACGGCGTATCCTGGCGCATCCTGTTTGAGGACATTGCAGCGGGGTACGA GCAGGCAATGGAATGGACAAGCAATCGTCTTCCACAAAGACCGATTCTGTATCTTGTATGGTCTGAGCAAGCGACGA AGTATGCAGCAGGGCTGCTCTGGACAAGGAGCGTGCATACTGGCAGCTGATCGAGGCGGATTTTGGCTCCACTG CCGAAGGATGAGGATCAGAAAGCCGGCACCAATTCGGGATACCTGAATCGGTTACGGTAACGTGGTCTGCGCAGGAAA CTGACCTGCTGTGGACAAGCGAACCCGGCGTATCATACGGAGACGAATGACTTGTCTTGTACTGCTCTGGGGCA GCCATTACAGCGCTGGACAGGCATGGAGCAGATTTTGGTCAATCTTGAAGGACATGGACGGGAAATAATCGTACCCAGA CCTGGATAATACCCGTACCGTGGTTGGTTTCCACAAACCCAGTATCCAGTTCTGTGAACTGCAAGGCAGACAGGAAGT ATCTGCGGAAATCAAGCGCATCAAGGAGATTTCGAGAGGTTCCGCATAAAGGAATCGGCTACGGTCTTCTGAAAT ATATGGCACCGGAGAAAAGTGTCCGACTCGGCGTGGAGCCGGAATTTCCCTTCAATTAATCTTGGGCAAGTTTGATCAG GATTTGGAGGGTAATGCCCTTAGCCTATCCACACATTCAGTTGGTAAAGCGCTCAGCGATCTCACACCCACAGCAATAT GCTCTGGATGTGAATGGCATGATTGCCGAAGCCAGCTATCATCTGACGATTACGTACAGCAGCAGGCAGTATCGTAA GGAGACGGTGAGTCAATTTTGTGAATTAATACAGTCAAGCCTTAGTGAGGTCACTCCGTCAATGTGTGGCTCAGGAGCG TTCACAGCTTACACCAAGTGTATGTTCTGTTCCAAAGGATTAACATTGGAGCAGCTTGAATCGACTCAGCGGCGCAGACGGC TCACATCGGAGAGATTGAGGATGTGTACAAAGCTGACGCCGATGCAGAAAGGGAATGCTGTTCACAGCCTACTGGAGC CGGGCTCCTTCATACCTTCGAACAGGCAACGTTTGAAGCTGCGTGGCAGCTTCGATGTAGATACCTTCTTCGAGAGCT TCCAGGCTCTGGTGCAACGACATGCCATACCTACGTACCGGCTTTTACAACAACATTTGCTGATGTACCGCTGCAAGTTG TCTTTAAGCAACGGTTAATCCCTCTGCACTACGTAGATTTCGGCGACGCACTACGCAGGAACAAGAGCCCGAATCA AGGCTTATATTGCTGAAGATATGGTTAAGGGTTTCGGCTGTGCAAGATCCCGTGTATGCGGGTGACCGCTCTTGACGA AGGATCAAGCTGCTTGTATTGTGGAGCTTCCACCAATATTGTCAATGGATGGCTGGTGTATCCCGATCATTAACACAGG AGCTGTTCTGATTATTATCTGCCAAGAAACAGCAAGTACAGCCTGTCTCTACCGCCAGCTCAGCCCTATAGTCTGTTATA TCGAGTGGCTTGATGCACAGGATGATCAAGAGCTTCAACGTATTGGAGCCAAATATCTCGAAGATTATGACGGGAAT ACTGTAATGCCGGAAGTAAACGAAATCTCAAGCCAAAGAGCGGGCTATGTTCTAAAAGAGCATGTTCTCTCCATCT GGGTGTATCTTTGACAGGTAAAATGGATGTTGTCTCGGAAGCGCAATCACGTGACCGTCAACACACTCATGACAGACAG

Strain	SEQ ID NO:	Sequence
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Strain	SEQ ID NO:	Sequence
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NRRL B-67721	2	ATGAATGACATGCAGTTATATGATTTAACAAATGGGCAGAAAGCGTATATGGTATACCGAATTACTCTACCCAGATAC GTCAGTGTACAGCTTTCCGGTACAGCTAAGATGAAGGGCACATCAATATTGCTGCCTTTATGTCAGTCCCATTAATTT GATTATCAACAGTATGATGCGTTCCGCATCCGTATTACCTCAGTGAAGGAGTGGCTCAGCAGTACGTCGTCCTTA TGAAAGAGACAGCTGAGTGCCTGGATCTTAGCCACTATGAAAGTGTATCTGAGGTGGAAAGCCTTACTTGAGCAAC ACAAAGCAAGCCCTTGCCCTGTTGGATTCTGAGCTCTCCAGTTTTTAATTGTGAAGATTAGCGAGGAAGAGTATT GGATTAAATATCAAGATGCACCATATTATTCTGACGGAATATCAATGGTGGTCTATGGCAATCAGCTGACAGCATTTT ACATGGAGTTAATTCAAGGAATGAACCGAAGCTGGGCGACGATTGCTCGTATATTCAATATATTGCTGATGAGAAAT GCATACGAACCTTCTGACAGATACCAAAAGGATAAGGCTTACTGGCTGGATAAATTTCTGATTTGCCCTGAGCTTACG GGTTGGAAGTCATATAATCCGTTATCTTTAAGCACCCACGCCGTTCCGGAGCAITTTTACCCTACCAGAAAGTGTATAT CACGAGCTGCAAGCAATTTTGCCAACAGAAACAGAAATTTCTTTGTTCCAGTTCTTCAATGGGTGCGATGTATATCTACATA CACAAATGACGAATCAGCCGATGTGGTATGGAACCTTCGTTCCGTAACCGGGGAAACAAAAGAGAAAGCAAA AGATAGGTATGTTCTGTCAGCACCGCTGCTGCCAGAACATACGTCAAAAGGATATAGATGATTGAGCTTCCTGCAG GATGAGCCAGAGATCAGATGTCAGTCTCGGCGATCAGAAATATCCATACAAATCAGTTAATTCAGGATCTTAGAGA AATGCATGGGAACAAGGATATTCAGCGGCTTTTGGCGTTTCCATGGAAATATCGTCTTATCAATTGGGTGATTTGGA TGATGTGCGTATTTTGACAGATTATGATTCTGCGGGGACGAAGTGAACGATTTCTGCTGCTTATATCGTGGAGATTCT GGATGAAGGCGAACTGTAAGTGTGATTATCGGACAGAGCTGTTTGAACGCAAGTGAAGTTAAGGACATGGTTT CCCAGTTGCTTACGATCGCCGAGCAGATCATCTACCTCAGCTTTCTATTGACAGAGGTAACCTTATTGGGTGAAC CAGAAAGAGCAATCCATTTTGGCTCTTTTCGGAAGGCGCCGAGTCGATTATCCACGTGAGAAAGACCATTCATGGCTTAT TCGAGGAACAAGCCGAGCGCACACAGATCACGTAGCCGTTTCAGATGGACGAGCAGATTCATACCAAGCTCT

Strain	SEQ ID NO:	Sequence
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Strain	SEQ ID NO:	Sequence
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Strain	SEQ ID NO:	Sequence
		GTCACGGTTACTGCAGGCCGGCTATCGGTTAGAGATGAAGCAGCTGTTCAATCGCCAAACCAATTGCCGAGCTAGGCG CGGAAATTCAAACGGCTGTGCAATATGGCTGAACAGGGAGTTGTGCGTGGAACGACTCGCTTGACTCCAGTCCACACAG TGGTCTTTGGACGGAAGCAGGCATCATCTTCAATCAAGCGTTATGCTGTATCGTGAACAGGATTTGAG GAAAGGCCCTTGCAATCAGGTGCTAAGAAACTCGCTGAGCATCATGACGCCCTTCGCAATGTTTCCGTCAGACAGA GCATGGCTACGAAGCTTGAATCGTGATCTTGAAGAAGGAGAGTTGTATAGCCTATTCAACCGCTGATTTACGGAATG AATCCGATCCGGCTGCAGCCATTACATCGCTGTCGGATGACATTCAGCGCATATCAATCTGGCAGAAGTCCGCTGC TGAAAGTTAGGACTTTTCCATTGTCAGGATGGAGACCCTTCTAATCGTGATCCACCATTGTTGGTGGACGGAGTAT CCTGGCGGATTTTGTTCGAGGATATTGCAGCAGGCTATGAGCAGGTGATTCAAGGACAAGCGCTGACATTCGCCGAG AAGACGGATTCTTCCTGACTGGGGAGACGCCCTTGTCTGTTATTTCGGAAGTCTCTGAAATGGAGACTCATCGGGC GTATTGGAGAGAGCTGGAGGATCAGCCACTCGAACAGTTACCGAAGGATGAGGCTGTGGAAGCCCTTCTTTACAGG ATAGCAAAGTAGTAACAGCACAAATGGACTCTAGAAGAAACCGACCAATTGTTGAGAAAGCCCATCGTCTTATCAA ACAGAGACGAATGATCTGCTATTGACTGCTCTGGGCATGGCGGTATCCAAATGGTCTGGCATCGGAAAGTTGCTGT GAATCTGGAAGGACACGGTCGTGAGCCGATTATACCGAATATCGACATCACCCGTACCGTAGGCTGGTTACAAAGTC AATATCCGGTGATTTAGACTTGGGGGATAACCCGGAAGTGGCCTCCTTGATCAAGTCTGTGAAGAAGGGCTGCCG CGAATTCGGAACAAAGGTATTGGCTACGGGTGCTTAAAGATGGCAAGTCAAGTTGGATAAAGACAGCTTCAGCTT GCAGCTGAGATTCTTTTAACTATTGGGGCAATTGATCAGGATTGCAAGGAAGCTCGTTGCAAGATTCTCTCTTAT CCGACCGGAAGCGCCCAAGCTTGTGGAGAACCGGCTATACGCTAGATATCAATGGCATGGTGACGGACGGAG CCCTGACTCTGACGATTACTTATAACGGAACACAGTATAAGTCACTACGATGGAACAGCTCGCTGGATATATTGAA AAAAGCCTGCGGAGCTTCTCCAGCATGGCGTAACCCAGAAACCCGATTGACACCAAGCGACGTGCTTGGCGAA GGGTCTAAGCAATTGCCGATCTGGAGGAGCTTCTAAGCAGACCGCACATAGCGGATATTGAGAAATGTATATAGTC TGACGCCGATGCAGAAGGCAATGCTGTTCCATGATATGTTTGAGCCGCATACAGGTGCTTATTGAGCAGGCTGCCT TTGACTTTAAGGGTAGCTTTGATCCGACCGCTTCGGACACAGTCTGGATGCAGTGTGGAGCGTCATGCCATCCTGC GCACGAACCTTTACAGCGGATGGGCGAGCGCTTTGACAGTTGTATTTCGGCACAGAGCGCTAAATGGTGTAC GAAGACCTGCGTGAGATGAATGCATCGCAGCGGAAGCTTACCTGAAGACATTTGGTGCTAAGGACAAAGCACAGG GCTTCAACCTAGCTGAAGCAGCTTCTCCGTGTATCAATTTTACAACAGATGAAGAGAGCTTCCGCCCTTATGGA GCTTTCACCAACATCGTCAATGGATGGCTGTGTTCGGTTAATTACGCGAGGAGTATTGGAACACTATTTTGCCCCCT GGAAAGGAAGAGCCGCGAGCTGGCAGAGGTTTCATCCGTACAGTCGATATATCGAATGGCTGGAACAGCAGGATGAA GCAGTTGCGTCCAACTATTGGAGCCGATATCTGGCCGGTTACGAGCAGCAGACGCTTTTACCTCAAGTCGGTGGAGC AAGTAAGGGAGAAAGGCTATGTAGCAGAAAGCTGAATTATCCTCTCAGCAGGGAATTGACTGAGCGCCTTGAAAAG GTGGCCAGGGATGCTCATGTACAGATGAATATATTGCTGCAGTCCCTCTGGGGCATTTGGCTTCAACGCTACAACGGT

Strain	SEQ ID NO:	Sequence
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Strain	SEQ ID NO:	Sequence
		ACAGCGGAGCGAGAGCATTATCCATTGTCTCTCGGCCCAAAAACGACTGTTTATTCTAAGTCAGCTGGAAGGTGG AGAGCTGAGCTACAATATGCCGGGTATCCTTACCGTTGAGGGAGCTTTGGATCGGGAACGGCTAGAGCAGGCATTCC GTCGTCTAATTCATCGTCATGTTCCGTACTCGTTTGTGACCGTGAAACGGTGAAACCTGTACAGCAGCTCCTGA CGGATGTTCCGTTTACTGTGGAATATGCGGAGTTGAGCGAGGAAGAGGCTACCCCTTCAGCAGTGTGTCCTGT CCTTTGATTAGGTAGCTCCATTGCTCGGGTCTGGCCTTATTCGAAATTGCACATGAGCGCCATTACTATTGTTTG ACATGCATCATAATTGTCTCAGATGGGTTTCTATGAATATTCTCATAGAAGAGTTTCTCCGCTTCTACCAAGAGGAGG ACGTATTCCCTGAACACTACAGATCCAGTACACAGACTATGCTGTATGGCAGCAAGAGCAGCTCGGAAGCGAGCGTCTT AAGCCCCAGGAAGCTTACTGGCTGGATGCTTTCCCGGGAAGCTTGCCAGTGTGATTGCCCAGGAGATGAAGTTCCG TCCTGGGTGCGAAGCTTTGCGGGGATCGAATCGACTTCCAAATTGATTCTCTGTAGTGTCTTCACTTCAGGAGCT GGCTACCCGAAACGGGTTCCACTCTGTTTCAATGTTACTGTGTGAGCCTATACGGCGCTCTTACACAAGTACACAGGTCA GGAAGATGTCATTGTGCGTTTCACTGTGCGAGGAAGATCCCATGCGACACTCGAAGGCCCTCATCGGTATGTTCTCGG CACAGTGGCACTTCGTACTTATCCAGAAAGGAGAGAGCCCTTCGAGGCTTATCTGCAGAAAGTGAAGGAACAACAGCGC TGCGGGCTATGAAAACCAAGGATTACCCGTTCCGAGGAGCTGTAGACAAGCTGGAGCTTCAGCGTGAATTTGAGCCGT AACCCTGATTGTATACCATGTTTGTCTGCAAAATATTGAGCAGGGAGAACAAAGAAATAGAAGATTGCGCTTCAC TCCTTACGATAATGTACATCCGGCTGCCAAGTTGATCTCACGCTGACCGTGAAGTGAAGCAGCGGGGTATTGAACGTG CACGCTTGAGTACGCGACTGCGATCTACAAAAGAGAGACTGCCACGCGGATGCGAGGCCACTTTGTACAGCTTATTTC GGGAAGCCGTCTCCAATCCGGGAATGCCGTTGTCTATCCCTTGATATCGTGACACCTCAGGAAAAATCAAGGCTGATG AAAGCCCGGACGAAGCCAAAGGCAGATTATCCTCGTGACAAGACGATCCATGCGTGTTCGAGGAACAGGCTGCAC GTACTCCGAATGCAGTGGCAGTCGTATGTGAAAATGCAGCCCTGTCTACAGCGAGCTGAACGAGCGGGCCAAATGGA CTTGCCAGAACGCTAAGGGAACGTGTTTGCACACGACGGTTTGGCTGGAATCATGGCGGATCGTTCCCTTGAAAT GGTGTGCGGAATTTAGCCAATCTTGAAGGCAGGCGGAGCCCTATGTCCCTGTAGACCCCTGAATATCCAGAGGACCGCA TTCGCTTTATGCTTGAGGATTGCGGAGCCAAAGCTACTGCTGACACAAGCGCATCTGGAGCAACGTGCTCTCTTCGCTG GGGACATCGTGAGTCTGGATAAAATGGCTTCCTATAAGGAAGATGTCTCAACCTGCAGCCTGCAGCCGGACCCGGAG CATCTTGCCCTACGTCATCTACATCAGGTACGACAGGCAAGCCAAAGGGAACGCTGATCGAGCATAAAATGTAGT TCGCTTGCTCTTTAATGATAAAATATGTTTGACTTTGGTCCCTCAGGATACGTGGACACTGTTCCTCATCTCTGTTT GACTTCTCTGTATGGGAATGTACGGAGCATTTGCTGAACGGAGGACGGTTGGTTCATCGTTCCATCGCTTACCGCGAAG AGTCCAGATCGTTTCTTGCAATTGCTTAAGGATCAGAAGGTACCCGTTTGAACCCAGACACCGACGTACTTCTATCAG TTGCTACAGGAAGAGCTCGGTATCAGGCGGCAGAACTGAGCCTCCGTATGATATCTTCGGTGGAGAGGCATTAGC CCCGCCCTGCTCAAGGACTGGAGAACGAAGTATCCGCAAGTGCAGCTCATTAACATGTACGGCATTACCGAAACGA CCGTGCATGTAAACATACAAGGAATTACAGAGTTGGAAATTGAACAGGGCCGCGAGCAATATCGGCCACACGATTCCA

Strain	SEQ ID NO:	Sequence
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Strain	SEQ ID NO:	Sequence
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Strain	SEQ ID NO:	Sequence
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NRRL B-67723	3	ATGAATGACATGCAGTTATATGATTTAACAAATGCGCAGAAACGTATATGGTATACCGAATTAATCTATATCCAGATACG TCAGTGTCAACAGCTTTCCGGTACAGCCAAGATGAAGGCCGTATCCATATCGCTGCCCTTCATGCAGTCCATTAAATTG ATTATCAAAACAGTATGATGCGTTCCGCAATTCGTATCACCTCAGTGGATGGAGTGCCTCAGCAGTATGTCTGTTCTTAT GAAAGAGACAGTTGGAGTATCTGGACCTTACCCACTATGAAGTATCTCTGAGGTGGAAGCCTTACTTGAGCAACA CAAAAGCAAAACCTTGCACACTGCTGGATTCTGAGCTATTCAGTATTTTGTGAAAGATTAGCGAGGATGAGTATTG GATTAATACCAAGATGCACCATAATTTCTGACGGGATCTCAATGGTGATCTATGGCAATCAATTGACGGAATTTTA CATGCAGATCATTCAGGAATGAACCGACGCTGAATGACGATTGCTCTTATATTCAAATATATTGCAGAAAGAGAACG CATACGAGCTTTCTGACAGATATCAAAAAGGACAAAGACATACCTGGCTCAATAAAATTTTCTGATTTACCTGAACTTACGG GTTGGAAGTCATACAAATCCGTTATCTCTGAGCACCCACGCGGTTCCGGAGCAATTTTACCGTGCACAGAGTGTGTATC ACGAGTTGCAGGCAATTTTGCCAAACAGAACAGGATTTCTCTGTTCCAGTTCTTCATGGGTGTGATGTATATCTACATAC ACAAAGTAACGAATCAGCCGATGTGGTATTGGTACTTCCGTAACCGTGGGAACAAAAAGAGAAAGCAAAA GATCGGTATGTTCTGTTAGTACGGCTGCAGCCAGAACATACGTCGAAAAGGACATGGATGTGCTGAGCTTCCTGCAGG

