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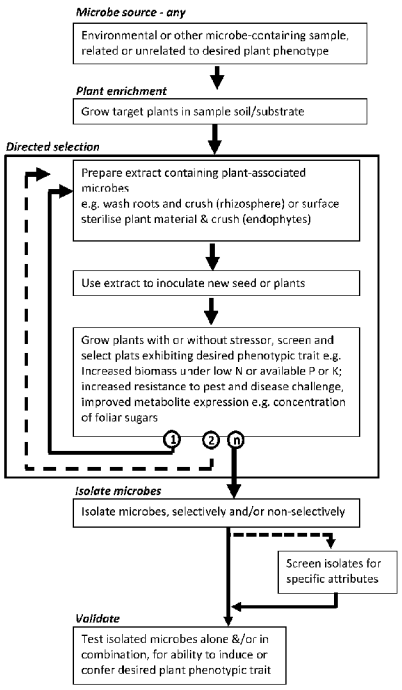
(54) Title: AGRICULTURALLY BENEFICIAL MICROBES, MICROBIAL COMPOSITIONS, AND CONSORTIA

(57) Abstract: The disclosure relates to isolated microorganisms -including novel strains of the microorganisms- microbial consortia, and agricultural compositions comprising the same. Furthermore, the disclosure teaches methods of utilizing the described microorganisms, microbial consortia, and agricultural compositions comprising the same, in methods for imparting beneficial properties to target plant species. In particular aspects, the disclosure provides methods of increasing desirable plant traits in agronomically important crop species.

FIG. 1



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AGRICULTURALLY BENEFICIAL MICROBES, MICROBIAL COMPOSITIONS, AND CONSORTIA

CROSS REFERENCE TO RELATED APPLICATIONS

[0001] The present application is a PCT International Patent Application claiming the benefit of priority to U.S. Provisional Patent Application No. 62/280,508, filed January 19, 2016, which is hereby incorporated by reference in its entirety for all purposes. The following applications are generally related to the instant disclosure: PCT International Patent Application No. PCT/US2016/043933, filed July 25, 2016, which claims the benefit of priority to U.S. Provisional Patent Application No. 62/196,951, filed July 25, 2015; PCT International Patent Application No. PCT/US2016/017204, filed February 9, 2016, which claims the benefit of priority to U.S. Provisional Patent Application No. 62/113,792, filed on February 9, 2015, U.S. Provisional Patent Application No. 62/165,620, filed May 22, 2015, and U.S. Provisional Patent Application No. 62/280,503, filed January 19, 2016, each of which is hereby incorporated by reference in its entirety for all purposes.

DESCRIPTION OF THE TEXT FILE SUBMITTED ELECTRONICALLY

[0002] The contents of the text file submitted electronically herewith are incorporated herein by reference in their entirety: A computer readable format copy of the Sequence Listing (filename: 16063-3 Sequence Listing_ST25.txt, date recorded January 19, 2017, file size 488 kilobytes).

FIELD

[0003] The present disclosure relates to isolated and biologically pure microorganisms that have application, *inter alia*, in agriculture. The disclosed microorganisms can be utilized in their isolated and biologically pure states, as well as being formulated into agriculturally acceptable compositions. Further, the disclosure provides agriculturally beneficial microbial consortia, containing at least two members of the disclosed microorganisms, as well as methods of utilizing said consortia in agricultural applications.

BACKGROUND

[0004] According to the United Nations World Food Program, there are close to 900 million malnourished people in the world. The malnourishment epidemic is particularly striking in the developing nations of the world, where one in six children is underweight. The paucity of available food can be attributed to many socioeconomic factors; however, regardless of ultimate cause, the fact remains that there is a shortage of food available to feed a growing world population, which is expected to reach 9 billion people by 2050. The United Nations estimates that agricultural yields must increase by 70-100% to feed the projected global population in 2050.

[0005] These startling world population and malnutrition figures highlight the importance of agricultural efficiency and productivity, in sustaining the world's growing population. The technological advancements achieved by modern row crop agriculture, which has led to never before seen crop yields, are impressive. However, despite the advancements made by technological innovations such as genetically engineered crops and new novel pesticidal and herbicidal compounds, there is a need for improved crop performance, in order to meet the demands of an exponentially increasing global population.

[0006] Scientists have estimated that if the global agricultural "yield gap" (which is the difference between the best observed yield and results elsewhere) could be closed, then worldwide crop production would rise by 45-70%. That is, if all farmers, regardless of worldwide location, could achieve the highest attainable yield expected for their respective regions, then a great majority of the deficiencies in worldwide food production could be addressed. However, solving the problem of how to achieve higher yields across a heterogenous worldwide landscape are difficult.

[0007] Often, yield gaps can be explained by inadequate water, substandard farming practices, inadequate fertilizers, and the non-availability of herbicides and pesticides. However, to vastly increase the worldwide use of water, fertilizers, herbicides, and pesticides, would not only be economically infeasible for most of the world, but would have negative environmental consequences.

[0008] Thus, meeting global agricultural yield expectations, by simply scaling up current high-input agricultural systems—utilized in most of the developed world—is simply not feasible.

[0009] There is therefore an urgent need in the art for improved methods of increasing crop performance and imparting beneficial traits to desired plant species.

SUMMARY OF THE DISCLOSURE

[0010] The present disclosure addresses this important issue of how to improve crop performance, thereby closing the worldwide yield gap, along with providing ways of imparting other beneficial traits to plant species.

[0011] The solution to increasing crop performance and increasing yield proffered by the present disclosure is not detrimental to the earth's resources, as it does not rely upon increased water consumption or increased input of synthetic chemicals into a system. Rather, the present disclosure utilizes microbes to impart beneficial properties, including increased yields, to desirable plants.

[0012] The disclosure therefore offers an environmentally sustainable solution that allows farmers to increase yields of important crops, which is not reliant upon increased utilization of synthetic herbicides and pesticides.

[0013] In embodiments, the disclosure provides for an efficient and broadly applicable agricultural platform utilizing microbes and microbial consortia that promote one or more desirable plant properties.

[0014] In some embodiments, a single microbe is utilized. In some aspects, the single microbe is isolated and purified. In some aspects, the single microbe is a taxonomic species of bacteria. In some aspects, the single microbe is an identifiable strain of a taxonomic species of bacteria. In some aspects, the single microbe is a novel, newly discovered strain of a taxonomic species of bacteria.

[0015] In some embodiments, a single microbe from **Table 1** is utilized. In other embodiments, a single microbe from **Table 2** is utilized. In yet other embodiments, a single microbe from **Table 3** is utilized. In additional embodiments, a single microbe from **Table 4** is utilized.

[0016] In some embodiments, a microbe from the genus *Bosea* is utilized.

[0017] In some aspects, the single microbe—whether a taxonomically identifiable species or strain—is combined with one or more other microbes of a different species or strain. In certain aspects, the combination of two or more microbes forms a consortia or consortium. The terms consortia and consortium are utilized interchangeably.

[0018] In certain aspects, the disclosure provides for the development of highly functional microbial consortia that help promote the development and expression of a desired phenotypic or genotypic plant trait. In some embodiments, the consortia of the present disclosure possess functional attributes that are not found in nature, when the individual microbes are living alone. That is, in various embodiments, the combination of particular microbial species into consortia, leads to the microbial combination possessing functional attributes that are not possessed by any one individual member of the consortia when considered alone.

[0019] In some embodiments, this functional attribute possessed by the microbial consortia is the ability to impart one or more beneficial properties to a plant species, for example: increased growth, increased yield, increased nitrogen utilization efficiency, increased stress tolerance, increased drought tolerance, increased photosynthetic rate, enhanced water use efficiency, increased pathogen resistance, modifications to plant architecture that don't necessarily impact plant yield, but rather address plant functionality, etc.

[0020] The ability to impart these beneficial properties upon a plant is not possessed, in some embodiments, by the individual microbes as they would occur in nature. Rather, in some embodiments, it is by the hand of man combining these microbes into consortia that a functional composition is developed, said functional composition possessing attributes and functional properties that do not exist in nature.

[0021] However, in other embodiments, the disclosure provides for individual isolated and biologically pure microbes that are able to impart beneficial properties upon a desired plant species, without the need to combine said microbes into consortia.

[0022] In embodiments, the microbial consortia can be any combination of individual microbes from **Table 1**. In other embodiments, the microbial consortia can be any combination of individual microbes from **Table 2**. In yet other embodiments, the

microbial consortia can be any combination of individual microbes from **Table 3**. In additional embodiments, the microbial consortia can be any combination of individual microbes from **Table 4**. In yet other embodiments, the microbial consortia can be any combination of individual microbes from any of **Tables 1-4.** In certain embodiments, the microbial consortia comprise two microbes, or three microbes, or four microbes, or five microbes, or six microbes, or seven microbes, or eight microbes, or nine microbes, or 10 microbes, or more than 10 microbes.

[0023] Another object of the disclosure relates to the use of the isolated microbes and microbial consortia as plant growth promoters. In other aspects, the isolated microbes and microbial consortia function as growth modifiers, which can, e.g. subvert normal senescence that leads to increased biomass.

[0024] Yet another object of the disclosure relates to the use of the isolated microbes and microbial consortia as soil health enhancers and plant health enhancers.

[0025] Another object of the disclosure is to design a microbial consortium, which is able to perform multidimensional activities in common. In certain aspects, the microbes comprising the consortium act synergistically. In aspects, the effect that the microbial consortium has on a certain plant characteristic is greater than the effect that would be observed had any one individual microbial member of the consortium been utilized singularly. That is, in some aspects, the consortium exhibit a greater than additive effect upon a desired plant characteristic, as compared to the effect that would be found if any individual member of the consortium had been utilized by itself.

[0026] In some aspects, the consortia lead to the establishment of other plant-microbe interactions, *e.g.* by acting as primary colonizers or founding populations that set the trajectory for the future microbiome development.

[0027] In embodiments, the disclosure is directed to synergistic combinations (or mixtures) of microbial isolates.

[0028] In some aspects, the consortia taught herein provide a wide range of agricultural applications, including: improvements in yield of grain, fruit, and flowers; improvements in growth of plant parts; improved resistance to disease; improved survivability in extreme climate; and improvements in other desired plant phenotypic characteristics. Significantly, these benefits to plants can be obtained without any hazardous side effects to the environment.

[0029] In some aspects, the individual microbes of the disclosure, or consortia comprising same, can be combined into an agriculturally acceptable composition.

[0030] In some embodiments, the agricultural compositions of the present disclosure include, but are not limited to: wetters, compatibilizing agents, antifoam agents, cleaning agents, sequestering agents, drift reduction agents, neutralizing agents, buffers, corrosion inhibitors, dyes, odorants, spreading agents, penetration aids, sticking agents, binders , dispersing agents, thickening agents, stabilizers, emulsifiers, freezing point depressants, antimicrobial agents, fertilizers, pesticides, herbicides, inert carriers, polymers, and the like.

[0031] In one embodiment of the present disclosure, the microbes (including isolated single species, or strains, or consortia), are supplied in the form of seed coatings or other applications to the seed. In embodiments, the seed coating may be applied to a naked and untreated seed. In other embodiments, the seed coating may be applied as a seed overcoat to a previously treated seed. Thus, in some embodiments, the present disclosure teaches a method of treating a seed comprising applying an isolated bacterial strain or a microbial consortium to a seed. In certain embodiments, the isolated bacterial strain or microbial consortium is applied as an agricultural composition including an agriculturally acceptable carrier.

[0032] In some embodiments, the applied microbes may become endophytic and consequently may be present in the growing plant that was treated and its subsequent offspring. In other embodiments the microbes might be applied at the same time as a co-treatment with seed treatments.

[0033] In one embodiment of the present disclosure, the microbes are supplied in the form of granules, or plug, or soil drench that is applied to the plant growth media. In other embodiments, the microbes are supplied in the form of a foliar application, such as a foliar spray or liquid composition. The foliar spray or liquid application may be applied to a growing plant or to a growth media, *e.g.* soil.

[0034] In embodiments, the agricultural compositions of the disclosure can be formulated as: (1) solutions; (2) wettable powders; (3) dusting powders; (4) soluble powders; (5) emulsions or suspension concentrates; (6) seed dressings, (7) tablets; (8) water-dispersible granules; (9) water soluble granules (slow or fast release); (10) microencapsulated granules or suspensions; and (11) as irrigation components, among

others. In certain aspects, the compositions may be diluted in an aqueous medium prior to conventional spray application. The compositions of the present disclosure can be applied to the soil, plant, seed, rhizosphere, rhizosheath, or other area to which it would be beneficial to apply the microbial compositions.

[0035] Still another object of the disclosure relates to the agricultural compositions being formulated to provide a high colony forming units (CFU) bacterial population or consortia. In some aspects, the agricultural compositions have adjuvants that provide for a pertinent shelf life. In embodiments, the CFU concentration of the taught agricultural compositions is higher than the concentration at which the microbes would exist naturally, outside of the disclosed methods. In another embodiment, the agricultural composition contains the microbial cells in a concentration of 10^3-10^{12} CFU per gram of the carrier or 10^5-10^9 CFU per gram of the carrier. In an aspect, the microbial cells are applied as a seed coat directly to a seed at a concentration of 10^5-10^9 CFU. In other aspects, the microbial cells are applied as a seed overcoat on top of another seed coat at a concentration of 10^5-10^9 CFU. In other aspects, the microbial cells are applied as a co-treatment together with nother seed treatment at a rate of 10^5-10^9 CFU.

[0036] In aspects, the disclosure is directed to agricultural microbial formulations that promote plant growth. In aspects, the disclosure provides for the taught isolated microbes, and consortia comprising same, to be formulated as an agricultural bioinoculant. The taught bioinoculants can be applied to plants, seeds, or soil. Suitable examples of formulating bioinoculants comprising isolated microbes can be found in U.S. Pat. No. 7,097,830, which is herein incorporated by reference.

[0037] The disclosed polymicrobial formulations can: lower the need for nitrogen containing fertilizers, solubilize minerals, protect plants against pathogens, and make available to the plant valuable nutrients, such as phosphate, thus reducing and eliminating the need for using chemical pesticides and chemical fertilizers.

[0038] In some embodiments, the isolated and biologically pure microbes of the present disclosure can be utilized, in a method of imparting one or more beneficial properties or traits to a desired plant species.

[0039] In some embodiments, the agriculturally acceptable composition containing isolated and biologically pure microbes of the present disclosure can be utilized, in a

method of imparting one or more beneficial properties or traits to a desired plant species.

[0040] In some embodiments, the consortia of the present disclosure can be utilized, in a method of imparting one or more beneficial properties or traits to a desired plant species.

[0041] In some embodiments, the agriculturally acceptable composition containing consortia of the present disclosure can be utilized, in a method of imparting one or more beneficial properties or traits to a desired plant species.

[0042] In some aspects, the isolated and biologically pure microbes of the present disclosure, and/or the consortia of the present disclosure, are derived from an accelerated microbial selection process ("AMS" process). The AMS process utilized in some aspects of the present disclosure is described, for example, in: (1) International Patent Application No. PCT/NZ2012/000041, published on September 20, 2012, as International Publication No. WO 2012125050 A1, and (2) International Patent Application No. PCT/NZ2013/000171, published on March 27, 2014, as International Publication No. WO 2014046553 A1, each of these PCT Applications is herein incorporated by reference in their entirety for all purposes. The AMS process is described in the present disclosure, for example, in **FIGS. 1-4**.

[0043] However, in other embodiments, the microbes of the present disclosure are not derived from an accelerated microbial selection process. In some aspects, the microbes utilized in embodiments of the disclosure are chosen from amongst members of microbes present in a database. In particular aspects, the microbes utilized in embodiments of the disclosure are chosen from microbes present in a database based upon particular characteristics of said microbes.

[0044] The present disclosure provides that a plant element or plant part can be effectively augmented, by coating said plant element or plant part with an isolated microbe or microbial consortia, in an amount that is not normally found on the plant element or plant part

[0045] Some embodiments described herein are methods for preparing an agricultural seed composition, or seed coating, comprising: contacting the surface of a seed with a formulation comprising a purified microbial population that comprises at least one isolated microbe that is heterologous to, or rarely present on the seed. Further

embodiments entail preparing an agricultural plant composition, comprising: contacting the surface of a plant with a formulation comprising a purified microbial population that comprises at least one isolated microbe that is heterologous to the plant.

[0046] In some aspects, applying an isolated microbe, microbial consortia, and/or agricultural composition of the disclosure to a seed or plant modulates a trait of agronomic importance. The trait of agronomic importance can be, e.g., disease resistance, drought tolerance, heat tolerance, cold tolerance, salinity tolerance, metal tolerance, herbicide tolerance, chemical tolerance, improved water use efficiency, improved nitrogen utilization, improved resistance to nitrogen stress, improved nitrogen fixation, pest resistance, herbivore resistance, pathogen resistance, increased yield, increased yield under water limited conditions, health enhancement, vigor improvement, growth improvement, photosynthetic capability improvement, nutrition enhancement, altered protein content, altered oil content, increased biomass, increased shoot length, increased root length, improved root architecture, increased seed weight, faster seed germination, altered seed carbohydrate composition, altered seed oil composition, number of pods, delayed senescence, stay-green, and altered seed protein composition. In some aspects, at least 2, 3, 4, or more traits of agronomic importance are modulated. In some aspects, the modulation is a positive effect on one of the aforementioned agronomic traits.

[0047] In some aspects, the isolated microbes, consortia, and/or agricultural compositions of the disclosure can be applied to a plant, in order to modulate or alter a plant characteristic such as altered oil content, altered protein content, altered seed carbohydrate composition, altered seed oil composition, altered seed protein composition, chemical tolerance, cold tolerance, delayed senescence, disease resistance, drought tolerance, ear weight, growth improvement, health enhancement, heat tolerance, herbicide tolerance, herbivore resistance, improved nitrogen fixation, improved nitrogen utilization, improved root architecture, improved water use efficiency, increased biomass, decreased biomass, increased root length, decreased root length, increased seed weight, increased shoot length, decreased shoot length, increased yield, increased yield under water-limited conditions, kernel mass, kernel moisture content, metal tolerance, number of ears, number of kernels per ear, number of pods, nutrition enhancement, pathogen resistance, pest resistance, photosynthetic

capability improvement, salinity tolerance, stay-green, vigor improvement, increased dry weight of mature seeds, increased fresh weight of mature seeds, increased number of mature seeds per plant, increased chlorophyll content, increased number of pods per plant, increased length of pods per plant, reduced number of wilted leaves per plant, reduced number of severely wilted leaves per plant, and increased number of non-wilted leaves per plant, a detectable modulation in the level of a metabolite, a detectable modulation in the level of a transcript, and a detectable modulation in the proteome relative to a reference plant.

[0048] In some embodiments, the agricultural formulations taught herein comprise at least one member selected from the group consisting of an agriculturally compatible carrier, a tackifier, a microbial stabilizer, a fungicide, an antibacterial agent, an herbicide, a nematicide, an insecticide, a plant growth regulator, a rodenticide, and a nutrient

[0049] The methods described herein can include contacting a seed or plant with at least 100 CFU or spores, at least 300 CFU or spores, at least 1,000 CFU or spores, at least 3,000 CFU or spores, at least 10,000 CFU or spores, at least 30,000 CFU or spores, at least 100,000 CFU or spores, at least 300,000 CFU or spores, at least 1,000,000 CFU or spores or more, of the microbes taught herein.

[0050] In some embodiments of the methods described herein, an isolated microbe of the disclosure is present in a formulation in an amount effective to be detectable within and/or on a target tissue of an agricultural plant. For example, the microbe is detected in an amount of at least 100 CFU or spores, at least 300 CFU or spores, at least 1,000 CFU or spores, at least 3,000 CFU or spores, at least 10,000 CFU or spores, at least 30,000 CFU or spores, at least 100,000 CFU or spores, at least 300,000 CFU or spores, at least 1,000,000 CFU or spores, or more, in and/or on a target tissue of a plant. Alternatively or in addition, the microbes of the disclosure may be present in a formulation in an amount effective to increase the biomass and/or yield of a plant that has had such a formulation applied thereto, by at least 1%, at least 2%, at least 3%, at least 5%, at least 10%, at least 15%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 100%, or more, when compared with a reference agricultural plant that has not had the formulations of the disclosure applied. Alternatively or in addition, the microbes of the disclosure may be present in a formulation in an amount effective to detectably

modulate an agronomic trait of interest of a plant that has had such a formulation applied thereto, by at least 1%, at least 2%, at least 3%, at least 5%, at least 10%, at least 15%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 100%, or more, when compared with a reference agricultural plant that has not had the formulations of the disclosure applied.

[0051] In some embodiments, the agricultural compositions taught herein are shelf-stable. In some aspects, the microbes taught herein are freeze dried. Also described herein are a plurality of isolated microbes confined within an object selected from the group consisting of: bottle, jar, ampule, package, vessel, bag, box, bin, envelope, carton, container, silo, shipping container, truck bed, and case.

[0052] In some aspects, combining a selected plant species with a disclosed microbe—operational taxonomic unit (OTU), strain, or composition comprising any of the aforementioned—leads to improved yield from crops and generation of products thereof. Therefore, in one aspect, the present disclosure provides a synthetic combination of a seed of a first plant and a preparation of a microbe(s) that is coated onto the surface of the seed of the first plant, such that the microbe is present at a higher level on the surface of the seed, than is present on the surface of an uncoated reference seed. In another aspect, the present disclosure provides a synthetic combination of a part of a first plant and a preparation of a microbe(s) that is coated onto the surface of the part of the first plant, such that the microbe is present at a higher level on the surface of the part of the first plant, than is present on the surface of an uncoated reference plant part. The aforementioned methods can be used alone, or in parallel with plant breeding and transgenic technologies.

[0053] In some embodiments, an isolated bacterial strain may be selected from the group consisting of *Brevibacterium frigoritolerans* deposited as NRRL Accession Deposit No. NRRL B-67360; *Bacillus megaterium* deposited as NRRL Accession Deposit No. NRRL B-67370; *Janibacter limosus* deposited as NRRL Accession Deposit No. NRRL B-67358; *Janibacter limosus* deposited as NRRL Accession Deposit No. NRRL B-67359; *Janibacter limosus* deposited as NRRL Accession Deposit No. NRRL B-67364; *Pseudomonas yamanorum* deposited as NRRL Accession Deposit No. NRRL B-67361; *Pseudomonas yamanorum* deposited as NRRL Accession Deposit No. NRRL B-67362; *Pseudomonas yamanorum* deposited as NRRL Accession Deposit No. NRRL B-67363.

[0054] In some embodiments, the isolated bacterial strain has substantially similar morphological and physiological characteristics as an isolated bacterial strain of the present disclosure. In some embodiments, the isolated bacterial strain has substantially similar genetic characteristics as an isolated bacterial strain of the present disclosure. In some embodiments, an isolated bacterial strain of the present disclosure is in substantially pure culture.

[0055] In some embodiments, progeny and/or mutants of an isolated bacterial strain of the present disclosure are contemplated. In some embodiments, an isolated bacterial strain of the present disclosure comprises a polynucleotide sequence sharing at least 97% sequence identity with any one of SEQ ID Nos: 1-315. In other embodiments, an isolate bacterial strain of the present disclosure comprises a polynucleotide sequence sharing at least 97% sequence identity with any one of SEQ ID NOs: 308-315.

[0056] In some embodiments, a cell-free or inactivated preparation of an isolated bacterial strain of the present disclosure is contemplated, or a mutant of said isolated bacterial strain. In some embodiments, a metabolite produced by an isolated bacterial strain of the present disclosure is contemplated, or a mutant of said isolated bacterial strain.

[0057] In some embodiments, an agricultural composition comprises an isolated bacterial strain and an agriculturally acceptable carrier. The isolated bacterial strain may be present in the composition at 1×10^{3} to 1×10^{12} CFU per gram. The agricultural composition may be formulated as a seed coating.

[0058] In some embodiments, a method of imparting at least one beneficial train upon a plant species comprises applying an isolated bacterial strain to the plant or to a growth medium in which said plant is located. In some embodiments, a method of imparting at least one beneficial trait upon a plant species comprises applying an agricultural composition of the present disclosure to the plant or to a growth medium in which the plant is located.

[0059] In some embodiments, the present disclosure teaches a method of growing a plant having at least one beneficial trait. In some embodiments, the method comprises applying an isolated bacterial strain or microbial consortium to the seed of a plant; sowing or planting the seed; and growing the plant. In certain embodiments, the isolated bacterial strain or microbial consortium is applied as an agricultural composition that further includes an agriculturally acceptable carrier.

[0060] In some embodiments a microbial consortium comprises at least two microbes selected from the groups consisting of: A) *Stenotrophomonas maltophilia, Rhodococcus erythropolis, Pantoea vagans, Pseudomonas oryzihabitans, Rahnella aquatilis, Duganella radicis, Exiguobacterium acetylicum, Arthrobacter pascens, Pseudomonas putida, Bacillus megaterium, Bacillus aryabhattai, Bacillus cereus, Novosphingobium sediminicola, Rhizobium etli, Ensifer adhaerens, Chitinophaga terrae, Variovorax ginsengisoli, Pedobacter terrae, Massilia albidiflava, Dyadobacter soli, Bosea robiniae, Microbacterium maritypicum, Microbacterium azadirachtae, Sphingopyxis alaskensis, Arthrobacter pascens, Chryseobacterium rhizosphaerae, Variovorax paradoxus, Hydrogenophaga atypica,* and *Microbacterium oleivorans;* and/or *B) Brevibacterium frigoritolerans, Bacillus megaterium, Janibacter limosus,* and *Pseudomonas yamanorum*; and combinations thereof, and wherein at least one microbe from B) is selected.

[0061] In some embodiments, the microbial consortium has substantially similar morphological and physiological characteristics as a microbial consortium of the present disclosure. In some embodiments, the microbial consortium has substantially similar genetic characteristics as a microbial consortium of the present disclosure. In some embodiments, the microbial consortium is in substantially pure culture. In some embodiments, a subsequent generation of any microbe of the microbial consortium is contemplated. In some embodiments, a mutant of any microbe of microbial consortium is contemplated. In some embodiments, a cell-free or inactivated preparation of the microbial consortium, or a mutant of any microbe in the microbial consortium, is contemplated. In some embodiments, a metabolite produced by the microbial consortium, or a mutant of any microbe in the microbial consortium, is contemplated.

[0062] In some embodiments, an agricultural composition comprises a microbial consortium and an agriculturally acceptable carrier. The microbial consortium of the agricultural composition may be present in the composition at 1×10^{3} to 1×10^{12} bacterial cells per gram. In some embodiments, the agricultural composition is formulated as a seed coating. In some embodiments, a method of imparting at least one beneficial train upon a plant species comprises applying a microbial consortium to said plant, or to a growth medium in which said plant is located. In some embodiments, a method of imparting at least one beneficial trait upon a plant species,

comprising applying the agricultural composition to the plant, or to a growth medium in which said plant is located.

[0063] In some embodiments, a microbial consortium comprises at least two microbes selected from the group consisting of *Brevibacterium frigoritolerans* deposited as NRRL Accession Deposit No. NRRL B-67360; *Bacillus megaterium* deposited as NRRL Accession Deposit No. NRRL B-67370; *Janibacter limosus* deposited as NRRL Accession Deposit No. NRRL B-67358; *Janibacter limosus* deposited as NRRL Accession Deposit No. NRRL B-67359; *Janibacter limosus* deposited as NRRL Accession Deposit No. NRRL B-67364; *Pseudomonas yamanorum* deposited as NRRL Accession Deposit No. NRRL B-67361; *Pseudomonas yamanorum* deposited as NRRL Accession Deposit No. NRRL B-67362; *Pseudomonas yamanorum* deposited as NRRL Accession Deposit No. NRRL B-67363.

[0064] In one embodiment, the microbial consortium comprises *Brevibacterium frigoritolerans* deposited as NRRL Accession Deposit No. NRRL B-67360; *Bacillus megaterium* deposited as NRRL Accession Deposit No. NRRL B-67370; *Janibacter limosus* deposited as NRRL Accession Deposit No. NRRL B-67359; *Pseudomonas yamanorum* deposited as NRRL Accession Deposit No. NRRL B-67362.

[0065] In some embodiments, a method of imparting at least one beneficial trait upon a plant species comprises applying at least one isolated bacterial species to the plant, or to a growth medium in which the plant is located, wherein at least one isolated bacterial species is selected from the group consisting of: *Brevibacterium frigoritolerans, Bacillus megaterium, Janibacter limosus,* and *Pseudomonas yamanorum* and combinations thereof. In a further embodiment, at least one isolated bacterial species is a strain selected from the group consisting of: *Brevibacterium frigoritolerans* deposited as NRRL Accession Deposit No. NRRL B-67360; *Bacillus megaterium* deposited as NRRL Accession Deposit No. NRRL B-67370; *Janibacter limosus* deposited as NRRL Accession Deposit No. NRRL B-67358; *Janibacter limosus* deposited as NRRL Accession Deposit No. NRRL B-67359; *Janibacter limosus* deposited as NRRL Accession Deposit No. NRRL B-67364; *Pseudomonas yamanorum* deposited as NRRL Accession Deposit No. NRRL B-67361; *Pseudomonas yamanorum* deposited as NRRL Accession Deposit No. NRRL B-67362; *Pseudomonas yamanorum* deposited as NRRL Accession Deposit No. NRRL B-67363.

[0066] In some embodiments, an isolated bacterial strain is selected from Table 3. In some embodiments, an isolated bacterial strain is contemplated having substantially similar morphological and physiological characteristics as an isolated bacterial strain selected from Table 3. In some embodiments, an isolated bacterial strain is contemplated having substantially similar genetic characteristics as an isolated bacterial strain from Table 3. In some embodiments, a substantially pure culture is contemplated of an isolated bacterial strain from Table 3. In some embodiments, a progeny or a mutant of an isolated bacterial strain from Table 3 is contemplated. In some embodiments, a cell-free or inactivated preparation is contemplated from an isolated bacterial strain, or a mutant thereof, from Table 3. In some embodiments, a metabolite produced by an isolated bacterial strain, or a mutant thereof, from Table 3.

[0067] In some embodiments, an agricultural composition comprises an isolated bacterial strain from Table 3 and an agriculturally acceptable carrier. In some embodiments, the isolated bacterial strain is present in the agricultural composition at 1×10^{3} to 1×10^{12} CFU per gram. In some embodiments, the agricultural composition is formulated as a seed coating. In some embodiments, a method of imparting at least one beneficial train upon a plant species comprises applying an isolated bacterial strain from Table 3 to the plant, or to a growth medium in which said plant is located. In some embodiments, a method of imparting at least one beneficial trait upon a plant species comprises applying an agricultural composition of the present disclosure to the plant, or to a growth medium in which said plant is located.

[0068] In some embodiments, a microbial consortium comprises at least two microbes selected from those listed in Table 3. In some embodiments, a microbial consortium is selected from the consortia listed in Table 5, wherein the consortium comprises at least one microbe listed in Table 3. In some embodiments, a microbial consortium is selected from the consortia listed in Table 6, wherein the consortium comprises at least one microbe listed in Table 3. In some embodiments, a microbial consortium is selected from the consortia listed in Table 7, wherein the consortium comprises at least one microbe listed in Table 3. In some embodiments, a microbial consortium is selected from the consortia listed in Table 8, wherein the consortium comprises at least one microbe listed in Table 3. In some embodiments, a microbial consortium is selected from the consortia listed in Table 9, wherein the consortium comprises at least one microbe listed in Table 3. In some embodiments, a microbial consortium is selected from the consortia listed in Table 10, wherein the consortium

comprises at least one microbe listed in Table 3. In some embodiments, a microbial consortium is selected from the consortia listed in Table 11, wherein the consortium comprises at least one microbe listed in Table 3.

[0069] In some embodiments, a plant seed enhanced with a microbial seed coating comprises a plant seed and a seed coating applied onto said plant seed, wherein the seed coating comprises at least two microbes as listed in Tables 1-4, and wherein at least one microbe is selected from Table 3. In a further embodiment, the seed coating comprises a consortium of microbes as listed in Tables 5-11. In a further embodiment, the seed coating comprises at least one microbe as listed in Table 3 at a concentration of 1×10^5 to 1×10^9 CFU per seed. In some embodiments, a microbe selected from Table 3 is used in agriculture. In some embodiments, a synthetic combination of a plant and microbe comprises at least one plant and at least one microbe selected from Table 3.

[0070] In some embodiments, a method of increasing or promoting a desirable phenotypic trait of a plant species comprises applying at least one bacteria selected from Table 3 to said plant, or to a growth medium in which said plant is located. In a further embodiment, the method of applying the at least one bacteria occurs by coating a plant seed with said bacteria, coating a plant part with said bacteria, spraying said bacteria onto a plant part, spraying said bacteria into a furrow into which a plant or seed will be placed, drenching said bacteria onto a plant part or into an area into which a plant will be placed, spreading said bacteria onto a plant part or into an area into which a plant will be placed, broadcasting said bacteria onto a plant part or into an area into which a plant will be placed, and combinations thereof.

[0071] In any of the methods, the microbe can include a 16S rRNA nucleic acid sequence having at least 97% sequence identity to a 16S rRNA nucleic acid sequence of a bacteria selected from a genus provided in Table 3.

BRIEF DESCRIPTION OF THE FIGURES

[0072] FIG. 1 shows a generalized process schematic of a disclosed method of accelerated microbial selection (AMS), also referred to herein as directed microbial selection. When the process is viewed in the context of a microbial consortium, the schematic is illustrative of a process of directed evolution of a microbial consortium.

The process is one method, by which the beneficial microbes of the present disclosure were obtained.

[0073] FIG. 2 shows a generalized process flow chart of an embodiment, by which the beneficial microbes of the present disclosure were obtained.

[0074] FIG. 3 shows a graphic representation and associated flow chart of an embodiment, by which the beneficial microbes of the present disclosure were obtained.

[0075] FIG. 4 shows a graphic representation and associated flow chart of an embodiment, by which the beneficial microbes of the present disclosure were obtained.

[0076] FIG. 5 shows a graphic representation of the average total biomass of wheat, in grams of fresh weight, at seven days post inoculation with individual microbial strains (BCIs).

[0077] FIG. 6A and **FIG. 6B** shows a graphic representation of the average wheat shoot (A) and root (B) biomass, in grams of fresh weight, at six days post inoculation (DPI) with individual microbial strains. Seeds were inoculated, placed on wet germination paper and rolled. Rolls were incubated at 25°C in sealed plastic bins. Each individual strain was tested in triplicates of 30 seeds each. The horizontal red line represents the water control.

[0078] FIG. 7A and **FIG. 7B** shows a graphic representation of average corn shoot biomass, in grams of fresh weight, at six days post inoculation (DPI) with individual microbial strains. Seeds were inoculated, placed on wet germination paper and rolled. Rolls were incubated at 25°C in sealed plastic bins. Each individual strain was tested in triplicates of 30 seeds each. Due to the amount of samples tested, rolls were placed in two independent bins with a respective water control, represented individually in Figure 7 by graphs A and B. The horizontal red line represents the water control.

[0079] FIG. 8A and **FIG. 8B** shows a graphic representation of average corn root biomass, in grams of fresh weight, at six days post inoculation (DPI) with individual microbial strains. Seeds were inoculated, placed on wet germination paper and rolled. Rolls were incubated at 25°C in sealed plastic bins. Each individual strain was tested in triplicates of 30 seeds each. Due to the amount of samples tested, rolls were placed

in two independent bins with a respective water control, represented individually in Figure 8 by graphs A and B. The horizontal red line represents the water control.

[0080] FIG. 9 shows a graphic representation of the average shoot length, in millimeters, of maize at 4 days post treatment with individual microbial strains. Maize seeds were inoculated with individual microbial strains (BDNZ numbers) and subjected to a germination test. Seeds were inoculated, placed on wet paper towels and rolled. Rolls were incubated in sealed plastic bags at 25°C. Each individual strain was tested in duplicates of 30 seeds each. Shoot length was measured at 4 days post inoculation (DPI). Standard error bars are shown. Results show that germination rates were good for all strains tested and some strains caused a relative increase in shoot length at 4 days post inoculation (DPI) compared to the water control *in vivo*.

[0081] FIG. 10 shows a graphic representation of the average root length, in millimeters, of maize at 4 days post treatment with individual microbial strains. Maize seeds were inoculated with individual microbial strains (BDNZ numbers) and subjected to a germination test. Seeds were inoculated, placed on wet paper towels and rolled. Rolls were incubated in sealed plastic bags at 25°C. Each individual strain was tested in duplicates of 30 seeds each. Root length was measured at 4 days post inoculation (DPI). Standard error bars are shown. Results show that e germination rates were good for all strains tested and some strains caused a relative increase in root length at 4 days post inoculation (DPI) compared to the water control *in vivo*.

[0082] FIG. 11 shows a graphic representation of the average shoot length, in millimeters, of wheat at 4 days post treatment with individual microbial strains. Wheat seeds were inoculated with individual microbial strains (BDNZ numbers) and subjected to a germination test. Seed were inoculated, placed on wet paper towels and rolled. Rolls were incubated in sealed plastic bags at 25°C. Each individual strain was tested in duplicates of 30 seeds each. Shoot length was measured at 4 days post treatment. Results show that germination rates were good for all strains tested (>90%) and some strains caused a relative increase in shoot length at 4 days post inoculation (DPI) compared to the water control *in vitro*.

[0083] FIG. 12 shows a graphic representation of the average root length, in millimeters, of wheat at 4 days post treatment with individual microbial strains. Wheat seeds were inoculated with individual microbial strains (BDNZ numbers) and

subjected to a germination test. Seed were inoculated, placed on wet paper towels and rolled. Rolls were incubated in sealed plastic bags at 25°C. Each individual strain was tested in duplicates of 30 seeds each. Root length was measured at 4 days post treatment. Results show that germination rates were good for all strains tested (>90%) and some strains caused a relative increase in root length at 4 days post inoculation (DPI) compared to the water control *in vitro*.

[0084] FIG. 13 shows a graphic representation of the average shoot length, in millimeters, of tomato at 4 days post treatment with individual microbial strains. Tomato seeds were inoculated with individual microbial strains (BDNZ numbers) and subjected to a germination test. Seeds were inoculated, placed on wet paper towels and rolled. Rolls were incubated in sealed plastic bags at 25°C. Each individual strain was tested in duplicates of 50 seeds each. Shoot length was measured at 4 days post treatment. The mean length of shoots of the water control seed can be seen in the far right bar labelled "H2O". Results show that germination rates were good for all strains tested and some strains caused a relative increase in shoot length at 4 days post inoculation (DPI) compared to the water control *in vitro*.

[0085] FIG. 14 shows a graphic representation of the average root length, in millimeters, of tomato at 4 days post treatment with individual microbial strains. Tomato seeds were inoculated with individual microbial strains (BDNZ numbers) and subjected to a germination test. Seeds were inoculated, placed on wet paper towels and rolled. Rolls were incubated in sealed plastic bags at 25°C. Each individual strain was tested in duplicates of 50 seeds each. Root length was measured at 4 days post treatment. The mean length of roots of the water control seed can be seen in the far right bar labelled "H2O". Results show that germination rates were good for all strains tested and some strains caused a relative increase in root length at 4 days post inoculation (DPI) compared to the water control *in vitro*.

[0086] FIG. 15A and **FIG. 15B** shows a graphic representation of average corn shoot length, in millimeters, at six days post inoculation (DPI) with individual microbial strains. Seeds were inoculated, placed on wet germination paper and rolled. Rolls were incubated at 25°C in sealed plastic bins. Each individual strain was tested in triplicates of 30 seeds each. Due to the amount of samples tested, rolls were placed in two independent bins with a respective water control, represented individually in Figure 15 by graphs A and B. The horizontal red line represents the water control.

[0087] FIG. 16A and **FIG. 16 B** shows a graphic representation of average corn root length, in millimeters, at six days post inoculation (DPI) with individual microbial strains. Seeds were inoculated, placed on wet germination paper and rolled. Rolls were incubated at 25°C in sealed plastic bins. Each individual strain was tested in triplicates of 30 seeds each. Due to the amount of samples tested, rolls were placed in two independent bins with a respective water control, represented individually in Figure 16 by graphs A and B. The horizontal red line represents the water control.

[0088] FIG. 17 shows a graphic representation of percentage differences compared to a water-treated control of tomato (*Solanum lycopersicum*) shoot biomass. Tomato seedlings were grown in ceramic growth media in a growth chamber and inoculated with individual microbial strains at 21 days post planting. Seedlings were grown for a further 10 days post inoculation before shoot biomass was measured. For each microbial treatment, tomato seedlings were drench-inoculated with 1 mL of a water-based suspension of microbes at 10^7 CFU/mL. A control treatment with water in the absence of a microbial inoculant was included. All plants were grown in a growth chamber at 25 ± 5°C, and on a 16/8 h day/night cycle for 10 days after inoculation. Treatments were arrayed using a Randomized Complete Block Design (RCBD) comprising 3 blocks and 8 replicates per block, per treatment.

[0089] FIG. 18 shows a graphic representation of the effect of microbial treatments on corn (*Zea mays*) shoot biomass. The graph shows average corn shoot fresh-weight in grams at 10 days post first inoculation with individual microbial strains. Corn seedlings were raised in ceramic growth media in a growth room and inoculated with individual strains at 5 and 10 days post planting. Treatments were arrayed using a Randomized Complete Block Design (RCBD) comprising 3 blocks and 6 replicates per block, per treatment. Shoot above ground biomass was cut and weighed 10 days post first inoculation. Bars represent standard error. The horizontal orange line represents the average shoot weight of the un-inoculated water only control.

[0090] FIG. 19 shows a graphic representation of the effect of microbial treatments on wheat (*Triticum aestivum*) seedling shoot (left of each pair) and root (right of each pair) biomass. The graph shows percentage difference of wheat shoot and root biomass compared to an un-inoculated water-treated control. Wheat seeds were inoculated with individual microbes, placed on wet germination paper that was then rolled and incubated in plastic bins at 25°C for 6 days. Each individual strain was

tested in triplicate rolls of 20 seeds each. Total shoot and root fresh weight was measured at six days post treatment.

[0091] FIG. 20 shows a graphic representation of the effect of microbial treatments on corn seedling shoot and root biomass. The graph shows the percentage difference of corn shoot (left of each pair) and root (right of each pair) biomass compared to a water-treated control. Corn seeds were inoculated with individual microbes, placed on wet germination paper that was then rolled and incubated in plastic bins at 25°C. Each individual strain was tested in triplicate rolls of 20 seeds each. Shoot and root fresh weight was measured at six days post treatment.

BUDAPEST TREATY ON THE INTERNATIONAL RECOGNITION OF THE DEPOSIT OF MICROORGANISMS FOR THE PURPOSE OF PATENT PROCEDURES

[0092] The microorganisms described in this Application were deposited with the Agricultural Research Service Culture Collection (NRRL), which is an International Depositary Authority, located at 1815 North University Street, Peoria, IL 61604, USA.

[0093] The deposits were made under the terms of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purposes of Patent Procedure.

[0094] The deposits were made in accordance with, and to satisfy, the criteria set forth in 37 C.F.R. §§ 1.801-1.809 and the Manual of Patent Examining Procedure §§ 2402-2411.05.

[0095] The NRRL accession numbers, dates of deposit, and descriptions for the aforementioned Budapest Treaty deposits are provided in **Tables 1-4**.

Table 1

Microbial Species	Strains	Origin	Budapest Treaty International Depositary Authority Accession No. & Date of Deposit	Representative Deposited Species Available to the Public	SEQ ID No.
1. *Azotobacter chroococcum*	BDNZ 57597	NZ		DSM-2286*	289
2. *Pantoea*	BDNZ	NZ	NRRL B-67224 January 29, 2016		278

Microbial Species	Strains	Origin	Budapest Treaty International Depositary Authority Accession No. & Date of Deposit	Representative Deposited Species Available to the Public	SEQ ID No.
agglomerans (recently reassigned to *Pantoea vagans*)	54499 BDNZ 55529 BDNZ 57547				289 288
3. *Pantoea agglomerans* (recently reassigned to *Pantoea vagans*)	BCI 1208 BCI 1274 BCI 1355	US		DSM-23078*	62 68 90
4. *Pseudomonas fluorescens*	BDNZ 54480 BDNZ 56530 BDNZ 56249	NZ		DSM-50090*	276 285 284
5. *Pseudomonas fluorescens*	BCI 1352	US		DSM-50090*	88
6. *Pseudomonas oryzihabitans*	BDNZ 55530	NZ	NRRL B-67225 January 29, 2016		283
7. *Pseudomonas oryzihabitans*	BCI 1184 BCI 1195 BCI 1199	US		DSM-6835*	58 59 60
8. *Pseudomonas putida*	BDNZ 60303	NZ		DSM-291*	294
9. *Pseudomonas putida*	BCI 159 BCI 178 BCI 234 BCI 235 BCI 244 BCI 357 BCI 360 BCI 363 BCI 365 BCI 367 BCI 368 BCI 369 BCI 370 BCI 372 BCI 375 BCI 458 BCI 459 BCI 460	US		DSM-291*	100 104 109 110 112 124 126 127 128 129 130 131 132 134 135 144 145 147

Microbial Species	Strains	Origin	Budapest Treaty International Depositary Authority Accession No. & Date of Deposit	Representative Deposited Species Available to the Public	SEQ ID No.
	BCI 461 BCI 462 BCI 467 BCI 469 BCI 470 BCI 571 BCI 593 BCI 731 BCI 791 BCI 802 BCI 805 BCI 806 BCI 809 BCI 1312 BCI 1314 BCI 1315 BCI 1319 BCI 1330 BCI 1333 BCI 1351 BCI 1353 BCI 1356 BCI 1358 BCI 1363				148 149 150 151 152 162 168 198 205 208 210 211 213 73 74 75 77 82 84 87 89 91 93 96
10. *Rahnella aquatilis*	BDNZ 56532 BDNZ 57157 BDNZ 58013	NZ	NRRL B-67228 January 29, 2016 NRRL B-67229 January 29, 2016		286 287 293
11. *Rahnella aquatilis*	BCI 29 BCI 1158	US	NRRL B-67165 December 18, 2015		118 54
12. *Rhizobium etli*	BDNZ 60473	NZ		DSM-11541*	295
13. *Rhodococcus*	BDNZ	NZ	NRRL B-67227 January 29, 2016		274 275

Microbial Species	Strains	Origin	Budapest Treaty International Depositary Authority Accession No. & Date of Deposit	Representative Deposited Species Available to the Public	SEQ ID No.
erythropolis	54093 BDNZ 54299				
14. *Rhodococcus erythropolis*	BCI 1182	US		DSM-43066*	57
15. *Stenotrophomonas maltophilia*	BDNZ 54073	NZ	NRRL B-67226 January 29, 2016		273
16. *Stenotrophomonas maltophilia*	BCI 7	US		DSM-50170*	194
	BCI 64				183
	BCI 77				201
	BCI 115				52
	BCI 120				61
	BCI 164				102
	BCI 171				103
	BCI 181				105
	BCI 271				114
	BCI 343				122
	BCI 344				123
	BCI 380				136
	BCI 539				157
	BCI 545				158
	BCI 551				159
	BCI 574				163
	BCI 588				165
	BCI 590				167
	BCI 601				170
	BCI 602				171
	BCI 606				172
	BCI 607				173
	BCI 610				176
	BCI 617				177
	BCI 618				178
	BCI 619				179
	BCI 620				181
	BCI 623				182
	BCI 665				185
	BCI 693				193
	BCI 787				202
	BCI 790				204
	BCI 793				206
	BCI 795				207
	BCI 808				212
	BCI 903				218
	BCI 908				219

Microbial Species	Strains	Origin	Budapest Treaty International Depositary Authority Accession No. & Date of Deposit	Representative Deposited Species Available to the Public	SEQ ID No.
	BCI 970				224
	BCI 996				226
	BCI 997				227
	BCI 1032				37
	BCI 1092				45
	BCI 1096				46
	BCI 1116				50
	BCI 1224				64
	BCI 1279				69
	BCI 1316				76
	BCI 1320				79
	BCI 1322				80
	BCI 1325				81
	BCI 1331				83
	BCI 1344				85
	BCI 1350				86
	BCI 1357				92
	BCI 1362				95

*Denotes a microbial species that has been deposited and is available to the public, but said species is not a deposit of the exact BCI or BDNZ strain.

TABLE 2

Microbial Species	Strain	Origin	Budapest Treaty International Depositary Authority Accession No. & Date of Deposit	Representative Deposited Species Available to the Public	SEQ ID No.
1. *Azospirillum lipoferum*	BDNZ57661 BDNZ66460	NZ		DSM-1838*	291 300
2. *Bacillus megaterium*	BDNZ55076	NZ		DSM-32*	279
3. *Bacillus megaterium*	BCI 251 BCI 255 BCI 262 BCI 264	US		DSM-32*	113 114 115 116
4. *Bacillus psychrosaccharolyticus*	BDNZ 66518 BDNZ 66544	NZ		DSM-13778*	303 306
5. *Duganella zoogloeoides*	BDNZ 66500	NZ		DSM-16928*	302
6. *Herbaspirillum huttiense*	BDNZ 54487	NZ		DSM-10281*	277
7. *Herbaspirillum huttiense*	BCI 9	US		DSM-10281*	217

Microbial Species	Strain	Origin	Budapest Treaty International Depositary Authority Accession No. & Date of Deposit	Representative Deposited Species Available to the Public	SEQ ID No.
8. *Paenibacillus chondroitinus*	BDNZ 57634	NZ		DSM-5051*	290
9. *Paenibacillus polymyxa*	BDNZ 55146 BDNZ 66545	NZ		DSM-36*	280 304
10. *Paenibacillus polymyxa*	BCI 1118	US		DSM-36*	51

*Denotes a microbial species that has been deposited and is available to the public, but said species is not a deposit of the exact BCI or BDNZ strain.

TABLE 3

Microbial Species	Strain	Origin	Budapest Treaty International Depositary Authority Accession No. & Date of Deposit	Representative Deposited Species Available to the Public	SEQ ID No.
1. *Flavobacterium glaciei*	BDNZ 66487	NZ		DSM-19728*	301
2. *Massilia niastensis*	BDNZ 55184 BCI 1217	NZ US	NRRL B-67235 February 8, 2016 NRRL B-67199 December 29, 2015		281 63
3. *Massilia kyonggiensis* (*Massilia albidiflava*)	BCI 36	US		DSM-17472*	125
4. *Sphingobium yanoikuyae*	BDNZ 57662	NZ		DSM-7462*	292
5. *Bacillus subtilis*	BDNZ 66347	NZ		DSM-1088*	263
6. *Bacillus subtilis*	BCI 395 BCI 989 BCI 1089	US		DSM-1088*	138 225 43
7. *Bosea minatitlanensis*	BDNZ 66354	NZ		DSM-13099*	264

Microbial Species	Strain	Origin	Budapest Treaty International Depositary Authority Accession No. & Date of Deposit	Representative Deposited Species Available to the Public	SEQ ID No.
8. *Bosea thiooxidans*	BDNZ 54522	NZ		DSM-9653*	240
9. *Bosea thiooxidans*	BCI 703 BCI 985 BCI 1111	US	NRRL B-67187 December 29, 2015		196 36 49
10. *Bosea robinae*	BCI 1041 BCI 689 BCI 765	US	NRRL B-67186 December 29, 2015		38 190 200
11. *Bosea eneae*	BCI 1267	US	NRRL B-67185 December 29, 2015		67
12. *Caulobacter henrici*	BDNZ 66341	NZ		DSM-4730*	262
13. *Pseudoduganella violaceinigra*	BDNZ 66361	NZ		DSM-15887*	265
14. *Luteibacter yeojuensis*	BDNZ 57549	NZ		DSM-17673*	235
15. *Mucilaginibacter gossypii*	BDNZ66321	NZ			297
16. *Mucilaginibacter gossypii*	BCI 142 BCI 1156 BCI 1307	US			99 53 71
17. *Paenibacillus amylolyticus*	BDNZ 66316	NZ		DSM-11730*	296
18. *Polaromonas ginsengisoli*	BDNZ 66373 BDNZ 66821	NZ NZ	NRRL B-67231 February 8, 2016 NRRL B-67234 February 8, 2016	DSM-14656*	266 270
19. *Ramlibacter henchirensis*	BDNZ 66331	NZ		DSM-14656*	261

Microbial Species	Strain	Origin	Budapest Treaty International Depositary Authority Accession No. & Date of Deposit	Representative Deposited Species Available to the Public	SEQ ID No.
20. *Ramlibacter henchirensis*	BCI 739	US	NRRL B-67208 December 29, 2015		199
21. *Leifsonia shinshuensis* (previously *Rhizobium leguminosarum bv. trifolii)*	BDNZ 61433	NZ		DSM-15165*	250
22. *Rhizobium pisi*	BDNZ 66326	NZ		DSM-30132*	260
23. *Rhodoferax ferrireducens*	BDNZ 66374	NZ		DSM-15236*	267
24. *Sphingobium chlorophenolicum*	BDNZ 61473	NZ		DSM-24952*	251
25. *Sphingobium quisquiliarum*	BDNZ 66576	NZ		DSM-24952*	269
26. *Herbaspirillum frisingense*	BDNZ 50525	NZ		DSM-13128*	234
27. *Caulibacter henrici*	BDNZ 66341	NZ		DSM-4730*	262
28. *Chitinophaga arvensicola*	BDNZ 56343	NZ		DSM-3695*	246
29. *Duganella violaceinigra*	BDNZ 66361 BDNZ 58291	NZ NZ	NRRL B-67232 February 8, 2016 NRRL B-67233 February 8, 2016	DSM-15887*	265 248
30. *Frateuria sp.*	BDNZ 52707 BDNZ 60517	NZ		DSM-6220* *(Frateuria aurantia)* DSM-26515* *(Frateuria terrea)*	238 249
31. *Janthinobacterium sp.*	BDNZ 54456 BDNZ 63491	NZ			239 252
32. *Luteibacter rhizovicinus*	BDNZ 65069	NZ		DSM-16549*	255
33. *Lysinibacillus fusiformis*	BDNZ 63466	NZ		DSM-2898*	254
34. *Novosphingobium rosa*	BDNZ 65589 BDNZ 65619	NZ		DSM-7285*	258 259
35. *Rhizobium miluonense*	BDNZ 65070	NZ			256

Microbial Species	Strain	Origin	Budapest Treaty International Depositary Authority Accession No. & Date of Deposit	Representative Deposited Species Available to the Public	SEQ ID No.
36. *Stenotrophomonas chelatiphaga*	BDNZ 54952	NZ		DSM-21508*	243
37. *Stenotrophomonas chelatiphaga*	BDNZ 47207	NZ		DSM-21508*	232
38. *Stenotrophomonas chelatiphaga*	BDNZ 64212	NZ		DSM-21508*	253
39. *Stenotrophomonas chelatiphaga*	BNDZ 64208	NZ		DSM-21508*	305
40. *Stenotrophomonas chelatiphaga*	BDNZ 58264	NZ		DSM-21508*	247
41. *Stenotrophomonas rhizophila*	BDNZ 50839	NZ		DSM-14405*	236
42. *Stenotrophomonas rhizophila*	BDNZ 48183	NZ		DSM-14405*	233
43. *Stenotrophomonas rhizophila*	BDNZ 45125	NZ		DSM-14405*	228
44. *Stenotrophomonas rhizophila*	BDNZ 46120	NZ		DSM-14405*	230
45. *Stenotrophomonas rhizophila*	BDNZ 46012	NZ		DSM-14405*	229
46. *Stenotrophomonas rhizophila*	BDNZ 51718	NZ		DSM-14405*	237
47. *Stenotrophomonas rhizophila*	BDNZ 56181	NZ		DSM-14405*	245
48. *Stenotrophomonas rhizophila*	BDNZ 54999	NZ		DSM-14405*	244
49. *Stenotrophomonas rhizophila*	BDNZ 54850	NZ		DSM-14405*	242
50. *Stenotrophomonas rhizophila*	BDNZ 54841	NZ		DSM-14405*	241
51. *Stenotrophomonas rhizophila*	BDNZ 66478	NZ		DSM-14405*	268
52. *Stenotrophomonas rhizophila*	BDNZ 46856	NZ		DSM-14405*	231
53. *Stenotrophomonas rhizophila*	BDNZ 65303	NZ		DSM-14405*	257
54. *Stenotrophomonas terrae*	BDNZ 68599	NZ		DSM-15236*	271
55. *Stenotrophomonas terrae*	BDNZ 68741	NZ		DSM-18941*	272
56. *Achromobacter spanius*	BCI 385	US		DSM-23806*	137
57. *Acidovorax soli*	BCI 690	US	NRRL B-67182 Dec. 29, 2015		191
58. *Arthrobacter cupressi*	BCI 59	US	NRRL B-67183 Dec. 29, 2015		166

Microbial Species	Strain	Origin	Budapest Treaty International Depositary Authority Accession No. & Date of Deposit	Representative Deposited Species Available to the Public	SEQ ID No.
59. *Arthrobacter mysorens*	BCI 700	US		DSM-12798*	195
60. *Arthrobacter pascens*	BCI 682	US		DSM-20545*	187
61. *Bacillus oleronius*	BCI 1071	US		DSM-9356*	42
62. *Bacillus cereus or Bacillus thuringiensis (In Taxonomic Flux)*	BCI 715	US		DSM-2046*	197
63. *Chitinophaga terrae*	BCI 79	US	NRRL B-67188 December 29, 2015		203
64. *Delftia lacustris*	BCI 124	US	NRRL B-67190 December 29, 2015		65
65. *Duganella radicis*	BCI 105	US	NRRL B-67192 December 29, 2015		39
66. *Duganella radicis*	BCI 57	US			161
67. *Duganella radicis*	BCI 31	US	NRRL B-67166 January 13, 2016		21
68. *Dyadobacter soli*	BCI 68	US	NRRL B-67194 December 29, 2015		186
69. *Exiguobacterium acetylicum*	BCI 23	US		DSM-20416*	108
70. *Exiguobacterium acetylicum*	BCI 83	US		DSM-20416*	216
71. *Exiguobacterium acetylicum*	BCI 125	US		DSM-20416*	66
72. *Exiguobacterium aurantiacum*	BCI 50	US	NRRL B-67175 December 18, 2015		155
73. *Exiguobacterium sp.* (In Taxonomic Flux)	BCI 81	US		DSM-27935*	214
74. *Exiguobacterium sibiricum*	BCI 116	US	NRRL B-67167 December 18, 2016		16
75. *Herbaspirillum chlorophenolicum*	BCI 58	US	NRRL B-67236 February 8, 2016	DSM-17796*	164

Microbial Species	Strain	Origin	Budapest Treaty International Depositary Authority Accession No. & Date of Deposit	Representative Deposited Species Available to the Public	SEQ ID No.
76. *Kosakonia radicincitans*	BCI 107	US		DSM-16656*	41
77. *Massilia kyonggiensis (Massilia albidiflava)*	BCI 97	US	NRRL B-67198 December 29, 2015		32
78. *Microbacterium sp.*	BCI 688	US		DSM-16050*	189
79. *Microbacterium oleivorans*	BCI 132	US	NRRL B-67170 December 18, 2015		78
80. *Mucilaginibacter gossypii*	BCI 142	US			98
81. *Novosphigobium lindaniclasticum*	BCI 684	US	NRRL B-67201 December 29, 2015		188
82. *Novosphingobium resinovorum*	BCI 557	US	NRRL B-67202 December 29, 2015		160
83. *Novosphingobium sediminicola*	BCI 136	US		DSM-27057*	94
84. *Novosphingobium sediminicola*	BCI 82	US		DSM-27057*	215
85. *Novosphingobium sediminicola*	BCI 130	US	NRRL B-67168 December 18, 2015		28
86. *Paenibacillus glycanilyticus*	BCI 418	US	NRRL B-67204 December 29, 2015		141
87. *Pedobacter rhizosphaerae (Pedobacter soli)*	BCI 598	US	NRRL B-67205 December 29, 2015		169
88. *Pedobacter terrae*	BCI 91	US	NRRL B-67206 December 29, 2015		220
89. *Pseudomonas jinjuensis*	BCI 804	US	NRRL B-67207 December 29, 2015		209
90. *Rhizobium grahamii*	BCI 691	US			192
91. *Rhizobium lemnae* (taxonomic name changed December 2015 to *Rhizobium rhizoryzae*)	BCI 34	US	NRRL B-67210 December 29, 2015		121

Microbial Species	Strain	Origin	Budapest Treaty International Depositary Authority Accession No. & Date of Deposit	Representative Deposited Species Available to the Public	SEQ ID No.
92. *Agrobacterium fabrum or Rhizobium pusense* (In Taxonomic Flux)	BCI 106	US	NRRL B-67212 December 29, 2015	DSM-22668*	40
93. *Agrobacterium fabrum or Rhizobium pusense* (In Taxonomic Flux)	BCI 11	US		DSM-22668*	47
94. *Agrobacterium fabrum or Rhizobium pusense* (In Taxonomic Flux)	BCI 609	US		DSM-22668*	175
95. *Ensifer adhaerens*	BCI 131	US	NRRL B-67169 December 18, 2015		72
96. *Sphingopyxis alaskensis*	BCI 914	US	NRRL B-67215 December 29, 2015	DSM-13593*	221
97. *Variovorax ginsengisoli*	BCI 137	US	NRRL B-67216 December 29, 2015		97
98. *Bacillus niacini*	BCI 4718	US	NRRL B-67230 February 8, 2016	DSM-2923*	153
99. *Exiguobacterium sibiricum*	BCI 116	US	NRRL B-67167 December 18, 2015		16
100. *Chryseobacterium daecheongense*	BCI 45	US	NRRL B-67172 December 18, 2015		1
101. *Achromobacter pulmonis*	BCI 49		NRRL B-67174 December 18, 2015		15
102. *Acidovorax soli*	BCI 648		NRRL B-67181 December 29, 2015		184
103. *Arthrobacter cupressi*	BCI 62		NRRL B-67184 December 29, 2015		180
104. *Chininophaga terrae*	BCI 109		NRRL B-67189 December 29, 2015		44

Microbial Species	Strain	Origin	Budapest Treaty International Depositary Authority Accession No. & Date of Deposit	Representative Deposited Species Available to the Public	SEQ ID No.
105. *Delftia lacustris*	BCI 2350		NRRL B-67191 December 29, 2015		111
106. *Duganella violaceinigra*	BCI 2204		NRRL B-67193 December 29, 2015		107
107. *Dyadobacter soli*	BCI 96		NRRL B-67195 December 29, 2015		222
108. *Flavobacterium glacei*	BCI 4005		NRRL B-67196 December 29, 2015		139
109. *Herbaspirillum chlorophenolicum*	BCI 162		NRRL B-67197 December 29, 2015		101
110. *Novosphingobium lindaniclasticum*	BCI 608		NRRL B-67200 December 29, 2015		30
111. *Nocosphingobium resinovorum*	BCI 3709		NRRL B-67203 December 29, 2015		133
112. *Ramlibacter henchirensis*	BCI 1959		NRRL B-67209 December 29, 2015		106
113. *Rhizobium rhizoryzae*	BCI 661		NRRL B-67211 December 29, 2015		35
114. *Sinorhizobium chiapanecum (Ensifer adhaerens)*	BCI 111		NRRL B-67213 December 29, 2015		48
115. *Sphingopyxis alaskensis*	BCI 412		NRRL B-67214 December 29, 2015		140
116. *Variovorax ginsengisoli*	BCI 3078		NRRL B-67217 December 29, 2015		119
117. *Kosakonia radicincitans*	BCI 44		NRRL B-67171 December 18, 2015		142
118. *Pedobacter terrae*	BCI 53		NRRL B-67176 December 18, 2015	DSM17933*	20

Microbial Species	Strain	Origin	Budapest Treaty International Depositary Authority Accession No. & Date of Deposit	Representative Deposited Species Available to the Public	SEQ ID No.
119. *Agrobacterium fabrum* or *Rhizobium pusense* (In Taxonomic Flux) (previously Rhizobium sp.)	BCI 46		NRRL B-67173 December 18, 2015		146
120. *Brevibacterium frigoritolerans*[1]	BCI 4468		NRRL B-67360 January 5, 2016	DSM 8801* ATCC 25097*	308
121. *Bacillus megaterium*	BCI 4473		NRRL B-67370 January 16, 2016	DSM 32 ATCC 14581	309
122. *Janibacter limosus*	BCI 3103 BCI 4708 BCI 3105		NRRL B-67358 January 5, 2016 NRRL B-67359 January 5, 2016 NRRL B-67364 January 5, 2016	DSM 11140* ATCC 700321*	310 311 312
123. *Pseudomonas yamanorum*	BCI 5446 BCI 4853 BCI 3523		NRRL B-67361 January 5, 2016 NRRL B-67362 January 5, 2016 NRRL B-67363 January 5, 2016	DSM 16768*	313 314 315

*Denotes a microbial species that has been deposited and is available to the public, but said species is not a deposit of the exact BCI or BDNZ strain.
[1] In taxonomic flux, potential synonym of *Bacillus muralis*

TABLE 4

Microbial Species	Strain	Origin	Budapest Treaty International Depositary Authority Accession No. & Date of Deposit	Representative Deposited Species Available to the Public	SEQ ID No.
1. *Chryseobacterium daecheongense*	BCI 191	US	NRRL B-67291 July 14, 2016	DSM15235*	2
2. *Chryseobacterium rhizosphaerae*	BCI 597 BCI 615	US US	NRRL B-67288 July 14, 2016 NRRL B-67287 July 14, 2016		3 4
3. *Frigidibacter albus* or *Delfulviimonas dentrificans* (In Taxonomic Flux)	BCI 712 BCI 402 BCI 745	US US US	NRRL B-67285 July 14, 2016 NRRL B-67283 July 14, 2016 NRRL B-67284 July 14, 2016		5 6 7
4. *Arthrobacter nicotinovorans*	BCI 717 BCI 3189	US US	NRRL B-67289 July 14, 2016 NRRL B-67290 July 14, 2016	DSM420*	8 9
5. *Pseudomonas helmanticensis*	BCI 616 BCI 2945 BCI 800	US US US	NRRL B-67295 July 14, 2016 NRRL B-67296 July 14, 2016 NRRL B-67297 July 14, 2016	DSM28442*	10 11 12
6. *Agrobacterium fabrum* or *Rhizobium pusense* (In Taxonomic Flux) (previously *Rhizobium sp.*)	BCI 958	US	NRRL B-67286 July 14, 2016	DSM22668*	14
7. *Exiguobacterium sibiricum*	BCI 718	US	NRRL B-67294 July 14, 2016	DSM17290*	17
8. *Exiguobacterium antarcticum*	BCI 63 BCI 225	US US	NRRL B-67292 July 14, 2016 NRRL B-67293 July 14, 2016	DSM14480*	18 19
9. *Leifsonia lichenia*	BDNZ 72243 BDNZ 72289	NZ NZ	NRRL B-67298 July 21, 2016 NRRL B-67299 July 21, 2016		22 23

10. *Tumebacillus permanentifrigoris*	BDNZ 72229 BDNZ 74542 BDNZ 72366 BDNZ 72287	NZ NZ NZ NZ	NRRL B-67302 July 22, 2016 NRRL B-67300 August 4, 2016 NRRL B-67303 July 22, 2016 NRRL B-67301 August 4, 2016	DSM118773*	24 25 26 307
11. *Bacillus asahii*	BCI 928	US			27
12. *Novosphingobium sediminicola*	BDNZ 71628	NZ		DSM27057*	29
13. *Novosphingobium lindaniclasticum*	BDNZ 71222	NZ		DSM25409*	31
14. *Massilia kyonggiensis*	BCI 94 BDNZ 73021	US NZ		DSM101532*	33 34

*Denotes a microbial species that has been deposited and is available to the public, but said species is not a deposit of the exact BCI or BDNZ strain.

