

REVIEW PAPER

Symbiosis between cyanobacteria and plants: from molecular studies to agronomic applications

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Abstract

Nitrogen-fixing cyanobacteria from the order Nostocales are able to establish symbiotic relationships with diverse plant species. They are promiscuous symbionts, as the same strain of cyanobacterium is able to form symbiotic biological nitrogen-fixing relationships with different plants species. This review will focus on the different types of cyanobacterial–plant associations, both endophytic and epiphytic, and provide insights from a structural viewpoint, as well as our current understanding of the mechanisms involved in the symbiotic crosstalk. In all these symbioses, the benefit for the plant is clear; it obtains from the cyanobacterium fixed nitrogen and other bioactive compounds, such as phytohormones, polysaccharides, siderophores, or vitamins, leading to enhanced plant growth and productivity. Additionally, there is increasing use of different cyanobacterial species as bio-inoculants for biological nitrogen fixation to improve soil fertility and crop production, thus providing an eco-friendly, alternative, and sustainable approach to reduce the over-reliance on synthetic chemical fertilizers.

Keywords: Biofertilizer, cyanobacteria, heterocyst, *Nostoc*, PGPR, symbiosis.

Introduction

Cyanobacteria are a distinct group of oxygenic prokaryotes that can be classified on the basis of their morphology into unicellular (Sections I and II) and filamentous species (Section III, IV and V). Filamentous cyanobacteria can be further divided into species that are non-heterocystous (do not form heterocysts, Section III), and species that possess heterocysts along either non-branched filaments (Section IV) or filaments with lateral branches (Section V). Nostocales cyanobacteria represent a

monophyletic order of filamentous cyanobacteria from Section IV in the classical cyanobacterial classification (Rippka *et al.*, 1979; Fugita and Uesaka, 2022). They are commonly found in a wide range of aquatic and terrestrial environments, where they can live freely and/or in symbiosis with a variety of organisms, including animals, plants, and fungi (Adams and Duggan, 2012).

Nostoc sp. can differentiate into four different cell types, depending on prevailing conditions (Fig. 1). In the presence

of combined nitrogen, the cyanobacterium grows as long trichomes, composed of chains of photosynthetically competent vegetative cells that are capable of fixing CO₂. When external combined nitrogen is limited, some cells in the trichome transform into heterocysts, which are cells capable of fixing nitrogen and providing vegetative cells with combined nitrogen. Heterocysts develop from vegetative cells in a semi-regular pattern (typically, one heterocyst every 10–15 vegetative cells) in a process controlled by positive regulators (hetR), and negative diffusible peptides (PatS and HetN) that control the heterocyst pattern (Yoon and Golden, 1998; Corrales-Guerrero *et al.*, 2013; Flores *et al.*, 2019). When in symbiosis with plants, the pattern of heterocyst spacing is altered, and an increase in heterocyst frequency, with respect to the free-living state, is commonly observed (Söderbäck *et al.*, 1990; Johansson and Bergman, 1992; Meeks and Elhai, 2002; Álvarez *et al.*, 2020). Additionally, cyanobacterium metabolism shifts from photoautotrophic to heterotrophic, as the plant provides the cyanobiont with soluble sugars (Khamar *et al.* 2010), leading to enhanced N₂ fixation, with a tendency to release fixed nitrogen to the host (Tredici *et al.*, 1989; Söderbäck *et al.*, 1990; Warshan *et al.*, 2017). This has the effect of maximizing the rate of nitrogen fixation at the expense of cyanobacterial growth.

Nostoc species also possess the ability to differentiate hormogonia. Hormogonia are short, motile trichomes that lack heterocysts to facilitate cyanobacterial dispersal and colonization of new habitats. They are produced from both the

vegetative trichomes and the heterocyst-containing trichomes. Hormogonia are known as the ‘infection units’, as they exhibit positive chemotaxis to root exudates prior to infection and colonization of plant partners (Knight and Adams, 1996; Watts *et al.*, 1999; Nilsson *et al.*, 2006). Hormogonia can be distinguished by the presence of tapered terminal cells, smaller cell sizes (compared with vegetative cells), and presence of gas vesicles within the cells (Meeks *et al.*, 2002). Hormogonium differentiation can be induced by different factors, such as dilution of the medium, changes in light, deprivation of combined nitrogen, or by plant exudates containing hormogonium-inducing factors (HIFs) (Campbell and Meeks, 1989; Gantar *et al.*, 1993; Rasmussen *et al.*, 1994; Nilsson *et al.*, 2006). In the presence of HIFs, large-scale transcriptional reprogramming occurs (with thousands of genes up- and down-regulated in <24 h); differentiation is rapid and unequivocal, with multiple rounds of cell division without DNA replication (Herdman and Rippka, 1988; Campbell *et al.*, 2008; Harwood and Risser, 2021). Additionally, there is an immediate cessation of net biomass increase, followed by a peptidoglycan-based reorganization of the cell wall, culminating in the fragmentation of the parental filament at the junctions between heterocysts and vegetative cells (Damerval *et al.*, 1991; Meeks *et al.*, 2002). Mature hormogonia remain motile for 48–72 h after induction, followed by differentiation of the tapered cells into heterocysts. The remaining cells then resume growth as