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		GTACGAAGACCTGCGGAGATGGACGAACGACGCGGAAGCTTATTGTGAAGACATTTGCTGCAAAAGGACAAAGGCA CAGGGCTTCAACTTATCTGAGGATGAGCTTCTACGTGTTTCGATTTTGTGTACAGGTGAGGAGAGCTTCCGCTCTTGT GGAGCTTTCACCAACATCGTCATGGATGGATGGTTCGTTAAATTACGACGAGGATATTGAACATTTATTTTGCCCC TCCTGGAAGGAAGAGAGCCTCAGTTGGCAGAGGTTACGCCGTACAGTCGATATATTGAATGGCTGGAACAGCAGGAT GAAAGCAGCTGCGTCCAACCTATTGGAGTCGATATCTGGCCGGTTACGAGCAGCAGACGCTTTTACCTCAAGTCGGGGA AGCAAGTAAAGGAAGGGTACGTATCAGAAAAGCAGAATTACATCCTCGCAGGGGAATTAACCTGGACGTCTGGAG AAGTAGCCAGAGATGCTCATGTCACGATGAATATATTGCTGCAATCCATATGGGGCATTTGCACCTCAACGCTATAAC GGTAAGCCGGGATGTCGTATACGGAAGTGTAGTATCAGGCAGACCCAGCAGAAATTCCGGGCATTGATCGGATGATCGG TTTGTTTCATCAATACGATTCCAGTCCGTGTGAAGACGGAGGAAATCTCCCCCTTCTCAGTTTGTGATGAAGCAGCAGCA GGAAACAATTTATGGCTTCCCATATGTATGACACCTACCCGCTGTTGAGATTCAAGGCTCAGACCGATCAGAAACAGGA CTTAATCTCACATAATTATGGTGTGAGAACTATCCTGTGAGGAGGAGTAGAACGCTCTGGGTGGTGGCGAGGCTGA CTTTGAGATTGAGGACGCCGAGCTTCTGGAGCAACGAAATACGATTTTAACTTAATTATCCTGCCTGGCAAAAGAGAT GAGATTGCTATTCCAGTACAATGCATTGTGTATGATCAAGTGACGATTGAGCAATCAAGGACATCTGTTTCACTT CATGGAACAAATTGTGGAGAAATCCTGCAATTTCCGTGGATGCTCTGGAATTGGTCAACGCCGACGAGGAGAGAGCTGA TTCTGGACGTATGGGTAAACACGAAAGTCAGTTACGAGCACTGTAAACAGCTTCCACGGGCTGTTGGAGGAACAGGCG GGACGAACGCCGAGGCGACTGCCAATTGTGTTTCGAGGATGAGATGCTGACCTATGCGCGAGCTCAATGCAAAAGCCAA CGGACTGGCAAGAAACTGCGTAATCAGGGAATCCAGAGGAGATCTGGTGGGCTGATTGCTGACCGTTCGTCGG AAATGATCGTTGGAAATCTACGGCAATTATGAAAGCCGGAGGTGCTATGTTCCAAATTGATCCAGAGTATCCGAAAGAA CGGATCAGTTACATGCTTGAAGATTCCGGAGCAAAAGCTGGTCTTACACAGGCCCGCTCTTGGAGCATCTTGGATGG ACGGAAATGTTTTGTGCTGGATGAACCATCGACATATGATGCCGATACCTCGAATTTGAAGGATACCTGTGGCCCG GATAATCTGGCTTATGTGATCTATACTTCAGGTACGACGGGTACGCCCTAAGGGCGTATTAGTCCGAACATCGGGGACTA CAAAATCTTTCGGACGTATACGGGACATACTTCGAAGTTACACCGCAGGACCGAATCGTTTCAAGTTTGCAGTCTGTCA TTTGATGCATCGGTTTCGGAAAGTTTAAACGGCACTAAGCCATGGGGCTGCTGTGTCATCCCTTCTACACAAGACATT TTAGATTATGCCCTTGTTCGAACAGTTTCATAACGACAAGGGAATTACGATAGCGACTCTGCCACCGCTTACGCTATC CACCTTGAGCCTGAGCGCTGCCAGCACTGCGATGTCTGCTTACCGCCGATCAGCCGCTCTGTCTCGAGTTGATCGAA AAGTGGAGGAAGCATGTACGCTACTCCAATGGCTACGGCCCCAACGGAGGACTCTATTTCGACCCACAATCTGGTCTGT TCCGGATAGCGAGGAACGCTGGAGACAGTATCCATTGGCCGACCTATTGCTAACCAATAGTGTGTACGTGTTGGATG AGCATCTCAGATTGCAGCCTGTCCGGCTAGTTGGAGAGCTATGCATTTACAGGTATCGGGTTAGCACGGGGTATCATA ACCGACCTGCATTAATGGACGAGAAAGTTTCGTCGAAAATCCGTTCACTCCAGGGGAGCGTATGTATCGGACAGGTGAC TTGGTTCCGCTGGTTACCGAACGGTACCATCGAATACGTGGGCCGAAATAGATCATCAAGTCAAAATTCGCGGCTATCG

Strain	SEQ ID NO:	Sequence
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Strain	SEQ ID NO:	Sequence
		TCTTGCTACGTACATCGGTACGACAGGCAAGCCAAAGGGAACACTGATCGACACAAAAATGTAGTTC GCTTGCTCTTAATGATAAAAAATATGTTGATTTCGGTCTCAGGATACGTGGACGCTGTTCCATTCTGCTTGA CTTCTCCGTATGGGAGATGATGGGGCAATTGCTGAATGGAGTCTGTCATCGTTCCATCGCTTACCGCGAAGAG TCCAGATCGTTTCTTGCAATTGCTAAAGGACCAAGGTCACCGTCTTGAAACAGACGCGGACATACCTTCTACCAAGTT ACTACAGGAAGAGCTTGTCATCACGCGGAGAACTGAGTCTCCGTATGATTATCTTCGGTGGCGAGGCAATTAAGCC CGGCTTGCTCAAGGACTGGAGAACGAAGTACCCACAAAGTGCACTCAACATGTACGGCATACCGAAACAACC GTGCATGTAAACATAAGGAAATTACAGATCTGGAATTGAAACAGGGCCGCAATATCGGTACCAAGATTCCGAC GCTGCGTGATACATTTCTGGATGAACAACGTCGTCCACAGCCGATTGGCATTCAGGTGAACCTCTACGTGGCGCG AAGACTGGCGCGGCTACCTGAACCGACCGGAATTGACGGAAGAAAGTTGTGCTCATCCGTTTGACGCGGCG GAGCGTATGTACCGCTCGGTGACCTGGCACGCTGGCTGATGGAAGCATGGAGTATTGGGACGGATTGACCA CCAGGTTAAATCCGGGTTACCGCATCGAGCTGGGGAAGTGGAACGCAAGCTGCTCCATGCTCCGTCTGTAAAGG AGGCTGTAGTCTCGCTCAGGAGGATGGAAGTGGAACAAAGGTGCTGTGCGCTATTTACAGCCGATCAGATACTG ACGGTAGCGGAATTGAGAAAGCCTTGGCCGAGAGCTGCCAGTTATATGATTCGCTTACTTTCATGCAATTGGAA CAGATGCCATTGACGCCAATGGCAAGCTGGATCGCAAGCACTTCGGCTCCGGAGGCCAATGTGCAAGACAGGAG CGGTTTATGAACGCCAAGGACGAAGGCTGAGGAAGCTCTGGCTCCGTATGGCAAGGGTGTCTGGGAGCACAGAA GGTCGGCATCCATGATCATTTCTTCGATCTGGTGGTGACTCCATCAAGCGCATCCAGGTATCCTCAAGATTGTTCCA AGCCGGGTATAAGCTAGAGATGAAGGATCTCTCAAAATATCCGACAATTGCTGAGCTAAGCCCGTATCTTCAAGTAG CCGGACGCACAGCAACAGGGTGAAATTAAGGCGCAGAGAGCTGATGCCAATTCAGCGGTGTTCTTTGAGCGGT CATACAGAGGAGCCGATCATTAATCATGCGCTCATGCTCTATCGGAAAGACGGCTTTGACGAGGCTGCACCTCCG GTTGACAAATGACCCAATTGCTACCCACCATGACGCGCTGCGTATGCTCTCCGGTCTACAGAGCCGGATATGCAGC CTGGAATCGTGGAACGGATGAAGCGGAGCTCTATACATTGGATATAGACGATGTGCGACAGGCAGAAAGACCAAGTT GCTGCCGTTCAAGCCAAAGCCGATGCCATTCAAGCAAGCTTCCACTTGGAAGACGGCCCGCTGTTCAAGCTAGGCTT GTTCCATTGTGAAGATGGGATCATTTATTAATTGTTATCCATCACCTTCTAGTTGACGGGTATCCTGGCGCATCCTG TTTGAGGACATCGCAACGGGATACGAGCAGGCGTTGAATGGACAAGCGATTGTCTTCCACAAAAGACAGATTCTGA TCTTGTATGCTGTGAACAAGCGCGGAAGTATGACAGCAGGCGCTGCACTGGACAAGGAGCGTGCATCTGGCAGCAGA TCGAGGATACAATTCTGGCCCTACTGCCAAAAGATGAAGATCAGGAGCCAGGCACCATTCGGGATACCGAGTCCGTA ACGGTAAACGTGTGCGCAGGAAACAGACCTGTCTGTGCGACAAGCGAACCGGGCGTATCATACGGAGACGAATG ATTTGCTTTTGACTGCTCTGGGAGCAGCAATTCAGCGCTGGACAGGCAATGGAGCAGATTGTTGTTCAATCTTGAAGGCG ATGGACGGGAAATGATCATACCGGAACCTGGATATCACCCGTACCGTGGGCTGTTTCAACAAACCCAGTATCCGGTTCTG CTGAACCTTCAAGACGGACAGGAAGTATCTGACACGAATCAAGCGTATCAAGGAGAAATTTGGCCGACAGATTCCGCAAA

Strain	SEQ ID NO:	Sequence
		AGGAATCGGCTACGGCCTTCTGAAGTATATAGCACTGGAGAAAAGTGGCGGTTCGGCGTAGAGCCGGAGATTTCCT TCAACTATCTTGGACAGTTTGATCAGGATTTGGAGGGAATGCACCTACGCTATCCACACATTCAGTCGGTAAGGCGC TCAGCGACCACACACACAGCATGTCTCTGGATGTGAATGGCATGATTGCCGAAGGCCAGCTATCACTGACGGTT ACGTACAGCAGCAGGAGTATCGCAAGGAGACGGTGAATCATTTTGCCGAATTTATACAGTCCAGCCTTAGCGAGGT TATCCGGCAATTGCGTGCGCAGGAGCGCTACAGCTTACGCCAAGTGATGTTTTGTTCCAGGGAATTAGCGCTGGAGCA GCTGATCGACTTACGGAGCAGAGCGGCCACATTTGGAGAGATTGAAGATGTGTACAAGCTTACGCCAATGCAGAAAG GGATGCTGTTTACAGCCTGCTGGAGCCAGACTCTTCTCATACTTCGAGCAGGCTACGTTCGAGCTGCGAGGCAAGCT TCGATGTAGAGACCTTCTTCGAGAGCTTCCAAAGCTTTGGTGCAAAGACATGCCATACCTGCTACCAACTTTTACAACA ACATTTGGTGATTACCGCTGCAAGTCGCTTTTAAAGCAACGGCCAATCCCATTTGCATACGTAGATCTGCTGCCGCA CTTTGCAAGAGCAAGAAGCCAGATCAAGGCTTACACTGCTGAGGATATGGCTAAGGGGTTTCAGCTTGTCCGGAAGAT CCGCTGATCGGGTAAGCGTCTTGCAAACAGAAACAAAGCTCTCTGCTGTTATATGGAGCTTCCATCATATTGTCATGGAT GGCTGGTGATCCCGATCATACACAGGAGCTATTCGATTAATTTCTGCTCTGCGCCAGCAAGTACAGCCTGTGCTG CCGCCAGCTCAGCCCTATAGCCGTTATATTGAGTGGCTTGATGCACAGGATGATGAGGAAGCTTCCACGTATTGGAGC CAATACCTCAAGGACTATGATGGGAATACCGTATTGCCGGAAGGCAAAACGAAATCTCAAGCTAAAGAAAGCGGGCT ATGTTCTGAATGAGCATGTTCTCCATCTGGTGCACTCTTGACCGGTAAATGGATACCTGCTGCTAAGCGAAACCCAG TGACCGTCAACACACTCATGCAGACAGCCTGGGACTGATTCTTCAACGTTACAAATGCCAGCTCGGATGTGGTTTTCG GCGGCGTTGTATCGGCGAGACCGGCTGAGATTGCAGGATCGAAATATGTTGGTCTGTTCATTAATACAGTACCT ATCCGTGTACAGTCTCCAAAGACGAAGCCTTTGTGAGGTGATGAACGTACACAGGCACAGTCATTTGGCTAGTCG TGCCACGACACCTATCCACTGTATGAGATTCAAGGGGAAACACCCAAAGCAGGACCTGTATTTCTCATATTATGAT CTTTGAAAATTATCCGCTCGACGAGCAGGTGGAGCAATCGGGTAATCAAAATGAGGACAATCTCGAAAGTCGCGAACT TCACCATGTTTGAAACAACGAACCTATGACTTTAACCTGGTTGTGATTCCAGGCGAGGATATCAAGGTTTGCAATTCGTT ACAATGCTTTGGTCTACGAACAAGAAAGCATTTGCACGAATCGGTGACACTTGATGCAAAATGCTCGATCAGGTAGCT ACCGTCCGCGCAGGAGTCATAAAGGAACCTGGAGCTTGTAACCTCTGATGAACGAATGCAATTGCTAGACTGGGCGG CAAGGCCATACACCTATCCAAAGTATCAGGGTCTGCATACCTTGTTTGAAGAACAGGTTGTCCTACGCCAGATAAGAT TGCACTGTGTTAACGGCGATATTCAAGTCAAGTATCGGAGCTGAACGAGCAGGCAACAGATTGGCCCTCCACCTTGA TCGCCAGGAACTTCGGAGTGAACAAGTGTGCTGTTGGCGGATCGGCTGTGGAACTGCTTGTCCGCAATTAATGG GTGTGCTCAAGCGGCGGGTCTATGTACCTATTGATCTCTGAATATCCGAGGAACGGATTCAAGTATATCTAAAGG ATTCCGGCGCTGAGATTTGTCTACACAGAGCCACTTGACGGAGCTGGCTCTTTGAGGGAACGGTTATGGAATTGG ATTCCCCGCACATCTACGGAGACGGGGGGATAACCCCTAATCTACCTGTGAGAGGAACGATCTGGTGATTTAATC TATACATCGGGTACAACAGGAAATCCGAAGGGAACCATGATTAAACCATAAAGGGATCGTGAACTACATCTGTGGTGGC

Strain	SEQ ID NO:	Sequence
		CAATAAGTCTACTGTGCAGGGAACCAACAGATTTCCTCGTGTACTCGTCCATTTCATTGACCTGACGCTGACATC AATTTTCACTCCATTAAATTAACGGAGGATTAGTACGGATTACGATGGTATAGATAAGGCGGAGGTTGTTTCAGCATAT TTTGCGCGAAAATGCGGTGGACATTCTCAAGCTGACGCCAACTCATCTCAGTCTGATTAAGATATGACCATCCCGGC GGAAAGTCGCAATTCAGCAGCTCAATTGTGGGTGGAGAGAAATTTGACCAACATTTGTGCGAAACCAATCACAGATCTCTT TGGCGCAAGATCAAAATCTACAAATGAATACGGTCTCTACCGAAACGGTCTGCTGCGATGATTCACCTTTATGATCC TGTGAAGGATACACGTGAATCCGTACCTATTGGATTGCGGGCAGACAACATATACATCCATATCTGATGACCAAGCT TCGTCTGTACCATTAGCGGTGGAGGGGAAATGTACATCGCCGGGACGGGTAGCCCGCGGATACCTGAACCCGTC CTGAGCTTACCGCAGAAAATTCATTAGAGACCCGTTCCCTCGGAAGAAATATGTATCGAACCCGGGATTGGCC CGTCTCTTCTAATGGAGACATTGAGTACATTGGACGTATTGACCATCAAGTTAAATACGGGGCTATCGTATAGAG CTTGGTGAGATTGAGGCCAAGCTGCTGGATAATCCACTTATCGAGGAAGCTCTCGTTGTTGCGTGGCGAGATGCCCAT GGACAGAAAGTCTGTGTGCTACTTCTGTAGCTGATCGGGAATGTCTGTACGCGAGCTGCGGAACGAACTTTCTTGG CTGCTGCATATATGATCCCGTCTCTACTTCGTCCACTGACGTGATGCTTTGACACCGAAATGGCAAGCTGGACCGT AAGGCACTGCTGAACCGAATCTCGGTGTGAAGCGGGCGGCTTACTGCTCCGCGACGGATGTGGAGAACAT TTTGGCTTCGATCTGGCAGGTGTGATGTTCCGCTTGTGCGCATACATGACAAATTTCTTTGAGCTCGGAGCGGA CTCGATCAAAATCCATTCAAGTCTCATCAAGGCTGCTCCAAAGCAGGCTATAAACTTGAGATGAAGGATTTGTTCAGCTA TCCGACCAATTGCAGAGCTGGCCCCAGCGTGTAAAGGCGGTGACGCCGAATTGCGGATCAGAGCGAGGTACACGGAGCG GTAAAGACTGGGACCTGCCAGTGCAGATTTCGACGAGCAGTCGACGGACCTGCACCACTTTAATCAGTCGGTCATG TTGTACCGTCGGGAAGGCTTCGATACCGATGCGCTCGCCAAGTTGTTCGGAATAATTGCAGAACATCATGATGCGCT GCGACTGGTGTTCGCGCAAGGAGAGCGGGGATTGAAGCCTGGAAACCGCAGCTTAGGTGAGGTGAGCTTTATAGCC TCCAGATCCACGATCTGCAGGATGAACAGACCCGGCTTCGGCAATAGAACGAGGTGTGGAAGCCATTGAGCGCAGC ATCTCTCTCGGTGATGGACCTCTCTTAAGATTGGGCTGTTCGCGTGCAGGAAAGCGAAATCTGCTAATCGTTATT CATCATCTGCTGTTGATGGCGTATCCTGGCGCATCCTCTTTGAGGACCTGCAGGAAGGCTACGAGCAGGCAAGCAG CGGAGAAAGCTGTCAAGCTTCCGCGAGAGACGGATTCTGACCGTGCATGGCCCGAGGAATCACACAATATGCGAAC AGTCCGGCGGTGAACAAGAACCGAGCTATTGGGCAGAGGTAGAAGGGGATGGCTTCGCCCTCTTCCAAAAGACA AGGTAGACGACGCTCTTCTCATCAAGACAGCGGACGGTTACGGTGAGATGTTGTCACCAAGAGACAGACAGCAGTT CCTGAAAGAGGCGAACCCGCACTTACACACGGAAGTTAACGATTGCTCTGACGGCCCTCGGCAATGGCTGTTACG AGTGACCGGGATCGAACGTGTAGGCATCCTTCTGTGAAGGACATGGACGGGAGCCTGTGTACCTGAACCTGGATATC ACTCGCACTATAGGCTGGTTTACAAGTCAATACCTGTGCGCCCTTGAGATGAAGAGGAACCTGGAGATCGGCGCTAG AATCAAGCGTGTCAAGGAAGGCTTGCCTCATCTTCAACAAAGGTGTGCGATATGTTTGAATAATTGAGCG ACGTATCCGATGTCTCTCTCTGCTGAACCGGAGATTATCTTCAACTACCTGGGACAGTTTCGACCAAGGATCTTGC

Strain	SEQ ID NO:	Sequence
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Strain	SEQ ID NO:	Sequence
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NRRL B-67724	4	ATGAATGACATGCAGTTATATGATTTAAACAAATCGCGCAGAAAGCGTATATGGTATACCGAAATTAATCTTACCCAGATAC GTCAAGTGTACAGCTTTCCGGTACAGCTAAGATGAAGGGCATATCAATATTGCTGCCCTTATGTCAGTCCATTAATTT GATTATCAACAGATATGATGCGTTCGCCATCCGTATTAACCTCAGTGGATGGAGTGCCCTCAGCAGTACGTCGTTCCCTTA TGAAAGAGACAGTTGGAGTGCCTGGATCTTATGTCACATATGAAAGTGTATCTGAGGTGGAAAGCTTACTTGTGAGCAAC ACAAAGAAACCCCTTGCCCTGCTGGATTCTGAGCTCTTCCAGTTTAAATTGTGAAGATTAGCGAGGAAAGAGTATT

Strain	SEQ ID NO:	Sequence
		GGATTAATCAAGATGCACCATATTATTCTGACGGGATCTCAATGGTGGTCTATGGCAATCAGCTGACAGCATTTT ACATGGAGTTAATTCAAGGAAATGAACCGGAGCTGGGCGACGATTGCTCGTATATTCAATATATTGCAGATGAGAAT GCATACGAACCTTTCTGACAGATACCAAAAGGATAAGGCTTACTGGCTAGATAAATTTCCGATTTGCCCTGAGCTTACG GGTTGGAAGTCATATAATCCGTTATCTTTAAGCACCCACGCCGTTCCGGAGCAATTTTACCGTACCAGAAAGTGCTATAT CACGAGCTGCAAGCAATTTTGCCAAACAGAAATAGGAATTTCTTTTGTTCCAGTTCTTCAATGGTGCAGTATATCTACATA CACAAAATGACGAATCAGCCGATGTGGTATGGCACTTCGTTCCGTAACCCGGGGAACAAAAGAGAGAACAAA AGATAGGTATGTTCTGTCAGCACCGCTGCTGCCAGAACATACGTCAAAAAGGATATAGATGTGTGAGCTTCCTGCAG GATGAGCCAGAGATCAGATGTCAGTCTCGGCGATCAGAAATATCCATACAAATCAGTTAATTCAGGATCTTAGAGA AATGCATGGGAACAAGGATATTACAGCGGCTTTTGGCGTTTCAATGGAATATCGTCTTATCAATTTGGGTTGATTTGGA TGATGTGCGTATTTTGACAGATTATGATTCTCGGGGACGAAGTGAACGATTTCTGCTTCATATATCGTGGAGATCCT GGATGAAGGCGAACTGGTACTGATGTCGATTATCGGACAGAGCTGTTGAACGCAAGTGAAGTAAAGGACATGGTTT CCCAGTTGCTTACGATCGCCGAGCAGATCATTCATTCACCTCAGCTTTCTATCGCAGAGGTAAGCTTATTAGGTGAAC CAGAAAGACAATCCATTTTGGCTCTTTTCGGAAGGCCGCGCAGTCGATTTATCCACGAGAGAAAGACCATTCATGGCTTAT TCGAGGAACAAGCCGAGCACACGCCAGATCACGTAGCCGTTTCAGATGGACGAGCAGATTCATACCAAGCTCT AAACGAGCAGGCTAACCAAGCTTGCGAGATATTTCGCTCCGAGGGAGTAGGGGCAAGATACGCTCGTAGGGATTTATGG CTGACCGTTCCCTTGAGATGGTCAATCGGATGTTGGCCATTTTGAAGCAGGTGGTGCCTATGTACCAATTTGACCCCG ATTATCCCGAAGAGCGTATCCACTATATGCTGAGGATTCAGGTGAAGTCTGTGCTCACCCAAAGTCATCTATGGG AGAGCACCACTTTTGACGGAAAGCTTGTGATCTGGACGAAGCTGCAACGTATACAGGAGATGCTTCCAAATCTGGAG AGTATTTCCGGGACCAAGCCATCTGGCCATGTTATCTACACGTCGGGTACGACTGGCAAGCCGAAGGGCACGCTGAT TGAAACACAAAATGTAGTTCGACTGCTCTTTAACGATAAAAATTTATTGACTTCAACTCTCAGGATACGTGGACGCT GTTCCATTCTGCTTCTCGATTCTCCGTTTGGGAGATGTACGGAGCGCTTCTTTACGGAGGGGAAAATTTGGTGTGTT CCATCTCTACAGCCAAGAGCCCAAGCAGCTTTCTTGAGTTGTGAAAAGACAACCAAGTCACCATCTTAAATCAGAC GCCGACGTATTTTATCAGGTGCTACAGGAAGAGTTAATGCACCTCTCGACAGAGCTTGGCCTTAGAAAAATCATTTT TGGTGGAGAGGCTTTAAGTCCATCTCTCTTGAGAAAAGTGGCGGTCAAGTATCCTGATGTGCAGCTGATTAAATATGTA CGGAATTACGGAAACAACGGTTTCATGTCACTTAAAGGAAATCAGGAAACATGAGATTGAAGCGGGGAAAAGCAAT ATTGGCAGAACGATCCCAACACTTAGCGCTTACATCTCGATGAGCAAGACGCTGCAGCCTGTGCGGTTCCAGG AGAGCTATACATTGCGGGAGACGGTCTTGCCCGTGGGTATTGAAATCGGCCGGAATTTGACGTCTGAGAAAATTCGTTGA GCATCCGTATCGGTGGGAGAGCGGCTGTACCGAAGTGGGATCTTGCTCGTTGTTGCTGATGGCAATATTGAATA TTTGGGGGGATCGACCATCAGGTCAAAATTCGGGCTACCGAATTGAGCTTGGCGAGGTAGAAGCCCAAAATCTCA AGGCTCCAAGCGTACGAGAAAACGATTGTCTCGCACGGGAAGACGAACAGGGCCAAAATTTGCTGTGCGCCTACTAT

