



Nitrogen-fixing Bacteria and Trends in Agricultural Applications

Junjarus Sermsathanaswadi*

Department of Chemical Technology, Faculty of Science and Technology, Suan Dusit University, Bangkok, 10300 Thailand

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Abstract

Bacteria that can increase the number of nutrients in the soil are important to plants, especially nitrogen-fixing bacteria that fix atmospheric nitrogen and change into the form that plants can use. In recent years, the use of nitrogen-fixing bacteria in agriculture has received a lot of attention because it offers an economically attractive and environmentally friendly method. Many species of nitrogen-fixing bacteria, symbiotic and non-symbiotic, that promote plant growth are used on a regular basis in order to improve crop yields. In addition to agricultural benefits, there are also potential benefits for environmental applications. Many nitrogen-fixing bacteria which grow and multiply within plant tissues are called endophytes. They illustrate the tight association with the plant tissues without causing damage. Therefore, different types of endophytes which produce plant growth hormone provide benefit for many plants.

Introduction

Nitrogen is one of the most abundant elements in the Earth's atmosphere. Air is composed of 78 percent nitrogen, predominately in the form of nitrogen gas (N_2). Nitrogen is an essential element for all living organisms. Nitrogen exists either in the reduced or oxidized forms in the global nitrogen cycle as shown in Fig. 1. In plants, nitrogen is a major element of amino acids which are the building blocks of proteins such as enzymes, cell membranes, transport proteins, hormones, nucleic acids and ATP (energy currency of the cell). Moreover, nitrogen is also an essential element in chlorophyll, which is the most crucial pigment for photosynthesis. When plants lack nitrogen, the leaves will appear yellow and/or pale green because plants are unable to produce the

chlorophyll. Plants will also develop and grow more slowly than we would normally expect. Although the atmosphere contains a large amount of nitrogen, plants cannot use that nitrogen gas. Plants can use nitrogen in the form of nitrogen compounds in the soil, but it is tiny amount (Graham & Vance, 2000). About 90 percent of the nitrogen compounds in the soil are in the form of organic matter or organic nitrogen. When they are transformed into inorganic nitrogen, nitrate ion (NO_3^-) and ammonium ion (NH_4^+), they will be beneficial to the plants. Most plants prefer nitrogen in the form of NO_3^- rather than NH_4^+ . Plants can absorb NO_3^- better than NH_4^+ , which is toxic for plants (Ruan et al., 2007; Babourina et al. 2007). However, both NH_4^+ and NO_3^- contained in the soil are limited and easily lost by processes such as leaching and other procedures such as

* Corresponding Author
e-mail: junjarus_ser@dusit.ac.th

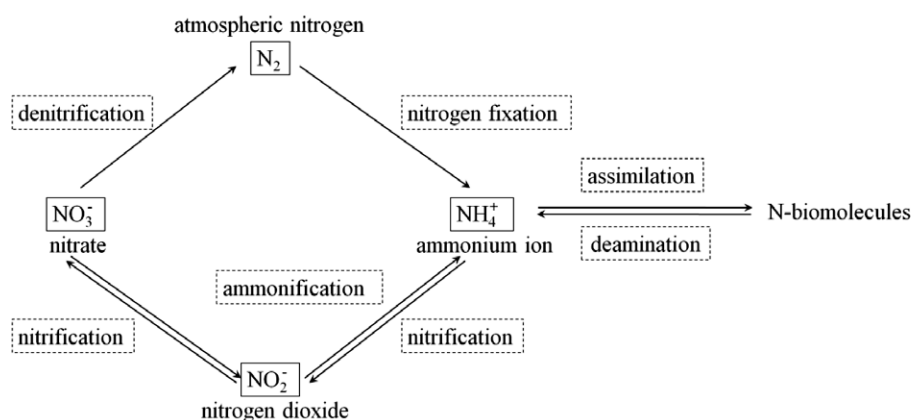
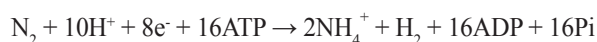