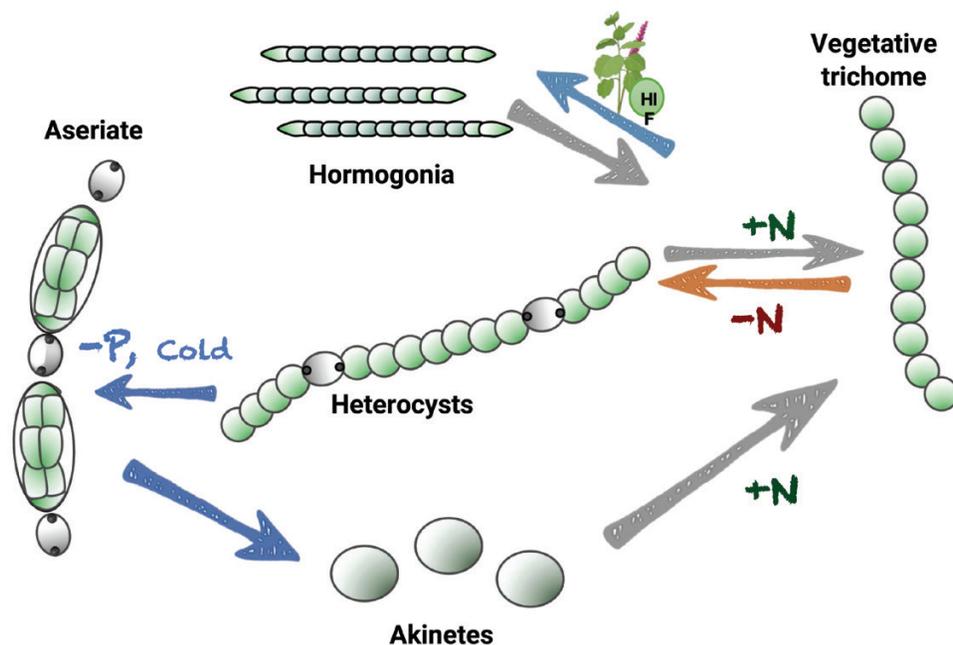


Fig. 1. Schematic illustration of the Nostocales life cycle. The vegetative trichome is composed of vegetative cells performing oxygenic photosynthesis. Heterocysts develop from vegetative cells in response to nitrogen deprivation, and they are arranged in the trichome in a semi-regular pattern. The vegetative cells develop into motile hormogonia (plant infection units) in response to changes in external conditions or in response to plant factors; their ability to move facilitates colonization of new habitats. Akinetes are produced to endure harsh conditions for long periods of time.

normal vegetative cells, resulting in filaments with regularly spaced heterocysts (Campbell and Meeks, 1989; Christman *et al.*, 2011).

The ability to form spore-like resting cells, called akinetes, enables *Nostoc* species to survive harsh, unfavourable environmental conditions while dormant, and germinate again to give rise to vegetative trichomes when the environmental conditions become favourable (Meeks *et al.*, 2002; Kaplan-Levy *et al.*, 2010; Garg and Maldener, 2021). Akinetes are characterized as thick-walled, non-motile cells with a larger size compared with vegetative cells, and conspicuous granulation (Fig. 1). Cellular metabolism is drastically reduced in mature akinetes compared with vegetative cells, and they contain substantial amounts of food reserves that are gradually consumed during the extended period of dormancy (Kaplan-Levy *et al.*, 2010; Perez *et al.*, 2016).

Symbiotic interactions between Nostocales cyanobacteria and plants

Unlike diazotrophic rhizobia or *Frankia* spp., which establish symbiosis exclusively with legumes and actinorhizal plants, respectively, Nostocales cyanobacteria exhibit a broad diversity of associations with plants distributed throughout the entire plant kingdom (Adams and Duggan, 2012; Santi *et al.*, 2013; Warshan *et al.*, 2018). They include spore-forming bryophytes (hornworts, mosses, liverworts; Kimura and Nakano, 1990; Warshan *et al.*, 2017; Chatterjee *et al.*, 2022) and ferns (*Azolla* spp.; Peters and Meeks, 1989; Eily *et al.*, 2019), as well as seed-producing plants, comprising gymnosperms (cycads; Lindblad *et al.*, 1985; Chang *et al.*, 2019) and angiosperms (*Gunnera* spp., Johansson and Bergman, 1992; *Oryza* spp., Álvarez *et al.*, 2020). In all these symbioses, the cyanobacterium provides the plant with fixed nitrogen. In return, the host plant provides the cyanobacteria with a protective environment and a stable source of nutrients (Silvester *et al.*, 1996; Khamar *et al.*, 2010; Liu and Rousk, 2022).

From an evolutionary viewpoint, symbiosis between cyanobacteria and plants has an ancestral origin, with ancient lineages found in symbiotic associations with bryophytes [~470 million years ago (Mya); Warshan *et al.*, 2018], which could imply a long history of co-evolution between plants and cyanobacteria through extracellular to intracellular associations (Fig. 2). In the most ancient lineages, such as non-vascular plants (liverworts and hornworts), the cyanobacterium is established extracellularly in specialized compartments, while it colonizes intracellularly in seed plants (monocots and dicots).