Strain	SEQ ID NO:	Sequence
		GTAGCCTCAGTGACCTTTCCGCCGGGGAATTGCGGTCTCAGCTGGCGGGGAACTCCCGCTTACATGATTCCTTCT TATTTGTCCGGTGGAGCAAAATGCCGCTTACACCAAAATGGCAAACTGGATCGCGTGGCTTCCCGCTCCTGAAAGC AGGTACAAATCCGGTGGAGCTTATTTGGCTCCGAGAACTGCTGTGGAAGCTCAGATGTACTCATCTGGCAAGATATC TTGGCGTTGCTGCTGTCAGAGATAAATTTCTTTGAAATTGCTGTCACCTCTTTGGGGGCAACAGTGTCTGTTT CACGGATTACAAAAGAAATTGGGATGTAGCAATTTCCGCTGCGTGAAGTGTTCAGTCACTACGGTCGAATCCTTTGGCGC AACTTGTGAAAAACACATTCGACCAATGTACGAATCCATCCACAGGCAACGAAAGCGAGGCTTACCCAGTGTCC TCAGCGCAAAAGCGGTTATACGTGCTGAGACAGATGACGGGGAGAGCTCAGCTACAATATGCCAGGGGTCTTCAC AGTGATGGACCGTTGGATCGACCGGCTGGAGTCTGCGTTCACGGCACTGATCCAGCGTCATGAATCCCTGAGAA CCGGCTTTTATATGCAGGATGGAGAGCTTGTTCAGCTGTGCATAGGAATGTGCCGTTTGGCTTGAACACACAGAGG CTTTGCTGAGGAGACGGATACGCTCAATTCACAACTTTATTCGTGCTTGTATCTGAGCCAGGCTCCATTACTGCGTG TTAGCTTGGTGAAGCTCCAGGAGGCGTCACTGTGCTGTTGTATGATATGCATCACATCATTTTCAGATGGGTTTCTAT TCAAATATTGATAGAGAACTTACTCATTTGTATCAAGGAACAGCTCCAGAGCTGCACATCCAGTACAAGGAT ATGCCGTATGGCAACGGGAACAGTCAGAGAACCAATGGCAAGATCTTGAGAAATATTGGCTGCAATCCTTTGAAGGA GAGTTGCCGGTATTGGATTGGCTACAGACTTCCAAACGACTTCAAGTTCGGAGCTTCGAGGTAGCCGAATTGATTTT ACATTGGAATGATCTGGCAATAAGGGGATACAAAGAGCTTGCATCCGTACAGGTACTACACTGTATATGTAATTGCTG GCCGCTATTTCGTAATCTGTCACAAATAATACAGGACAGGAGGACATCGTCTAGGTTCTCCAGTAGCCGGGAAGACC GCAGGCTGAGCTTGAGGGCATCATCGGGATGTTGTCAACACACTGGCTTGGCAGCTACCCGGCAGGAGATAAAA CCTTTCAGGATTATCTTCTGGAATCAAGGAACGGCGCTCAAGGCTTGGAGCATCAGGATTACCTTTTGAAGAAAT TGGTCGAAAGCTGGCGTAGGACGTGATGTCAGCCGCAATCCGCTCTTTGACACCTATTGGTATTACAAATACCG AGCAGGAAGAGCAGGAATGGACGGAGTGCACTTACTCCTTACTTGTATGGACACCGTCAAGCCAAATTGACCTG TCCCTCAAATGTAGAGGAGAAGGGGTCAAATTAAGCCTTTGGCTCGAGTATAGTACGGCTTTATATCGGCGTGAAAC CGTAGAGCGACTTGCAACGCACCTTGTCCGGGTTCTGCATGCAGTCTCGGCAATCCTCAGTTGCAACTGGCCGAGAT AGAAATGATCACACCGGAGGAGAAAGTACAGATCGTTGAAGTATTTAACGCGACATCGGCTCCTTATCCAAAGGACA AGACCATTCATGAGCTGTTCTAGAACAAAGTCAATCGTACACAGAGCAGCGGCTTGTATTCCGGCGATGTCCAG CTAACGTACCTTGAATTGCAAGACAAGGGGAGCCGACTGGCCCAACACTGCTGCTTTGGGAAACGTTGAGGGAGCA GCCTGTGGCCGTGATGGCGGACGAAGCAATTGAGATGGTCAATTGGTATGCTCGGGTGTCTCAAGCGGGTGGAGCCT ATGTGCCGATTGATCCTGATTACCCGGAAGATCGGGTTCGTTATATGCTTAAATGATTCCGACGCCAAGCTATTATTGG TGCAAAAGGGCGAGCTTATAAGTGTAGACTACGGTATACCGATTGTCGATCTTAGCAGTGAAGAGGCCATATGCAGCT GAACCTGCCCCAGCCGAGACTGCTCAGGGATCGCAGGGGCTTGTCTATGTCATCTATACATCGGGTACGACGGGTAG ACCGAAGGGCGTTATGTTTGAACACCGGAAACGTGGTCCGCTTAGTCAAAAGAGACCAACTATGTGGAGCTGAATGAAT

Strain	SEQ ID NO:	Sequence
		CCACACGAATTTTGCAGACAGGAGCCGTGGCCCTTTGATGCTTCTACATTCGAAATATGGGGAGCGTTACTTAAACGGTG GGCAGCTCTATTTCGTGGAGAACGACGATATCCTGATTGCCGATAGGCTAAAAGCGGCCATTACCAAGTACGGGATT ACAAACAATGTGGCTTACTTCACCGCTTTTCAATCAGCTTTCCTTGCAGGATGAGTACCTGTTTCAGAGGCTAAACAA TTGCTGGTCCGGGAGACGTACTGTCCAATATCTCATATGAACCGTGTAAATCGAGGCTAAATCCTGATCTTGTCCCTATC AATGGCTATGGTCCGACAGAGAAATACGACCTTCTCCACCACTCAACAGATTTCTGGGTGCTGCCGAAAGGGGTCTGTGCC GATTGGCCGCCCAATTAGTAATTTCTACCGCTTATGTGTCATATGGATCGTCAATACAGCCTATTTGGTGTCTGGGG TGAACTCATTTGTGCGGGTGAAGGTGTAGCGCGGGATATCTCAATCGTCTGATCTCACAGCAGAGAAATTTGTTC TAGTCTGTGAAGGACGGAGAACCTTGCTACAGAACTGGGATTTGGTACGCTGGCTTCCAGATGGGAATTTGGAGT TTAAAGGAAGAATTGATGAGCAGGTCAAAATACGTGTTACCGCATCGAATCCTCTGAAATCGAGGCCCAACTGGCC AAGATGGAGTCAGTAATCGACGCCGTAGTGTGCTTCCGCGGATGAGCTTGGCGAGAAAGCAACTTTGCGCTTATTA TGTGGCGGATCGTACGCTCACGGCAGCGGAAGTACGTCTTTCCTATCGCAGGTACTTCCAGGCTATATGATTCCTATC CTACTTTATCCAGATGGATCGTATGCCATTAACTGTCAAACGGAAAGTGGACCGGAGTCTCTGCCGGCTCCTCAAGT AGCGCGCATACAGACGGAAATACAGCTCTCGTACACCGCTGAGGAAGCTTTGGCATCTGTCTGGCAAGGGG TGCTGGGTGCCGAACAGGTGGTATCCATGACAAATTTCTTTGAAATGGCGGAGACTCCATAAAGCTATTACAGGTGT CGTACCGTTACTGCAGGCCGGCTATCGTTAGAGATGAAGCAGCTGTTCAAAATCGCCAACCAATGCGCAGCTAGGC GCGGAAATTCAACGGCTGTGCTATATGGCTGAACAGGAGTTGTGCGTGGAACGACTCGCTTGAACCTCCAGTCCAAACA GTGGTCTTTGGACGGAAGCAGGACAGCGCTCATCACTTCAATCAAGCGGTTATGCTGTATCGTGAACAGGATTTGA GGAAAGGCCCTTGCAATCAGGTGCTAAGAAACTCGCTGAGCATCATGACGCCCTTCGCATGGTTTCCGTCAGACAG AGCATGGCTACGAAGCTTGGAAATCGTGATCTTGAAGAAAGGAGAGTTGTATAGCCTATTCACCCGTGATTTACGGAAAT GAATCCGATCCGACTGTAGCCATTACATCGCTGTGCGATGACATTCAGTGCAATCAATCTGGCAGAAAGTCCGCTG CTGAAGTTAGGACTTTTCCATTGTCAAGGATGGAGACCACTTCTGATCGTGATCCACCAATTTGGTGTGGACGGAGTA TCCTGGCGGATTTGTTCGAGGATATTGCAGCAGGTTATGAGCAGGTGATTCAAGGACAAGCGCTGACATTCGCCCA GAAGACGGATTCTCCGTGATTGGGAGACGCCCTTGCTCGTTATTCGGAAGGTCCAGAAATGGAGACTCATCGGG CGTATTGGAGAGAGCTGGAGATCAGCCACTCGAACAGTTGCCGAAGGATGAGGCTGTGGAAAGCCTTCTTGTACAG GATAGCAAGTAGTAACAGCACAATGGACTCTAGAAAGAAACCGACCAATATTATGAGAAAGCCCACTCGTGCTTATCA AACAGAGACGAATGATCTGCTATTGACTGCTGGGCAATGGCGGTATCCAAATGTGCTGGCATCGGAAAGGTTGCTG TGAAATCTGGAAGGACACGGTCTGTAGCCGATTATACCGAATATCGACATCACCCGTACCGTAGGCTGGTTTACAAAGT CAATATCCGGTGATTTTAGACTTGGGAATAACCCGGAAGTGGCTCCTTGATCAAGTCTGTGAAAGAAAGGGCTGCG CCGAATTCCGAACAAAGGTATTGGCTACGGTTGCTCAAAACGATGGCAAGTCAGTTGGATGAAGGCAGCTTCAGCT TGCAGCCTGAGATTTCTTTAACTATCTGGGGCAATTTGATCAGGATTTGCAAGGAAGCTGTTGCAGATTTCTCTCTTA

Strain	SEQ ID NO:	Sequence
		TCCGACCGGAAGCGCGCAAGCTTGTGGAGGAACCGGCCCTATACGCTAGATATCAATGGCATGGTGACGACGGA GCCCTGACTCTGACGATTACTTATAACGGAAACAGTATAAGTCATCTACGATGGAACAGCTCGCTGGATATATTGA AGAAAGCCTGGGGAACCTTCTCCAGCATTCGTAACCCAGAAACACCGTATTGACACCAAGCGACGTGCTTGCGGA AGGTCTGAGCATTCGCCGATCTGGAGGAGCTTTCTAAGCAGACGAGTCACATTGGCGATATTGAGAAATGTATATAGT CTGACGCCAATGCAGAAAGGCAATGCTGTTCATGATATGTTTGAAGCCGCATACAGGTGCTTATTTTGAGCAGGCCGCT TTTGATTTTAAAGGTAGCTTTGATCCGATCCGCTTCGGGCACAGTCTGGATGCAGTAGTGAGCGTCATGCTATCCTG CGCACGAACCTTTACAGCGGATGGGCGAGCGCTTTCAGAGTTGTATTTCGGCACAGAGGCGCTAAAATTGGTGTA CGAAGACCTGGGAGATGAATGCATCGCAGCGGAAGCTTACCTGAAGACATTTGGTGCTAAGGACAAAGCAGCTG GGCTTCAACCTAGCTGAAGACGAGCTTCTCCGTGTATCCATTTTACAAACAGATGAAGAGAGCTTCCGTCTTATGG AGTTTTCACACATCGTATGATGGTGTGTGTTCCGTTAATTACGACGAGGATATTGAAACACTATTTTGCCCTCC TGGAAGGTAGAGACCGCAGTTGGCAGAGGTTTCATCCGTACAGTCGATATATCGAATGGCTCGAACAGCAGGATGA AGCAATTGCGTCCAACTATTGGAGCCGATATCTGGCCGTTACGAGCAGCAGACGCTTTTACCTCAAGTCGGTGAG CAAGTAAGGGAGAAGGCTATGTAGCAGAAAGCTGAATATCTCTCAGCAGGGAATTGACTGAGCGCTTGAAAA GGTGCCAGGGATGCTCATGTACGATGAATATATTGCTGCAGTCCCTCTGGGGCATTCGCTTCAACGCTATAACGG TAGCCGAGATGTCGTACGGAAGTGTAGTATCAGGCAGACAGCAAAATCCGGGCAATTGATCGGATGATCGGTT TGTTCAATCAATACGATTCCCGTTCGTGTGAAGACAGAGGAGAAATCTCCCTTCACAGTTCTGATGAAGCAGCAGCAGG AACAAATATATGCTTCTCATATGATGACACCTACCCGTTGTTTGAGATTCAGGCTCAGACGGATCAGAAAGCAGGATC TAATCTCCACATATGCTGTTTGAGAACTATCTGTGGAGGAGGAGGTAGAGCTGCTGGTGGTGGCGAGGCTGCC TTTGAGATTGAGGAAGCGGAGCTTCTTGAGCAAAACGAATTATGATTTTAAATTTAATTGTCTCCCTGGCGAAGAAATG AGATTGCTGTTCCAGTACAAATGCATTGTTTATGACCCAGTGACAATTGAGCAAAATCAAGGGCCATCTGGTTTACCTC ATGGAACAATAATTGTAGAGAACCTGCTCCGTTGATGCACTAGAAATTAGTCAAGCCGCAAGGAGAGAGAACAGAT TCTGAACGTATGGGAAATACAAAGGCAATTAACGAGCACTGTAAACAGTTCCACGGGCTGTTGGAGGAACAGGCGG GACGAACGCCGGATGCGACTGCCCTTGGTTCGAGGACAAGAGTCTGACCTATGCCGAGCTCAATGCAAAAGCCAAC GGACTGGCGAAGGCTCCGTACTCAGGGAATCAAGACGGGAGATCTGGTGGGACTGATTGCTGAACGGTCCGCTCG AAATGATCGTTGGGATCTACGGCATATGAAAGCCGGGGTGCCTATGTTCCAAATCGATCCAGAGTATCCGAAAGAA CGAATCAGTTACATGCTTGAAGATTCGGGGCGAAGCTGATCCTTACACAGGCCCATCTCTTGAGAGCATCTCGGATGG ACGGAAATGTTTTGCTGCTGGATGAATCATCGACCTATGATGCCGACACCTCGAAATTTGAGAGCTACTGCTGGCCCCG GATGATCTGGCTTACGTGATCTACACTTCAGGTACGACGGGTACGCCCTAAGGGCGTATTAGTCGAGCATCGGGGACT ACCGAATCTTTCGGACGTATACGGGACACACTTCGAAGTTACACCCGAGGATCGGATCGTTTCAAGTTGCAAGTCTGTC GTTTGATGCATCGGTTTCGGAAATTTTAAACGGCGCTGAGCCACGGGGCTGCTCTGTGCATCCCTTCTACACAAGATAT

Strain	SEQ ID NO:	Sequence
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Strain	SEQ ID NO:	Sequence
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Strain	SEQ ID NO:	Sequence
		GAGGACATTGCAGCGGGGTACGAGCAGGCATTGAATGGACAAAGCAATCGTCCCTCCACAAAAGACCGATTCTGATCTGTGATGCTGAGCAAGCGAAGTATGCAGCAGGCGCTCTGTGACAAAGGAGCGTGCTACTGGCAGCTGATCGAAGAGCGGATTTGGCCCCACTGCCGAAGGATGAGATCAGAAAGCGGGCACCAATCCGGGATACTGAATCGGTTACGGTAACGTGTCTGCGCAGGAACAGACCTGTCTTGCGGCAAGCGAACCGGGGTATCATACGGAGACGAACGACTTGCTTGACTGCTCTGGGGCAGCCATTACGCGCTGACAGGCATGGAGCAGATTTTGGTCAATCTTGAAGGGCATGACGGGAAATGATCGTACAGACCTGGATATTACCCGTACCGTCCGTTGTTTCAACCCAGTATCCAGTTCTGCTGACCTGCAAGGGACAGGAAGTATCTGCGGCATCAAGCGCATCAAGGAGAAATTTGGAGAGGTTCCGCACAAAGGAATCGGCTACGGTCTTCTGAAGTATATGGCACCGGAGAAAGTGTGCGAATTTGGCGTGGAGCCGAAATTTCCTTCAATTATCTTGGCAGTTTGATCAGGATCTGGAGGGTAAATGCCCTTAGCCCTATCCACACATTCAGTTGTAAGGGCTCAACGGACCTACAGCAATAATGCTCTGGATGTGAATGGCATGATTGCTGAAGCGCGGTATCACTGACGATTACGTACAGCAGCAGTATCGTAACGAGACGGTGAGTCAATTTGCTGAATTTATACAGTCAAGCCTTAGTGAGGTCATCCTGTCATTGTGGCTCAGGAGCGTTTACACAGCTTACACCAAGTATGTTCTGTCCAAAGGATTAACATTTGGAGCAGCTTGATGAGTCAAGCGGCGCAGACGGCTCACATCGGAGAGATTGAGGATGTGTACAGTACGCCAATGCAGAAAGGAAATGCTGTTTCAAGCCTGCTGGAGCCGACTCTTCTCACTTCTGAAACAGGCAACGTTTGAGCTGCTGATGTAGATATCTTCTCGAGAGCTTCCAGGCTTTGGTGCAACGACATGCCATACACTACCGGATTTTACAACAATTTGCTGATGTACCGCTGCAAGTTGTCTTTAAGCAACGGTTAATCCCTCTGCACCAAGTATGCTGCTGACGCACTATGCAGGAACAAGAGCCGAAATCAAGGCTTATATGCTGAAGATATGTTAAGGGGTTCAAGCTTGTCAGAAAGATCCGCTGATGCGAGTGACCGTCTTGCAAGGATCAAGCTGTCTTGTATTGTGGAGCTTCCACCATAATTGTCAATGGATGGCTGGTATCCCGATCATACACAGGAGCTGTTCGATTATTTCTGCCAAGAAACAGCAAGCACAGCCTGTCTACCGCAGCTCAGCCCTATAGCCGTTATATCGAGTGGCTTGTATGCGCAGGATGATCAAGAAAGCTTCAACATATTGGAGCCAAATATCTTGAAAGATTATGACGGGAACCCGTATTACCGGAAGGTAAAACGAAATCTCAAGCAAAAAGCGGGCTATGTCTAAAAGAGCATGTTCTCCATCTGGGTGCATCTTTGACAGGTAAAATGGATGTTGTCGGAAGCGCAATCACGTAACCGTCAATACACTCATGACAGACAGCTTGGGACTGATTCTTCAACGTTATATGCCAGCTCGGATGTCGTTTTCGGCGGCGTTGTGTCGGGTAGACCCGCTGAGATTGCAAGGATCGAAAATATGGTGGTCTGTTCATCAATACAGTACCTATCCGTGTACAGTCATCCAAAGACGAAGCCTTCGTCGAAGTGAACGTACACAGGCACAGTCAATGGCTGTGCTGCGCTACGACACCTATCCACTGTATGAGATTCAAGGGAAACAAACCCAAAGCAGGACCTGATTTCTCATATTATGATCTTTGAAAATTACCCGCTCGACGAGCAGGTGAGCAATCCGGTAAATCAACGGAGGACAAATCTCGAAGTTTCCAACTTCAACCATGTTTGAACAACCAACTATGACTTTAAACCTGGTTGATTTCCAGGCGAAGACATCAAGGTCTGCTGCTATCGCTATAATGCTTCGGTTTACGAGCAAGAAAGCATTGCAACGTATCGGAGGACACTTGTGTCAGATGCTCGATCAGGTGCTGCTCGTCCGAGCGACGATACAGGAACTGGAGATTGTAACTCCGAGGAACGGATAAACCTGCTTGACTGGGGGGCAAGG