Fig. 1 Steps involved in global nitrogen cycle (modified from Igarashi & Seefeldt, 2003).

biological reduction of NO_3^- (denitrification). Therefore, it can be explained that nitrogen is an element that limits the growth of plants. Even though nitrogen is the most abundant element in the world, plants can only utilize combined nitrogen or reduced forms of nitrogen. Plants acquire these forms of nitrogen from two main sources, first is from the soil through adding fertilizers such as ammonia, manure and/or decomposition of organic substances to the soil. The second source is the conversion of atmospheric nitrogen through nitrogen fixation, such as chemical fixation via the Haber-Bosch process, which reduces N_2 to ammonia using both high temperature and pressure. In other cases, chemical nitrogen fixation can be achieved by oxidation reaction which fixes N_2 by oxidation to nitrate. In nature, lightning strike transforms N_2 into oxide of nitrogen in various forms (finally to NO_3^-). The other nitrogen fixation is symbiotic nitrogen fixation or biological nitrogen fixation by free-living or plant-associated bacteria (Sprent, 2007; Santi et al., 2013). Beijerinck (1901) discovered the biological nitrogen fixation (BNF) for the first time in 1901. It was found that the operation was carried out by a group of prokaryotes including cyanobacteria (*Anabaena* and *Nostoc*) and some bacteria. They have the nitrogenase (EC 1.18.6.1, EC 1.19.6.1), enzymes that catalyze the reduction of N_2 to produce ammonia (NH_3), which is the key step in nitrogen fixation processes. Then, NH_3 will be modified by bacteria to create their organic compounds. The overall reaction of nitrogenase is described by the equation below (Morrison et al., 2017).



Some prokaryotes are able to convert nitrogen in the atmosphere to ammonia which can be used by plants through a biological nitrogen fixation (BNF) which are called diazotrophs (Lam et al., 1996; Franche et al., 2009). These prokaryotes include aquatic organisms, free-living soil bacteria and bacteria that interactions with plants, legumes and other legumes (Postgate, 1982). Nitrogen-fixing bacteria can be divided into three broad categories based on the degree of intimacy and interdependency between them. The first is the free-living bacteria (nonsymbiotic), such as *Azotobacter*, *Beijerinckia* and *Clostridium*. The second category is endophytic bacteria that can colonize interior the plant tissues and provide benefits to the plant. The third is the endosymbiosis bacteria or mutualistic bacteria (symbiotic), such as *Rhizobium* which are associated with leguminous plants.

Endosymbiosis bacteria

Symbiotic nitrogen fixation is a fixation of nitrogen from the air that relies on microorganisms and plant roots. Many diazotrophs can be found in the rhizosphere, the region of soil around plant roots that influence growth, respiration and nutrient exchange of a plant. The diazotrophs show a tremendous competitive advantage over other bacteria in the rhizosphere, mainly when nitrogen in the soil is limited due to their ability to fix nitrogen from the atmosphere (Döbereiner & Pedrosa, 1987). The habitat of diazotrophs are not only in the rhizosphere, area around the root plant but also in the phyllosphere which are all the above-ground parts of

plants (Ruinen, 1956). The well-known mutualistic relationship between bacteria and plant is the association between legume and *Rhizobium* (Fig. 2). The leguminous plants produce the energy from photosynthesis to drive the nitrogen-fixing process and the *Rhizobia* fix the N_2 from the atmosphere, supplying both the bacteria and the plants. Most of the leguminous plants such as soybeans, peanuts, alfalfa, clover and lentils can fix N_2 in association with the *Rhizobia*. The *Rhizobia* have been classified on the species of legume that they nodulate. This type of grouping is called “cross-inoculation”. The plants were divided into cross-inoculation groups and *Rhizobium* species would inoculate plants in the same group (Table 1). The interactions between plants and nitrogen-fixing bacteria are the purest form of nitrogen-fixing symbiosis. Plants create the root areas for the symbiotic nitrogen-fixing bacteria which are embedded into the root hairs of plants (generally do not invade the plant tissues). The symbiotic