DETAILED DESCRIPTION

Definitions

[0096] While the following terms are believed to be well understood by one of ordinary skill in the art, the following definitions are set forth to facilitate explanation of the presently disclosed subject matter.

[0097] The term "a" or "an" refers to one or more of that entity, *i.e.* can refer to a plural referents. As such, the terms "a" or "an", "one or more" and "at least one" are used interchangeably herein. 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 is present, unless the context clearly requires that there is one and only one of the elements.

[0098] As used herein the terms "microorganism" or "microbe" should be taken broadly. These terms are used interchangeably and include, but are not limited to, the two prokaryotic domains, Bacteria and Archaea, as well as eukaryotic fungi and protists. In some embodiments, the disclosure refers to the "microbes" of **Tables 1-4**, or the "microbes" of various other tables present in the disclosure. This characterization can refer to not only the identified taxonomic bacterial genera of the tables, but also the identified taxonomic species, as well as the various novel and newly identified bacterial strains of said tables.

[0099] The term "microbial consortia" or "microbial consortium" refers to a subset of a microbial community of individual microbial species, or strains of a species, which can be described as carrying out a common function, or can be described as participating in, or leading to, or correlating with, a recognizable parameter or plant phenotypic trait. The community may comprise two or more species, or strains of a species, of microbes. In some instances, the microbes coexist within the community symbiotically.

[00100] The term "microbial community" means a group of microbes comprising two or more species or strains. Unlike microbial consortia, a microbial community does not have to be carrying out a common function, or does not have to be participating in, or leading to, or correlating with, a recognizable parameter or plant phenotypic trait.

[00101] The term "accelerated microbial selection" or "AMS" is used interchangeably with the term "directed microbial selection" or "DMS" and refers to the iterative selection methodology that was utilized, in some embodiments of the disclosure, to derive the claimed microbial species or consortia of said species.

[00102] As used herein, "isolate," "isolated," "isolated microbe," and like terms, are intended to mean that the one or more microorganisms has been separated from at least one of the materials with which it is associated in a particular environment (for example soil, water, plant tissue).

[00103] Thus, an "isolated microbe" does not exist in its naturally occurring environment; rather, it is through the various techniques described herein that the microbe has been removed from its natural setting and placed into a non-naturally occurring state of existence. Thus, the isolated strain may exist as, for example, a biologically pure culture, or as spores (or other forms of the strain) in association with an agricultural carrier.

[00104] In certain aspects of the disclosure, the isolated microbes exist as isolated and biologically pure cultures. It will be appreciated by one of skill in the art, that an isolated and biologically pure culture of a particular microbe, denotes that said culture is substantially free (within scientific reason) of other living organisms and contains only the individual microbe in question. The culture can contain varying concentrations of said microbe. The present disclosure notes that isolated and

biologically pure microbes often "necessarily differ from less pure or impure materials." *See, e.g. In re Bergstrom*, 427 F.2d 1394, (CCPA 1970)(discussing purified prostaglandins), see also, *In re Bergy*, 596 F.2d 952 (CCPA 1979)(discussing purified microbes), see also, *Parke-Davis & Co. v. H.K. Mulford & Co.*, 189 F. 95 (S.D.N.Y. 1911) (Learned Hand discussing purified adrenaline), *aff'd in part, rev'd in part*, 196 F. 496 (2d Cir. 1912), each of which are incorporated herein by reference. Furthermore, in some aspects, the disclosure provides for certain quantitative measures of the concentration, or purity limitations, that must be found within an isolated and biologically pure microbial culture. The presence of these purity values, in certain embodiments, is a further attribute that distinguishes the presently disclosed microbes from those microbes existing in a natural state. *See, e.g., Merck & Co. v. Olin Mathieson Chemical Corp.*, 253 F.2d 156 (4th Cir. 1958) (discussing purity limitations for vitamin B12 produced by microbes), incorporated herein by reference.

[00105] As used herein, "individual isolates" should be taken to mean a composition, or culture, comprising a predominance of a single genera, species, or strain, of microorganism, following separation from one or more other microorganisms. The phrase should not be taken to indicate the extent to which the microorganism has been isolated or purified. However, "individual isolates" can comprise substantially only one genus, species, or strain, of microorganism.

[00106] The term "growth medium" as used herein, is any medium which is suitable to support growth of a plant. By way of example, the media may be natural or artificial including, but not limited to: soil, potting mixes, bark, vermiculite, hydroponic solutions alone and applied to solid plant support systems, and tissue culture gels. It should be appreciated that the media may be used alone or in combination with one or more other media. It may also be used with or without the addition of exogenous nutrients and physical support systems for roots and foliage.

[00107] In one embodiment, the growth medium is a naturally occurring medium such as soil, sand, mud, clay, humus, regolith, rock, or water. In another embodiment, the growth medium is artificial. Such an artificial growth medium may be constructed to mimic the conditions of a naturally occurring medium; however, this is not necessary. Artificial growth media can be made from one or more of any number and combination of materials including sand, minerals, glass, rock, water, metals, salts,

nutrients, water. In one embodiment, the growth medium is sterile. In another embodiment, the growth medium is not sterile.

[00108] The medium may be amended or enriched with additional compounds or components, for example, a component which may assist in the interaction and/or selection of specific groups of microorganisms with the plant and each other. For example, antibiotics (such as penicillin) or sterilants (for example, quaternary ammonium salts and oxidizing agents) could be present and/or the physical conditions (such as salinity, plant nutrients (for example organic and inorganic minerals (such as phosphorus, nitrogenous salts, ammonia, potassium and micronutrients such as cobalt and magnesium), pH, and/or temperature) could be amended.

[00109] As used herein, the term "plant" includes the whole plant or any parts or derivatives thereof, such as plant cells, plant protoplasts, plant cell tissue cultures from which plants can be regenerated, plant calli, embryos, pollen, ovules, fruit, flowers, leaves, seeds, roots, root tips and the like.

[00110] As used herein, the term "cultivar" refers to a variety, strain, or race, of plant that has been produced by horticultural or agronomic techniques and is not normally found in wild populations.

[00111] As used herein, the terms "dicotyledon," "dicot" and "dicotyledonous" refer to a flowering plant having an embryo containing two cotyledons. As used herein, the terms "monocotyledon," "monocot" and "monocotyledonous" refer to a flowering plant having an embryo containing only one cotyledon. There are of course other known differences between these groups, which would be readily recognized by one of skill in the art.

[00112] As used herein, "improved" should be taken broadly to encompass improvement of a characteristic of a plant, as compared to a control plant, or as compared to a known average quantity associated with the characteristic in question. For example, "improved" plant biomass associated with application of a beneficial microbe, or consortia, of the disclosure can be demonstrated by comparing the biomass of a plant treated by the microbes taught herein to the biomass of a control plant not treated. Alternatively, one could compare the biomass of a plant treated by the microbes taught herein to the average biomass normally attained by the given plant, as represented in scientific or agricultural publications known to those of skill

in the art. In the present disclosure, "improved" does not necessarily demand that the data be statistically significant (*i.e.* $p < 0.05$); rather, any quantifiable difference demonstrating that one value (*e.g.* the average treatment value) is different from another (*e.g.* the average control value) can rise to the level of "improved."

[00113] As used herein, "inhibiting and suppressing" and like terms should not be construed to require complete inhibition or suppression, although this may be desired in some embodiments.

[00114] As used herein, the term "genotype" refers to the genetic makeup of an individual cell, cell culture, tissue, organism (*e.g.*, a plant), or group of organisms.

[00115] As used herein, the term "allele(s)" means any of one or more alternative forms of a gene, all of which alleles relate to at least one trait or characteristic. In a diploid cell, the two alleles of a given gene occupy corresponding loci on a pair of homologous chromosomes. Since the present disclosure, in embodiments, relates to QTLs, *i.e.* genomic regions that may comprise one or more genes or regulatory sequences, it is in some instances more accurate to refer to "haplotype" (*i.e.* an allele of a chromosomal segment) instead of "allele", however, in those instances, the term "allele" should be understood to comprise the term "haplotype". Alleles are considered identical when they express a similar phenotype. Differences in sequence are possible but not important as long as they do not influence phenotype.

[00116] As used herein, the term "locus" (loci plural) means a specific place or places or a site on a chromosome where for example a gene or genetic marker is found.

[00117] As used herein, the term "genetically linked" refers to two or more traits that are co-inherited at a high rate during breeding such that they are difficult to separate through crossing.

[00118] A "recombination" or "recombination event" as used herein refers to a chromosomal crossing over or independent assortment. The term "recombinant" refers to a plant having a new genetic makeup arising as a result of a recombination event.

[00119] As used herein, the term "molecular marker" or "genetic marker" refers to an indicator that is used in methods for visualizing differences in characteristics of nucleic acid sequences. Examples of such indicators are restriction fragment length

polymorphism (RFLP) markers, amplified fragment length polymorphism (AFLP) markers, single nucleotide polymorphisms (SNPs), insertion mutations, microsatellite markers (SSRs), sequence-characterized amplified regions (SCARs), cleaved amplified polymorphic sequence (CAPS) markers or isozyme markers or combinations of the markers described herein which defines a specific genetic and chromosomal location. Mapping of molecular markers in the vicinity of an allele is a procedure which can be performed by the average person skilled in molecular-biological techniques.

[00120] As used herein, the term "trait" refers to a characteristic or phenotype. For example, in the context of some embodiments of the present disclosure, yield of a crop relates to the amount of marketable biomass produced by a plant (*e.g.*, fruit, fiber, grain). Desirable traits may also include other plant characteristics, including but not limited to: water use efficiency, nutrient use efficiency, production, mechanical harvestability, fruit maturity, shelf life, pest/disease resistance, early plant maturity, tolerance to stresses, etc. A trait may be inherited in a dominant or recessive manner, or in a partial or incomplete-dominant manner. A trait may be monogenic (*i.e.* determined by a single locus) or polygenic (*i.e.* determined by more than one locus) or may also result from the interaction of one or more genes with the environment.

[00121] A dominant trait results in a complete phenotypic manifestation at heterozygous or homozygous state; a recessive trait manifests itself only when present at homozygous state.

[00122] In the context of this disclosure, traits may also result from the interaction of one or more plant genes and one or more microorganism genes.

[00123] As used herein, the term "homozygous" means a genetic condition existing when two identical alleles reside at a specific locus, but are positioned individually on corresponding pairs of homologous chromosomes in the cell of a diploid organism. Conversely, as used herein, the term "heterozygous" means a genetic condition existing when two different alleles reside at a specific locus, but are positioned individually on corresponding pairs of homologous chromosomes in the cell of a diploid organism.

[00124] As used herein, the term "phenotype" refers to the observable characteristics of an individual cell, cell culture, organism (*e.g.*, a plant), or group of organisms which results from the interaction between that individual's genetic makeup (*i.e.*, genotype) and the environment.

[00125] As used herein, the term "chimeric" or "recombinant" when describing a nucleic acid sequence or a protein sequence refers to a nucleic acid, or a protein sequence, that links at least two heterologous polynucleotides, or two heterologous polypeptides, into a single macromolecule, or that re-arranges one or more elements of at least one natural nucleic acid or protein sequence. For example, the term "recombinant" can refer to an artificial combination of two otherwise separated segments of sequence, *e.g.*, by chemical synthesis or by the manipulation of isolated segments of nucleic acids by genetic engineering techniques.

[00126] As used herein, a "synthetic nucleotide sequence" or "synthetic polynucleotide sequence" is a nucleotide sequence that is not known to occur in nature or that is not naturally occurring. Generally, such a synthetic nucleotide sequence will comprise at least one nucleotide difference when compared to any other naturally occurring nucleotide sequence.

[00127] As used herein, the term "nucleic acid" refers to a polymeric form of nucleotides of any length, either ribonucleotides or deoxyribonucleotides, or analogs thereof. This term refers to the primary structure of the molecule, and thus includes double- and single-stranded DNA, as well as double- and single-stranded RNA. It also includes modified nucleic acids such as methylated and/or capped nucleic acids, nucleic acids containing modified bases, backbone modifications, and the like. The terms "nucleic acid" and "nucleotide sequence" are used interchangeably.

[00128] As used herein, the term "gene" refers to any segment of DNA associated with a biological function. Thus, genes include, but are not limited to, coding sequences and/or the regulatory sequences required for their expression. Genes can also include non-expressed DNA segments that, for example, form recognition sequences for other proteins. Genes can be obtained from a variety of sources, including cloning from a source of interest or synthesizing from known or predicted sequence information, and may include sequences designed to have desired parameters.

[00129] As used herein, the term "homologous" or "homologue" or "ortholog" is known in the art and refers to related sequences that share a common ancestor or family member and are determined based on the degree of sequence identity. The terms "homology," "homologous," "substantially similar" and "corresponding substantially" are used interchangeably herein. They refer to nucleic acid fragments wherein changes in one or more nucleotide bases do not affect the ability of the nucleic acid fragment to mediate gene expression or produce a certain phenotype. These terms also refer to modifications of the nucleic acid fragments of the instant disclosure such as deletion or insertion of one or more nucleotides that do not substantially alter the functional properties of the resulting nucleic acid fragment relative to the initial, unmodified fragment. It is therefore understood, as those skilled in the art will appreciate, that the disclosure encompasses more than the specific exemplary sequences. These terms describe the relationship between a gene found in one species, subspecies, variety, cultivar or strain and the corresponding or equivalent gene in another species, subspecies, variety, cultivar or strain. For purposes of this disclosure homologous sequences are compared. "Homologous sequences" or "homologues" or "orthologs" are thought, believed, or known to be functionally related. A functional relationship may be indicated in any one of a number of ways, including, but not limited to: (a) degree of sequence identity and/or (b) the same or similar biological function. Preferably, both (a) and (b) are indicated. Homology can be determined using software programs readily available in the art, such as those discussed in Current Protocols in Molecular Biology (F.M. Ausubel *et al.*, eds., 1987) Supplement 30, section 7.718, Table 7.71. Some alignment programs are MacVector (Oxford Molecular Ltd, Oxford, U.K.), ALIGN Plus (Scientific and Educational Software, Pennsylvania) and AlignX (Vector NTI, Invitrogen, Carlsbad, CA). Another alignment program is Sequencher (Gene Codes, Ann Arbor, Michigan), using default parameters.

[00130] As used herein, the term "nucleotide change" refers to, *e.g.*, nucleotide substitution, deletion, and/or insertion, as is well understood in the art. For example, mutations contain alterations that produce silent substitutions, additions, or deletions, but do not alter the properties or activities of the encoded protein or how the proteins are made.

[00131] As used herein, the term "protein modification" refers to, *e.g.*, amino acid substitution, amino acid modification, deletion, and/or insertion, as is well understood in the art.

[00132] As used herein, the term "at least a portion" or "fragment" of a nucleic acid or polypeptide means a portion having the minimal size characteristics of such sequences, or any larger fragment of the full length molecule, up to and including the full length molecule. A fragment of a polynucleotide of the disclosure may encode a biologically active portion of a genetic regulatory element. A biologically active portion of a genetic regulatory element can be prepared by isolating a portion of one of the polynucleotides of the disclosure that comprises the genetic regulatory element and assessing activity as described herein. Similarly, a portion of a polypeptide may be 4 amino acids, 5 amino acids, 6 amino acids, 7 amino acids, and so on, going up to the full length polypeptide. The length of the portion to be used will depend on the particular application. A portion of a nucleic acid useful as a hybridization probe may be as short as 12 nucleotides; in some embodiments, it is 20 nucleotides. A portion of a polypeptide useful as an epitope may be as short as 4 amino acids. A portion of a polypeptide that performs the function of the full-length polypeptide would generally be longer than 4 amino acids.

[00133] Variant polynucleotides also encompass sequences derived from a mutagenic and recombinogenic procedure such as DNA shuffling. Strategies for such DNA shuffling are known in the art. *See*, for example, Stemmer (1994) PNAS 91:10747-10751; Stemmer (1994) Nature 370:389-391; Crameri *et al.*(1997) Nature Biotech. 15:436-438; Moore *et al.*(1997) J. Mol. Biol. 272:336-347; Zhang *et al.*(1997) PNAS 94:4504-4509; Crameri *et al.*(1998) Nature 391:288-291; and U.S. Patent Nos. 5,605,793 and 5,837,458. For PCR amplifications of the polynucleotides disclosed herein, oligonucleotide primers can be designed for use in PCR reactions to amplify corresponding DNA sequences from cDNA or genomic DNA extracted from any plant of interest. Methods for designing PCR primers and PCR cloning are generally known in the art and are disclosed in Sambrook *et al.*(1989) Molecular Cloning: A Laboratory Manual (2nd ed., Cold Spring Harbor Laboratory Press, Plainview, New York). See also Innis *et al.*, eds. (1990) PCR Protocols: A Guide to Methods and Applications (Academic Press, New York); Innis and Gelfand, eds. (1995) PCR Strategies (Academic Press, New York); and Innis and Gelfand, eds. (1999) PCR

Methods Manual (Academic Press, New York). Known methods of PCR include, but are not limited to, methods using paired primers, nested primers, single specific primers, degenerate primers, gene-specific primers, vector-specific primers, partially-mismatched primers, and the like.

[00134] The term "primer" as used herein refers to an oligonucleotide which is capable of annealing to the amplification target allowing a DNA polymerase to attach, thereby serving as a point of initiation of DNA synthesis when placed under conditions in which synthesis of primer extension product is induced, *i.e.*, in the presence of nucleotides and an agent for polymerization such as DNA polymerase and at a suitable temperature and pH. The (amplification) primer is preferably single stranded for maximum efficiency in amplification. Preferably, the primer is an oligodeoxyribonucleotide. The primer must be sufficiently long to prime the synthesis of extension products in the presence of the agent for polymerization. The exact lengths of the primers will depend on many factors, including temperature and composition (A/T vs. G/C content) of primer. A pair of bi-directional primers consists of one forward and one reverse primer as commonly used in the art of DNA amplification such as in PCR amplification.

[00135] The terms "stringency" or "stringent hybridization conditions" refer to hybridization conditions that affect the stability of hybrids, *e.g.*, temperature, salt concentration, pH, formamide concentration and the like. These conditions are empirically optimized to maximize specific binding and minimize non-specific binding of primer or probe to its target nucleic acid sequence. The terms as used include reference to conditions under which a probe or primer will hybridize to its target sequence, to a detectably greater degree than other sequences (*e.g.* at least 2-fold over background). Stringent conditions are sequence dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. Generally, stringent conditions are selected to be about 5° C lower than the thermal melting point (Tm) for the specific sequence at a defined ionic strength and pH. The Tm is the temperature (under defined ionic strength and pH) at which 50% of a complementary target sequence hybridizes to a perfectly matched probe or primer. Typically, stringent conditions will be those in which the salt concentration is less than about 1.0 M Na+ ion, typically about 0.01 to 1.0 M Na + ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C for short

probes or primers (*e.g.* 10 to 50 nucleotides) and at least about 60° C for long probes or primers (*e.g.* greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. Exemplary low stringent conditions or "conditions of reduced stringency" include hybridization with a buffer solution of 30% formamide, 1 M NaCl, 1% SDS at 37° C and a wash in 2×SSC at 40° C. Exemplary high stringency conditions include hybridization in 50% formamide, 1M NaCl, 1% SDS at 37° C, and a wash in 0.1×SSC at 60° C. Hybridization procedures are well known in the art and are described by *e.g.* Ausubel *et al.*, 1998 and Sambrook *et al.*, 2001. In some embodiments, stringent conditions are hybridization in 0.25 M Na2HPO4 buffer (pH 7.2) containing 1 mM Na2EDTA, 0.5-20% sodium dodecyl sulfate at 45°C, such as 0.5%, 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 11%, 12%, 13%, 14%, 15%, 16%, 17%, 18%, 19% or 20%, followed by a wash in 5×SSC, containing 0.1% (w/v) sodium dodecyl sulfate, at 55°C to 65°C.

[00136] As used herein, "promoter" refers to a DNA sequence capable of controlling the expression of a coding sequence or functional RNA. The promoter sequence consists of proximal and more distal upstream elements, the latter elements often referred to as enhancers. Accordingly, an "enhancer" is a DNA sequence that can stimulate promoter activity, and may be an innate element of the promoter or a heterologous element inserted to enhance the level or tissue specificity of a promoter. Promoters may be derived in their entirety from a native gene, or be composed of different elements derived from different promoters found in nature, or even comprise synthetic DNA segments. It is understood by those skilled in the art that different promoters may direct the expression of a gene in different tissues or cell types, or at different stages of development, or in response to different environmental conditions. It is further recognized that since in most cases the exact boundaries of regulatory sequences have not been completely defined, DNA fragments of some variation may have identical promoter activity.

[00137] As used herein, a "plant promoter" is a promoter capable of initiating transcription in plant cells whether or not its origin is a plant cell, *e.g.* it is well known that Agrobacterium promoters are functional in plant cells. Thus, plant promoters include promoter DNA obtained from plants, plant viruses and bacteria such as *Agrobacterium* and *Bradyrhizobium* bacteria. A plant promoter can be a constitutive promoter or a non-constitutive promoter.

[00138] As used herein, a "constitutive promoter" is a promoter which is active under most conditions and/or during most development stages. There are several advantages to using constitutive promoters in expression vectors used in plant biotechnology, such as: high level of production of proteins used to select transgenic cells or plants; high level of expression of reporter proteins or scorable markers, allowing easy detection and quantification; high level of production of a transcription factor that is part of a regulatory transcription system; production of compounds that requires ubiquitous activity in the plant; and production of compounds that are required during all stages of plant development. Non-limiting exemplary constitutive promoters include, CaMV 35S promoter, opine promoters, ubiquitin promoter, alcohol dehydrogenase promoter, etc.

[00139] As used herein, a "non-constitutive promoter" is a promoter which is active under certain conditions, in certain types of cells, and/or during certain development stages. For example, tissue specific, tissue preferred, cell type specific, cell type preferred, inducible promoters, and promoters under development control are non-constitutive promoters. Examples of promoters under developmental control include promoters that preferentially initiate transcription in certain tissues, such as stems, leaves, roots, or seeds.

[00140] As used herein, "inducible" or "repressible" promoter is a promoter which is under chemical or environmental factors control. Examples of environmental conditions that may effect transcription by inducible promoters include anaerobic conditions, or certain chemicals, or the presence of light.

[00141] As used herein, a "tissue specific" promoter is a promoter that initiates transcription only in certain tissues. Unlike constitutive expression of genes, tissue-specific expression is the result of several interacting levels of gene regulation. As such, in the art sometimes it is preferable to use promoters from homologous or closely related plant species to achieve efficient and reliable expression of transgenes in particular tissues. This is one of the main reasons for the large amount of tissue-specific promoters isolated from particular plants and tissues found in both scientific and patent literature.

[00142] As used herein, the term "operably linked" refers to the association of nucleic acid sequences on a single nucleic acid fragment so that the function of one is

regulated by the other. For example, a promoter is operably linked with a coding sequence when it is capable of regulating the expression of that coding sequence (i.e., that the coding sequence is under the transcriptional control of the promoter). Coding sequences can be operably linked to regulatory sequences in a sense or antisense orientation. In another example, the complementary RNA regions of the disclosure can be operably linked, either directly or indirectly, 5′ to the target mRNA, or 3′ to the target mRNA, or within the target mRNA, or a first complementary region is 5′ and its complement is 3′ to the target mRNA.

[00143] As used herein, the phrases "recombinant construct", "expression construct", "chimeric construct", "construct", and "recombinant DNA construct" are used interchangeably herein. A recombinant construct comprises an artificial combination of nucleic acid fragments, *e.g.*, regulatory and coding sequences that are not found together in nature. For example, a chimeric construct may comprise regulatory sequences and coding sequences that are derived from different sources, or regulatory sequences and coding sequences derived from the same source, but arranged in a manner different than that found in nature. Such construct may be used by itself or may be used in conjunction with a vector. If a vector is used then the choice of vector is dependent upon the method that will be used to transform host cells as is well known to those skilled in the art. For example, a plasmid vector can be used. The skilled artisan is well aware of the genetic elements that must be present on the vector in order to successfully transform, select and propagate host cells comprising any of the isolated nucleic acid fragments of the disclosure. The skilled artisan will also recognize that different independent transformation events will result in different levels and patterns of expression (Jones *et al.*, (1985) EMBO J. 4:2411-2418; De Almeida *et al.*, (1989) Mol. Gen. Genetics 218:78-86), and thus that multiple events must be screened in order to obtain lines displaying the desired expression level and pattern. Such screening may be accomplished by Southern analysis of DNA, Northern analysis of mRNA expression, immunoblotting analysis of protein expression, or phenotypic analysis, among others. Vectors can be plasmids, viruses, bacteriophages, pro-viruses, phagemids, transposons, artificial chromosomes, and the like, that replicate autonomously or can integrate into a chromosome of a host cell. A vector can also be a naked RNA polynucleotide, a naked DNA polynucleotide, a polynucleotide composed of both DNA and RNA within the same strand, a poly-

lysine-conjugated DNA or RNA, a peptide-conjugated DNA or RNA, a liposome-conjugated DNA, or the like, that is not autonomously replicating. As used herein, the term "expression" refers to the production of a functional end-product *e.g.*, an mRNA or a protein (precursor or mature).

[00144] In some embodiments, the cell or organism has at least one heterologous trait. As used herein, the term "heterologous trait" refers to a phenotype imparted to a transformed host cell or transgenic organism by an exogenous DNA segment, heterologous polynucleotide or heterologous nucleic acid. Various changes in phenotype are of interest to the present disclosure, including but not limited to modifying the fatty acid composition in a plant, altering the amino acid content of a plant, altering a plant's pathogen defense mechanism, increasing a plant's yield of an economically important trait (*e.g.*, grain yield, forage yield, etc.) and the like. These results can be achieved by providing expression of heterologous products or increased expression of endogenous products in plants using the methods and compositions of the present disclosure

[00145] A "synthetic combination" can include a combination of a plant and a microbe of the disclosure. The combination may be achieved, for example, by coating the surface of a seed of a plant, such as an agricultural plant, or host plant tissue (root, stem, leaf, etc.), with a microbe of the disclosure. Further, a "synthetic combination" can include a combination of microbes of various strains or species. Synthetic combinations have at lest one variable that distinguishes the combination from any combination that occurs in nature. That variable may be, *inter alia*, a concentration of microbe on a seed or plant tissue that does not occur naturally, or a combination of microbe and plant that does not naturally occur, or a combination of microbes or strains that do not occur naturally together. In each of these instances, the synthetic combination demonstrates the hand of man and possesses structural and/or functional attributes that are not present when the individual elements of the combination are considered in isolation.

[00146] In some embodiments, a microbe can be "endogenous" to a seed or plant. As used herein, a microbe is considered "endogenous" to a plant or seed, if the microbe is derived from the plant specimen from which it is sourced. That is, if the microbe is naturally found associated with said plant. In embodiments in which an endogenous microbe is applied to a plant, then the endogenous microbe is applied in an amount

that differs from the levels found on the plant in nature. Thus, a microbe that is endogenous to a given plant can still form a synthetic combination with the plant, if the microbe is present on said plant at a level that does not occur naturally.

[00147] In some embodiments, a microbe can be "exogenous" (also termed "heterologous") to a seed or plant. As used herein, a microbe is considered "exogenous" to a plant or seed, if the microbe is not derived from the plant specimen from which it is sourced. That is, if the microbe is not naturally found associated with said plant. For example, a microbe that is normally associated with leaf tissue of a maize plant is considered exogenous to a leaf tissue of another maize plant that naturally lacks said microbe. In another example, a microbe that is normally associated with a maize plant is considered exogenous to a wheat plant that naturally lacks said microbe.

[00148] Microbes can also be "exogenously disposed" on a given plant tissue. This means that the microbe is placed upon a plant tissue that it is not naturally found upon. For instance, if a given microbe only naturally occurs on the roots of a given plant, then that microbe could be exogenously applied to the above-ground tissue of a plant and would thereby be "exogenously disposed" upon said plant tissue. As such, a microbe is deemed exogenously disposed, when applied on a plant that does not naturally have the microbe present or does not naturally have the microbe present in the number that is being applied

[00149] The compositions and methods herein may provide for an improved "agronomic trait" or "trait of agronomic importance" to a host plant, which may include, but not be limited to, the following: altered oil content, altered protein content, altered seed carbohydrate composition, altered seed oil composition, and altered seed protein composition, chemical tolerance, cold tolerance, delayed senescence, disease resistance, drought tolerance, ear weight, growth improvement, health enhancement, heat tolerance, herbicide tolerance, herbivore resistance, improved nitrogen fixation, improved nitrogen utilization, improved root architecture, improved water use efficiency, increased biomass, increased root length, increased seed weight, increased shoot length, increased yield, increased yield under water-limited conditions, kernel mass, kernel moisture content, metal tolerance, number of ears, number of kernels per ear, number of pods, nutrition enhancement, pathogen resistance, pest resistance, photosynthetic capability improvement, salinity tolerance,

stay-green, vigor improvement, increased dry weight of mature seeds, increased fresh weight of mature seeds, increased number of mature seeds per plant, increased chlorophyll content, increased number of pods per plant, increased length of pods per plant, reduced number of wilted leaves per plant, reduced number of severely wilted leaves per plant, and increased number of non-wilted leaves per plant, a detectable modulation in the level of a metabolite, a detectable modulation in the level of a transcript, and a detectable modulation in the proteome, compared to an isoline plant grown from a seed without said seed treatment formulation.

Ability to Impart Beneficial Traits Upon a Given Plant Species by Microbes and Consortia of the Disclosure

[00150] The present disclosure utilizes microbes to impart beneficial properties (or beneficial traits) to desirable plant species, such as agronomic species of interest. In the current disclosure, the terminology "beneficial property" or "beneficial trait" is used interchangeably and denotes that a desirable plant phenotypic or genetic property of interest is modulated, by the application of a microbe or microbial consortia as described herein. As aforementioned, in some aspects, it may very well be that a metabolite produced by a given microbe is ultimately responsible for modulating or imparting a beneficial trait to a given plant.

[00151] There are a vast number of beneficial traits that can be modulated by the application of microbes of the disclosure. For instance, the microbes may have the ability to impart one or more beneficial properties to a plant species, for example: increased growth, increased yield, increased nitrogen utilization efficiency, increased stress tolerance, increased drought tolerance, increased photosynthetic rate, enhanced water use efficiency, increased pathogen resistance, modifications to plant architecture that don't necessarily impact plant yield, but rather address plant functionality, causing the plant to increase production of a metabolite of interest, etc.

[00152] In aspects, the microbes taught herein provide a wide range of agricultural applications, including: improvements in yield of grain, fruit, and flowers, improvements in growth of plant parts, improved resistance to disease, improved survivability in extreme climate, and improvements in other desired plant phenotypic characteristics.

[00153] In some aspects, the isolated microbes, consortia, and/or agricultural compositions of the disclosure can be applied to a plant, in order to modulate or alter a plant characteristic such as altered oil content, altered protein content, altered seed carbohydrate composition, altered seed oil composition, altered seed protein composition, chemical tolerance, cold tolerance, delayed senescence, disease resistance, drought tolerance, ear weight, growth improvement, health enhancement, heat tolerance, herbicide tolerance, herbivore resistance, improved nitrogen fixation, improved nitrogen utilization, improved root architecture, improved water use efficiency, increased biomass, increased root length, increased seed weight, increased shoot length, increased yield, increased yield under water-limited conditions, kernel mass, kernel moisture content, metal tolerance, number of ears, number of kernels per ear, number of pods, nutrition enhancement, pathogen resistance, pest resistance, photosynthetic capability improvement, salinity tolerance, stay-green, vigor improvement, increased dry weight of mature seeds, increased fresh weight of mature seeds, increased number of mature seeds per plant, increased chlorophyll content, increased number of pods per plant, increased length of pods per plant, reduced number of wilted leaves per plant, reduced number of severely wilted leaves per plant, and increased number of non-wilted leaves per plant, a detectable modulation in the level of a metabolite, a detectable modulation in the level of a transcript, and a detectable modulation in the proteome relative to a reference plant.

[00154] In some aspects, the isolated microbes, consortia, and/or agricultural compositions of the disclosure can be applied to a plant, in order to modulate in a negative way, a particular plant characteristic. For example, in some aspects, the microbes of the disclosure are able to decrease a phenotypic trait of interest, as this functionality can be desirable in some applications. For instance, the microbes of the disclosure may possess the ability to decrease root growth or decrease root length. Or the microbes may possess the ability to decrease shoot growth or decrease the speed at which a plant grows, as these modulations of a plant trait could be desirable in certain applications.

Isolated Microbes – Tables 1-4

[00155] In aspects, the present disclosure provides isolated microbes, including novel strains of identified microbial species, presented in **Tables 1-4**.

[00156] In other aspects, the present disclosure provides isolated whole microbial cultures of the species and strains identified in **Tables 1-4**. These cultures may comprise microbes at various concentrations.

[00157] In aspects, the disclosure provides for utilizing a microbe selected from **Tables 1-4** in agriculture.

[0157] In some embodiments, the disclosure provides isolated microbial species belonging to genera of: Achromobacter, Agrobacterium, Arthrobacter, Azotobacter, Azospirillum, Bacillus, Bosea, Brevibacterium, Caulobacter, Chryseobacterium, Delfulviimonas, Duganella, Exiguobacterium, Flavobacterium, Frigidibacter, Herbaspirillum, Janibacter, Leifsonia, Luteibacter, Massilia, Mucilaginibacter, Novosphingobium, Pantoeo, Paenibacillus, Pedobacter, Polaromonas, Pseudoduganella, Pseudomonas, Rahnella, Ramlibacter, Rhizobium, Rhodococcus, Rhodoferax, Sphingobium, Stenotrophomonas and Tumebacillus.

[0158] In some embodiments, the disclosure provides isolated microbial species belonging to genera of: *Achromobacter, Agrobacterium, Arthrobacter, Bacillus, Brevibacterium, Chryseobacterium, Delfulviimonas, Exiguobacterium, Frigidibacter, Janibacter, Leifsonia, Massilia, Novosphingobium, Pedobacter, Pseudomonas,* and *Tumebacillus*.

[0159] In some embodiments, a microbe from the genus *Bosea* is utilized in agriculture to impart one or more beneficial properties to a plant species.

[0160] In some embodiments, the disclosure provides isolated microbial species, selected from the group consisting of: *Achromobacter pulmonis, Agrobacterium fabrum (*previously *Rhizobium pusense), Arthrobacter nicotinovorans, Azotobacter chroococcum, Bacillus megaterium, Brevibacterium frigoritolerans, Chryseobacterium daecheongense, Chryseobacterium rhizosphaerae, Duganella radicis, Exiguobacterium antarcticum, Exiguobacterium sibiricum, Frigidibacter albus (*previously *Delfulviimonas dentrificans), Janibacter limosus, Leifsonia lichenia, Pantoea agglomerans* (recently reassigned to *Pantoea vagans*), *Pedobacter terrae, Pseudomonas fluorescens, Pseudomonas helmanticensis, Pseudomonas yamanorum, Pseudomonas oryzihabitans, Pseudomonas putida, Rahnella aquatilis, Rhizobium etli, Rhodococcus erythropolis, Stenotrophomonas maltophilia* and *Tumebacillus permanentifrigoris*.

[0161] In some embodiments, the disclosure provides isolated microbial species, selected from the group consisting of: *Achromobacter pulmonis, Agrobacterium fabrum* (previously *Rhizobium pusense*), *Arthrobacter nicotinovorans, Bacillus megaterium, Brevibacterium frigoritolerans, Chryseobacterium daecheongense, Chryseobacterium rhizosphaerae, Exiguobacterium antarcticum, Exiguobacterium sibiricum, Frigidibacter albus (*previously *Delfulviimonas dentrificans), Janibacter limosus, Leifsonia lichenia, Massilia kyonggiensis, Novosphingobium lindaniclasticum, Novosphingobium sediminicola, Pedobacter terrae, Pseudomonas helmanticensis, Pseudomonas yamanorum,* and *Tumebacillus permanentifrigoris.*

[0162] In some embodiments, the disclosure provides novel isolated microbial strains of species, selected from the group consisting of: *Achromobacter, Agrobacterium, Arthrobacter, Azotobacter, Azospirillum, Bacillus, Bosea, Brevibacterium, Caulobacter, Chryseobacterium, Delfulviimonas, Duganella, Exiguobacterium, Flavobacterium, Frigidibacter, Herbaspirillum, Janibacter, Leifsonia, Luteibacter, Massilia, Mucilaginibacter, Novosphingobium, Pantoea, Paenibacillus, Pedobacter, Polaromonas, Pseudoduganella, Pseudomonas, Rahnella, Ramlibacter, Rhizobium, Rhodococcus, Rhodoferax, Sphingobium, Stenotrophomonas* and *Tumebacillus.* Particular novel strains of these aforementioned species can be found in **Tables 1-4**.

[0163] Furthermore, the disclosure relates to microbes having characteristics substantially similar to that of a microbe identified in **Tables 1-4**.

[0164] The isolated microbial species, and novel strains of said species, identified in the present disclosure, are able to impart beneficial properties or traits to target plant species.

[0165] For instance, the isolated microbes described in **Tables 1-4**, or consortia of said microbes, are able to improve plant health and vitality. The improved plant health and vitality can be quantitatively measured, for example, by measuring the effect that said microbial application has upon a plant phenotypic or genotypic trait.

Microbial Consortia – Tables 1-4

[0166] In aspects, the disclosure provides microbial consortia comprising a combination of at least any two microbes selected from amongst the microbes identified in **Table 1**.

[0167] In other aspects, the disclosure provides microbial consortia comprising a combination of at least any two microbes selected from amongst the microbes identified in **Table 2**.

[0168] In yet other aspects, the disclosure provides microbial consortia comprising a combination of at least any two microbes selected from amongst the microbes identified in **Table 3**.

[0169] In additional aspects, the disclosure provides microbial consortia comprising a combination of at least any two microbes selected from amongst the microbes identified in **Table 4**.

[0170] Also, the disclosure provides microbial consortia comprising a combination of at least any two microbes selected from amongst the microbes identified in **Tables 1-4**.

[0171] In certain embodiments, the consortia of the present disclosure comprise two microbes, or three microbes, or four microbes, or five microbes, or six microbes, or seven microbes, or eight microbes, or nine microbes, or ten or more microbes. Said microbes of the consortia are different microbial species, or different strains of a microbial species.

[0172] In some embodiments, the disclosure provides consortia, comprising: at least two isolated microbial species belonging to genera of: *Achromobacter*, *Agrobacterium*, *Arthrobacter*, *Azotobacter*, *Azospirillum*, *Bacillus*, *Bosea*, *Brevibacterium*, *Caulobacter*, *Chryseobacterium*, *Delfulviimonas*, *Duganella*, *Exiguobacterium*, *Flavobacterium*, *Frigidibacter*, *Herbaspirillum*, *Janibacter*, *Leifsonia*, *Luteibacter*, *Massilia*, *Mucilaginibacter*, *Novosphingobium*, *Pantoea*, *Paenibacillus*, *Pedobacter*, *Polaromonas*, *Pseudoduganella*, *Pseudomonas*, *Rahnella*, *Ramlibacter*, *Rhizobium*, *Rhodococcus*, *Rhodoferax*, *Sphingobium*, *Stenotrophomonas* and *Tumebacillus*.

[0173] In some embodiments, the disclosure provides consortia, comprising: at least two isolated microbial species, selected from the group consisting of: *Azotobacter chroococcum*, *Bacillus megaterium*, *Brevibacterium frigoritolerans*, *Chryseobacterium daecheongense*, *Chryseobacterium rhizosphaerae*, *Duganella radicis*, *Janibacter limosus*, *Leifsonia lichenia*, *Massilia kyonggiensis*, *Novosphingobium sediminicola*, *Pantoea agglomerans* (recently reassigned to

Pantoea vagans), *Pedobacter terrae, Pseudomonas fluorescens, Pseudomonas yamanorum, Pseudomonas oryzihabitans, Pseudomonas putida, Rahnella aquatilis, Rhizobium etli, Rhodococcus erythropolis* and *Stenotrophomonas maltophilia*.

[0174] In some embodiments, the disclosure provides consortia, comprising: at least two novel isolated microbial strains of species, selected from the group consisting of: *Azotobacter chroococcum, Bacillus megaterium, Brevibacterium frigoritolerans, Chryseobacterium daecheongense, Chryseobacterium rhizosphaerae, Duganella radicis, Janibacter limosus, Leifsonia lichenia, Massilia kyonggiensis, Novosphingobium sediminicola, Pantoea agglomerans* (recently reassigned to *Pantoea vagans*), *Pedobacter terrae, Pseudomonas fluorescens, Pseudomonas yamanorum, Pseudomonas oryzihabitans, Pseudomonas putida, Rahnella aquatilis, Rhizobium etli, Rhodococcus erythropolis,* and *Stenotrophomonas maltophilia*. Particular novel strains of these aforementioned species can be found in **Tables 1-4**.

[0175] In some embodiments, the disclosure provides consortia, comprising: at least two isolated microbial species selected from **Tables 1-4**, and further comprising a *Bradyrhizobium* species.

[0176] In particular aspects, the disclosure provides microbial consortia, comprising species as grouped in **Tables 5-11**. With respect to **Tables-5-11**, the letters **A** through **I** represent a non-limiting selection of microbes of the present disclosure, defined as:

[0177] **A** = *Rahnella aquatilis* and associated novel strains identified in **Table 1**;

[0178] **B** = *Bacillus megaterium* and associated novel strains identified in **Tables 2 and 3**;

[0179] **C** = *Bacillus niacini* and associated novel strains identified in **Table 3**;

[0180] **D** = *Brevibacterium frigoritolerans* (in taxonomic flux, potential synonym of *Bacillus muralis*) and associated novel strains identified in **Table 3**;

[0181] **E** = *Frigidibacter albus* or *Delfulviimonas dentrificans* (In Taxonomic Flux) and associated novel strains identified in **Table 4**;

[0182] **F** = *Janibacter limosus* and associated novel strains identified in **Table 3**;

[0183] **G** = *Leifsonia lichenia* and associated novel strains identified in **Table 4**;

[0184] **H** = *Pseudomonas yamanorum* and associated novel strains identified in **Table 3**; and

[0185] **I** = *Novosphingobium sediminicola* and associated novel strains identified in **Table 4**.

Table 5: Eight and Nine Strain Consortia

A,B,C,D,E,F,G,H	A,B,C,D,E,F,G,I	A,B,C,D,E,F,H,I	A,B,C,D,E,G,H,I	A,B,C,D,F,G,H,I	A,B,C,E,F,G,H,I
A,B,D,E,F,G,H,I	A,C,D,E,F,G,H,I	B,C,D,E,F,G,H,I	A,B,C,D,E,F,G,H,I		

Table 6: Seven Strain Consortia

A,B,C,D,E,F,G	A,B,C,D,E,F,H	A,B,C,D,E,F,I	A,B,C,D,E,G,H	A,B,C,D,E,G,I	A,B,C,D,E,H,I
A,B,C,D,F,G,H	A,B,C,D,F,G,I	A,B,C,D,F,H,I	A,B,C,D,G,H,I	A,B,C,E,F,G,H	A,B,C,E,F,G,I
A,B,C,E,F,H,I	A,B,C,E,G,H,I	A,B,C,F,G,H,I	A,B,D,E,F,G,H	A,B,D,E,F,G,I	A,B,D,E,F,H,I
A,B,D,E,G,H,I	A,B,D,F,G,H,I	A,B,E,F,G,H,I	A,C,D,E,F,G,H	A,C,D,E,F,G,I	A,C,D,E,F,H,I
A,C,D,E,G,H,I	A,C,D,F,G,H,I	A,C,E,F,G,H,I	A,D,E,F,G,H,I	B,C,D,E,F,G,H	B,C,D,E,F,G,I
B,C,D,E,F,H,I	B,C,D,E,G,H,I	B,C,D,F,G,H,I	B,C,E,F,G,H,I	B,D,E,F,G,H,I	C,D,E,F,G,H,I

Table 7: Six Strain Consortia

A,B,C,D,E,F	A,B,C,D,E,G	A,B,C,D,E,H	A,B,C,D,E,I	A,B,C,D,F,G	A,B,C,D,F,H	A,B,C,D,F,I
A,B,C,D,G,H	A,B,C,D,G,I	A,B,C,D,H,I	A,B,C,E,F,G	A,B,C,E,F,H	A,B,C,E,F,I	A,B,C,E,G,H
A,B,C,E,G,I	A,B,C,E,H,I	A,B,C,F,G,H	A,B,C,F,G,I	A,B,C,F,H,I	A,B,C,G,H,I	A,B,D,E,F,G
A,B,D,E,F,H	A,B,D,E,F,I	A,B,D,E,G,H	A,B,D,E,G,I	A,B,D,E,H,I	A,B,D,F,G,H	A,B,D,F,G,I
D,E,F,G,H,I	C,E,F,G,H,I	A,B,D,F,H,I	A,B,D,G,H,I	A,B,E,F,G,H	A,B,E,F,G,I	A,B,E,F,H,I
A,B,E,G,H,I	A,B,F,G,H,I	A,C,D,E,F,G	A,C,D,E,F,H	A,C,D,E,F,I	A,C,D,E,G,H	A,C,D,E,G,I
A,C,D,E,H,I	A,C,D,F,G,H	A,C,D,F,G,I	A,C,D,F,H,I	A,C,D,G,H,I	A,C,E,F,G,H	A,C,E,F,G,I
A,C,E,F,H,I	A,C,E,G,H,I	A,C,F,G,H,I	A,D,E,F,G,H	A,D,E,F,G,I	A,D,E,F,H,I	A,D,E,G,H,I
A,D,F,G,H,I	A,E,F,G,H,I	B,C,D,E,F,G	B,C,D,E,F,H	B,C,D,E,F,I	B,C,D,E,G,H	B,C,D,E,G,I
B,C,D,E,H,I	B,C,D,F,G,H	B,C,D,F,G,I	B,C,D,F,H,I	B,C,D,G,H,I	B,C,E,F,G,H	B,C,E,F,G,I
B,C,E,F,H,I	B,C,E,G,H,I	B,C,F,G,H,I	B,D,E,F,G,H	B,D,E,F,G,I	B,D,E,F,H,I	B,D,E,G,H,I
B,D,F,G,H,I	B,E,F,G,H,I	C,D,E,F,G,H	C,D,E,F,G,I	C,D,E,F,H,I	C,D,E,G,H,I	C,D,F,G,H,I

Table 8: Five Strain Consortia

A,B,C,D,E	A,B,C,D,F	A,B,C,D,G	A,B,C,D,H	A,B,C,D,I	A,B,C,E,F	A,B,C,E,G	A,B,C,E,H
A,B,C,F,H	A,B,C,F,G	A,B,C,F,I	A,B,C,G,H	A,B,C,G,I	A,B,C,H,I	A,B,D,E,F	A,B,D,E,G
A,B,D,E,I	A,B,D,F,G	A,B,D,F,H	A,B,D,F,I	A,B,D,G,H	A,B,D,G,I	A,B,D,H,I	A,B,E,F,G
A,B,E,F,I	A,B,E,G,H	A,B,E,G,I	A,B,E,H,I	A,B,F,G,H	A,B,F,G,I	A,B,F,H,I	A,B,G,H,I
A,C,D,E,G	A,C,D,E,H	A,C,D,E,I	A,C,D,F,G	A,C,D,F,H	A,C,D,F,I	A,C,D,G,H	A,C,D,G,I
A,C,E,F,G	A,C,E,F,H	A,C,E,F,I	A,C,E,G,H	A,C,E,G,I	A,C,E,H,I	A,C,F,G,H	A,C,F,G,I
A,C,G,H,I	A,D,E,F,G	A,D,E,F,H	A,D,E,F,I	A,D,E,G,H	A,D,E,G,I	A,D,E,H,I	A,D,F,G,H
A,D,F,H,I	A,D,G,H,I	A,E,F,G,H	A,E,F,G,I	A,E,F,H,I	A,E,G,H,I	A,F,G,H,I	B,C,D,E,F
B,C,D,E,H	B,C,D,E,I	B,C,D,F,G	B,C,D,F,H	B,C,D,F,I	B,C,D,G,H	B,C,D,G,I	B,C,D,H,I

B,C,E,F,H	B,C,E,F,I	B,C,E,G,H	B,C,E,G,I	B,C,E,H,I	B,C,F,G,H	B,C,F,G,I	B,C,F,H,I
B,D,E,F,G	B,D,E,F,H	B,D,E,F,I	B,D,E,G,H	B,D,E,G,I	B,D,E,H,I	B,D,F,G,H	B,D,F,G,I
B,D,G,H,I	B,E,F,G,H	B,E,F,G,I	B,E,F,H,I	B,E,G,H,I	B,F,G,H,I	C,D,E,F,G	C,D,E,F,H
C,D,E,G,H	C,D,E,G,I	C,D,E,H,I	C,D,F,G,H	C,D,F,G,I	C,D,F,H,I	C,D,G,H,I	C,E,F,G,H
C,E,F,H,I	C,E,G,H,I	C,F,G,H,I	D,E,F,G,H	D,E,F,G,I	D,E,F,H,I	D,E,G,H,I	D,F,G,H,I
A,B,C,E,I	A,B,D,E,H	A,B,E,F,H	A,C,D,E,F	A,C,D,H,I	A,C,F,H,I	A,D,F,G,I	B,C,D,E,G
B,C,E,F,G	B,C,G,H,I	B,D,F,H,I	C,D,E,F,I	C,E,F,G,I	E,F,G,H,I		

Table 9: Four Strain Consortia

A,B,C,D	A,B,C,E	A,B,C,F	A,B,C,G	A,B,C,H	A,B,C,I	A,B,D,E	A,B,D,F	D,G,H,I
A,B,D,G	A,B,D,H	A,B,D,I	A,B,E,F	A,B,E,G	A,B,E,H	A,B,E,I	A,B,F,G	E,F,G,H
A,B,F,H	A,D,F,H	A,D,F,I	A,D,G,H	A,D,G,I	A,D,H,I	A,E,F,G	A,E,F,H	E,F,G,I
A,B,F,I	A,B,G,H	A,B,G,I	A,B,H,I	A,C,D,E	A,C,D,F	A,C,D,G	A,C,D,H	E,F,H,I
A,C,D,I	A,C,E,F	A,C,E,G	A,C,E,H	A,C,E,I	A,C,F,G	A,C,F,H	A,C,F,I	E,G,H,I
A,C,G,H	A,C,G,I	A,C,H,I	A,D,E,F	A,D,E,G	A,D,E,H	A,D,E,I	A,D,F,G	F,G,H,I
A,E,F,I	A,E,G,H	A,E,G,I	A,E,H,I	A,F,G,H	A,F,G,I	A,F,H,I	A,G,H,I	D,E,F,H
B,C,D,E	B,C,D,F	B,C,D,G	B,C,D,H	B,C,D,I	B,C,E,F	B,C,E,G	B,C,E,H	D,E,F,I
B,C,E,I	B,C,F,G	B,C,F,H	B,C,F,I	B,C,G,H	B,C,G,I	B,C,H,I	B,D,E,F	D,E,G,H
B,D,E,G	B,D,E,H	B,D,E,I	B,D,F,G	B,D,F,H	B,D,F,I	B,D,G,H	B,D,G,I	D,E,G,I
B,D,H,I	B,E,F,G	B,E,F,H	B,E,F,I	B,E,G,H	B,E,G,I	B,E,H,I	B,F,G,H	D,E,H,I
B,F,G,I	B,F,H,I	B,G,H,I	C,D,E,F	C,D,E,G	C,D,E,H	C,D,E,I	C,D,F,G	D,F,G,H
C,D,F,H	C,D,F,I	C,D,G,H	C,D,G,I	C,D,H,I	C,E,F,G	C,E,F,H	C,E,F,I	D,F,G,I
C,E,G,H	C,E,G,I	C,E,H,I	C,F,G,H	C,F,G,I	C,F,H,I	C,G,H,I	D,E,F,G	D,F,H,I

Table 10: Three Strain Consortia

A,B,C	A,B,D	A,B,E	A,B,F	A,B,G	A,B,H	A,B,I	A,C,D	A,C,E	G,H,I	E,F,H
A,C,F	A,C,G	A,C,H	A,C,I	A,D,E	A,D,F	A,D,G	A,D,H	A,D,I	F,H,I	E,F,G
A,E,F	A,E,G	A,E,H	A,E,I	A,F,G	A,F,H	A,F,I	A,G,H	A,G,I	F,G,I	D,H,I
A,H,I	B,C,D	B,C,E	B,C,F	B,C,G	B,C,H	B,C,I	B,D,E	B,D,F	F,G,H	D,G,I
B,D,G	B,D,H	B,D,I	B,E,F	B,E,G	B,E,H	B,E,I	B,F,G	B,F,H	E,H,I	E,F,I
B,F,I	B,G,H	B,G,I	B,H,I	C,D,E	C,D,F	C,D,G	C,D,H	C,D,I	E,G,I	D,G,H
C,E,F	C,E,G	C,E,H	C,E,I	C,F,G	C,F,H	C,F,I	C,G,H	C,G,I	E,G,H	D,F,I
C,H,I	D,E,F	D,E,G	D,E,H	D,E,I	D,F,G	D,F,H				

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Table 11: Two Strain Consortia

A,B	A,C	A,D	A,E	A,F	A,G	A,H	A,I	B,C	B,D	B,E	B,F	B,G	B,H	B,I	C,D
C,E	C,F	C,G	C,H	C,I	D,E	D,F	D,G	D,H	D,I	E,F	E,G	E,H	E,I	F,G	F,H
F,I	G,H	G,I	H,I												

[0186] In some embodiments, the microbial consortia may be selected from any member group from **Tables 5-11**.

Isolated Microbes – Source Material

[0187] The microbes of the present disclosure were obtained, among other places, at various locales in New Zealand and the United States.

Isolated Microbes – Microbial Culture Techniques

[0188] The microbes of **Tables 1-4** were identified by utilizing standard microscopic techniques to characterize the microbes' phenotype, which was then utilized to identify the microbe to a taxonomically recognized species.