Epiphytic associations

Considering that diversification of mosses took place ~470 Mya (Liu *et al.*, 2019), epiphytic associations between nitrogen-fixing cyanobacteria and mosses could be among the earliest symbiotic relationships between cyanobacteria and plants. In ecosystems that are dominated by mosses, such as arctic tundra

and boreal forests, the biomass of the symbiotic cyanobacteria usually scales well with nitrogen fixation activity (Rousk, 2022). Nitrogen fixation through symbiotic cyanobacteria has been reported both in pleurocarpous feathermosses (e.g. *Pleurozium schreberi* and *Hylocomium splendens*) and in acrocarpous mosses (e.g. *Sphagnum fuscum*) (Solheim and Zielke, 2002; Warshan *et al.*, 2017). However, nitrogen fixation associated with *Sphagnum* can be several orders of magnitude higher than in other widespread mosses (Liu and Rousk, 2022). The main reason for these differences is that in *Sphagnum*, cyanobacteria are found within water-filled hyalocysts (Fig. 3), whereas they are found only on the leaf surfaces in other mosses (Warshan *et al.*, 2018; Rousk, 2022). In these epiphytic associations, the moss provides a stable, moist substrate for cyanobacteria to adhere to, and from which to absorb water and nutrients. Additionally, *Sphagnum* moss also helps to regulate the pH levels of the surrounding environment, thereby providing a favourable environment for the cyanobacteria (Solheim and Zielke, 2002; Liu and Rousk, 2022).

Endophytic associations

Endophytic associations can involve the cyanobacteria living in specialized extracellular compartments, or intracellularly within the plant cells. Extracellular associations between *Nostoc* spp. and plants are ubiquitous, and extended into non-vascular plants (hornworts and liverworts) and vascular plants (pteridophytes and gymnosperms) (Fig. 2). Hornworts and liverworts exist as a flattened gametophyte thallus a few centimetres in length, and symbiotic colonies are seen as small, dark spots, that are visible to the naked eye (Fig. 3; Adams and Duggan, 2012; Chatterjee *et al.*, 2022). In the liverwort *Blasia*, the cyanobacteria occupy roughly spherical structures known as auricles located on the underside of the thallus (Liaimer *et al.*, 2016; Pratte and Thiel, 2021), whereas cyanobacteria are found in slime cavities positioned within the thallus, that open to the ventral surface via slit-like pores or mucilage clefts in the hornworts *Anthoceros* and *Phaeoceros* (Fig. 3; Adams *et al.*, 2013; Chatterjee *et al.*, 2022). The mucilaginous slime cavities are typically large chambers that provide a protective environment for the cyanobacteria to reside in, and for nutrient exchange (Adams, 2002; Frangedakis *et al.*, 2021). *Azolla* plants are small, floating ferns containing symbiotic cyanobacteria, generally *Nostoc azolla*, in the periphery of an extracellular cavity on the dorsal side of the fronds (Perkins and Peters, 1993; Pratte and Thiel, 2021). This symbiosis is unique among cyanobacterial-plant symbioses because it is the only case of a perpetual symbiosis, where the cyanobiont, *N. azollae*, is unable to exist outside of the plant due to genome reduction (Bergman *et al.*, 2007; Ran *et al.*, 2010; de Vries and de Vries, 2022). However, the fern is able to host other cyanobacterial strains, such as *Nostoc punctiforme* and *Nostoc* sp. 2RC (Pratte and Thiel, 2021).

Symbiosis between cyanobacteria and cycads is the only case of endophytic, extracellular association of cyanobacteria with