Fig. 2 Nitrogen-fixing bacteria (*Rhizobium*) nodules on peanut roots.

bacteria stimulate the formation of roots nodules when they grow and multiply. In the root nodules, bacteria can turn free nitrogen into ammonia which the plant can absorb and utilize for growth and development. Typically, *Rhizobia* have two sets of genes, *nod* genes for nodulation and *nif* genes for nitrogen fixation (Masson-Boivin et al., 2009). The *Rhizobia* secrete the Nod factors to stimulate the re-orientation of cell wall of the growing root hairs lead to curled root hairs and induce the formation of infection threads. The *Rhizobia* use these tubular structures to enter leguminous plants (Fig. 3). In the actinorhizal plant, a group of angiosperms, is associated with *Frankia* acts similar to legumes and *Rhizobium* (Benson & Silvester, 1993).

Table 1 The cross-inoculation groups

Cross-inoculation Groups	Leguminous plant	<i>Rhizobium</i> species
Clover group	<i>Trifolium</i> sp. (clovers, trefoil)	<i>Rhizobium trifolii</i>
Alfalfa group	<i>Medicago</i> sp. (alfalfa, burclover) <i>Melilotus</i> sp. (melilot, sweet clover, kumoniga)	<i>Rhizobium meliloti</i>
Bean group	<i>Phaseolus</i> sp. (bean, wild bean)	<i>Rhizobium phaseoli</i>
Lupine group	<i>Ornithopus</i> sp. (lupines, serradella)	<i>Rhizobium lupine</i>
Pea group	pea, sweet pea, lentil, vetch	<i>Rhizobium leguminosarum</i>
Soybean group	<i>Glycine max</i> (soybean)	<i>Rhizobium japonicum</i>
Cowpea group	cowpea, pegionpea, lespedza, groundnut, kudzu	<i>Rhizobium</i> sp.

Remark: modified from Somasegaran, 1994.

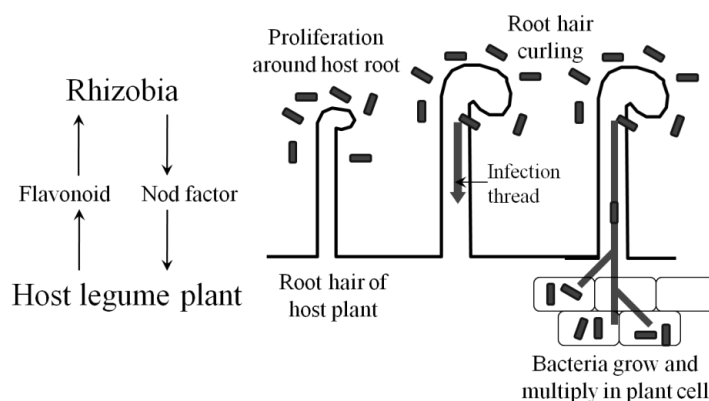


Fig. 3 Scheme of chemical signal exchanges and infection processes involving rhizobia. (modified from Okasaki et al., 2004)