[0189] The isolation, identification, and culturing of the microbes of the present disclosure can be effected using standard microbiological techniques. Examples of such techniques may be found in Gerhardt, P. (ed.) Methods for General and Molecular Microbiology. American Society for Microbiology, Washington, D.C. (1994) and Lennette, E. H. (ed.) Manual of Clinical Microbiology, Third Edition. American Society for Microbiology, Washington, D.C. (1980), each of which is incorporated by reference.

[0190] Isolation can be effected by streaking the specimen on a solid medium (*e.g.*, nutrient agar plates) to obtain a single colony, which is characterized by the phenotypic traits described hereinabove (*e.g.*, Gram positive/negative, capable of forming spores aerobically/anaerobically, cellular morphology, carbon source metabolism, acid/base production, enzyme secretion, metabolic secretions, etc.) and to reduce the likelihood of working with a culture which has become contaminated.

[0191] For example, for isolated bacteria of the disclosure, biologically pure isolates can be obtained through repeated subculture of biological samples, each subculture followed by streaking onto solid media to obtain individual colonies. Methods of preparing, thawing, and growing lyophilized bacteria are commonly known, for example, Gherna, R. L. and C. A. Reddy. 2007. Culture Preservation, p 1019-1033. In C. A. Reddy, T. J. Beveridge, J. A. Breznak, G. A. Marzluf, T. M. Schmidt, and L. R. Snyder, eds. American Society for Microbiology, Washington, D.C., 1033 pages; herein incorporated by reference. Thus freeze dried liquid formulations and cultures stored long term at −70° C in solutions containing glycerol are contemplated for use in providing formulations of the present inventions.

[0192] The bacteria of the disclosure can be propagated in a liquid medium under aerobic conditions. Medium for growing the bacterial strains of the present disclosure includes a carbon source, a nitrogen source, and inorganic salts, as well as specially

required substances such as vitamins, amino acids, nucleic acids and the like. Examples of suitable carbon sources which can be used for growing the bacterial strains include, but are not limited to, starch, peptone, yeast extract, amino acids, sugars such as glucose, arabinose, mannose, glucosamine, maltose, and the like; salts of organic acids such as acetic acid, fumaric acid, adipic acid, propionic acid, citric acid, gluconic acid, malic acid, pyruvic acid, malonic acid and the like; alcohols such as ethanol and glycerol and the like; oil or fat such as soybean oil, rice bran oil, olive oil, corn oil, sesame oil. The amount of the carbon source added varies according to the kind of carbon source and is typically between 1 to 100 gram(s) per liter of medium. Preferably, glucose, starch, and/or peptone is contained in the medium as a major carbon source, at a concentration of 0.1-5% (W/V). Examples of suitable nitrogen sources which can be used for growing the bacterial strains of the present invention include, but are not limited to, amino acids, yeast extract, tryptone, beef extract, peptone, potassium nitrate, ammonium nitrate, ammonium chloride, ammonium sulfate, ammonium phosphate, ammonia or combinations thereof. The amount of nitrogen source varies according to the type of nitrogen source, typically between 0.1 to 30 gram per liter of medium. The inorganic salts, potassium dihydrogen phosphate, dipotassium hydrogen phosphate, disodium hydrogen phosphate, magnesium sulfate, magnesium chloride, ferric sulfate, ferrous sulfate, ferric chloride, ferrous chloride, manganous sulfate, manganous chloride, zinc sulfate, zinc chloride, cupric sulfate, calcium chloride, sodium chloride, calcium carbonate, sodium carbonate can be used alone or in combination. The amount of inorganic acid varies according to the kind of the inorganic salt, typically between 0.001 to 10 gram per liter of medium. Examples of specially required substances include, but are not limited to, vitamins, nucleic acids, yeast extract, peptone, meat extract, malt extract, dried yeast and combinations thereof. Cultivation can be effected at a temperature, which allows the growth of the bacterial strains, essentially, between 20°C and 46°C. In some aspects, a temperature range is 30°C-37°C. For optimal growth, in some embodiments, the medium can be adjusted to pH 7.0-7.4. It will be appreciated that commercially available media may also be used to culture the bacterial strains, such as Nutrient Broth or Nutrient Agar available from Difco, Detroit, MI. It will be appreciated that cultivation time may differ depending on the type of culture medium used and the concentration of sugar as a major carbon source.

[0193] In aspects, cultivation lasts between 24-96 hours. Bacterial cells thus obtained are isolated using methods, which are well known in the art. Examples include, but are not limited to, membrane filtration and centrifugal separation. The pH may be adjusted using sodium hydroxide and the like and the culture may be dried using a freeze dryer, until the water content becomes equal to 4% or less. Microbial co-cultures may be obtained by propagating each strain as described hereinabove. It will be appreciated that the microbial strains may be cultured together when compatible culture conditions can be employed.

Isolated Microbes – Microbial Strains

[0194] Microbes can be distinguished into a genus based on polyphasic taxonomy, which incorporates all available phenotypic and genotypic data into a consensus classification (Vandamme *et al.* 1996. Polyphasic taxonomy, a consensus approach to bacterial systematics. *Microbiol Rev* 1996, 60:407-438). One accepted genotypic method for defining species is based on overall genomic relatedness, such that strains which share approximately 70% or more relatedness using DNA-DNA hybridization, with 5°C or less ΔT_m (the difference in the melting temperature between homologous and heterologous hybrids), under standard conditions, are considered to be members of the same species. Thus, populations that share greater than the aforementioned 70% threshold can be considered to be variants of the same species.

[0195] The 16S rRNA sequences are often used for making distinctions between species, in that if a 16S rRNA sequence shares less than a specified % sequence identity from a reference sequence, then the two organisms from which the sequences were obtained are said to be of different species.

[0196] Thus, one could consider microbes to be of the same species, if they share at least 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity across the 16S or 16S rRNA or rDNA sequence. In some aspects, a microbe could be considered to be the same species only if it shares at least 95% identity.

[0197] Further, one could define microbial *strains* of a species, as those that share at least 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity across the 16S rRNA sequence. Comparisons may also be made with 23S rRNA sequences against reference sequences. In some aspects, a microbe could be considered to be the same

strain only if it shares at least 95% identity. In some embodiments, "substantially similar genetic characteristics" means a microbe sharing at least 95% identity.

[0198] In one embodiment, microbial strains of the present disclosure include those that comprise polynucleotide sequences that share at least 70%, 75%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity with any one of SEQ ID NOs:-308-315; or any one of SEQ ID NOs:1-307.

[0199] In one embodiment, microbes of the present disclosure include those that comprise polynucleotide sequences that share at least 70%, 75%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity with any one of SEQ ID NOs: 308-315; or any one of SEQ ID NOs:1-307.

[0200] In one embodiment, microbial consortia of the present disclosure include two or more microbes those that comprise polynucleotide sequences that share at least 70%, 75%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity with any one of SEQ ID NOs: 308-315; or any one of SEQ ID NOs: 1-307.

[0201] Unculturable microbes often cannot be assigned to a definite species in the absence of a phenotype determination, the microbes can be given a *candidatus* designation within a genus provided their 16S rRNA sequences subscribes to the principles of identity with known species.

[0202] One approach is to observe the distribution of a large number of strains of closely related species in sequence space and to identify clusters of strains that are well resolved from other clusters. This approach has been developed by using the concatenated sequences of multiple core (house-keeping) genes to assess clustering patterns, and has been called multilocus sequence analysis (MLSA) or multilocus sequence phylogenetic analysis. MLSA has been used successfully to explore clustering patterns among large numbers of strains assigned to very closely related species by current taxonomic methods, to look at the relationships between small numbers of strains within a genus, or within a broader taxonomic grouping, and to address specific taxonomic questions. More generally, the method can be used to ask whether bacterial species exist – that is, to observe whether large populations of

similar strains invariably fall into well-resolved clusters, or whether in some cases there is a genetic continuum in which clear separation into clusters is not observed.

[0203] In order to more accurately make a determination of genera, a determination of phenotypic traits, such as morphological, biochemical, and physiological characteristics are made for comparison with a reference genus archetype. The colony morphology can include color, shape, pigmentation, production of slime, etc. Features of the cell are described as to shape, size, Gram reaction, extracellular material, presence of endospores, flagella presence and location, motility, and inclusion bodies. Biochemical and physiological features describe growth of the organism at different ranges of temperature, pH, salinity and atmospheric conditions, growth in presence of different sole carbon and nitrogen sources. One of ordinary skill in the art would be reasonably apprised as to the phenotypic traits that define the genera of the present disclosure. For instance, colony color, form, and texture on a particular agar (*e.g.* YMA) was used to identify species of *Rhizobium*.

[0204] In one embodiment, the microbes taught herein were identified utilizing 16S rRNA gene sequences. It is known in the art that 16S rRNA contains hypervariable regions that can provide species/strain-specific signature sequences useful for bacterial identification. In the present disclosure, many of the microbes were identified *via* partial (500 – 1200 bp) 16S rRNA sequence signatures. In aspects, each strain represents a pure colony isolate that was selected from an agar plate. Selections were made to represent the diversity of organisms present based on any defining morphological characteristics of colonies on agar medium. The medium used, in embodiments, was R2A, PDA, Nitrogen-free semi-solid medium, or MRS agar. Colony descriptions of each of the 'picked' isolates were made after 24-hour growth and then entered into our database. Sequence data was subsequently obtained for each of the isolates.

[0205] Phylogenetic analysis using the 16S rRNA gene was used to define "substantially similar" species belonging to common genera and also to define "substantially similar" strains of a given taxonomic species. Further, we recorded physiological and/or biochemical properties of the isolates that can be utilized to highlight both minor and significant differences between strains that could lead to advantageous behavior on plants.

Agricultural Compositions

[0206] In some embodiments, the microbes of the disclosure are combined into agricultural compositions. In some embodiments, the agricultural compositions of the present disclosure include, but are not limited to: wetters, compatibilizing agents (also referred to as "compatibility agents"), antifoam agents, cleaning agents, sequestering agents, drift reduction agents, neutralizing agents and buffers, corrosion inhibitors, dyes, odorants, spreading agents (also referred to as "spreaders"), penetration aids (also referred to as "penetrants"), sticking agents (also referred to as "stickers" or "binders"), dispersing agents, thickening agents (also referred to as "thickeners"), stabilizers, emulsifiers, freezing point depressants, antimicrobial agents, and the like.

[0207] In some embodiments, the agricultural compositions of the present disclosure are solid. Where solid compositions are used, it may be desired to include one or more carrier materials with the active isolated microbe or consortia. In some embodiments, the present disclosure teaches the use of carriers including, but not limited to: mineral earths such as silicas, silica gels, silicates, talc, kaolin, attaclay, limestone, chalk, loess, clay, dolomite, diatomaceous earth, calcium sulfate, magnesium sulfate, magnesium oxide, ground synthetic materials, fertilizers such as ammonium sulfate, ammonium phosphate, ammonium nitrate, thiourea and urea, products of vegetable origin such as cereal meals, tree bark meal, wood meal and nutshell meal, cellulose powders, attapulgites, montmorillonites, mica, vermiculites, synthetic silicas and synthetic calcium silicates, or compositions of these.

[0208] In some embodiments, the agricultural compositions of the present disclosure are liquid. Thus in some embodiments, the present disclosure teaches that the agricultural compositions disclosed herein can include compounds or salts such as monoethanolamine salt, sodium sulfate, potassium sulfate, sodium chloride, potassium chloride, sodium acetate, ammonium hydrogen sulfate, ammonium chloride, ammonium acetate, ammonium formate, ammonium oxalate, ammonium carbonate, ammonium hydrogen carbonate, ammonium thiosulfate, ammonium hydrogen diphosphate, ammonium dihydrogen monophosphate, ammonium sodium hydrogen phosphate, ammonium thiocyanate, ammonium sulfamate or ammonium carbamate.

[0209] In some embodiments, the present disclosure teaches that agricultural compositions can include binders such as: polyvinylpyrrolidone, polyvinyl alcohol, partially hydrolyzed polyvinyl acetate, carboxymethylcellulose, starch, vinylpyrrolidone/vinyl acetate copolymers and polyvinyl acetate, or compositions of these; lubricants such as magnesium stearate, sodium stearate, talc or polyethylene glycol, or compositions of these; antifoams such as silicone emulsions, long-chain alcohols, phosphoric esters, acetylene diols, fatty acids or organofluorine compounds, and complexing agents such as: salts of ethylenediaminetetraacetic acid (EDTA), salts of trinitrilotriacetic acid or salts of polyphosphoric acids, or compositions of these.

[0210] In some embodiments, the agricultural compositions comprise surface-active agents. In some embodiments, the surface-active agents are added to liquid agricultural compositions. In other embodiments, the surface-active agents are added to solid formulations, especially those designed to be diluted with a carrier before application. Thus, in some embodiments, the agricultural compositions comprise surfactants. Surfactants are sometimes used, either alone or with other additives, such as mineral or vegetable oils as adjuvants to spray-tank mixes to improve the biological performance of the microbes on the target. The types of surfactants used for bioenhancement depend generally on the nature and mode of action of the microbes. The surface-active agents can be anionic, cationic, or nonionic in character, and can be employed as emulsifying agents, wetting agents, suspending agents, or for other purposes. In some embodiments, the surfactants are non-ionics such as: alky ethoxylates, linear aliphatic alcohol ethoxylates, and aliphatic amine ethoxylates. Surfactants conventionally used in the art of formulation and which may also be used in the present formulations are described, in *McCutcheon's Detergents and Emulsifiers Annual*, MC Publishing Corp., Ridgewood, N.J., 1998, and in *Encyclopedia of Surfactants*, Vol. I-III, Chemical Publishing Co., New York, 1980-81. In some embodiments, the present disclosure teaches the use of surfactants including alkali metal, alkaline earth metal or ammonium salts of aromatic sulfonic acids, for example, ligno-, phenol-, naphthalene- and dibutylnaphthalenesulfonic acid, and of fatty acids of arylsulfonates, of alkyl ethers, of lauryl ethers, of fatty alcohol sulfates and of fatty alcohol glycol ether sulfates, condensates of sulfonated naphthalene and its derivatives with formaldehyde, condensates of naphthalene or of the naphthalenesulfonic acids with phenol and formaldehyde, condensates of phenol

or phenolsulfonic acid with formaldehyde, condensates of phenol with formaldehyde and sodium sulfite, polyoxyethylene octylphenyl ether, ethoxylated isooctyl-, octyl- or nonylphenol, tributylphenyl polyglycol ether, alkylaryl polyether alcohols, isotridecyl alcohol, ethoxylated castor oil, ethoxylated triarylphenols, salts of phosphated triarylphenolethoxylates, lauryl alcohol polyglycol ether acetate, sorbitol esters, lignin-sulfite waste liquors or methylcellulose, or compositions of these.

[0211] In some embodiments, the present disclosure teaches other suitable surface-active agents, including salts of alkyl sulfates, such as diethanolammonium lauryl sulfate; alkylarylsulfonate salts, such as calcium dodecylbenzenesulfonate; alkylphenol-alkylene oxide addition products, such as nonylphenol-C_{18} ethoxylate; alcohol-alkylene oxide addition products, such as tridecyl alcohol-C_{16} ethoxylate; soaps, such as sodium stearate; alkylnaphthalene-sulfonate salts, such as sodium dibutyl-naphthalenesulfonate; dialkyl esters of sulfosuccinate salts, such as sodium di(2-ethylhexyl)sulfosuccinate; sorbitol esters, such as sorbitol oleate; quaternary amines, such as lauryl trimethylammonium chloride; polyethylene glycol esters of fatty acids, such as polyethylene glycol stearate; block copolymers of ethylene oxide and propylene oxide; salts of mono and dialkyl phosphate esters; vegetable oils such as soybean oil, rapeseed/canola oil, olive oil, castor oil, sunflower seed oil, coconut oil, corn oil, cottonseed oil, linseed oil, palm oil, peanut oil, safflower oil, sesame oil, tung oil and the like; and esters of the above vegetable oils, particularly methyl esters.

[0212] In some embodiments, the agricultural compositions comprise wetting agents. A wetting agent is a substance that when added to a liquid increases the spreading or penetration power of the liquid by reducing the interfacial tension between the liquid and the surface on which it is spreading. Wetting agents are used for two main functions in agrochemical formulations: during processing and manufacture to increase the rate of wetting of powders in water to make concentrates for soluble liquids or suspension concentrates; and during mixing of a product with water in a spray tank or other vessel to reduce the wetting time of wettable powders and to improve the penetration of water into water-dispersible granules. In some embodiments, examples of wetting agents used in the agricultural compositions of the present disclosure, including wettable powders, suspension concentrates, and water-dispersible granule formulations are: sodium lauryl sulphate; sodium dioctyl sulphosuccinate; alkyl phenol ethoxylates; and aliphatic alcohol ethoxylates.

[0213] In some embodiments, the agricultural compositions of the present disclosure comprise dispersing agents. A dispersing agent is a substance which adsorbs onto the surface of particles and helps to preserve the state of dispersion of the particles and prevents them from re-aggregating. In some embodiments, dispersing agents are added to agricultural compositions of the present disclosure to facilitate dispersion and suspension during manufacture, and to ensure the particles redisperse into water in a spray tank. In some embodiments, dispersing agents are used in wettable powders, suspension concentrates, and water-dispersible granules. Surfactants that are used as dispersing agents have the ability to adsorb strongly onto a particle surface and provide a charged or steric barrier to re-aggregation of particles. In some embodiments, the most commonly used surfactants are anionic, non-ionic, or mixtures of the two types.

[0214] In some embodiments, for wettable powder formulations, the most common dispersing agents are sodium lignosulphonates. In some embodiments, suspension concentrates provide very good adsorption and stabilization using polyelectrolytes, such as sodium naphthalene sulphonate formaldehyde condensates. In some embodiments, tristyrylphenol ethoxylate phosphate esters are also used. In some embodiments, such as alkylarylethylene oxide condensates and EO-PO block copolymers are sometimes combined with anionics as dispersing agents for suspension concentrates.

[0215] In some embodiments, the agricultural compositions of the present disclosure comprise polymeric surfactants. In some embodiments, the polymeric surfactants have very long hydrophobic 'backbones' and a large number of ethylene oxide chains forming the 'teeth' of a 'comb' surfactant. In some embodiments, these high molecular weight polymers can give very good long-term stability to suspension concentrates, because the hydrophobic backbones have many anchoring points onto the particle surfaces. In some embodiments, examples of dispersing agents used in agricultural compositions of the present disclosure are: sodium lignosulphonates; sodium naphthalene sulphonate formaldehyde condensates; tristyrylphenol ethoxylate phosphate esters; aliphatic alcohol ethoxylates; alky ethoxylates; EO-PO block copolymers; and graft copolymers.

[0216] In some embodiments, the agricultural compositions of the present disclosure comprise emulsifying agents. An emulsifying agent is a substance, which stabilizes a

suspension of droplets of one liquid phase in another liquid phase. Without the emulsifying agent the two liquids would separate into two immiscible liquid phases. In some embodiments, the most commonly used emulsifier blends include alkylphenol or aliphatic alcohol with 12 or more ethylene oxide units and the oil-soluble calcium salt of dodecylbenzene sulphonic acid. A range of hydrophile-lipophile balance ("HLB") values from 8 to 18 will normally provide good stable emulsions. In some embodiments, emulsion stability can sometimes be improved by the addition of a small amount of an EO-PO block copolymer surfactant.

[0217] In some embodiments, the agricultural compositions of the present disclosure comprise solubilizing agents. A solubilizing agent is a surfactant, which will form micelles in water at concentrations above the critical micelle concentration. The micelles are then able to dissolve or solubilize water-insoluble materials inside the hydrophobic part of the micelle. The types of surfactants usually used for solubilization are non-ionics: sorbitan monooleates; sorbitan monooleate ethoxylates; and methyl oleate esters.

[0218] In some embodiments, the agricultural compositions of the present disclosure comprise organic solvents. Organic solvents are used mainly in the formulation of emulsifiable concentrates, ULV formulations, and to a lesser extent granular formulations. Sometimes mixtures of solvents are used. In some embodiments, the present disclosure teaches the use of solvents including aliphatic paraffinic oils such as kerosene or refined paraffins. In other embodiments, the present disclosure teaches the use of aromatic solvents such as xylene and higher molecular weight fractions of C9 and C10 aromatic solvents. In some embodiments, chlorinated hydrocarbons are useful as co-solvents to prevent crystallization of pesticides when the formulation is emulsified into water. Alcohols are sometimes used as co-solvents to increase solvent power.

[0219] In some embodiments, the agricultural compositions comprise gelling agents. Thickeners or gelling agents are used mainly in the formulation of suspension concentrates, emulsions, and suspoemulsions to modify the rheology or flow properties of the liquid and to prevent separation and settling of the dispersed particles or droplets. Thickening, gelling, and anti-settling agents generally fall into two categories, namely water-insoluble particulates and water-soluble polymers. It is possible to produce suspension concentrate formulations using clays and silicas. In

some embodiments, the agricultural compositions comprise one or more thickeners including, but not limited to: montmorillonite, e.g. bentonite; magnesium aluminum silicate; and attapulgite. In some embodiments, the present disclosure teaches the use of polysaccharides as thickening agents. The types of polysaccharides most commonly used are natural extracts of seeds and seaweeds or synthetic derivatives of cellulose. Some embodiments utilize xanthan and some embodiments utilize cellulose. In some embodiments, the present disclosure teaches the use of thickening agents including, but are not limited to: guar gum; locust bean gum; carrageenam; alginates; methyl cellulose; sodium carboxymethyl cellulose (SCMC); hydroxyethyl cellulose (HEC). In some embodiments, the present disclosure teaches the use of other types of anti-settling agents such as modified starches, polyacrylates, polyvinyl alcohol, and polyethylene oxide. Another good anti-settling agent is xanthan gum.

[0220] In some embodiments, the presence of surfactants, which lower interfacial tension, can cause water-based formulations to foam during mixing operations in production and in application through a spray tank. Thus, in some embodiments, in order to reduce the tendency to foam, anti-foam agents are often added either during the production stage or before filling into bottles/spray tanks. Generally, there are two types of anti-foam agents, namely silicones and non-silicones. Silicones are usually aqueous emulsions of dimethyl polysiloxane, while the non-silicone anti-foam agents are water-insoluble oils, such as octanol and nonanol, or silica. In both cases, the function of the anti-foam agent is to displace the surfactant from the air-water interface.

[0221] In some embodiments, the agricultural compositions comprise a preservative.

[0222] Further, the individual microbes, or microbial consortia, or microbial communities, developed according to the disclosed methods can be combined with known actives available in the agricultural space, such as: pesticide, herbicide, bactericide, fungicide, insecticide, virucide, miticide, nemataicide, acaricide, plant growth regulator, rodenticide, anti-algae agent, biocontrol or beneficial agent. Further, the microbes, microbial consortia, or microbial communities developed according to the disclosed methods can be combined with known fertilizers. Such combinations may exhibit synergistic properties. Further still, the individual microbes, or microbial consortia, or microbial communities, developed according to the disclosed methods

can be combined with inert ingredients. Also, in some aspects, the disclosed microbes are combined with biological active agents.

Metabolites Produced by Microbes and Consortia of the Disclosure

[0223] In some cases, the microbes of the present disclosure may produce one or more compounds and/or have one or more activities, e.g., one or more of the following: production of a metabolite, production of a phytohormone such as auxin, production of acetoin, production of an antimicrobial compound, production of a siderophore, production of a cellulase, production of a pectinase, production of a chitinase, production of a xylanase, nitrogen fixation, or mineral phosphate solubilization.

[0224] For example, a microbe of the disclosure may produce a phytohormone selected from the group consisting of an auxin, a cytokinin, a gibberellin, ethylene, a brassinosteroid, and abscisic acid.

[0225] Thus, a "metabolite produced by" a microbe of the disclosure, is intended to capture any molecule (small molecule, vitamin, mineral, protein, nucleic acid, lipid, fat, carbohydrate, etc.) produced by the microbe. Often, the exact mechanism of action, whereby a microbe of the disclosure imparts a beneficial trait upon a given plant species is not known. It is hypothesized, that in some instances, the microbe is producing a metabolite that is beneficial to the plant. Thus, in some aspects, a cell-free or inactivated preparation of microbes is beneficial to a plant, as the microbe does not have to be alive to impart a beneficial trait upon the given plant species, so long as the preparation includes a metabolite that was produced by said microbe and which is beneficial to a plant.

[0226] In one embodiment, the microbes of the disclosure may produce auxin (e.g., indole-3-acetic acid (IAA)). Production of auxin can be assayed. Many of the microbes described herein may be capable of producing the plant hormone auxin indole-3-acetic acid (IAA) when grown in culture. Auxin plays a key role in altering the physiology of the plant, including the extent of root growth.

[0227] Therefore, in an embodiment, the microbes of the disclosure are present as a population disposed on the surface or within a tissue of a given plant species. The microbes may produce a metabolite in an amount effective to cause a detectable increase in the amount of metabolite that is found on or within the plant, when compared to a reference plant not treated with the microbes or cell-free or inactive

preparations of the disclosure. The metabolites produced by said microbial population may be beneficial to the plant species.

Plant Growth Regulators and Biostimulants

[0228] In some embodiments, the agricultural compositions of the present disclosure comprise plant growth regulators and/or biostimulants, used in combination with the taught microbes.

[0229] In some embodiments, the individual microbes, or microbial consortia, or microbial communities, developed according to the disclosed methods can be combined with known plant growth regulators in the agricultural space, such as: auxins, gibberellins, cytokinins, ethylene generators, growth inhibitors, and growth retardants.

[0230] For example, in some embodiments, the present disclosure teaches agricultural compositions comprising one or more of the following active ingredients including: ancymidol, butralin, alcohols, chloromequat chloride, cytokinin, daminozide, ethepohon, flurprimidol, giberrelic acid, gibberellin mixtures, indole-3-butryic acid (IBA), maleic hydrazide, mefludide, mepiquat chloride, mepiquat pentaborate, naphthalene-acetic acid (NAA), 1-napthaleneacetemide, (NAD), n-decanol, placlobutrazol, prohexadione calcium, trinexapac-ethyl, uniconazole, salicylic acid, abscisic acid, ethylene, brassinosteroids, jasmonates, polyamines, nitric oxide, strigolactones, or karrikins among others.

[0231] In some embodiments, the individual microbes, or microbial consortia, or microbial communities, developed according to the disclosed methods can be combined with seed inoculants known in the agricultural space, such as: QUICKROOTS®, VAULT®, RHIZO-STICK®, NODULATOR®, DORMAL®, SABREX®, among others. In some embodiments, a *Bradyrhizobium* inoculant is utilized in combination with any single microbe or microbial consortia disclosed here. In particular aspects, a synergistic effect is observed when one combines one of the aforementioned inoculants, e.g. QUICKROOTS® or *Bradyrhizobium*, with a microbe or microbial consortia as taught herein.

[0232] In some embodiments, the agricultural compositions of the present disclosure comprise a plant growth regulator, which contains: kinetin, gibberellic acid, and indole butyric acid, along with copper, manganese, and zinc.

[0233] In some aspects, the agricultural compositions comprising microbes of the disclosure (e.g. any microbe or combination thereof from **Tables 1-4**) and kinetin, gibberellic acid, and indole butyric acid, along with copper, manganese, and zinc, exhibit the ability to act synergistically together.

[0234] In some embodiments, the present disclosure teaches agricultural compositions comprising one or more commercially available plant growth regulators, including but not limited to: Abide®, A-Rest®, Butralin®, Fair®, Royaltac M®, Sucker-Plucker®, Off-Shoot®, Contact-85®, Citadel®, Cycocel®, E-Pro®, Conklin®, Culbac®, Cytoplex®, Early Harvest®, Foli-Zyme®, Goldengro®, Happygro®, Incite®, Megagro®, Ascend®, Radiate®, Stimulate®, Suppress®, Validate®, X-Cyte®, B-Nine®, Compress®, Dazide®, Boll Buster®, BollD®, Cerone®, Cotton Quik®, Ethrel®, Finish®, Flash®, Florel®, Mature®, MFX®, Prep®, Proxy®, Quali-Pro®, SA-50®, Setup®, Super Boll®, Whiteout®, Cutless®, Legacy®, Mastiff®, Topflor®, Ascend®, Cytoplex®, Ascend®, Early Harvest®, Falgro®, Florgib®, Foli-Zyme®, GA3®, GibGro®, Green Sol®, Incite®, N-Large®, PGR IV®, Pro-Gibb®, Release®, Rouse®, Ryzup®, Stimulate®, BVB®, Chrysal®, Fascination®, Procone®, Fair®, Rite-Hite®, Royal®, Sucker Stuff®, Embark®, Sta-Lo®, Pix®, Pentia®, DipN Grow®, Goldengro®, Hi-Yield®, Rootone®, Antac®, FST-7®, Royaltac®, Bonzi®, Cambistat®, Cutdown®, Downsize®, Florazol®, Paclo®, Paczol®, Piccolo®, Profile®, Shortstop®, Trimmit®, Turf Enhancer®, Apogee®, Armor Tech®, Goldwing®, Governor®, Groom®, Legacy®, Primeraone®, Primo®, Provair®, Solace®, T-Nex®, T-Pac®, Concise®, and Sumagic®.

[0235] In some embodiments, the present invention teaches a synergistic use of the presently disclosed microbes or microbial consortia with plant growth regulators and/or stimulants such as phytohormones or chemicals that influence the production or disruption of plant growth regulators.

[0236] In some embodiments, the present invention teaches that phytohormones can include: Auxins (e.g., Indole acetic acid IAA), Gibberellins, Cytokinins (e.g., Kinetin), Abscisic acid, Ethylene (and its production as regulated by ACC synthase and disrupted by ACC deaminase).

[0237] In some embodiments, the present invention teaches additional plant-growth promoting chemicals that may act in synergy with the microbes and microbial consortia disclosed herein, such as: humic acids, fulvic acids, amino acids, polyphenols and protein hydrolysates.

[0238] In some embodiments, the present disclosure teaches that the individual microbes, or microbial consortia, or microbial communities, developed according to the disclosed methods—including any single microorganism or combination of microorganisms disclosed in **Tables 1-4** of the specification—can be combined with Ascend® or other similar plant growth regulators. Ascend® is described as comprising 0.090% cytokinin as kinetin, 0.030% gibberellic acid, 0.045% indole butyric acid, and 99.835% other ingredients.

[0239] Thus, in some embodiments, the disclosure provides for the application of the taught microbes in combination with Ascend® upon any crop. Further, the disclosure provides for the application of the taught microbes in combination with Ascend® upon any crop and utilizing any method or application rate.

[0240] In some embodiments, the present disclosure teaches agricultural compositions with biostimulants.

[0241] As used herein, the term "biostimulant" refers to any substance that acts to stimulate the growth of microorganisms that may be present in soil or other plant growing medium.

[0242] The level of microorganisms in the soil or growing medium is directly correlated to plant health. Microorganisms feed on biodegradable carbon sources, and therefore plant health is also correlated with the quantity of organic matter in the soil. While fertilizers provide nutrients to feed and grow plants, in some embodiments, biostimulants provide biodegradable carbon, e.g., molasses, carbohydrates, e.g., sugars, to feed and grow microorganisms. Unless clearly stated otherwise, a biostimulant may comprise a single ingredient, or a combination of several different ingredients, capable of enhancing microbial activity or plant growth and development, due to the effect of one or more of the ingredients, either acting independently or in combination.

[0243] In some embodiments, biostimulants are compounds that produce non-nutritional plant growth responses. In some embodiments, many important benefits of

biostimulants are based on their ability to influence hormonal activity. Hormones in plants (phytohormones) are chemical messengers regulating normal plant development as well as responses to the environment. Root and shoot growth, as well as other growth responses are regulated by phytohormones. In some embodiments, compounds in biostimulants can alter the hormonal status of a plant and exert large influences over its growth and health. Thus, in some embodiments, the present disclosure teaches sea kelp, humic acids, fulvic acids, and B Vitamins as common components of biostimulants. In some embodiments, the biostimulants of the present disclosure enhance antioxidant activity, which increases the plant's defensive system. In some embodiments, vitamin C, vitamin E, and amino acids such as glycine are antioxidants contained in biostimulants.

[0244] In other embodiments, biostimulants may act to stimulate the growth of microorganisms that are present in soil or other plant growing medium. Prior studies have shown that when certain biostimulants comprising specific organic seed extracts (e.g., soybean) were used in combination with a microbial inoculant, the biostimulants were capable of stimulating growth of microbes included in the microbial inoculant. Thus, in some embodiments, the present disclosure teaches one or more biostimulants that, when used with a microbial inoculant, is capable of enhancing the population of both native microbes and inoculant microbes. For a review of some popular uses of biostimulants, please see Calvo et al., 2014, Plant Soil 383:3-41.

[0245] In some embodiments, the present disclosure teaches that the individual microbes, or microbial consortia, or microbial communities, developed according to the disclosed methods—including any single microorganism or combination of microorganisms disclosed in **Tables 1-4** of the specification—can be combined with any plant biostimulant.

[0246] In some embodiments, the present disclosure teaches agricultural compositions comprising one or more commercially available biostimulants, including but not limited to: Vitazyme®, Diehard™ Biorush®, Diehard™ Biorush® Fe, Diehard™ Soluble Kelp, Diehard™ Humate SP, Phocon®, Foliar Plus™, Plant Plus™, Accomplish LM®, Titan®, Soil Builder™, Nutri Life, Soil Solution TM, Seed Coat TM PercPlus TM, Plant Power, CropKarb®, Thrust™, Fast2Grow®, Baccarat®, and Potente® among others.

[0247] In some embodiments, the present disclosure teaches that the individual microbes, or microbial consortia, or microbial communities, developed according to the disclosed methods—including any single microorganism or combination of microorganisms disclosed in **Tables 1-4** of the specification—can be combined with ProGibb® or other similar plant growth regulators. ProGibb® is described as comprising 4.0% Gibberellic Acid and 96.00% other ingredients.

[0248] In some embodiments, the present disclosure teaches that the individual microbes, or microbial consortia, or microbial communities, developed according to the disclosed methods—including any single microorganism or combination of microorganisms disclosed in **Tables 1-4** of the specification—can be combined with Release® or other similar plant growth regulators. Release® is described as comprising 10.0% Gibberellic Acid and 90.00% other ingredients.

[0249] In some embodiments, the present disclosure teaches that the individual microbes, or microbial consortia, or microbial communities, developed according to the disclosed methods—including any single microorganism or combination of microorganisms disclosed in **Tables 1-4** of the specification—can be combined with RyzUp SmartGrass® or other similar plant growth regulators. RyzUp SmartGrass® is described as comprising 40.0% Gibberellin A_3 and 60.00% other ingredients.

[0250] In some embodiments, the present disclosure teaches that the individual microbes, or microbial consortia, or microbial communities, developed according to the disclosed methods—including any single microorganism or combination of microorganisms disclosed in **Tables 1-4** of the specification—can be combined with X-CYTE™ or other similar plant growth regulators. X-CYTE™ is described as comprising 0.04% Cytokinin, as kinetin and 99.96% other ingredients.

[0251] In some embodiments, the present disclosure teaches that the individual microbes, or microbial consortia, or microbial communities, developed according to the disclosed methods—including any single microorganism or combination of microorganisms disclosed in **Tables 1-4** of the specification—can be combined with N-Large™ or other similar plant growth regulators. N-Large™ is described as comprising 4.0% Gibberellin A_3 and 96.00% other ingredients.

[0252] In some embodiments, when the microbe or microbial consortia identified according to the taught methods is combined with an active chemical agent one

witnesses an additive effect on a plant phenotypic trait of interest. In other embodiments, when the microbe or microbial consortia identified according to the taught methods is combined with an active chemical agent one witness a synergistic effect on a plant phenotypic trait of interest.

[0253] In some embodiments, when the microbe or microbial consortia identified according to the taught methods is combined with a fertilizer one witnesses an additive effect on a plant phenotypic trait of interest. In other embodiments, when the microbe or microbial consortia identified according to the taught methods is combined with a fertilizer one witness a synergistic effect on a plant phenotypic trait of interest.

[0254] In some embodiments, when the microbe or microbial consortia identified according to the taught methods is combined with a plant growth regulator, one witnesses an additive effect on a plant phenotypic trait of interest. In some embodiments, when the microbe or microbial consortia identified according to the taught methods is combined with a plant growth regulator, one witnesses a synergistic effect. In some aspects, the microbes of the present disclosure are combined with Ascend® and a synergistic effect is observed for one or more phenotypic traits of interest.

[0255] In some embodiments, when the microbe or microbial consortia identified according to the taught methods is combined with a biostimulant, one witnesses an additive effect on a plant phenotypic trait of interest. In some embodiments, when the microbe or microbial consortia identified according to the taught methods is combined with a biostimulant, one witnesses a synergistic effect.

[0256] The synergistic effect obtained by the taught methods can be quantified according to Colby's formula (*i.e.* (E) =X+Y-(X*Y/100). *See* Colby, R. S., "Calculating Synergistic and Antagonistic Responses of Herbicide Combinations," 1967 Weeds, vol. 15, pp. 20-22, incorporated herein by reference in its entirety. Thus, by "synergistic" is intended a component which, by virtue of its presence, increases the desired effect by more than an additive amount.

[0257] The isolated microbes and consortia of the present disclosure can synergistically increase the effectiveness of agricultural active compounds and also agricultural auxiliary compounds.

[0258] In other embodiments, when the microbe or microbial consortia identified according to the taught methods is combined with a fertilizer one witnesses a synergistic effect.

[0259] Furthermore, in certain embodiments, the disclosure utilizes synergistic interactions to define microbial consortia. That is, in certain aspects, the disclosure combines together certain isolated microbial species, which act synergistically, into consortia that impart a beneficial trait upon a plant, or which are correlated with increasing a beneficial plant trait.

[0260] The agricultural compositions developed according to the disclosure can be formulated with certain auxiliaries, in order to improve the activity of a known active agricultural compound. This has the advantage that the amounts of active ingredient in the formulation may be reduced while maintaining the efficacy of the active compound, thus allowing costs to be kept as low as possible and any official regulations to be followed. In individual cases, it may also possible to widen the spectrum of action of the active compound since plants, where the treatment with a particular active ingredient without addition was insufficiently successful, can indeed be treated successfully by the addition of certain auxiliaries along with the disclosed microbial isolates and consortia. Moreover, the performance of the active may be increased in individual cases by a suitable formulation when the environmental conditions are not favorable.

[0261] Such auxiliaries that can be used in an agricultural composition can be an adjuvant. Frequently, adjuvants take the form of surface-active or salt-like compounds. Depending on their mode of action, they can roughly be classified as modifiers, activators, fertilizers, pH buffers, and the like. Modifiers affect the wetting, sticking, and spreading properties of a formulation. Activators break up the waxy cuticle of the plant and improve the penetration of the active ingredient into the cuticle, both short-term (over minutes) and long-term (over hours). Fertilizers such as ammonium sulfate, ammonium nitrate or urea improve the absorption and solubility of the active ingredient and may reduce the antagonistic behavior of active ingredients. pH buffers are conventionally used for bringing the formulation to an optimal pH.

[0262] For further embodiments of agricultural compositions of the present disclosure, *See* "Chemistry and Technology of Agrochemical Formulations," edited by D. A. Knowles, copyright 1998 by Kluwer Academic Publishers, hereby incorporated by reference.

Seed Treatments

[0263] In some embodiments, the present disclosure also concerns the discovery that treating seeds before they are sown or planted with a combination of one or more of the microbes or agricultural compositions of the present disclosure can enhance a desired plant trait, *e.g.* plant growth, plant health, and/or plant resistance to pests.

[0264] Thus, in some embodiments, the present disclosure teaches the use of one or more of the microbes or microbial consortia as seed treatments. The seed treatment can be a seed coating applied directly to an untreated and "naked" seed. However, the seed treatment can be a seed overcoat that is applied to a seed that has already been coated with one or more previous seed coatings or seed treatments. The previous seed treatments may include one or more active compounds, either chemical or biological, and one or more inert ingredients.

[0265] The term "seed treatment" generally refers to application of a material to a seed prior to or during the time it is planted in soil. Seed treatment with microbes, and other agricultural compositions of the present disclosure, has the advantages of delivering the treatments to the locus at which the seeds are planted shortly before germination of the seed and emergence of a seedling.

[0266] In other embodiments, the present disclosure also teaches that the use of seed treatments minimizes the amount of microbe or agricultural composition that is required to successfully treat the plants, and further limits the amount of contact of workers with the microbes and compositions compared to application techniques such as spraying over soil or over emerging seedlings.

[0267] Moreover, in some embodiments, the present disclosure teaches that the microbes disclosed herein are important for enhancing the early stages of plant life (*e.g.*, within the first thirty days following emergence of the seedling). Thus, in some embodiments, delivery of the microbes and/or compositions of the present disclosure as a seed treatment places the microbe at the locus of action at a critical time for its activity.

[0268] In some embodiments, the microbial compositions of the present disclosure are formulated as a seed treatment. In some embodiments, it is contemplated that the seeds can be substantially uniformly coated with one or more layers of the microbes and/or agricultural compositions disclosed herein, using conventional methods of mixing, spraying, or a combination thereof through the use of treatment application equipment that is specifically designed and manufactured to accurately, safely, and efficiently apply seed treatment products to seeds. Such equipment uses various types of coating technology such as rotary coaters, drum coaters, fluidized bed techniques, spouted beds, rotary mists, or a combination thereof. Liquid seed treatments such as those of the present disclosure can be applied via either a spinning "atomizer" disk or a spray nozzle, which evenly distributes the seed treatment onto the seed as it moves though the spray pattern. In aspects, the seed is then mixed or tumbled for an additional period of time to achieve additional treatment distribution and drying.

[0269] The seeds can be primed or unprimed before coating with the microbial compositions to increase the uniformity of germination and emergence. In an alternative embodiment, a dry powder formulation can be metered onto the moving seed and allowed to mix until completely distributed.

[0270] In some embodiments, the seeds have at least part of the surface area coated with a microbiological composition, according to the present disclosure. In some embodiments, a seed coat comprising the microbial composition is applied directly to a naked seed. In some embodiments, a seed overcoat comprising the microbial composition is applied to a seed that already has a seed coat applied thereon. In some aspects, the seed may have a seed coat comprising, *e.g.* clothianidin and/or *Bacillus firmus*-I-1582, upon which the present composition will be applied on top of, as a seed overcoat. In some aspects, the taught microbial compositions are applied as a seed overcoat to seeds that have already been treated with PONCHO™ VOTiVO™. In some aspects, the seed may have a seed coat comprising, *e.g.* Metalaxyl, and/or clothianidin, and/or *Bacillus firmus*-I-1582, upon which the present composition will be applied on top of, as a seed overcoat. In some aspects, the taught microbial compositions are applied as a seed overcoat to seeds that have already been treated with ACCELERON™.

[0271] In some embodiments, the microorganism-treated seeds have a microbial spore concentration, or microbial cell concentration, from about: 10^3 to 10^{12}, 10^3 to

10^{11}, 10^3 to 10^{10}, 10^3 to 10^9, 10^3 to 10^8, 10^3 to 10^7, 10^3 to 10^6, 10^3 to 10^5, or 10^3 to 10^4 per seed.

[0272] In some embodiments, the microorganism-treated seeds have a microbial spore concentration, or microbial cell concentration, from about: 10^4 to 10^{12}, 10^4 to 10^{11}, 10^4 to 10^{10}, 10^4 to 10^9, 10^4 to 10^8, 10^4 to 10^7, 10^4 to 10^6, or 10^4 to 10^5 per seed.

[0273] In some embodiments, the microorganism-treated seeds have a microbial spore concentration, or microbial cell concentration, from about: 10^5 to 10^{12}, 10^5 to 10^{11}, 10^5 to 10^{10}, 10^5 to 10^9, 10^5 to 10^8, 10^5 to 10^7, or 10^5 to 10^6 per seed.

[0274] In some embodiments, the microorganism-treated seeds have a microbial spore concentration, or microbial cell concentration, from about: 10^5 to 10^9 per seed.

[0275] In some embodiments, the microorganism-treated seeds have a microbial spore concentration, or microbial cell concentration, of at least about: 1×10^3, or 1×10^4, or 1×10^5, or 1×10^6, or 1×10^7, or 1×10^8, or 1×10^9 per seed.

[0276] In some embodiments, the amount of one or more of the microbes and/or agricultural compositions applied to the seed depend on the final formulation, as well as size or type of the plant or seed utilized. In some embodiments, one or more of the microbes are present in about 2% w/w/ to about 80% w/w of the entire formulation. In some embodiments, the one or more of the microbes employed in the compositions is about 5% w/w to about 65% w/w, or 10% w/w to about 60% w/w by weight of the entire formulation.

[0277] In some embodiments, the seeds may also have more spores or microbial cells per seed, such as, for example about 10^2, 10^3, 10^4, 10^5, 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15}, 10^{16}, or 10^{17} spores or cells per seed.

[0278] In some embodiments, the seed coats of the present disclosure can be up to 10μm, 20μm, 30μm, 40μm, 50μm, 60μm, 70μm, 80μm, 90μm, 100μm, 110μm, 120μm, 130μm, 140μm, 150μm, 160μm, 170μm, 180μm, 190μm, 200μm, 210μm, 220μm, 230μm, 240μm, 250μm, 260μm, 270μm, 280μm, 290μm, 300μm, 310μm, 320μm, 330μm, 340μm, 350μm, 360μm, 370μm, 380μm, 390μm, 400μm, 410μm, 420μm, 430μm, 440μm, 450μm, 460μm, 470μm, 480μm, 490μm, 500μm, 510μm, 520μm, 530μm, 540μm, 550μm, 560μm, 570μm, 580μm, 590μm, 600μm, 610μm, 620μm, 630μm, 640μm, 650μm, 660μm, 670μm, 680μm, 690μm, 700μm, 710μm, 720μm, 730μm, 740μm, 750μm, 760μm, 770μm, 780μm, 790μm, 800μm, 810μm,

820μm, 830μm, 840μm, 850μm, 860μm, 870μm, 880μm, 890μm, 900μm, 910μm, 920μm, 930μm, 940μm, 950μm, 960μm, 970μm, 980μm, 990μm, 1000μm, 1010μm, 1020μm, 1030μm, 1040μm, 1050μm, 1060μm, 1070μm, 1080μm, 1090μm, 1100μm, 1110μm, 1120μm, 1130μm, 1140μm, 1150μm, 1160μm, 1170μm, 1180μm, 1190μm, 1200μm, 1210μm, 1220μm, 1230μm, 1240μm, 1250μm, 1260μm, 1270μm, 1280μm, 1290μm, 1300μm, 1310μm, 1320μm, 1330μm, 1340μm, 1350μm, 1360μm, 1370μm, 1380μm, 1390μm, 1400μm, 1410μm, 1420μm, 1430μm, 1440μm, 1450μm, 1460μm, 1470μm, 1480μm, 1490μm, 1500μm, 1510μm, 1520μm, 1530μm, 1540μm, 1550μm, 1560μm, 1570μm, 1580μm, 1590μm, 1600μm, 1610μm, 1620μm, 1630μm, 1640μm, 1650μm, 1660μm, 1670μm, 1680μm, 1690μm, 1700μm, 1710μm, 1720μm, 1730μm, 1740μm, 1750μm, 1760μm, 1770μm, 1780μm, 1790μm, 1800μm, 1810μm, 1820μm, 1830μm, 1840μm, 1850μm, 1860μm, 1870μm, 1880μm, 1890μm, 1900μm, 1910μm, 1920μm, 1930μm, 1940μm, 1950μm, 1960μm, 1970μm, 1980μm, 1990μm, 2000μm, 2010μm, 2020μm, 2030μm, 2040μm, 2050μm, 2060μm, 2070μm, 2080μm, 2090μm, 2100μm, 2110μm, 2120μm, 2130μm, 2140μm, 2150μm, 2160μm, 2170μm, 2180μm, 2190μm, 2200μm, 2210μm, 2220μm, 2230μm, 2240μm, 2250μm, 2260μm, 2270μm, 2280μm, 2290μm, 2300μm, 2310μm, 2320μm, 2330μm, 2340μm, 2350μm, 2360μm, 2370μm, 2380μm, 2390μm, 2400μm, 2410μm, 2420μm, 2430μm, 2440μm, 2450μm, 2460μm, 2470μm, 2480μm, 2490μm, 2500μm, 2510μm, 2520μm, 2530μm, 2540μm, 2550μm, 2560μm, 2570μm, 2580μm, 2590μm, 2600μm, 2610μm, 2620μm, 2630μm, 2640μm, 2650μm, 2660μm, 2670μm, 2680μm, 2690μm, 2700μm, 2710μm, 2720μm, 2730μm, 2740μm, 2750μm, 2760μm, 2770μm, 2780μm, 2790μm, 2800μm, 2810μm, 2820μm, 2830μm, 2840μm, 2850μm, 2860μm, 2870μm, 2880μm, 2890μm, 2900μm, 2910μm, 2920μm, 2930μm, 2940μm, 2950μm, 2960μm, 2970μm, 2980μm, 2990μm, or 3000μm thick.

[0279] In some embodiments, the seed coats of the present disclosure can be 0.5mm, 1mm, 1.5mm, 2mm, 2.5mm, 3mm, 3.5mm, 4mm, 4.5mm, or 5mm thick.

[0280] In some embodiments, the seed coats of the present disclosure can be at least 0.5%, 1%, 1.5%, 2%, 2.5%, 3%, 3.5%, 4%, 4.5%, 5%, 5.5%, 6%, 6.5%, 7%, 7.5%, 8%, 8.5%, 9%, 9.5%, 10%, 10.5%, 11%, 11.5%, 12%, 12.5%, 13%, 13.5%, 14%, 14.5%, 15%, 15.5%, 16%, 16.5%, 17%, 17.5%, 18%, 18.5%, 19%, 19.5%, 20%, 20.5%, 21%, 21.5%, 22%, 22.5%, 23%, 23.5%, 24%, 24.5%, 25%, 25.5%, 26%, 26.5%, 27%, 27.5%, 28%, 28.5%, 29%, 29.5%, 30%, 30.5%, 31%, 31.5%, 32%,

32.5%, 33%, 33.5%, 34%, 34.5%, 35%, 35.5%, 36%, 36.5%, 37%, 37.5%, 38%, 38.5%, 39%, 39.5%, 40%, 40.5%, 41%, 41.5%, 42%, 42.5%, 43%, 43.5%, 44%, 44.5%, 45%, 45.5%, 46%, 46.5%, 47%, 47.5%, 48%, 48.5%, 49%, 49.5%, or 50% of the uncoated seed weight.

[0281] In some embodiments, the microbial spores and/or cells can be coated freely onto the seeds or they can be formulated in a liquid or solid composition before being coated onto the seeds. For example, a solid composition comprising the microorganisms can be prepared by mixing a solid carrier with a suspension of the spores until the solid carriers are impregnated with the spore or cell suspension. This mixture can then be dried to obtain the desired particles.

[0282] In some other embodiments, it is contemplated that the solid or liquid microbial compositions of the present disclosure further contain functional agents *e.g.*, activated carbon, nutrients (fertilizers), and other agents capable of improving the germination and quality of the products or a combination thereof.

[0283] Seed coating methods and compositions that are known in the art can be particularly useful when they are modified by the addition of one of the embodiments of the present disclosure. Such coating methods and apparatus for their application are disclosed in, for example: U.S. Pat. Nos. 5,916,029; 5,918,413; 5,554,445; 5,389,399; 4,759,945; 4,465,017, and U.S. Pat. App. No. 13/260,310, each of which is incorporated by reference herein.

[0284] Seed coating compositions are disclosed in, for example: U.S. Pat. Nos. 5,939,356; 5,876,739, 5,849,320; 5,791,084, 5,661,103; 5,580,544, 5,328,942; 4,735,015; 4,634,587; 4,372,080, 4,339,456; and 4,245,432, each of which is incorporated by reference herein.

[0285] In some embodiments, a variety of additives can be added to the seed treatment formulations comprising the inventive compositions. Binders can be added and include those composed of an adhesive polymer that can be natural or synthetic without phytotoxic effect on the seed to be coated. The binder may be selected from polyvinyl acetates; polyvinyl acetate copolymers; ethylene vinyl acetate (EVA) copolymers; polyvinyl alcohols; polyvinyl alcohol copolymers; celluloses, including ethylcelluloses, methylcelluloses, hydroxymethylcelluloses, hydroxypropylcelluloses and carboxymethylcellulose; polyvinylpyrolidones; polysaccharides, including starch,

modified starch, dextrins, maltodextrins, alginate and chitosans; fats; oils; proteins, including gelatin and zeins; gum arabics; shellacs; vinylidene chloride and vinylidene chloride copolymers; calcium lignosulfonates; acrylic copolymers; polyvinylacrylates; polyethylene oxide; acrylamide polymers and copolymers; polyhydroxyethyl acrylate, methylacrylamide monomers; and polychloroprene.

[0286] Any of a variety of colorants may be employed, including organic chromophores classified as nitroso; nitro; azo, including monoazo, bisazo and polyazo; acridine, anthraquinone, azine, diphenylmethane, indamine, indophenol, methine, oxazine, phthalocyanine, thiazine, thiazole, triarylmethane, xanthene. Other additives that can be added include trace nutrients such as salts of iron, manganese, boron, copper, cobalt, molybdenum and zinc.

[0287] A polymer or other dust control agent can be applied to retain the treatment on the seed surface.

[0288] In some specific embodiments, in addition to the microbial cells or spores, the coating can further comprise a layer of adherent. The adherent should be non-toxic, biodegradable, and adhesive. Examples of such materials include, but are not limited to, polyvinyl acetates; polyvinyl acetate copolymers; polyvinyl alcohols; polyvinyl alcohol copolymers; celluloses, such as methyl celluloses, hydroxymethyl celluloses, and hydroxymethyl propyl celluloses; dextrins; alginates; sugars; molasses; polyvinyl pyrrolidones; polysaccharides; proteins; fats; oils; gum arabics; gelatins; syrups; and starches. More examples can be found in, for example, U.S. Pat. No. 7,213,367, incorporated herein by reference.

[0289] Various additives, such as adherents, dispersants, surfactants, and nutrient and buffer ingredients, can also be included in the seed treatment formulation. Other conventional seed treatment additives include, but are not limited to: coating agents, wetting agents, buffering agents, and polysaccharides. At least one agriculturally acceptable carrier can be added to the seed treatment formulation such as water, solids, or dry powders. The dry powders can be derived from a variety of materials such as calcium carbonate, gypsum, vermiculite, talc, humus, activated charcoal, and various phosphorous compounds.

[0290] In some embodiments, the seed coating composition can comprise at least one filler, which is an organic or inorganic, natural or synthetic component with

which the active components are combined to facilitate its application onto the seed. In aspects, the filler is an inert solid such as clays, natural or synthetic silicates, silica, resins, waxes, solid fertilizers (for example ammonium salts), natural soil minerals, such as kaolins, clays, talc, lime, quartz, attapulgite, montmorillonite, bentonite or diatomaceous earths, or synthetic minerals, such as silica, alumina or silicates, in particular aluminium or magnesium silicates.

[0291] In some embodiments, the seed treatment formulation may further include one or more of the following ingredients: other pesticides, including compounds that act only below the ground; fungicides, such as captan, thiram, metalaxyl, fludioxonil, oxadixyl, and isomers of each of those materials, and the like; herbicides, including compounds selected from glyphosate, carbamates, thiocarbamates, acetamides, triazines, dinitroanilines, glycerol ethers, pyridazinones, uracils, phenoxys, ureas, and benzoic acids; herbicidal safeners such as benzoxazine, benzhydryl derivatives, N,N-diallyl dichloroacetamide, various dihaloacyl, oxazolidinyl and thiazolidinyl compounds, ethanone, naphthalic anhydride compounds, and oxime derivatives; chemical fertilizers; biological fertilizers; and biocontrol agents such as other naturally-occurring or recombinant bacteria and fungi from the genera *Rhizobium, Bacillus, Pseudomonas, Serratia, Trichoderma, Glomus, Gliocladium* and mycorrhizal fungi. These ingredients may be added as a separate layer on the seed, or alternatively may be added as part of the seed coating composition of the disclosure.

[0292] In some embodiments, the formulation that is used to treat the seed in the present disclosure can be in the form of a suspension; emulsion; slurry of particles in an aqueous medium (*e.g.*, water); wettable powder; wettable granules (dry flowable); and dry granules. If formulated as a suspension or slurry, the concentration of the active ingredient in the formulation can be about 0.5% to about 99% by weight (w/w), or 5-40%, or as otherwise formulated by those skilled in the art.

[0293] As mentioned above, other conventional inactive or inert ingredients can be incorporated into the formulation. Such inert ingredients include, but are not limited to: conventional sticking agents; dispersing agents such as methylcellulose, for example, serve as combined dispersant/sticking agents for use in seed treatments; polyvinyl alcohol; lecithin, polymeric dispersants (*e.g.*, polyvinylpyrrolidone/vinyl acetate); thickeners (*e.g.*, clay thickeners to improve viscosity and reduce settling of particle suspensions); emulsion stabilizers; surfactants; antifreeze compounds (*e.g.*,

urea), dyes, colorants, and the like. Further inert ingredients useful in the present disclosure can be found in McCutcheon's, vol. 1, "Emulsifiers and Detergents," MC Publishing Company, Glen Rock, N.J., U.S.A., 1996, incorporated by reference herein.

[0294] The seed coating formulations of the present disclosure can be applied to seeds by a variety of methods, including, but not limited to: mixing in a container (*e.g.*, a bottle or bag), mechanical application, tumbling, spraying, and immersion. A variety of active or inert material can be used for contacting seeds with microbial compositions according to the present disclosure.

[0295] In some embodiments, the amount of the microbes or agricultural composition that is used for the treatment of the seed will vary depending upon the type of seed and the type of active ingredients, but the treatment will comprise contacting the seeds with an agriculturally effective amount of the inventive composition.

[0296] As discussed above, an effective amount means that amount of the inventive composition that is sufficient to affect beneficial or desired results. An effective amount can be administered in one or more administrations.

[0297] In some embodiments, in addition to the coating layer, the seed may be treated with one or more of the following ingredients: other pesticides including fungicides and herbicides; herbicidal safeners; fertilizers and/or biocontrol agents. These ingredients may be added as a separate layer or alternatively may be added in the coating layer.

[0298] In some embodiments, the seed coating formulations of the present disclosure may be applied to the seeds using a variety of techniques and machines, such as fluidized bed techniques, the roller mill method, rotostatic seed treaters, and drum coaters. Other methods, such as spouted beds may also be useful. The seeds may be pre-sized before coating. After coating, the seeds are typically dried and then transferred to a sizing machine for sizing. Such procedures are known in the art.

[0299] In some embodiments, the microorganism-treated seeds may also be enveloped with a film overcoating to protect the coating. Such overcoatings are known in the art and may be applied using fluidized bed and drum film coating techniques.

[0300] In other embodiments of the present disclosure, compositions according to the present disclosure can be introduced onto a seed by use of solid matrix priming. For example, a quantity of an inventive composition can be mixed with a solid matrix material and then the seed can be placed into contact with the solid matrix material for a period to allow the composition to be introduced to the seed. The seed can then optionally be separated from the solid matrix material and stored or used, or the mixture of solid matrix material plus seed can be stored or planted directly. Solid matrix materials which are useful in the present disclosure include polyacrylamide, starch, clay, silica, alumina, soil, sand, polyurea, polyacrylate, or any other material capable of absorbing or adsorbing the inventive composition for a time and releasing that composition into or onto the seed. It is useful to make sure that the inventive composition and the solid matrix material are compatible with each other. For example, the solid matrix material should be chosen so that it can release the composition at a reasonable rate, for example over a period of minutes, hours, or days.

Microorganisms

[0301] As used herein the term "microorganism" should be taken broadly. It includes, but is not limited to, the two prokaryotic domains, Bacteria and Archaea, as well as eukaryotic fungi and protists.

[0302] By way of example, the microorganisms may include: Proteobacteria (such as *Pseudomonas, Enterobacter, Stenotrophomonas, Burkholderia, Rhizobium, Herbaspirillum, Pantoea, Serratia, Rahnella, Azospirillum, Azorhizobium, Azotobacter, Duganella, Delftia, Bradyrhizobiun, Sinorhizobium* and *Halomonas),* Firmicutes (such as *Bacillus, Paenibacillus, Lactobacillus, Mycoplasma,* and *Acetobacterium*), Actinobacteria (such as *Brevibacterium*, *Janibacter*, *Streptomyces, Rhodococcus, Microbacterium,* and *Curtobacterium),* and the fungi Ascomycota (such as *Trichoderma, Ampelomyces, Coniothyrium, Paecoelomyces, Penicillium, Cladosporium, Hypocrea, Beauveria, Metarhizium, Verticullium, Cordyceps, Pichea,* and *Candida,* Basidiomycota (such as *Coprinus, Corticium,* and *Agaricus)* and Oomycota (such as *Pythium, Mucor,* and *Mortierella).*

[0303] In a particular embodiment, the microorganism is an endophyte, or an epiphyte, or a microorganism inhabiting the plant rhizosphere or rhizosheath. That is, the microorganism may be found present in the soil material adhered to the roots of a

plant or in the area immediately adjacent a plant's roots. In one embodiment, the microorganism is a seed-borne endophyte.