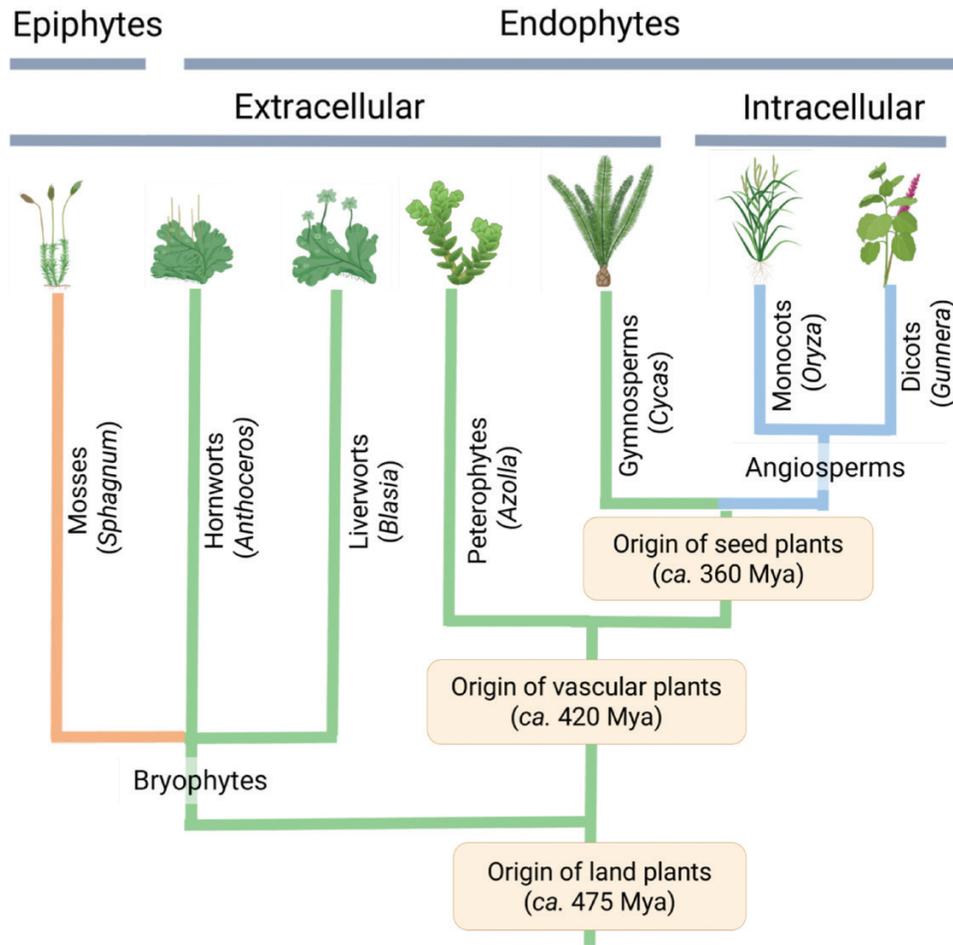


Fig. 2. Symbiotic interactions between Nostocales cyanobacteria and plants. Simplified green plant phylogeny inferred by Davis et al. (2014). The most representative genera in each plant division with which the symbiosis is established is indicated in parentheses. The line in orange denotes epiphytic associations, which is established with mosses. The green line denotes endophytic, extracellular associations, which is extended into non-vascular plants (hornworts and liverworts) and vascular plants (pteridophytes and gymnosperms). The blue lines denote endophytic, intracellular associations, restricted to angiosperms. Created with Biorender.com.

seed plants (Fig. 2). Cycads belong to the most ancient members of seed plants, with fossil records from the late Paleozoic era (~280 Mya), and are the only members of gymnosperms currently capable of forming new associations with cyanobacteria. All known species of cycads form highly specialized lateral roots called coralloid roots (named for their resemblance to corals) to house endosymbiotic cyanobacteria (Lindblad et al., 1985; Chang et al., 2019; Gutiérrez-García et al., 2019). Within the collaroid roots, the nitrogen-fixing cyanobacteria are found in the extracellular space between the inner and outer coralloid root cortex (cyanobacterial zone), and they are visible as a dark blue-green band (Adams and Duggan, 2012; Chang et al., 2019). Cyanobionts found in collaroid roots are mainly *Nostoc* spp., although *Calothrix* and *Scytonema* have also been observed (Costa et al., 1999; Zheng et al., 2002; Gehringer et al., 2010; Chang et al., 2019).

Intracellular *Nostoc*-plant associations are restricted to angiosperms, the most recently derived plant group that

originated ~140 Mya (Sauquet et al., 2017). In the context of cyanobacteria-angiosperm associations, the intracellular symbiotic interaction between *Nostoc* and *Gunnera* spp., which was first described by Reinke in 1873, has been extensively studied (reviewed in Bergman et al., 1992, 2007; Rai et al., 2000; Bonnett, 2002; Osborne and Bergman, 2008). In contrast to other cyanobacterial-plant symbioses, the *Nostoc*-*Gunnera* symbiosis is exclusively intracellular; the cyanobacterium penetrates and resides within the cells of specialized stem glands, which are found at the base of leaf petioles, and *Nostoc* has been identified as the sole cyanobiont (Reinke, 1873; Bergman et al., 1992; Johansson and Bergman, 1992; Rasmussen et al., 1994). The stem glands are composed of a central papilla surrounded by 7–9 smaller papillae (Johansson and Bergman, 1992), and they are unique to *Gunnera*, suggesting that they arose during the co-evolution of *Gunnera* and *Nostoc* (Chapman and Margulis, 1998). These pre-formed glands harbour channels from which the motile hormogonia are guided into the stem