Strain	SEQ ID NO:	Sequence
		CCCATACCTATCCAAGTGATCAGGGTCTGCATACCTTGTGTTTGAAGAACAGGTTGTCCGTACGCCGGATAAGATTGCCG CTGTAAATGGGGACACTCAGATCACGTATTGGGAGCTGAACGAGCAGCGCAACAGACTAGCTTCCACCTTGATAGAC CAAGGACTACAGAGTGAACAAAGTGTAGTCTGTGGCAGATCGGTCTGTAGAGCTGCTTGTCCGCATCATGGGTGT ACTCAAAGCGGTGAGCCTATGTACCTATTGATCCTGAATATCCGCAGGAGCGGATTACGTATATTTTGAAGGATTTC TGGCGCTGAAATCCTGCTCACACAGAGCCACCTAACCGAGTTGGCCTCTTTTGAGGGAACGGTTATGGAATTGGATTTC CCGTACATCTACGGAACCGAGGTGGATAATCCCAATATTCTGTGGAGGAAACGATCTGGTGTACTTAATCTATAC CTCGGGTACAACCGGAAATCCGAAGGGAACCATGATTAAACCAAAAGGATCGTGAACTACATCTGTGGGCCAAT AAGTCTATTGTGCTGGAACCAACGGATTTCCTGTTGATTTCATCCATTTCTGTTGACTTGACGTGACATCAATGT TTACTCCGTTAATAACGGAGGAATAGTACGGATTATGATGTTATAGATAAGCAGAGGTCGTTACAGCATATTTTGC GCGAAAATGCGGTGATATTCTCAAGCTGACCGCACGATCTCAGTCTCATAAAGACATGACCATTTCCAGCAGAA AGTCGCATTCAACAGCTCATTTGTGGTGGAGAGATTGTGACCACACATTTGTCCAAAACGATTACCGATCTCTTTGGT GGCAACATCAAAATCTACAATGAATATGGACCAACCGAAACGGTCGTCGGTGCATGATTCACCTGTACAATCCTGC GAAGGATACCGGTGAATCTGTACCGATTGGTTGCCAGCAGACAATATATACATCCATATTCTGGATGAACAGCTTC GTCTGTACCGTTAGCGGTGAGGGTGAATGTACATCGCCGGGACGGGTAGCCCGTGATATCTGAACCGTCT GAGCTTACCGCAGATAAATTCATTAGAAATCCGTTCCGTTCCGGAAGGAAATATGTATCGCACTGGGATTTGGCTCGT CGCCTTCCTAATGGAGACATTGAGTACAATTGGACGCATTGACCAACCAAGTTAAAATACGGGGCTATCGTATTGAGCTT GGTGAGATTGAGGCCAAGCTGCTGGACATTCACCTGTGCGAGGAAGCTCTCGTTGTTGCTGGACAGATGCTCATGG GCAGAAATCGCTGTGCTTACTTCGTAGCTAATCGCGAAATGTCTGTACGAGAGCTGAGAGACGAACCTGTCTGCCG GACTGCCGTGCATATATGATTCCGCTTACTTCGTCCAACCTGGACGTGATGCCCTTGACACCCGAATGGTAAGCTGGATC GCAAGGCACTGCTGAACCGAATCTCGGTATAAAGCGGGAGCAGACTTTACCGTCCGCGCACGGATGTGGAGAA CATTTTGGCTTCAAATCTGGCAGGGTGTACTCGCGGTGCGCGCTTGTGGCAATTCTATGATAATTTCTTTGAGCTTGGAGGT GACTCGATCAAATCCAATTCATCCTCAAGGCTTCTCCAAGCAGGCTATAAGCTTGAAATGAAGGATTGTTCGGT TATCCGACAATTGCAGAGCTGGCACAGCGCGTTAGTGTGTCAGCCGAATTGCGGACCAAGCGAGGTACACGGAGC GGTAAGACTGGGACCTGCTCAGCACAGATTCTTCGATGAACAGTCGATGGATCTGCATCACTTTAATCAGTCGGTCAT GTTGTACCGACGGGATGGCTTCAATACCGATGCGCTCGCGAGGTGTTTCGGAAATTTGCAGAGCATCATGATGCTTT ACGACTGGTGTTCGCCCAAGGAGAGCAGGATTGGAGGCCCTGGAACCGGAGCATGGATGAGGGTGAGCTCTATAGC CTCCAGATCCACGACCTGCGGGAATGAGACAGACCCGCTTCAAGCAATAGAAGCAGGTGCGGGAAGCCATTCAAGCGCA GCATCTCTCTGGAGGATGGACCTCTCTTTAGACTGGGTCTGTCCGCTGTGCGGAAGGTGAACATCTGTGTGATCGTTA TTCATCATCTGGCTGTGGATGCGGTATCTCTTTGAGGACCTGCAGGATGGCTACGAGCAGGACGAGCAGC GTGGAGAAAGCGGTCAAGCTTCCACAGAAAGACGGATTCTGTACCGTGCATGGGTTGAGGGAATCACACAATTTGCGAAT

Strain	SEQ ID NO:	Sequence
		AGTCTGGCGGTGAACAAACGCAGCTATTGGGCAGAGGTAGAGGAGATGGCTTTGTCCCTCTTCCCAAGACAA GGTAGACGGGCTCTTCTCATCAAGACAGTGAGGCTGTACGGTGAGATGGTCACCAGAGAGACAGACAGATTCC TGAAAGAACCGCACTTACAATACGGAGGTCAACGATCTGCTCTGACGGCTCTGGGTATGGCTGTTCACGAG TGGACGGGAATCGAACGTGTAGGCACTCTTCTGAGGACATGGACGGAGCCTGTTGTGCCGGAACCTGGATATTAC TCGCACAAATAGGCTGTTTACAAAGTCAATACCTGTGCGCCCTTGAGATGGAGGGGAATTGGAGATCGCGCCAGAA TCAAGCACGTCAAGGAAGGCTTGCCTGATATCCGAACAAGGTGTCGGATATGGTATTTTGAATAATTAAAGCGAC GGTTCCGATATCTCCTCTCTCGGCTGAACCGGAGATTACCTTCAACTACTTGGGACAGTTCGACCAGGATCTTGCA GGAGGGATGATGGAAGTATCGCCTTACTCAGTAGGACCTGAGGTCACTGAGCAGATGGTGCAGCATCAGGCATTGAA CATTAAATGGACTGATTGCCGAAGGACAGCTTCAACTTTCGGTCAAGCTATAACCGTCATCAGCTCGACGGGAGTCCGT GGCTAAGTTTGTGGCAATCTGAAGAACCCTCTTAGCGAAGTTATTGGACATTGCGTAAGTAAGGAAGAACAGAAC TTACACCAAGCGATGTACTCTCAAGATATACAGCTTGGAAAAGATTGAGGAGTTAGAAAGCAGACACGGCATATC GGCAGTATTGAAAATATGTATAAAGTACCGCGATGCAAAAAGGAATGTTGTCCACAGCTTGTGGAGCCTCATTC GGAAGTCTACTTTGAGCAGGCCAAATTTGAAATTCAGGGAGCATCTATCCTGAGGATTTCAAACGCAGCTTAAAT ATCTGATGAACCGCATGCCATATTGAGAACGAATTTCCATGCCGGTGGGGCGATTCCCTATTTCAGATTGTGTCA AAGAAAGAGCGTGTGACTTCGTATACGAGGATCTGCACGAGCTGGAAACCGATGAAATTCAAAGCGCTCTTGCAGCT TATACTGCTCAGGACAAAGCAAGAGGCTTTAATCTTGCTGAAGAACGATGCTGCGTGTGCTATTCTACGTACAGCA GAAGAGGCTTACCATCTGCTGTGAGCTCTCATCATCATCTTTTGATGGCTGGTGTATGCCGCTTGTGCTCCAGGA GTGTTTGAGACGTATGGGGTTCTGCGTGAGCAAAAGGAGCCTGAGCTTCCGAGCTGTATCGTACAGCCAGTATATT CAATGGTTGGAGAAAGCAAGCGAGGAAGAGGCACTCTTACTGGAGAGGTACCTGGAAGGCTACGAGCAGCAGA CGAAGCTGCCACAAGCCATCACACAGCCATCAGCAAAAGCAGAGCCTATGTGTGGGAGAAAGTATTACCGTTG GATCGGAATTGACCGATCGCTGGAACAGGTGGCCAAACAGCATCAGGTGACGATGATATACATTGATGCAAGCAG CCTGGGAATCGTGTGTCAGCGCTACAATAGAAGCCAGGATATCGTCTTCGGAAGTGTAGTATCGGGGAGACCTGCC GAGATTCCGGGTATCGAAAAGTATGATCGGTCTCTTATCAATACAGTTCGGTTCGGGTTTCAGGCCGAGGGAAGTGAT TCGTTCTCCCATGTGATGAAAAGACAGCAGGAATATATTTGGCAGGACATGCTTATGATTCCTATCCGCTCTATGAG ATTCAAGCACAGAGCGAAACAAAGCAAGATTGTGATTTCTCATATTTAGGTGTTCCGAAAATTACCCGGTAGAAGACA TCTGGAAGAGAAAATTGCTAGTGAAGAGGCTGAATACAGAAATTACGGATGTTTCAGATGTTTGAACAGACGAATTATG ATTTTAACCTCATTTGTGTCGCGGGCCGTAACTCTGGAGTTCTTGTACCGTTACAAATGCCCGCGTCTATGATCGGGAGA GCGTGGAACGCAATCAAGGACACTTGACGAGAAATCTGACAGCGTTGCTGTTCACCTACCATCCGTATTGATGAGC TGGAGTTGATCACCCAGAAAGAGAAATCGCAGATTATAGAGGTGTGGGGCGATACAGCAGCTCCTTATCCGCGTGAG CAGACCTTCACGGTATATTTGAGGAAAAGCAGCGCTCACACCGGATCGTACAGCACTTATTTACGGTGAAACCGGA

Strain	SEQ ID NO:	Sequence
		GCTTACCTATGGAGAACTCGATCAGCAGGGGAACCGTCTCGCACGTACGCTGCGTGCCCAAGGGGTCTCAGACCGGACC AACAGTCGGCATCATGGTCGAGCGCTCGCTTGAGATGATCATTTGGTATTCTATGCCATTCTAAAAGCTGGCGGGCCCT ATGTACCGATTGATCCGAGATTCCAGAGATCGTATTCCGCCACATGCTGGAGGATTCGGGAGCGAAGCTTCTGCTG ACGAAGAACCATCTCAAGATCGTTTTCTCGTTCACTGTACGATTCTGGCACTTGATGATCCGAGGCGTATCATATCGG GATAGCTCGAAACTGGAGCCAAATTGGGGGCGGAGCATCTGGCGTATATCATTTACACGTCAGGTTCAACCCGGCAA GCCGAAAGGGGTAATGATTGAGCATCGCGTCCGTCATACGCTGAGTCAGTTGGAAGCTGAATATCCGATGTTGG CAGGCGACCGTTTCTGCTCAAAACGACATTACCTTTGACTTCTCCGTGCCGAGCTGTTCTGCTGCTGTTCTTTGGACA AGGACTCTCGTGATCCTGCCACAAGCGTGGACAAGACCCGATGGCACTGCTAGAGCCGTGGATACGAACCCGTA TCACGCATCTCAATTTGGTGCCGTGATGCTCAGTGTCTGTTCAATCTTGAAGAAGCGGCAACCAAGGATTCTC TTACTCTGAATAACCTGTTTGGCTGCGGAGACGCTGCCGCCAACTTGTGGAAGAGTATTATAAAGTATCTCCTT ACGCAGTACTGGAAACATCTACGGTCTCTACGGAAGCAGCGTATATGCGACTCGGTATACAAAGAGCCTTGAGACT GCGGCTCTAACGCATGTGCCGATCGGCAAAACCGTACGCTAACGTCCAAGTATGATGATGGACAGCGCTTCTCAGGT ATCACCTGTGGGGTACCGGGAGAATCTGTGATTGCGGGCAAGGGGTAGCGGGGGTATTTCACACAGTCGGACC TGACGGCAGAGAAATTCTATCTCTCACCCGTACAAACCGGGAGCACGAAATTTACCGAACGGCGGATTTGGCCCCGATGG CTACCAGACGGGAATTGAGTATTTGGGGCGGATCGATCACAGGTAATAATCCGGGTTACCGCATTGAGCTGGG AGAAAGTGGAAGCACAAATTTCTGAAGGTGCCATCGGTGCAGGAAGCGGTTGTTCTAGCACTGGCTGACTCCACCCGAA GTACTCAACTTTGTGCATACTTTGTGGCCGAAGAGGGGCTTGACAGCGGGCGTGTACCGAAAGTACTGGCCAGCGAG CTGCCAAGCTACATGATTCGGACTGCTTTCGTACAGTTGGCAACAATGCCGCTGAATCCGAATGGCAAAATGGATCGC AAAGCGCTACCGGCACCGGAACACATTTCTGCGGAGCACAGCGGAGTATATCGCGCCGCTACGCAGACAGAAAGTAG AGCTCGCTCAGATTTGGTCCGAGGTGCTGGCGTACAGGAAATCGGGATCAGAGATCATTTCTTCGAACTTGGGGGC CATTCCTGAAAGTATTGGGCTTGATCCAAGGATTTCTGTCGGTATGGGCGTCCAGCTACCACTCCAAAGTCGTGTTT AATCTGCCGACTGTGAAGAAATGGCGCATGAATATCCAAGTTGCAGCAACAACCTGCTGCTAATGAAGAGGAAA TGGAATATATCCGCTTCCAGGGAAGGAACACTCAAGTGTGTTTGTCTTCCCTCCACGGGTAGGCCACTCTCTGGGT ACTATGAGATGGCCAGGAGCTGGAAGGGCTTTGCGAGGTGTACGGGATGGAATTTATCGGGCATCGTTTCCAGGGC CAAGATATGCTGGATCGATACATCGATGCCATCGTGGATATTCAAGCAGAGGGCCCGTATATATTCCTGGGATACCTCA CTTGGAGGAAATCTCGCCTTCGAGGTAGCTAAGCCATGGAAAGCCGAGGTACCAATGTTAGCGACCTTATTATGTT AGATGCTATGAGAAAGATGTCCAAAGGATGAATCGACACCGGAGGAGCTTGAAAGAGATTGTGAGATGTTACTGGAC AGCATTAGGGACCAGTACAAAGCATTCCTCGCCGATCCAGTGGACAGGAGCGAGTCAATGGACAAATGTTGGTGT CTCCACCTACCGCGATGAGCTTATTAAACGCAGGTGAAGTTTCATGCCAATATCCATGCTCTGATTGCAGAGGATGATAG TATTGGTCCGGATACATCATTAGATAAAATTGTTATGGCAACAGGCGACACTTGGTCAATACAAAGAATACGAAGTCA

Strain	SEQ ID NO:	Sequence
		TCGGAACGCATGATGTGCTGCTTGATTCCGGTTTTATTGGGGAATAATGCTAAAGTACTGAGACAGATACTTGGCAAG GTCACAGAGGCTTCATCTAATAACAAGCCCCATTTTGTCTAA

Table 6. Nucleotide sequences of genes encoding an NRPS (*triE*) involved in the biosynthesis of tridecaptin in *Paenibacillus* sp. strains NRRL B-50374, NRRL B-67721, NRRL B-67723, and NRRL B-67724.

Strain	SEQ ID NO:	Sequence
NRRL B-50374	5	TTGAAAGCCTTATTTGAGAAAGGAAAAAATTACTGGAGTCATAAACTGGAATCTGAGGATCATATCATCTGCCTGCC ATACACCAACCAATGTGTCCAGAAAGTACAACGTGTAACGAGTTTAAATTCCTCATACGTACACACTCACATTTTCCAACTGA AATTTCCCAAAGAATATCATCTATAACAGGTGGCGTCCATGGGCCGTGTTATGGTCTCTGCTGGAGTAGAGAG CTTATTGCATAAATACACAGGTGAGGAACGTGTGCTGGCATCCCGGTAGCCAAAGTCTGGCAACGGTGTCTACAA AGCCGATCAACCATCTGCTTTATTGAAAAAATACGCTGGATTCCAGTACAACCTTCAAAGCTTTGCTGTCTCAAATCA AAACCTCTGTGGCGAAGCTATTGAACATCAAAACATTCTTTTGGAACTATTCTGAATTAATTGACATTCAAACGTA ATGAGGATGAAAAGCCTCTTATTACACACACAGTATCCTTGGCAAATAATTCTGATTTTCTGATTTTAAATCACGTACA ATCTGAACCTGGATTTCAGTTTCAATGGGAACATGAAGCAGTCTCCCTGAACGTAAAGTATAGTAGCGACCGTTATAG CGAGACGACGATTGAGCACCTTTGTGAGCAGCTTCTGCGGCTGTACACTATTGTTTGCAGCAGCCAGAGTTGGCGAT TTCCACAGCACAGTACTGTGAGAGCAAGAAAGTAGACAGCTGGTCCATACCTTCAACGATACAAATGTGGATTATC CATGTATGCGTCTATTCTATGAATTGTTCTGTGAACAGGCGAAGCAGGCACACAGCAGGTGGCGGTAGTGTGTGGG CAAGATAGCCTAACCTATGCAGAAATTGAATGAAAAGGCCAACCGACTGGCTCATTTCTTACGTAAGCAGGGAATCCG CACCGAGCAGACGGTCGGCATTTGAGCTGAACGCTCGATCGAGATGATTGTCGGTATGCTCGGAATTCTCAAAGCAG GTGGAGCGTATGTACCCATTGATTCTGATTACCCGGATGAGCGTATACGCTATTGCTGCAGGATTCGGGTGCGGACA TACTGCTCGTGCAAGCAATGGAACATCGGCCCACTGATTTTAAAGGAATGGTCTTGACCTTAGCGATGCTGCAATTT ATGGAACGGATGATGCTGATCGTTACGATCCAAATTTGCCGAATGATCACGGGACGAATACTGATCCGGGATACGTG GACTGCCTAGATCCGTTCTACTCCAATTTCCGCCAGTCCCGAATTTGCTTCTACGACAACCATACAAACAGAACCATG CAACCAAAGCTACGCAATCAGAAACAAGCAGAAACAATACAGCAGGCTTATGCACTGGAGAAACAACCGAAGGCGA GCGCAGCTGGTCGTTTGGCCTATATTATGTACACCTCAGGGACTACAGGCCAGCCCAAGGGGTTATGGTGGAGCAC CGTAATGTCGTGCGTTTGGTGACAAACACAAATTATGCACGCTTGAATGCCGACACGCGCATTTTGCAGACCGGTCT GTTGTCTTTGACGGTCCACCTTCGAAATTTGGGTGCGTTATTGAACGGTGGACAGCTGGTGTGCTGAGTCAGGAT GTTATTTTGGACGCTCCCAAGCTCAAGGAAGTTGTTCGCAATCAGCGCAATCAGCGAATACACAGATGTGGCTGACCGCACCTC TTTAATCAGCTATCCAGCAGGACTTGGAACTATTGAGGGGATGCGGGAGCTATTGGTTGGTGTGATGTGCTGTCC GTACCGCATATTAAACCGGGTATTGGAGGCCCATCCGAACTACATATCAATTAACGGCTACGGTCCGACGGAAAAATAC GACCTTTTCCACCACACATGCCATTACCGGCGTTCAATCGGCATCTGTGCCATTGGTAGCCCGATCCATAACTCGAC GGCATATGTCGTGACCGTTCGATGCAGCTTACGCCATTGAGCGTGGGGGAGCTGATCGTCGGCGGTGACGGG TGGCTCGGGGATATCGCAACCGCCAGACCTGACGACCCGAAAAGTTTCATCGACAGCCCGTTCCGTTGGCGGCGAACGC