[0304] Endophytes may benefit host plants by preventing pathogenic organisms from colonizing them. Extensive colonization of the plant tissue by endophytes creates a "barrier effect," where the local endophytes outcompete and prevent pathogenic organisms from taking hold. Endophytes may also produce chemicals which inhibit the growth of competitors, including pathogenic organisms.

[0305] In certain embodiments, the microorganism is unculturable. This should be taken to mean that the microorganism is not known to be culturable or is difficult to culture using methods known to one skilled in the art.

[0306] Microorganisms of the present disclosure may be collected or obtained from any source or contained within and/or associated with material collected from any source.

[0307] In an embodiment, the microorganisms are obtained from any general terrestrial environment, including its soils, plants, fungi, animals (including invertebrates) and other biota, including the sediments, water and biota of lakes and rivers; from the marine environment, its biota and sediments (for example sea water, marine muds, marine plants, marine invertebrates (for example sponges), marine vertebrates (for example, fish)); the terrestrial and marine geosphere (regolith and rock, for example crushed subterranean rocks, sand and clays); the cryosphere and its meltwater; the atmosphere (for example, filtered aerial dusts, cloud and rain droplets); urban, industrial and other man-made environments (for example, accumulated organic and mineral matter on concrete, roadside gutters, roof surfaces, road surfaces).

[0308] In another embodiment the microorganisms are collected from a source likely to favor the selection of appropriate microorganisms. By way of example, the source may be a particular environment in which it is desirable for other plants to grow, or which is thought to be associated with terroir. In another example, the source may be a plant having one or more desirable traits, for example a plant which naturally grows in a particular environment or under certain conditions of interest. By way of example, a certain plant may naturally grow in sandy soil or sand of high salinity, or under extreme temperatures, or with little water, or it may be resistant to

certain pests or disease present in the environment, and it may be desirable for a commercial crop to be grown in such conditions, particularly if they are, for example, the only conditions available in a particular geographic location. By way of further example, the microorganisms may be collected from commercial crops grown in such environments, or more specifically from individual crop plants best displaying a trait of interest amongst a crop grown in any specific environment, for example the fastest-growing plants amongst a crop grown in saline-limiting soils, or the least damaged plants in crops exposed to severe insect damage or disease epidemic, or plants having desired quantities of certain metabolites and other compounds, including fiber content, oil content, and the like, or plants displaying desirable colors, taste, or smell. The microorganisms may be collected from a plant of interest or any material occurring in the environment of interest, including fungi and other animal and plant biota, soil, water, sediments, and other elements of the environment as referred to previously. In certain embodiments, the microorganisms are individual isolates separated from different environments.

[0309] In one embodiment, a microorganism or a combination of microorganisms, of use in the methods of the disclosure may be selected from a pre-existing collection of individual microbial species or strains based on some knowledge of their likely or predicted benefit to a plant. For example, the microorganism may be predicted to: improve nitrogen fixation; release phosphate from the soil organic matter; release phosphate from the inorganic forms of phosphate (*e.g.* rock phosphate); "fix carbon" in the root microsphere; live in the rhizosphere of the plant thereby assisting the plant in absorbing nutrients from the surrounding soil and then providing these more readily to the plant; increase the number of nodules on the plant roots and thereby increase the number of symbiotic nitrogen fixing bacteria (*e.g. Rhizobium* species) per plant and the amount of nitrogen fixed by the plant; elicit plant defensive responses such as ISR (induced systemic resistance) or SAR (systemic acquired resistance) which help the plant resist the invasion and spread of pathogenic microorganisms; compete with microorganisms deleterious to plant growth or health by antagonism, or competitive utilization of resources such as nutrients or space; change the color of one or more part of the plant, or change the chemical profile of the plant, its smell, taste or one or more other quality.

[0310] In one embodiment a microorganism or combination of microorganisms is selected from a pre-existing collection of individual microbial species or strains that provides no knowledge of their likely or predicted benefit to a plant. For example, a collection of unidentified microorganisms isolated from plant tissues without any knowledge of their ability to improve plant growth or health, or a collection of microorganisms collected to explore their potential for producing compounds that could lead to the development of pharmaceutical drugs.

[0311] In one embodiment, the microorganisms are acquired from the source material (for example, soil, rock, water, air, dust, plant or other organism) in which they naturally reside. The microorganisms may be provided in any appropriate form, having regard to its intended use in the methods of the disclosure. However, by way of example only, the microorganisms may be provided as an aqueous suspension, gel, homogenate, granule, powder, slurry, live organism or dried material.

[0312] The microorganisms of the disclosure may be isolated in substantially pure or mixed cultures. They may be concentrated, diluted, or provided in the natural concentrations in which they are found in the source material. For example, microorganisms from saline sediments may be isolated for use in this disclosure by suspending the sediment in fresh water and allowing the sediment to fall to the bottom. The water containing the bulk of the microorganisms may be removed by decantation after a suitable period of settling and either applied directly to the plant growth medium, or concentrated by filtering or centrifugation, diluted to an appropriate concentration and applied to the plant growth medium with the bulk of the salt removed. By way of further example, microorganisms from mineralized or toxic sources may be similarly treated to recover the microbes for application to the plant growth material to minimize the potential for damage to the plant.

[0313] In another embodiment, the microorganisms are used in a crude form, in which they are not isolated from the source material in which they naturally reside. For example, the microorganisms are provided in combination with the source material in which they reside; for example, as soil, or the roots, seed or foliage of a plant. In this embodiment, the source material may include one or more species of microorganisms.

[0314] In some embodiments, a mixed population of microorganisms is used in the methods of the disclosure.

[0315] In embodiments of the disclosure where the microorganisms are isolated from a source material (for example, the material in which they naturally reside), any one or a combination of a number of standard techniques which will be readily known to skilled persons may be used. However, by way of example, these in general employ processes by which a solid or liquid culture of a single microorganism can be obtained in a substantially pure form, usually by physical separation on the surface of a solid microbial growth medium or by volumetric dilutive isolation into a liquid microbial growth medium. These processes may include isolation from dry material, liquid suspension, slurries or homogenates in which the material is spread in a thin layer over an appropriate solid gel growth medium, or serial dilutions of the material made into a sterile medium and inoculated into liquid or solid culture media.

[0316] Whilst not essential, in one embodiment, the material containing the microorganisms may be pre-treated prior to the isolation process in order to either multiply all microorganisms in the material, or select portions of the microbial population, either by enriching the material with microbial nutrients (for example, by pasteurizing the sample to select for microorganisms resistant to heat exposure (for example, bacilli), or by exposing the sample to low concentrations of an organic solvent or sterilant (for example, household bleach) to enhance the survival of spore-forming or solvent-resistant microorganisms). Microorganisms can then be isolated from the enriched materials or materials treated for selective survival, as above.

[0317] In an embodiment of the disclosure, endophytic or epiphytic microorganisms are isolated from plant material. Any number of standard techniques known in the art may be used and the microorganisms may be isolated from any appropriate tissue in the plant, including for example root, stem and leaves, and plant reproductive tissues. By way of example, conventional methods for isolation from plants typically include the sterile excision of the plant material of interest (*e.g.* root or stem lengths, leaves), surface sterilization with an appropriate solution (*e.g.* 2% sodium hypochlorite), after which the plant material is placed on nutrient medium for microbial growth (See, for example, Strobel G and Daisy B (2003) Microbiology and Molecular Biology Reviews 67 (4): 491-502; Zinniel DK *et al.*(2002) Applied and Environmental Microbiology 68 (5): 2198-2208).

[0318] In one embodiment of the disclosure, the microorganisms are isolated from root tissue. Further methodology for isolating microorganisms from plant material are detailed hereinafter.

[0319] In one embodiment, the microbial population is exposed (prior to the method or at any stage of the method) to a selective pressure. For example, exposure of the microorganisms to pasteurisation before their addition to a plant growth medium (preferably sterile) is likely to enhance the probability that the plants selected for a desired trait will be associated with spore-forming microbes that can more easily survive in adverse conditions, in commercial storage, or if applied to seed as a coating, in an adverse environment.

[0320] In certain embodiments, as mentioned herein before, the microorganism(s) may be used in crude form and need not be isolated from a plant or a media. For example, plant material or growth media which includes the microorganisms identified to be of benefit to a selected plant may be obtained and used as a crude source of microorganisms for the next round of the method or as a crude source of microorganisms at the conclusion of the method. For example, whole plant material could be obtained and optionally processed, such as mulched or crushed. Alternatively, individual tissues or parts of selected plants (such as leaves, stems, roots, and seeds) may be separated from the plant and optionally processed, such as mulched or crushed. In certain embodiments, one or more part of a plant which is associated with the second set of one or more microorganisms may be removed from one or more selected plants and, where any successive repeat of the method is to be conducted, grafted on to one or more plant used in any step of the plant breeding methods.

Plants That Are Able to Benefit from the Application of the Disclosed Microbes, Consortia, and Compositions Comprising the Same

[0321] Any number of a variety of different plants, including mosses and lichens and algae, may be used in the methods of the disclosure. In embodiments, the plants have economic, social, or environmental value. For example, the plants may include those used as: food crops, fiber crops, oil crops, in the forestry industry, in the pulp and paper industry, as a feedstock for biofuel production, and as ornamental plants.

[0322] In other embodiments, the plants may be economically, socially, or environmentally undesirable, such as weeds. The following is a list of non-limiting examples of the types of plants the methods of the disclosure may be applied to:

Food crops:

[0323] *Cereals e.g* maize, rice, wheat, barley, sorghum, millet, oats, rye, triticale, and buckwheat;

[0324] *Leafy vegetables e.g.* brassicaceous plants such as cabbages, broccoli, bok choy, rocket; salad greens such as spinach, cress, and lettuce;

[0325] *Fruiting and flowering vegetables e.g.* avocado, sweet corn, artichokes; curcubits *e.g.* squash, cucumbers, melons, courgettes, pumpkins; solanaceous vegetables/fruits *e.g.* tomatoes, eggplant, and capsicums;

[0326] *Podded vegetables e.g.* groundnuts, peanuts, peas, soybeans, beans, lentils, chickpea, okra;

[0327] *Bulbed and stem vegetables e.g.* asparagus, celery, *Allium* crops e.g garlic, onions, and leeks;

[0328] *Roots and tuberous vegetables e.g.* carrots, beet, bamboo shoots, cassava, yams, ginger, Jerusalem artichoke, parsnips, radishes, potatoes, sweet potatoes, taro, turnip, and wasabi;

[0329] Sugar crops including sugar beet (*Beta vulgaris*), sugar cane (*Saccharum officinarum*);

[0330] Crops grown for the production of non-alcoholic beverages and stimulants *e.g.* coffee, black, herbal, and green teas, cocoa, marijuana, and tobacco;

[0331] *Fruit crops* such as true berry fruits (*e.g.* kiwifruit, grape, currants, gooseberry, guava, feijoa, pomegranate), citrus fruits (*e.g.* oranges, lemons, limes, grapefruit), epigynous fruits (*e.g.* bananas, cranberries, blueberries), aggregate fruit (blackberry, raspberry, boysenberry), multiple fruits (*e.g.* pineapple, fig), stone fruit crops (*e.g.* apricot, peach, cherry, plum), pip-fruit (*e.g.* apples, pears) and others such as strawberries, sunflower seeds;

[0332] *Culinary and medicinal herbs e.g.* rosemary, basil, bay laurel, coriander, mint, dill, *Hypericum,* foxglove, alovera, rosehips, and cannabis;

[0333] *Crop plants producing spices e.g.* black pepper, cumin cinnamon, nutmeg, ginger, cloves, saffron, cardamom, mace, paprika, masalas, star anise;

[0334] *Crops grown for the production of nuts e.g.* almonds and walnuts, Brazil nut, cashew nuts, coconuts, chestnut, macadamia nut, pistachio nuts; peanuts, pecan nuts;

[0335] Crops grown for production of beers, wines and other alcoholic beverages *e.g* grapes, and hops;

[0336] *Oilseed crops e.g.* soybean, peanuts, cotton, olives, sunflower, sesame, lupin species and brassicaeous crops (*e.g.* canola/oilseed rape); and, *edible fungi e.g.* white mushrooms, Shiitake and oyster mushrooms;

Plants used in pastoral agriculture:

[0337] *Legumes: Trifolium* species, *Medicago* species, and *Lotus* species; White clover *(T.repens);* Red clover *(T. pratense);* Caucasian clover *(T. ambigum);* subterranean clover *(T.subterraneum);* Alfalfa/Lucerne *(Medicago sativum);* annual medics; barrel medic; black medic; Sainfoin *(Onobrychis viciifolia);* Birdsfoot trefoil *(Lotus corniculatus);* Greater Birdsfoot trefoil *(Lotus pedunculatus);*

[0338] Seed legumes/pulses including Peas (*Pisum sativum*), Common bean (*Phaseolus vulgaris*), Broad beans (*Vicia faba*), Mung bean (*Vigna radiata*), Cowpea (*Vigna unguiculata*), Chick pea (*Cicer arietum*), Lupins (*Lupinus species*); Cereals including Maize/com (*Zea mays*), Sorghum (*Sorghum spp.*), Millet (*Panicum miliaceum, P. sumatrense*), Rice (*Oryza sativa indica, Oryza sativa japonica*), Wheat (*Triticum aestivum*), Barley (*Hordeum vulgare*), Rye (*Secale cereale*), Triticale (*Triticum X Secale*), Oats (*Avena sativa*);

[0339] Forage and Amenity grasses: Temperate grasses such as *Lolium* species; *Festuca* species; *Agrostis* spp., Perennial ryegrass (*Lolium perenne*); hybrid ryegrass (*Lolium hybridum*); annual ryegrass (*Lolium multiflorum*), tall fescue (*Festuca arundinacea*); meadow fescue (*Festuca pratensis*); red fescue (*Festuca rubra*); *Festuca ovina*; *Festuloliums* (*Lolium X Festuca crosses*); Cocksfoot (*Dactylis glomerata*); Kentucky bluegrass *Poa pratensis*; *Poa palustris*; *Poa nemoralis*; *Poa trivialis*; *Poa compresa*; *Bromus* species; *Phalaris* (*Phleum* species); *Arrhenatherum elatius*; *Agropyron* species; *Avena strigosa*; *Setaria italic*;

[0340] *Tropical grasses* such as: *Phalaris* species; *Brachiaria* species; *Eragrostis* species; *Panicum* species; Bahai grass *(Paspalum notatum); Brachypodium* species; and, grasses used for biofuel production such as Switchgrass *(Panicum virgatum)* and *Miscanthus* species;

Fiber crops:

[0341] Cotton, hemp, jute, coconut, sisal, flax (*Linum* spp.), New Zealand flax (*Phormium* spp.); plantation and natural forest species harvested for paper and engineered wood fiber products such as coniferous and broadleafed forest species;

Tree and shrub species used in plantation forestry and bio-fuel crops:

[0342] Pine *(Pinus* species); Fir *(Pseudotsuga* species); Spruce *(Picea* species); Cypress *(Cupressus* species); Wattle *(Acacia* species); Alder *(Alnus* species); Oak species *(Quercus* species); Redwood *(Sequoiadendron* species); willow *(Salix* species); birch *(Betula* species); Cedar *(Cedurus* species); Ash *(Fraxinus* species); Larch *(Larix* species); *Eucalyptus* species; Bamboo (*Bambuseae* species) and Poplars *(Populus* species).

Plants grown for conversion to energy, biofuels or industrial products by extractive. biological. physical or biochemical treatment:

[0343] Oil-producing plants such as oil palm, jatropha, soybean, cotton, linseed; Latex-producing plants such as the Para Rubber tree, *Hevea brasiliensis* and the Panama Rubber Tree *Castilla elastica;* plants used as direct or indirect feedstocks for the production of biofuels *i.e.* after chemical, physical (*e.g.* thermal or catalytic) or biochemical (*e.g.* enzymatic pre-treatment) or biological (*e.g.* microbial fermentation) transformation during the production of biofuels, industrial solvents or chemical products *e.g.* ethanol or butanol, propane dials, or other fuel or industrial material including sugar crops (*e.g.* beet, sugar cane), starch producing crops (*e.g.* C3 and C4 cereal crops and tuberous crops), cellulosic crops such as forest trees (*e.g.* Pines, Eucalypts) and Graminaceous and Poaceous plants such as bamboo, switch grass, miscanthus; crops used in energy, biofuel or industrial chemical production via gasification and/or microbial or catalytic conversion of the gas to biofuels or other industrial raw materials such as solvents or plastics, with or without the production of biochar (*e.g.* biomass crops such as coniferous, eucalypt, tropical or broadleaf forest trees, graminaceous and poaceous crops such as bamboo, switch grass, miscanthus,

sugar cane, or hemp or softwoods such as poplars, willows; and, biomass crops used in the production of biochar;

Crops producing natural products useful for the pharmaceutical. Agricultural nutraceutical and cosmeceutical industries:

[0344] Crops producing pharmaceutical precursors or compounds or nutraceutical and cosmeceutical compounds and materials for example, star anise (shikimic acid), Japanese knotweed (resveratrol), kiwifruit (soluble fiber, proteolytic enzymes);

Floricultural, Ornamental and Amenity plants grown for their aesthetic or environmental properties:

[0345] Flowers such as roses, tulips, chrysanthemums;

[0346] Ornamental shrubs such as Buxus, Hebe, Rosa, Rhododendron, Hedera

[0347] Amenity plants such as Platanus, Choisya, Escallonia, Euphorbia, Carex

[0348] Mosses such as sphagnum moss

Plants grown for bioremediation:

[0349] Helianthus, Brassica, Salix, Populus, Eucalyptus

Hybrid and GM Plant Improvement

[0350] In certain aspects, the microbes of the present disclosure are applied to hybrid plants to increase beneficial traits of said hybrids. In other aspects, the microbes of the present disclosure are applied to genetically modified plants to increase beneficial traits of said GM plants. The microbes taught herein are able to be applied to hybrids and GM plants and thus maximize the elite genetics and trait technologies of these plants.

[0351] It should be appreciated that a plant may be provided in the form of a seed, seedling, cutting, propagule, or any other plant material or tissue capable of growing. In one embodiment the seed may be surface-sterilised with a material such as sodium hypochlorite or mercuric chloride to remove surface-contaminating microorganisms. In one embodiment, the propagule is grown in axenic culture before being placed in the plant growth medium, for example as sterile plantlets in tissue culture.

Methods of Application

[0352] The microorganisms may be applied to a plant, seedling, cutting, propagule, or the like and/or the growth medium containing said plant, using any appropriate technique known in the art.

[0353] However, by way of example, an isolated microbe, consortia, or composition comprising the same may be applied to a plant, seedling, cutting, propagule, or the like, by spraying or dusting.

[0354] In another embodiment, the isolated microbe, consortia, or composition comprising the same may applied directly to a plant seed prior to sowing.

[0355] In another embodiment, the isolated microbe, consortia, or composition comprising the same may applied directly to a plant seed, as a seed coating.

[0356] In one embodiment of the present disclosure, the isolated microbe, consortia, or composition comprising the same is supplied in the form of granules, or plug, or soil drench that is applied to the plant growth media.

[0357] In other embodiments, the the isolated microbe, consortia, or composition comprising the same are supplied in the form of a foliar application, such as a foliar spray or liquid composition. The foliar spray or liquid application may be applied to a growing plant or to a growth media, *e.g.* soil.

[0358] In another embodiment, the isolated microbe, consortia, or composition comprising the same may be formulated into granules and applied alongside seeds during planting. Or the granules may be applied after planting. Or the granules may be applied before planting.

[0359] In some embodiments, the isolated microbe, consortia, or composition comprising the same are administered to a plant or growth media as a topical application and/or drench application to improve crop growth, yield, and quality. The topical application may be via utilization of a dry mix or powder or dusting composition or may be a liquid based formulation.

[0360] In embodiments, the the isolated microbe, consortia, or composition comprising the same can be formulated as: (1) solutions; (2) wettable powders; (3) dusting powders; (4) soluble powders; (5) emulsions or suspension concentrates; (6) seed dressings or coatings, (7) tablets; (8) water-dispersible granules; (9) water soluble granules (slow or fast release); (10) microencapsulated granules or

suspensions; and (11) as irrigation components, among others. In in certain aspects, the compositions may be diluted in an aqueous medium prior to conventional spray application. The compositions of the present disclosure can be applied to the soil, plant, seed, rhizosphere, rhizosheath, or other area to which it would be beneficial to apply the microbial compositions. Further still, ballistic methods can be utilized as a means for introducing endophytic microbes.

[0361] In aspects, the compositions are applied to the foliage of plants. The compositions may be applied to the foliage of plants in the form of an emulsion or suspension concentrate, liquid solution, or foliar spray. The application of the compositions may occur in a laboratory, growth chamber, greenhouse, or in the field.

[0362] In another embodiment, microorganisms may be inoculated into a plant by cutting the roots or stems and exposing the plant surface to the microorganisms by spraying, dipping, or otherwise applying a liquid microbial suspension, or gel, or powder.

[0363] In another embodiment, the microorganisms may be injected directly into foliar or root tissue, or otherwise inoculated directly into or onto a foliar or root cut, or else into an excised embryo, or radicle, or coleoptile. These inoculated plants may then be further exposed to a growth media containing further microorganisms; however, this is not necessary.

[0364] In other embodiments, particularly where the microorganisms are unculturable, the microorganisms may be transferred to a plant by any one or a combination of grafting, insertion of explants, aspiration, electroporation, wounding, root pruning, induction of stomatal opening, or any physical, chemical or biological treatment that provides the opportunity for microbes to enter plant cells or the intercellular space. Persons of skill in the art may readily appreciate a number of alternative techniques that may be used.

[0365] In one embodiment, the microorganisms infiltrate parts of the plant such as the roots, stems, leaves and/or reproductive plant parts (become endophytic), and/or grow upon the surface of roots, stems, leaves and/or reproductive plant parts (become epiphytic) and/or grow in the plant rhizosphere. In one embodiment, the microorganisms form a symbiotic relationship with the plant.

EXAMPLES

I. Increased Yield in Agriculturally Important Crops

[0366] In certain embodiments of the disclosure, the present methods aim to increase the yields for a given crop.

[0367] The methodologies presented herein—based upon utilizing the disclosed isolated microbes, consortia, and compositions comprising the same—have the potential to increase the yield of important agricultural crops. These yield increases can be realized without the need for further fertilizer addition.

Example 1: Increasing Ryegrass Biomass with Isolated Microbes and Microbial Consortia

A. Seed Treatment with Isolated Microbe

[0368] In this example, an isolated microbe from **Tables 1-4** will be applied as a seed coating to seeds of ryegrass (*Lolium perenne*). Upon applying the isolated microbe as a seed coating, the ryegrass will be planted and cultivated in the standard manner.

[0369] A control plot of ryegrass seeds, which did not have the isolated microbe applied as a seed coating, will also be planted.

[0370] It is expected that the ryegrass plants grown from the seeds treated with the seed coating will exhibit a quantifiably higher biomass than the control ryegrass plants.

[0371] The biomass from the treated plants may be about 1-10% higher, 10-20% higher, 20-30% higher, 30-40% higher, 40-50% higher, 50-60% higher, 60-70% higher, 70-80% higher, 80-90% higher, or more.

[0372] The biomass from the treated plants may equate to about a 1 bushel per acre increase over the controls, or a 2 bushel per acre increase, or a 3 bushel per acre increase, or a 4 bushel per acre increase, or a 5 bushel per acre increase, or more.

[0373] In some aspects, the biomass increase is statistically significant. In other aspects, the biomass increase is not statistically significant, but is still quantifiable.

B. Seed Treatment with Microbial Consortia

[0374] In this example, a microbial consortium, comprising at least two microbes from **Tables 1-4** will be applied as a seed coating to seeds of ryegrass (*Lolium*

perenne). Upon applying the microbial consortium as a seed coating, the ryegrass will be planted and cultivated in the standard manner.

[0375] A control plot of ryegrass seeds, which did not have the microbial consortium applied as a seed coating, will also be planted.

[0376] It is expected that the ryegrass plants grown from the seeds treated with the seed coating will exhibit a quantifiably higher biomass than the control ryegrass plants.

[0377] The biomass from the treated plants may be about 1-10% higher, 10-20% higher, 20-30% higher, 30-40% higher, 40-50% higher, 50-60% higher, 60-70% higher, 70-80% higher, 80-90% higher, or more.

[0378] The biomass from the treated plants may equate to about a 1 bushel per acre increase over the controls, or a 2 bushel per acre increase, or a 3 bushel per acre increase, or a 4 bushel per acre increase, or a 5 bushel per acre increase, or more.

[0379] In some aspects, the biomass increase is statistically significant. In other aspects, the biomass increase is not statistically significant, but is still quantifiable.

C. Treatment with Agricultural Composition Comprising Isolated Microbe

[0380] In this example, an isolated microbe from **Tables 1-4** will be applied as an agricultural composition, administered to the ryegrass seed at the time of sowing.

[0381] For example, it is anticipated that a farmer will apply the agricultural composition to the ryegrass seeds simultaneously upon broadcasting said seeds into the field. This can be accomplished, for example, by applying the agricultural composition to a hopper or spreader, which contains the ryegrass seeds and which is configured to broadcast the same.

[0382] A control plot of ryegrass seeds, which are not administered the agricultural composition, will also be planted.

[0383] It is expected that the ryegrass plants grown from the seeds treated with the agricultural composition will exhibit a quantifiably higher biomass than the control ryegrass plants.

[0384] The biomass from the treated plants may be about 1-10% higher, 10-20% higher, 20-30% higher, 30-40% higher, 40-50% higher, 50-60% higher, 60-70% higher, 70-80% higher, 80-90% higher, or more.

[0385] The biomass from the treated plants may equate to about a 1 bushel per acre increase over the controls, or a 2 bushel per acre increase, or a 3 bushel per acre increase, or a 4 bushel per acre increase, or a 5 bushel per acre increase, or more.

[0386] In some aspects, the biomass increase is statistically significant. In other aspects, the biomass increase is not statistically significant, but is still quantifiable.

D. Treatment with Agricultural Composition Comprising Microbial Consortia

[0387] In this example, a microbial consortium, comprising at least two microbes from **Tables 1-4** will be applied as an agricultural composition, administered to the ryegrass seed at the time of sowing.

[0388] For example, it is anticipated that a farmer will apply the agricultural composition to the ryegrass seeds simultaneously upon broadcasting said seeds into the field. This can be accomplished, for example, by applying the agricultural composition to a hopper or spreader, which contains the ryegrass seeds and which is configured to broadcast the same.

[0389] A control plot of ryegrass seeds, which are not administered the agricultural composition, will also be planted.

[0390] It is expected that the ryegrass plants grown from the seeds treated with the agricultural composition will exhibit a quantifiably higher biomass than the control ryegrass plants.

[0391] The biomass from the treated plants may be about 1-10% higher, 10-20% higher, 20-30% higher, 30-40% higher, 40-50% higher, 50-60% higher, 60-70% higher, 70-80% higher, 80-90% higher, or more.

[0392] The biomass from the treated plants may equate to about a 1 bushel per acre increase over the controls, or a 2 bushel per acre increase, or a 3 bushel per acre increase, or a 4 bushel per acre increase, or a 5 bushel per acre increase, or more.

[0393] In some aspects, the biomass increase is statistically significant. In other aspects, the biomass increase is not statistically significant, but is still quantifiable.

Example 2: Increasing Maize Biomass with Isolated Microbes and Microbial Consortia

A. Seed Treatment with Isolated Microbe

[0394] In this example, an isolated microbe from **Tables 1-4** will be applied as a seed coating to seeds of corn (*Zea mays*). Upon applying the isolated microbe as a seed coating, the corn will be planted and cultivated in the standard manner.

[0395] A control plot of corn seeds, which did not have the isolated microbe applied as a seed coating, will also be planted.

[0396] It is expected that the corn plants grown from the seeds treated with the seed coating will exhibit a quantifiably higher biomass than the control corn plants.

[0397] The biomass from the treated plants may be about 1-10% higher, 10-20% higher, 20-30% higher, 30-40% higher, 40-50% higher, 50-60% higher, 60-70% higher, 70-80% higher, 80-90% higher, or more.

[0398] The biomass from the treated plants may equate to about a 1 bushel per acre increase over the controls, or a 2 bushel per acre increase, or a 3 bushel per acre increase, or a 4 bushel per acre increase, or a 5 bushel per acre increase, or more.

[0399] In some aspects, the biomass increase is statistically significant. In other aspects, the biomass increase is not statistically significant, but is still quantifiable.

B. Seed Treatment with Microbial Consortia

[0400] In this example, a microbial consortium, comprising at least two microbes from **Tables 1-4** will be applied as a seed coating to seeds of corn (*Zea mays*). Upon applying the microbial consortium as a seed coating, the corn will be planted and cultivated in the standard manner.

[0401] A control plot of corn seeds, which did not have the microbial consortium applied as a seed coating, will also be planted.

[0402] It is expected that the corn plants grown from the seeds treated with the seed coating will exhibit a quantifiably higher biomass than the control corn plants.

[0403] The biomass from the treated plants may be about 1-10% higher, 10-20% higher, 20-30% higher, 30-40% higher, 40-50% higher, 50-60% higher, 60-70% higher, 70-80% higher, 80-90% higher, or more.

[0404] The biomass from the treated plants may equate to about a 1 bushel per acre increase over the controls, or a 2 bushel per acre increase, or a 3 bushel per acre increase, or a 4 bushel per acre increase, or a 5 bushel per acre increase, or more.

[0405] In some aspects, the biomass increase is statistically significant. In other aspects, the biomass increase is not statistically significant, but is still quantifiable.

C. Treatment with Agricultural Composition Comprising Isolated Microbe

[0406] In this example, an isolated microbe from **Tables 1-4** will be applied as an agricultural composition, administered to the corn seed at the time of sowing.

[0407] For example, it is anticipated that a farmer will apply the agricultural composition to the corn seeds simultaneously upon planting the seeds into the field. This can be accomplished, for example, by applying the agricultural composition to a hopper/bulk tank on a standard 16 row planter, which contains the corn seeds and which is configured to plant the same into rows. Alternatively, the agricultural composition can be contained in a separate bulk tank on the planter and sprayed into the rows upon planting the corn seed.

[0408] A control plot of corn seeds, which are not administered the agricultural composition, will also be planted.

[0409] It is expected that the corn plants grown from the seeds treated with the agricultural composition will exhibit a quantifiably higher biomass than the control corn plants.

[0410] The biomass from the treated plants may be about 1-10% higher, 10-20% higher, 20-30% higher, 30-40% higher, 40-50% higher, 50-60% higher, 60-70% higher, 70-80% higher, 80-90% higher, or more.

[0411] The biomass from the treated plants may equate to about a 1 bushel per acre increase over the controls, or a 2 bushel per acre increase, or a 3 bushel per acre increase, or a 4 bushel per acre increase, or a 5 bushel per acre increase, or more.

[0412] In some aspects, the biomass increase is statistically significant. In other aspects, the biomass increase is not statistically significant, but is still quantifiable.

D. Treatment with Agricultural Composition Comprising Microbial Consortia

[0413] In this example, a microbial consortium, comprising at least two microbes from **Tables 1-4** will be applied as an agricultural composition, administered to the corn seed at the time of sowing.

[0414] For example, it is anticipated that a farmer will apply the agricultural composition to the corn seeds simultaneously upon planting the seeds into the field. This can be accomplished, for example, by applying the agricultural composition to a hopper/bulk tank on a standard 16 row planter, which contains the corn seeds and which is configured to plant the same into rows. Alternatively, the agricultural composition can be contained in a separate bulk tank on the planter and sprayed into the rows upon planting the corn seed.

[0415] A control plot of corn seeds, which are not administered the agricultural composition, will also be planted.

[0416] It is expected that the corn plants grown from the seeds treated with the agricultural composition will exhibit a quantifiably higher biomass than the control corn plants.

[0417] The biomass from the treated plants may be about 1-10% higher, 10-20% higher, 20-30% higher, 30-40% higher, 40-50% higher, 50-60% higher, 60-70% higher, 70-80% higher, 80-90% higher, or more.

[0418] The biomass from the treated plants may equate to about a 1 bushel per acre increase over the controls, or a 2 bushel per acre increase, or a 3 bushel per acre increase, or a 4 bushel per acre increase, or a 5 bushel per acre increase, or more.

[0419] In some aspects, the biomass increase is statistically significant. In other aspects, the biomass increase is not statistically significant, but is still quantifiable.

Example 3: Increasing Soybean Biomass with Isolated Microbes and Microbial Consortia

A. Seed Treatment with Isolated Microbe

[0420] In this example, an isolated microbe from **Tables 1-4** will be applied as a seed coating to seeds of soybean (*Glycine max*). Upon applying the isolated microbe as a seed coating, the soybean will be planted and cultivated in the standard manner.

[0421] A control plot of soybean seeds, which did not have the isolated microbe applied as a seed coating, will also be planted.

[0422] It is expected that the soybean plants grown from the seeds treated with the seed coating will exhibit a quantifiably higher biomass than the control soybean plants.

[0423] The biomass from the treated plants may be about 1-10% higher, 10-20% higher, 20-30% higher, 30-40% higher, 40-50% higher, 50-60% higher, 60-70% higher, 70-80% higher, 80-90% higher, or more.

[0424] The biomass from the treated plants may equate to about a 1 bushel per acre increase over the controls, or a 2 bushel per acre increase, or a 3 bushel per acre increase, or a 4 bushel per acre increase, or a 5 bushel per acre increase, or more.

[0425] In some aspects, the biomass increase is statistically significant. In other aspects, the biomass increase is not statistically significant, but is still quantifiable.

B. Seed Treatment with Microbial Consortia

[0426] In this example, a microbial consortium, comprising at least two microbes from **Tables 1-4** will be applied as a seed coating to seeds of soybean (*Glycine max*). Upon applying the microbial consortium as a seed coating, the soybean will be planted and cultivated in the standard manner.

[0427] A control plot of soybean seeds, which did not have the microbial consortium applied as a seed coating, will also be planted.

[0428] It is expected that the soybean plants grown from the seeds treated with the seed coating will exhibit a quantifiably higher biomass than the control soybean plants.

[0429] The biomass from the treated plants may be about 1-10% higher, 10-20% higher, 20-30% higher, 30-40% higher, 40-50% higher, 50-60% higher, 60-70% higher, 70-80% higher, 80-90% higher, or more.

[0430] The biomass from the treated plants may equate to about a 1 bushel per acre increase over the controls, or a 2 bushel per acre increase, or a 3 bushel per acre increase, or a 4 bushel per acre increase, or a 5 bushel per acre increase, or more.

[0431] In some aspects, the biomass increase is statistically significant. In other aspects, the biomass increase is not statistically significant, but is still quantifiable.

C. Treatment with Agricultural Composition Comprising Isolated Microbe

[0432] In this example, an isolated microbe from **Tables 1-4** will be applied as an agricultural composition, administered to the soybean seed at the time of sowing.

[0433] For example, it is anticipated that a farmer will apply the agricultural composition to the soybean seeds simultaneously upon planting the seeds into the field. This can be accomplished, for example, by applying the agricultural composition to a hopper/bulk tank on a standard 16 row planter, which contains the soybean seeds and which is configured to plant the same into rows. Alternatively, the agricultural composition can be contained in a separate bulk tank on the planter and sprayed into the rows upon planting the soybean seed.

[0434] A control plot of soybean seeds, which are not administered the agricultural composition, will also be planted.

[0435] It is expected that the soybean plants grown from the seeds treated with the agricultural composition will exhibit a quantifiably higher biomass than the control soybean plants.

[0436] The biomass from the treated plants may be about 1-10% higher, 10-20% higher, 20-30% higher, 30-40% higher, 40-50% higher, 50-60% higher, 60-70% higher, 70-80% higher, 80-90% higher, or more.

[0437] The biomass from the treated plants may equate to about a 1 bushel per acre increase over the controls, or a 2 bushel per acre increase, or a 3 bushel per acre increase, or a 4 bushel per acre increase, or a 5 bushel per acre increase, or more.

[0438] In some aspects, the biomass increase is statistically significant. In other aspects, the biomass increase is not statistically significant, but is still quantifiable.

D. Treatment with Agricultural Composition Comprising Microbial Consortia

[0439] In this example, a microbial consortium, comprising at least two microbes from **Tables 1-4** will be applied as an agricultural composition, administered to the soybean seed at the time of sowing.

[0440] For example, it is anticipated that a farmer will apply the agricultural composition to the soybean seeds simultaneously upon planting the seeds into the field. This can be accomplished, for example, by applying the agricultural

composition to a hopper/bulk tank on a standard 16 row planter, which contains the soybean seeds and which is configured to plant the same into rows. Alternatively, the agricultural composition can be contained in a separate bulk tank on the planter and sprayed into the rows upon planting the soybean seed.

[0441] A control plot of soybean seeds, which are not administered the agricultural composition, will also be planted.

[0442] It is expected that the soybean plants grown from the seeds treated with the agricultural composition will exhibit a quantifiably higher biomass than the control soybean plants.

[0443] The biomass from the treated plants may be about 1-10% higher, 10-20% higher, 20-30% higher, 30-40% higher, 40-50% higher, 50-60% higher, 60-70% higher, 70-80% higher, 80-90% higher, or more.

[0444] The biomass from the treated plants may equate to about a 1 bushel per acre increase over the controls, or a 2 bushel per acre increase, or a 3 bushel per acre increase, or a 4 bushel per acre increase, or a 5 bushel per acre increase, or more.

[0445] In some aspects, the biomass increase is statistically significant. In other aspects, the biomass increase is not statistically significant, but is still quantifiable.

Example 4: Modifying Wheat Seedling Biomass with Isolated Microbes

A. Seed Treatment with Isolated Microbe

[0446] In this example, wheat seeds were inoculated with individual microbial strains (BCIs), and allowed to germinate (Figure 5).

[0447] The seeds were inoculated and placed on wet paper towels and rolled. The rolls were then incubated at 25°C in plastic bins covered with wet towels. Each strain appearing in Figure 5 was tested in triplicate, with 20 seeds per replicate test.

[0448] Total biomass was measured at seven days post treatment. An uninoculated 'water' control treatment was run and measured simultaneously. The solid line parallel to the x axis and bisecting the bars near the top of the y-axis of Figure 5 represents uninoculated control seeds. Some of the inoculated strains revealed relative increases in biomass at seven days post inoculation (DPI) compared to untreated control *in vitro*.

[0449] Table 12 provides a breakout of the biomass increase in wheat having been inoculated as described above, relative to a water-only treatment control (H2O) and an untreated (Unt) control. The two columns immediately to the right of the species reflect the percentage increase over control (%IOC) for the water-only treatment control and the untreated control. Both increases and decreases in the biomasses are reflected in the data of **Table 12**. A smaller plant reflects potential for in-field conservation of nutrients and water where these resources may be limited by drought or local conditions, thus decreases are hypothesized to be yield relevant.

[0450] The results demonstrated that ~19 strains caused a relative increase in total biomass of wheat at seven days post inoculation (DPI) compared to the water-only and untreated controls *in vitro*. Eight strains showed greater than a 5% increase over both controls, whereas 19 strains showed greater than a 5% decrease in biomass over the water control.

Table 12

Strain	Species	%IOC UNT	%IOC H2O	Strain	Species	%IOC UNT	% IOC H2O
557	*Novosphingobium resinovorum*	*26.2*	10.9	**1217**	*Massilia niastensis*	10.4	-3.0
55529	*Pantoea vagans*	*25.7*	10.4	**914**	*Sphingopyxis alaskensis*	10.1	-3.3
2204	*Duganella violaceinigra*	*24.3*	9.2	**23**	*Exiguobacterium acetylicum*	9.8	-3.5
50	*Exiguobacterium aurantiacum*	*22.7*	7.8	**79**	*Chitinophaga terrae*	9.7	-3.6
116	*Exiguobacterium sibiricum*	*21.5*	6.7	**412**	*Sphingopyxis alaskensis*	9.3	-4.0
3078	*Variovorax ginsengisoli*	*21.3*	6.6	**124**	*Delftia lacustris*	8.7	-4.5
82	*Novosphingobium sediminicola*	*20.4*	5.7	**53**	*Pedobacter terrae*	8.6	-4.6
418	*Paenibacillus glycanilyticus*	*19.9*	5.3	**130**	*Novosphingobium sediminicola*	8.4	-4.8
648	*Acidovorax soli*	*19.3*	4.8	**131**	*Ensifer adhaerens*	7.4	-5.7
137	*Variovorax ginsengisoli*	*19.0*	4.6	**31**	*Duganella radicis*	7.3	-5.8
385	*Achromobacter spanius*	*18.6*	4.1	**29**	*Rahnella aquatilis*	5.7	-7.2
598	*Pedobacter rhizosphaerae*	*17.2*	3.0	**44**	*Kosakonia radicincitans*	5.6	-7.3
109	*Chitinophaga terrae*	*16.7*	2.5	**59**	*Arthrobacter cupressi*	4.7	-8.0
62	*Arthrobacter cupressi*	*16.4*	2.2	**83**	*Exiguobacterium acetylicum*	4.7	-8.0

703	*Bosea thiooxidans*	*15.8*	1.7	**91**	*Pedobacter terrae*	4.7	-8.0
690	*Acidovorax soli*	*15.2*	1.2	**34**	*Rhizobium rhizoryzae*	4.7	-8.1
3709	*Novosphingobium resinovorum*	*14.2*	0.3	**132**	*Microbacterium oleivorans*	3.0	-9.5
96	*Dyadobacter soli*	*14.1*	0.2	**2350**	*Delftia lacustris*	2.8	-9.7
162	*Herbaspirillum chlorophenolicum*	*13.9*	0.1	**689**	*Bosea robiniae*	2.3	-10.1
H2O		13.8	0.0	**105**	*Duganella radicis*	1.9	-10.5
97	*Massilia albidiflava*	13.5	-0.3	**46**	*Agrobacterium fabrum* or *Rhizobium pusense* (In Taxonomic Flux) (previously *Rhizobium sp.*)	1.7	-10.7
54073	*Stenotrophomonas maltophilia*	13.5	-0.3	**45**	*Chryseobacterium daecheongense*	1.2	-11.1
608	*Novosphingobium lindaniclasticum*	13.2	-0.5	**UNT**		0.0	-12.2
684	*Novosphingobium lindaniclasticum*	13.1	-0.7	**661**	*Rhizobium rhizoryzae*	-0.3	-12.4
54093	*Rhodococcus erythropolis*	13.0	-0.8	**1267**	*Bosea eneae*	-0.4	-12.5
55530	*Pseudomonas oryzihabitans*	11.6	-1.9	**68**	*Dyadobacter soli*	-1.8	-13.8
81	*Exiguobacterium sp.*	10.9	-2.6	**49**	*Achromobacter pulmonis*	-5.0	-16.5
804	*Pseudomonas jinjuensis*	10.4	-3.0				

Example 5: Modifying Wheat Seedling Shoot and Root Biomass with Isolated Microbes

A. Seed Treatment with Isolated Microbe

[0451] In this example, wheat seeds were inoculated with individual microbial strains (BCIs), and subjected to a germination test (Figure 6 A and Figure 6 B).

[0452] The seeds were inoculated, placed on wet germination paper, and rolled. The rolls were then incubated at 25°C in plastic bins. Each strain in Figure 6 was tested in triplicate, with 30 seeds per replicate.

[0453] Shoot and root biomass was measured at six days post treatment. An uninoculated 'water' control treatment was run and measured simultaneously. The solid line parallel to the x axis and bisecting the bars near the top of the y-axis in each figure represents the average of values for the water-treated control seeds. Some of the inoculated strains revealed relative increases in shoot and/or root biomass at six days post inoculation (DPI) compared to untreated control *in vitro*.

[0454] Table 13 provides a breakout of the shoot and root biomass increase in wheat having been inoculated and treated as described above, relative to a water-only control (H2O). The two columns immediately to the right of the species reflect the percentage increase over control (%IOC). Both increases and decreases in biomass are reflected in the data of table 13. A smaller plant reflects potential for in-field conservation of nutrients and water where these resources may be limited by drought or local conditions, thus decreases are hypothesized to be yield relevant.

[0455] The results demonstrated that 16 strains caused a relative increase in shoot biomass of wheat at six days post inoculation (DPI) compared to the water-only controls *in vitro*. Twelve strains showed greater than a 5% increase over water control, whereas 10 strains showed greater than a 5% decrease in shoot biomass over the water control.

[0456] The results demonstrated that 26 strains caused a relative increase in root biomass of wheat at six days post inoculation (DPI) compared to the water-only control *in vitro*. Eighteen strains showed greater than a 5% increase over control, whereas 2 strains showed greater than a 5% decrease in biomass relative to the water control.

Table 13

BCI Strain #	Crop	Species	Shoot Biomass% IOC Control	Root Biomass% IOC Control
49	Wheat	*Achromobacter pulmonis*	9.03	18.55
46	Wheat	*Agrobacterium fabrum* or *Rhizobium pusense* (In Taxonomic Flux) (previously *Rhizobium sp.*)	3.31	18.55
958	Wheat	*Agrobacterium fabrum* or *Rhizobium pusense* (In Taxonomic Flux) (previously *Rhizobium sp.*)	13.55	21.26
5222	Wheat	*Agrobacterium fabrum* or *Rhizobium pusense* (In Taxonomic Flux) (previously *Rhizobium sp.*)	-10.54	0.90
717	Wheat	*Arthrobacter nicotinovorans*	13.85	11.76
3189	Wheat	*Arthrobacter nicotinovorans*	2.41	19.90
3444	Wheat	*Arthrobacter nicotinovorans*	-3.32	4.07
45	Wheat	*Chryseobacterium daecheongense*	-2.41	5.88

191	Wheat	*Chryseobacterium daecheongense*	-3.92	2.71
774	Wheat	*Chryseobacterium daecheongense*	-8.14	0.90
597	Wheat	*Chryseobacterium rhizosphaerae*	-1.81	6.78
615	Wheat	*Chryseobacterium rhizosphaerae*	-17.17	-4.98
1075	Wheat	*Chryseobacterium rhizosphaerae*	5.42	4.97
402	Wheat	*Frigidibacter albus* or *Delfulviimonas dentrificans* (In Taxonomic Flux)	-7.23	8.14
745	Wheat	*Frigidibacter albus* or *Delfulviimonas dentrificans* (In Taxonomic Flux)	-19.28	-2.27
31	Wheat	*Duganella radicis*	-15.97	-8.60
105	Wheat	*Duganella radicis*	6.32	22.62
63	Wheat	*Exiguobacterium antarcticum*	-6.03	-5.43
718	Wheat	*Exiguobacterium sibircum or antarcticum*	12.04	18.55
116	Wheat	*Exiguobacterium sibiricum*	11.14	12.66
225	Wheat	*Exiguobacterium soli*	-10.24	-3.17
712	Wheat	*Frigidibacter albus*	1.20	15.83
3231	Wheat	*Massilia kyonggiensis*	12.04	21.71
94	Wheat	*Massilia kyonggiensis*	9.94	11.31
97	Wheat	*Massilia kyonggiensis*	-1.51	0.90
138	Wheat	*Novosphingobium sediminicola*	-3.32	5.43
53	Wheat	*Pedobacter terrae*	5.72	12.21
91	Wheat	*Pedobacter terrae*	-10.24	-0.91
110	Wheat	*Pedobacter terrae*	-7.83	4.52
616	Wheat	*Pseudomonas helmanticensis*	9.33	15.38
800	Wheat	*Pseudomonas helmanticensis*	8.73	14.47
2945	Wheat	*Pseudomonas helmanticensis*	0.60	4.97

Example 6: Modifying Corn Seedling Shoot and Root Biomass with Isolated Microbes

A. Seed Treatment with Isolated Microbe

[0457] In this example, corn seeds were inoculated with individual microbial strains (BCIs), and subjected to a germination test (Figures 7 A, 7 B, 8 A and 8 B).

[0458] The seeds were inoculated, placed on wet germination paper, and rolled. The rolls were then incubated at 25°C in plastic bins. Each strain appearing in Figures 7 A, 7 B, 8 A and 8 B was tested in triplicates, with 30 seeds per replicate test. Due to the amount of samples tested, rolls were placed in two independent bins with a respective water control, represented individually in Figures 7 A, 7 B, 8 A and 8 B.

[0459] Shoot and root biomass was measured at six days post treatment. An uninoculated 'water' control treatment was run and measured simultaneously. The solid line parallel to the x axis and bisecting the bars near the top of the y-axis in each figure represents the average of values for the water-treated control seeds. Some of the inoculated strains revealed relative increases in shoot and/or root biomass at six days post inoculation (DPI) compared to untreated control *in vitro*.

[0460] Table 14 provides a breakout of the shoot and root biomass changes in corn having been inoculated and treated as described above, relative to a water-only control (H2O). The two columns immediately to the right of the species reflect the percentage increase over control (%IOC). Both increases and decreases in the biomasses are reflected in the data of table 14. A smaller plant reflects potential for in-field conservation of nutrients and water where these resources may be limited by drought or local conditions, thus decreases are hypothesized to be yield relevant.

[0461] The results demonstrated that 25 strains caused a relative increase in shoot biomass of corn at six days post inoculation (DPI) compared to the water-only control *in vitro*. Twenty-two strains showed greater than a 10% increase, whereas 7 strains caused a decrease in biomass relative the water control.

[0462] The results demonstrated that 15 strains caused a relative increase in root biomass of corn at six days post inoculation (DPI) compared to the water-only control *in vitro*. Eight strains showed greater than a 5% increase over water control, whereas 11 strains showed greater than a 5% decrease in root biomass over the water control.

[0463] Results demonstrated that a number of strains isolated from superior plants caused a significant increase over the water control in root and/or shoot biomass ($p<0.05$ Dunnett's Multiple Comparisons Test). Statistically significant results are labeled with an asterisk. In one embodiment, superior plants are defined as a subset of individual plants observed in an AMS process to exhibit a phenotype of interest that is improved relative to the plurality of plants screened in the same assay. Phenotypes of interest may be screened in the absence or presence of biotic or abiotic stress and include early vigor, as manifested by improved germination rate, foliar and or root biomass; chlorophyll content; leaf canopy temperature; and water use efficiency.

Table 14

BCI Strain #	Crop	Species	Shoot Biomass% IOC	Root Biomass% IOC
49	Corn	*Achromobacter pulmonis*	-4.28	-16.12
46	Corn	*Agrobacterium fabrum* or *Rhizobium pusense (In Taxonomic Flux) (previously Rhizobium sp.)*	15.10	-4.41
958	Corn	*Agrobacterium fabrum* or *Rhizobium pusense (In Taxonomic Flux) (previously Rhizobium sp.)*	17.31	-0.63
5222	Corn	*Agrobacterium fabrum* or *Rhizobium pusense (In Taxonomic Flux) (previously Rhizobium sp.)*	22.22	-2.52
717	Corn	*Arthrobacter nicotinovorans*	26.21	22.61*
3189	Corn	*Arthrobacter nicotinovorans*	74.15*	14.05
3444	Corn	*Arthrobacter nicotinovorans*	6.48	-15.54
45	Corn	*Chryseobacterium daecheongense*	31.48	-3.60
191	Corn	*Chryseobacterium daecheongense*	19.44	-14.86
774	Corn	*Chryseobacterium daecheongense*	21.58	1.17
597	Corn	*Chryseobacterium rhizosphaerae*	15.53	3.15
615	Corn	*Chryseobacterium rhizosphaerae*	17.52	1.89
1075	Corn	*Chryseobacterium rhizosphaerae*	73.79*	11.26
402	Corn	*Frigidibacter albus* or *Delfulviimonas dentrificans (In Taxonomic Flux)*	11.25	2.97
745	Corn	*Frigidibacter albus* or *Delfulviimonas dentrificans (In Taxonomic Flux)*	8.76	-17.75
31	Corn	*Duganella radicis*	35.68*	-2.07
105	Corn	*Duganella radicis*	19.73	5.05
63	Corn	*Exiguobacterium antarcticum*	17.17	2.61
718	Corn	*Exiguobacterium sibircum or antarcticum*	1.29	-12.27
116	Corn	*Exiguobacterium sibiricum*	77.56*	24.05*
225	Corn	*Exiguobacterium soli*	15.67	-7.75
138	Corn	*Exiguobacterium sp.*	16.31	0.81
712	Corn	*Frigidibacter albus*	15.24	4.77
3231	Corn	*Massilia kyonggiensis*	-12.84	-10.53
94	Corn	*Massilia kyonggiensis*	-6.44	-8.54
97	Corn	*Massilia kyonggiensis*	-2.29	-13.74
53	Corn	*Pedobacter terrae*	-7.90	-14.58
91	Corn	*Pedobacter terrae*	50.64*	23.87*
110	Corn	*Pedobacter terrae*	-0.17	-7.64
616	Corn	*Pseudomonas helmanticensis*	16.67	14.05
800	Corn	*Pseudomonas helmanticensis*	-3.21	-2.88
2945	Corn	*Pseudomonas helmanticensis*	14.60	5.68

*Statistically significant results

Example 7: Increasing Root and Shoot Length of Maize, Wheat, and Tomato with Isolated Microbes

A. Seed Treatment with Isolated Microbe

[0464] In this example, seeds of maize, wheat, and tomato were inoculated with individual microbial strains (BDNZ strains), and allowed to germinate.

[0465] The seeds were inoculated, placed on wet paper towels and rolled. The rolls were then incubated at 25°C in sealed plastic bags. Each strain appearing in table 15 was tested in germination tests in duplicate, with 30 seeds per replicate test for wheat and maize and 50 seeds for tomato.

[0466] Root length and shoot length (RL and SL) were measured at four days post treatment. Some of the inoculated strains revealed relative increases in root and/or shoot length at four days point inoculation (DPI) compared to untreated control.

[0467] Each strain applied to maize seed was tested in duplicates of 30 seeds each. Results show that while germination rates were good for all strains tested, some strains caused a relative increase in root and/or shoot length at 4 days post inoculation (DPI) compared to the water control *in vitro* (See Figures 9 and 10).

[0468] Each strain applied to wheat seed was tested in duplicates of 30 seeds each. Root and shoot length were measured at 4 days post treatment. Results show that germination rates were good for all strains tested (>90%), and some strains caused a relative increase in root and/or shoot length at 4 days post inoculation (DPI) compared to the water control *in vitro* (See Figures 11 and 12).

[0469] Each strain applied to tomato seed was tested in duplicates of 50 seeds each. Root and shoot length were measured at 4 days post inoculation (DPI). Results show that germination rates were good for all strains tested, and some strains caused a relative increase in root and/or shoot length at 4 days post inoculation (DPI) compared to the water control *in vitro* (See Figures 13 and 14).

[0470] Table 15 provides a breakout of the root and shoot length increase (in mm) after inoculation and treatment as described above, relative to a water-only control (H2O). The columns immediately to the right of the species reflect the percentage increase over control (%IOC) for the water-only control. Both increases and decreases are reflected in the data. A smaller plant reflects potential for in-field conservation of

nutrients and water where these resources may be limited by drought or local conditions, thus decreases are hypothesized to be yield relevant.

[0471] The results demonstrated that a number of strains isolated from superior plants caused a significant increase over the water control in root and/or shoot length ($p<0.1$, Fisher's LSD) at four days post inoculation (DPI). Twenty strains isolated from superior plants caused a significant increase over the water control in maize root length and 19 caused a significant increase in maize shoot length. Four strains caused a significant increase over control in root and shoot length of wheat. Four strains caused a significant increase over control in root and shoot length of tomato.

Table 15

BDNZ Strain #	Crop	Species	%IOC RL	%IOC SL
54073	Maize	*Stenotrophomonas maltophilia*	61.8	5
54093	Maize	*Rhodococcus erythropolis*	54.6	29.7
54137	Maize	*Pantoea agglomerans*	36.1	-10.5
54299	Maize	*Rhodococcus erythropolis*	102.7	40.7
55529	Maize	*Pantoea agglomerans*	142.4	47.3
55530	Maize	*Pseudomonas oryzihabitans*	52.3	0.6
56343	Maize	*Chitinophaga arvensicola*	188.6	54.3
56654	Maize	*Paenibacillus chondroitinus*	72.1	3.1
56682	Maize	*Paenibacillus chondroitinus*	192.5	61.8
57157	Maize	*Rahnella aquatilis*	58.5	23.2
57494	Maize	*Bosea minatitlanensis*	298.9	93.8
57549	Maize	*Luteibacter yeojuensis*	183	35.9
57570	Maize	*Caulobacter henricii*	30.5	30.6
58001	Maize	*Stenotrophomonas maltophilia*	78	50.5
58013	Maize	*Rahnella aquatilis*	67	-9
60510	Maize	*Dyella ginsengisoli*	118	58.2

60517	Maize	*Frateuria sp.*	278.5	96.9
65589	Maize	*Novosphingobium rosa*	223	33.2
65600	Maize	*Herbaspirillum huttiense*	23	18
65619	Maize	*Novosphingobium rosa*	22.4	-19.3
66374	Maize	*Albidiferax sp.*	75.3	10.9
68775	Maize	*Rhodoferax ferrireducens*	93	63.1
68999	Maize	*Chitinophaga arvensicola*	65.4	14.5
71420	Maize	*Luteibacter yeojuensis*	42.3	11.6
74038	Maize	*Pseudomonas oryzihabitans*	92.2	40.7
54456	Wheat	*Janthinobacterium sp.*	7.7	0.5
54660	Wheat	*Paenibacillus amylolyticus*	-4	-3.9
55184	Wheat	*Massilia niastensis*	16.1	12.2
56699	Wheat	*Massilia niastensis*	0.8	3.6
66487	Wheat	*Flavobacterium saccharophilum*	7.2	13
69132	Wheat	*Flavobacterium glaciei*	-10.2	-6.8
63491	Wheat	*Janthinobacterium sp.*	10.2	13.9
66821	Wheat	*Polaromonas ginsengisoli*	-3.1	11.1
56782	Tomato	*Sphingobium quisquiliarum*	14.1	7
58291	Tomato	*Duganella violaceinigra*	13.4	-3.5
58577	Tomato	*Ramlibacter sp.*	5.6	-8
66316	Tomato	*Paenibacillus amylolyticus*	28.1	16.2
66341	Tomato	*Caulobacter henricii*	-4.8	-17.4
66354	Tomato	*Bosea minatitlanensis*	9.4	3.4
66361	Tomato	*Duganella violaceinigra*	34.9	24.6
66373	Tomato	*Polaromonas ginsengisoli*	23.5	34
66576	Tomato	*Sphingobium quisquiliarum*	28.1	35.4
68599	Tomato	*Stenotrophomonas terrae*	15.9	9.6
68741	Tomato	*Stenotrophomonas terrae*	15.8	20.3

[0472] In Table 15, the root and shoot length were assessed to evaluate the effect of the microbe treatments on early plant development. Both increases and decreases in biomass have been noted to reflect the possibility that decreases are hypothesized to be yield relevant; for example a smaller plant reflects potential for in-field conservation of nutrients and water where these may be limited by drought or local conditions. Results show that of all strains tested, some 40 strains caused a relative increase in root length at 4 days post inoculation (DPI) and 35 strains caused a relative increase in shoot length compared to water controls *in vitro*. Four tomato strains, three wheat strains and 17 maize strains caused a significant increase in both shoot length and root length ($p<0.1$, Fishers least squared difference).

Example 8: Modifying Root and Shoot Length of Corn with Isolated Microbes

A. Seed Treatment with Isolated Microbe

[0473] In this example, corn seeds were inoculated with individual microbial strains and allowed to germinate (Figures 15A, 15B, 16A and 16B).

[0474] The seeds were inoculated, placed on wet germination paper, and rolled. The rolls were then incubated at 25°C in plastic bins. Each strain appearing in figures 15 and 16 was tested in germination tests in triplicates, with 30 seeds per replicate. Due to the amount of samples tested, rolls were placed in two independent bins with a respective water control, represented individually in Figures 15 and 16 by graphs A and B.

[0475] Root length and shoot length (RL and SL) were measured at six days post treatment. A control treatment was included comprising seeds treated with water in the absence of a microbial inoculant of the present disclosure. Some of the inoculated strains revealed relative increases in root and/or shoot length at six days point inoculation (DPI) compared to untreated control (Figures 15 and 16).

[0476] Table 16 provides a breakout of the root and shoot length increase (in mm) after inoculation and treatment as described above, relative to a water-only control (H2O). The columns immediately to the right of the species reflect the percentage increase over control (%IOC). Both increases and decreases are reflected in the data. A smaller plant reflects potential for in-field conservation of nutrients and water

where these resources may be limited by drought or local conditions, thus decreases are hypothesized to be yield relevant.

[0477] Results demonstrated that a number of strains listed in Table 16 which were origanly isolated from superior plants caused a significant increase, over the water-only control, in root and/or shoot length ($p<0.05$, Fisher's LSD) at six days post inoculation (DPI). Statistically significant results are labeled with an asterisk. Ten strains isolated from superior plants caused a significant increase over the water control in corn shoot length and 5 caused a significant increase in corn root length.