Endophytic bacteria

Although biological nitrogen-fixation using endosymbiosis bacteria is very beneficial for a plant, not all plants have acquired a symbiosis with the *Rhizobia* due to the specificity between *Rhizobia* and host plant (Mylona et al., 1995). The *Rhizobia* require nodules to fix nitrogen from the atmosphere, but in case of some bacteria, endophytic, they not need nodules. It has been reported that the plant-bacteria association can enhance the nitrogen-fixing efficacy of both legume and non-legume plants (Udvarc & Poole, 2013; Santi et al., 2013). In 1961, the diazotrophs in the non-legume plant were first reported by Döbereiner J., Brazilian researcher, and he found the diazotrophs in the rhizosphere of sugarcane (*Saccharum officinarum*) (Döbereiner J., 1961). In subsequent researches, many diazotrophs were isolated from the rhizosphere of sugarcane such as *Azospirillum lipoferum*, *A. amazonense*, *Bacillus azotofixans*, *Enterobacter cloacae*, *Erwinia herbicola*, and *Paenibacillus polymyxa* (Puri et al., 2017). Many diazotrophic bacteria have evolved to grow, spread and multiply within plant tissues without causing damage or causing plant defense responses such as *Azoarcus*, *Herbaspirillum* and *Gluconacetobacter*. These bacteria illustrate the tight association with plant tissues and they are classified as endophytes (Pedraza, 2008). They enter to plant tissues through stomata on leaves or through the lateral root (Fig. 4).

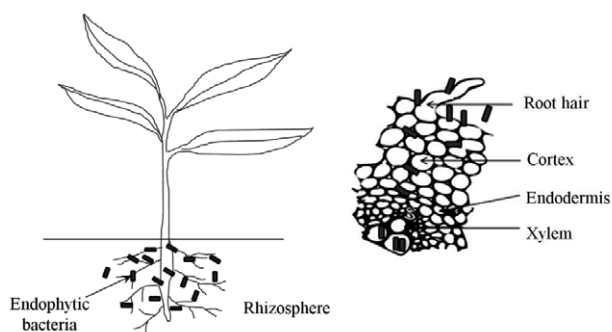


Fig. 4 Plant colonization routes by endophytic bacteria (modified from Audi pudi et al., 2017)

Endophytes are often found as epiphytes, suggesting that endophytes may also colonize surrounding environments of host plants. Many endophytes originate from the rhizosphere and move into the plant cell due to the presence of root exudates and through root

colonization. Besides, inside the surface of the stem and leaf can produce exudates that attract microbes as well. Then, bacteria can be found in both areas as well. However, UV light, lack of nutrients and desiccation generally reduce the colonization of the leaf surface.

The most studied association system in the non-legume plant is the association between sugarcane and *Gluconoacetobacter diazotrophicus*. It has been reported that living *G. diazotrophicus* can produce some molecules that activate the sugarcane defense response, protecting the plant against *Xanthomonas albilineans* (pathogenic) attack (Arencibia et al., 2006). This relationship has resulted in increasing of sugarcane production without adding nitrogen fertilizers. There are many experiments which have illustrated that nitrogen-fixing bacteria are beneficial to plants. In 2014, Szilagyi-Zecchin et al. (2014) isolated and identified six endophytic strains from roots of corn growing in the southern Brazilian region of Campo Largo, PR. Out of these six endophytic isolates were found the presence of *nifH* gene and shown nitrogen-fixing activity. Interestingly, they found that two strains, identified as *Bacillus* sp., showed other plant growth-promotion (PGP) characteristics, like production of indole-3-acetic acid (IAA) or auxin plant hormone. It stimulates plant growth, cell division and cell elongation, siderophores and lytic enzymes and antagonism against pathogenic fungi. In 2013, Gupta and coworkers isolated the endophytic diazotrophic strains from pearl millet plants growing in a nutrient-deficient sandy clay loam soil located in Rajasthan. They found that the most dominant diazotrophic strain in pearl millet plants was *Pseudomonas aeruginosa* strain PM389. This strain can migrate and live in the stem tissues. *P. aeruginosa* strain PM389 has the ability not only on nitrogen fixation, but also possesses other PGP characteristics such as mineral phosphate solubilization, siderophore production, and antagonistic activity against many pathogenic bacteria and fungi. Moreover, when *P. aeruginosa* strain PM389 was inoculated into wheat, it can promote wheat growth by increasing the, seed germination rate, and root and shoot length (Gupta et al., 2013). The association of endophytic diazotrophic bacteria and their host plants, especially agricultural crops are shown in Table 2.