Strain	SEQ ID NO:	Sequence
		TGCTATCGTACAGGGACCTGGTGGTTGGAATGCGGATGGGACGCTGGAATATAAGGGACGAATCGACGCGCAGGT GAAATTCGAGGCTACCGGATTGAGCTGGCGAGGTGGAAGCACAGCTGTTGAAGCTGGAGGCAGTCCGAGAAAGCT GTTGTAATTGCACATGAAGATGAGCAGGGGCAAAAGCTGCTCTGCGCATATGTGGTCAACCCATGCGGAAGTAGCGAC AAGTAGCTGCGTAGTGTCTTGTAGTCAGGAGCTGCCGGCTACATGTACCGTCTGTAATTTGTACAGCTGGAGCAATT GCCACTGACGCCCAACGGCAAGGTGGATCGCCGAGCGTTGCCACAGCCAGAGGGAGGTGTAAGCTCAGGCGCAGAA TATGTACCTCCTCAAAATCAATTACAAGCACAACTGGCTAGCATCTGGAAGATGTGCTGGAGCTTGAGCGCATTTGG GATTAAGGATAACTTTTGTAGGCAAGGAGACATCCCTGCGGGCACACATGTCATATCACTCATCTATAAGGAATT GCATAAAATGTGCAGCTAAAGGATTTGTTCAGCATCCGACAAATTGAACAGCTGGCGCAGGTTATTGAAGCACTGG AGCAAACCACTATGAATCCATCCCTGTACGGAGAAATAGCCATTTTATGCGGTCTCTTCGGCTCAAAACGGATGT ATATCCTCAATCAGCTTGATGAGCGGGAATTAGCTATAACATACCTGTGCCCCCTGACTCTGACCGGTTCACTTGATC ACAAGGCACTGGATAACGCGTTCCGTCAGCTTATTGAACGCCATGAACATTTGCGCACAAAGTTTGTAGACCATGAAC GGTGAACCTGTCCAGCGAGTGATGACGAGGTTCCTTTTCGCATGGAATTGACCTATGCTACGGAGCTGCCCAAG GAAACGGATGAGCTGTACATAACTTTGTTACGCCGTTCCGATCTGGGGCAAGCTCCGTTATTCGAGTTGGTTTGATT GAAACAGACCCAGAGCATCATATTTGCTCATAGATATGCATCATATCATTTTCGGACGGTACCTCTATAAATGTACTG ATTCAGGACTTCAATTCATTTATATGCAGGGGACACGCTGCCATCGCTGCGCATTCAGTATAAAGACTACGCCGCTTGG CAACAGAGCAGCAAAAGTGAACGCTACCGGGAACAAGGAAACTACTGGCTCAATACCTTCGCAAGGAGAGCTAC CTGTGCTTGATCTACCGACTGATTATTACGCCCAGCGGTGAGAAGCTTTGAAGGAGATGTGCTGGAAATTTACGCTTG ACCAACGACAAAGTGAAGGCTTAAAGCATTCGCGTGACAGCGGAATCGACATTTATATGCTGCTGTTGGCTGCC TATTCGGCTTTGCTTAGCCACTATAGCGGGCAGGAAGATATTATTGTCGGTTCCGCAATTGCAGGGCGGCCCATGCA GATCTTGGCAGTGTGATCGGGATGTTCTGTGAATACACTGGCAATCCGTAATATCCAGAAAGCGGGGAAACGTTCCG CGAGTATGTGTTGGAGGTCAAGGATAACGCGTTAACAGCTTTTGAACATCAGGATTAATCCGTTTGAAGAGCTGGTGG AGAACTGGGCGTGATCGAGATTTAAGCCGTAATCCGTTATTGTATACCATGTTTGCACTGCAAAACTTAGAGCAAA AAGAGCAGCAGCTGGCGGGTTGCAATTGGCATCCTATCCAAAGTGAACAAACGACGGCCAAATTTGATTTGAGTCTG TTCCGAGTGGAGGATGGAGAACAAATTTCTGTGCTCTTCAATACGGAACCTCGGCTGTACAAACGGGAAACCATTTGA ACGACTGACTGAACAATTTGCAGCAGCTTATCAATGCGGTTATAGAACAGCCGGATATCGTTCTTTCCGGCTATTGAAAT GGTTTCGGCCCAAGAAAGAGCTGCTTGTGTCAGAGATTCAATGATACGGTAGCAGACTATCCGTATCCACGAGATC AAGCACTGCATGTGCTGTTTCGAGGAACAGGTAGTGCAATCACCCAGATCGGCTGGCCGTCACCTTTGCGGACACGCGAG CTTACCTACCGGAGCTGAATGAACGTGCCAACCGTCTGGCACGCATACCTGCTTCCCATGGGATACGGCGCGGTCC GAGCCAGAGACACAGCGAGTAGGGATTATGGCTGAACGCTCCATTGAAATGTCGTCGGTATGCTGGCGGATTTTGAA GGTCGGAGGGGCTTACGTTCCCATTTGATCCTGATTATCCTGAGGAGCGGTATCCGTTATTTACTGGAGGATTCCAGTGC

Strain	SEQ ID NO:	Sequence
		TGGGCTGTACTGTTACAGCGACGTGAGCAGATTCCCTTTTGAACCCCGGCATTCCGATCATCGATTGAGTGATGAACA GCGATGCAATAGCAATCTGAATGTGACGCTCAGACGGATGGAACAATTGCGATTACAACAGGGGGATCTTCCTCCG ATCTTGCGTACGTGATACACCTCTGTCAGACAGCAAGCCGAGGGGTGATGATTGAGCACCCTAATGTCGTG CGCCTAGTGAAAAACAAGCTATGCCATGCTTGATGAATAACACGTATGCTGCAATTGGGCGCAGTTGTGTTCGA TGCCCTCCACATTTGAAAATTTGGGAACGCTGCTGAACGGGGACAACCTGTATGTGTAAGTCAATGACACTATTCTGGA TGCCCTCCAAAGCTCAAGCAGCGGATTGACAAAGTATCGTGTAAACAGATGTTCATGACCAACGGCTTTATTCATCAATCAGTA TTCGCAGCAAGAAATCGGAGTGTGCTTGAAGGAGTTGCTCGTGGGTGGTGTATGATTGCTGTACCAACACGT CAATCGTGTGTTGAAGGAGTACCCGACGCTTCGCCAATATTTATGGGCCGACGGAGAACACCACTTTTCCAC CATCTATGACATTACAGAACCGCAACCCAGGCTATTCCCATTGGACGTCCAATTGATCACTCGACCGCTTATGTGGT CAATCGTTCTGTTGAAGCTGCAACCTATCGGAGCCCTGGGAGAGCTGATCGTGGCGACGGGCTTGGGCGGAGGAT ATCTGAATCGGCCGAGCTTACGGCGGAAAAATTTATTGAAAAGTCCATTCCGGTCTGGAGAATATTGCTATCGTACAG GGGACTTAGTGGCTGGCTGATGTTGTAAGTGTACAAAGGGAAGAAATGGATGAACAGGTCAAAATTCGGGGC TACCGCATTTGAATGAAATGAAACCCGTTTGTCCACGATCCAGGTGTAAGGAATCGGTTGTTACCGTGGCG CAGGATGATCAGGACAAACACAGCTGTGCTTATTTGCAACAGACAGTGAATTGAGCGCCAGCGACTTACGTAA CATTTGTGCGAGGATCTGCCGTGCTATATGTTGCGCTTACTTTGTGACGCTCTCCAGACTGCCCTTTGACGCTGAAT GGCAAGTAGACCGCAGGGCACTGCCCGCACTGAGCACAACTCTCGATACAGGTATGGATTATATGGCACCTGAGAC GGATGTCCAAACAGGCACTGGCTACGGCTTGGGAGCCATTCTTGGTATCCCGAAAGTCGGAATACAGGATAACTTTT CCATTGGGTGGTGACTCCATCAAGGCCATCCAAAGTATCGTCTCGCTTTCAGGGTGGATACAAGCTGGAAATGAA GGACTTGTTCAAATACCCGACAAATTCGGGACTAAGCACATAATTCAAGCTGTTAACCGAATAGCCGAGCAGGGCG AGGTTACAGGAATGTAGTCTTACACCGATTACAGCGCTGGTTTGTGAACAGCCAACGGGAGAACCACTATTTTA ACCAATCTGTCA TGCTCTATCGTCAGGAAGGCTATGACGAACAGGCACTACGGGCGGCGATCCATCAGATTACATCG CACCATGATGCAATTGCGTATGTTTGTGTCGGAGAACGGATGTACAGCATGGAACCGCAGTATAGAGGAAGG CGAACCGTACCATCTGGAGTCTTTGACTATAATGACAGCGATGTAAACAAGCAAGATTGCGGAAGATAATTGAAG CGAAATGCAATGAAATCTGATTTCCCTAAGCGAAGGTCCTGTAGACTGGGGCTGTTCCTGTTGCCCGG ATGGAGATCATCTGCTGCTGATTCAATCTTGGCGGTGACGGGTATCTTGGCGCATTTTATTCGAGGATTGG CGACTGCCCTATGATCAAGCCCTCCAAGGTGAACAGGTGATTCAAGCTGCCCTCATAAACAGATTCTGTTCCAAACGTTG GCCGAGCAGCTGCACGCTTACGCCAACAGTCCAGCTATGGAACGTGAGCGAGCGTATTGGGGGAAACTTGCACAAGC GGAACTGGCTCCTTTGCCGAGGATTACGGGCATAACGAGCACGAAAGCCATTGATTGGCGATAGTGAGTCGGTTA CTGCTTTGTGGACACATGCTGAGACAGAGCAGCTGCTCAAGCAGGCCAATCGTGCCTACCGTACAGAAATTAATGAC CTGTTGTTGACGGCGGTAGGAATGGCAATTGCAAGCATGGAGCGGACATGAGCGTTTCTGTATTATCTGGAGGGACA

Strain	SEQ ID NO:	Sequence
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Strain	SEQ ID NO:	Sequence
		TTGCTATTTTGACGGACAGATTGTCAATCTGAATGAGGATACGTCCTACAGTGCAGATGCTTCCAATCTGGGTATAGA TGGAGCGGGTAATCATGCTGCTTATGTCAATTTATACCTCAGGTTCAACAGGTAAGCCTAAGGGTGTCTGTTGTGAGCA TCAAAGTGTCTGCGCCTTGTCGCAATACGAATTAATGTGCCATTTGATGAATCGACCCGAATGCTGCAGACTTGCGC GTTTGTATTGTATCTACGTTTGAATTTGGGCGCGCTGCTGAACGGCGGTGAGCTTGTCTTGTGTCATAAAGGAT GATCTATTGACGCGGCCAAGCTTAAAGAGACGATACGGGATCATCGCGTCACCATGATGTGGCTGACACACACCGTT ATTTAATCAGCTTTCACAGCAGGATAGTAACTTTTCGGCGATGTGAAGTATTTGCTGTTGGTGGTGAATGTTTGTCT GCACCCCATATTACCGGGTTCTGCGGATAATCCGGACATCAACATCATTACGGCTATGGGCCAACGGAAAATAC AACCTTTTCGACGACGTATCATTACGGAAGAACAGCTGGAATCTGTGCCGATCGGACGCCCATCCGCAATTCGAC GGCGTATGTTGTGATTCTGTCATTTAACCTGCAACCGGTGAGACTTGGGGTGAAGCTTGTGCGGAGACGGAGT TGCACGTGGTTATCTAAACCGTCTGAGCTGACGGCTGAGAGATTCTTGTCTAACCCGTGGTGGACGGAGATCGCCT GTA CTGTACGGGAGACCTTGTTCGCTGGCTGAAGACGGCATACTGGAATACGCTGGACGGATTGATCAACAGGTTA AAATTCGCGGTTACCGGATTGAGCTGGCGAGGTGGAGCGCGCTGGCAAGTGTACCGTCCGTGCGGGATAGCGTT GTTATCGCTTTGCGGGATGGAGCAGGTCAGCAGCAATTATGTGCTTACTTCACTGCCGATGAACAGCTGACCATCCGT GAGATTGAGCTGCGATGTCGGCCAGTCTGCCGAGCTATATGATCCATCCGCAATTTGTACAGCTGGATCGGTTTCCG CTGACGACAAACGGCAAAATCGACCCGAAAGCTTTACCTGTGCCGACAAAGGGCTGCACACGGGTATAGAATAATGT CGCACCGCGAACCGATGTGGAACAGTTGCTGGCAGCCATTGTCGAGGAAGTACTTGAATTCACAAAGTGGGTATCC ACGATGACTTTTTCACGTTAGGTGGACATTCCTTAAAGTACTGGAGCTTATACGCAAGTTCACCTTGCTACAGATA TTGAGCTTCCCATCCGATAGTGTCTGGACTTCCCACTATAGAACGCGCAGCGCTCACATTAATTGAAAGCCGATCTGG AGTACAAGGCCGATAGTCCAATCATTCGGTTGAATGAACACGGTCCGATCTCCATCTTCTGCTTCTCCTATGCTTGG ATACGGCTGTCTGCGGAGCTTGCGAAACAACTGGATCAGGACGCAAGTGTGATGGGTTGGAGTTCGTAGATG ATGCTGCGGATGAGCAGGCCATGCTGGCACGTTACGTTGATTTGATCGTCAGCACGCAAGCGCAAGGTCCGTATGTG CTGCTTGGTTATTCCATAGGTGTAATCTGGCGCATAAAGGTTGCTGACACACTGGAACGTCAAGGTCACTACTGTATCC GATATTTTATGCTCGATTTCGGTCAAAAGGGCGGAAGCCCTGCCCTTCACAGTTGAAGAAACAGAGCATGAAATTCAT GACATGCTGGAACAAAGTTCCGACTCTACCGTGAGCTGTTGAATGAACAGTACCAACGTAAAATGATCGCTTACGC GGTATATGGCAACAGCTTGTGAATACAGAGAGCGTTACAGCGAATATTCACGGCTTGTGCGCGTTGGATCAGAAA CGGTCAAGGGTACAGGAGATAATCGACTTTTATGGAAGACGCTACACAAGGTAGCTATGAAGAGCATAGCTTGATT GGCAATCATATTATGAACTGCTGGAACCCGGATTATTCGAGGAAATGTAAAAGTATCCGTGCCACAATACAAAAGAT AACTCGGAACACGGACAAAGACATGACACAAGACTTGGCACATCAATAATCTTGA
NRRL B-67721	6	TTGAAAGCCTTATTGAGAAAGGAAAAAATTACTGGAGTCATAAACTGGAATCTGAGGATCATATCATCTGCCCTACC ATACACCAACCATGTGTCCAGAAAGTACAACTGTAACGAGTTTAAATTCCCATACGTACACACTCACATTTCCAACTGA

Strain	SEQ ID NO:	Sequence
		AATTCCCAAAGAATATCATCTATAACAGGTGGCGCTCCATGGGCCGTGTTTATGGTCCCTGCTTGTGGAGTAGAGAG CTTATTGCATAAATACACAGGTGAGGAACGTGTGCTGTGGCATCCCGGTAGCCAAAGTCTGGCAACGGTGTCTACAA AGCCGATCAACCATCTGCTTTATTGAAAATAACGCTGGATTCCAGCACAACTTCAAAAGCTTGTCTCAAAATCA AAACCTCTGTGGCGAAGCTATTGAACATCAAAACATTCCTTTTGGAACTATTCTGAATTAATTGACATTCACACGTA ATGAGGATGGAAAGCCCTCTTATTACACCCACAGTATCCTTGGCAAAATATTCAATATATCTGAATTTTGAATCACGTAC AATCCGAACATACTTCCAGTTTCAATGGGAACATGAAGCGTCTCCCTGAACGTAAAGTATAGTAGCGACCGTTATA GGGAGACGACGATTGAGCACTTTGTGAGCAGCTTCTGCGGCTGTACACTATTGTTTTCAGCAGCCAGAGTTGGCGA TTTCCACAGCACAAAGTACTGTCAGAGCAAGAAGTAGAGCAGCTGGTCCATACCTTCAACGATACAACTGTGGATTAT CCACGTCAATGCGTCTATTTCATGAAATGTTTCGTGAACAGGGCAAGCAGGCCACCAAGCAGGTGGCGGTAGTGTGG GCAAGATCGCCTAACCTATGCAGAAATGAAATGAAGGCCAACCGACTGGCTCATTTCTTACGTAAAGCAGGGAAATCC GCACTGAGCAGACGGTCCGCAATGTAGCTGAACGCTCGATTGAGATGATTGCTCGGTATGCTCGGAATTCCTCAAAGCA GGTGAGCGTATGTACCCATTGATTCTGATTACCCGATGAGCGTATACGCTATTGCTGCAGGATTCGGTGGGAC ATACTGCTCGTCAGCGAATGGAACATCGGCCACTGATTTTAAAGGATTGGTGTGACCTTAGCGATGTCGCAATT TACGGAAACGGATGATGCTGATCGTTACGATCCAAATTTGCGCAATGATCAGCGGACGAATACTGATCCGGGATACGT GGACTGCTAGATCCGTTCTACTCCATTTTCGCCAGTCCCGAACTTGCTTCTACGACAACCATACAAACCGAAACCAT GCAACCAAAAGCTACGCAATCAGAACAAAGCAGAACAAATACAGCAGGCTTATGCAAGCTGGAGAACAAACCGAAGGCG AGCGCAGCTGCTGTTGGCCTATATTATGTACACCTCAGGGACTACAGGCCAGCCCAAGGGGTTATGTTGGAGCA CCGTAATGTCGTGCTTTGGTGACAAACACAATATATGCACGCTTGAATGCCGACACCGCGCATTTTTCAGACCGGGTC TGTTGCTTTTGACCGCTCCACCTTCGAAATTTGGGTGCGTTATTGAACGGTGGACAGCTGGTGTGTCAGTCAGGA TGTTATTTTGGACCGGCCCAAGCTCAAGGAAGTTGTTCGCAATCACGGCATTACCAAGATGTGGCTGACCGCACCGCT CTTTAATCAGCTATCCACAGCAAGGACTTTGGAAGTATTGAGGGGATGCGGGAGCTATTGTTGGTGGTGTGCTGTCTC CGTACCGCATATTAAACCGGGTATTGGAGGCCCATCCGAATCTACATATCATTAACGGCTACGGTCCGACGGAAATA CGACCTTTTCCACCACACATGCCATTACCGCGGTTCAATCGGCATCTGTGCCATTTGGTAGCCCGATCCATAACTCGA CGGCATATGTCGTGAACCGTTGATGCAGCTCCAGCCTGTGAGCGGTGGGAGAACTGATCGTCGGCGGTGACGGG GTGGCTCGGGATACCGCAACCGCCAGAACTGACGACCGGAAAGTTCAATTGACAGTCCGTTTCGTGGCGGGGAAACG CTGCTATCGAACAGGGGACCTGTGCGTTGGAATGCGGACGGGACGCTGGAATATAGGAGCAATATCGACGCAACAG GTGAAAATTTCGAGGCTACCGGATTGAGCTGGCGAGGTGGAAGCACTGCTGTGAAAGCTGGAGGCAATCCGAGAAG CTGTTGTAAATTGCACATGAAGATGAGCAGGGGCAAAAGCTGCTCTGCGCATATGTGCTCACCCATGCGGAAGTAGCG ACAAAGTGAGCTGCGTAGTCTTTGAGTCAGGAGCTGCGGGGCTACATGGTACCGTCTGTTTGTACAGCTGGAGCA ATTGCCACTGACGCCCCAACGGCAAGGTGGATCGCCGAGCGTTGCCACAGCCAGAGGGAGGTGTAAAGCTCAGGGCGCA

Strain	SEQ ID NO:	Sequence
		GAATATGTACCTCCTCAAAATCAATTACAAGCACAACTGGGTAGCATCTGGAAAGATGTGCTGGAGCTTGAGCGCAT TGGGATTAAAGGATAACTTTTGTAGGCAGGAGGACATTCCTCTCGGGGACACATGTTCATATCACTCATTTTATAAGGA ATTGCATAAAAATGTGCAGCTAAAGGATTGTTCAGCATCCGACAAATTGAACAGCTGGCGCAGGTTATTGAAGCAC TGGAGCAAACCACTATGAATCCATCCCTGTACGGAGAAATAAGCCATTTTATGCGGTCTCTTCGGCTCAAAAACGGA TGTATATCCTCAATCAGCTTGTATGAGAGGGAATTAGCTATAACATACCTGTGCTGCTGACTCTGACCGGTTCACTTG ATCACAAGGCACTGGATAACGCTTCCGTACGCTTATTGAACGCCATGAAACATTTGCGCACAAAGTTTGTAGACCATG AACGGTGAACCTGTCCAGCGAGTGATGACGAGGTTCCTTTTCGCATGGAATTGACCTATGCTCACGGAGCTGCCCA AAGGAAACGGATGAGCTGGTACGTAACTTTGTTCAAGCGTTTCGATCTGGAGCAGGCTCCGTTATTCGGAGTTGGTTG ATTGAAACAGACCCAGAGCATCATATTTGCTCATAGATATGCATCATATCATTTTCGGACGTAACCTCTATAAATGTA CTGATTTCAGGACTTTCATTTATATGCAGGCGACACGCTGCCATCGCTGCGCATTCAGTATAAAGACTACGCCGCT TGGCAACAGAAAGCAGCAAAAGTGAACGCTACCGAGAACAGGAAAACTACTGGCTCAATACCTTCGCGGGGAGC TACCAGTGTCTTCCGACTGATTATCCACGCCCGCGGTGAGAAAGCTTTGAAAGGAGATGTGCTGGAAATTTACGC TTGACCAACGACAAAAGTGAAGGCTTAAAAGCAATTGCGGTGAAGACGGAATCGACATATATATGGTGTGTTGGCT GCCTATTCCGGCTTTGCTTAGCCACTATAGCGGGCAGGAAGATATTTATGTCGGTTCGCCAAATTGCAGGCGGCCCAT GCGGATCTTGGCAGTGTGATCGGGATGTTCTGTAATACACTGGCAATCCGTAATTATCCAGAAAGCGGGGAAAACGTT CCGCGATTATGTGTTGGAGGTCAAGGAAAATGCGTTAAAGGCTTTTGAACATCAGGATTATCCGTTTGAAGAGCTGGT GGAGAAAGCTGGGCTAGATCGAGATTAAAGCCGTAATCCGTTATTGTATACCATGTTTGCACCTACAAAACATAGAGC AAAAGAGCAGCAGCTGGCGGGCTGCAATTGGCATCTTATCCAAAGTGAGCAAAACGACGCCAAATTTGATTGAGT CTGTTCCGAGTGGAGATGGAGAACAAATTTCTGTGCTCTTCAATACGGAACTCGGCTGTACAAACGGGAAACCAT TGAAACGACTGACTGAACATTTGACAGCAGCTTATCAATGCGGTTATAAAGACCGGATATCGCTCTTTTCGGCTATAGA AATGTTTTCGGCCCAAGAAAAGAGCTGCTTGTGACAGAGATTCAATGATACGGTAGCAGACTATCCGTATCCACGAG ATCAAGCACTGCATGTGTTGTTTCGAGGAACAGGTAGCGCAATCACAGATCGGCTGCCCTCACCTTTGCGGACATG CAGCTTACCTACCGGAGCTGAATGAACGTGCCGACCGTCTGCGCACACATACCTGCTTCCCATGGGATACGGCGCG CTCCGAGCCAGACACAGCGAGTAGGATTATGGCTGAACGCTCCATTGAATGCTGCTCGGTATGCTGGCGATT TAAAGGTCGGAGGGCTTACGTTCCCATTTGATCCCGATTATCCTGAGGAGCGTATCCGTTATTTACTGGAGGATTCCA GTGCTGGGCTGTTACTGTTACAGCAGCGACGTGAACAGATGCTTTTGAACCGGCAATCCGGTCAATCGATTGAGTGTG AACAAAGATGGAATAGCAAAATCTGAAGGTGACGCTCATACCGATGGAAACAATTGCGATTACAAACAGGGGATCTTCC TCCGATCTTGGTACGTGATCTACACCTCTGGTACGACAGGCAAGCCGAAGGGCGTGTGATGATGAGCACCGTAATGT CGTGGCCTAGTGAAAAACAAAGCTATGCCATGCTTGATGAAAAATACAGTATGCTGCAATTTGGCGCAGTTGTGT TCGATGCCCTCCACATTTGAAAATTTGGGGAACGCTGCTGAACGGGGGACAACTGTATGTGGTAAGCCATGACACTATTC