Table 16

Strain	Crop	Species	% IOC SL	% IOC RL
49	Corn	*Achromobacter pulmonis*	23.30	-0.84
46	Corn	*Agrobacterium fabrum* or *Rhizobium pusense* (In Taxonomic Flux) (previously *Rhizobium sp.*)	21.79	1.56
958	Corn	*Agrobacterium fabrum* or *Rhizobium pusense* (In Taxonomic Flux) (previously *Rhizobium sp.*)	47.76*	6.25
5222	Corn	*Agrobacterium fabrum* or *Rhizobium pusense* (In Taxonomic Flux) (previously *Rhizobium sp.*)	38.31*	17.55*
717	Corn	*Arthrobacter nicotinovorans*	60.20*	53.32*
3189	Corn	*Arthrobacter nicotinovorans*	N/A	N/A
3444	Corn	*Arthrobacter nicotinovorans*	21.04	3.36
45	Corn	*Chryseobacterium daecheongense*	39.99*	11.43
191	Corn	*Chryseobacterium daecheongense*	17.91	-1.62
774	Corn	*Chryseobacterium daecheongense*	45.65*	6.84
597	Corn	*Chryseobacterium rhizosphaerae*	20.90	5.29
615	Corn	*Chryseobacterium rhizosphaerae*	25.57	9.98
1075	Corn	*Chryseobacterium rhizosphaerae*	N/A	N/A
402	Corn	*Frigidibacter albus* or *Delfulviimonas dentrificans* (In Taxonomic Flux)	44.78*	18.96*
745	Corn	*Frigidibacter albus* or *Delfulviimonas dentrificans* (In Taxonomic Flux)	15.92	-0.36
31	Corn	*Duganella radicis*	22.39	12.81
105	Corn	*Duganella radicis*	36.02	7.51
63	Corn	*Exiguobacterium antarcticum*	42.29*	4.59
718	Corn	*Exiguobacterium sibircum or antarcticum*	18.12	-6.56
116	Corn	*Exiguobacterium sibiricum*	N/A	N/A

225	Corn	*Exiguobacterium soli*	23.88	9.48
138	Corn	*Exiguobacterium sp.*	37.11	20.56*
712	Corn	*Frigidibacter albus*	38.81*	10.24
3231	Corn	*Massilia kyonggiensis*	-13.92	-10.76
94	Corn	*Massilia kyonggiensis*	16.50	-9.92
97	Corn	*Massilia kyonggiensis*	11.72	-4.68
53	Corn	*Pedobacter terrae*	3.88	4.33
91	Corn	*Pedobacter terrae*	N/A	N/A
110	Corn	*Pedobacter terrae*	12.30	4.87
616	Corn	*Pseudomonas helmanticensis*	42.79*	56.95*
800	Corn	*Pseudomonas helmanticensis*	6.97	2.62
2945	Corn	*Pseudomonas helmanticensis*	38.81*	8.22

*Statistically significant results

[0478] In table 16, the root and shoot length were assessed to evaluate the effect of the microbe treatments on early plant development. Both increases and decreases have been noted to reflect the possibility that decreases are hypothesized to be yield relevant; for example a smaller plant reflects potential for in-field conservation of nutrients and water where these may be limited by drought or local conditions. Results show that of all strains tested, some 21 strains caused a relative increase in root length at six days post inoculation (DPI) and 27 strains caused a relative increase in shoot length compared to water controls *in vitro*. A total of six strains tested on corn caused a significant increase in both shoot length and root length ($p<0.1$, Fishers least squared difference). Asterisks show significance ($p<0.1$, Dunnette's Multtiple-Comparison Test).

Example 9: Modifying Tomato Seedling Shoot Biomass with Isolated Microbes

A. Seedling Drench Treatment with Isolated Microbe

[0479] In this example, tomato seedlings were grown in ceramic growth media (50 mL volume; Profile Greens Grade, Profile, Buffalo Grove, IL, U.S.A.) in a growth chamber and inoculated with individual microbial strains at 21 days post planting (DPP). Seedlings were grown for a further 10 days post inoculation (DPI) before FW measurements were taken (Figure 17).

[0480] For each microbial treatment the tomato seedlings were drench-inoculated with 1 mL of a water-based suspension of microbes at a concentration of 10^7 CFU/mL. A control treatment with water in the absence of a microbial inoculant was

included. All plants were grown in a growth chamber at 25 ± 5 ^{0}C, and on a 16/8 h day/night cycle for 31 day growth period. Treatments were arrayed using a Randomized Complete Block Design (RCBD) comprising 3 blocks and 8 replicates per block, per treatment.

[0481] Plants were destructively harvested 31 days post planting and shoot biomass (fresh weight) determined.

[0482] Results show that many of the tested strains caused a relative increase in shoot biomass compared to the water control at 10 DPI.

[0483] Table 17 provides a breakout of the shoot fresh weight relative to a water-only control treatment. The columns immediately to the right of the species reflect the percentage increase over the water control (% IOC). Both increases and decreases are reflected in the data. A smaller plant reflects potential for in-field conservation of nutrients and water where these resources may be limited by drought or local conditions, thus decreases are hypothesized to be yield relevant.

[0484] Three strains isolated from superior plants gave a greater than 5% increase over the control in shoot biomass. These included two strains of *Janibacter limosus* (3105 and 4708), and one strain of *Pseudomonas yamanorum* (5446).

Table 17

Strain BCI#	Crop	Species	% IOC H20 Shoot Biomass
3103	Tomato	*Janibacter limosus*	1.50
3105	Tomato	*Janibacter limosus*	6.81
3523	Tomato	*Pseudomonas yamanorum*	-3.82
4468	Tomato	*Brevibacterium frigoritolerans*[*]	3.84
4473	Tomato	*Bacillus megaterium*	2.20
4708	Tomato	*Janibacter limosus*	6.87
4853	Tomato	*Pseudomonas yamanorum*	3.79
5446	Tomato	*Pseudomonas yamanorum*	7.98

[*] In taxonomic flux, potential synonym of *Bacillus muralis*

Example 10: Modifying Corn Seedling Shoot Biomass with Isolated Microbes

A. Seedling Drench Treatment with Isolated Microbes

[0485] In this example, seedlings of *Zea mays* were grown in 128 well plug trays in ceramic growth media (Profile Greens Grade, Profile, Buffalo Grove, IL, U.S.A.) in a

growth chamber and inoculated with individual microbial strains at 5 and 13 days after planting (Figure 18).

[0486] For each microbial treatment, seedlings were drench-inoculated using 1.75 mL of a water-based suspension of microbes at 10^7 CFU/mL. A control treatment with water in the absence of a microbial inoculant was included. Plants were grown in a growth room at 25 ± 5°C, on a 16/8 h day/night cycle. Treatments were arrayed using a Randomized Complete Block Design (RCBD) comprising 3 blocks and 6 replicates per block, per treatment.

[0487] Plants were destructively harvested 15 days post planting and shoot (above ground biomass) (fresh weight) determined.

[0488] Results show that the majority of tested strains caused a relative increase in shoot biomass compared to the water control at 10 days post inoculation (DPI). Two showed biomass increases of > 5% and two strains showed increases of > 10%.

[0489] Table 18 provides a breakout of the shoot fresh weight relative to the water-only control treatment. The columns immediately to the right of the species reflect the percentage increase over control (%IOC). Both increases and decreases are reflected in the data. A smaller plant reflects potential for in-field conservation of nutrients and water where these resources may be limited by drought or local conditions, thus decreases are hypothesized to be yield relevant.

Table 18

Strain (BCI#)	Crop	Species	%IOC H20 Shoot Biomass
3103	Corn	*Janibacter limosus*	2.50
3105	Corn	*Janibacter limosus*	12.44
4468	Corn	*Brevibacterium frigoritolerans*[*]	-6.84
4708	Corn	*Janibacter limosus*	16.01

[*]In taxonomic flux, potential synonym of *Bacillus muralis*

Example 11: Modifying Wheat Seedling Biomass with Isolated Microbes

A. Seed Treatment with Isolated Microbe

[0490] In this example wheat (*Triticum aestivum*) seeds were inoculated with individual microbial strains and subjected to a paper germination test. (Figure 19).

[0491] The seeds were inoculated, placed on wet germination paper that was then rolled and incubated in plastic bins at 25°C for 6 days. Each individual strain appearing in Figure 19 was tested in triplicate rolls of 20 seeds each.

[0492] Total shoot and root fresh weight was measured at six days post treatment. An uninoculated 'water' control treatment was prepared and measured simultaneously. Figure 18 displays percent increase over control. Most of the inoculated strains increased plant biomass at six days post inoculation (DPI) compared to the untreated control.

[0493] Table 19 provides a breakout of the biomass percent increase in wheat having been inoculated as described above, relative to a water-treated control. The two columns immediately to the right of the species reflect the percentage increase over control (%IOC) for shoot and root biomass. Both increases and decreases in biomass are presented. A smaller plant reflects potential for in-field conservation of nutrients and water where these resources may be limited by drought or local conditions, thus decreases are hypothesized to be yield relevant.

[0494] The results demonstrated that four strains caused a relative increase in total shoot biomass of wheat at six days post inoculation (DPI) compared to the water-treated controls. Four strains caused a relative increase in total root biomass of wheat at six days post inoculation (DPI) compared to the water-treated controls *in vitro*.

Table 19

Strain (BCI)	Species	Shoot biomass IOC	Root biomass IOC
4473	*Bacillus megaterium*	-3.67%	-2.04%
4468	*Brevibacterium frigoritolerans*[*]	9.49%	8.77%
3103	*Janibacter limosus*	1.20%	-1.19%
3105	*Janibacter limosus*	6.22%	5.28%
4708	*Janibacter limosus*	6.67%	3.90%
3523	*Pseudomonas yamanorum*	-13.81%	-8.92%
4853	*Pseudomonas yamanorum*	-1.04%	-9.27%
5446	*Pseudomonas yamanorum*	-11.93%	-14.62%

[*] In taxonomic flux, potential synonym of *Bacillus muralis*

Example 12: Modifying Corn Seedling Shoot and Root Biomass with Isolated Microbes

A. Seed Treatment with Isolated Microbe

[0495] In this example, corn (*Zea mays*) seeds were inoculated with individual microbial strains (BCIs), and subjected to a paper germination test (Figure 20).

[0496] The seeds were inoculated, placed on wet germination paper that was then rolled and incubated in a plastic bin at 25°C. Each individual strain appearing in Figure 20 was tested in triplicate rolls of 20 seeds each.

[0497] Shoot and root fresh weight was measured at six days post treatment. A water-treated control was run and measured simultaneously. Figure 20 displays percent increase over control. Some of the inoculated strains increased shoot and/or root biomass at six days post inoculation (DPI) compared to water-treated control.

[0498] Table 20 provides a breakout of the shoot and root biomass changes in corn having been inoculated and treated as described above, relative to a water-treated control (H2O). The two columns immediately to the right of the species reflect the percentage increase over control (%IOC) for shoot and root biomass. Both increases and decreases in biomass are presented. A smaller plant reflects potential for in-field conservation of nutrients and water where these resources may be limited by drought or local conditions, thus decreases are hypothesized to be yield relevant.

[0499] The results demonstrated that five strains caused a relative increase in shoot biomass of corn at six days post inoculation (DPI) compared to the water-treated control. Three strains caused a decrease in shoot biomass relative to the water control.

[0500] The results demonstrated that four strains caused a relative increase in root biomass of corn at six days post inoculation (DPI) compared to the water-treated control *in vitro*. Whereas four strains showed greater than a decrease in root biomass over the water control.

Table 20

Strain (BCI)	Species	Shoot biomass IOC	Root biomass IOC
4473	*Bacillus megaterium*	-20.75%	-14.38%
4468	*Brevibacterium frigoritolerans*[*]	16.23%	0.45%
3103	*Janibacter limosus*	12.45%	2.60%
3105	*Janibacter limosus*	43.92%	12.84%
4708	*Janibacter limosus*	-21.13%	-15.98%
3523	*Pseudomonas yamanorum*	8.85%	0.71%
4853	*Pseudomonas yamanorum*	-39.49%	-16.55%
5446	*Pseudomonas yamanorum*	15.05%	-3.78%

[*] In taxonomic flux, potential synonym of *Bacillus muralis*

Example 13: Biochemical Characterization of Microbial Isolates

A. *In vitro* analysis of plant beneficial properties of a microbe in US trials

[0501] In this example, microbes from Table 3 were tested in duplicate for phosphate, potassium, and zinc solubilization, Indole Acetic Acid (IAA) production, and the ability to grow on low nitrogen media and the ability to use phytate as a sole source of phosphorus. All isolates were grown for six days at 25°C.

[0502] Table 21 provides a summary of the growth response of each isolate, having been grown as described above. Plate-based solubilization assays were performed using NBRIP medium (inorganic phosphate) according to the method by Islam et al., (2007); Phytate utilization as the sole source of phosphorus for growth was assessed using media containing (g/L): phytic acid (10) $NaNO_3$ (3); KCl (0.5); $FeSO_4.7H_2O$ (0.01); $MgSO_4.7H_2O$ (0.5); glucose (10) and noble agar (15), pH 7.5.media containing (g/L): phytic acid (10) $NaNO_3$ (3); KCl (0.5); $FeSO_4.7H_2O$ (0.01); $MgSO_4.7H_2O$ (0.5); glucose (10) and noble agar (15), pH 7.5; Alexandrov medium supplemented with Mica (potassium); minimal medium supplemented with insoluble Zn compounds according to methods by Goteti et al., (2013); low nitrogen medium (nitogen aquisition) according to methods by Dobereiner et al., 1976 without Bromothymol blue, solidified with 0.175% agar. IAA production was measured against a standard curve in a colorimetric assay based on methods by Gordon and Weber (1951).

[0503] Within table 21, a (+) symbol represents a positive response in the respective trait element, (-) symbol, no activity and N/A, no growth observed on the respective media.

[0504] Results show that microbes on table 3 exhibit a broad spectrum of known plant-beneficial biochemical activities (Rana et al., 2012, Rodriguez and Reynaldo, 1999) including solubilization of mineral nutrients and secretion of plant-like hormones. By enhancing nutrient availability for plant growth promotion, the microbes exhibit a potential for increasing plant yields.

Table 21

Strain BCI	Species	Nitrogen mobiliza-tion	Phytate utiliza-tion	Potassium solubilize-tion	Phosphate solubilize-tion	Zinc solubilize-tion	IAA produc-tion
4468	*Brevibacterium frigoritolerans**	+	+	-	+	N/A	-

Strain BCI	Species	Nitrogen mobiliza-tion	Phytate utiliza-tion	Potassium solubilize-tion	Phosphate solubilize-tion	Zinc solubilize-tion	IAA produc-tion
3103	*Janibacter limosus*	+	+	N/A	N/A	+	+
3105	*Janibacter limosus*	+	+	N/A	N/A	+	-
4708	*Janibacter limosus*	+	+	N/A	-	+	+
3523	*Pseudomonas yamanorum*	+	+	+	+	+	+
4853	*Pseudomonas yamanorum*	+	+	+	+	+	+
5446	*Pseudomonas yamanorum*	+	+	+	+	+	+
4473	*Bacillus megaterium*	+	+	+	-	N/A	+

*In taxonomic flux, potential synonym of *Bacillus muralis*

B. Further *In vitro* analysis of plant beneficial properties of a microbe in US trials

[0505] In this example, isolated microbes from Table 4 were grown on minimal or nutrient-deficient agar plates supplemented with insoluble nutrient substrates to determine biochemical activity (Table 22).

[0506] Isolates were tested, in triplicate, for phosphate, potassium, and zinc solubilization, siderophore production and the ability to grow on low nitrogen media. Plates were incubated at 25°C for six days.

[0507] Table 22 provides a summary of the growth response of each isolate, having been grown as described above. Tests are abbreviated as follows: Mica (K solubilization) - isolates were grown on modified Alexandrov medium supplemented with Mica (Parmar and Sindhu 2013); PO4 - isolates were grown on NBRIP media (Nautiyal, 1999) containing insoluble tri-calcium phosphate as the sole source of P; ZnO and ZnO3 (Zn solubilization) - isolates were grown on minimal media supplemented with insoluble Zn as described by Goteti et al., (2013); NfA - isolates were grown on Nfb media (Dobereiner et al., 1976) without Bromothymol blue, solidified with 12.5% agar; CAS agar - isolates were grown on Chrome Azurol-s agar for detection of iron chelation according to the method of Perez-Miranda et al (2007).

[0508] Within table 22, a (+) symbol represents an isolates ability to grow under the test conditions and solubilize the respective element, (–) symbol represents a lack of solubilization, (N/A) represents no isolate growth observed on the respective media.

[0509] Results show that microbes on table 4 exhibit a broad spectrum of known plant-beneficial biochemical activities (Rana et al., 2012, Rodriguez and Reynaldo, 1999) including solubilization of mineral nutrients and chelation of micronutrients. By enhancing nutrient availability for plant growth promotion, the microbes exhibit a potential for increasing plant yields.

Table 22

Strain	Species	Media					
BCI #		Mica (K)	PO4	ZnO	ZnCO3	NfA	CAS agar
49	*Achromobacter pulmonis*	N/A	+	+	+	+	-
46	*Agrobacterium fabrum* or *Rhizobium pusense*	-	-	+	-	+	-
958	*Agrobacterium fabrum* or *Rhizobium pusense*	-	-	+	+	+	-
717	*Arthrobacter nicotinovorans*	-	+	+	+	+	-
3189	*Arthrobacter nicotinovorans*	-	+	+	+	+	-
3444	*Arthrobacter nicotinovorans*	-	+	+	+	+	-
774	*Chryseobacterium daecheongense*	-	N/A	N/A	N/A	N/A	-
615	*Chryseobacterium rhizosphaerae*	N/A	N/A	N/A	N/A	N/A	+
1075	*Chryseobacterium rhizosphaerae*	N/A	N/A	N/A	N/A	N/A	+
597	*Chryseobacterium rhizosphaerae*	N/A	N/A	N/A	N/A	N/A	+
402	*Frigidibacter albus* or *Delfulviimonas dentrificans* (In Taxonomic Flux)	-	-	N/A	N/A	+	-
745	*Frigidibacter albus* or *Delfulviimonas dentrificans* (In Taxonomic Flux)	-	-	N/A	N/A	+	-
31	*Duganella radicis*	-	N/A	+	+	+	-
105	*Duganella radicis*	-	N/A	+	+	+	-
712	*Frigidibacter albus*	-	-	N/A	N/A	+	-
3231	*Massilia kyonggiensis*	-	+	N/A	N/A	+	-
94	*Massilia kyonggiensis*	-	+	+	+	+	-
97	*Massilia kyonggiensis*	-	-	N/A	N/A	N/A	+
53	*Pedobacter terrae*	-	N/A	+	+	+	-
91	*Pedobacter terrae*	-	-	+	+	+	-
110	*Pedobacter terrae*	-	-	+	+	+	-
616	*Pseudomonas helmanticensis*	+	+	N/A	N/A	+	-
800	*Pseudomonas helmanticensis*	+	+	N/A	N/A	+	-

Strain	Species	Media					
BCI #		Mica (K)	PO4	ZnO	ZnCO3	NfA	CAS agar
2945	*Pseudomonas helmanticensis*	+	+	N/A	+	+	+
5222	*Agrobacterium fabrum* or *Rhizobium pusense*	-	-	+	+	+	-

C. *In vitro* analysis of plant beneficial properties of microbial strains from New Zealand

[0510] Microbes from Table 23 were grown on minimal or nutrient-deficient agar plates supplemented with insoluble nutrient substrates to determine biochemical activity.

[0511] Phosphate solubilization was determined using NBRIP media containing 5 g/L tri-calcium phosphate according to the method Islam et al., (2007). The ability to use phytate as the sole source of phosphorus for growth was assessed using media containing (g/L): phytic acid (10) $NaNO_3$ (3); KCl (0.5); $FeSO_4.7H_2O$ (0.01); $MgSO_4.7H_2O$ (0.5); glucose (10) and noble agar (15), pH 7.5. Growth on low-nitrogen media (Low N) was assessed using NfA media as described above.

[0512] Within table 23, a (+) symbol represents an isolates ability to grow under the test conditions and solubilize the respective element, (–) symbol represents a lack of solubilization.

Table 23

Strain	Species	Media		
BDNZ		low N	Tri Ca (P)	Phytic (P)
74542	*Tumebacillus permanentifrigoris*	-	-	-
72366	*Tumebacillus permanentifrigoris*	+	+	+
72229	*Tumebacillus permanentifrigoris*	+	-	+
72287	*Tumebacillus permanentifrigoris*	+	-	-
72243	*Leifsonia lichenia*	+	-	+
72289	*Leifsonia lichenia*	+	-	+
73021	*Massilia kyonggiensis*	+	-	-
71222	*Novosphingobium lindaniclasticum*	+	+	+
71628	*Novosphingobium sediminicola*	+	-	+

II. Increased Drought Tolerance and H_20 Use Efficiency in Agriculturally Important Crops

[0513] In certain embodiments of the disclosure, the present methods aim to increase the drought tolerance and water use efficiency for a given crop.

[0514] The methodologies presented herein—based upon utilizing the disclosed isolated microbes, consortia, and compositions comprising the same—have the potential to increase the drought tolerance and water use efficiency of important agricultural crops. This will enable a more sustainable agricultural system and increase the regions of the world that are suitable for growing important crops.

Example 1: Increasing Ryegrass Drought Tolerance and H_20 Use Efficiency with Isolated Microbes and Microbial Consortia

A. Seed Treatment with Isolated Microbe

[0515] In this example, an isolated microbe from **Tables 1-4** will be applied as a seed coating to seeds of ryegrass (*Lolium perenne*). Upon applying the isolated microbe as a seed coating, the ryegrass will be planted and cultivated in the standard manner.

[0516] A control plot of ryegrass seeds, which did not have the isolated microbe applied as a seed coating, will also be planted.

[0517] It is expected that the ryegrass plants grown from the seeds treated with the seed coating will exhibit a quantifiable and superior ability to tolerate drought conditions and/or exhibit superior water use efficiency, as compared to the control ryegrass plants.

[0518] The drought tolerance and/or water use efficiency can be based on any number of standard tests from the art, *e.g* leaf water retention, turgor loss point, rate of photosynthesis, leaf color and other phenotypic indications of drought stress, yield performance, and various root morphological and growth patterns.

B. Seed Treatment with Microbial Consortia

[0519] In this example, a microbial consortium, comprising at least two microbes from **Tables 1-4** will be applied as a seed coating to seeds of ryegrass (*Lolium perenne*). Upon applying the microbial consortium as a seed coating, the ryegrass will be planted and cultivated in the standard manner.

[0520] A control plot of ryegrass seeds, which did not have the microbial consortium applied as a seed coating, will also be planted.

[0521] It is expected that the ryegrass plants grown from the seeds treated with the seed coating will exhibit a quantifiable and superior ability to tolerate drought

conditions and/or exhibit superior water use efficiency, as compared to the control ryegrass plants.

[0522] The drought tolerance and/or water use efficiency can be based on any number of standard tests from the art, *e.g* leaf water retention, turgor loss point, rate of photosynthesis, leaf color and other phenotypic indications of drought stress, yield performance, and various root morphological and growth patterns.

C. Treatment with Agricultural Composition Comprising Isolated Microbe

[0523] In this example, an isolated microbe from **Tables 1-4** will be applied as an agricultural composition, administered to the ryegrass seed at the time of sowing.

[0524] For example, it is anticipated that a farmer will apply the agricultural composition to the ryegrass seeds simultaneously upon broadcasting said seeds into the field. This can be accomplished, for example, by applying the agricultural composition to a hopper or spreader, which contains the ryegrass seeds and which is configured to broadcast the same.

[0525] A control plot of ryegrass seeds, which are not administered the agricultural composition, will also be planted.

[0526] It is expected that the ryegrass plants grown from the seeds treated with the with the agricultural composition will exhibit a quantifiable and superior ability to tolerate drought conditions and/or exhibit superior water use efficiency, as compared to the control ryegrass plants.

[0527] The drought tolerance and/or water use efficiency can be based on any number of standard tests from the art, *e.g* leaf water retention, turgor loss point, rate of photosynthesis, leaf color and other phenotypic indications of drought stress, yield performance, and various root morphological and growth patterns.

D. Treatment with Agricultural Composition Comprising Microbial Consortia

[0528] In this example, a microbial consortium, comprising at least two microbes from **Tables 1-4** will be applied as an agricultural composition, administered to the ryegrass seed at the time of sowing.

[0529] For example, it is anticipated that a farmer will apply the agricultural composition to the ryegrass seeds simultaneously upon broadcasting said seeds into

the field. This can be accomplished, for example, by applying the agricultural composition to a hopper or spreader, which contains the ryegrass seeds and which is configured to broadcast the same.

[0530] A control plot of ryegrass seeds, which are not administered the agricultural composition, will also be planted.

[0531] It is expected that the ryegrass plants grown from the seeds treated with the with the agricultural composition will exhibit a quantifiable and superior ability to tolerate drought conditions and/or exhibit superior water use efficiency, as compared to the control ryegrass plants.

[0532] The drought tolerance and/or water use efficiency can be based on any number of standard tests from the art, *e.g* leaf water retention, turgor loss point, rate of photosynthesis, leaf color and other phenotypic indications of drought stress, yield performance, and various root morphological and growth patterns.

Example 2: Increasing Maize Drought Tolerance and H_20 Use Efficiency with Isolated Microbes and Microbial Consortia

A. Seed Treatment with Isolated Microbe

[0533] In this example, an isolated microbe from **Tables 1-4** will be applied as a seed coating to seeds of corn (*Zea mays*). Upon applying the isolated microbe as a seed coating, the corn will be planted and cultivated in the standard manner.

[0534] A control plot of corn seeds, which did not have the isolated microbe applied as a seed coating, will also be planted.

[0535] It is expected that the corn plants grown from the seeds treated with the seed coating will exhibit a quantifiable and superior ability to tolerate drought conditions and/or exhibit superior water use efficiency, as compared to the control corn plants.

[0536] The drought tolerance and/or water use efficiency can be based on any number of standard tests from the art, *e.g* leaf water retention, turgor loss point, rate of photosynthesis, leaf color and other phenotypic indications of drought stress, yield performance, and various root morphological and growth patterns.

B. Seed Treatment with Microbial Consortia

[0537] In this example, a microbial consortium, comprising at least two microbes from **Tables 1-4** will be applied as a seed coating to seeds of corn (*Zea mays*). Upon

applying the microbial consortium as a seed coating, the corn will be planted and cultivated in the standard manner.

[0538] A control plot of corn seeds, which did not have the microbial consortium applied as a seed coating, will also be planted.

[0539] It is expected that the corn plants grown from the seeds treated with the seed coating will exhibit a quantifiable and superior ability to tolerate drought conditions and/or exhibit superior water use efficiency, as compared to the control corn plants.

[0540] The drought tolerance and/or water use efficiency can be based on any number of standard tests from the art, *e.g* leaf water retention, turgor loss point, rate of photosynthesis, leaf color and other phenotypic indications of drought stress, yield performance, and various root morphological and growth patterns.

C. Treatment with Agricultural Composition Comprising Isolated Microbe

[0541] In this example, an isolated microbe from **Tables 1-4** will be applied as an agricultural composition, administered to the corn seed at the time of sowing.

[0542] For example, it is anticipated that a farmer will apply the agricultural composition to the corn seeds simultaneously upon planting the seeds into the field. This can be accomplished, for example, by applying the agricultural composition to a hopper/bulk tank on a standard 16 row planter, which contains the corn seeds and which is configured to plant the same into rows. Alternatively, the agricultural composition can be contained in a separate bulk tank on the planter and sprayed into the rows upon planting the corn seed.

[0543] A control plot of corn seeds, which are not administered the agricultural composition, will also be planted.

[0544] It is expected that the corn plants grown from the seeds treated with the with the agricultural composition will exhibit a quantifiable and superior ability to tolerate drought conditions and/or exhibit superior water use efficiency, as compared to the control corn plants.

[0545] The drought tolerance and/or water use efficiency can be based on any number of standard tests from the art, *e.g* leaf water retention, turgor loss point, rate of photosynthesis, leaf color and other phenotypic indications of drought stress, yield performance, and various root morphological and growth patterns.

D. Treatment with Agricultural Composition Comprising Microbial Consortia

[0546] In this example, a microbial consortium, comprising at least two microbes from **Tables 1-4** will be applied as an agricultural composition, administered to the corn seed at the time of sowing.

[0547] For example, it is anticipated that a farmer will apply the agricultural composition to the corn seeds simultaneously upon planting the seeds into the field. This can be accomplished, for example, by applying the agricultural composition to a hopper/bulk tank on a standard 16 row planter, which contains the corn seeds and which is configured to plant the same into rows. Alternatively, the agricultural composition can be contained in a separate bulk tank on the planter and sprayed into the rows upon planting the corn seed.

[0548] A control plot of corn seeds, which are not administered the agricultural composition, will also be planted.

[0549] It is expected that the corn plants grown from the seeds treated with the with the agricultural composition will exhibit a quantifiable and superior ability to tolerate drought conditions and/or exhibit superior water use efficiency, as compared to the control corn plants.

[0550] The drought tolerance and/or water use efficiency can be based on any number of standard tests from the art, *e.g* leaf water retention, turgor loss point, rate of photosynthesis, leaf color and other phenotypic indications of drought stress, yield performance, and various root morphological and growth patterns.

Example 3: Increasing Soybean Drought Tolerance and H_20 Use Efficiency with Isolated Microbes and Microbial Consortia

A. Seed Treatment with Isolated Microbe

[0551] In this example, an isolated microbe from **Tables 1-4** will be applied as a seed coating to seeds of soybean (*Glycine max*). Upon applying the isolated microbe as a seed coating, the soybean will be planted and cultivated in the standard manner.

[0552] A control plot of soybean seeds, which did not have the isolated microbe applied as a seed coating, will also be planted.

[0553] It is expected that the soybean plants grown from the seeds treated with the seed coating will exhibit a quantifiable and superior ability to tolerate drought conditions and/or exhibit superior water use efficiency, as compared to the control soybean plants.

[0554] The drought tolerance and/or water use efficiency can be based on any number of standard tests from the art, *e.g* leaf water retention, turgor loss point, rate of photosynthesis, leaf color and other phenotypic indications of drought stress, yield performance, and various root morphological and growth patterns.

B. Seed Treatment with Microbial Consortia

[0555] In this example, a microbial consortium, comprising at least two microbes from **Tables 1-4** will be applied as a seed coating to seeds of soybean (G*lycine max*). Upon applying the microbial consortium as a seed coating, the soybean will be planted and cultivated in the standard manner.

[0556] A control plot of soybean seeds, which did not have the microbial consortium applied as a seed coating, will also be planted.

[0557] It is expected that the soybean plants grown from the seeds treated with the seed coating will exhibit a quantifiable and superior ability to tolerate drought conditions and/or exhibit superior water use efficiency, as compared to the control soybean plants.

[0558] The drought tolerance and/or water use efficiency can be based on any number of standard tests from the art, *e.g* leaf water retention, turgor loss point, rate of photosynthesis, leaf color and other phenotypic indications of drought stress, yield performance, and various root morphological and growth patterns.

C. Treatment with Agricultural Composition Comprising Isolated Microbe

[0559] In this example, an isolated microbe from **Tables 1-4** will be applied as an agricultural composition, administered to the soybean seed at the time of sowing.

[0560] For example, it is anticipated that a farmer will apply the agricultural composition to the soybean seeds simultaneously upon planting the seeds into the field. This can be accomplished, for example, by applying the agricultural composition to a hopper/bulk tank on a standard 16 row planter, which contains the soybean seeds and which is configured to plant the same into rows. Alternatively, the

agricultural composition can be contained in a separate bulk tank on the planter and sprayed into the rows upon planting the soybean seed.

[0561] A control plot of soybean seeds, which are not administered the agricultural composition, will also be planted.

[0562] It is expected that the soybean plants grown from the seeds treated with the with the agricultural composition will exhibit a quantifiable and superior ability to tolerate drought conditions and/or exhibit superior water use efficiency, as compared to the control soybean plants.

[0563] The drought tolerance and/or water use efficiency can be based on any number of standard tests from the art, *e.g* leaf water retention, turgor loss point, rate of photosynthesis, leaf color and other phenotypic indications of drought stress, yield performance, and various root morphological and growth patterns.

D. Treatment with Agricultural Composition Comprising Microbial Consortia

[0564] In this example, a microbial consortium, comprising at least two microbes from **Tables 1-4** will be applied as an agricultural composition, administered to the soybean seed at the time of sowing.

[0565] For example, it is anticipated that a farmer will apply the agricultural composition to the soybean seeds simultaneously upon planting the seeds into the field. This can be accomplished, for example, by applying the agricultural composition to a hopper/bulk tank on a standard 16 row planter, which contains the soybean seeds and which is configured to plant the same into rows. Alternatively, the agricultural composition can be contained in a separate bulk tank on the planter and sprayed into the rows upon planting the soybean seed.

[0566] A control plot of soybean seeds, which are not administered the agricultural composition, will also be planted.

[0567] It is expected that the soybean plants grown from the seeds treated with the with the agricultural composition will exhibit a quantifiable and superior ability to tolerate drought conditions and/or exhibit superior water use efficiency, as compared to the control soybean plants.

[0568] The drought tolerance and/or water use efficiency can be based on any number of standard tests from the art, *e.g* leaf water retention, turgor loss point, rate of photosynthesis, leaf color and other phenotypic indications of drought stress, yield performance, and various root morphological and growth patterns.

III. Increased Nitrogen Use Efficiency in Agriculturally Important Crops

[0569] In certain embodiments of the disclosure, the present methods aim to decrease the amount of nitrogen that must be deposited into a given agricultural system and yet achieve the same or better yields for a given crop.

[0570] The methodologies presented herein—based upon utilizing the disclosed isolated microbes, consortia, and compositions comprising the same—have the potential to reduce the amount of nitrogen fertilizer that is lost by farmers every year due to nitrogen leaching into the air, soil, and waterways. This will enable a more sustainable agricultural system that is still able to produce yield results consistent with today's agricultural expectations.

Example 1: Increasing Ryegrass NUE with Isolated Microbes and Microbial Consortia

A. Seed Treatment with Isolated Microbe

[0571] In this example, an isolated microbe from **Tables 1-4** will be applied as a seed coating to seeds of ryegrass (*Lolium perenne*). Upon applying the isolated microbe as a seed coating, the ryegrass will be planted and cultivated in the standard manner.

[0572] A control plot of ryegrass seeds, which did not have the isolated microbe applied as a seed coating, will also be planted.

[0573] It is expected that the ryegrass plants grown from the seeds treated with the seed coating will exhibit a quantifiable and superior ability to utilize nitrogen, as compared to the control ryegrass plants.

[0574] The nitrogen use efficiency can be quantified by recording a measurable change in any of the main nitrogen metabolic pool sizes in the assimilation pathways (*e.g.*, a measurable change in one or more of the following: nitrate, nitrite, ammonia, glutamic acid, aspartic acid, glutamine, asparagine, lysine, leucine, threonine, methionine, glycine, tryptophan, tyrosine, total protein content of a plant part, total nitrogen content of a plant part, and/or chlorophyll content), or where the treated plant is shown to provide the same or elevated biomass or harvestable yield at lower

nitrogen fertilization levels compared to the control plant, or where the treated plant is shown to provide elevated biomass or harvestable yields at the same nitrogen fertilization levels compared to a control plant.

B. Seed Treatment with Microbial Consortia

[0575] In this example, a microbial consortium, comprising at least two microbes from **Tables 1-4** will be applied as a seed coating to seeds of ryegrass (*Lolium perenne*). Upon applying the microbial consortium as a seed coating, the ryegrass will be planted and cultivated in the standard manner.

[0576] A control plot of ryegrass seeds, which did not have the microbial consortium applied as a seed coating, will also be planted.

[0577] It is expected that the ryegrass plants grown from the seeds treated with the seed coating will exhibit a quantifiable and superior ability to utilize nitrogen, as compared to the control ryegrass plants.

[0578] The nitrogen use efficiency can be quantified by recording a measurable change in any of the main nitrogen metabolic pool sizes in the assimilation pathways (*e.g.*, a measurable change in one or more of the following: nitrate, nitrite, ammonia, glutamic acid, aspartic acid, glutamine, asparagine, lysine, leucine, threonine, methionine, glycine, tryptophan, tyrosine, total protein content of a plant part, total nitrogen content of a plant part, and/or chlorophyll content), or where the treated plant is shown to provide the same or elevated biomass or harvestable yield at lower nitrogen fertilization levels compared to the control plant, or where the treated plant is shown to provide elevated biomass or harvestable yields at the same nitrogen fertilization levels compared to a control plant.

C. Treatment with Agricultural Composition Comprising Isolated Microbe

[0579] In this example, an isolated microbe from **Tables 1-4** will be applied as an agricultural composition, administered to the ryegrass seed at the time of sowing.

[0580] For example, it is anticipated that a farmer will apply the agricultural composition to the ryegrass seeds simultaneously upon broadcasting said seeds into the field. This can be accomplished, for example, by applying the agricultural composition to a hopper or spreader, which contains the ryegrass seeds and which is configured to broadcast the same.

[0581] A control plot of ryegrass seeds, which are not administered the agricultural composition, will also be planted.

[0582] It is expected that the ryegrass plants grown from the seeds treated with the agricultural composition will exhibit a quantifiable and superior ability to utilize nitrogen, as compared to the control ryegrass plants.

[0583] The nitrogen use efficiency can be quantified by recording a measurable change in any of the main nitrogen metabolic pool sizes in the assimilation pathways (*e.g.*, a measurable change in one or more of the following: nitrate, nitrite, ammonia, glutamic acid, aspartic acid, glutamine, asparagine, lysine, leucine, threonine, methionine, glycine, tryptophan, tyrosine, total protein content of a plant part, total nitrogen content of a plant part, and/or chlorophyll content), or where the treated plant is shown to provide the same or elevated biomass or harvestable yield at lower nitrogen fertilization levels compared to the control plant, or where the treated plant is shown to provide elevated biomass or harvestable yields at the same nitrogen fertilization levels compared to a control plant.

D. Treatment with Agricultural Composition Comprising Microbial Consortia

[0584] In this example, a microbial consortium, comprising at least two microbes from **Tables 1-4** will be applied as an agricultural composition, administered to the ryegrass seed at the time of sowing.

[0585] For example, it is anticipated that a farmer will apply the agricultural composition to the ryegrass seeds simultaneously upon broadcasting said seeds into the field. This can be accomplished, for example, by applying the agricultural composition to a hopper or spreader, which contains the ryegrass seeds and which is configured to broadcast the same.

[0586] A control plot of ryegrass seeds, which are not administered the agricultural composition, will also be planted.

[0587] It is expected that the ryegrass plants grown from the seeds treated with the agricultural composition will exhibit a quantifiable and superior ability to utilize nitrogen, as compared to the control ryegrass plants.

[0588] The nitrogen use efficiency can be quantified by recording a measurable change in any of the main nitrogen metabolic pool sizes in the assimilation pathways (*e.g.*, a measurable change in one or more of the following: nitrate, nitrite, ammonia, glutamic acid, aspartic acid, glutamine, asparagine, lysine, leucine, threonine, methionine, glycine, tryptophan, tyrosine, total protein content of a plant part, total nitrogen content of a plant part, and/or chlorophyll content), or where the treated plant is shown to provide the same or elevated biomass or harvestable yield at lower nitrogen fertilization levels compared to the control plant, or where the treated plant is shown to provide elevated biomass or harvestable yields at the same nitrogen fertilization levels compared to a control plant.

Example 2: Increasing Maize NUE with Isolated Microbes and Microbial Consortia

A. Seed Treatment with Isolated Microbe

[0589] In this example, an isolated microbe from **Tables 1-4** will be applied as a seed coating to seeds of corn (*Zea mays*). Upon applying the isolated microbe as a seed coating, the corn will be planted and cultivated in the standard manner.

[0590] A control plot of corn seeds, which did not have the isolated microbe applied as a seed coating, will also be planted.

[0591] It is expected that the corn plants grown from the seeds treated with the seed coating will exhibit a quantifiable and superior ability to utilize nitrogen, as compared to the control corn plants.

[0592] The nitrogen use efficiency can be quantified by recording a measurable change in any of the main nitrogen metabolic pool sizes in the assimilation pathways (*e.g.*, a measurable change in one or more of the following: nitrate, nitrite, ammonia, glutamic acid, aspartic acid, glutamine, asparagine, lysine, leucine, threonine, methionine, glycine, tryptophan, tyrosine, total protein content of a plant part, total nitrogen content of a plant part, and/or chlorophyll content), or where the treated plant is shown to provide the same or elevated biomass or harvestable yield at lower nitrogen fertilization levels compared to the control plant, or where the treated plant is shown to provide elevated biomass or harvestable yields at the same nitrogen fertilization levels compared to a control plant.

B. Seed Treatment with Microbial Consortia

[0593] In this example, a microbial consortium, comprising at least two microbes from **Tables 1-4** will be applied as a seed coating to seeds of corn (*Zea mays*). Upon applying the microbial consortium as a seed coating, the corn will be planted and cultivated in the standard manner.

[0594] A control plot of corn seeds, which did not have the microbial consortium applied as a seed coating, will also be planted.

[0595] It is expected that the corn plants grown from the seeds treated with the seed coating will exhibit a quantifiable and superior ability to utilize nitrogen, as compared to the control corn plants.

[0596] The nitrogen use efficiency can be quantified by recording a measurable change in any of the main nitrogen metabolic pool sizes in the assimilation pathways (*e.g.*, a measurable change in one or more of the following: nitrate, nitrite, ammonia, glutamic acid, aspartic acid, glutamine, asparagine, lysine, leucine, threonine, methionine, glycine, tryptophan, tyrosine, total protein content of a plant part, total nitrogen content of a plant part, and/or chlorophyll content), or where the treated plant is shown to provide the same or elevated biomass or harvestable yield at lower nitrogen fertilization levels compared to the control plant, or where the treated plant is shown to provide elevated biomass or harvestable yields at the same nitrogen fertilization levels compared to a control plant.

C. Treatment with Agricultural Composition Comprising Isolated Microbe

[0597] In this example, an isolated microbe from **Tables 1-4** will be applied as an agricultural composition, administered to the corn seed at the time of sowing.

[0598] For example, it is anticipated that a farmer will apply the agricultural composition to the corn seeds simultaneously upon planting the seeds into the field. This can be accomplished, for example, by applying the agricultural composition to a hopper/bulk tank on a standard 16 row planter, which contains the corn seeds and which is configured to plant the same into rows. Alternatively, the agricultural composition can be contained in a separate bulk tank on the planter and sprayed into the rows upon planting the corn seed.

[0599] A control plot of corn seeds, which are not administered the agricultural composition, will also be planted.

[0600] It is expected that the corn plants grown from the seeds treated with the agricultural composition will exhibit a quantifiable and superior ability to utilize nitrogen, as compared to the control corn plants.

[0601] The nitrogen use efficiency can be quantified by recording a measurable change in any of the main nitrogen metabolic pool sizes in the assimilation pathways (*e.g.*, a measurable change in one or more of the following: nitrate, nitrite, ammonia, glutamic acid, aspartic acid, glutamine, asparagine, lysine, leucine, threonine, methionine, glycine, tryptophan, tyrosine, total protein content of a plant part, total nitrogen content of a plant part, and/or chlorophyll content), or where the treated plant is shown to provide the same or elevated biomass or harvestable yield at lower nitrogen fertilization levels compared to the control plant, or where the treated plant is shown to provide elevated biomass or harvestable yields at the same nitrogen fertilization levels compared to a control plant.

D. Treatment with Agricultural Composition Comprising Microbial Consortia

[0602] In this example, a microbial consortium, comprising at least two microbes from **Tables 1-4** will be applied as an agricultural composition, administered to the corn seed at the time of sowing.

[0603] For example, it is anticipated that a farmer will apply the agricultural composition to the corn seeds simultaneously upon planting the seeds into the field. This can be accomplished, for example, by applying the agricultural composition to a hopper/bulk tank on a standard 16 row planter, which contains the corn seeds and which is configured to plant the same into rows. Alternatively, the agricultural composition can be contained in a separate bulk tank on the planter and sprayed into the rows upon planting the corn seed.

[0604] A control plot of corn seeds, which are not administered the agricultural composition, will also be planted.

[0605] It is expected that the corn plants grown from the seeds treated with the agricultural composition will exhibit a quantifiable and superior ability to utilize nitrogen, as compared to the control corn plants.

[0606] The nitrogen use efficiency can be quantified by recording a measurable change in any of the main nitrogen metabolic pool sizes in the assimilation pathways (*e.g.*, a measurable change in one or more of the following: nitrate, nitrite, ammonia, glutamic acid, aspartic acid, glutamine, asparagine, lysine, leucine, threonine, methionine, glycine, tryptophan, tyrosine, total protein content of a plant part, total nitrogen content of a plant part, and/or chlorophyll content), or where the treated plant is shown to provide the same or elevated biomass or harvestable yield at lower nitrogen fertilization levels compared to the control plant, or where the treated plant is shown to provide elevated biomass or harvestable yields at the same nitrogen fertilization levels compared to a control plant.

Example 3: Increasing Soybean NUE with Isolated Microbes and Microbial Consortia

A. Seed Treatment with Isolated Microbe

[0607] In this example, an isolated microbe from **Tables 1-4** will be applied as a seed coating to seeds of soybean (*Glycine max*). Upon applying the isolated microbe as a seed coating, the soybean will be planted and cultivated in the standard manner.

[0608] A control plot of soybean seeds, which did not have the isolated microbe applied as a seed coating, will also be planted.

[0609] It is expected that the soybean plants grown from the seeds treated with the seed coating will exhibit a quantifiable and superior ability to utilize nitrogen, as compared to the control soybean plants.

[0610] The nitrogen use efficiency can be quantified by recording a measurable change in any of the main nitrogen metabolic pool sizes in the assimilation pathways (*e.g.*, a measurable change in one or more of the following: nitrate, nitrite, ammonia, glutamic acid, aspartic acid, glutamine, asparagine, lysine, leucine, threonine, methionine, glycine, tryptophan, tyrosine, total protein content of a plant part, total nitrogen content of a plant part, and/or chlorophyll content), or where the treated plant is shown to provide the same or elevated biomass or harvestable yield at lower nitrogen fertilization levels compared to the control plant, or where the treated plant is shown to provide elevated biomass or harvestable yields at the same nitrogen fertilization levels compared to a control plant.

B. Seed Treatment with Microbial Consortia

[0611] In this example, a microbial consortium, comprising at least two microbes from **Tables 1-4** will be applied as a seed coating to seeds of soybean (*Glycine max*). Upon applying the microbial consortium as a seed coating, the soybean will be planted and cultivated in the standard manner.

[0612] A control plot of soybean seeds, which did not have the microbial consortium applied as a seed coating, will also be planted.

[0613] It is expected that the soybean plants grown from the seeds treated with the seed coating will exhibit a quantifiable and superior ability to utilize nitrogen, as compared to the control soybean plants.

[0614] The nitrogen use efficiency can be quantified by recording a measurable change in any of the main nitrogen metabolic pool sizes in the assimilation pathways (*e.g.*, a measurable change in one or more of the following: nitrate, nitrite, ammonia, glutamic acid, aspartic acid, glutamine, asparagine, lysine, leucine, threonine, methionine, glycine, tryptophan, tyrosine, total protein content of a plant part, total nitrogen content of a plant part, and/or chlorophyll content), or where the treated plant is shown to provide the same or elevated biomass or harvestable yield at lower nitrogen fertilization levels compared to the control plant, or where the treated plant is shown to provide elevated biomass or harvestable yields at the same nitrogen fertilization levels compared to a control plant.

C. Treatment with Agricultural Composition Comprising Isolated Microbe

[0615] In this example, an isolated microbe from **Tables 1-4** will be applied as an agricultural composition, administered to the soybean seed at the time of sowing.

[0616] For example, it is anticipated that a farmer will apply the agricultural composition to the soybean seeds simultaneously upon planting the seeds into the field. This can be accomplished, for example, by applying the agricultural composition to a hopper/bulk tank on a standard 16 row planter, which contains the soybean seeds and which is configured to plant the same into rows. Alternatively, the agricultural composition can be contained in a separate bulk tank on the planter and sprayed into the rows upon planting the soybean seed.

[0617] A control plot of soybean seeds, which are not administered the agricultural composition, will also be planted.

[0618] It is expected that the soybean plants grown from the seeds treated with the agricultural composition will exhibit a quantifiable and superior ability to utilize nitrogen, as compared to the control soybean plants.

[0619] The nitrogen use efficiency can be quantified by recording a measurable change in any of the main nitrogen metabolic pool sizes in the assimilation pathways (*e.g.*, a measurable change in one or more of the following: nitrate, nitrite, ammonia, glutamic acid, aspartic acid, glutamine, asparagine, lysine, leucine, threonine, methionine, glycine, tryptophan, tyrosine, total protein content of a plant part, total nitrogen content of a plant part, and/or chlorophyll content), or where the treated plant is shown to provide the same or elevated biomass or harvestable yield at lower nitrogen fertilization levels compared to the control plant, or where the treated plant is shown to provide elevated biomass or harvestable yields at the same nitrogen fertilization levels compared to a control plant.

D. Treatment with Agricultural Composition Comprising Microbial Consortia

[0620] In this example, a microbial consortium, comprising at least two microbes from **Tables 1-4** will be applied as an agricultural composition, administered to the soybean seed at the time of sowing.

[0621] For example, it is anticipated that a farmer will apply the agricultural composition to the soybean seeds simultaneously upon planting the seeds into the field. This can be accomplished, for example, by applying the agricultural composition to a hopper/bulk tank on a standard 16 row planter, which contains the soybean seeds and which is configured to plant the same into rows. Alternatively, the agricultural composition can be contained in a separate bulk tank on the planter and sprayed into the rows upon planting the soybean seed.

[0622] A control plot of soybean seeds, which are not administered the agricultural composition, will also be planted.

[0623] It is expected that the soybean plants grown from the seeds treated with the agricultural composition will exhibit a quantifiable and superior ability to utilize nitrogen, as compared to the control soybean plants.

[0624] The nitrogen use efficiency can be quantified by recording a measurable change in any of the main nitrogen metabolic pool sizes in the assimilation pathways (*e.g.*, a measurable change in one or more of the following: nitrate, nitrite, ammonia, glutamic acid, aspartic acid, glutamine, asparagine, lysine, leucine, threonine, methionine, glycine, tryptophan, tyrosine, total protein content of a plant part, total nitrogen content of a plant part, and/or chlorophyll content), or where the treated plant is shown to provide the same or elevated biomass or harvestable yield at lower nitrogen fertilization levels compared to the control plant, or where the treated plant is shown to provide elevated biomass or harvestable yields at the same nitrogen fertilization levels compared to a control plant.

IV. Increased Metabolite Expression in Agriculturally Important Crops

[0625] In certain embodiments of the disclosure, the present methods aim to increase the production of a metabolite of interest for a given crop.

[0626] The methodologies presented herein—based upon utilizing the disclosed isolated microbes, consortia, and compositions comprising the same—have the potential to increase the production of a metabolite of interest for a given crop.

Example 1: Increasing Sugar Content in Basil with Isolated Microbes and Microbial Consortia

A. Seed Treatment with Isolated Microbe

[0627] In this example, an isolated microbe from **Tables 1-4** will be applied as a seed coating to seeds of basil (*Ocium basilicum*). Upon applying the isolated microbe as a seed coating, the basil will be planted and cultivated in the standard manner.

[0628] A control plot of basil seeds, which did not have the isolated microbe applied as a seed coating, will also be planted.

[0629] It is expected that the basil plants grown from the seeds treated with the seed coating will exhibit a quantifiable increase in water-soluble carbohydrate content, as compared to the control basil plants.

B. Seed Treatment with Microbial Consortia

[0630] In this example, a microbial consortium, comprising at least two microbes from **Tables 1-4** will be applied as a seed coating to seeds of basil (*Ocium basilicum*).

Upon applying the microbial consortium as a seed coating, the basil will be planted and cultivated in the standard manner.

[0631] A control plot of basil seeds, which did not have the microbial consortium applied as a seed coating, will also be planted.

[0632] It is expected that the basil plants grown from the seeds treated with the seed coating will exhibit a quantifiable increase in water-soluble carbohydrate content, as compared to the control basil plants.

V. Synergistic Effect Achievable with Combination of Microbes and Ascend®

A. Seed Treatment with Isolated Microbe Combined with Ascend®

[0633] In this example, an isolated microbe from **Tables 1-4** will be combined with Ascend® and applied as a seed coating to seeds of a plant. Upon applying the isolated microbe/Ascend® combination as a seed coating, the plant will be planted and cultivated in the standard manner.

[0634] A control plot of plant seeds, which did not have the isolated microbe/Ascend® combination applied as a seed coating, will also be planted.

[0635] It is expected that the plants grown from the seeds treated with the seed coating will exhibit a quantifiable increase in a phenotypic trait of interest, as compared to the control plants. It is expected that a synergistic effect may be observed for the phenotypic trait of interest.

B. Seed Treatment with Microbial Consortia Combined with Ascend®

[0636] In this example, a microbial consortium, comprising at least two microbes from **Tables 1-4** will be combined with Ascend® and then applied as a seed coating to seeds of a plant. Upon applying the microbial consortium/Ascend® combination as a seed coating, the plant will be planted and cultivated in the standard manner.

[0637] A control plot of plant seeds, which did not have the microbial consortium/Ascend® combination applied as a seed coating, will also be planted.

[0638] It is expected that the plants grown from the seeds treated with the seed coating will exhibit a quantifiable increase in a phenotypic trait of interest, as

compared to the control plants. It is expected that a synergistic effect may be observed for the phenotypic trait of interest.

VI. Microbial Consortia

[0639] The microbial consortia utilized in the examples are presented in Table 24 in a non-limiting matter, while recognizing that the microbial consortia may comprise any one or more microbes presented in tables 1-4.

Table 24: Consortia Compositions

ID	Microbes		ID	Microbes
D1	*Stenotrophomonas maltophilia* BDNZ 54073 *Rhodococcus erythropolis* BDNZ 54093 *Pantoea vagans* BDNZ 55529 *Pseudomonas oryzihabitans* BDNZ 55530		**D2**	*Rhodococcus erythropolis* BDNZ 54093 *Pseudomonas oryzihabitans* BDNZ 55530 *Rahnella aquatilis* BDNZ 56532
D3	*Stenotrophomonas maltophilia* BDNZ 54073 *Rhodococcus erythropolis* BDNZ 54093 *Pantoea vagans* BDNZ 55529 *Rahnella aquatilis* BDNZ 56532		**D4**	*Stenotrophomonas maltophilia* BDNZ 54073 *Rhodococcus erythropolis* BDNZ 54093 *Pseudomonas fluorescens* BDNZ 56530 *Pantoea agglomerans* BDNZ 57547
D5	*Rhodococcus erythropolis* BDNZ 54093 *Pseudomonas fluorescens* BDNZ 56530 *Pantoea agglomerans* BDNZ 57547		**D6**	*Rahnella aquatilis* BDNZ 57157 *Rahnella aquatilis* BDNZ 58013 *Rhizobium etli* BDNZ 60473
D7	*Stenotrophomonas maltophilia* BDNZ 54073 *Rhodococcus erythropolis* BDNZ		**D8**	*Stenotrophomonas maltophilia* BDNZ 54073 *Rhodococcus erythropolis* BDNZ

ID	Microbes		ID	Microbes
	54093 *Pantoea vagans* BDNZ 55529 *Pseudomonas oryzihabitans* BDNZ 55530 *Rahnella aquatilis* BDNZ 56532			54093 *Pantoea vagans* BDNZ 55529 *Pseudomonas oryzihabitans* BDNZ 55530 *Rahnella aquatilis* BDNZ 57157 *Rahnella aquatilis* BDNZ 58013 *Rhizobium etli* BDNZ 60473
D9	*Rahnella aquatilis* BDNZ 56532		**D10**	*Rhodococcus erythropolis* BDNZ 54093 *Pantoea vagans* BDNZ 55529 *Pseudomonas oryzihabitans* BDNZ 55530 *Rahnella aquatilis* BDNZ 56532
D11	*Exiguobacterium aurantiacum* BCI 50 *Duganella radicis* BCI 105 *Rhizobium pusense* BCI 106 *Kosakonia radicincitans* BCI 107 *Delftia lacustris* BCI 124		**D12**	*Rahnella aquatilis* BCI 29 *Duganella radicis* BCI 31 *Exiguobacterium sibiricum* BCI 116 *Novosphingobium sediminicola* BCI 130 *Ensifer sp.* BCI 131 *Microbacterium oleivorans* BCI 132
D13	*Chitinophaga terrae* BCI 79 *Exiguobacterium sp.* BCI 81 *Novosphingobium sediminicola* BCI 82 *Exiguobacterium acetylicum* BCI 83 *Variovorax ginsengisoli* BCI 137		**D14**	*Exiguobacterium acetylicum* BCI 23 *Rahnella aquatilis* BCI 29 *Rhizobium lemnae* BCI 34 *Achromobacter spanius* BCI 385
D15	*Dyadobacter soli* BCI 68		**D16**	*Rhodococcus erythropolis* BDNZ

ID	Microbes		ID	Microbes
	Chitinophaga terrae BCI 79 *Pedobacter terrae* BCI 91 *Massilia albidiflava* BCI 97 *Novosphingobium sediminicola* BCI 136			54093 *Pantoea vagans* BDNZ 55529 *Pseudomonas oryzihabitans* BDNZ 55530
D17	*Rhodococcus erythropolis* BDNZ 54093 *Rahnella aquatilis* BDNZ 56532 *Rahnella aquatilis* BDNZ 58013 *Rhizobium etli* BDNZ 60473		**D18**	*Exiguobacterium acetylicum* BCI125 *Bacillus megaterium* BCI 255 *Paenibacillus glycanilyticus* BCI 418
D19	*Agrobacterium fabrum* BCI 608 *Acidovorax soli* BCI 690 *Rhizobium grahamii* BCI 691 *Bacillus subtilis* BCI 989		**D20**	*Arthrobacter pascens* BCI 682 *Novosphingobium lindaniclasticum* BCI 684 *Bosea robiniae* BCI 688 *Microbacterium maritypicum* BCI 689 *Sphingopyxis alaskensis* BCI 914
D21	*Chryseobacterium rhizosphaerae* BCI 615 *Hydrogenophaga atypica* BCI 687 *Bosea robiniae* BCI 689 *Microbacterium maritypicum* BCI 688 *Agrobacterium fabrum* BCI 958		**D22**	*Novosphingobium resinovorum* BCI 557 *Arthrobacter mysorens* BCI 700 *Bosea thiooxidans* BCI 703 *Bacillus oleronius* BCI 1071
D23	*Pedobacter rhizosphaerae* BCI 598 *Bacillus sp.* BCI 715 *Pseudomonas jinjuensis* BCI 804 *Pseudomonas putida* BCI 805		**D24**	*Novosphingobium sediminicola* BCI 130 *Ensifer sp.* BCI 131 *Microbacterium oleivorans* BCI 132
D25	*Arthrobacter cupressi* BCI 59		**D26**	*Bosea robiniae* BCI 689

ID	Microbes		ID	Microbes
	Dyadobacter soli BCI 68			*Bosea thiooxidans* BCI 703 *Bosea eneae* BCI 1267
D27	*Pseudomonas helmanticensis* BCI 616 *Arthrobacter pascens* BCI 682 *Bosea robiniae* BCI 689 *Pseudomonas putida* BCI 791 *Agrobacterium fabrum* BCI 958		**D28**	*Chryseobacterium rhizosphaerae* BCI 597 *Defluviimonas denitrificans* BCI 712 *Arthrobacter nicotinovorans* BCI 717 *Pseudomonas putida* BCI 802
D29	*Pseudomonas florescens* BDNZ 71627 *Novosphingobium sediminicola* BDNZ 71628 *Microbacterium azadirachtae* BDNZ 71629		**D30**	*Rhodococcus erythropolis* BDNZ 74552 *Tumebacillus permanentifrigoris* BDNZ 74542
D31	*Tumebacillus permanentifrigoris* BDNZ 72229		**D32**	*Rhodococcus erythropolis* BNDZ 72250 *Bacillus megatarium* BDNZ 72242 *Leifsonia lichenia* BDNZ 72243
D33	*Bacillus megatarium* BDNZ 72242 *Leifsonia lichenia* BDNZ 72243 *Bacillus aryabhattai* BDNZ 72259		**D34**	*Novosphingobium lindaniclasticum* BDNZ 71222
D35	*Rhodococcus erythropolis* BDNZ 71221 *Novosphingobium lindaniclasticum* BDNZ 71222 *Microbacterium azadirachtae* BDNZ 71663		**D36**	*Bacillus cereus* BDNZ 71220 *Rhodococcus erythropolis* BNDZ 71221 *Novosphingobium lindaniclasticum* BDNZ 71222
D37	*Massilia kyonggiensis* BDNZ 73021 *Microbacterium azadirachtae* BDNZ 72996		**D38**	*Variovorax paradoxus* BDNZ 72150 *Tumebacillus permanentifrigoris* BDNZ 72366

ID	Microbes		ID	Microbes
	Rhizobium tibeticum BDNZ 72135			
D39	*Tumebacillus permanentifrigoris* BDNZ 72287 *Bacillus megatarium* BDNZ 72255			
A1	*Stenotrophomonas maltophilia* BDNZ 54073 *Rhodococcus erythropolis* BDNZ 54093 *Pantoea vagans* BDNZ 55529 *Pseudomonas oryzihabitans* BDNZ55530		**A2**	*Flavobacterium glaciei* BDNZ 66487 *Massilia niastensis* BDNZ 55184 *Pseudomonas fluorescens* BDNZ 54480
A3	*Azospirillum lipoferum* BDNZ 57661 *Herbaspirillum huttiense* BDNZ 54487 *Pantoea agglomerans* BDNZ 54499 *Pseudomonas fluorescens* BDNZ 54480		**A4**	*Janthinobacterium sp.* BDNZ 54456 *Mucilaginibacter dorajii* BDNZ 66513 *Pseudomonas psychrotolerans* BDNZ 54517
A5	*Janthinobacterium sp.* BDNZ 54456 *Mucilaginibacter dorajii* BDNZ 66513 *Pseudomonas psychrotolerans* BDNZ 54517		**A6**	*Rhizobium etli* BDNZ 61443 *Caulobacter henrici* BDNZ 66341 *Duganella violaceinigra* BDNZ 66361
A7	*Duganella violaceinigra* BDNZ 66361		**A8**	*Ramlibacter henchirensis* BDNZ 66331 *Rhizobium pisi* BDNZ 66326 *Mucilaginibacter gosypii* BDNZ 66321 *Paenibacillus amylolyticus* BDNZ 66316
A9	*Polaromonas ginsengisoli* BDNZ 66373		**A10**	*Sphingobium quisquiliarum* BDNZ 66576

ID	Microbes		ID	Microbes
				Bacillus subtilis BDNZ 66347 *Azospirillum lipoferum* BDNZ 66297
A11	*Rhodoferax ferrireducens* BDNZ 66374 *Mucilaginibacter gosypii* BDNZ 66321 *Paenibacillus amylolyticus* BDNZ 66316 *Azospirillum lipoferum* BDNZ66315		**A12**	*Rhodococcus erythropolis* BDNZ 54093 *Pseudomonas oryzihabitans* BDNZ 55530 *Rahnella aquatilis* BDNZ 56532
A13	*Rhodococcus erythropolis* BDNZ 54093 *Rahnella aquatilis* BDNZ 57157 *Azotobacter chroococcum* BDNZ57597		**A14**	*Rhodococcus erythropolis* BDNZ54299 *Rahnella aquatilis* BDNZ58013 *Herbaspirillum huttiense* BDNZ 65600
A15	*Rhodococcus erythropolis* BDNZ 54093 *Pseudomonas oryzihabitans* BDNZ 55530 *Rahnella aquatilis* BDNZ 56532		**A16**	*Brevibacterium frigoritolerans* BCI 4468 *Janibacter limosus* BCI 4708 *Pseudomonas yamanorum* BCI 4853 *Bacillus megaterium* BCI 4473

VII. Effects of Microbial Consortia on Plant Phenotypes

Example 1: Evaluation of Phenotype of Plants Exposed to Microbial Consortia in U.S. Trials

[0640] Plants disclosed in Table 25 were grown in a controlled environment in a rooting volume of 167ml and typically in a soil substrate. The chamber photoperiod was set to 16 hours for all experiments on all species. The light intensity ranged from 180 µmol PAR m^{-2} s^{-1} to approximately 200 µmol PAR m^{-2} s^{-1} as plant height increased during experiments.