Because Thailand is the largest rice producer and exporter in the world, then a lot of research focuses on endophytic diazotrophic bacteria and rice. Koomnok et al. (2007) reported that they can be isolated the diazotrophic bacteria which are composed of *Azospirillum*,

Table 2 List of endophytic diazotrophic bacteria recently isolated and associated with agricultural plants.

Endophytic diazotrophic bacteria	Isolated from	Reference
- <i>Paenibacillus kribbensis</i> HS-R01, HS-R04; <i>Bacillus aryabhattai</i> HS-S05; <i>Bacillus megaterium</i> KW7-R08; <i>Klebsiella pneumoniae</i> KW7-S06, KW7-S22, KW7-S27, KW7-S33; <i>Bacillus subtilis</i> CB-R05; <i>Microbacterium binotii</i> CB-S18; <i>Microbacterium trichotecenolyticum</i> SW521-L21, SW521-L37	Rice (<i>Oryza sativa</i> var. Japonica c.v. ilpum)	Ji et al. (2014)
- <i>Enterobacter dissolvens</i> ; <i>Brevundimonas aurantiaca</i> ; <i>Pantoea agglomerans</i> ; <i>Pseudomonas</i> spp.	Rice (<i>Oryza sativa</i> L. cultivar KDML-105)	Prakamhang et al. (2009)
- <i>Bacillus</i> sp. BPSAC3, BPSAC6, BPSAC14; <i>Paenibacillus</i> sp. BPSAC45; <i>Bacillus thuringiensis</i> BPSAC46; <i>Lysinibacillus sphaericus</i> BPSAC60; <i>Pseudomonas</i> sp. BPSAC75; <i>Pseudomonas stutzeri</i> BPSAC43; <i>Staphylococcus</i> sp. BPSAC18, BPSAC155	East Indian glory bower (<i>Clerodendrum colebrookianum</i>)	Passari et al. (2016)
- <i>Bacillus amyloliquefaciens</i> MBL_B26; <i>Bacillus subtilis</i> MBL_B4; <i>Bacillus firmus</i> MBL_B5; <i>Brevibacterium</i> sp. MBL_B7; <i>Micrococcus</i> sp. MBL_B10, MBL_B11; <i>Bacillus pumilus</i> MBL_B12; <i>Bacillus subtilis</i> MBL_B13; <i>Bacillus</i> sp. MBL_15, MBL_16, MBL_17, MBL_20, MBL_21; <i>Micrococcus luteus</i> MBL_B18; <i>Micrococcus lylae</i> MBL_B1; <i>Kocuria</i> sp. MBL_19; <i>Pseudomonas psychrotolerans</i> MBL_B23, MBL_27; <i>Pseudomonas monteilii</i> MBL_B24; <i>Ralstonia solanacearum</i> MBL_B6; <i>Staphylococcus arletiae</i> MBL_B2, MBL_B3, MBL_B14, MBL_B22; <i>Staphylococcus hominis</i> MBL_B8; <i>Staphylococcus saprophyticus</i> MBL_B9; <i>Staphylococcus warneri</i> MBL_B25;	Jute (<i>Corchorus olitorius</i>)	Haidar et al. (2018)
- <i>Bacillus aryabhattai</i> ; <i>Pantoea cyrripedii</i> ; <i>Bacillus licheniformis</i> ; <i>Klebsiella</i> sp.; <i>Pantoea dispersa</i> ; <i>Klebsiella variicola</i> ; <i>Pantoea</i> sp.; <i>Agrobacterium larrymoorei</i> ; <i>Bacillus</i> sp., <i>Bacillus amyloliquefaciens</i> ; <i>Lactococcus lactis</i> ; <i>Bacillus cereus</i> ; <i>Staphylococcus homini</i>	Maize (<i>Zea mays</i> L.)	Marag & Suman (2018)
- <i>Ancylobacter</i> sp. UT3R1; <i>Ochrobactrum</i> sp. C7HL1; <i>Novosphingobium sediminicola</i> C2HL2; <i>Novosphingobium capsulatum</i> C34MR1	Sugarcane (<i>Saccharum officinarum</i> L.)	Muangthong et al. (2015)
- <i>Mycobacterium</i> spp.; <i>Streptomyces thermolineatus</i> ; <i>Micromonospora endolithica</i> ; <i>Micromonospora peucetica</i> ; <i>Gordonia polyisoprenivorans</i>	Wheat (<i>Triticum aestivum</i>)	Conn & Franco (2004)