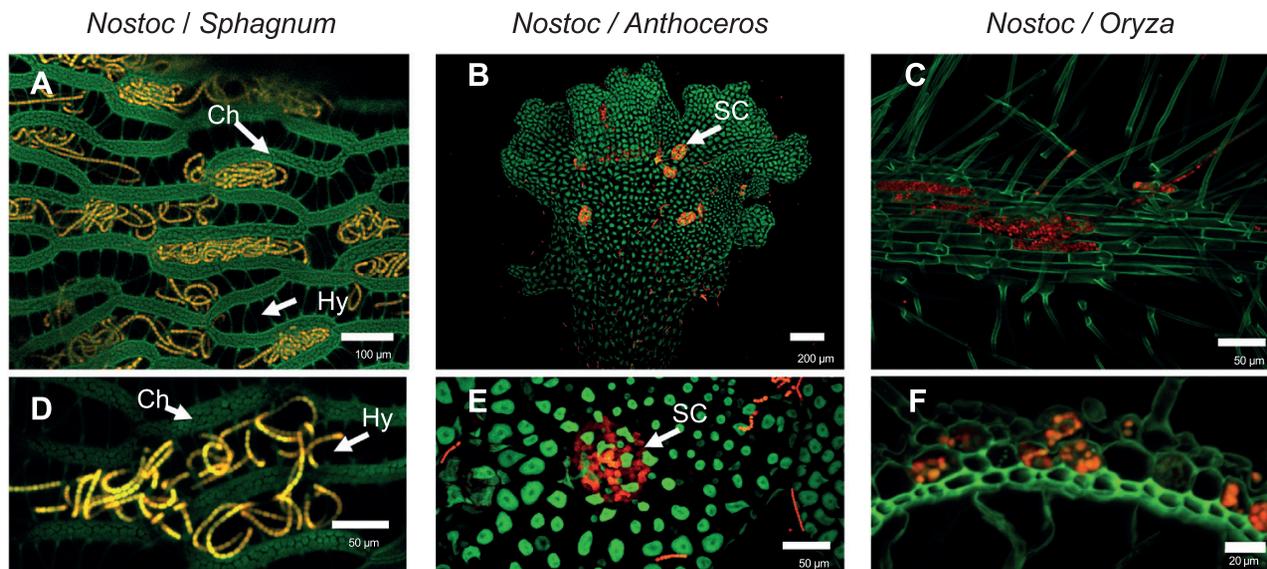


Fig. 3. Multihost symbiotic competence of *Nostoc punctiforme* with plants. (A, D) Epiphytic association of *N. punctiforme* (red/yellow) with *Sphagnum palustre*. Hy, hyalocysts; Chl, chlorocysts. The cyanobacterium is allocated within hyalocysts, which are empty structures connected with the environment. (B, E) Endophytic, extracellular association of *N. punctiforme* with *Anthoceros agrestis*. Cyanobacterial trichomes (in red) are found in the slime cavities (SC), which provide a protective environment for the cyanobacteria to reside. (C, F) Endophytic, intracellular symbiosis between *N. punctiforme* and *O. sativa*; cyanobacterial filaments (in red) are enclosed inside the root epidermal cells (in green).

glands for subsequent colonization of the gland cells (Silvester and McNamara, 1976; Bonnett and Silvester, 1981; Towata, 1985; Johansson and Bergman, 1992; Uheda and Silvester, 2001). *Gunnera* stem glands secrete a viscous, carbohydrate-rich mucilage (that has little or no inhibitory effect on hormogonia differentiation), which creates a suitable microenvironment to facilitate cyanobiont colonization, in addition to providing a moist and nutrient-rich substrate to support cyanobiont growth and symbiotic nitrogen fixation (Wouters *et al.*, 2000; Chiu *et al.*, 2005; Khamar *et al.*, 2010). In addition to supporting cyanobacterial growth, the nutrient-rich mucilage also plays a pivotal role in stimulating hormogonia differentiation, which is essential for intracellular colonization of *Gunnera* stem gland cells (Rasmussen *et al.*, 1994). Once in symbiosis, the frequency of heterocysts has been observed to increase to ~60% of the cyanobacterial cell population, a much higher frequency than in the free-living state (~10% of the cyanobacterial cell population) (Söderbäck *et al.*, 1990). The volume of the *Nostoc* cells also increases several fold, while the growth rate is retarded (Söderbäck *et al.*, 1990; Johansson and Bergman, 1992).

More recently, Álvarez *et al.* (2020, 2022) reported the endophytic and intracellular association of *Nostoc* with hydroponically grown rice. They first observed strong adherence of *Nostoc* with rice roots 7 days post-inoculation (dpi), in agreement with previous observations by Nilsson *et al.* (2002). This adherence is focused on adventitious roots, which are likely to act as the primary sites of colonization. Intracellular colonization of rice roots was observed at 35 dpi, with plant trichoblasts and atrichoblasts entirely colonized by filaments containing an increased number of heterocysts, compared with the free-living

state (Álvarez *et al.*, 2020, 2022; Fig. 3). Ultrastructural analysis of this association showed that *Nostoc* is able to colonize intracellularly cells in the epidermis and endodermis of the roots, but does not transverse the sclerenchyma layer, suggesting an apoplasmic route for the colonization of the plant cells (Álvarez *et al.*, 2020).

Signalling pathway for cyanobacteria-plant symbiosis

The association between *Nostoc* and host plants requires two phase changes, firstly the differentiation of the vegetative filaments to hormogonia, followed by development of heterocysts (Fig. 1). This developmental phase change from vegetative filaments to motile hormogonia is initiated following the sensing of plant-derived metabolites called HIFs. Interestingly, the motile hormogonia have been shown to exhibit positive chemotaxis towards extracts from host plants (*Blasia pusilla*, *Gunnera manicata*, *Cycas revoluta*, and *Oryza sativa*) and non-host plants (*Trifolium repens* and *Arabidopsis thaliana*) (Nilsson *et al.*, 2006).

The full nature of host-derived HIFs remains largely elusive, although it would appear from studies conducted to date that it is unlikely to be a common factor. For example, Hashidoko *et al.* (2019) showed that 1-palmitoyl-2-linoleoyl-*sn*-glycerol extracted from collaroid roots of the cycad *C. revoluta* could induce the formation of hormogonia in *Nostoc* sp. strain Yaku-1. However, the receptor protein(s) responsible for sensing this cycad-derived HIF has not been identified. Warshan *et al.* (2017) showed that nitric oxide (NO) could be a potential

feathermoss HIF from transcriptomics data showing up-regulation in the expression of genes encoding proteins involved in NO binding and signalling, such as haem-NO binding. Following the sensing of the HIFs, a tripartite, hierarchical gene regulatory network (GRN) comprising the sigma factors, *sigC*, *sigJ*, and *sigF*, activates the differentiation of vegetative filaments to the motile hormogonia in *N. punctiforme* (Gonzalez *et al.*, 2019).

Once the cyanobacterial hormogonia have colonized the plant, further hormogonia formation is repressed; this is achieved through the activation of a transcription factor involved in hexuronic acid metabolism (the *hrm* locus; Campbell *et al.*, 2003), thereby facilitating the transition to filaments containing heterocysts (Meeks *et al.*, 2002). In *Gunnera*, the high levels of soluble sugars (sucrose, fructose, and glucose) present in stem glands function to negatively regulate hormogonia formation (Gagunashvili and Andrésson, 2018). Studies by Khamar *et al.* (2010) showed higher expression levels of genes encoding enzymes involved in sugar and starch metabolism, such as starch phosphorylases, cell wall invertases, α -amylases, and sucrose synthase, and high levels of soluble sugars such as glucose and fructose in N-starved *Gunnera* stem segments with glands. Another genetic locus in *N. punctiforme* encoding a polyketide, which acts as an autogenic repressor of hormogonium differentiation, could also function in symbiosis (Liaimer *et al.*, 2016).