Strain	SEQ ID NO:	Sequence
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Strain	SEQ ID NO:	Sequence
		GAGGCCAAGTGGTCTGACGATTAGCTATAGTCGTACCACTATAGACCGGAGACCATCGAGCGATTGGCGAAATTCCTGGAATCGAGCCCTGCGTGAAATTTGGCGCATTCATCCATAAAGAACACCCGAGCTTACCCCAAGTGATATTTCCATAAGGAAATGAGTGGAGCCCTTGGACAGTCTTATCTGAAATGGGTGCTGCGGTGAGATCGACAATGTATATGCACTGACCCCGATGCAGAAAGGATGCTGTTTCACAGCCAGCTAGATAGTCAAGCAGCTGCAATGACCGGTATTGAGCAGGTTTCTTATGATATGCGAGGTCAGATGGACATTCGGGCTTTTGCAGAAAGCCTGAATATTCTGTTCCGGC GACATGAGGGCGCTGCGTACACATTTGTATTTTGGCAGAGATACGGAACCGTTGCAAGGTGGTGAATAATTTCAAGCTACA TGCGGCTTTCAATATGAAGATTTACACCATCTAGATGAGGATGCAAAAGATACCTGGGTGAAATAATTTCAAGCTACA AGATAAGCACGGGGCTTTGATCTGCGTCGGGATGTCTTGTGCTGCTAGCGATTTTACGTACCGGAGAAAGACAGCT ATCATTTTGTATGGAGCTTTTCATCATATCGTCAATGGACGGCTGTCTGTCCCTTATAACAAAGAGTGTGTTGAAA GCTATGCAGCACTTCAGGAGGGCAGAGTACCAGAACTGGCACCCGCACTGCCGTACAGCCGCTTTTATTGAAATGGCTG GAAGCACAGGATCGCAAGGGCGCAACCGACTACTGGAGCAGCTATTATCCGGATATGAGCAGCAACACAGCGTTAC CAGCTGTAAAATCCGGTCGCAAGAGTGAAAGGCAACACGGCTAGTATGGGTGACGGTTTGGAAACGTGAGTTGACC CTCCGGGTGGAGAGACGGCTAAGCGATATCAAGTGACCATGAATACGTTATTACAACCGCATGGGGATTGTGCT GCAAAAATATAACAACACAGTGA TGTCGTATTTGGCAGTGTCTCAGCCGTCCTCAGATATATTCGGGGTAG AGGATATTATCGGCTTGTTCAATTAATACCAATCCCGTTCCGATCTTAGTAGGCAGGGGAATCTTTTGCAGAAATTTAT GAAAGAAACGCAGGAGCAGCGCTGGCTTCTCATGCTATATGATACGTAATCCACTGTTTGGAGATTCAAGGCATTGACCGG ACCAGAAACAGGATTTAATTAAACCATATTATGGTGTGTTGAAAATTTATCCAGTAGATGAGCAGTCGAGGAACTGGGA AGTGACGGGCAGGATACATTTCTCGATTTCATGCAATGTTGGTGGCTGCAGAGCAGACTAACTATGATCTGAGCTTATGTCGTT ATGCCGGGAGAAATGCATCAAGATTCGTTTATGATAACCGCTTAAGTTATGATCAACACAGGCATTGAGCGTCTGCAT GGACATTTTGTGAACCTGTTGGAGCAAGTTTGTCTAACCCGAAATGTTTGGCTAGAGAGCTGGAACCTGGTTACAGCG GCGGAAACAAACAAATTACAGGAGAGTTTAAATGACACTGCCCTGTGCAATATCCAAAGCAATCACACGATCCAAAACCT GTTTGAGGAGCAGGAGAGCGCACGCCGATCATATTGCCGTAGCTTTGGGTCAATCAATCATTTGACCTATCGGGAAC TCAATGAGACAGCAACCGTTTACCGCATACCGTGGCTGATGCGAGGGTGAAATCCGATGAACCTGTGGCATTTTIG ACGGAGCGCTCACTGGATATGATACGGGAACACTCGCTATTTTGAAGGTGGTGGCGGTATGTGCCGTAGACCC TCAATATCCGGAGGACCGTATCCGTTATATGCTGGAGGACTCGGGAGCCAAAGTGTGCTGGCTCAGCAGGATTTACT GGATCGTTGCTATTTTGAATGGACAGATTGTCAATCTGAATGAGGATACGTCTTACAGTGCAGATGCTTCCAAATCTGGG TATAGATGAGCGGGTAAATCATGCTGCTTATGTCTATTATACCTCAGGTTCAACAGGTAAGCCTAAGGGTGTCTGTTGT TGAGCATCAAAAGTGTGCTGCGCCTTGTCCGCAATACGGATTATGTGCCATTGTGATGAATCGACCCGAATGCTGCAGAC TTGCGCGTTTGTATTGTATCTACGTTTGAATTTGGGGCGGCTGTGTAACGGGGTCAAGCTTGTCTTGTGTCAT AAGGATGATCTATTGGACCGGCCAAAGCTTAAAGAGACGATACGGGATCATCGCGTCACCATGATGTGGCTGACCAC

Strain	SEQ ID NO:	Sequence
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NRRL B-67723	7	TTGAAAGCCTTATTTGAGAGGAAATAAATTAAGTGGATCATAAAGCTGGAATCTGAGGATCATATCATCTGCTGCTG CATATACCAACACGTGTCCAAGGATGCAACTGCAACGAATTTAAATTCCTTACGTACACGCTCACATTTCCATCT GAAATTTCCGGACGAATATTGTCTATAACAGGTGGCGCTCCATGGGAGTGTATATGTTCTGCTGCTGGAGTAG AAAGCCTGTTACATAAATACACAGGTGAGGAACGTGTGCTGTTGGGCATTCGCGTAGCCAAAGTCTGGCAACGGTGC TACAAAGCCGATCAATCATCTGCTCATACTGAAAACACTCGCTGATCTACAAAGCCTTCAAGCCTTGTGCTCTC AAATCAAAACCTCTGTGAGCGGAAGCGATTGAGCACCAAAATATACCTTTTGGAACTATACCGAGGGCTTGAAAT TCCACGTAAACGAGGTGAACAGCCTCTTATTACACACCGGATCCTTGTGCAAAACATCCATATTTCCGATTTTTCGA

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Strain	SEQ ID NO:	Sequence
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Strain	SEQ ID NO:	Sequence
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Strain	SEQ ID NO:	Sequence
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NRRL B-67724	8	TTGAAAGCCTTATTTGAGAAAGGAAAAAATTAACCTGGAGCCATAAACTGGAATCTGAGGATCATATCATCTGTCTTCCA TATACTAACAAACGTGTCCAAAAGTACAACTGCAACGAGTTTAAATTCACACACATACACACTCACATTTCCATCTGAA ATTTCCCAAAGAATATCATCTATAACAGGTGGCGCTCCATGGGCCGTGTTATGGTCTGCTGCTGGAGTAGAGAGC TTATTGTCATAAATACACATGTGAGGAACGTGTGCTGCTGGGCAATCCGGTAGCCAAAGTCTAGCAACGGTGTCTACAAA GCCGATCAACCATCTGCTTTTATTGAATAATACGCTGTGATTCCAGCACAACTTCAAGCCTTGTGCTCTCAAATCAA AACCTCTGTCGGGAAGCTATTGAACATCAAAACATTCCTTTTGGAACTATTCTGAATTACTTGACATTTCAACGTAA TGAGGATGGAAGCCCTCTTATTCACACCACAGTATCCTTGCAAAATATTCATATTTCTGATTTTGTGAATCACGTACAA CCTGAACCTAGATTCCAGTTTCAATGGGAACATGAAGCGGTCTCCCTGAACGTAAAGTATAATAGCGACCGTTATAGC GAGACGCGATTGAGCACCTTTGTTGAGCAGCTTCTGCGGCTGTACACTATTGTTTTCAGCAGCCAGAGATTGGCGGATT

Strain	SEQ ID NO:	Sequence
		TCCACAGCACAGTGTCTCAGAGCAAGAGTAGAGCAGCTGCTCCATACCTTCAACGATACAAATGTGGATTATCC ACGTCAATGCGTCTATTCAATGATTGTCGAGAAACAGGTGAAGCAGACACACAGCAGGTGGCGGTAGTGTGTGGGC AAGATAGCCTAACCTATGCAGATTGAAATGAAAAGGCCAACCGACTGGCTCATTTCTTACGTAAAGCAGGAAATCCGC ACCGAGCAGACGGTCGGCATTTGAGCTGAACGCTCGATTGAGATGATTGTCGGTATGCTCGGAATTCTCAAGCAGG TGGAGCGTATGTACCTATTGATTCTGATTACCCGGATGAGCGTGTACGCTATTACTGAAGGATTCGGTGGCGACAT ACTGCTCGTGCAGCGAATGGAACATCGGCCACTGATTTAAGGGAAGGTGCTTGACCTTAGCGATGCTGCAATTTA TGGAACGGATGATGCTGATCGTTACGATCCCATTTTGCCGAATGATCACGGAACGAATACTGATCCGGGATACGTGG ACTGCCTAGATCCGTTCTACTCCATTTCCGCCAGTCCCGAACTTGCTTCTACGACACCAATACACAGAAACATGC AACCAGAGCTACGCAATCAGAACAGCAAAATAACAGCAGACTTATGCAGCTAAGAACACCCGAAGGCGAG CGCAGCTGATTGCTTGGCCTATATTATGTACACCTCAGGGACTACAGGCCAGCCCAAGGGGTTATGTTGGAGCAC GTAATGTGCTGCGTTTGTGACAAATACAACTATGCACGCTTGAATGCCGACACACCGCATTTTGCAGACCGGGTCTG TTGTCTTTGACGCTCCACCTTCGAAATTTGGGTGCGCTATTGAACGGTGGACAGCTTGTGCTGGTGAATCAGGATG TTATTTTGGACGGCCCAAGCTCAAGGAAGTTGTTCGCAATCACGGCAATACACGATGTGGCTGACCGCACCACTCT TTAATCAGCTATCCCAAGCAGGACTTGGAACTATTGTAGGGAATGCAGGAGCTGTGGTGGTGTGATGTGCTGTCCG TACCGCATATTAAACCGGTATTGGAGGCCATCCGAATCTACATATTATTAACGGCTACGTTCCGACGGAATAACG ACCTTTTCCACCCACATGCCAATTACCGGCGTTCAATCGGCAATCTGTGCCCATTTGTAGCCCCGATCCATAACTCGACG GCATATGTTGTGACGGTTCGATGCAGCTCCAGCTGTTGGAGCGTGGGAGAACTGATCGTCGGCGGTGACGGGT GGCTCGCGGATACCGCAACCGCCAGAACTGACGACCGAAAGTTCAATTGACAGTCCGTTCCGTGGCGGCGAACGCT GCTATCGAACAGGGACCTGGTGGATTGGAATGCGGACGGGACGCTGGAATATAAGGACGAATCGACGCGCAGGT GAAATTTCGAGGCTACCGGATTGAGCTGGCGGAGGTGGAAGCACAGCTGTTGAAAGCTGGAGGCACTCCGAGAGCT GTTGTAATTGCACATGAAGATGAGCAGGGGCAAAAGCTGCTCTGCGCATATGTGGTCAACCCATGCGGAAGTAGCGAC AAGTGAGCTGCGTAGTGTCTTGAAGCCAGGAGCTACCGGGTACATGTAACCGTCTGTAATTTGTGACGCTGGAGCAATT GCCACTGACGCCCAATGGCAAGGTGATCGCCGAGCGTTGCCACACACAGAGGAGGTGTAAAGCTCAGGCGCAGAA TATGTACCTCCTCAAAATCAATTACAAGCACAACTGGTAGCATCTGGAAAGATGTGCTGGAGCTTGAGCGCATGG GATTAAAGGATAACTTTTTTGAAGCAGGAGGACATTCCTTGGCGGACACATGTCATATCACTCATCTATAAGGAATT GCATAAAATGTGCAACTAAAGGATCTGTTCAGCATCCGACAAATTGAACAGCTGGCGCAGGTTATTGAAGCAGCTG AGCAAAACCACTATGAATCCATCCCTGTTACGGAGAAATAGCCATTTTATGCGGTTTCTTCAAGCTCAAAACGGATGT ATATCCTCAATCAGCTTGATGGAGCGGGAATTAGCTATAACATACCTGTTGCCCTGACTCTGACCGGTTCACTTGATC ACAAAGGCACTGGATAACGCGTTCGTCAGCTTATTGACCGCCATGAACATTTGGCGCACAAAGTTTGGAGACCATGAAC GGTGAACTGTCCAGCGAGTACATGACGAGGTTCTTTTGTGATGGAAATTGACCTATGCTCACGGAGCTGCCCCAAAG

Strain	SEQ ID NO:	Sequence
		GAAACGGATGAGCTGGTACGTAACTTTGTCCAAACCATTCGATCTGGGGCAGGCCCCGTTATTCCGAGTTGGTTTGATT GAAACAGACCCAGAGCATCATATTTTGCTCATGGACATGCATCATATCATTTTCGGACGGCACCTCTATAAATGTACTA ATTACAGGACTTTATTATATGCAGGGGACACACTGCCATCGCTACGCATTACGTATAAAGACTACGCCGCTTGG CAACAGAAAGCAGCAAAAGTGAACGCTACCGGGAACAGGAAACTACTGGCTCAATACCTTCGCAGGAGAGCTAC CTGTGCTTGATCTACCGACTGATTATCCACGCCAGCGGTGAGAAAGCTTTGAAGGAGATGTGCTGGAAATTAACGCTTG ACCAACGACAAGCGAAGGCTTAAAGCATTTGCGGTGACAGCGGAATCGACATTATATATGCTGTGCTGGCTGCC TATTCGGCTTTGCTTAGCCACTATAGCGGGCAGGAGAAATTAATGTGCTGGTTCCCAATTGACAGGGGCCCCCATGCC GATCTTGGCAGTCTGATCGGGATGTTCTGTGAATACACTGGCAATCCGTAATTATCCAGAAAGCGGGGAAAACGTTCCG CGATTATGTGTGGAGGTCAAGGAAACGCGTTAAGGCTTTTGAACATCAGGATTATCCGTTTGAAGAGCTGGTGG AGAAAGCTGGCGTGCATCGAGATTAAAGCCGTAATCCGTTATTGATACCAATGTTGCACTGCAAAAATTAGAGCAA AAAGAGCAACAGCTGGCGGCTTCAATTGGCATCCTATCCAAAGTGAACAAACGACGGCCAAATTTGATTGAGTCT GTTCCGAGTGGAGATGGAGAACAAATTTCTGTGCTCTGCAATACGGAACCTCGGTGTACAAACGGGAAACCATTG AACGACTGACTGAACATTTGCAGCAGCTTATCAATGCGGTTATAGAACAGCCGGATATCGTTCTTTCCGGCTATTGAAA TGGTTTCGGCCCCAAGAAAAGAGCTGCTGTGCAGAGATTCAATGATACGGTAGCAGACTATCCGTATCCACGAGAT CAAGCACTGCATGTGCTGTTCGAGAACAGGTAGCGCAATCACAGATCGGCTGGCGTCACTTTTGGGACATGCA GCTTACCTACCGCGAGCTGAATGAACGTGCCAACCGTCTGGCACGCAATACCTCGCTTCCCAATGGGATACGGCGCGGT GCGAGCCAGAGACACAGCGAGTAGGGAATTATGGCTGAACGCTCCATTGAAATGGTCGCTGATGCTGGCGATTITG AAGTTCGGAGGGCTTACGTTCCCATTGATCCCGATTATCCTGAGGAGCGTATCCGTTATTTACTGGAGGATCCAGT GCGGGGCTGTTACTGTTACAGCGACGTGAGCAGATGCCTTTGAACCCGGCATTCGGTCAATTGATTTGAGTGATGAA CAACGATGGAATAGCAATCTGAATGTGACACTCATACCGATGGAACAATTGCGATTACAACAGGGGGAATCTCCTC AGATCTTGGCTATGTGATCTACACCTCTGCTACGACAGGCAAAACCGAAGGCGTGTGATGATTGAGCACCGTAATGTG TGCGGCTAGTGAAAACAAAGCTATGCCATGCTTGTGATGAAATACACGATGCTGCAATTTGGCGCAGTTGTGTTT GATGCCCTCCACATTTGAAATCTGGGAAACGCTGCTGAACGGGGACAACTGTATGTGTAAGCCATGACACTATTCT GGATGCCCTCCAAGCTCAAGCAGGCGATTGACAAGTATCGTGTAAACACGATGTTTCATGACACCGCTTTATTCAATCA GTATTCCGACGAAGAAATCGGAGTGTTTGCGTCTTGAAGGAGTTGCTCGTGGTGGTGTGATGTGTGTCTGTACCCACA CGTCAATCGTGTGTGAAGGAGTACCCGACGCTTCGCTGGCCAAATATTTATGGGCCGACGGAGAACACACCTTTTC CACCATCTATGACATTACAGAAACCGCAACCCCTGGCTATTTCCCAATTGGACGTTCCAAATTGATCACTCGACCGCTTATGT GGTCAATCGTTCGTTGAAGCTGCAACCTATCGGAGCCCTGGGAGAGATTGATCGTGGTGGCGACGGTGTGGGCGGAG GATATCTGAATCGGGCCGAGCTTACGGCGGAAAATTTATTGAAAGTCCATTCCGGTCTGGAGAAATATTGCTATCGTA CAGGAGACTTAGTGCGTTGGCGTGTGATGCTGACTGGAGTACAAGGGAGAAATGGATGAACAGGTCAAAATTCGC