Herbaspirillum, *Beijerinckia* and *Pseudomonas* from cultivated rice (khao dawk mali 105, purple glutinous rice kum doi saket and bue polo) and wild rice (*Oryza granulata*, *O. rufipogon*, *O. rufipogon* 18883 and *O. nivara* 18852). In 2016, Raweekul et al. reported that 126 endophytic bacteria isolated from rice (*Oryza sativa*) roots and stems consist of the members of phyla *Firmicutes*, *Proteobacteria*, *Bacteroidete* and *Actinobacteria*. From these phyla, 12 members of isolated in genera *Bacillus*, *Micrococcus* and *Acinetobacter* showed the increased

fresh weight of rice seedlings when compared to the water-treated control group. These genera contain *nifH* gene, siderophore production, IAA synthesis and ACC-deaminase activity which represented their potential application as biofertilizers (Raweekul et al., 2016). Many studies showed that endophytic diazotrophic bacteria have the ability to nitrogen-fixation and can act as biofertilizer, especially for highly N-demanding crops such as sugarcane, corn, and rice. Moreover, they present PGP characteristics which can enhance plant growth and antagonistic activity against many pathogenic microorganisms.

Free-living bacteria

There are many free-living microorganisms can fix N₂ from the atmosphere. The free-living nitrogen-fixers live in soil or on soil surfaces such as *Cyanobacteria*, *Proteobacteria*, *Archaea* and *Firmicutes*. The free-living nitrogen-fixing bacteria is a group of bacteria that lives independently in soil or other environments. Nitrogen can be fixed from the air without using carbohydrates or energy sources from plants. These microbes rely on energy sources from organic matters in the soil. Therefore, the activity of these microorganisms does not require coexistence with plants (non-symbiotic). The vital enzyme in atmospheric nitrogen fixation is nitrogenase. There are many factors affect the nitrogenase activity, enzymes which convert N₂ to NH₃ or NH₄⁺, the composition of free-living nitrogen-fixer communities including nutrients in soil, soil pollution, plant rhizosphere, plant species and temperature (Zhan & Sun, 2012). This nitrogenase enzyme complex is composed of three subunits Nitrogenase 1 which encoded by the *nif* gene and it is dependent on iron and molybdenum. Nitrogenase 2 which encoded by *vnf* gene and it is dependent on vanadium. Nitrogenase 3 which encoded by *anf* gene and it is dependent on iron. In free-living nitrogen-fixing bacteria, the *nif* genes are responsible for encoding highly conserved subunits (Franchet et al., 2009). Due to the high conservation of *nif* gene, it has been used to characterize the genetic diversity of diazotrophs using *16S rRNA* gene (Zehr et al., 2003). The significant factor that affects the nitrogenase enzyme complex activity is the high sensitivity to oxygen. The major problem of free-living nitrogen-fixing bacteria is inhibition of nitrogenase by oxygen, especially aerobic species such as cyanobacteria (blue-green algae) and the free-living aerobic bacteria,