[0641] The air temperature was typically 28°C during the photoperiod, decreasing to 23°C during the night for *Zea mays, Glycine max,* and *Sorghum bicolor* experiments. Air temperature was typically 24°C during the photoperiod, decreasing to 20°C during the night for *Triticum aestivum* experiments.

[0642] Phenotypes were measured during early vegetative growth, typically before the V3 developmental stage.

[0643] Leaf chlorophyll content was measured midway along the youngest fully-expanded leaf, non-destructively using a meter providing an index of leaf chlorophyll content (CCM-200, Opti Sciences, Hudson, NH, US).

[0644] Whole plant, shoot, and root dry weight was measured after plants had been dried to a constant weight in a drying oven set to 80°C. At least 10 replicate plants were measured for each phenotype measured in each experiment.

[0645] For evaluations on *Glycine max*, the number of nodules were counted.

[0646] A control treatment of uninoculated seeds was run in each experiment for comparison with plants grown from seeds inoculated with microbial consortia.

Table 25

				Controlled Environment Efficacy (%)					
Consortia	**Crop**	**Assay**	**Evaluations**	**Plant**	**Shoot**	**Root**	**Chlorophyll**	**T leaf**	**Nodulation**
D1	Zea mays	early vigor	21			74		25	
D6	Zea mays	early vigor	15			36	36	22	
D7	Zea mays	early vigor	15	72	63	65	25	0	
D11	Zea mays	early vigor	17			60		20	
D13	Zea mays	early vigor	12		40		33	0	
D14	Zea mays	early vigor	15	62	69		22	10	
D15	Zea mays	early vigor	12			70	25	0	
D25	Zea mays	early vigor	13			63	22	0	
D2	Zea mays	early vigor	5 / 4*	100	100	100*	60	_	
D3	Zea mays	early vigor	5 / 4*	80	100	75*	60	_	
D4	Zea mays	early vigor	5 / 4*	80	80	75*	60	_	
D5	Zea mays	early vigor	5 / 4*	60	80	100*	80	_	
D8	Zea mays	early vigor	5 / 4*	60	80	75*	40	_	
D12	Zea mays	early vigor	3	100	100	100	66	_	
D24	Zea mays	early vigor	2	100	100	100	0	0	
D1	Sorghum bicolor	early vigor	5	60	80	80	40	20	
D11	Sorghum bicolor	early vigor	3	60	80	80	40	20	
D13	Sorghum bicolor	early vigor	5	80	60	80	60	40	
D14	Sorghum bicolor	early vigor	5	80	80	100	40	20	
D15	Sorghum bicolor	early vigor	3	100	66	100	33	0	
D6	Sorghum bicolor	early vigor	3	100	100	100	33	66	
D7	Sorghum bicolor	early vigor	3	33	33	33	33	66	
D25	Sorghum bicolor	early vigor	3	66	100	66	33	66	
D9	Triticum aestivum	early vigor	8 / 6*		38	63	33*	_	
D10	Triticum aestivum	early vigor	8 / 6*	63	38	63		_	
D16	Triticum aestivum	early vigor	8 / 6*			63	33*	_	

				Controlled Environment Efficacy (%)					
Consortia	Crop	Assay	Evaluations	Plant	Shoot	Root	Chlorophyll	T leaf	Nodulation
D17	Triticum aestivum	early vigor	8 / 6*	76	63	75	33*	–	
D18	Triticum aestivum	early vigor	8 / 6*		50	50	33*	–	
D26	Triticum aestivum	early vigor	8 / 6*		66	66	0*	–	
D19	Glycine max	early vigor	2	0	0	0		–	
D20	Glycine max	early vigor	2	100	100	100	0	–	
D21	Glycine max	early vigor	2	0	0	0	0	–	
D22	Glycine max	early vigor	2			0		–	
D23	Glycine max	early vigor	2		100			–	
D27	Glycine max	cold tolerance	3		100				
D28	Glycine max	cold tolerance	12/3*				67*		75
A1	Zea mays	early vigor	5	–	80	80	–	–	
A2	Triticum aestivum	cold tolerance	4	–	75	75	–	–	
A3	Triticum aestivum	cold tolerance	4	–	75	75	–	–	
A4	Triticum aestivum	cold tolerance	2	–	100	100	–	–	
A5	Triticum aestivum	early vigor	2	–	50	50	–	–	
A6	Solanum sp.	early vigor	2	–	100	100	–	–	
A7	Solanum sp.	early vigor	3	–	100	100	–	–	
A8	Solanum sp.	early vigor	3	–	100	66	–	–	
A9	Solanum sp.	early vigor	3	–	66	100	–	–	
A10	Solanum sp.	early vigor	3	–	66	66	–	–	
A11	Solanum sp.	early vigor	3	–	100	66	–	–	
A12	Solanum sp.	early vigor	2	–	100	50	–	–	
A13	Triticum aestivum	early vigor	2	–	0	0	–	–	
A14	Triticum aestivum	early vigor	2	–			–	–	

[0647] The data presented in table 25 describes the percentage of time (efficiency) a particular consortium changed a phenotype of interest relative to a control run in the same experiment. The measured phenotypes were whole plant dry weight (plant), shoot dry weight (shoot), root dry weight (root), leaf chlorophyll content (chlorophyll), leaf temperature (Tleaf), and nodulation.

[0648] The data presented is averaged across the number of times a specific consortium was tested against a control (evaluations). For consortia where different phenotypes were measured in a different number of evaluations, an asterisk was placed next to data points to match the phenotype with the number of evaluations. Evaluations have been broken down and displayed for specific crop species (crop).

[0649] The presented data identifies consortia that have increased a phenotype of interest in greater than 60% of evaluations (hit rate >59) and consortia that decreased a phenotype of interest in greater than 60% of evaluations (hit rate<41). Both increases and decreases in a phenotype of interest were recorded to reflect the possibility that decreases in select phenotypes of interest are yield relevant. Improvement in canopy photosynthesis through decreased leaf chlorophyll, and improvement in drought tolerance through decreased shoot biomass constitute two examples.

Example 2: Further Evaluation of Phenotype of Plants Exposed to Microbial Consortia in U.S. Trials

A. Evaluation of microbial effects on stem diameter of *Zea mays*

[0650] Microbial consortia disclosed in Table 26 were evaluated on three different seed sources each planted into 4.5L pots containing one of two soils, a low fertility topsoil and a clay loam. The combination of 3 seed sources and 2 soils yielded six unique testing combinations.

[0651] Ten replicate plants were used for each seed and soil testing combination. All plants were grown in a greenhouse throughout the duration of the experiment. All plants were irrigated at least daily to minimize water stress, and fertilized weekly beginning when the V1 leaf was developed.

[0652] Stem diameter was measured to the nearest 0.5mm using calipers. Measurements were made immediately beneath the V3 leaf for all plants when the V3 leaf was fully developed in all control plants. Because the stem is not perfectly

circular the calipers were rotated around the stem and the widest measurement taken. Microbial consortia that increased stem diameter in at least 60% of test combinations are identified in Table 26.

Table 26

Consortia	Crop	Growth Environment	Trait	Phenotype	Tests (n)	Wins
A16	Corn	Greenhouse	Early Vigor	Increased stem diameter	6	66%

Example 3: Evaluation of Phenotype of Plants Exposed to Microbial Consortia in New Zealand Trials

[0653] A. Seed Treatment with Microbial Consortia

[0654] The inoculants were prepared from isolates grown as spread plates on R2A incubated at 25°C for 48 to 72 hours. Colonies were harvested by blending with sterile distilled water (SDW) which was then transferred into sterile containers. Serial dilutions of the harvested cells were plated and incubated at 25°C for 24 hours to estimate the number of colony forming units (CFU) in each suspension. Dilutions were prepared using individual isolates or blends of isolates (consortia) to deliver ~$1x10^5$ cfu/microbe/seed and seeds inoculated by either imbibition in the liquid suspension or by overtreatment with 5% vegetable gum and oil.

[0655] Seeds corresponding to the plants of table 27 were planted within 24 to 48 hours of treatment in agricultural soil, potting media or inert growing media. Plants were grown in small pots (28 mL to 200 mL) in either a controlled environment or in a greenhouse. Chamber photoperiod was set to 16 hours for all experiments on all species. Air temperature was typically maintained between 22-24°C.

[0656] Unless otherwise stated, all plants were watered with tap water 2 to 3 times weekly. Growth conditions were varied according to the trait of interest and included manipulation of applied fertilizer, watering regime and salt stress as follows:

- Low N – seeds planted in soil potting media or inert growing media with no applied N fertilizer
- Moderate N – seeds planted in soil or growing media supplemented with commercial N fertilizer to equivalent of 135 kg/ha applied N

- Insol P – seeds planted in potting media or inert growth substrate and watered with quarter strength Pikovskaya's liquid medium containing tri-calcium phosphate as the only form phosphate fertilizer.
- Cold Stress – seeds planted in soil, potting media or inert growing media and incubated at 10°C for one week before being transferred to the plant growth room.
- Salt stress - seeds planted in soil, potting media or inert growing media and watered with a solution containing between 100 to 200 mg/L NaCl.

[0657] Untreated (no applied microbe) controls were prepared for each experiment. Plants were randomized on trays throughout the growth environment. Between 10 and 30 replicate plants were prepared for each treatment in each experiment. Phenotypes were measured during early vegetative growth, typically before the V3 developmental stage and between 3 and 6 weeks after sowing. Foliage was cut and weighed. Roots were washed, blotted dry and weighed. Results indicate performance of treatments against the untreated control.

Table 27

				Shoot	Root
Microbe sp.	**Strain ID**	**Crop**	**Assay**	**IOC (%)**	**IOC (%)**
Bosea thiooxidans overall	**1**	**2**	**3**	**Efficacy 100%**	**Efficacy 100%**
Bosea thiooxidans	54522	Wheat	Early vigor - insol P	30-40	_
Bosea thiooxidans	54522	Ryegrass	Early vigor	50-60	50-60
Bosea thiooxidans	54522	Ryegrass	Early vigor - moderate P	0-10	0-10
Duganella violaceinigra overall	**1**	**1**	**1**	**Efficacy 100%**	**Efficacy 100%**
Duganella violaceinigra	66361	Tomato	Early vigor	0-10	0-10
Duganella violaceinigra	66361	Tomato	Early vigor	30-40	40-50
Duganella violaceinigra	66361	Tomato	Early vigor	20-30	20-30
Herbaspirillum huttiense overall	**2**	**2**	**2**	**Efficacy 100%**	**_**
Herbaspirillum huttiense	54487	Wheat	Early vigor - insol P	30-40	_
Herbaspirillum huttiense	60507	Maize	Early vigor - salt stress	0-10	0-10
Janthinobacterium sp. Overall	**2**	**2**	**2**	**Efficacy 100%**	**_**
Janthinobacterium sp.	54456	Wheat	Early vigor - insol P	30-40	_
Janthinobacterium sp.	54456	Wheat	Early vigor - insol P	0-10	_
Janthinobacterium sp.	63491	Ryegrass	Early vigor - drought stress	0-10	0-10
Massilia niastensis overall	**1**	**1**	**2**	**Efficacy 80%**	**Efficacy 80%**
Massilia niastensis	55184	Wheat	Early vigor - salt stress	0-10	20-30
Massilia niastensis	55184	Winter wheat	Early vigor - cold stress	0-10	10-20
Massilia niastensis	55184	Winter wheat	Early vigor - cold stress	20-30	20-30

				Shoot	Root
Microbe sp.	**Strain ID**	**Crop**	**Assay**	**IOC (%)**	**IOC (%)**
Massilia niastensis	55184	Winter wheat	Early vigor - cold stress	10-20	10-20
Massilia niastensis	55184	Winter wheat	Early vigor - cold stress	<0	<0
Novosphingobium rosa overall	**2**	**1**	**1**	**Efficacy 100%**	**Efficacy 100%**
Novosphingobium rosa	65589	Maize	Early vigor - cold stress	0-10	0-10
Novosphingobium rosa	65619	Maize	Early vigor - cold stress	0-10	0-10
Paenibacillus amylolyticus overall	**1**	**1**	**1**	**Efficacy 100%**	**Efficacy 100%**
Paenibacillus amylolyticus	66316	Tomato	Early vigor	0-10	0-10
Paenibacillus amylolyticus	66316	Tomato	Early vigor	10-20	10-20
Paenibacillus amylolyticus	66316	Tomato	Early vigor	0-10	0-10
Pantoea agglomerans	**3**	**2**	**3**	**Efficacy 33%**	**Efficacy 50%**
Pantoea agglomerans	54499	Wheat	Early vigor - insol P	40-50	_
Pantoea agglomerans	57547	Maize	Early vigor - low N	<0	0-10
Pantoea vagans (formerly P. agglomerans)	55529	Maize	Early vigor	<0	<0
Polaromonas ginsengisoli	**1**	**1**	**1**	**Efficacy 66%**	**Efficacy 100%**
Polaromonas ginsengisoli	66373	Tomato	Early vigor	0-10	0-10
Polaromonas ginsengisoli	66373	Tomato	Early vigor	20-30	30-40
Polaromonas ginsengisoli	66373	Tomato	Early vigor	<0	10-20
Pseudomonas fluorescens	**1**	**2**	**2**	**Efficacy 100%**	_
Pseudomonas fluorescens	54480	Wheat	Early vigor - insol P	>100	_
Pseudomonas fluorescens	56530	Maize	Early vigor - moderate N	0-10	_

				Shoot	Root
Microbe sp.	**Strain ID**	**Crop**	**Assay**	**IOC (%)**	**IOC (%)**
Rahnella aquatilis	**3**	**3**	**4**	**Efficacy 80%**	**Efficacy 63%**
Rahnella aquatilis	56532	Maize	Early vigor - moderate N	10-20	_
Rahnella aquatilis	56532	Maize	Early vigor - moderate N	0-10	0-10
Rahnella aquatilis	56532	Wheat	Early vigor - cold stress	0-10	10-20
Rahnella aquatilis	56532	Wheat	Early vigor - cold stress	<0	0-10
Rahnella aquatilis	56532	Wheat	Early vigor - cold stress	10-20	<0
Rahnella aquatilis	57157	Ryegrass	Early vigor	<0	_
Rahnella aquatilis	57157	Maize	Early vigor - low N	0-10	0-10
Rahnella aquatilis	57157	Maize	Early vigor - low N	0-10	<0
Rahnella aquatilis	58013	Maize	Early vigor	0-10	10-20
Rahnella aquatilis	58013	Maize	Early vigor - low N	0-10	<0
Rhodococcus erythropolis	**3**	**1**	**3**	**Efficacy 66%**	**_**
Rhodococcus erythropolis	54093	Maize	Early vigor - low N	40-50	_
Rhodococcus erythropolis	54299	Maize	Early vigor - insol P	>100	_
Rhodococcus erythropolis	54299	Maize	Early vigor	<0	<0
Stenotrophomonas chelatiphaga	**6**	**1**	**1**	**Efficacy 60%**	**Efficacy 60%**
Stenotrophomonas chelatiphaga	54952	Maize	Early vigor	0-10	0-10
Stenotrophomonas chelatiphaga	47207	Maize	Early vigor	<0	0
Stenotrophomonas chelatiphaga	64212	Maize	Early vigor	0-10	10-20
Stenotrophomonas chelatiphaga	64208	Maize	Early vigor	0-10	0-10
Stenotrophomonas chelatiphaga	58264	Maize	Early vigor	<0	<0

				Shoot	Root
Microbe sp.	**Strain ID**	**Crop**	**Assay**	**IOC (%)**	**IOC (%)**
Stenotrophomonas maltophilia	**6**	**1**	**2**	**Efficacy 43%**	**Efficacy 66%**
Stenotrophomonas maltophilia	54073	Maize	Early vigor - low N	50-60	_
Stenotrophomonas maltophilia	54073	Maize	Early vigor	<0	0-10
Stenotrophomonas maltophilia	56181	Maize	Early vigor	0-10	<0
Stenotrophomonas maltophilia	54999	Maize	Early vigor	0-10	0-10
Stenotrophomonas maltophilia	54850	Maize	Early vigor	0	0-10
Stenotrophomonas maltophilia	54841	Maize	Early vigor	<0	0-10
Stenotrophomonas maltophilia	46856	Maize	Early vigor	<0	<0
Stenotrophomonas rhizophila	**8**	**1**	**1**	**Efficacy 12.5%**	**Efficacy 37.5%**
Stenotrophomonas rhizophila	50839	Maize	Early vigor	<0	<0
Stenotrophomonas rhizophila	48183	Maize	Early vigor	<0	<0
Stenotrophomonas rhizophila	45125	Maize	Early vigor	<0	<0
Stenotrophomonas rhizophila	46120	Maize	Early vigor	<0	0-10
Stenotrophomonas rhizophila	46012	Maize	Early vigor	<0	<0
Stenotrophomonas rhizophila	51718	Maize	Early vigor	0-10	0-10
Stenotrophomonas rhizophila	66478	Maize	Early vigor	<0	<0
Stenotrophomonas rhizophila	65303	Maize	Early vigor	<0	0-10
Stenotrophomonas terrae	**2**	**2**	**1**	**Efficacy 50%**	**Efficacy 50%**
Stenotrophomonas terrae	68741	Maize	Early vigor	<0	<0
Stenotrophomonas terrae	68599	Maize	Early vigor	<0	0-10
Stenotrophomonas terrae	68599	Capsicum *	Early vigor	20-30	20-30
Stenotrophomonas terrae	68741	Capsicum *	Early vigor	10-20	20-30

[0658] The data presented in table 27 describes the efficacy with which a microbial species or strain can change a phenotype of interest relative to a control run in the same experiment. Phenotypes measured were shoot fresh weight and root fresh weight for plants growing either in the absence of presence of a stress (assay). For each microbe species, an overall efficacy score indicates the percentage of times a strain of that species increased a both shoot and root fresh weight in independent evaluations. For each species, the specifics of each independent assay is given, providing a strain ID (strain) and the crop species the assay was performed on (crop). For each independent assay the percentage increase in shoot and root fresh weight over the controls is given.

B. Seed Treatment with Microbial Consortia

[0659] The inoculants were prepared from isolates grown as spread plates on R2A incubated at 25°C for 48 to 72 hours. Colonies were harvested by blending with sterile distilled water (SDW) which was then transferred into sterile containers. Serial dilutions of the harvested cells were plated and incubated at 25°C for 24 hours to estimate the number of colony forming units (CFU) in each suspension. Dilutions were prepared using individual isolates or blends of isolates (consortia) to deliver ~$1x10^5$ cfu/microbe/seed and seeds inoculated by either imbibition in the liquid suspension or by overtreatment in combination with 0.1 – 1% vegetable gum.

[0660] Seeds corresponding to the plants of table 28 were planted within 24 to 48 hours of treatment in agricultural soil, potting media or inert growing media. Plants were grown in small pots (28 mL) in a controlled environment. The chamber photoperiod was set to 16 hours for all experiments on all species. Air temperature was typically maintained between 22-24°C.

[0661] All plants were watered with tap water 2 to 3 times weekly. Plants were subjected to either no stress (NS) or limited nitrogen to investigate nitrogen use efficiency (NUE). Growth conditions were varied according to the trait of interest and included manipulation of applied fertilizer as follows:

- Low N – seeds planted in soil potting media or inert growing media with no applied N fertilizer
- Moderate N – seeds planted in soil or growing media supplemented with commercial N fertilizer to equivalent of 135 kg/ha applied N

[0662] Untreated (no applied microbe) controls were prepared for each experiment. Plants were randomized on trays throughout the growth environment. Between 10 and 30 replicate plants were prepared for each treatment in each experiment. Phenotypes were measured during early vegetative growth, typically before the V3 developmental stage and between 3 and 6 weeks after sowing. Fresh foliar weight was measured 18h after watering substrate to saturation. Dry root weight was measured after drying to a constant weight at 80°C. Results indicate performance of treatments against the untreated control.

Table 28

				Controlled Environment Efficacy (%)	
Consortia	**Crop**	**Assay**	**Evaluations**	**Foliar Weight**	**Root Weight**
D29	Wheat	NS	7	71	57
D36	Wheat	NS	1	100	100
D32	Wheat	NS	8	88	63
D33	Wheat	NS	9	78	33
D35	Wheat	NS	1	100	100
D34	Wheat	NS	1	100	100
D37	Wheat	NS	1	100	100
D38	Wheat	NS	1	100	100
D39	Wheat	NS	6	67	50
D39	Wheat	NUE	8	100	75
D31	Wheat	NS	7	71	43
D31	Wheat	NUE	8	75	50
D30	Tomato	NS	6 (FW) 3 RW	50	33

[0663] The data presented in table 28 describes the percentage of time a particular consortium changed a phenotype of interest relative to an inert-only control run in the same experiment. The measured phenotypes were fresh shoot weight, measured 18 hours after watering to saturation, and dry root weight, measured after drying to a constant state at 80 degrees Celsius.

[0664] The presented data identifies consortia that have increased a phenotype of interest in greater than 60% of evaluations (hit rate >59) and consortia that decreased a phenotype of interest in greater than 60% of evaluations (hit rate<41). Both increases and decreases in a phenotype of interest were recorded to reflect the possibility that decreases in select phenotypes of interest are yield relevant.

Example 4: Evaluation of Yield Effect of Maize Exposed to Microbial Consortia in U.S. Field Trials

[0665] The data presented in Table 29 summarizes the changes in final yield relative to a control for six consortia tested in eight locations in the mid-West of the United States. Also presented is final yield data from two drought trials performed in California in the United States. Data is expressed as the percentage of trials in which a yield effect in bushels per acre of a particular magnitude was observed. All field trials were run in accordance with standard agronomic practices.

Table 29

Consortia	Trials	Field Trial Yield Increases (%) > 6 bu ac	0-6 bu ac	< 0 bu ac
D1	8 Yield	62.5	25	12.2
D6	8 Yield	25	25	50
D7	8 Yield	25	37.5	37.5
D2	8 Yield	25	37.5	37.5
D3	8 Yield	25	25	50
D4	8 Yield	25	37.5	37.5
D5	8 Yield	25	50	25
D12	2 Drought	100	_	_

Example 5: Evaluate Yield Effect of Maize Exposed to Microbial Consortia in New Zealand Field Trials

[0666] The data presented in Table 30 summarizes the results of New Zealand field trials for select consortia. The presented data describes the number of trials in which a particular consortia has been tested relative to a control, and the number of trials in which the consortia treatment increased the final yield relative to the control treatment. All field trials were run in accordance with standard agronomic practices.

Table 30

Consortia	Trials	Trials with yield > control
A1	3	3
D6	2	1
A13	2	1
A14	1	1
A15	3	3

Example 6: Evaluation of Yield Effect of Sorghum Exposed to Microbial Consortia in U.S. Field Trials

[0667] The data presented in Table 31 summarizes the changes in final grain yield of Sorghum relative to a control for one consortia tested in two field locations in the mid-West of the United States. Data is expressed as the number of trials in which a yield effect in bushels per acre of a particular magnitude was observed. All field trials were run in accordance with standard agronomic practices.

Table 31

Consortia	Trials	Field Trial Grain Yield Increases > 6 bu ac	3-6 bu ac	< 3 bu ac
A16	2 Yield	1	1	0

Example 7: Microbes Deposited with the ARS Culture Collection (NRRL)

[0668] In one experimental embodiment, the inventors utilized the following microbial species in applications of the present disclosure. Table 32 details microbial species of the present disclosure which have been deposited with the United States Department of Agriculture ARS Culture Collection (NRRL).

Table 32

	Taxonomy	BCI (US)	BDNZ (NZ)	Deposited date	Accession number	USDA Viability Date
1	Acidovorax soli	648		12.29.2015	**NRRL B-67181**	1.4.2016
2	Acidovorax soli	690		12.29.2015	**NRRL B-67182**	1.4.2016
3	Arthrobacter cupressi	59		12.29.2015	**NRRL B-67183**	1.4.2016
4	Arthrobacter cupressi	62		12.29.2015	**NRRL B-67184**	1.4.2016
5	Bosea eneae	1267		12.29.2015	**NRRL B-67185**	1.4.2016
6	Bosea robiniae	689		12.29.2015	**NRRL B-67186**	1.4.2016
7	Bosea thiooxidans	703		12.29.2015	**NRRL B-67187**	1.4.2016
8	Chitinophaga terrae	79		12.29.2015	**NRRL B-67188**	1.4.2016
9	Chitinophaga terrae	109		12.29.2015	**NRRL B-67189**	1.4.2016
10	Delftia lacustris	124		12.29.2015	**NRRL B-67190**	1.4.2016
11	Delftia lacustris	2350		12.29.2015	**NRRL B-67191**	1.4.2016
12	Duganella radicis	105		12.29.2015	**NRRL B-67192**	1.4.2016
13	Duganella violaceinigra	2204		12.29.2015	**NRRL B-67193**	1.4.2016
14	Dyadobacter soli	68		12.29.2015	**NRRL B-67194**	1.4.2016

	Taxonomy	BCI (US)	BDNZ (NZ)	Deposited date	Accession number	USDA Viability Date
15	Dyadobacter soli	96		12.29.2015	**NRRL B-67195**	1.4.2016
16	Flavobacterium glacei	4005		12.29.2015	**NRRL B-67196**	1.4.2016
17	Herbaspirillum chlorophenolicum	162		12.29.2015	**NRRL B-67197**	1.4.2016
18	Massilia kyonggiensis (deposited as Massilia albidiflava)	97		12.29.2015	**NRRL B-67198**	1.4.2016
19	Massilia niastensis	1217		12.29.2015	**NRRL B-67199**	1.4.2016
20	Novosphingobium lindaniclasticum	684		12.29.2015	**NRRL B-67201**	1.4.2016
21	Novosphingobium lindaniclasticum	608		12.29.2015	**NRRL B-67200**	1.4.2016
22	Novosphingobium resinovorum	557		12.29.2015	**NRRL B-67202**	1.4.2016
23	Novosphingobium resinovorum	3709		12.29.2015	**NRRL B-67203**	1.4.2016
24	Paenibacillus glycanilyticus	418		12.29.2015	**NRRL B-67204**	1.4.2016
25	Pedobacter rhizosphaerae (deposited as Pedobacter soli)	598		12.29.2015	**NRRL B-67205**	1.4.2016
26	Pedobacter terrae	91		12.29.2015	**NRRL B-67206**	1.4.2016
27	Pseudomonas jinjuensis	804		12.29.2015	**NRRL B-67207**	1.4.2016
28	Ramlibacter henchirensis	739		12.29.2015	**NRRL B-67208**	1.4.2016
29	Ramlibacter henchirensis	1959		12.29.2015	**NRRL B-67209**	1.4.2016
30	Rhizobium rhizoryzae (previously R. lemnae)	34		12.29.2015	**NRRL B-67210**	1.4.2016
31	Rhizobium rhizoryzae (previously R. lemnae)	661		12.29.2015	**NRRL B-67211**	1.4.2016
32	Rhizobium sp.	106		12.29.2015	**NRRL B-67212**	1.4.2016
33	Sinorhizobium Chiapanecum (now Ensifer adhaerens)	111		12.29.2015	**NRRL B-67213**	1.4.2016
34	Sphingopyxis alaskensis	412		12.29.2015	**NRRL B-67214**	1.4.2016
35	Sphingopyxis	914		12.29.2015	**NRRL B-67215**	1.4.2016

	Taxonomy	BCI (US)	BDNZ (NZ)	Deposited date	Accession number	USDA Viability Date
	alaskensis					
36	Variovorax ginsengisoli	137		12.29.2015	**NRRL B-67216**	1.4.2016
37	Variovorax ginsengisoli	3078		12.29.2015	**NRRL B-67217**	1.4.2016
38	Achromobacter pulmonis	49		12.18.15	**NRRL B-67174**	12.21.2015
39	Chryseobacterium daecheongense	45		12.18.15	**NRRL B-67172**	12.21.2015
40	Duganella radicis	31		1.13.16	**NRRL B-67166**	1.15.2016
41	Exiguobacterium aurantiacum	50		12.18.15	**NRRL B-67175**	12.21.2015
42	Exiguobacterium sibiricum	116		12.18.15	**NRRL B-67167**	12.21.2015
43	Kosakonia radicincitans	44		12.18.15	**NRRL B-67171**	12.21.2015
44	Microbacterium oleivorans	132		12.18.15	**NRRL B-67170**	12.21.2015
45	Novosphingobium sediminicola	130		12.18.15	**NRRL B-67168**	12.21.2015
46	Pedobacter terrae	53		12.18.15	**NRRL B-67176**	12.21.2015
47	Rahnella aquatilis	29		12.18.15	**NRRL B-67165**	12.21.2015
48	*Agrobacterium fabrum* or *Rhizobium pusense* (In Taxonomic Flux) (previously *Rhizobium sp.*)	46		12.18.15	**NRRL B-67173**	12.21.2015
49	Sinorhizobium chiapanecum (Ensifer adhaerens - current classification)	131		12.18.15	**NRRL B-67169**	12.21.2015
50	Pantoea vagans		55529	1.29.2016	**NRRL B-67224**	2.4.2016
51	Pseudomonas oryzihabitans		55530	1.29.2016	**NRRL B-67225**	2.4.2016
52	Stenotrophomonas maltophilia		54073	1.29.2016	**NRRL B-67226**	2.4.2016
53	Rahnella aquatilis		58013	1.29.2016	**NRRL B-67229**	2.4.2016
54	Rahnella aquatilis		56532	1.29.2016	**NRRL B-67228**	2.4.2016
55	Rhodococcus erythropolis		54093	1.29.2016	**NRRL B-67227**	2.4.2016
56	Herbaspirillum chlorophenolicum	58		2.8.2016	**NRRL B-67236**	2.10.2016
57	Bacillus niacini	4718		2.8.2016	**NRRL B-67230**	2.10.2016
58	Polaromonas ginsengisoli		66373	2.8.2016	**NRRL B-67231**	2.10.2016

	Taxonomy	BCI (US)	BDNZ (NZ)	Deposited date	Accession number	USDA Viability Date
59	Polaromonas ginsengisoli		66821	2.8.2016	**NRRL B-67234**	2.10.2016
60	Duganella violaceinigra		66361	2.8.2016	**NRRL B-67232**	2.10.2016
61	Duganella violaceinigra		58291	2.8.2016	**NRRL B-67233**	2.10.2016
62	Massilia niastensis		55184	2.8.2016	**NRRL B-67235**	2.10.2016
63	Agrobacterium fabrum or Rhizobium pusense	958		7.14.2016	**NRRL B-67286**	7.17.2016
64	Arthrobacter nicotinovorans	717		7.14.2016	**NRRL B-67289**	7.17.2016
65	Arthrobacter nicotinovorans	3189		7.14.2016	**NRRL B-67290**	7.17.2016
66	Chryseobacterium daecheongense	191		7.14.2016	**NRRL B-67291**	7.17.2016
67	Chryseobacterium rhizosphaerae	597		7.14.2016	**NRRL B-67288**	7.17.2016
68	Chryseobacterium rhizosphaerae	615		7.14.2016	**NRRL B-67287**	7.17.2016
69	*Frigidibacter albus* or *Delfulviimonas dentrificans* (In Taxonomic Flux)	712		7.14.2016	**NRRL B-67285**	7.17.2016
70	*Frigidibacter albus* or *Delfulviimonas dentrificans* (In Taxonomic Flux)	402		7.14.2016	**NRRL B-67283**	7.17.2016
71	*Frigidibacter albus* or *Delfulviimonas dentrificans* (In Taxonomic Flux)	745		7.14.2016	**NRRL B-67284**	7.17.2016
72	*Exiguobacterium antarcticum*	63		7.14.2016	**NRRL B-67292**	7.17.2016
73	*Exiguobacterium antarcticum*	225		7.14.2016	**NRRL B-67293**	7.17.2016
74	*Exiguobacterium sibiricum*	718		7.14.2016	**NRRL B-67294**	7.17.2016
75	*Pseudomonas helmanticensis*	616		7.14.2016	**NRRL B-67295**	7.17.2016
76	*Pseudomonas helmanticensis*	2945		7.14.2016	**NRRL B-67296**	7.17.2016
77	*Pseudomonas helmanticensis*	800		7.14.2016	**NRRL B-67297**	7.17.2016
78	*Leifsonia lichenia*		72243	7.21.2016	**NRRL B-67298**	7.22.2016
79	*Leifsonia lichenia*		72289	7.21.2016	**NRRL B-67299**	7.22.2016
80	*Tumebacillus*		72229	7.21.2016	**NRRL B-67302**	In process

	Taxonomy	BCI (US)	BDNZ (NZ)	Deposited date	Accession number	USDA Viability Date
	permanetifrigoris					
81	*Tumebacillus permanetifrigoris*		74542	7.21.2016 redeposited 8.4.2016	**NRRL B-67300**	8.5.2016
82	*Tumebacillus permanetifrigoris*		72366	7.22.2016	**NRRL B-67303**	7.25.2016
83	*Tumebacillus permanetifrigoris*		72287	7.21.2016 redeposited 8.4.2016	**NRRL B-67301**	8.5.2016
84	*Brevibacterium frigoritolerans*		4468	1.5.2017	**NRRL B-67360**	1.7.2017
86	*Janibacter limosus*		4708	1.5.2017	**NRRL B-67359**	1.7.2017
87	*Janibacter limosus*		3103	1.5.2017	**NRRL B-67358**	1.7.2017
89	*Janibacter limosus*		3105	1.5.2017	**NRRL B-67364**	1.7.2017
90	*Pseudomonas yamanorum*		4853	1.5.2017	**NRRL B-67362**	1.7.2017
91	*Pseudomonas yamanorum*		3523	1.5.2017	**NRRL B-67363**	1.7.2017
92	*Pseudomonas yamanorum*		5446	1.5.2017	**NRRL B-67361**	1.7.2017
93	*Bacillus megaterium*		4473	xxxx	NRRL B-67370	xxxx

Example 8: Novel Microbial Species Deposited with the ARS Culture Collection (NRRL)

[0669] In one experimental embodiment, the inventors utilized the following microbial species in applications of the present disclosure.

Table 33

Taxonomy	BCI (US)	BDNZ (NZ)
Achromobacter pulmonis	49	
Acidovorax soli	648	
Acidovorax soli	690	
Agrobacterium fabrum or Rhizobium pusense (in Taxonomix flux)	46	
Agrobacterium fabrum or Rhizobium pusense (in Taxonomix flux)	958	
Arthrobacter cupressi	59	
Arthrobacter cupressi	62	
Arthrobacter nicotinovorans	717	

Taxonomy	BCI (US)	BDNZ (NZ)
Arthrobacter nicotinovorans	3189	
Bacillus megaterium	4473	
Bacillus niacini	4718	
Bosea eneae	1267	
Bosea robiniae	689	
Bosea thiooxidans	703	
Brevibacterium frigoritolerans	4468	
Chitinophaga terrae	79	
Chitinophaga terrae	109	
Chryseobacterium daecheongense	45	
Chryseobacterium daecheongense	191	
Chryseobacterium rhizospaerae	597	
Chryseobacterium rhizospaerae	615	
Delftia lacustris	124	
Delftia lacustris	2350	
Frigidibacter albus or Delfulviimonas dentrificans (In Taxonomic Flux)	712	
*Frigidibacter albus or Delfulviimonas dentrificans (*In Taxonomic Flux)	402	
Frigidibacter albus or Delfulviimonas dentrificans (In Taxonomic Flux)	745	
Duganella radicis	105	
Duganella radicis	31	
Duganella violaceinigra	2204	
Duganella violaceinigra		66361
Duganella violaceinigra		58291
Dyadobacter soli	68	
Dyadobacter soli	96	
Exiguobacterium antarcticum	63	
Exiguobacterium antarcticum	225	
Exiguobacterium aurantiacum	50	
Exiguobacterium sibiricum	116	
Exiguobacterium sibiricum	718	
Flavobacterium glacei	4005	
Herbaspirillum chlorophenolicum	162	
Herbaspirillum chlorophenolicum	58	
Janibacter limosus	3103	
Janibacter limosus	4708	
Janibacter limosus	3105	
Kosakonia radicincitans	44	
Leifsonia lichenia		72243
Leifsonia lichenia		72289
Massilia kyonggiensis (deposited as *Massilia albidiflava;* new taxonomy is kyonggiensis)	97	
Massilia niastensis	1217	

Taxonomy	BCI (US)	BDNZ (NZ)
Massilia niastensis		55184
Microbacterium oleivorans	132	
Novosphingobium lindaniclasticum	684	
Novosphingobium lindaniclasticum	608	
Novosphingobium resinovorum	557	
Novosphingobium resinovorum	3709	
Novosphingobium sediminicola	130	
Paenibacillus glycanilyticus	418	
Pantoea vagans		55529
Pedobacter rhizosphaerae (deposited as *Pedobacter soli)*	598	
Pedobacter terrae	91	
Pedobacter terrae	53	
Polaromonas ginsengisoli		66373
Polaromonas ginsengisoli		66821
Pseudomonas helmanticensis	616	
Pseudomonas helmanticensis	2945	
Pseudomonas helmanticensis	800	
Pseudomonas jinjuensis	804	
Pseudomonas oryzihabitans		55530
Pseudomonas yamanorum	5446	
Pseudomonas yamanorum	4853	
Pseudomonas yamanorum	3523	
Rahnella aquatilis	29	
Rahnella aquatilis		58013
Rahnella aquatilis		56532
Ramlibacter henchirensis	739	
Ramlibacter henchirensis	1959	
Rhizobium rhizoryzae	34	
Rhizobium rhizoryzae	661	
Rhizobium sp.	106	
Rhodococcus erythropolis		54093
Sinorhizobium chiapanecum (now *Ensifer adhaerens)*	131	
Sinorhizobium Chiapanecum (now *Ensifer adhaerens)*	111	
Sphingopyxis alaskensis	412	
Sphingopyxis alaskensis	914	
Stenotrophomonas maltophilia		54073
Tumebacillus permanentifrigoris		72229
Tumebacillus permanentifrigoris		74542
Tumebacillus permanentifrigoris		72366
Tumebacillus permanentifrigoris		72287
Variovorax ginsengisoli	137	
Variovorax ginsengisoli	3078	

Example 9: Deposited Microbial Species Novel to Agriculture

[0670] In one experimental embodiment, the inventors utilized the following microbial species in applications of the present disclosure. Table 34 notes microbial organisms of the present disclosure which have been deposited with the NRRL, ATCC, and/or DSMZ depositories with the respective accession numbers.

Table 34

Species novel to Agriculture (in Tables 1, 2, 3, 4)	NRRL #	DSMZ #	ATTC #
Achromobacter pulmonis	NRRL B-67174	DSM29617	
Acidovorax soli	NRRL B-67181 NRRL B-67182		
*Agrobacterium fabrum or Rhizobium pusense (*In Taxonomic Flux) (previously *Rhizobium sp.)*	NRRL B-67173 NRRL B-67286	DSM22668	
Arthrobacter cupressi	NRRL B-67183 NRRL B-67184		
Arthrobacter nicotinovorans	NRRL B-67289 NRRL B-67290	DSM420	49919
Bosea eneae	NRRL B-67185		
Bosea minatitlanensis		DSM-13099	700918
Bosea robinae	NRRL B-67186		
Caulobacter henricii		DSM-4730	15253
Chitinophaga arvensicola		DSM-3695	51264
Chitinophaga terrae	NRRL B-67188		
Chryseobacterium daecheongense	NRRL B-67172 NRRL B-67291	DSM15235	
Chryseobacterium rhizophaerae	NRRL B-67288 NRRL B-67287		
Delftia lacustris	NRRL B-67190 NRRL B-67191		
Frigidibacter albus or Delfulviimonas dentrificans (In Taxonomic Flux)	NRRL B-67285 NRRL B-67283 NRRL B-67284		
Duganella radicis	NRRL B-67192 NRRL B-67166		
Duganella violaceinigra (Pseudoduganella violaceinigra)	NRRL B-67193 NRRL B-67232 NRRL B-67233		
Dyadobacter soli	NRRL B-67193 NRRL B-67194		
Exiguobacterium antarcticum	NRRL B-67292 NRRL B-67293	DSM14480	

Species novel to Agriculture (in Tables 1, 2, 3, 4)	NRRL #	DSMZ #	ATTC #
Exiguobacterium sibiricum	NRRL B-67167 NRRL B-67294	DSM17290	
Flavobacterium glaciei	NRRL B-67196		
Frateuria aurantia		DSM-6220	
Frateuria terrea		DSM-26515	
Herbaspirillum chlorophenolicum	NRRL B-67197 NRRL B-67236		
Janibacter limosus	NRRL B-67358 NRRL B-67359 NRRL B-67364	DSM-11140	700321
Janthinobacterium agaricidamnosum		DSM-9628	
Janthinobacterium lividum		DSM-1522	
Leifsonia lichenia	NRRL B-67298 NRRL B-67299		
Luteibacter yeojuensis		DSM-17673	
Massilia kyongggiensis (previously *Massilia albidiflava)*	NRRL B-67198	DSM101532	
Massilia niastensis	NRRL B-67199 NRRL B-67235		
Microbacterium sp. (*OLIEVORANS* DEPOSITED)		DSM-16050	31001
Novosphingobium lindaniclasticum	NRRL B-67201 NRRL B-67200	DSM25409	
Novosphingobium resinovorum	NRRL B-67202 NRRL B-67203		
Novosphingobium rosa		DSM-7285	51837
Novosphingobium sediminicola	NRRL B-67168	DSM27057	
Paenibacillus amylolyticus		DSM-11730	9995
Paenibacillus chondroitinus		DSM-5051	51184
Paenibacillus glycanilyticus	NRRL B-67204		
Pedobacter rhizosphaerae (Pedobacter soli)	NRRL B-67205		
Pedobacter terrae	NRRL B-67206 NRRL B-67176		
Polaromonas ginsengisoli	NRRL B-67231 NRRL B-67234		
Pseudomonas helmanticensis	NRRL B-67295 NRRL B-67296 NRRL B-67297	DSM28442	
Pseudomonas jinjuensis	NRRL B-67207		
Pseudomonas yamanorum	NRRL B-67361 NRRL B-67362 NRRL B-67363	DSM-16768	
Ramlibacter henchirensis	NRRL B-67208		

Species novel to Agriculture (in Tables 1, 2, 3, 4)	NRRL #	DSMZ #	ATTC #
Rhizobium rhizoryzae	NRRL B-67210 NRRL B-67211		
Rhodoferax ferrireducens		DSM-15236	BAA-621
Sinorhizobium chiapanecum (Ensifer adhaerens)	NRRL B-67213 NRRL B-67169		
Sphingobium quisquiliarum		DSM-24952	
Sphingopyxis alaskensis	NRRL B-67214 NRRL B-67215		
Stenotrophomonas terrae		DSM-18941	
Tumebacillus permanentifrigoris	NRRL B-67302 NRRL B-67300 NRRL B-67303 NRRL B-67301	DSM118773	
Variovorax ginsengisoli	NRRL B-67216 NRRL B-67217		

Example 10: Microbial Consortia Embodiments

[0671] In one experimental embodiment, the inventors utilized the following microbial consortia in applications of the present disclosure. Table 35 notes microbial consortia A16 of the present disclosure. Underneath each of the consortia designations are the specific strain numbers that identify the microbes present in each of the consortia.

Table 35

Strain BCI#	Strain BDNZ#	Microbe identity	A16
4468		*Brevibacterium frigoritolerans* (4468)	4468
4708		*Janibacter limosus* (4708)	4708
4853		*Pseudomonas yamanorum* (4853)	4853
4473		*Bacillus megaterium* (4473)	4473

Example 11: Microbial Strain and Microbial Species Embodiments

[0672] In one experimental embodiment, the inventors utilized the following microbial species and/or strains in applications of the present disclosure. Table 36

notes specific microbial species and strains utilized in experimental studies which are novel to agriculture and have exhibited positive results in controlled environment screening experiments of the present disclosure.

Table 36

Individual species of note	Strain	Strain		Individual strains of note	Strain	Strain
Species	**BDNZ#**	**BCI#**		**Species**	**BDNZ#**	**BCI#**
Duganella violaceinigra	66361			*Frigidibacter albus* or *Delfulviimonas dentrificans* (In Taxonomic Flux)		712
Bosea thiooxidans	54522	703		*Frigidibacter albus* or *Delfulviimonas dentrificans* (In Taxonomic Flux)		402
Massilia niastensis	55184	1217		*Frigidibacter albus* or *Delfulviimonas dentrificans* (In Taxonomic Flux)		745
Polaromonas ginsengisoli	66373			*Exiguobacterium antarcticum*		63
Novosphingobium resinovorum		557		*Exiguobacterium antarcticum*		225
Duganella violaceinigra		2204		*Exiguobacterium sibiricum*		116
Exiguobacterium aurantiacum		50		*Exiguobacterium sibiricum*		718
Exiguobacterium sibiricum		116		*Leifsonia lichenia*	72243	
Variovorax ginsengisoli		3078		*Leifsonia lichenia*	72289	
Pedobacter rhizosphaerae		598		*Pedobacter terrae*	-	53
Duganella radicis		31		*Pseudomonas helmanticensis*		616
Paenibacillus glycanilyticus		418		*Pseudomonas helmanticensis*		2945
Bacillus niacini		1718		*Pseudomonas helmanticensis*		800
Stenotrophomonas maltophilia	54073			*Tumebacillus permanentifrigoris*	72229	
Rhodococcus erythropolis	54093			*Tumebacillus permanentifrigoris*	74542	
Pantoea vagans	55529			*Tumebacillus permanentifrigoris*	72366	
Pseudomonas oryzihabitans	55530			*Tumebacillus permanentifrigoris*	72287	
Achromobacter pulmonis		49		*Brevibacterium frigoritolerans*		4468

Individual species of note	Strain	Strain		Individual strains of note	Strain	Strain
Species	BDNZ#	BCI#		Species	BDNZ#	BCI#
Agrobacterium fabrum or *Rhizobium pusense* (In Taxonomic Flux) (previously *Rhizobium sp.*)		46		*Janibacter limosus*		4708
Agrobacterium fabrum or *Rhizobium pusense* (In Taxonomic Flux) (previously *Rhizobium sp.*)		958		*Janibacter limosus*		3103
Arthrobacter nicotinovorans		717		*Janibacter limosus*		3105
Arthrobacter nicotinovorans		3189		*Pseudomonas yamanorum*		4853
Chryseobacterium daecheongense		45		*Pseudomonas yamanorum*		3523
Chryseobacterium daecheongense		191		*Pseudomonas yamanorum*		5446
Chryseobacterium rhizosphaerae		597		*Bacillus megaterium*		4473
Chryseobacterium rhizosphaerae		615				

INCORPORATION BY REFERENCE

[0673] All references, articles, publications, patents, patent publications, and patent applications cited herein are incorporated by reference in their entireties for all purposes.

[0674] However, mention of any reference, article, publication, patent, patent publication, and patent application cited herein is not, and should not be taken as, an acknowledgment or any form of suggestion that they constitute valid prior art or form part of the common general knowledge in any country in the world.

REFERENCES

[0675] Ascend® plant growth regulator product sheet. EPA reg. No. 9776-335

[0676] Calvo, P., Nelson, L., Kloepper, J. W., 2014 Agricultural uses of plant biostimulants. Plant soil 383, 3-41.

[0677] "Chemistry and Technology of Agrochemical Formulations," edited by D. A. Knowles, copyright 1998 by Kluwer Academic Publishers.

[0678] Colby, R. S., "Calculating Synergistic and Antagonistic Responses of Herbicide Combinations, 1967 Weeds, vol. 15, pp. 20-22.

[0679] Current Protocols in Molecular Biology (F.M. Ausubel *et al.*, eds., 1987).

[0680] Crameri *et al.*(1997) Nature Biotech. 15:436-438.

[0681] Crameri *et al.*(1998) Nature 391:288-291.

[0682] De Almeida *et al.*, (1989) Mol. Gen. Genetics 218:78-86).

[0683] Dobereiner J, Marriel E and Nery M 1976 Ecological distribution of *Spirillum lipoferum* Beijerinck. Can. J. Microbiol. 22, 1464–1473.

[0684] Fahraeus, G. (1957). *J. Gen Microbiol.* 16: 374-381.

[0685] Gerhardt, P. (ed.) Methods for General and Molecular Microbiology. American Society for Microbiology, Washington, D.C. (1994).

[0686] Gherna, R. L. and C. A. Reddy. 2007. Culture Preservation, p 1019-1033. In C. A. Reddy, T. J. Beveridge, J. A. Breznak, G. A. Marzluf, T. M. Schmidt, and L. R. Snyder, eds. American Society for Microbiology, Washington, D.C., 1033 pages.

[0687] Gordon, Solon A., and Robert P. Weber. "COLORIMETRIC ESTIMATION OF INDOLEACETIC ACID." *Plant Physiology* 26.1 (1951): 192–195. Print.

[0688] Goteti, P. K. et al., (2013). International Journal of Microbiology 2013: 1-7 Article ID 869697.

[0689] Hartmann A., Baldani J.I. The genus Azospirillum // The Prokaryotes, V. 5: Proteobacteria Alpha and Beta Subclasses // Eds. M. Dworkin, S. Falkow, E. Rosenberg, K.H. Schleifer, E. Stackebrandt. – Springer Verlag, New York, USA, 2006. p. 115–140.

[0690] Innis *et al.*, eds. (1990) PCR Protocols: A Guide to Methods and Applications (Academic Press, New York).

[0691] Innis and Gelfand, eds. (1995) PCR Strategies (Academic Press, New York).

[0692] *In re Bergstrom*, 427 F.2d 1394, (CCPA 1970).

[0693] *In re Bergy*, 596 F.2d 952 (CCPA 1979).

[0694] Islam, M. T., Deora, A., Hashidoko, Y., Rahman, A., Ito, T., and Tahara, S. (2007) Isolation and Identification of Potential Phosphate Solubilizing Bacteria from

the Rhizoplane of Oryza sativa L. cv. BR29 of Bangladesh. Zeitschrift fur Naturforschung C 62(1-2):103-10.

[0695] Jones *et al.*, (1985) EMBO J. 4:2411-2418.

[0696] Lennette, E. H. (ed.) Manual of Clinical Microbiology, Third Edition. American Society for Microbiology, Washington, D.C. (1980).

[0697] *McCutcheon's Detergents and Emulsifiers Annual*, MC Publishing Corp., Ridgewood, N.J., 1998, and in *Encyclopedia of Surfactants*, Vol. I-III, Chemical Publishing Co., New York, 1980-81.

[0698] McCutcheon's, vol. 1, "Emulsifiers and Detergents," MC Publishing Company, Glen Rock, N.J., U.S.A., 1996.

[0699] Merck & Co. v. Olin Mathieson Chemical Corp., 253 F.2d 156 (4th Cir. 1958).

[0700] Miche, L and Balandreau, J (2001). Effects of rice seed surface sterilisation with hypochlorite on inoculated *Burkholderia vietamiensis*. *Appl. Environ. Microbiol.***67(7):** p3046-3052.

[0701] Moore *et al.*(1997) J. Mol. Biol. 272:336-347.

[0702] Nautiyal, C.S. (1999), FEMS Microbiology Letters 170 (1999) 265-270.

[0703] N-Large™ plant growth regulator product sheet. EPA Reg. No. 57538-18.

[0704] Parke-Davis & Co. v. H.K. Mulford & Co., 189 F. 95 (S.D.N.Y. 1911).

[0705] Parmar, P. and Sindhu, S. S. (2013) Potassium Solubilization by Rhizosphere Bacteria: Influence of Nutritional and Environmental Conditions. Journal of Microbiology Research, 3(1): 25-31.

[0706] PCT/NZ2012/000041, published on September 20, 2012, as International Publication No. WO 2012125050 A1.

[0707] PCT/NZ2013/000171, published on March 27, 2014, as International Publication No. WO 2014046553 A1.

[0708] Perez-Miranda, S. et al., (2007). Journal of Microbiological Methods 70: 127-131.

[0709] Pikovskaya RI (1948). Mobilization of phosphorus in soil connection with the vital activity of some microbial species. *Microbiologia* 17:362–370.

[0710] ProGibb® plant growth regulator product sheet. EPA Reg. No. 73049-15.

[0711] Rana, A. et al. (2012) Enhancing Micronutrient Uptake and Yield of Wheat Through Bacterial PGPR Consortia, Soil Science and Plant Nutrition, 58:5, 573-582.

[0712] Release® plant growth regulator product sheet. EPA Reg. No. 73049-6.

[0713] Rodriguez, H. and Reynaldo, F. (1999). Phosphate Solubilizing Bacteria and their Role in Plant Growth Promotion. Biotechnology Advances. 17. 319-339.

[0714] Ruth Eckford, R., Cook, F.D., Saul, D., Aislabie J., and J. Foght (2002) Free-living Heterotrophic Bacteria Isolated from Fuel-Contaminated Antarctic Soils. *Appl. Environ. Microbiol* 68(10):5181.

[0715] RyzUp SmartGrass® plant growth regulator product sheet. EPA Reg. No. 73049-1.

[0716] Sambrook *et al.*(1989) Molecular Cloning: A Laboratory Manual (2nd ed., Cold Spring Harbor Laboratory Press, Plainview, New York).

[0717] Shanware, A.S. et al., 2014 Int.J.Curr.Microbiol.App.Sci 3(9) 622-629.

[0718] Stemmer (1994) Nature 370:389-391.

[0719] Stemmer (1994) PNAS 91:10747-10751.

[0720] Strobel G and Daisy B (2003) Microbiology and Molecular Biology Reviews 67 (4): 491-502.

[0721] U.S. Pat. No. 8,652,490 "Pasteuria Strain" issued February 18, 2014.

[0722] U.S. Pat. No. 8,383,097 "Bacteria Cultures and Compositions Comprising Bacteria Cultures" issued February 26, 2013.

[0723] Vandamme *et al.* 1996. Polyphasic taxonomy, a consensus approach to bacterial systematics. *Microbiol Rev* 1996, 60:407-438.

[0724] Bergey's Manual of Systematic Bacteriology 2nd Edition Volume 1 (2001) The Archaea and the deeply branching and phototrophic Bacteria. Editor-in-Chief: George M. Garrity. Editors: David R. Boone and Richard W. Castenholz. ISBN 0-387-98771-1.

[0725] Bergey's Manual of Systematic Bacteriology 2nd Edition Volume 2 (2005) The Proteobacteria. Editor-in-Chief: George M. Garrity. Editors: Don J. Brenner, Noel R. Krieg and James T. Staley. ISBN 0-387-95040-0.

[0726] Bergey's Manual of Systematic Bacteriology 2nd Edition Volume 3 (2009) The Firmicutes. Editors: Paul De Vos, George Garrity, Dorothy Jones, Noel R. Krieg, Wolfgang Ludwig, Fred A. Rainey, Karl-Heinz Schleifer and William B. Whitman. ISBN 0-387-95041-9.

[0727] Bergey's Manual of Systematic Bacteriology 2nd Edition Volume 4 (2011) The Bacteroidetes, Spirochaetes, Tenericutes (Mollicutes), Acidobacteria, Fibrobacteres, Fusobacteria, Dictyoglomi, Gemmatimonadetes, Lentisphaerae, Verrucomicrobia, Chlamydiae, and Planctomycetes. Editors: Noel R. Krieg, James T. Staley, Daniel R. Brown, Brian P. Hedlund, Bruce J. Paster, Naomi L. Ward, Wolfgang Ludwig and William B. Whitman. ISBN 0-387-95042-6

[0728] Bergey's Manual of Systematic Bacteriology 2nd Edition Volume 5 (2012) The Actinobacteria. Editors: Michael Goodfellow, Peter Kämpfer, Hans-Jürgen Busse, Martha E. Trujillo, Ken-ichiro Suzuki, Wolfgang Ludwig and William B. Whitman. ISBN 0-387-95042-7.

[0729] Yemm and Willis (Biochem. J. 1954, 57: 508–514).

[0730] X-CYTE™ plant growth regulator product sheet. EPA Reg. No. 57538-15.

[0731] Zhang *et al.*(1997) PNAS 94:4504-4509.

[0732] Zinniel DK *et al.*(2002) Applied and Environmental Microbiology 68 (5): 2198-2208).

[0733] Pikovskaya RI (1948). Mobilization of phosphorus in soil connection with the vital activity of some microbial species. *Microbiologia* 17:362–370.

CLAIMS

What is claimed is:

1. An isolated bacterial strain selected from the group consisting of:
    a) *Brevibacterium frigoritolerans* deposited as NRRL Accession Deposit No. NRRL B-67360;
    b) *Janibacter limosus* deposited as NRRL Accession Deposit No. NRRL B-67358;
    c) *Janibacter limosus* deposited as NRRL Accession Deposit No. NRRL B-67359;
    d) *Janibacter limosus* deposited as NRRL Accession Deposit No. NRRL B-67364;
    e) *Pseudomonas yamanorum* deposited as NRRL Accession Deposit No. NRRL B-67361;
    f) *Pseudomonas yamanorum* deposited as NRRL Accession Deposit No. NRRL B-67362;
    g) *Pseudomonas yamanorum* deposited as NRRL Accession Deposit No. NRRL B-67363;
    h) *Bacillus megaterium* deposited as NRRL Accession Deposit No. NRRL B-67370.