Strain	SEQ ID NO:	Sequence
		GGCTACCGCATTTGAACTGGGTGAAATTTGAAACCCGATTGTCCACAAATCCAGGTGTGAAGGAATCGGTGTTACCGT GCGCAGGATGATCAGGACAAAAACAGCTGTGTGCCTATTTTGCAACAGACAGTGAATTGAGCGCCAGCGACTTAC GTAACATTTTGTGCGAGGATCTGCCCTGGCTATATGGTCCGCTCCTACTTTGTGCACTCTCCAGACTGCGCTTTGACGCT GAATGGCAAAAGTAGACCGTAGGGCACTGCCCGACCTGAGCACAAATCTCGATACAGGTATGGATTAATGTGGCACCCG AGACGGATGTCCAACAGGCACTGGCTACGGCTTGGGAGCCATTTCTTGGTATCCCGAAAGTCGGAAATACAGGATAAC TTTTTCCATTTGGGTGGTGAATCAAGGCCATCCAAAGTATCGTCCCGCTTGTTCAGGCTGGATACAAAGCTGGAA ATGAAGGATTTGTTCAAAATACCCGACAAATGGCGGACTAAGCACATATATTCAGCCTGTTAACCGAATAGCCGAGCA GGCGAGGTTACAGGAAATGTAGTCTTACCCGATTACGGCTGGTTTTTGTGAACAGCCAAACGGAAGAACACACT ATTTTAACCAATCTGTCTATCTGTAGGAAGGCTATGACGAACAGGCACTACGGCGGCGCTCCATCAGATTATTA CTTCGCACCATGATGCAATTCGCTATGGTTTTTGTGTGGAGAAACGGATGTACAGCATGGAAACCGCAGTGTAGAGG AAGCGGAACCGTACCATCTGGATGCTTTGACTATAATGACAGCGATGTAAACAAGCAAGATTTGGCGAAGATAATT GAAGCGAAATGTAATGAAATTCATCTGTTATTTCCCTAAGCGAAGTCCGCTGATGAGACTGGGGCTGTCCGTTGC CCGATGGAGATCATCTGCTGGTCTGATTTCATCTTTGGCGGTGGACGGAGTATCCTGGCGCATATATTTCGAGGAT TTGGGACTGCCATGATCAAGCCTCCAAGGTGAACAGGTGATTCACTGCTCATATAAACAGATTCTGTTCCAAAC ATGGCCGAGCAGCTGACGCTTATGCCAACAGTCCAGCTATGGAACGTGAGCGAGCGTATTGGGGGAAACCTTGAC AAGCGGATCCGGCTCCTTTGCCGAGGATTACGGGCATAACGAGCACGAAAGCCATTGATTGGCGATAGTGAGTCG GTTACTGCTTTGTGGACACATGCAGAGACAGAGCAGCTGCTCAAGCAGGCCAATCGTGCCTACCGTACAGAAATTAA TGACCTGTTGTGACGGCGTAGGAATGGCAATGGCAATGGCAATGGAGTGGAAATGATCGTTTCTGATAAATCTAGAGG GACATGGACGTGAAGCCATTTTACCAGAGGTGGACATTAATCTGAAACGATAGGTGGTTTACAAGCCAAATATCCTGTTT TGCTCGATATGCCGGAAGAACTGGCACTTTTCGCAACGGATTAAAGCGTGTGAAGGAAGGACTGCGCGGCAATCCGCAA AAAGGGATTGGCTACGGTGTACTGAAATAATTTATCCGACCGTCAAGACACAGGCCACCAAGGCACTCTCCAACCATATT TACGACAGATCCGAAATCAGCTTTAACTATTTGGGACAGTTCGATCAGGATATGAAAGGGAACGACTTGCAATCAT CCTCATATGAGGTGGATGCCGCTGAGCCCGACCATGGCTCGAACGTATACGCTTGATTTTGGCGGCATCATTTCCGG GAGGCCAACTGGGTCTGACGATTAGCTATAGCCGTACCACTATAAACCCGAGACCATCGAGCGATTGGCGAAATTC CTGGAATCAAGCCTACGTGAAATTTTGGCGCATTTGCATCCATAAAGAACACCCGAGCTTACCCCAAGTGATATTTCT TATAAAGGAAATGAGTGTGAGGGCTTTGGACAGCCTCTTATCTGAAATGGGTGCTGCGGTGAGATCGACAAATGTATA TGCACTGACCCCATGCAGAAAGGGAATGCTGTTTTCACAGCCAGCTAGATAGTCAAGCAGCTGCGAATGACGCATATT TTGAGCAGGTTCTTATGATATGCGAGGTCAGATGGACATTCGGGCTTTTGCAGAAAGCCTGAATATCTGGTTCCGGC GACATGAGGGCTGCGTACACATTTTATTTTGGCAGAGATACGGAAACCGTTGCAAGGTGTATCGAAATCGGGATT GCGGCTTCAATATGAAGATTTACACCATCTGGATGAGGATGAAATAGATACCTGGGTGAAATAATTTCAAGCTACAA

Strain	SEQ ID NO:	Sequence
		GATAAGCACGGGCTTTGATCTGCGCGGGGATGTCTCTGCTGCTAGCGATTTTACGTACTGGAGAAACAGCCTA TCATTTTGTATGGAGCTTCCATCATATCGTCAATGGACGGCTGGTGTCTCTCCCTTATAAATAAAGAAAGTGTTTGAAAG CTATGCAGCACTTCAGGAGGGCAGAGTACCAGAGCTGGCACCGGCAAGTCCGTACAGCCGCTTATTGAAATGGCTGG AAGCACAGGATCGCAAGCGCGCAACCGACTACTGGAGCAAGCTATTTATCCGGATATGAGCAGCAACACAGCGTTACC AGCTGTAAATCCGGTCGCAAGAGTGAAGGCAACACGGCTAGTGATTTGGGTGACGGTTTGGAAACGTGAGTTGACCC TCCGGGTGGAGGAGACGGCTAAGCGATATCAAGTGACCATGAATACGTTATTACAAACCGCATGGGGGATTGTGCTG CAAAATATAACAACACAGTGATGTGCTATTTGGCAGTGTCTCAGCCGCTCCATCAGATATTATCGGGGTAGA GGATATTATCGGCTTTCATTAAATACCATCCCGTTCGCATTCTTAGTAAGGCAGGGGAACTCTTTGCAGAAAGTTATG AAGAAAACGCAGGAGCAGCGCTGGCTTCTCATGCAATATGATACGTATCCACTGTTGAGATTTCAGGCAATTGACCGA CCAGAAAACAGGATTTAATTAAACCATATTATGGTGTTTGAAAATTATCCGGTAGATGAGCAGGTGGAAGAACTGGGAA GTGCCGGCAGGATACATTCGCCGATTTCCAAACGTGTGGCTGCAGAGCAGACTAACTATGATCTGAGCTTAGTCGTTA TGCCGGGAGAAATGCATCAAGATTCGTTTATGTATAATGCGTTAAGTTATGATCAACAGGCATTGAGCGTCTGCATG GGCATTTTGTGAATCTGTTGGAGCAAGTTTGTCTAACCCGAATGTTTGGCTAGAAAGAGCTGGAACTCGTTACAGCGG CGGAAAACACAATAATTACAGGAGAGTTTAAATGACACTGCCTCTGCATATCCAAGCCATCACAGATCCCAAAACTG TTTGAGGAGCAGGACAGCGCACGCGCGATCATATTGCTGTAGCTTTGGGTCTATCAATCATTTGACCTATCGGGAACCTC AATGAGACAGCCAAACCGTTTAGCGCATACGCTACGTGATGCAAGGGGTGAAAATCCGATGAACCTGTGGGCATTTTGAC GGAGCGCTCACTGGATATGATTACGGGAACACTCGCTATTTTGAAGGCTGGAGCGCGTATGTGCCGGTAGACCCCTC AATATCCGGAGGACCGTATCCGTTATATGCTGGAGGACTCGGAGCTAAGCTGTCTGGCTCAGCAGGATTACTG GATCGTTGCTATTTGACGGACAGATTGTCAATCTGAATGAGGATACGTCTACAGTGCAGATGCTTCCAACTCTGGGT ATAGATGGAGCGGGTAATCATGTCTGCTTATGTCAATTTATACCTCAGGTTCAACAGGTAAGCCTAAGGTTGCTGTAGTT GAGCATCAAAAGTGTGCGCGCTTGTCCGCAATACGGATTATGTGCCAATTTGATGAATCGACCCGAATGCTGCAGACT TGCGCGTTTGTATTTGATGTATCTACGTTTGAAATTTGGGGTGCCTACTGAATGGTGTGAGCTTGTCTTGTGCATA AGGATGATCTATTGGACGCGGCCAAGCTTAAAGAGACGATACGGGATCATCAGTCACCATGATGTGCTGACCACA CCGTTATTTAATCAGCTTTCACAGCAGGATAGTAACTTTTCGGCGATGTGAAGTATTTGCTGGTTGGTGGTGTATGTTT TGTCTGCACCCCATATTAAACCGGGTCTGCGGATAATCCGGACATGAACATCATTAACGGCTATGGGCCAACGGAA AACACAACCTTTTCGACAACGTATCACAATTACGGAAGAACAGCTGGATTCTGTGCCGATCGGACGGCCCATCTGCAA TTCCGACGGCGTATGTTGTAGATTCTGTCATTTAACCTGCAACCGGTGCGAGCTTGGGGTGAAGCTGTGTCGCGCGGAGA CGGAGTTGCACGTGTTATCTAAATCGTCCTGAGCTGACGGCTGAGAGATTCTTGCTAACCCGTGGAGGGACGGAG ATCGCCTGTACTGTACGGGAGACCTTGTTCGCTGGCGTGAAGACGGCATACTGGAATACGCTGGACGGATTGATCAA CAGGTTAAATTCGGCGTTACCGGATTGAGCTGGGTGAGGTGGAGCGGAGGCTGGCAAGTGTACCGTCCGTGCGGGA

Strain	SEQ ID NO:	Sequence
		TAGCGTGGTTATTGCTTTGCGGGATGGAGCAGGTGAGCAGCAATTATGTGCTTACTTTACTGCCGATGAACAGCTGAC CATCCGTGAGATTCGAGCTGCGATGTCGGTCAGTCTGCCGAGCTATATGATTCCATCCGCAATTTGTACAGCTGGATCG GTTCCGCTGACGACCAACGGCAAAATCGACCGCAAAAGCTTTACCTGTGCCGGACAAAGGGCTGCACACGGGTATAG AATAATGTGCGCACCGCAACCGATGTGAGCAGTTGCTGGCATCTATTTGGCAGGAAGTGCTTGAAATTCCACAAAGTG GGTATCCATGATGACTTTTTCACGTTGGCGGACATTCCTTGAAAGTACTGGAGCTTATACGCAAAAGTTACACCTTGCC ACAGACATTGAGCTCCCATCCCATCCGTAAGTGAATGGACTTCCCGACTATAGAAAGAGCAGCGCTCACATTATTGAAAGC CGATCTGGAATACAAGGCCGATAGTCCAAATCATTCGGTTGAATGAACACGGTCCGATCTCCATCTTCTGCTTTCCTCC TATGCTTGGATACGGGCTGCTGCGGAGCTGGCGAAACAACCTGGATCAGGACGTCGTGTATGGATTAGAGT TCGTGGATGATGCTGCGGATGAGCAGGCCATGCTGGCACGTTACGTTGATTTGATCGTCAACGCAAGCGCAAGGT CCGTATGTGCTGCTTGGTTATTCCATAGGTGGTAATCTGGCGCATAGGTTGCTGACACACTGGAAACGTCAGGGCCAT GCTGTATCCGATATTTTATGCTCGATTCGGTCAAAGGGCGGAAGCCCTGCCCTTACAGTTGAAGAAACAGAGCAT GAAATTCAATGACATGCTGGAACAGGTTCCCGAATCCTACCGTGAGCTGTTGAATGAAACGTACCAACGTAAAAATGAT CGCTTACGCGGTGATGGCAACCAAGCTTGTGAATACAGAGCGGTTGAGGCGAATATTCACGGCTTTGTGCGCCGTTGG ATCGGAAACGGTGAGGGGTACAGGAGATAATCGACTTTTATGGAAGACGCTACACAAAGGTAGCTATGAAGAGCAT AGCTTGATTGGTAATCAATTAATGAACACTGGAACCCGGAATTTATCGAGGAAATGTAAAAAGTATCCGTGCGCCGAAT ACAAAAGATAACTCGGAACACGGACAAAGACATGACACAAAGATTGCGCACATCATAAATCTTGA

Example 5. Characterization of Fusaricidins in *Paenibacillus* sp. Strains NRRL B-50374, NRRL B-67721, NRRL B-67723, and NRRL B-67724

[0148] Whole broth cultures of *Paenibacillus* sp. strains NRRL B-50374, NRRL B-67721, NRRL B-67723, and NRRL B-67724 were prepared by culturing each strain in a soy-based medium as in Examples 1-3. Cell extracts of the whole broth cultures were prepared, and fusaricidin-like compounds were quantified in each cell extract.

[0149] A chromatographic method using ultra performance liquid chromatography/mass spectrometry triple time of flight (UPLC/MS Triple TOF) was utilized to fragment and quantify the fusaricidin-like molecules in the cell extracts: Column: YMC-Triart C8, 4.6 × 50 mm, 12 nm; Water (0.1% Formic Acid) and acetonitrile (0.1% Formic Acid); Gradient (%B): 0-5 min 10-70%; Wash. Mass fragmentation patterns obtained from an AB SCIEX TRIPLE TOF® mass spectrometer were analyzed to confirm the identity of each fusaricidin-like compound. The fusaricidin-like compounds analyzed included Fusaricidin A ("Fus A"), Fusaricidin B ("Fus B"), Fusaricidin C ("Fus C"), Fusaricidin D ("Fus D"), LiF05a, LiF05b, LiF06a, LiF06b, LiF07a, and LiF07b. These compounds are described in WO 2016/154297 where their structures are outlined in FIGs. 3, 4, and 12. The analytical method used to quantify the fusaricidin-like compounds did not distinguish between LiF05a and LiF06a or between LiF05b and LiF06b. Therefore, the signals produced by these two groups of compounds are referred to herein as LiF05/6a and LiF05/6b, respectively.

[0150] Quantification was performed using standard curves generated with known concentrations of the fusaricidin-like compounds. Quantification of LiF05/6a, LiF05/6b, LiF07a, and LiF07b was determined from the standard curve generated with Fusaricidin C. The lowest chemical standard used was at a concentration of 0.5 µg/g. When a signal was detected from an analyte in a cell extract but the intensity of the signal was below that produced with the lowest standard, the quantity of the analyte was determined to be Below the Level of Quantification (BLOQ). The results of the quantification of the fusaricidin-like compounds in each *Paenibacillus* sp. strain are presented in **Table 7**.

Table 7. Quantification of fusaricidin-like compounds in *Paenibacillus* sp. Strains NRRL B-50374, NRRL B-67721, NRRL B-67723, and NRRL B-67724.

	Fusaricidins (µg/g)								
Strain	Fus A	Fus B	Fus C	Fus D	LiF05/6a	LiF05/6b	LiF07a	LiF07b	Total
NRRL B-67724	287	78	127	31	168	32	64	8	795
NRRL B-67721	266	79	66	15	197	45	30	3	703
NRRL B-50374	167	35	53	9	217	32	23	1	536
NRRL B-67723	31	11	8	0.3	21	1	13	BLOQ	86

Example 6. Analysis of Nitrogen Fixation Gene Clusters in *Paenibacillus* sp. strains NRRL B-50374, NRRL B-67721, and NRRL B-67724

[0151] Additional analysis of the genomes of *Paenibacillus* sp. strains NRRL B-50374, NRRL B-67721, and NRRL B-67724 revealed that these strains also possess a nitrogen fixation gene cluster. The presence of a nitrogen fixation gene cluster was previously reported in the laboratory strain, *Paenibacillus* sp. WLY78. Wang L, Zhang L, Liu Z, Zhao D, Liu X, et al. (2013) A Minimal Nitrogen Fixation Gene Cluster from *Paenibacillus* sp. WLY78 Enables Expression of Active Nitrogenase in *Escherichia coli*. PLoS Genet 9(10): e1003865. In *Paenibacillus* sp. WLY78, the nitrogen fixation gene cluster contains *nifB*, *nifH*, *nifD*, *nifK*, *nifE*, *nifN*, *nifX*, *hesA*, and *nifV*. A similar gene cluster structure was found in *Paenibacillus* sp. strains NRRL B-50374, NRRL B-67721, and NRRL B-67724.

[0152] Without wishing to be bound to any theory, the presence of the nitrogen fixation gene cluster in the genomes of *Paenibacillus* sp. strains NRRL B-50374, NRRL B-67721, and NRRL B-67724 may contribute to the ability of these strains to promote efficient nitrogen uptake in plants and stimulate plant growth.

[0153] Comparison of the genome sequences for *nifB* encoding a nitrogen fixation protein showed that the *nifB* sequence in each strain shared at least 96.9% sequence identity with that of the other strains (see **Table 8**). The nucleotide sequences for the *nifB* sequences from the three strains are presented in **Table 9**.

Table 8. Percent identity matrix created with MAFFT for the *nifB* genes from *Paenibacillus* sp. strains NRRL B-50374, NRRL B-67721, and NRRL B-67724.

	Percent Sequence Identity		
Strain	NRRL B-67724	NRRL B-50374	NRRL B-67721
NRRL B-67724	100.00	97.27	96.93
NRRL B-50374	97.27	100.00	99.40
NRRL B-67721	96.93	99.40	100.00

Table 9. Nucleotide sequences of genes encoding a nitrogen fixing protein (*nifB*) in *Paenibacillus* sp. strains NRRL B-50374, NRRL B-67721, and NRRL B-67724.

Strain	SEQ ID NO:	Sequence
NRRL B-50374	9	ATGGACTCTTTAGCTGATCTCTCGGAAACCCCTTAGCAATTGGAAACCCCTCAGACGACATCCCCTGTTATAACGAAGAGGCACATCGCTATTTTGGCGCATTCATCTTCCAGTAGCCCGGCATGCAATATTC AATGCCATTATTGCAACCGCAAA TTCGATTGCGTCAATGAAGCCGTCCCGCGTTGTTAGTGA ACTGCTACGCCGGAGCAGCGCGGAGCAAGACCTA TGGCGTAGCGGCACAGCTGATGCAGCTGTCCGTTGTCCGCAATTGCCGACCTGGAGATCCGCTGGCCAAATGCGGAGG CAACCTTCGATAACCTTCCCGCGGTCCGTGAGACAGTTAAGGATGTCATATTCTGTCTCAGCACGAATGGCCTTACCT TGATCAGGCATA TCGACAGGATTGTAGAGCTGGGTATTTCGCATGTCACGATCAGATCAATGCTGTAGATCCAGTGG TGGGGAGCCGCAATTTATGGATGGGTCTACGATGAAGGAAAACGCTATG CAGGAGAGGAGCGCGCGCTGTTGATT GACCGCCAGCTGCGAGGCTTGAAAGATGCTGGCTTCGAGAGGCGTATTGTGCAAGGTGA ACTCGTGCTGATTCGCCGA AGTCAATGATGCCCCATCTGCCGGAAGGTAGCCAGGTAGTCAAGGAGCAGCGCGCAGTGCTGCACAACATTA TGCCGC TCATCATCGCACCTGTG TAGCCGTATGAGCAGGAAGGATGCGGGTCCCCGTCCCCGTCTGGTCCGGCAGCTGCAG GAGCAATGTGCTGAAGCGGGGCTGTCAATATGCGCCAATTGCCGTCA GTCAGGGCGGATGCGATTGGACTGCTGGG CGAGGATCGGAAATCAGGAATTTACATGGGAGAA CATA GCGGCTGCTCTCCCATGGATGAAGGGCAAGGGCACAAAT TTCAGAAAGAACTGGATGAGAAAGGTGAGAGTGAATGGAACGCAAGGAGGACAATCACACCACA AACAACCCGTC AACCCGGGCTGGCTGTAGTGCCCGTTATCGGGAGATAAGCCTGAAGCGAGCTTCACCTCAAAGCCAGTCCTAATCG CAGTGGCCAGTCGTGGCGGAGGAAAGGTGAATCAGCAATTCGGCCGTGCCAAGGAATTTATGATCTATGA AAGCGAC GGGACCATCGTA AATTTCATAGGCATTCGTAAGGTGCAATCCTACTGCCACGGGAAAGCCGATTGCAATGGGGACAA GGTCGAGACGATGAAGGAGATCCTTTCCATGTTCCATGCTGCAATGCTGCTGCTCGGCATAGGCGAAAGCCCC CAAAGAGGCATTGCAGGAAGCTGGCGTGTCTGCCTATTGTATCGCGCGGGGATATTGAGGAATCGGTTCTGGAATATG TGAAATTTCTGCGTTATATGATATCCTGTGCAGAGCAATAAAGGAAGTAAGCGCAATAAGGGAGTTAAGGGCAATCAT TCGGATTTACCCATTAAACATTTTGGAGGGCTGA
NRRL B-67721	10	ATGGACTCTTTAGCTGATCTCTCGGAAACCCCTTAGTATTGGAAACCCCTCAGACGACATCCCCTGTTATAACGAAGAGGCACATCGCTATTTTGGCGCATTCATCTTCCAGTAGCCCGGCATGCAATATTC AATGCCATTATTGCAACCGCAAA TTCGATTGCGTCAATGAAGCCGTCCCGCGTTGTTAGTGA ACTGCTACGCCGGAGCAGCGCGGAGCAAGACCTA TGGCGTAGCGGCACAGCTTATGCAGCTGTCCGTTGTCCGCAATTGCCGACCTGGAGATCCGCTGGCCAAATGCGGAGG CAACCTTCGATAACCTTCCCGCGGTCCGTGAGACAGTTAAGGATGTCATATTCTGTCTCAGCACAAATGGCCTTACCT TGATCAGGCATAATTGACAGGATTGTAGAGCTGGGTATTTCGCATGTCACGATCAGATCAATGCTGTAGATCCAGTGG TGGGGAGCCGCAATTTATGGATGGGTCTACGATGAAGGAAAACGCTATG CAGGAGAGGAGCGCGCGCTGTTGATT