such as *Azotobacter* and *Beijerinckia*. The aerobic bacteria have different methods to solve this problem. In *Azotobacter* species, the protection of nitrogenase is maintained a deficient concentration of oxygen in their cells by increased in respiration to decrease the oxygen concentration around nitrogenase. Another mechanism for nitrogenase protection is the production of extracellular polysaccharide and maintains water within the layer to limit oxygen diffusion into the cell (Bertsova et al., 2001). In the case of *Beijerinckia dextrii*, it contains two lipid structures consist of poly- β -hydroxybutyrate (PHB). It can produce polysaccharide slime which are exopolysaccharides that can protect the nitrogenase from oxygen, called protective O₂ barrier (Thuler et al., 2003). Most of the biological nitrogen fixation (BNF) is carried out by diazotrophs in symbiosis with legume plant. But in some conditions, free-living nitrogen fixer in soil may fix the massive amounts of nitrogen (up to 60 kg N ha⁻¹ year⁻¹) (Burgmann et al., 2004). The studies of free-living nitrogen-fixing bacteria are focused on both aerobic and anaerobic bacteria such as *Azotobacter vinelandii*, *Klebsiella pneumoniae*, *Clostridium pasteurianum* and *Rhodobacter capsulatus*. The two main steps of the free-living nitrogen-fixing bacteria are ammonia formation and nitrification. The NH₃ is formed by reducing the atmospheric nitrogen. When the bacteria die, NH₃ from bacteria is released from cells into the soil or surrounding ecosystems and can be converted to nitrates by nitrifying bacteria. Nitrates can be absorbed and beneficial to plants.

Application of endophytes in agriculture

Nowadays, modern agriculture has used pesticides excessively which has caused changes in soil microbial populations (Pampulha & Oliveira, 2006). It may have a direct effect on microbial growth and microbial diversity due to the overall changes in ecological structure. Recently, many endophytic bacteria have been studied for application in the agricultural field. They have the ability to produce plant growth-promoting substances to influence the growth of plants directly such as IAA production (Lee et al., 2004), siderophore and ammonia production, increase phosphate solubilization and nitrogen fixation. The endophytic bacteria can control phytopathogens, insects and nematodes through the production of new compounds and antifungal metabolites (Berg et al., 2005; Hallmann et al., 1998; Azevedo et al., 2000). They stimulate the host plant

growth by nitrogen fixation, enhance the solubility of minerals and phytohormones production (Audipudi et al., 2007). From the characters of the endophytic bacteria suggesting that they can be used as biofertilizers. Dhevendaran et al. (2013) reported that *Azotobacter chroococcum*, *Azotobacter beijerinckii* and *Azotobacter vinelandii* produced IAA, a growth-promoting hormone. The increasing pH stimulated the growth and synthesis of IAA lead to higher growth of the seedling of *Ocimum sanctum*. They suggest that the application of *Azotobacter* and *Azospirillum* species as biofertilizers is a testimony to the impact that IAA has on seed growth. From the IAA production of these bacteria dominates the application in agricultural in the next few years.

Pathogenic bacteria including pathogenic *Salmonella* sp., *Escherichia coli*, *Vibrio cholerae* and *Pseudomonas aeruginosa* were described as endophytic bacteria. They may be associated with the use of manures contaminated with fecal bacteria (Holden et al., 2009). The importance of agricultural practices for preserving the natural diversity of endophytic bacteria is emphasized that plants or crops may become the hosts for human pathogens and the source of foodborne illness (Brandl, 2006). The best methods for using endophytes in agriculture are not yet known. The most obvious way is adding bacteria into the soil or to soak the seeds in the culture solution. However, the addition of bacteria is often unsuccessful on the field level because of many factors in the environment (O'Callaghan, 2016). Many questions have not been answered about the use of endophytic bacteria as food supplements in the agricultural field. However, if properly managed, they can show the ability to pathogenic control and abiotic stress from climate change, osmotic stress, exposure to heavy metals and xenobiotic molecules (Howden et al., 2007; Johnson et al., 2013).

The endophytes show great potential in biotechnology. They produce substances that beneficial to plants and they can decompose contaminated molecules in the soil such as pesticides, makes them a promising tool for bioremediation. Moreover, the inoculation of endophytes in plants is economical because it increases productivity and utilizes low-cost farming techniques that have a little environmental impact. For the development of efficient endophytes in agricultural, the bacteria must be selected formulated concerning the agricultural field and environmental conditions.

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