In order for *Nostoc* to colonize and form intracellular associations with host plants, they must gain access to the plant cells, a process that requires the remodelling and breakdown of plant cell walls. Álvarez *et al.* (2022) showed differential accumulation of rice (*O. sativa*) proteins involved in cell wall biosynthesis, cell adhesion, and remodelling 7 dpi with the *Nostoc* cyanobiont. Differential accumulations of cell wall-modifying enzymes such as pullulanase and pectate lyase were also observed in the *Nostoc* cyanobiont (Álvarez *et al.*, 2022). The induction of pectate lyase was also previously reported by Warshan *et al.* (2017) in the exoproteome of *N. punctiforme* in association with the feathermoss, *P. scheberi*. These changes suggest a coordinated response between host plants and the *Nostoc* cyanobiont to facilitate intracellular association. To gain a better understanding of how *Nostoc* colonize and form intracellular associations, it is important to expand the proteome studies to include other host species such as cycads and *Gunnera* so that detailed comparative analyses can be conducted.

The typical response from plants encountering an invading microbe is the triggering of a highly localized and controlled cell death programme known as programmed cell death (PCD), in order to restrict the spread of the invading microbe (Chibucos *et al.*, 2009; Mukhtar *et al.*, 2016; Kacprzyk *et al.*, 2021). Biotrophic pathogens have evolved mechanisms to suppress PCD in order to obtain nutrients from the plants (Mukhtar *et al.*, 2016). Endophytic symbionts (symbiotic microbes) must also manipulate PCD, probably through regulating host defence responses (Chibucos *et al.*, 2009) in order to establish a stable

symbiotic association. This was supported by a recent study by Hernández-López *et al.* (2019) who showed that the cell death suppressor, Bax-inhibitor 1 (BI-1), when overexpressed in the common bean resulted in an increase in the number of *Rhizobium tropici* infection events in roots. It is likely that modulation of host PCD is also necessary for endophytic association of *Nostoc* with host plants. The ability of *N. punctiforme* to modulate PCD in plant cells was demonstrated by Belton *et al.* (2021), who showed that conditioned medium (CM) from *N. punctiforme* cultures was capable of attenuating PCD induced in *A. thaliana* suspension cell cultures, suggesting the presence of *Nostoc*-derived mediators for cross-species signalling to regulate PCD. In the context of cross-species signalling for pathogenic and symbiotic relationships, a growing body of evidence implicates sphingolipids functioning as the cross-species signals (Siebers *et al.*, 2016; Heaver *et al.*, 2018; Rossett *et al.*, 2021). However, Belton *et al.* (2022) showed that sphingolipids are unlikely to function as cross-species signals from nitrogen-fixing cyanobacteria to modulate plant PCD as *N. punctiforme* lacks the ability to synthesize sphingolipids. Additionally, transcriptomic analyses by Belton *et al.* (2022) suggested that the PCD attenuation by *Nostoc* CM is unlikely to be due to down-regulation in specific components of the plant PCD pathway, but more likely to be due to improved cellular redox homeostasis that increased the threshold for activation of PCD.

The establishment of stable symbiotic associations between host plants and arbuscular mycorrhizal fungi (AMF), and nitrogen-fixing rhizobia and actinobacteria appears to require a core set of signalling proteins that together make up the common symbiotic signalling pathway (CSSP; Fig. 4) (Oldroyd, 2013; Huisman and Geurts, 2020; Radhakrishnan *et al.*, 2020). The CSSP is activated by secreted lipochitooligosaccharides (LCOs) from rhizobia (Nod factors) and the actinobacterium, *Frankia*, and LCOs and chitin oligomers (COs) from AMF (Myc factors). The identity of the cyanobacterial factors (Cyn factors) remains to be determined, although Álvarez *et al.* (2022) observed an induction in the levels of a NodB-like protein (chitooligosaccharide deacetylase), four β -ketoacyl synthases (NodE-like protein), and six putative Ca^{2+} -binding proteins with homology to NodO, implicating LCOs as potential Cyn factors. The secreted Nod and Myc factors are sensed by heterodimeric complexes of lysine-motif domain-containing receptor-like kinases (LysM-RLKs) on the plasma membrane of host cells, although the identities of the LysM-RLKs for sensing *Frankia* LCOs remain to be determined (Fig. 4). The possible involvement of LCOs as Cyn factors also suggests the participation of a yet to be determined LysM-RLK for cyanobacterial-plant interactions. Downstream of the LysM-RLKs is the CSSP core module comprising SYMRK/DMI2, which are the LCOs receptors at the plant cytoplasmic membrane, CASTOR/POLLUX which are responsible for encoding Ca^{2+} signals in the form of oscillations (Ca^{2+} spiking), and CCamK/DMI3 and CYCLOPS/IPD3 which are responsible for decoding