Strain	SEQ ID NO:	Sequence
		GACGCCAGCTGGCAGGCTTGAAAGATGCTGGCTTCGAGAGGGCTATTGTGCAAGGTGAAC TCGGTGCTGATTCCCCGA AGTCAATGATGCCCATCTGCCGAGGTAGCCAGGGTGGTCAAGGAGCACGGTGCACTGCTGCACAACAATTATGCCCGC TCATCATCGCACCTGGTAGCCGGTATGAGCAGGAAGGATGCGGGCTCCCCGTCCCGTCTGCTCCGGCAGCTGCAG GAGCAATGTGCTGAAGCGGGGCTGTCATTATGCGCCATTGCCGTCACTGTCAGTGCAGGGCGGATGCGATTGGACTGCTGGG CGAGGATCGCAATCAGGATTTACATGGGAGAACATAGCGGTCTCTCCCATGGATGAAGGGCAAGGACACAAT TTCAGAAAGAACTGGATGAGAAAGGTGAGATGGAACGCAAGGAGGACAATCACACCAACAACAACCGTTC AACGGGGCTGGCTGAGCTGCCCGTTATCGGGAGATAAGCCTGAAAGCGAGCTTCACTCTCAAAGCCAGTCTAATCG CAGTGGCCAGTCTGGCGGAGGAAAGGTGAATCAGCAATTTCCGGCCGTGCCAAGGAAATTTATGATCTATGA AAGCGGAC GGGACCATCGTAAATTTCATAGGCATTCGTAAGGTGCAATCCTACTGCCACGGGAAAGCCGATTGCAATGGGGACAA GGTCGAGACGATGAAGGAGATCCTTTCATGTGTGCATGACTGTGCATTGCTGTCTCCGGCATAGCGGAAGCCC CCAAAGAGGCATTGCAGGAAGCTGGCTGTCCCTATTGTATCGCGGGGGATATTGAGGAATCGGTTCTGGAATAT GTGA AATTTCTCGGTTATATGTATCCTGTGCAGAGCAATAAAGGAAGTAAGCGCAATAAGGGAGTTAAGGGCAATCA TTCGGATTTACCCATTAAACAATTTTGGAGGCTGA
NRRL B-67724	11	ATGGACTCTTTAGCTGATCTCTCGGAAACCCCCCTTAGCAATTGGACACCCCTTAGACGACATCCCTGTTATAACGAAGAG GCACATCGCTATTTGCGCGCATTCATCTCCAGTAGCCCCGGCATGCAATATTCACTGCCATTATTGCAACCGCAAA TTCGATTGCGTCAATGAAGCCGTCCCGCGTTGTTAGTGAAC TGTCACTGCCGAGCAGCGCGGAGCAAGACCTA TGGCGTAGCGGCACAGCTGATGCAACTGTCCGTTGTCGGCAATTGCGGGAACCTGGAGATCCCGTGGCCAAATGCGGAGG CAACCTTCGATACCTTCCCGCGGTCCGTGAGACAGTTAAGGATGTCTATAATTCTGTCTCAGCACGAATGCCCTTACCT TGATCAGGCATATCGACAGGATTGTAGAGTTGGGTATTTCCGATGTCAACGATCACGATCAATGTCTGTAGATCCAGTGG TGGGAGCCGCATTTATGGATGGGTCTACGATGAAGGA AAAACGCTATGCAGGAGAGAGCGCGCGGCTGTTGATT GACCGCCAGCTGGCAGGCTTGAAGATGCTGGCTTCGAGAGGCGTATTGTGCAAGGTAAACTCGGTGCTGATTCCCCGA AGTCAATGATGCCCATCTGCCAGAGGTAGCCAGGGTGGTCAAGGACACGGCGCGGTACTGCACAACATTATGCCGC TCATCATCGCACCCCGCAGTCGGTATGAGCATGAAGGATGCGGGCCCCCGTCCCGTCTGTCGGCAGCTGCAG GAGCAATGTGCTGAGCGGGAGCTGTCAATTATGCGCCAATTGCCGTCA GTGCAAGGCGGATGCGATTGGACTGCTGGG CGAGGATCGCAATCAGGATTTTACATGGGAGAACATTGGGGCTGCTCTCCCATGGATGAAGAGGC AAGGGCACAAAT TTCAGAAAAGAACTGGATGAGAAAGGTGAGAGTGAGAAATGGAACGCAAGGAGGGACAATCGCACCAAAAACCGT CAACCGGGTTGGATGTAGTGCCCGTTATCGGAGGATAAGCCTGAAGCAAGCTTTACCTCAAAGCCAGTCCTAATC GCTGTGCCCAGTCGTGGCGGAGGGAAGGTGAATCAGCAATTTCCGTCGTGCCAAGGAATTCATGATCTATGAAAAGCGA CGGACTATCGTAAATTTCATAGGCATTCGT AAGGTGCAATCCTACTGCCATGGGAAGCCGATTGCAATGGAGACA AGGTCGAGACGATGAAGGAGATCCTTTCCATGGTGCACTGCTGCAATTGCTGCTGCTCGGCGCATAGGCGGAAGCC

Strain	SEQ ID NO:	Sequence
		CCCAAAGAGGCATTGCAGGATGCTGGCGTGCTGCCTATTGTATGCGGCGGGGATATTGAGGAATCCCGTTCTGGAATA TGTA AAA TTTCTGCGTTATATGTATCCTGTGCAGAGCAATAAGGGAAGTAAGCGCAATAAGGGAGTTAAGGGCAATC ATTGGGATTTACCCATTGAACATTTTGGAGGCTGA

Example 7. Plant Growth Promotion Properties of *Paenibacillus* sp. Strains NRRL B-50374, NRRL B-67721, NRRL B-67723, and NRRL B-67724

[0154] *Paenibacillus* sp. strain NRRL B-50374, *Paenibacillus* sp. strain NRRL B-67721, *Paenibacillus* sp. strain NRRL B-67723, and *Paenibacillus* sp. strain NRRL B-67724 were cultured in a soy-based medium to produce whole broths that were diluted in water to a concentrations of 20%. The diluted whole broths were applied to tomato plants as a drench at the time of planting. Several days later when the tomato seedlings had developed into young plants the average weights and standard deviations for forty whole tomato plants in each treatment group were measured. An untreated control group (“UTC”) and a group treated with the soy-based medium only (“Medium”) were included in the analysis for comparison.

[0155] Interestingly, *Paenibacillus* sp. strain NRRL B-50374, *Paenibacillus* sp. strain NRRL B-67721, and *Paenibacillus* sp. strain NRRL B-67724, each of which possesses a nitrogen fixation gene cluster, produced a significant increase in tomato plant growth compared to the UTC and Medium controls (see **FIG. 2**). In contrast, *Paenibacillus* sp. strain NRRL B-67723, which does not possess a nitrogen fixation gene cluster, did not increase tomato plant growth compared to the UTC and Medium controls.

[0156] Unless defined otherwise, all technical and scientific terms herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. All publications, patents, and patent publications cited are incorporated by reference herein in their entirety for all purposes.

[0157] It is understood that the disclosed invention is not limited to the particular methodology, protocols and materials described as these can vary. It is also understood that the terminology used herein is for the purposes of describing particular embodiments only and is not intended to limit the scope of the present invention which will be limited only by the appended claims.

[0158] Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

CLAIMS

We claim:

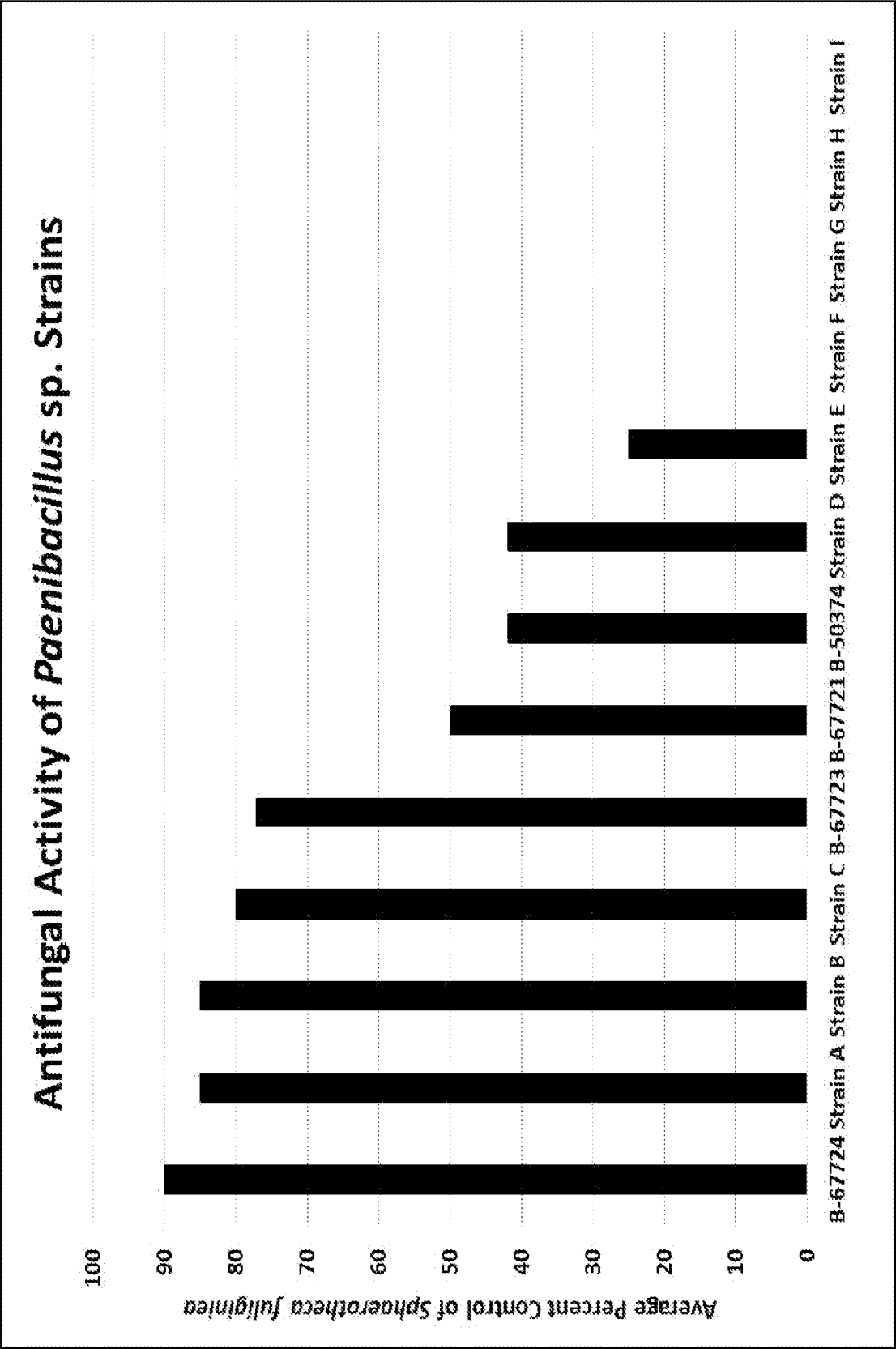
1. A composition comprising a biologically pure culture of a *Paenibacillus* sp. strain or a cell-free preparation thereof comprising a fusaricidin and a tridecaptin;
wherein the *Paenibacillus* sp. strain comprises a fusaricidin synthetase gene of *fusA* encoded by a DNA sequence exhibiting at least 90.5% sequence identity to SEQ ID NO: 3; and
the *Paenibacillus* sp. strain comprises a nonribosomal peptide synthetase (NRPS) gene of *triE* encoded by a DNA sequence exhibiting at least 90.0% sequence identity to SEQ ID NO: 7.
2. The composition according to Claim 1, comprising Fusaricidin A, Fusaricidin B, Fusaricidin C, Fusaricidin D, LiF05a, LiF05b, LiF06a, LiF06b, LiF07a, and/or LiF07b.
3. The composition according to Claim 1 or 2, wherein the composition effectively controls a plant disease caused by a fungus selected from the group consisting of *Botrytis cinerea*, *Sphaerotheca fuliginea*, and *Puccinia triticina*.
4. The composition according to any one of Claims 1 to 3, wherein the *Paenibacillus* sp. strain is *Paenibacillus* sp. strain NRRL B-50374, *Paenibacillus* sp. strain NRRL B-67721, *Paenibacillus* sp. strain NRRL B-67723, *Paenibacillus* sp. strain NRRL B-67724, or a fungicidal mutant strain thereof.
5. The composition according to Claim 4 comprising a fermentation product of *Paenibacillus* sp. strain NRRL B-50374, *Paenibacillus* sp. strain NRRL B-67721, *Paenibacillus* sp. strain NRRL B-67723, *Paenibacillus* sp. strain NRRL B-67724, or a fungicidal mutant strain thereof.
6. The composition according to Claim 4 or 5, wherein the fungicidal mutant strain has a genomic sequence with greater than about 90% sequence identity to *Paenibacillus* sp. strain NRRL B-50374, *Paenibacillus* sp. strain NRRL B-67721, *Paenibacillus* sp. strain NRRL B-67723, or *Paenibacillus* sp. strain NRRL B-67724 and/or the fungicidal mutant strain has fungicidal activity and/or levels of a fusaricidin that are comparable to or better than that of *Paenibacillus* sp. strain NRRL B-50374, *Paenibacillus* sp. strain NRRL B-67721, *Paenibacillus* sp. strain NRRL B-67723, or *Paenibacillus* sp. strain NRRL B-67724.

7. The composition according to any one of Claims 1 to 3, wherein the *Paenibacillus* sp. strain further comprises a nitrogen fixation gene cluster; and the nitrogen fixation gene cluster comprises a nitrogen fixation gene of *nifB* encoded by a DNA sequence exhibiting at least 96.9% sequence identity to SEQ ID NO: 10.
8. The composition according to Claim 7, wherein expression of the nitrogen fixation gene cluster contributes to enhanced plant growth, plant vigor, and/or crop yield.
9. The composition according to Claim 7 or 8, wherein the *Paenibacillus* sp. strain comprises a fusaricidin synthetase gene of *fusA* encoded by a DNA sequence exhibiting at least 97.3% sequence identity to SEQ ID NO: 1 and the *Paenibacillus* sp. strain comprises a NRPS gene of *triE* encoded by a DNA sequence exhibiting at least 97.5% sequence identity to SEQ ID NO: 5.
10. The composition according to any one of Claims 7 to 9, wherein the *Paenibacillus* sp. strain is *Paenibacillus* sp. strain NRRL B-50374, *Paenibacillus* sp. strain NRRL B-67721, *Paenibacillus* sp. strain NRRL B-67724, or a fungicidal mutant strain thereof.
11. The composition according to Claim 10 comprising a fermentation product of *Paenibacillus* sp. strain NRRL B-50374, *Paenibacillus* sp. strain NRRL B-67721, *Paenibacillus* sp. strain NRRL B-67724, or a fungicidal mutant strain thereof.
12. The composition according to Claim 10 or 11, wherein the fungicidal mutant strain has a genomic sequence with greater than about 90% sequence identity to *Paenibacillus* sp. strain NRRL B-50374, *Paenibacillus* sp. strain NRRL B-67721, or *Paenibacillus* sp. strain NRRL B-67724 and/or the fungicidal mutant strain has fungicidal activity and/or levels of a fusaricidin that are comparable to or better than that of *Paenibacillus* sp. strain NRRL B-50374, *Paenibacillus* sp. strain NRRL B-67721, or *Paenibacillus* sp. strain NRRL B-67724.
13. A method of treating an agricultural plant to control a disease, wherein the method comprises applying an effective amount of the composition according to any one of claims 1 to 12 to the plant, to a part of the plant and/or to a locus of the plant.
14. The method according to Claim 13, wherein the method comprises applying the composition to foliar plant parts.

15. The method according to Claim 13 or 14, wherein the composition is applied at about 1×10^{10} to about 1×10^{12} colony forming units (CFU) of the *Paenibacillus* sp. strain per hectare or at about 0.5 kg to about 5 kg fermentation solids per hectare.
16. The method according to any one of Claim 13 to 15, wherein the disease is a fungal disease or a bacterial disease.
17. A method for increasing the vigor and/or crop yield of an agricultural plant, wherein the plant, the plant propagule, the seed of the plant and/or a locus where the plant is growing or is intended to grow is treated with an effective amount of the composition according to any one of claims 1 to 12.
18. The method according to Claim 17, wherein the treatment is carried out as an in-furrow treatment, seed treatment, and/or foliar treatment.
19. The method according to any one of Claims 13 to 18, wherein the agricultural plant is selected from the group consisting of soybean, corn, wheat, triticale, barley, oat, rye, rape, millet, rice, sunflower, cotton, sugar beet, pome fruit, stone fruit, citrus, banana, strawberry, blueberry, almond, grape, mango, papaya, peanut, potato, tomato, pepper, cucurbit, cucumber, melon, watermelon, garlic, onion, broccoli, carrot, cabbage, bean, dry bean, canola, pea, lentil, alfalfa, trefoil, clover, flax, elephant grass, grass, lettuce, sugarcane, tea, tobacco and coffee; each in its natural or genetically modified form.
20. A seed treated with the composition according to any one of claims 1 to 12.

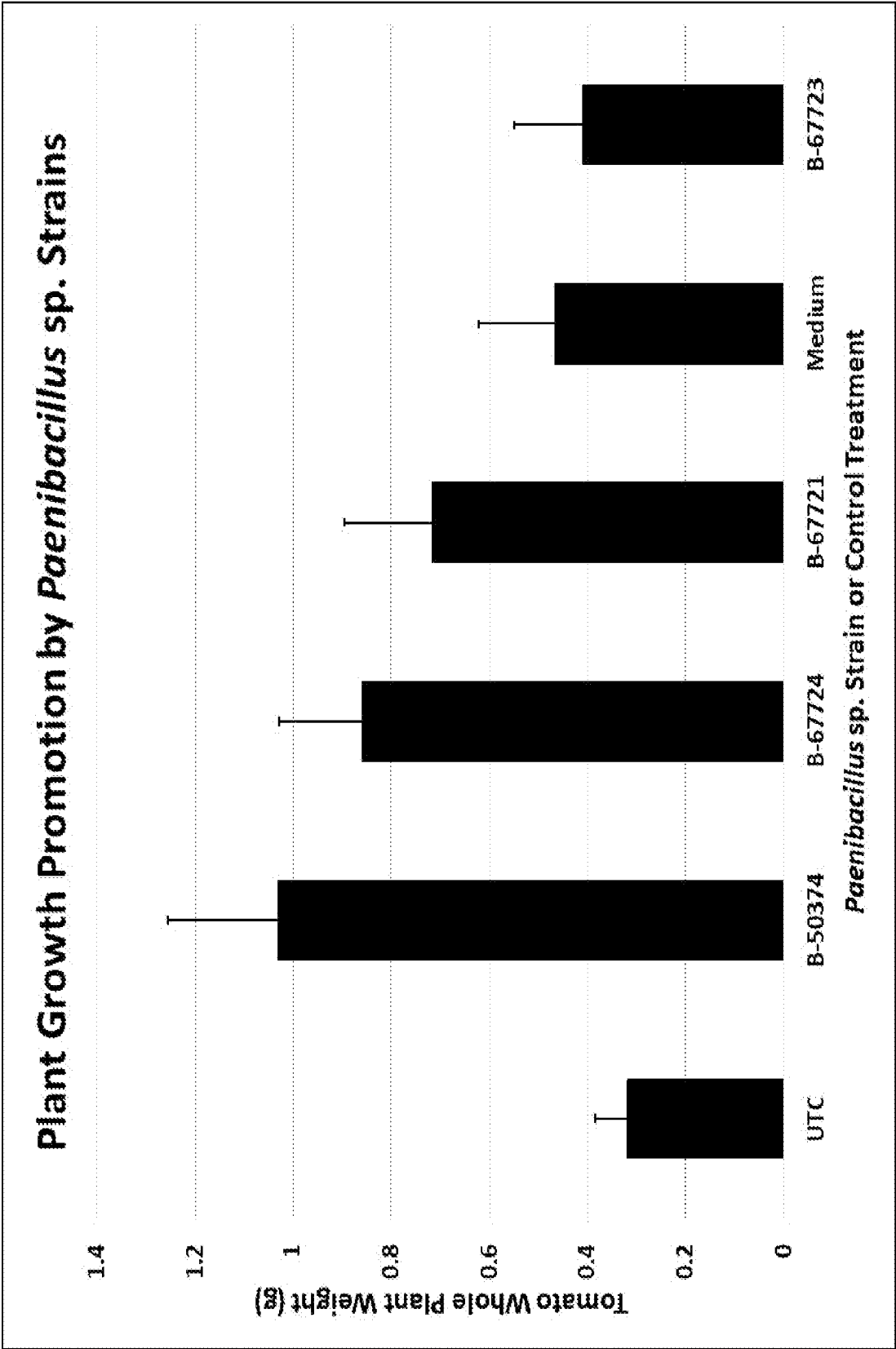
[SHEET 1 of 2]

FIG. 1



[SHEET 2 of 2]

FIG. 2



INTERNATIONAL SEARCH REPORT

International application No
PCT/US2020/021125

A. CLASSIFICATION OF SUBJECT MATTER
INV. A01N63/25
ADD.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
A01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

EPO-Internal

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	GAJENDER ALETI ET AL: "The Draft Genome Sequence of <i>Paenibacillus polymyxa</i> Strain CCI-25 Encompasses High Potential for Secondary Metabolite Production", GENOME ANNOUNCEMENTS, vol. 4, no. 3, 19 May 2016 (2016-05-19), XP055700841, DOI: 10.1128/genomeA.00366-16	1-20
Y	the whole document	1-20
Y	US 2018/146682 A1 (BEAU JEREMY [US] ET AL) 31 May 2018 (2018-05-31) cited in the application paragraphs [0082] - [0146]; claims; examples	1-20
	----- -/-	



Further documents are listed in the continuation of Box C.



See patent family annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

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"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search

15 June 2020

Date of mailing of the international search report

03/08/2020

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INTERNATIONAL SEARCH REPORT

International application No

PCT/US2020/021125

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	SEO HYEON LEE ET AL: "An antibiotic fusaricidin: a cyclic depsipeptide from Paenibacillus polymyxa E681 induces systemic resistance against Phytophthora blight of red-pepper", PHYTOPARASITICA., vol. 41, no. 1, 12 December 2012 (2012-12-12), pages 49-58, XP055274518, NL ISSN: 0334-2123, DOI: 10.1007/s12600-012-0263-z abstract page 50, paragraph 2 left-hand page 51, paragraph 2 right-hand -----	1-20

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Information on patent family members

International application No

PCT/US2020/021125

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