2. An isolated bacterial strain having substantially similar morphological and physiological characteristics as an isolated bacterial strain according to claim 1.

3. An isolated bacterial strain having substantially similar genetic characteristics as an isolated bacterial strain according to claim 1.

4. A substantially pure culture of an isolated bacterial strain according to claim 1.

5. A progeny of an isolated bacterial strain according to claim 1.

6. A mutant of an isolated bacterial strain according to claim 1.

7. An isolated bacterial strain comprising a polynucleotide sequence sharing at least 97% sequence identity with any one of SEQ ID Nos: 1-315.

8. A cell-free or inactivated preparation of an isolated bacterial strain according to claim 1 or a mutant of said isolated bacterial strain.

9. A metabolite produced by an isolated bacterial strain according to claim 1 or produced by a mutant of said isolated bacterial strain.

10. An agricultural composition, comprising:

a) an isolated bacterial strain according to claim 1; and

b) an agriculturally acceptable carrier.

11. The agricultural composition according to claim 10, wherein the isolated bacterial strain is present in the composition at 1×10^{3} to 1×10^{12} bacterial cells per gram.

12. The agricultural composition according to claim 10, wherein said agricultural composition is formulated as a seed coating.

13. A method of imparting at least one beneficial trait upon a plant species, comprising:

a) applying an isolated bacterial strain according to claim 1 to said plant, or to a growth medium in which said plant is located.

14. A method of imparting at least one beneficial trait upon a plant species, comprising:

a) applying the agricultural composition according to claim 10 to said plant, or to a growth medium in which said plant is located.

15. A microbial consortium, comprising at least two microbes selected from the groups consisting of:

A) *Stenotrophomonas maltophilia*, *Rhodococcus erythropolis*, *Pantoea vagans*, *Pseudomonas oryzihabitans*, *Rahnella aquatilis*, *Duganella radicis*,

Exiguobacterium acetylicum, Arthrobacter pascens, Pseudomonas putida, Bacillus megaterium, Bacillus aryabhattai, Bacillus cereus, Novosphingobium sediminicola, Rhizobium etli, Ensifer adhaerens, Chitinophaga terrae, Variovorax ginsengisoli, Pedobacter terrae, Massilia albidiflava, Dyadobacter soli, Bosea robiniae, Microbacterium maritypicum, Microbacterium azadirachtae, Sphingopyxis alaskensis, Arthrobacter pascens, Chryseobacterium rhizosphaerae, Variovorax paradoxus, Hydrogenophaga atypica, and *Microbacterium oleivorans;*

B) *Brevibacterium frigoritolerans, Janibacter limosus Pseudomonas yamanorum* and *Bacillus magaterium*;

and combinations thereof, and wherein at least one microbe from B) is selected.

16. A microbial consortium having substantially similar morphological and physiological characteristics as a microbial consortium according to claim 15.

17. A microbial consortium having substantially similar genetic characteristics as a microbial consortium according to claim 15.

18. A substantially pure culture of a microbial consortium according to claim 15.

19. A subsequent generation of any microbe recited in the microbial consortium according to claim 15.

20. A mutant of any microbe recited in the microbial consortium according to claim 15.

21. A cell-free or inactivated preparation of the microbial consortium according to claim 15 or a mutant of any microbe recited in the microbial consortium according to claim 15.

22. A metabolite produced by the microbial consortium according to claim 15 or a mutant of any microbe recited in the microbial consortium according to claim 15.

23. An agricultural composition, comprising:

a) a microbial consortium according to claim 15; and
b) an agriculturally acceptable carrier.

24. The agricultural composition according to claim 23, wherein the microbial consortium is present in the composition at 1×10^3 to 1×10^{12} bacterial cells per gram.

25. The agricultural composition according to claim 23, wherein said agricultural composition is formulated as a seed coating.

26. A method of imparting at least one beneficial trait upon a plant species, comprising:
a) applying a microbial consortium according to claim 15 to said plant, or to a growth medium in which said plant is located.

27. A method of imparting at least one beneficial trait upon a plant species, comprising:
a) applying the agricultural composition according to claim 23 to said plant, or to a growth medium in which said plant is located.

28. A microbial consortium comprising at least two microbes selected from the group consisting of:
a) *Brevibacterium frigoritolerans* deposited as NRRL Accession Deposit No. NRRL B-67360;
b) *Janibacter limosus* deposited as NRRL Accession Deposit No. NRRL B-67358;
c) *Janibacter limosus* deposited as NRRL Accession Deposit No. NRRL B-67359;
d) *Janibacter limosus* deposited as NRRL Accession Deposit No. NRRL B-67364;
e) *Pseudomonas yamanorum* deposited as NRRL Accession Deposit No. NRRL B-67361;
f) *Pseudomonas yamanorum* deposited as NRRL Accession Deposit No. NRRL B-67362;

g) *Pseudomonas yamanorum* deposited as NRRL Accession Deposit No. NRRL B-67363;

h) *Bacillus megaterium* deposited as NRRL Accession Deposit No. NRRL B-67370.

and combinations thereof.

29. The microbial consortium of claim 28, comprising *Brevibacterium frigoritolerans* deposited as NRRL Accession Deposit No. NRRL B-67360, *Janibacter limosus* deposited as NRRL Accession Deposit No. NRRL B-67359, *Pseudomonas yamanorum* deposited as NRRL Accession Deposit No. NRRL B-67362 and *Bacillus megaterium* deposited as NRRL Accession Deposit No. NRRL B-67370

30. A microbial consortium having substantially similar morphological and physiological characteristics as a microbial consortium according to claim 28.

31. A microbial consortium having substantially similar genetic characteristics as a microbial consortium according to claim 28.

32. A substantially pure culture of a microbial consortium according to claim 28.

33. A subsequent generation of any microbe recited in the microbial consortium according to claim 28.

34. A mutant of any microbe recited in the microbial consortium according to claim 28.

35. A cell-free or inactivated preparation of the microbial consortium according to claim 28 or a mutant of any microbe recited in the microbial consortium according to claim 28.

36. A metabolite produced by the microbial consortium according to claim 28 or a mutant of any microbe recited in the microbial consortium according to claim 28.

37. An agricultural composition, comprising:

a) a microbial consortium according to claim 28; and
b) an agriculturally acceptable carrier.

38. The agricultural composition according to claim 37, wherein the microbial consortium is present in the composition at 1×10^3 to 1×10^{12} bacterial cells per gram.

39. The agricultural composition according to claim 37, wherein said agricultural composition is formulated as a seed coating.

40. A method of imparting at least one beneficial trait upon a plant species, comprising:
a) applying a microbial consortium according to claim 8 to said plant, or to a growth medium in which said plant is located.

41. A method of imparting at least one beneficial trait upon a plant species, comprising:
a) applying the agricultural composition according to claim 37 to said plant, or to a growth medium in which said plant is located.

42. A method of imparting at least one beneficial trait upon a plant species, comprising: applying at least one isolated bacterial species to said plant, or to a growth medium in which said plant is located, wherein said at least one isolated bacterial species is selected from the group consisting of: *Brevibacterium frigoritolerans, Janibacter limosus, Pseudomonas yamanorum, Bacillus megaterium* and combinations thereof.

43. The method of claim 42, wherein said at least one isolated bacterial species is a strain selected from the group consisting of:
a) *Brevibacterium frigoritolerans* deposited as NRRL Accession Deposit No. NRRL B-67360;
b) *Janibacter limosus* deposited as NRRL Accession Deposit No. NRRL B-67358;
c) *Janibacter limosus* deposited as NRRL Accession Deposit No. NRRL B-67359;

d) *Janibacter limosus* deposited as NRRL Accession Deposit No. NRRL B-67364;
e) *Pseudomonas yamanorum* deposited as NRRL Accession Deposit No. NRRL B-67361;
f) *Pseudomonas yamanorum* deposited as NRRL Accession Deposit No. NRRL B-67362;
g) *Pseudomonas yamanorum* deposited as NRRL Accession Deposit No. NRRL B-67363
h) *Bacillus megaterium* deposited as NRRL Accession Deposit No. NRLL B-67370;

44. An isolated bacterial strain selected from **Table 3**.

45. An isolated bacterial strain having substantially similar morphological and physiological characteristics as an isolated bacterial strain according to claim 44.

46. An isolated bacterial strain having substantially similar genetic characteristics as an isolated bacterial strain according to claim 44.

47. A substantially pure culture of an isolated bacterial strain according to claim 44.

48. A progeny of an isolated bacterial strain according to claim 44.

49. A mutant of an isolated bacterial strain according to claim 44.

50. A cell-free or inactivated preparation of an isolated bacterial strain according to claim 44 or a mutant of such isolated bacterial strain.

51. A metabolite produced by an isolated bacterial strain according to claim 44 or produced by a mutant of such isolated bacterial strain.

52. An agricultural composition, comprising:
a) an isolated bacterial strain according to claim 44; and
b) an agriculturally acceptable carrier.

53. The agricultural composition according to claim 52, wherein the isolated bacterial strain is present in the composition at 1×10^{3} to 1×10^{12} bacterial cells per gram.

54. The agricultural composition according to claim 52, wherein said agricultural composition is formulated as a seed coating.

55. A method of imparting at least one beneficial trait upon a plant species, comprising:

a) applying an isolated bacterial strain according to claim 44 to said plant, or to a growth medium in which said plant is located.

56. A method of imparting at least one beneficial trait upon a plant species, comprising:

a) applying the agricultural composition according to claim 52 to said plant, or to a growth medium in which said plant is located.

57. A microbial consortium, comprising: at least two microbes selected from **Tables 1-4**, wherein at least one microbe is selected from **Table 3**.

58. A microbial consortium, comprising: at least two microbes selected from those listed in **Table 3**.

59. A microbial consortium selected from the consortia listed in **Table 5**, wherein the consortium comprises at least one microbe listed in **Table 3**.

60. A microbial consortium selected from the consortia listed in **Table 6**, wherein the consortium comprises at least one microbe listed in **Table 3**.

61. A microbial consortium selected from the consortia listed in **Table 7**, wherein the consortium comprises at least one microbe listed in **Table 3**.

62. A microbial consortium selected from the consortia listed in **Table 8**, wherein the consortium comprises at least one microbe listed in **Table 3**.

63. A microbial consortium selected from the consortia listed in **Table 9**, wherein the consortium comprises at least one microbe listed in **Table 3**.

64. A microbial consortium selected from the consortia listed in **Table 10**, wherein the consortium comprises at least one microbe listed in **Table 3**.

65. A microbial consortium selected from the consortia listed in **Table 11**, wherein the consortium comprises at least one microbe listed in **Table 3**.

66. A plant seed enhanced with a microbial seed coating, comprising:

a) a plant seed; and

b) a seed coating applied onto said plant seed,

wherein the seed coating comprises at least one microbe as listed in **Table 3**.

67. A plant seed enhanced with a microbial seed coating, comprising:

a) a plant seed; and

b) a seed coating applied onto said plant seed,

wherein the seed coating comprises at least two microbes as listed in **Tables 1-4**, and wherein at least one microbe is selected from **Table 3**.

68, The plant seed enhanced with a microbial seed coating according to claim 67, wherein the seed coating comprises a consortium of microbes as listed in **Tables 5-11**.

69. The plant seed enhanced with a microbial seed coating according to claim 66, wherein the microbial seed coating comprises at least one microbe as listed in **Table 3** at a concentration of 1×10^5 to 1×10^9 bacterial cells per seed.

70. A microbe selected from **Table 3** for use in agriculture.

71. A synthetic combination of a plant and microbe, comprising: at least one plant and at least one microbe selected from **Table 3**.

72. A method of increasing or promoting a desirable phenotypic trait of a plant species, comprising:

a) applying at least one bacteria selected from **Table 3** to said plant, or to a growth medium in which said plant is located.

73. The method of claim 72, wherein the applying occurs by: coating a plant seed with said bacteria, coating a plant part with said bacteria, spraying said bacteria onto a plant part, spraying said bacteria into a furrow into which a plant or seed will be placed, drenching said bacteria onto a plant part or into an area into which a plant will be placed, spreading said bacteria onto a plant part or into an area into which a plant will be placed, broadcasting said bacteria onto a plant part or into an area into which a plant will be placed, and combinations thereof.

FIG. 1

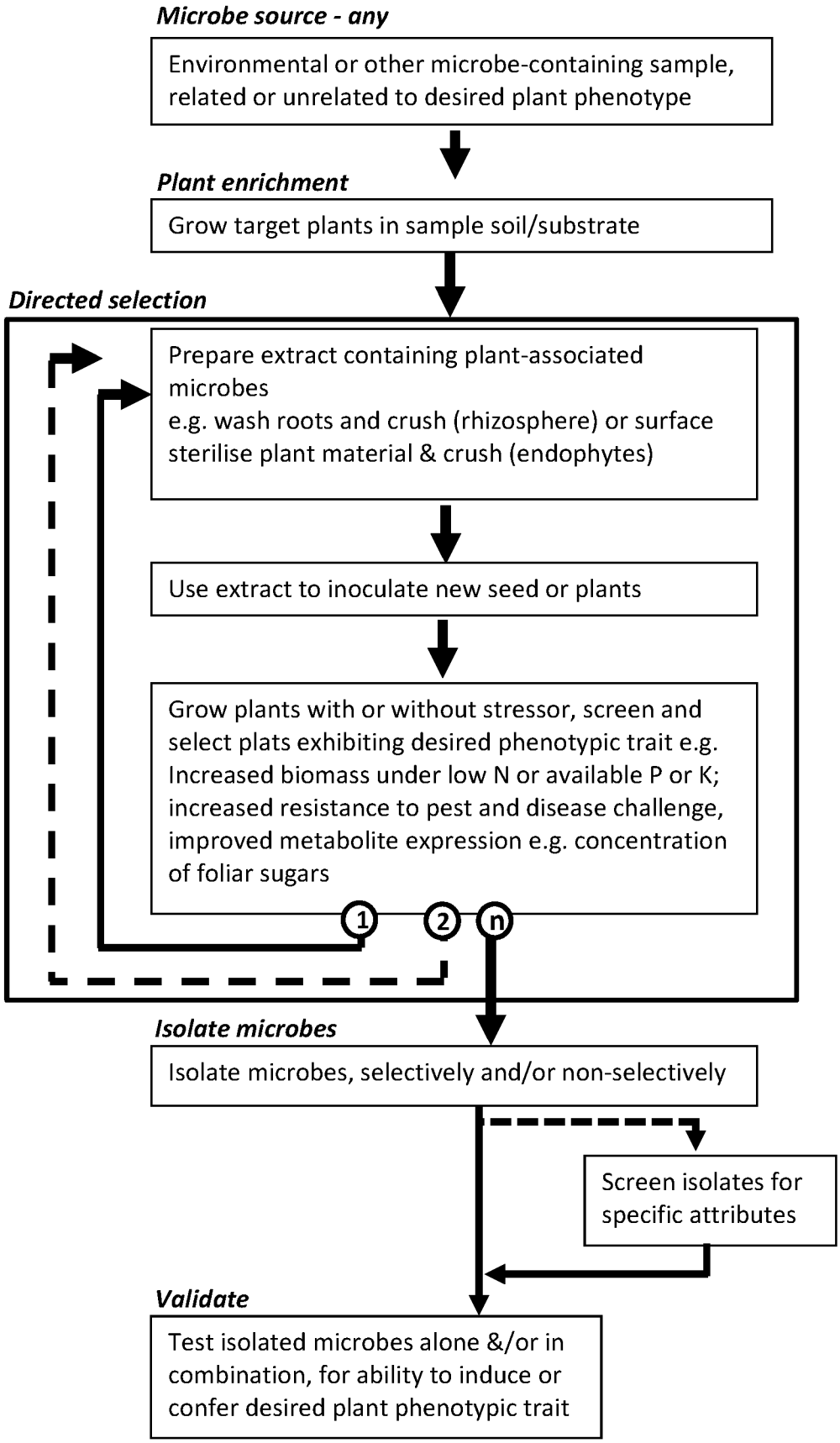

Microbe source - any
Environmental or other microbe-containing sample, related or unrelated to desired plant phenotype
Plant enrichment
Grow target plants in sample soil/substrate
Directed selection
Prepare extract containing plant-associated microbes
e.g. wash roots and crush (rhizosphere) or surface sterilise plant material & crush (endophytes)
Use extract to inoculate new seed or plants
Grow plants with or without stressor, screen and select plats exhibiting desired phenotypic trait e.g. Increased biomass under low N or available P or K; increased resistance to pest and disease challenge, improved metabolite expression e.g. concentration of foliar sugars
1
2
n
Isolate microbes
Isolate microbes, selectively and/or non-selectively
Screen isolates for specific attributes
Validate
Test isolated microbes alone &/or in combination, for ability to induce or confer desired plant phenotypic trait

FIG. 2

Microbe capture	Generate diverse plant-microbe associations in the target crop
Directed selection	Multiple rounds of iterative selection of plants/microbiomes best expressing the desired trait
Microbe isolation	On a range of media
Select key microbes	Single organisms and/or consortia
Trait validation	Identify leading microbes (consortia)

FIG. 3

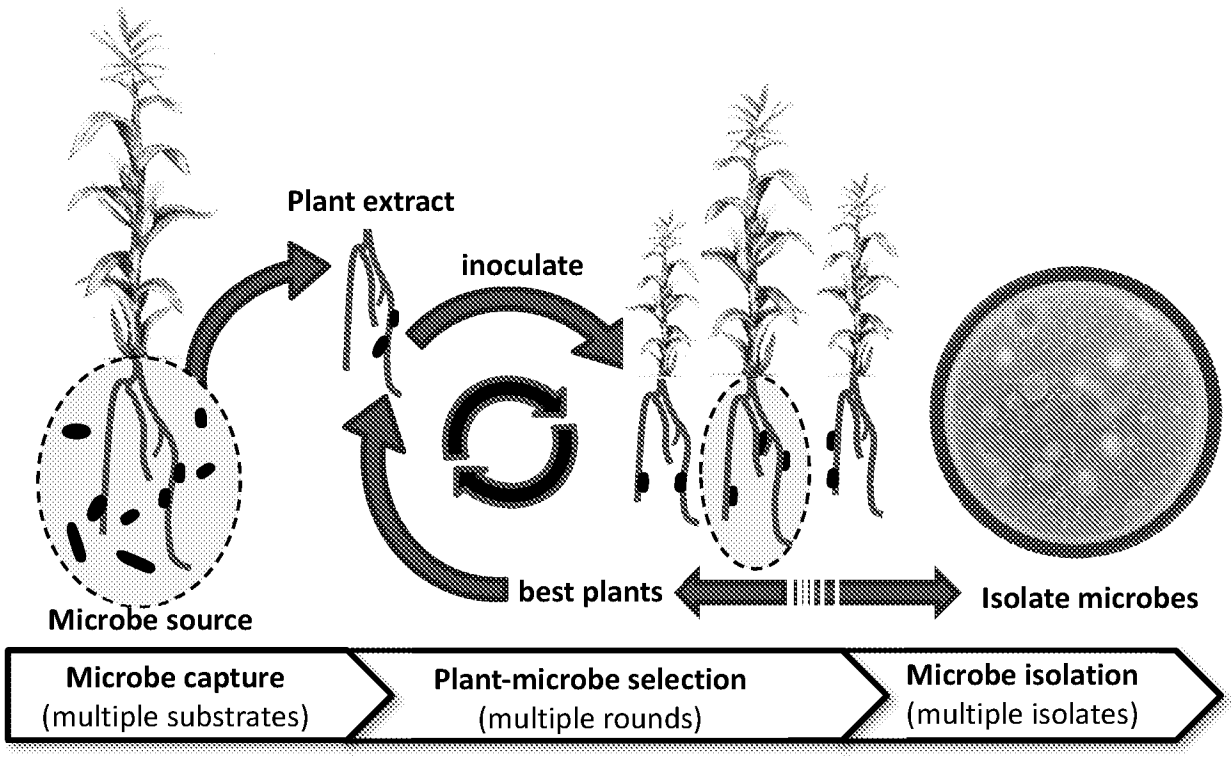
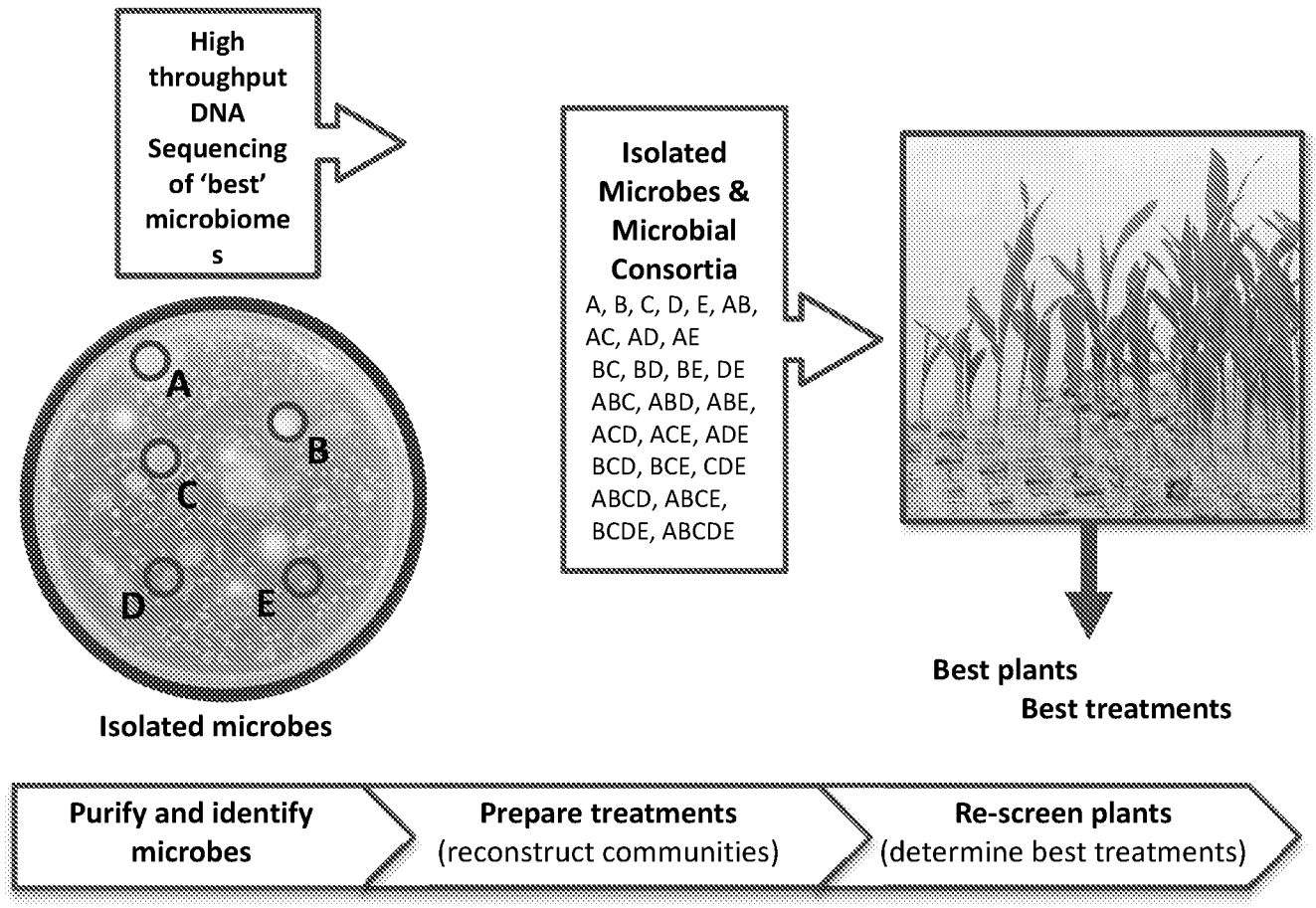
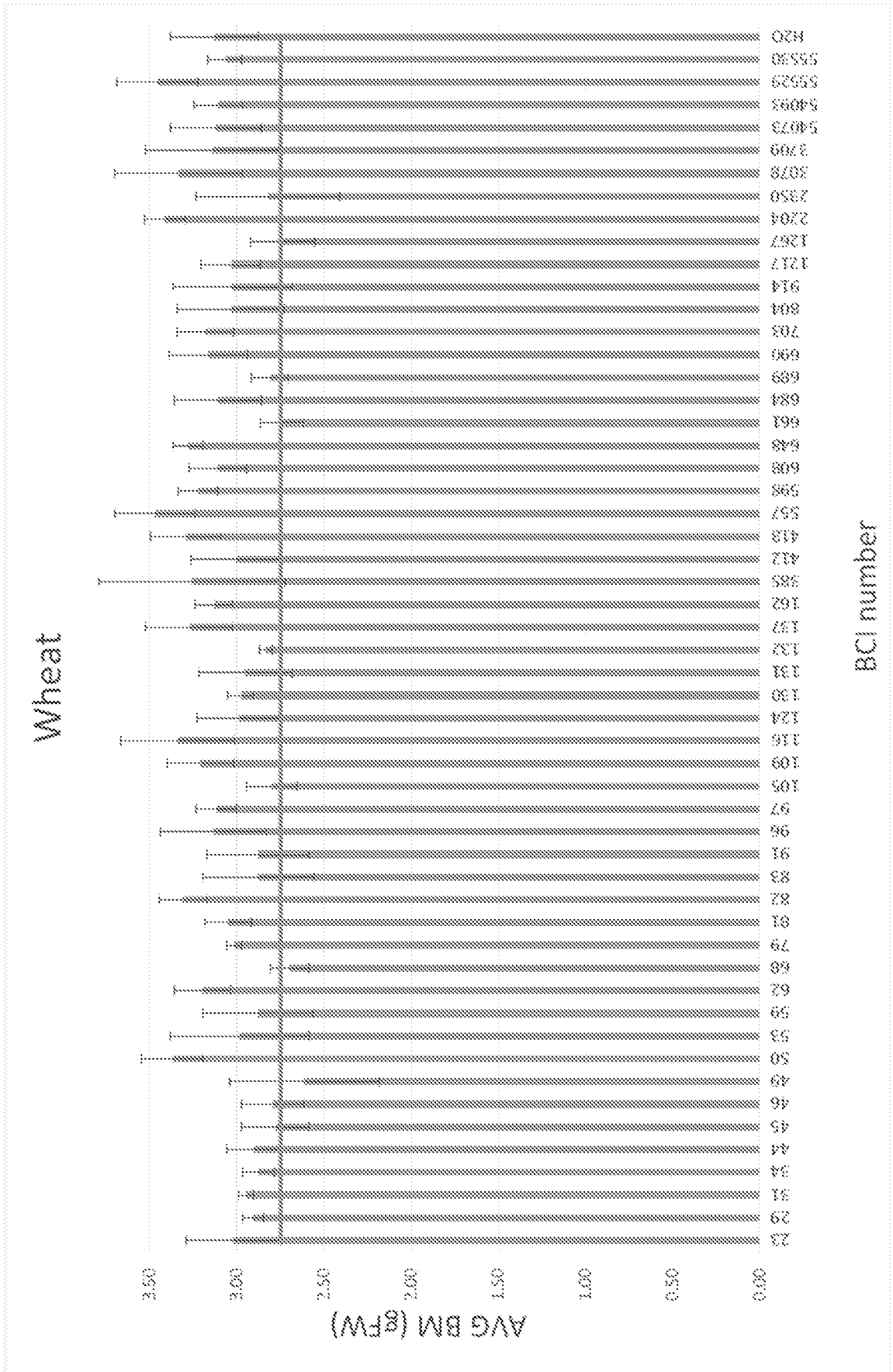

Plant extract
inoculate
Microbe source
best plants
Isolate microbes
Microbe capture
(multiple substrates)
Plant-microbe selection
(multiple rounds)
Microbe isolation
(multiple isolates)

FIG. 4


High throughput DNA Sequencing of 'best' microbiomes
A
B
C
D
E
Isolated microbes
Isolated Microbes & Microbial Consortia
A, B, C, D, E, AB, AC, AD, AE
BC, BD, BE, DE
ABC, ABD, ABE, ACD, ACE, ADE
BCD, BCE, CDE
ABCD, ABCE, BCDE, ABCDE
Best plants
Best treatments
Purify and identify microbes
Prepare treatments (reconstruct communities)
Re-screen plants (determine best treatments)


Wheat
AVG BM (gFW)
2.50
2.00
1.50
1.00
0.50
0.00
BCI number
23
29
31
34
44
45
46
49
50
53
59
62
66
79
81
82
83
91
96
97
105
109
116
124
130
131
132
137
162
165
412
413
557
598
608
648
661
684
689
690
705
804
914
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1267
2264
2350
3078
3709
5402
5409
5552
5553
H20

FIG. 5

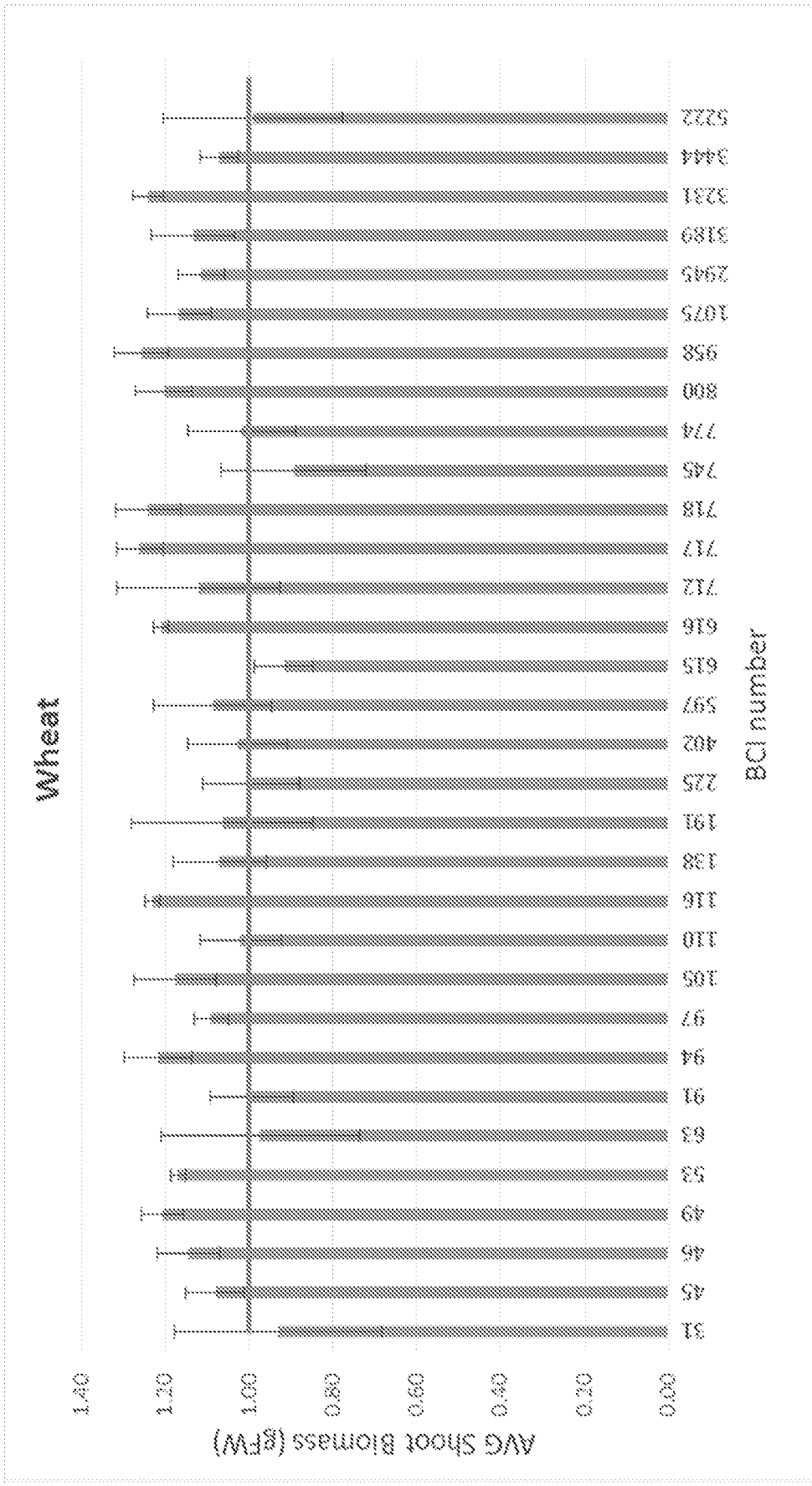

Wheat
BCI number
AVG Shoot Biomass (gFW)
1.40
1.20
1.00
0.80
0.60
0.40
0.20
0.00
31
45
46
49
53
63
91
94
97
105
110
116
138
191
225
402
597
615
616
712
717
718
745
774
800
958
1075
2945
3189
3231
3444
5222

FIG. 6 A

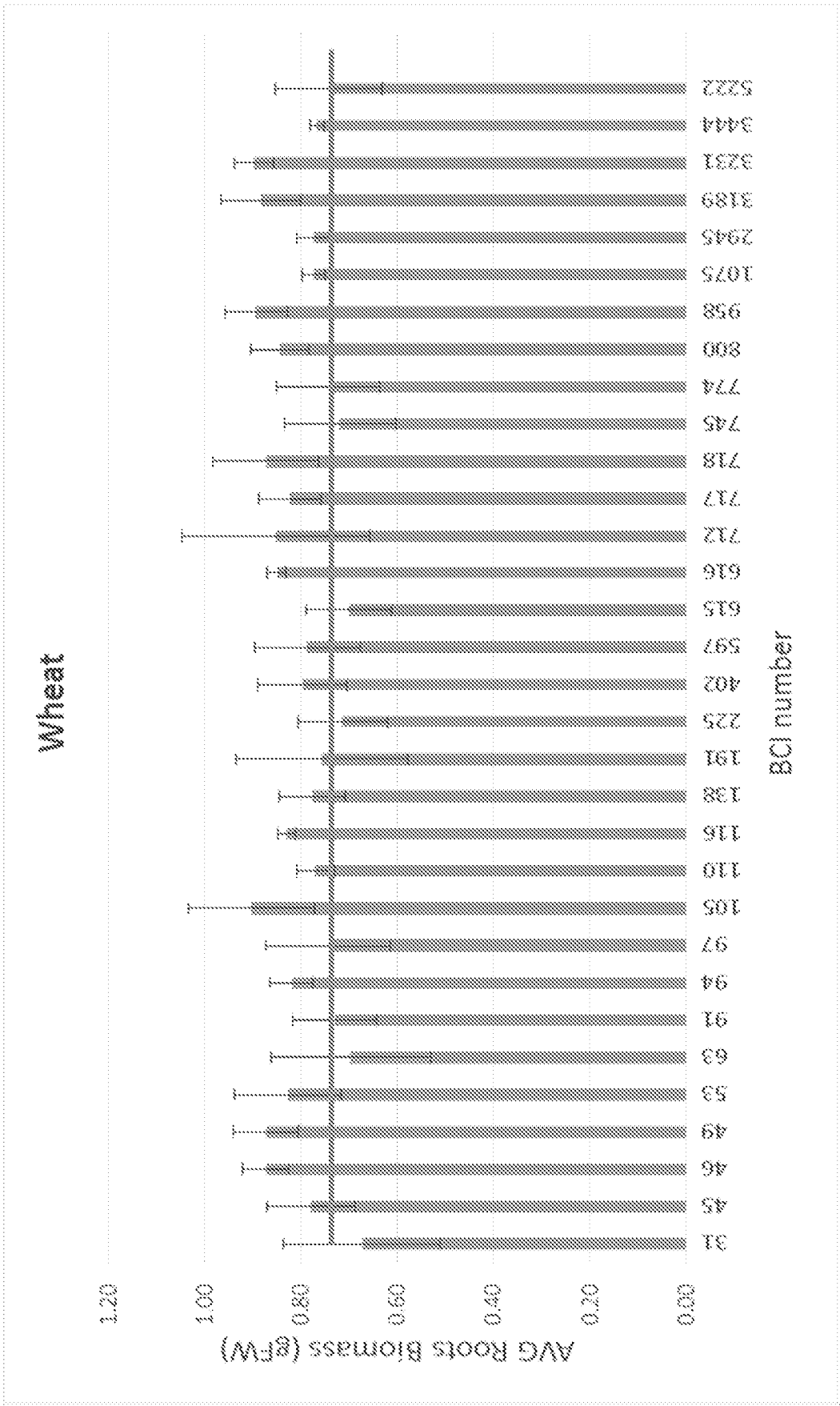

Wheat
AVG Roots Biomass (gFW)
1.20
1.00
0.80
0.60
0.40
0.20
0.00
BCI number
31
45
46
49
53
63
91
94
97
105
110
116
138
191
225
402
597
615
616
712
717
718
745
774
800
958
1075
2945
3189
3231
3444
5222

FIG.6 B

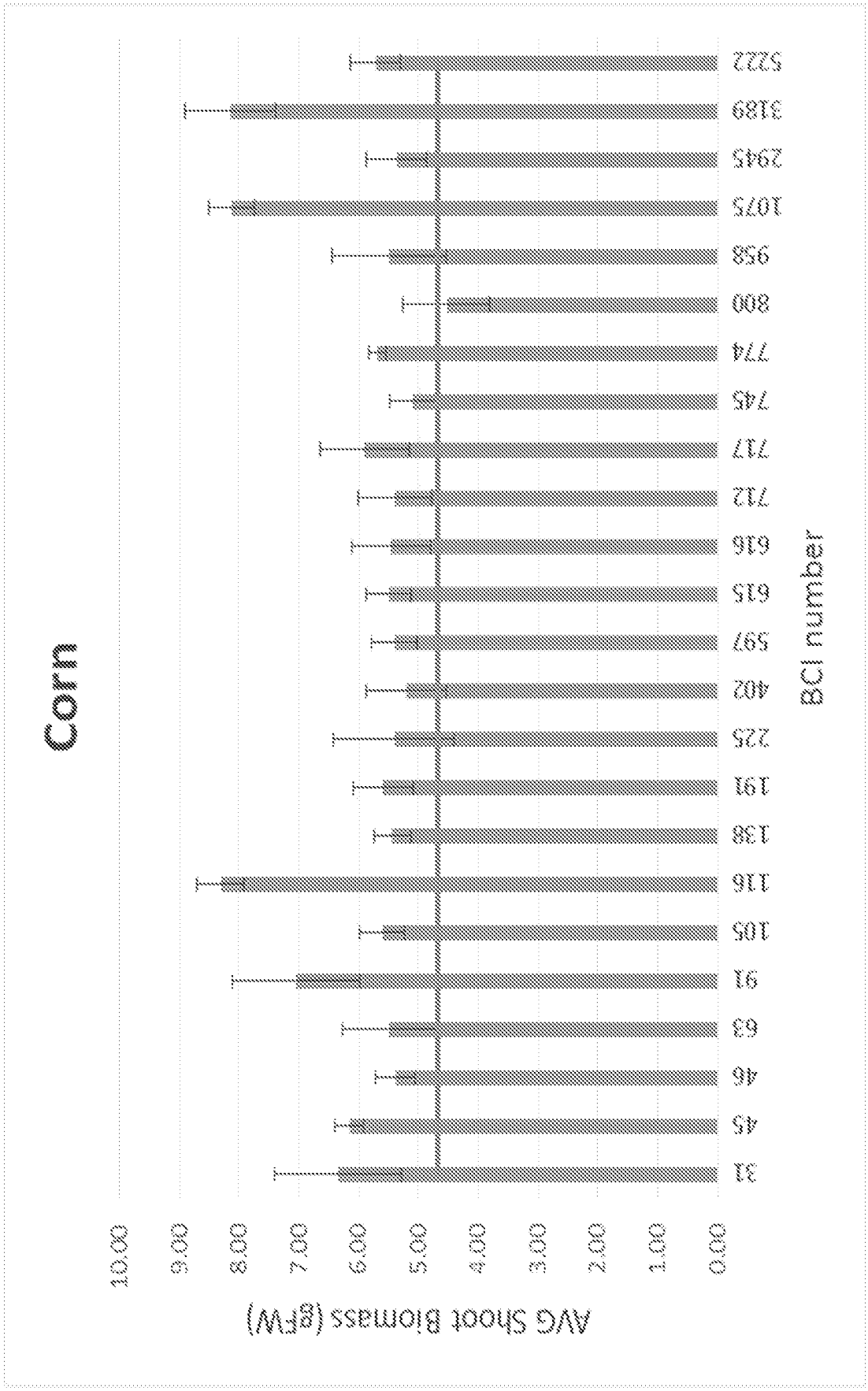

Corn
AVG Shoot Biomass (gFW)
10.00
9.00
8.00
7.00
6.00
5.00
4.00
3.00
2.00
1.00
0.00
BCI number
31
45
46
63
91
105
116
138
191
225
402
597
615
616
712
717
745
774
800
958
1075
2945
3189
5222

FIG. 7 A

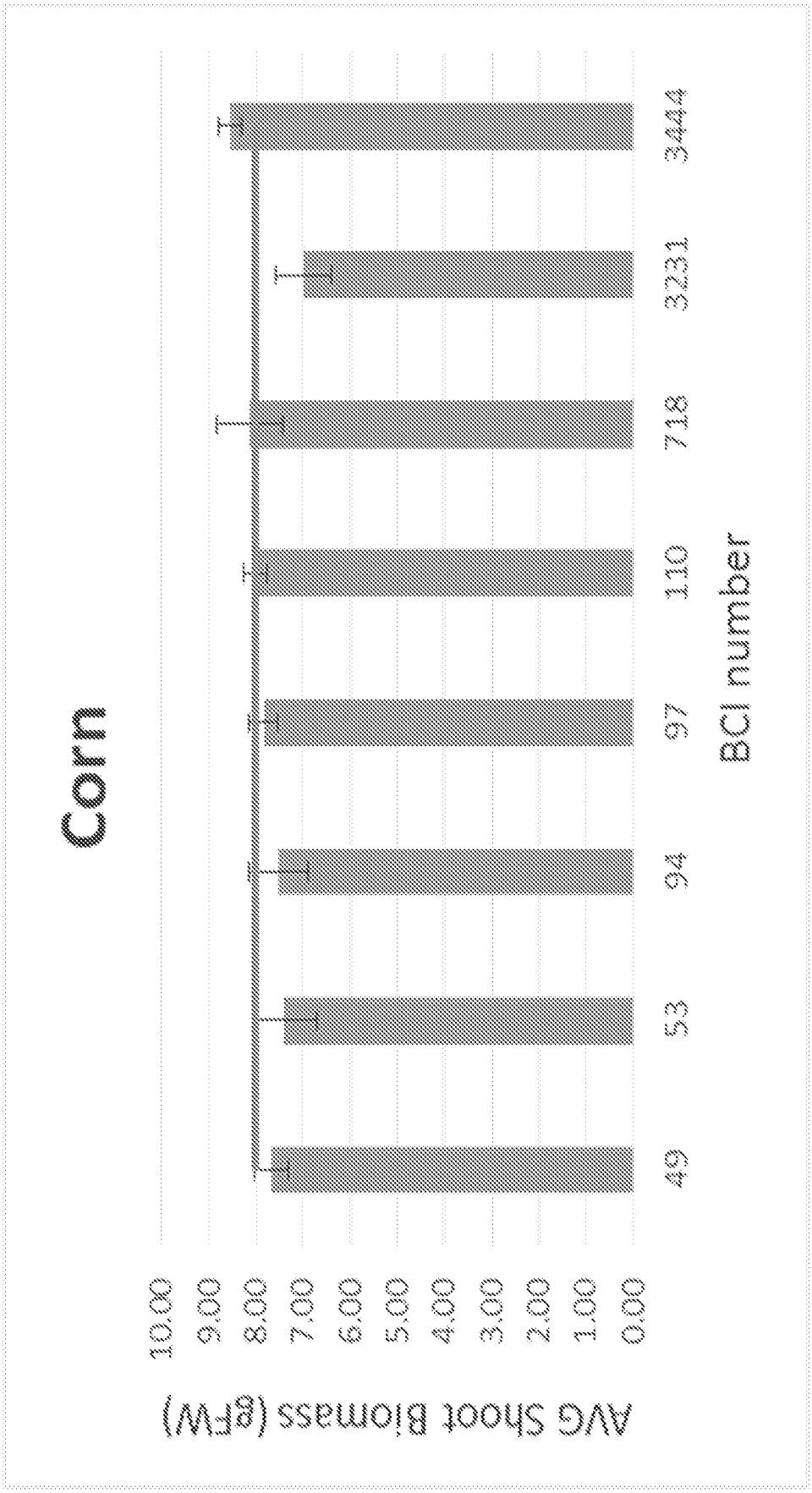

Corn
AVG Shoot Biomass (gFW)
10.00
9.00
8.00
7.00
6.00
5.00
4.00
3.00
2.00
1.00
0.00
BCI number
49
53
94
97
110
718
3231
3444

FIG. 7 B

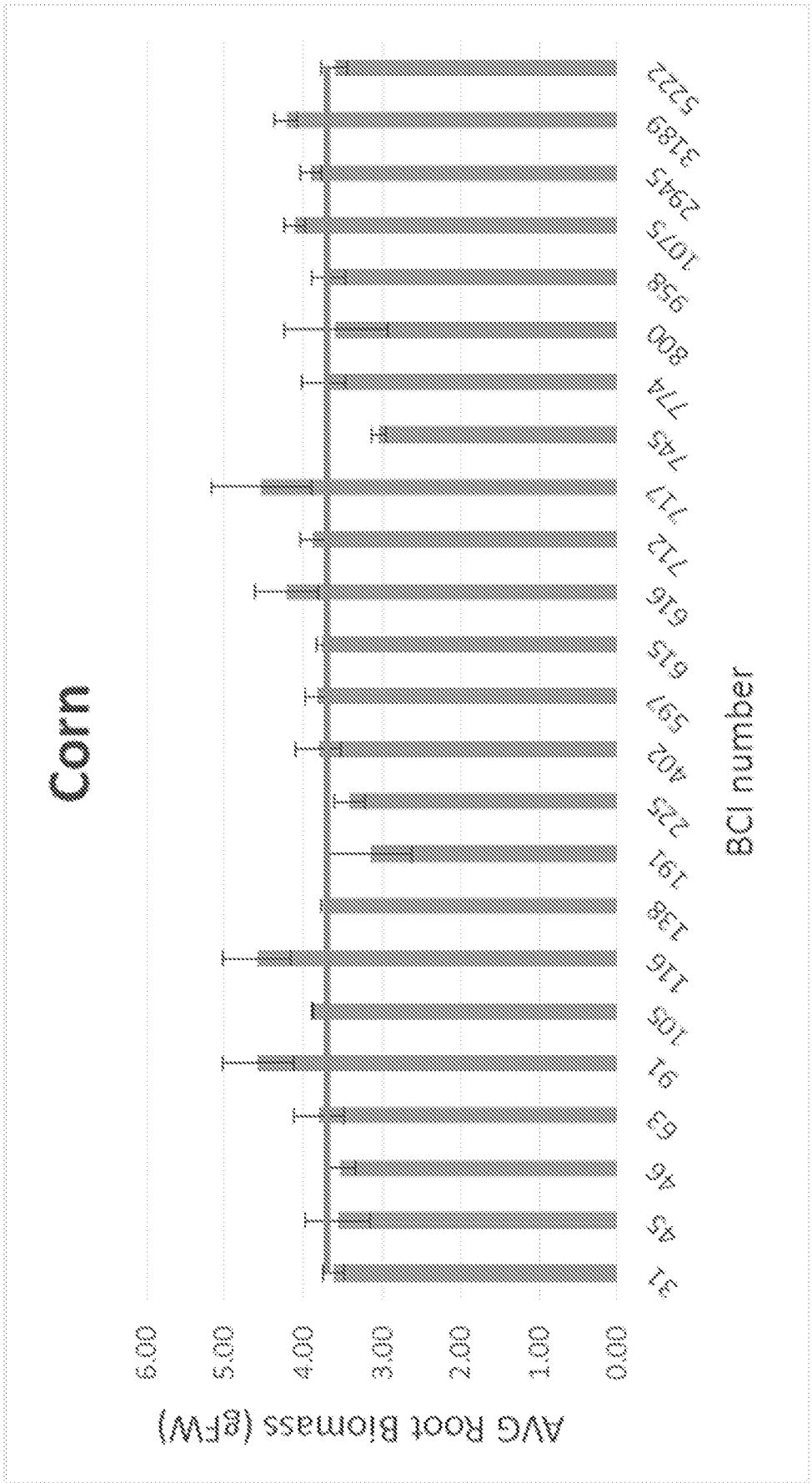

Corn
AVG Root Biomass (gFW)
6.00
5.00
4.00
3.00
2.00
1.00
0.00
BCI number
31
43
46
63
91
105
116
138
191
225
402
597
615
616
712
717
745
774
800
958
1075
2945
3189
5222

FIG. 8 A

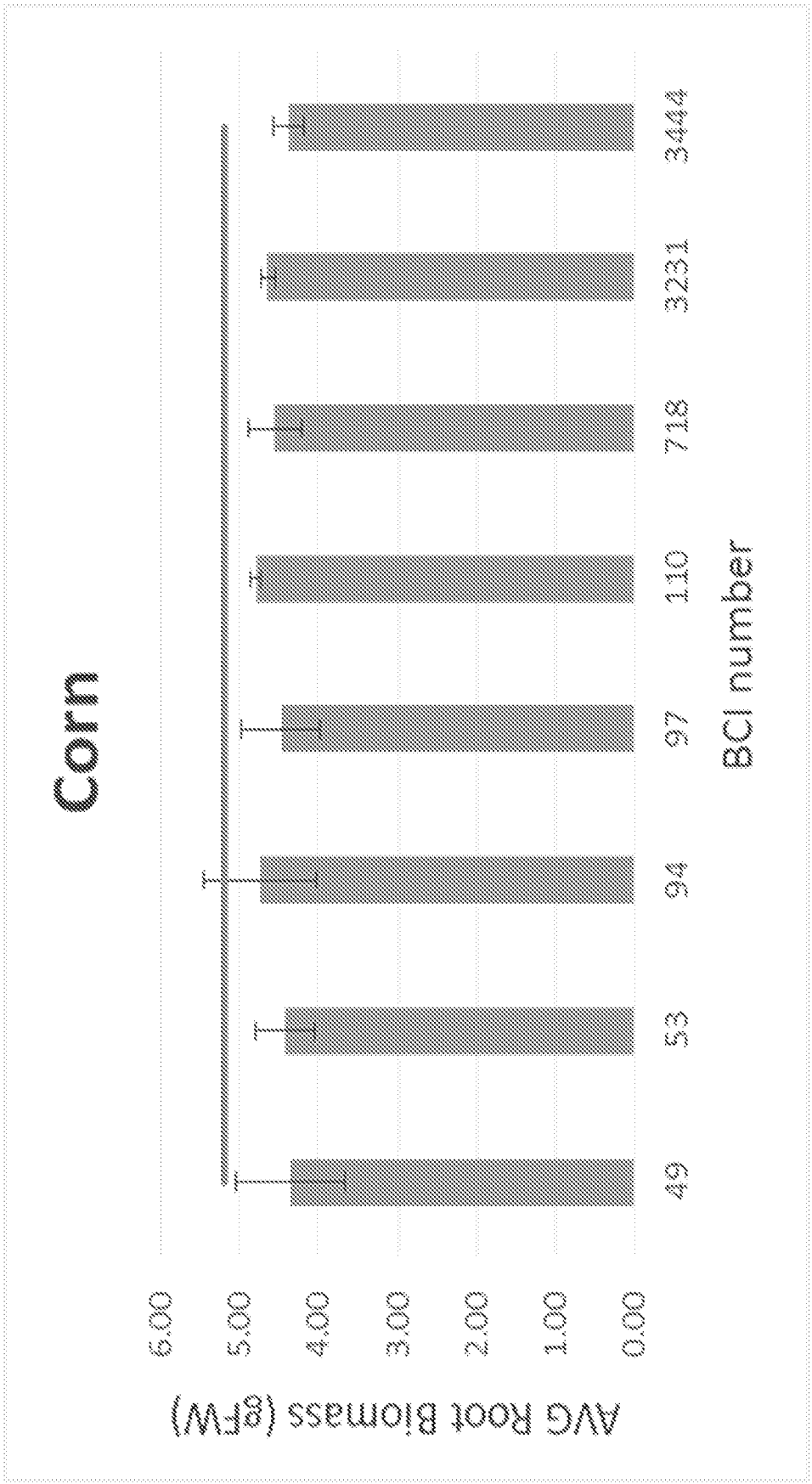

Corn
AVG Root Biomass (gFW)
6.00
5.00
4.00
3.00
2.00
1.00
0.00
BCI number
49
53
94
97
110
718
3231
3444

FIG. 8 B

FIG. 9

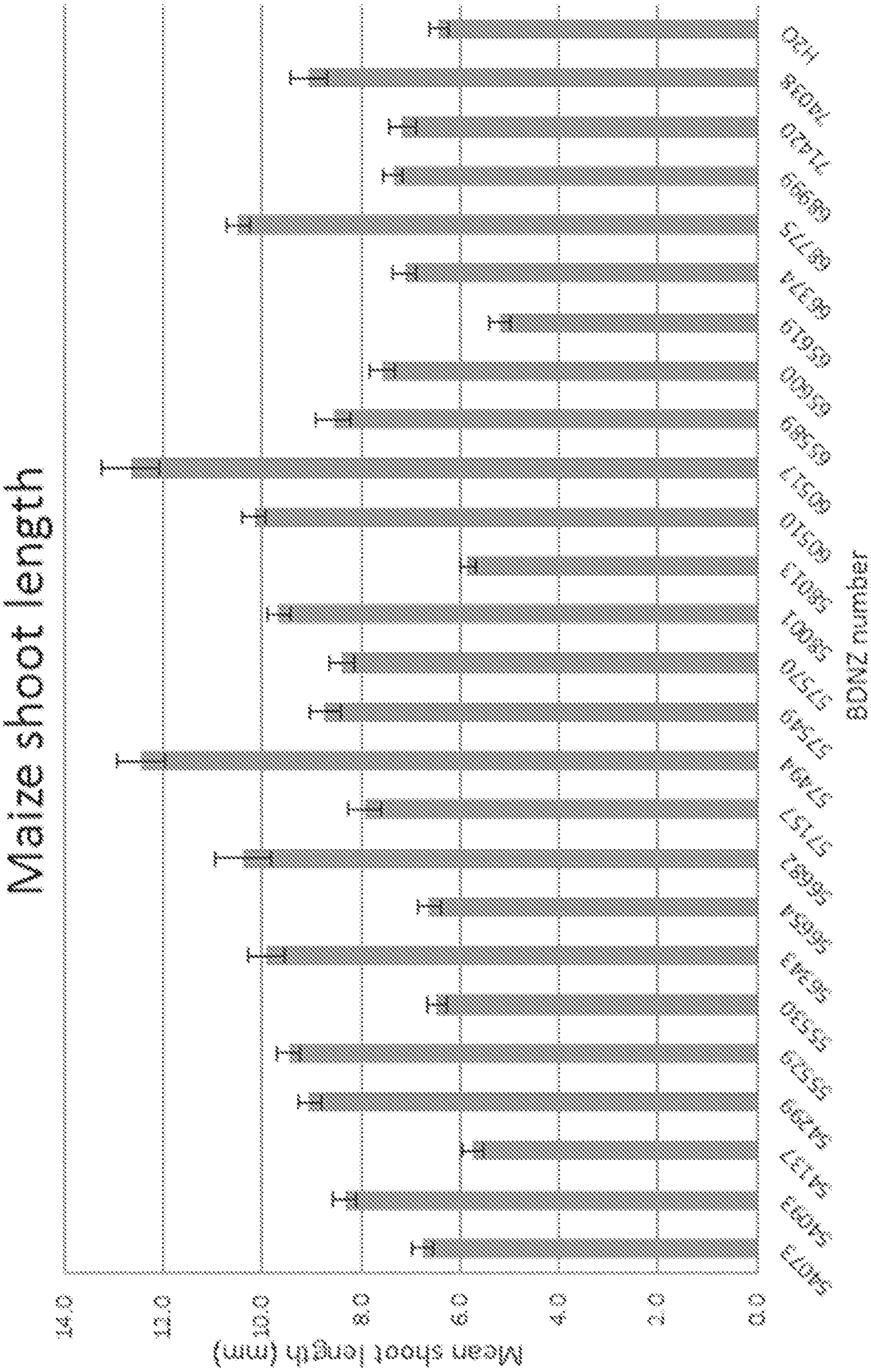
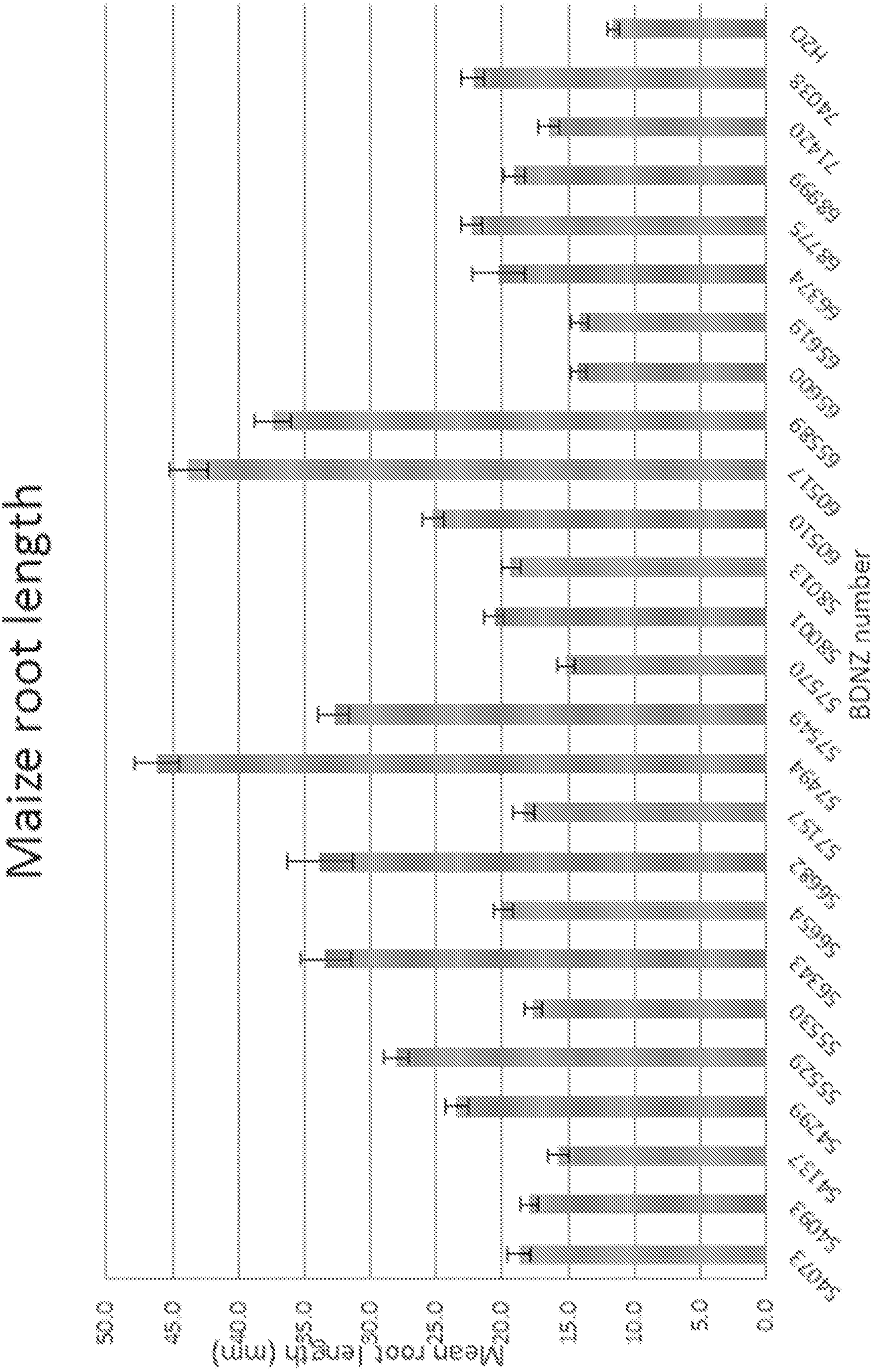

Maize shoot length
Mean shoot length (mm)
14.0
12.0
10.0
8.0
6.0
4.0
2.0
0.0
54073
54093
54137
54299
55529
55530
56343
56654
56682
57157
57494
57540
57570
58001
58013
60510
60517
65589
65600
65619
66374
68775
71420
H2O
BDNZ number

FIG. 10


Maize root length
Mean root length (mm)
BONZ number
50.0
45.0
40.0
35.0
30.0
25.0
20.0
15.0
10.0
5.0
0.0