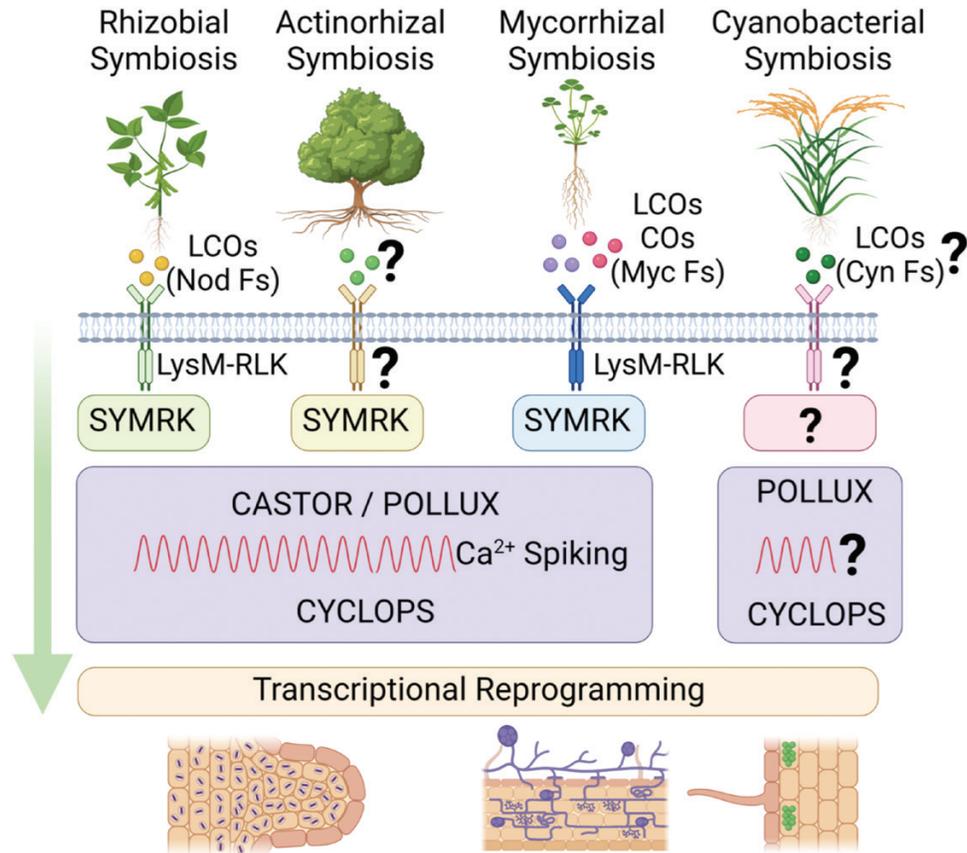


Fig. 4. Schematic illustration of the cyanobacterial symbiosis signalling pathway in the context of the common symbiosis signalling pathway (CSSP) in rhizobial, actinorhizal, and mycorrhizal symbiosis. Symbiosis is activated following the perception of secreted lipochitooligosaccharide (LCO) Nod factors (Nod Fs) from legumes and LCOs from *Alnus* spp., and LCOs and chitin oligomers (COs; Myc Fs) from plants by plasma membrane-localized heterodimeric LysM-RLKs. These LysM-RLKs interact with the leucine-rich repeat-type SYMBIOSIS RECEPTOR KINASE (SYMRK) to activate the CSSP core module. While the LysM-RLKs for rhizobial and mycorrhizal symbioses have been characterized, the identity of the LysM-RLK for actinorhizal symbiosis remains elusive. Calcium signalling is a hallmark of the CSSP, and nuclear Ca^{2+} oscillations (Ca^{2+} spiking) have been observed in rhizobial, actinorhizal, and mycorrhizal symbioses. SYMRK and CASTOR/POLLUX are responsible for encoding Ca^{2+} signals (Ca^{2+} spiking), while CcMk/DMI3 and CYCLOPS/IPD3 are responsible for decoding the calcium signals, followed by downstream transcriptional reprogramming, ultimately resulting in rhizobia and actinobacteria infection, colonization and nodulation in rhizobial and actinorhizal symbiosis, and arbuscular mycorrhizal fungal (AMF) infection and colonization in mycorrhizal symbiosis. In cyanobacterial symbiosis, only some components of the CSSP core module, POLLUX, CcaMK, and CYCLOPS, have been identified. Created with Biorender.com.

the calcium signals (Fig. 4) (Barker *et al.*, 2016; Huisman and Guerts, 2020). While the involvement of a SYMRK remains to be determined for *Nostoc*–rice symbiosis, Álvarez *et al.* (2022) showed, using rice mutants in components of the CSSP core module (POLLUX, CcaMK, and CYCLOPS), a significant reduction in the extent of intracellular colonization of rice roots by *N. punctiforme*. These observations provided evidence that endophytic association of *N. punctiforme* with rice probably requires a functioning CSSP.

Cyanobacteria in agriculture

Cyanobacterial biofertilizers

Cyanobacteria are ubiquitous in different soils, for example agricultural soils, rice paddy fields, and marshy soils, and they

form part of the community of prokaryotes known as plant growth-promoting rhizobacteria (PGPR). PGPR can enhance nutrient supply to support plant growth (Kawalekar, 2013), while simultaneously improving soil structure and texture, which in turns affects the soil water retention capacity (N.K. Singh *et al.*, 2016). PGPR achieve these through atmospheric nitrogen fixation, phytohormone (auxin, cytokinin, gibberellins, and ethylene) production, siderophore production (iron binding), mineral solubilization (e.g. P, K, and Zn), and bio-film formation with structural and protective functions (Hyder *et al.*, 2023). Cyanobacteria are characterized by their ability to reduce N_2 to ammonia, a biologically available source of nitrogen (Kumar *et al.*, 2010; Fugita and Uesaka, 2022). As such, they can be added as inoculants in biofertilizer formulations. Cyanobacterial nitrogen fixation is carried out in heterocysts by oxylabile nitrogenases that can be classified based on the

metal cofactor (Mo, V, or Fe) contained within their active metalcentre (Fugita and Uesaka, 2022). Compaoré and Stal (2010) showed, in *Crocospaera watsonii* and *Gloeotheca* sp., that nitrogenase activity was optimal at oxygen levels of 5–7.5%; no nitrogenase activity was detected at oxygen levels >15%. Consistent with the metalcentre serving as the active centre, Sadvakasova *et al.* (2022) showed that the cofactors Mo and Fe can enhance nitrogenase activity in *Trichormus variabilis* K-31 and *Nostoc* sp. J-14.