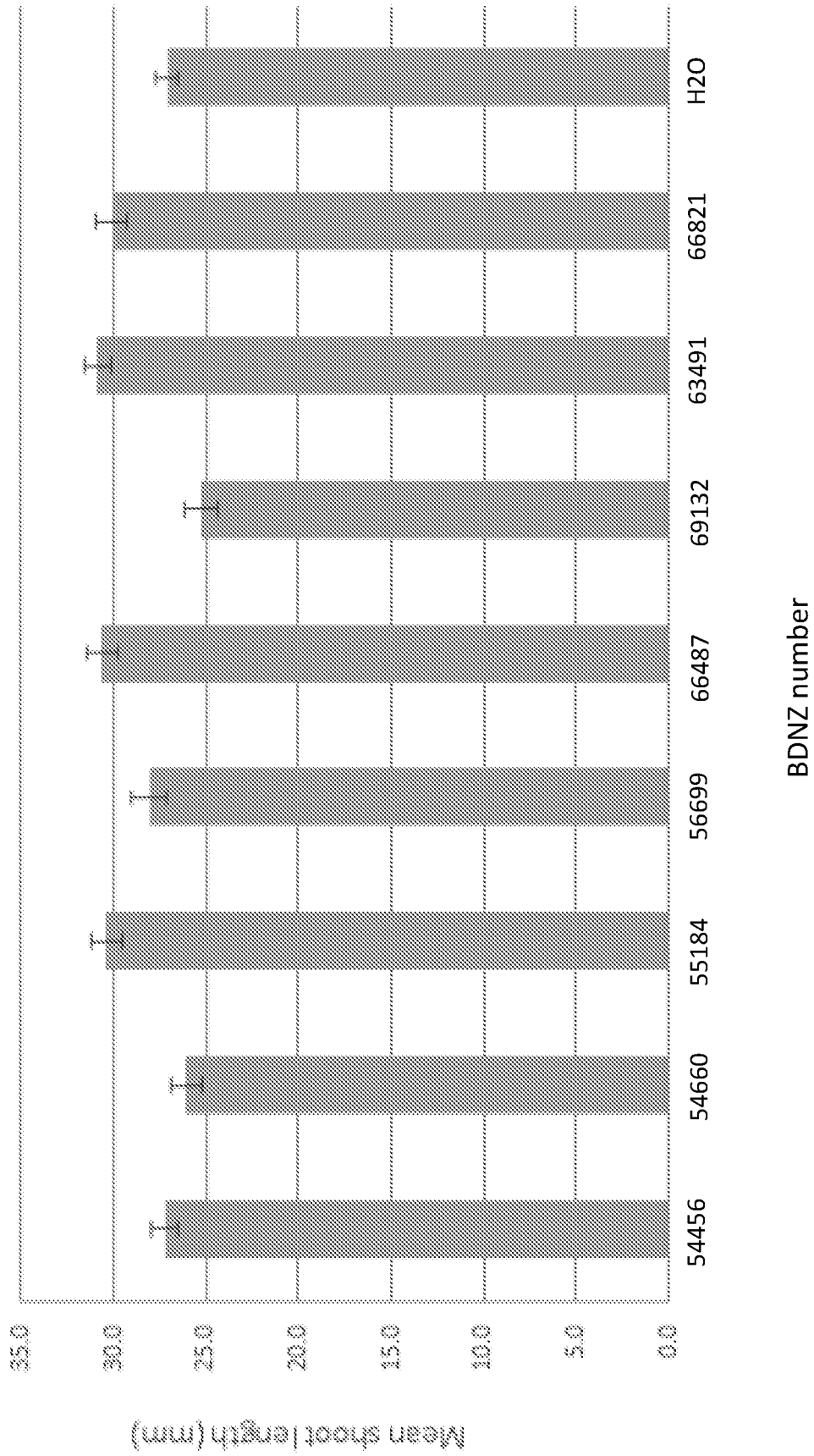

Wheat shoot length
Mean shoot length (mm)
35.0
30.0
25.0
20.0
15.0
10.0
5.0
0.0
54456
54660
55184
56699
66487
69132
63491
66821
H2O
BDNZ number

FIG. 11

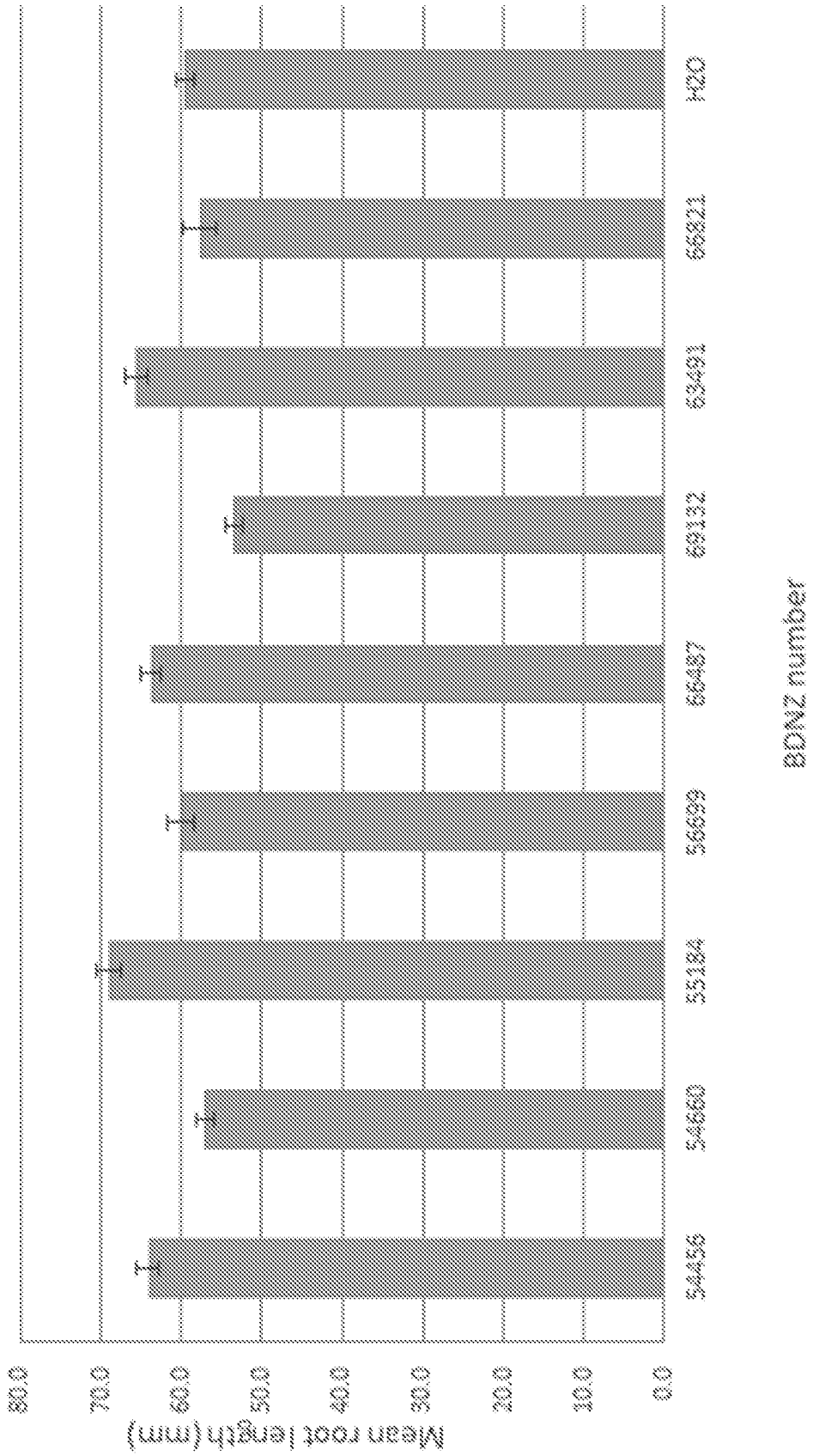

Wheat root length
Mean root length (mm)
80.0
70.0
60.0
50.0
40.0
30.0
20.0
10.0
0.0
54435
54660
55154
56639
66487
69132
63491
65921
H2O
BDNZ number

FIG. 12

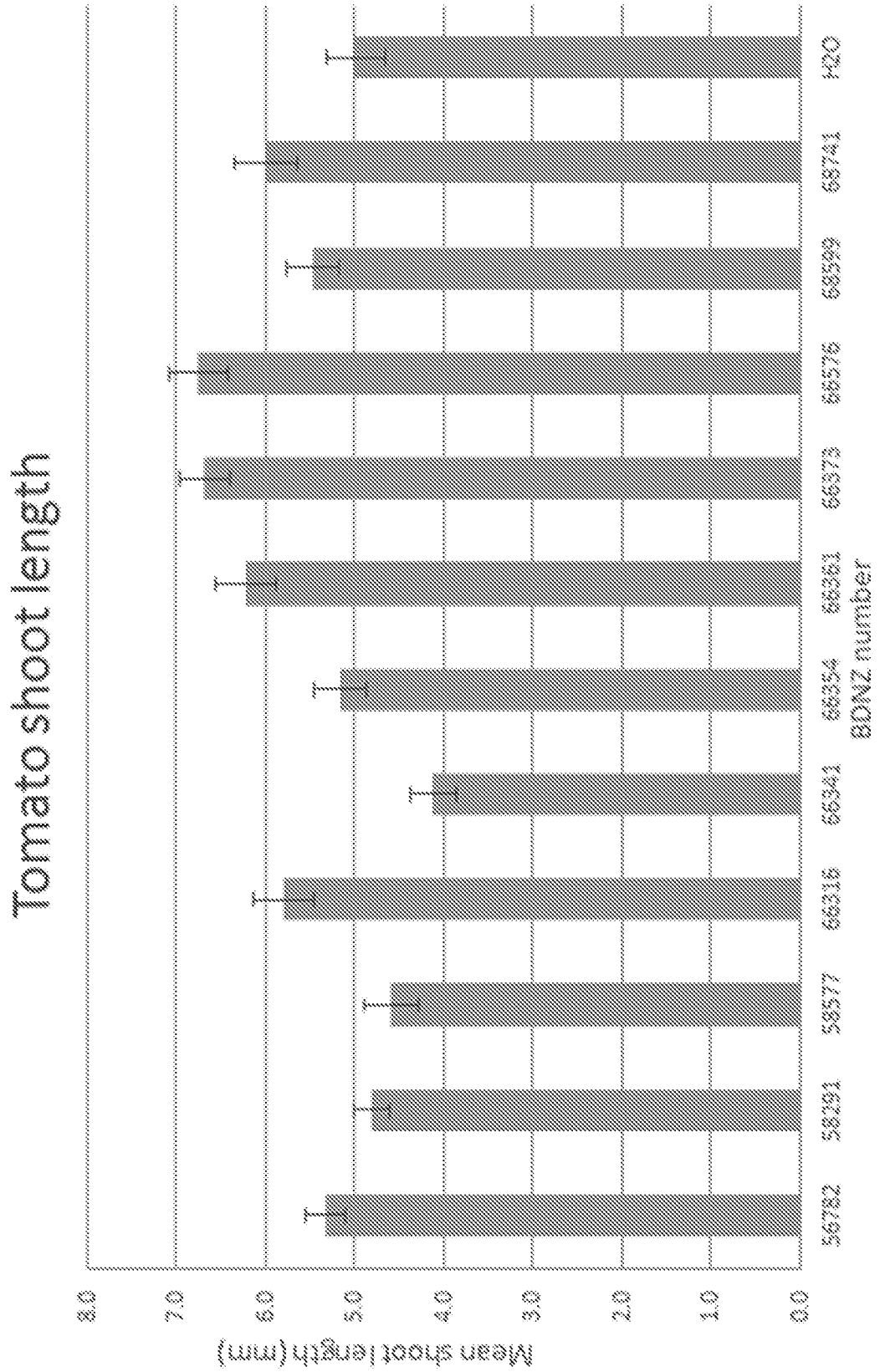
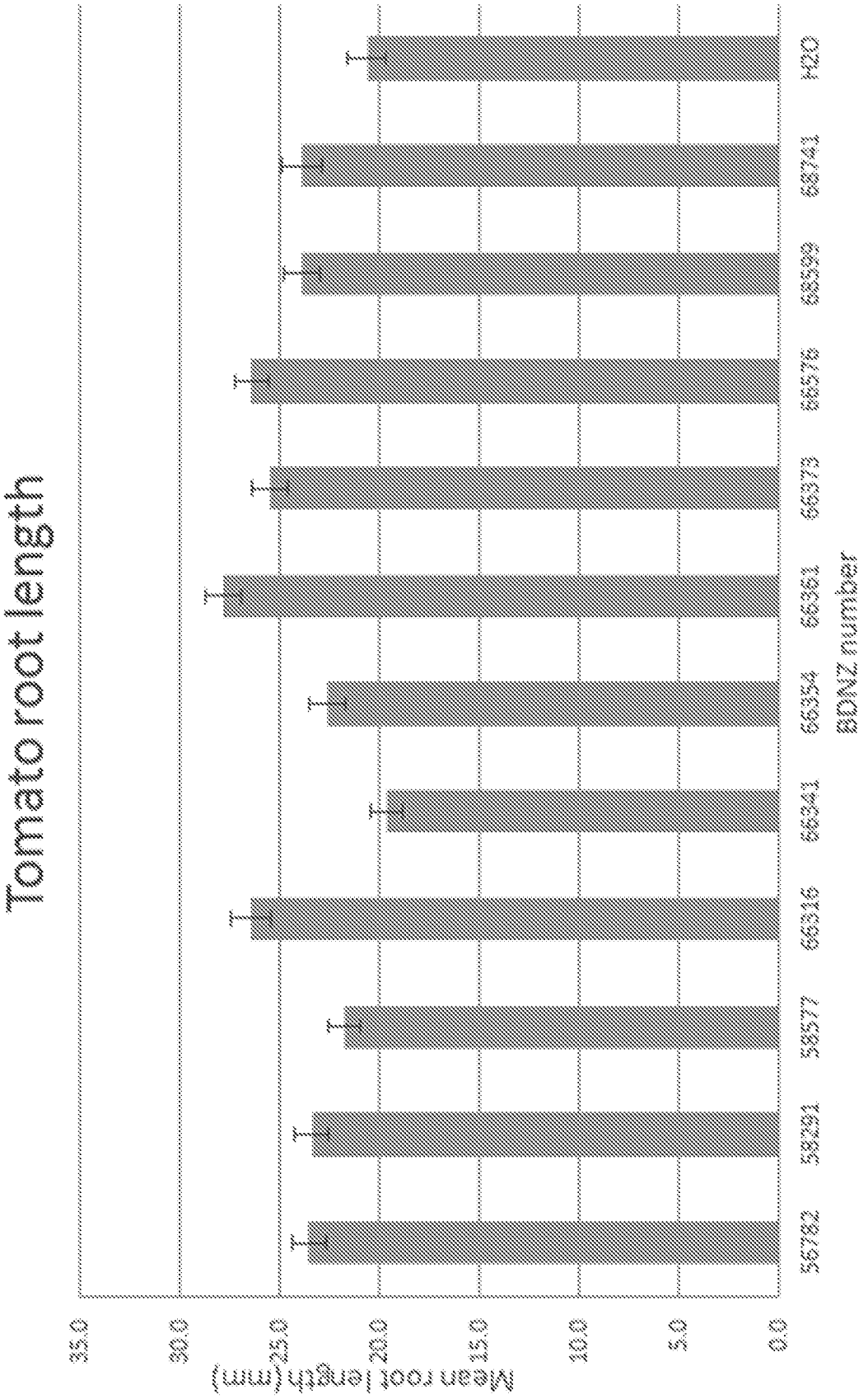

Tomato shoot length
Mean shoot length (mm)
8.0
7.0
6.0
5.0
4.0
3.0
2.0
1.0
0.0
56782
58191
58577
66316
66341
66354
66361
66373
66576
66599
68741
H2O
80NZ number

FIG. 13

FIG. 14


Tomato root length
Mean root length (mm)
35.0
30.0
25.0
20.0
15.0
10.0
5.0
0.0
56782
58291
58577
66316
66341
66354
66361
66373
66576
66599
66741
H2O
BDNZ number

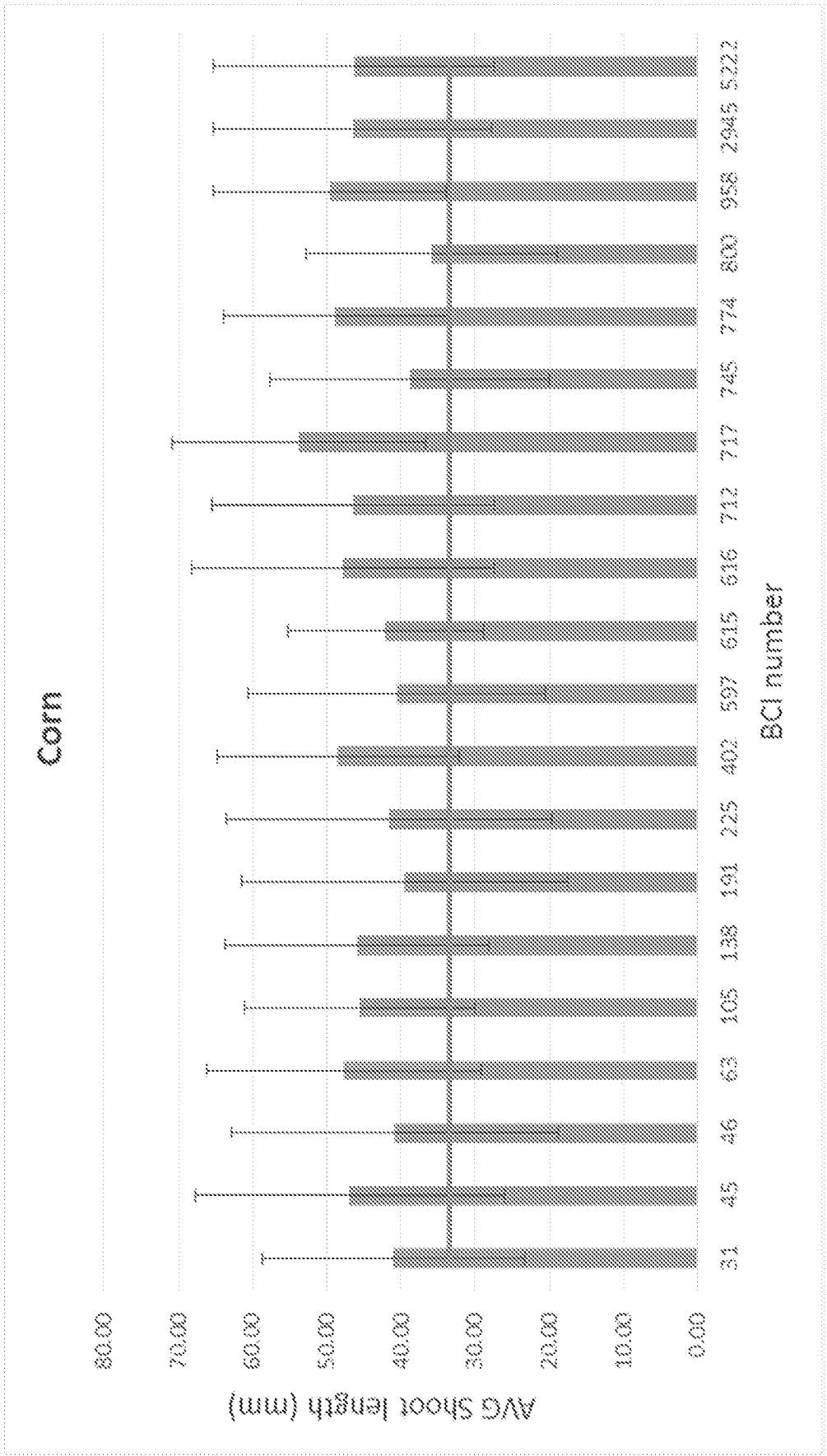

Corn
AVG Shoot length (mm)
80.00
70.00
60.00
50.00
40.00
30.00
20.00
10.00
0.00
BCI number
31
45
46
63
105
138
191
225
402
597
615
616
712
717
745
774
800
958
2945
5222

FIG. 15 A

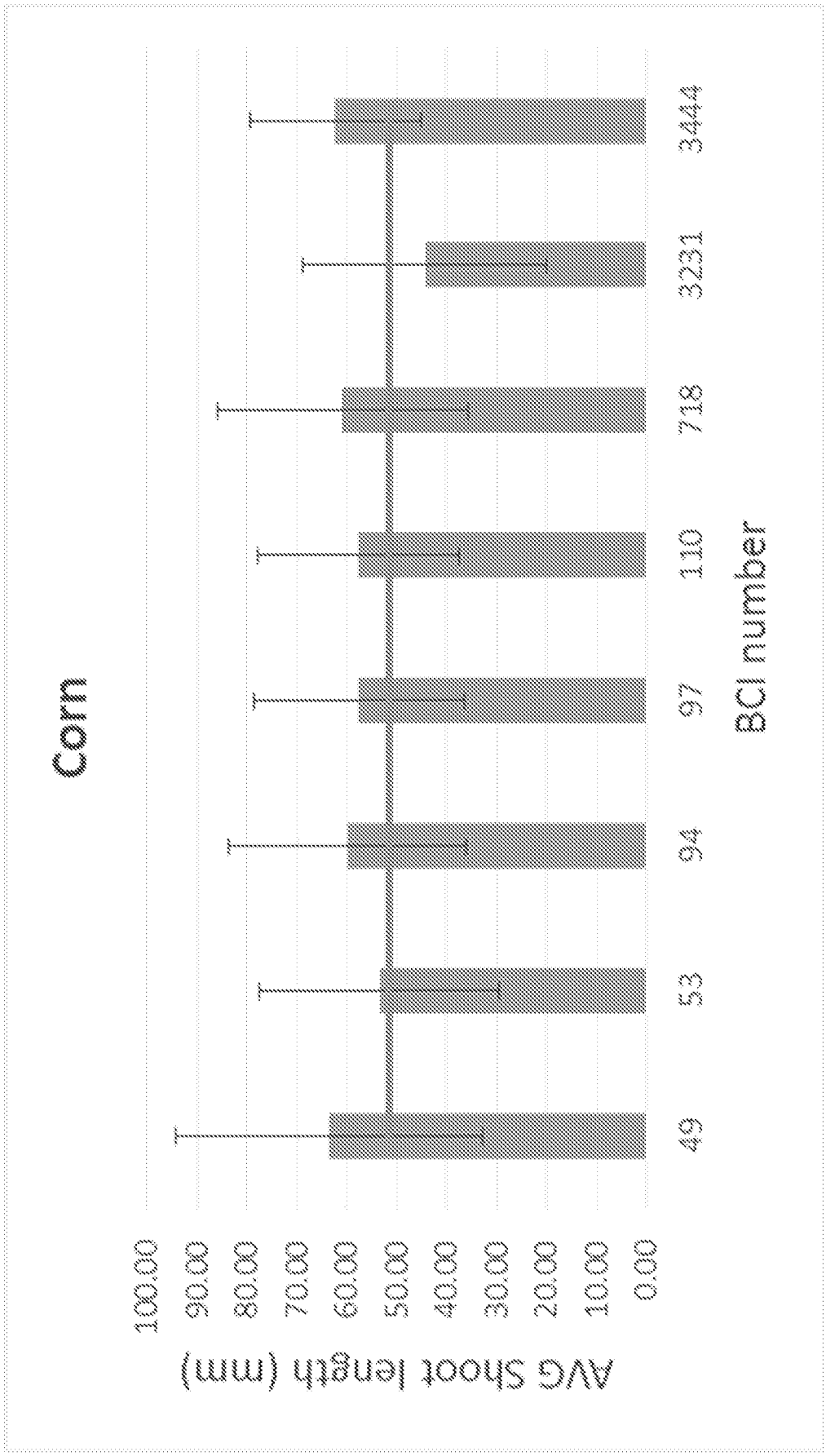

Corn
AVG Shoot length (mm)
100.00
90.00
80.00
70.00
60.00
50.00
40.00
30.00
20.00
10.00
0.00
49
53
94
97
110
718
3231
3444
BCI number

FIG. 15 B

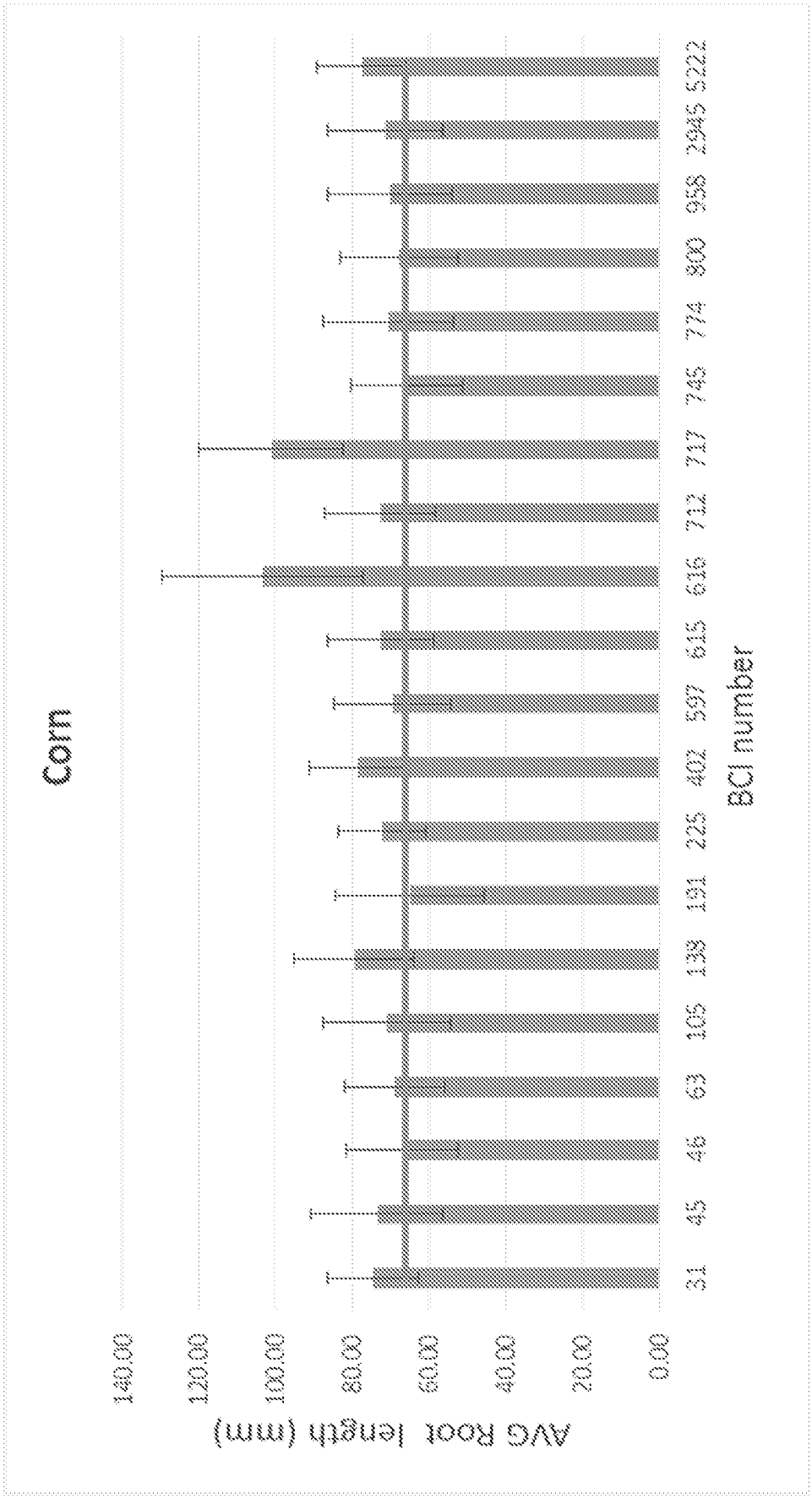

Corn
AVG Root length (mm)
140.00
120.00
100.00
80.00
60.00
40.00
20.00
0.00
BCI number
31
45
46
63
105
139
191
225
402
597
615
616
712
717
745
774
800
958
2945
5222

FIG. 16 A

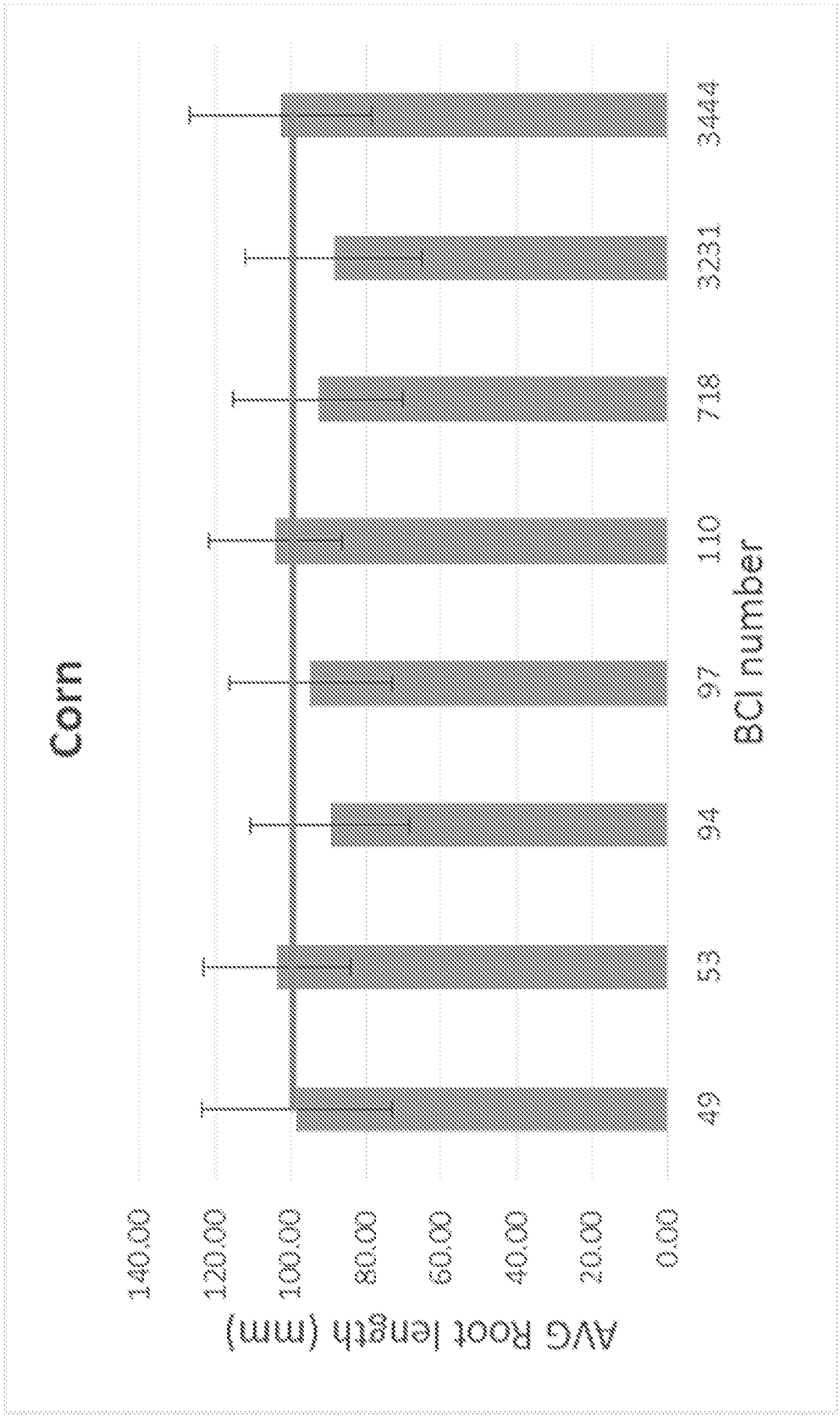

Corn
AVG Root length (mm)
140.00
120.00
100.00
80.00
60.00
40.00
20.00
0.00
BCI number
49
53
94
97
110
718
3231
3444

FIG. 16 B

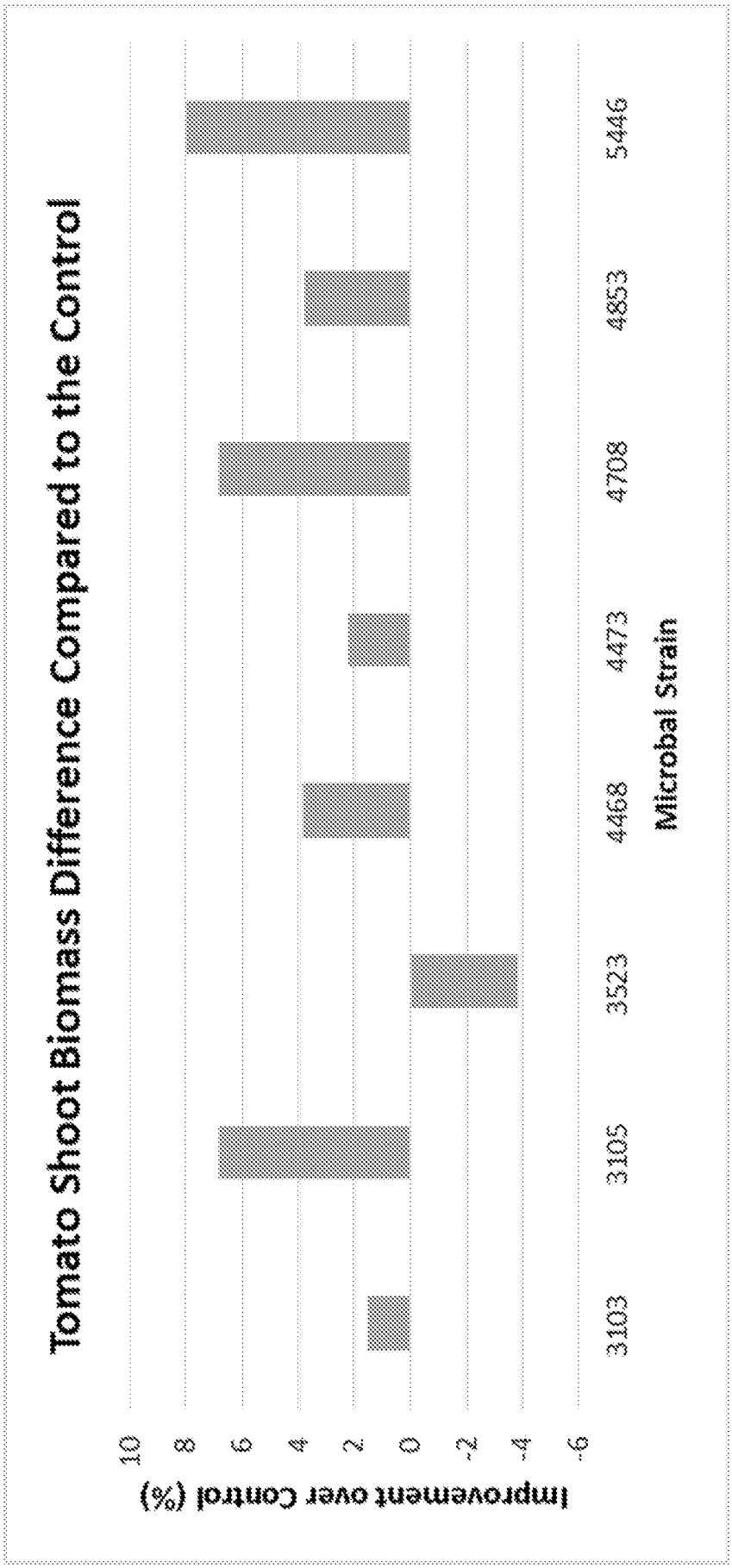

Tomato Shoot Biomass Difference Compared to the Control
Improvement over Control (%)
10
8
6
4
2
0
-2
-4
-6
3103
3105
3523
4468
4473
4708
4853
5446
Microbal Strain

FIG. 17

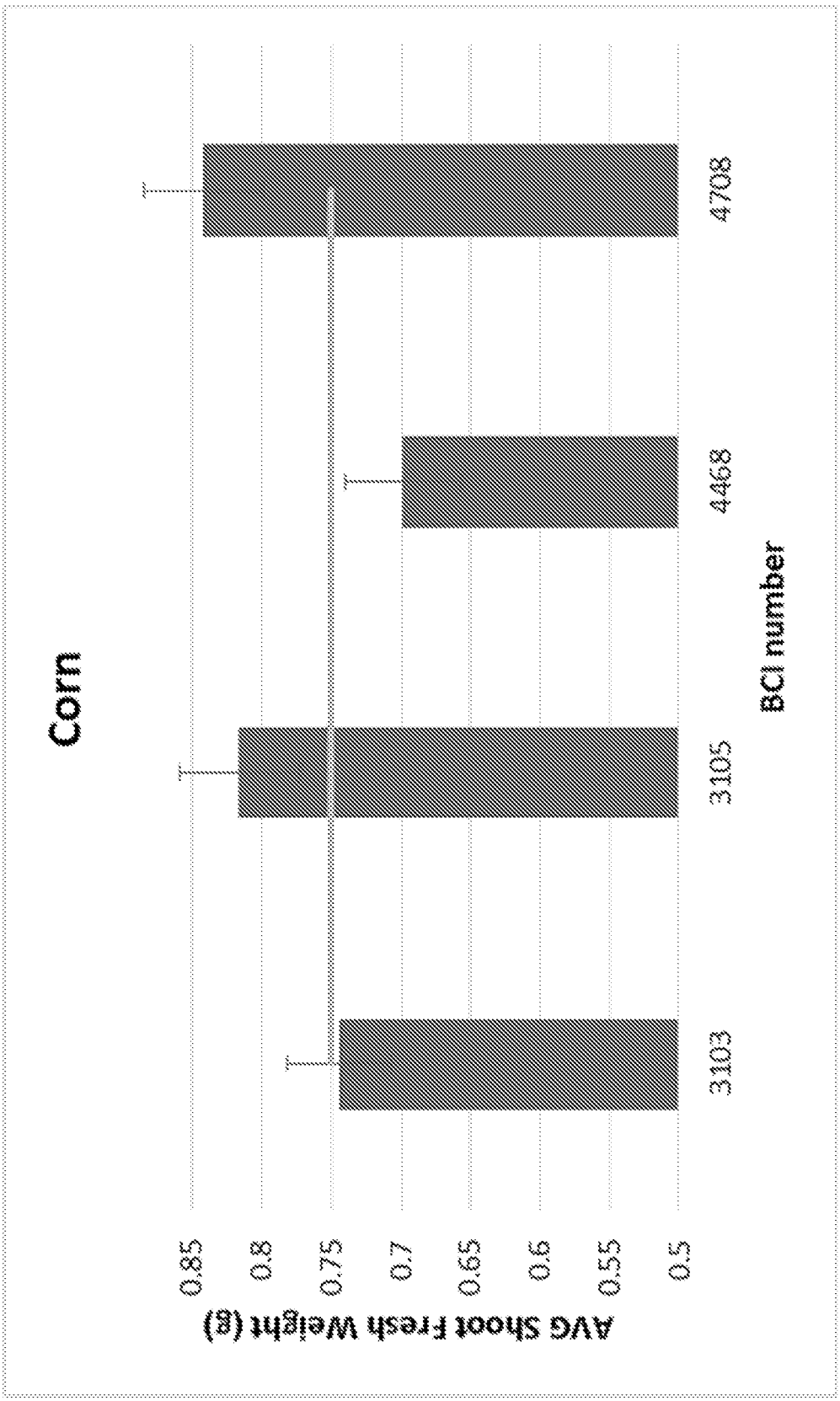

Corn
AVG Shoot Fresh Weight (g)
0.85
0.8
0.75
0.7
0.65
0.6
0.55
0.5
3103
3105
4468
4708
BCI number

FIG. 18

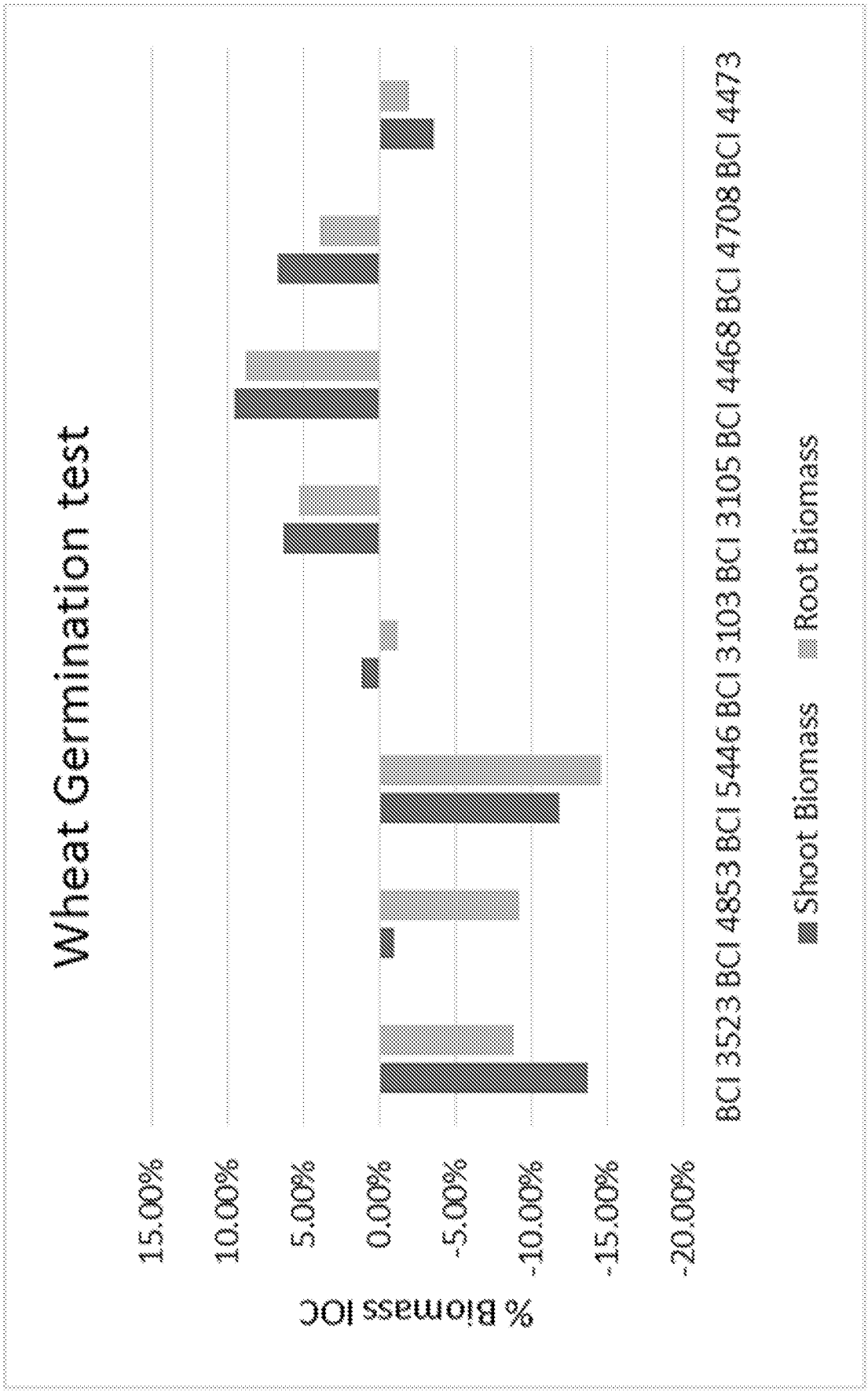

Wheat Germination test
% Biomass IOC
15.00%
10.00%
5.00%
0.00%
-5.00%
-10.00%
-15.00%
-20.00%
BCI 3523
BCI 4853
BCI 5446
BCI 3103
BCI 3105
BCI 4468
BCI 4708
BCI 4473
Shoot Biomass
Root Biomass

FIG. 19

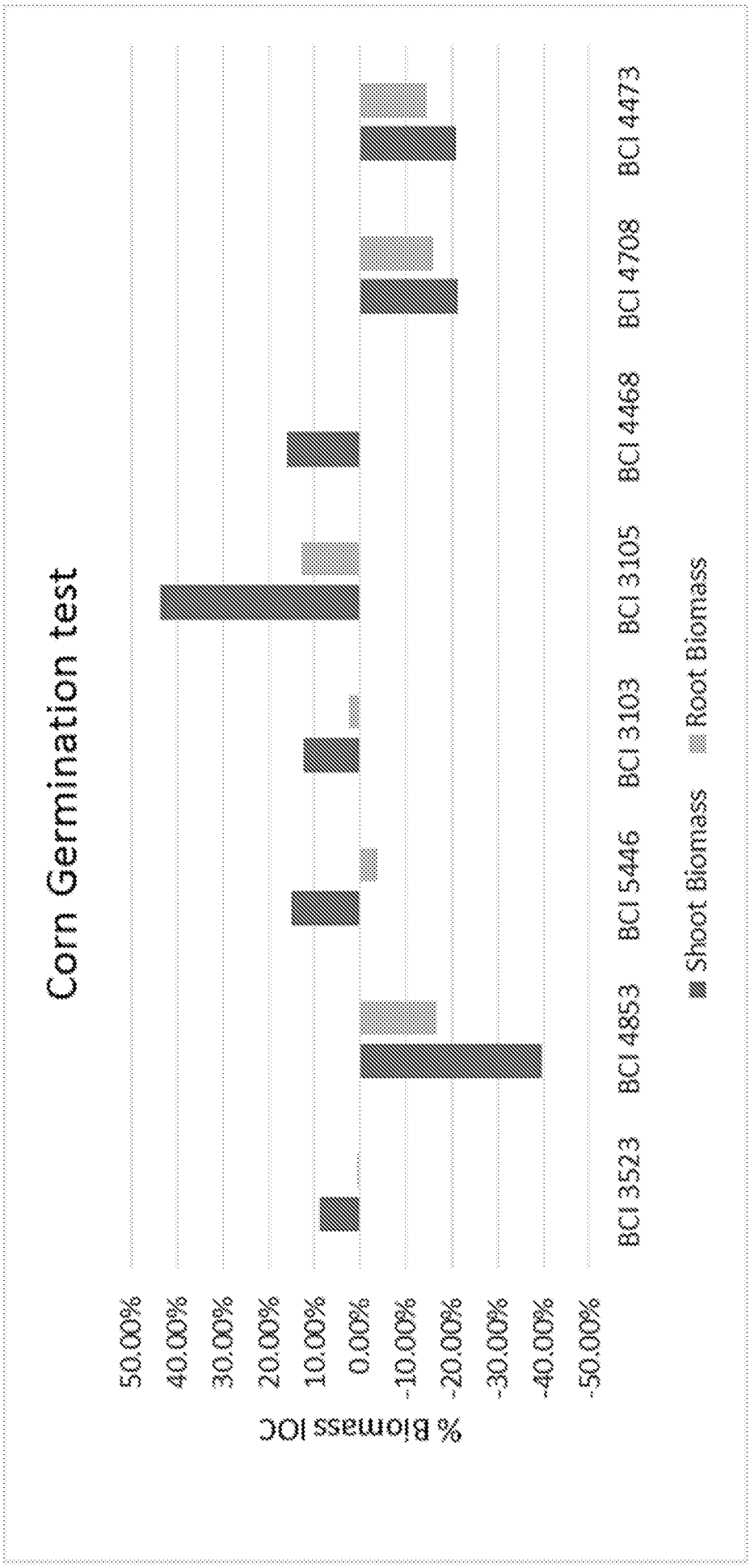

Corn Germination test
% Biomass IOC
50.00%
40.00%
30.00%
20.00%
10.00%
0.00%
-10.00%
-20.00%
-30.00%
-40.00%
-50.00%
BCI 3523
BCI 4853
BCI 5446
BCI 3103
BCI 3105
BCI 4468
BCI 4708
BCI 4473
Shoot Biomass
Root Biomass

FIG. 20

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US17/14119

A. CLASSIFICATION OF SUBJECT MATTER
IPC - C12N 1/20; A01N 63/00, 63/02; C12R 1/13 (2017.01)
CPC - C12N 1/20; A01N 63/00, 63/02; C12R 1/13

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)
See Search History document

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

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

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	US 2012/0149571 A1 (KLOEPPER JW et al.) June 14, 2012; paragraphs [0051], [0056]; SEQ ID NO: 5	7
Y	WO 2015/100431 A2 (SYMBIOTA, INC.) July 2, 2015; abstract; page 4, third paragraph; page 8, second and third paragraphs; page 11, sixth paragraph; page 19, first paragraph; page 23, fifth paragraph; page 49, second paragraph; page 61, fourth paragraph - page 62, first paragraph; page 84, second paragraph; page 85, second paragraph; page 110, second paragraph; page 118, third paragraph; page 142, fourth paragraph; page 156, second paragraph; page 157, first paragraph; Table 2; claim 30	15-27, 42
Y	CN 103952348 A (YANTAI DIYUAN BIOTECHNOLOGY CO., LTD) July 30, 2014; abstract	15-27, 42
A	(BEESLEY, CA et al.) Identification and Characterization of Clinical Bacillus spp. Isolates Phenotypically Similar to Bacillus anthracis. FEMS Microbiology Letters. 30 September 2010, Vol. 313, pages 47-53; page 48, second column, first paragraph; DOI:10.1111/j.1574-6968.2010.02120.x	1-6, 8-14, 43-56, 66, 69-73
A	(SWIDERSKI, J) [Brevibacterium] frigoritolerans strain DSM 8801 16S Ribosomal RNA Gene, Complete Sequence. Submitted 19 June 2007; downloaded from the internet < https://www.ncbi.nlm.nih.gov/nuccore/NR_115064.1> on 21 March 2017, page 1.	1-6, 8-14, 43-56, 66, 69-73

☐ 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
"E" earlier application or patent but published on or after the international filing date
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"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	Date of mailing of the international search report
19 May 2017 (19.05.2017)	09 JUN 2017
Name and mailing address of the ISA/ Mail Stop PCT, Attn: ISA/US, Commissioner for Patents P.O. Box 1450, Alexandria, Virginia 22313-1450 Facsimile No. 571-273-8300	Authorized officer Shane Thomas PCT Helpdesk: 571-272-4300 PCT OSP: 571-272-7774

Form PCT/ISA/210 (second sheet) (January 2015)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US17/14119

Box No. I Nucleotide and/or amino acid sequence(s) (Continuation of item 1.c of the first sheet)

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application, the international search was carried out on the basis of a sequence listing:

   a. ☒ forming part of the international application as filed:

      ☒ in the form of an Annex C/ST.25 text file.

      ☐ on paper or in the form of an image file.

   b. ☐ furnished together with the international application under PCT Rule 13*ter*.1(a) for the purposes of international search only in the form of an Annex C/ST.25 text file.

   c. ☐ furnished subsequent to the international filing date for the purposes of international search only:

      ☐ in the form of an Annex C/ST.25 text file (Rule 13*ter*.1(a)).

      ☐ on paper or in the form of an image file (Rule 13*ter*.1(b) and Administrative Instructions, Section 713).

2. ☐ In addition, in the case that more than one version or copy of a sequence listing has been filed or furnished, the required statements that the information in the subsequent or additional copies is identical to that forming part of the application as filed or does not go beyond the application as filed, as appropriate, were furnished.

3. Additional comments:

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US17/14119

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
-***-Please See Supplemental Page-***-

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
Groups I+, Claims 1-27, 42-56, 66, 69-73; Brevibacterium frigoritolerans NRRL B-67360 (bacterial strain), SEQ ID NO: 308 (nucleic acid)

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.

☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.

☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT
Information on patent family members

International application No.
PCT/US17/14119

-***-Continuation of Box No. III - Observations where unity of invention is lacking:

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Groups I+, Claims 1-73, Brevibacterium frigoritolerans NRRL B-67360 and SEQ ID NO: 308 are directed toward a bacterial strain, consortia comprising the strain, related strains, mutants and progeny, metabolites produced by the strain, compositions, plants and seeds comprising the strain, and a method comprising the strain.

The strain, consortia, mutants, progeny, metabolites, plants, seeds, compositions, and methods will be searched to the extent the strain encompasses Brevibacterium frigoritolerans deposited as NRRL Accession Deposit No. NRRL B-67360 (first exemplary bacterial strain), characterized by a nucleic acid encompassing SEQ ID NO: 308 (first exemplary nucleic acid). Applicant is invited to elect additional isolated bacterial strain(s), with specified identifying nucleic acid SEQ ID NO: for each, to be searched. Additional strain(s) and identifying sequence(s) will be searched upon the payment of additional fees. It is believed that claims 1 (in-part), 2 (in-part), 3 (in-part), 4 (in-part), 5 (in-part), 6 (in-part), 7 (in-part), 8 (in-part), 9 (in-part), 10 (in-part), 11 (in-part), 12 (in-part), 13 (in-part), 14 (in-part), 15 (in-part), 16 (in-part), 17 (in-part), 18 (in-part), 19 (in-part), 20 (in-part), 21 (in-part), 22 (in-part), 23 (in-part), 24 (in-part), 25 (in-part), 26 (in-part), 27 (in-part), 42 (in-part), 43 (in-part), 44 (in-part), 45 (in-part), 46 (in-part), 47 (in-part), 48 (in-part), 49 (in-part), 50 (in-part), 51 (in-part), 52 (in-part), 53 (in-part), 54 (in-part), 55 (in-part), 56 (in-part), 66 (in-part), 69 (in-part), 70 (in-part), 71 (in-part), 72 (in-part) and 73 (in-part) encompass this first named invention and thus these claims will be searched without fee to the extent that they encompass Brevibacterium frigoritolerans NRRL B-67360 (bacterial strain) and SEQ ID NO: 308 (nucleic acid). Applicants must specify the claims that encompass any additionally elected bacterial strain(s) and identifying sequence(s). Applicants must further indicate, if applicable, the claims which encompass the first named invention, if different than what was indicated above for this group. Failure to clearly identify how any paid additional invention fees are to be applied to the "+" group(s) will result in only the first claimed invention to be searched/examined. An exemplary election would be a bacterial strain encompassing Janibacter limosus deposited as NRRL Accession Deposit No. NRRL B-67358 (first exemplary elected bacterial strain) and identifying nucleic acid encompassing SEQ ID NO: 310 (first exemplary elected nucleic acid). Each strain in a specified consortium must be individually elected for the consortium to be searched.

No technical features are shared between the bacterial strains of Groups I+ and, accordingly, these groups lack unity a priori.

Groups I+ share the technical features including: an isolated bacterial strain for use in agriculture; a microbial consortium comprising at least two microbes; an isolated bacterial strain or consortium having substantially similar morphological and physiological characteristics as an isolated bacterial strain or consortium; and having substantially similar genetic characteristics as an isolated bacterial strain or consortium; a substantially pure culture of an isolated bacterial strain or consortium; a progeny of an isolated bacterial strain, or subsequent generation of any microbe of a consortium; a mutant of an isolated bacterial strain or any microbe of a consortium; a cell-free or inactivated preparation of an isolated bacterial strain or consortium; a metabolite produced by an isolated bacterial strain or consortium; an agricultural composition, comprising: a) an isolated bacterial strain or consortium; and b) an agriculturally acceptable carrier; a method of imparting, increasing or promoting at least one beneficial trait upon a plant species, comprising: a) applying an isolated bacterial strain or consortium or agricultural composition comprising an isolated bacterial strain or consortium to said plant, or to a growth medium in which said plant is located; a plant seed enhanced with a microbial seed coating, comprising: a) a plant seed; and b) a seed coating applied onto said plant seed, wherein the seed coating comprises at least one microbe or a consortium; and a synthetic combination of a plant and microbe, comprising: at least one plant and at least one microbe; and any one of SEQ ID NOs: 1-315.

-***-Continued on Next Supplemental Page-***-

-***-Continued from Previous Supplemental Page:

However, these shared technical features are previously disclosed by WO 2015/100431 A2 to Symbiota Inc. et al. (hereinafter 'Symbiota') in light of evidence provided by NCBI Reference Sequence NR_115064 (hereinafter 'NR_115064), and in view of US 2014/0349338 A1 (DEINOVE).

Symbiota discloses an isolated bacterial strain (an isolated bacterial strain; page 19, first paragraph) for use in agriculture (for providing benefit to a seed, seedling or plant (for use in agriculture); abstract); a microbial consortium comprising at least two microbes (a microbial consortium comprising at least two microbes; page 11, sixth paragraph; page 61, fourth paragraph - page 62, first paragraph); an isolated bacterial strain (an isolated bacterial strain; page 19, first paragraph) or consortium (or library (consortium); page 11, sixth paragraph) having substantially similar morphological and physiological characteristics as an isolated bacterial strain or consortium (having substantially similar morphological and physiological characteristics as an isolated bacterial strain or consortium; page 156, second paragraph; page 157, first paragraph); and having substantially similar genetic characteristics as an isolated bacterial strain or consortium (and having substantially similar genetic characteristics as an isolated bacterial strain or consortium; page 8, second and third paragraphs); a substantially pure culture of an isolated bacterial strain (a culture comprising an isolated bacterial strain (a substantially pure culture of an isolated bacterial strain); page 19, first paragraph; page 51, third paragraph) or consortium (or library (consortium); page 11, sixth paragraph; page 51, third paragraph); a progeny of an isolated bacterial strain (a progeny of an isolated bacterial strain; page 19, first paragraph; page 36, ninth paragraph), or subsequent generation of any microbe of a consortium (or subsequent generation of any microbe of a consortium; page 11, sixth paragraph; page 36, ninth paragraph); a mutant of an isolated bacterial strain (a mutant of an isolated bacterial strain; page 19, first paragraph; page 118, third paragraph) or any microbe of a consortium (or any microbe of a consortium; page 11, sixth paragraph; page 118, third paragraph); a metabolite produced by an isolated bacterial strain (a metabolite produced by an isolated bacterial strain; page 19, first paragraph; page 49, second paragraph) or consortium (or library (consortium); page 11, sixth paragraph; page 49, second paragraph); an agricultural composition (an agricultural composition; page 23, fifth paragraph), comprising: a) an isolated bacterial strain (comprising: a) an isolated bacterial strain; page 19, first paragraph; page 23, fifth paragraph) or consortium (or library (consortium); page 11, sixth paragraph; page 23, fifth paragraph); and b) an agriculturally acceptable carrier (and b) an agriculturally acceptable carrier; page 23, fifth paragraph); a method of imparting, increasing or promoting at least one beneficial trait upon a plant species (a method of imparting, increasing or promoting at least one beneficial trait upon a plant species; page 4, third paragraph), comprising: a) applying an isolated bacterial strain (comprising: a) applying an isolated bacterial strain; page 4, third paragraph; page 19, first paragraph) or consortium (or library (consortium); page 4, third paragraph; page 11, sixth paragraph) or agricultural composition comprising an isolated bacterial strain (or agricultural composition comprising an isolated bacterial strain; page 19, first paragraph; page 23, fifth paragraph) or consortium (or library (consortium); page 11, sixth paragraph; page 23, fifth paragraph) to said plant (to said plant; page 4, third paragraph); a plant seed enhanced with a microbial seed coating (a plant seed enhanced with a microbial seed coating; page 4, third paragraph), comprising: a) a plant seed; and b) a seed coating applied onto said plant seed (comprising: a) a plant seed; and b) a seed coating applied onto said plant seed; page 4, third paragraph), wherein the seed coating comprises at least one microbe (wherein the seed coating comprises at least one microbe; page 4, third paragraph; page 19, first paragraph) or a consortium (or a library (consortium); page 4, third paragraph; page 11, sixth paragraph); and a synthetic combination of a plant and microbe comprising: at least one plant and at least one microbe (a plant comprising one or more applied heterologous microbes (a synthetic combination of a plant and microbe comprising: at least one plant and at least one microbe); page 4, third paragraph). Symbiota further discloses a 16S nucleic acid sequence comprising SEQ ID NO: 308 (a 61S nucleic acid sequence of a bacterial endophyte of Table 2, including Brevibacterium frigoritolerans; page 8, second and third paragraphs; Table 2; wherein NR_115064 discloses the 16S ribosomal RNA sequence of a Brevibacterium frigoritolerans strain, comprises a sequence 100% identical (nucleotides 435-1446 in reverse order) to Applicants' SEQ ID NO: 308).

Symbiota does not disclose a cell-free or inactivated preparation of an isolated bacterial strain or consortium.

Deinove discloses a cell-free preparation of an isolated bacterial strain (a cell-free preparation of an isolated bacterial strain; paragraph [0023]), wherein the bacteria are useful for producing compounds of interest for agriculture (wherein the bacteria are useful for producing compounds of interest for agriculture; abstract).

It would have been obvious to a person of ordinary skill in the art at the time of the invention was made to have modified the disclosure of Symbiota to have included the production and use of a cell-free preparation, as disclosed by Deinove, from an isolated bacterial strain or consortium, as disclosed by Symbiota, in order to enable the conveyance of a metabolite to a plant in order to produce or enhance a beneficial trait in the plant, in the absence of the use of the intact strain, due to either difficulty colonizing the plant, or competition with other strains within the consortium.

Since none of the special technical features of the Groups I+ inventions is found in more than one of the inventions, and since all of the shared technical features are previously disclosed by a combination of the Symbiota and Deinove references, unity of invention is lacking.