There is good evidence for the biofertilizing potential of cyanobacteria in agriculture. The ability of cyanobacteria to catalyse N₂ fixation, decompose organic wastes and residues, detoxify heavy metals, pesticides, and other xenobiotics, catalyse nutrient cycling, suppress growth of pathogenic microorganisms in soil and water, and also produce some bioactive compounds (vitamins, hormones, or enzymes) which contribute to plant growth (reviewed in J.S. Singh *et al.*, 2016), make them good alternatives to synthetic chemical fertilizers for crop agriculture.

Cyanobacteria are ubiquitous in the flooded rice fields (Prasanna *et al.*, 2012; Vijayan and Ray, 2015; Iniesta-Pallarés *et al.*, 2021; Song *et al.*, 2022) where they are usually found in the column of floodwater or remain on the surface of soil layers. Some of them are capable of plant root association and possess plant growth-promoting abilities (Prasanna *et al.*, 2009, 2011; Priya *et al.*, 2015; Iniesta-Pallarés *et al.*, 2021; Toribio *et al.*, 2022). Rice paddy fields offer a favourable environment for cyanobacterial nitrogen fixation, and it has been estimated that cyanobacteria can contribute ~20–30 kg ha⁻¹ of fixed nitrogen (Venkataraman, 1972, 1975; Prasanna and Nayak, 2007; Prasanna *et al.*, 2009, 2011). The main species of nitrogen-fixing cyanobacteria that have been found in rice paddy fields include *Anabaena*, *Aulosira*, *Nostoc*, *Calothrix*, *Tolypothrix*, *Scytonema*, and *Plectonema* (Prasanna *et al.*, 2012; Sahu *et al.*, 2012; Vijayan and Ray, 2015; Iniesta-Pallarés *et al.*, 2021; Song *et al.*, 2022).

Calothrix sp., generally found in freshwater and also in cultivated soils, has been shown to be beneficial for rice growth. Priya *et al.* (2015) showed that growth, measured in terms of root and shoot length of 10-day-old rice plants, increased by 5-fold following *Calothrix* inoculation compared with non-inoculated controls. *Azolla* plants, containing *Nostoc azollae*, have also been used as a biofertilizer for rice cultivation (Bocchi and Malgioglio, 2010; Yadav *et al.*, 2014) in China, Thailand, Vietnam, and the Philippines (Fan, 1992; Tekle-Haimanot and Doku, 1995; Qiu and Yu, 2003; Nosheen *et al.*, 2021). Native cyanobacterial strains from southern Spanish rice paddy fields have also been isolated and used as bioinoculants for rice cultivation. Iniesta-Pallarés *et al.* (2021) selected cyanobacteria from five different phylogenetic groups (PG1, with high similarity to *Nostoc punctiforme*; PG2, genetically similar to *Nostoc* sp.; PG3, closely related to *Wolleea salina*; PG4, genetically close to *Anabaena cylindrica*; and PG5, closely related to *Calothrix membranacea*) for inoculating experimental plots. They observed that rice plants in inoculated plots were greener and healthier compared with the non-inoculated controls. Additionally,

measurements of rice panicles showed a significantly larger number of heavier grains per panicle. These results point to the utility of cyanobacterial biofertilizers as an eco-sustainable approach for rice cultivation.

The use of cyanobacterial inoculants as biofertilizers is not limited to rice paddy fields. Studies have also been conducted on their use in barley, wheat, oats, radish, cucumber, tomato, pumpkin, cotton, sugar cane, chilli, and lettuce, with positive results (Hashtroudi *et al.*, 2013; Prasanna *et al.*, 2013; Khadarate and Suryawanshi, 2016). Thus, a significant increase in yield was observed when lettuce was co-cultivated with *Anabaena cylindrica* PCC 7122 and *Nostoc* sp. (Xue *et al.*, 2017).

Cyanobacterial growth regulators

Cyanobacteria have also been reported to produce plant growth regulators such as auxin and cytokinin (Sergeeva *et al.*, 2002; Prasanna *et al.*, 2008, 2009, 2010; Tan *et al.*, 2021; Uniyal *et al.*, 2022). Like their plant counterparts, these cyanobacteria-derived regulators can promote plant growth, increase root development, and improve plant stress tolerance. Auxin [indole-3-acetic acid (IAA), indole-3-propionic acid (IPA), and indole-3-butyric acid (IBA)] biosynthesis has been detected in cyanobacteria (Hashtroudi *et al.*, 2013; Mazhar *et al.*, 2013; Ahmed *et al.*, 2014). Hussain *et al.* (2015) showed that *Nostoc ipdC* (a gene involved in IAA biosynthesis) knockout mutants exhibited a reduced capacity for *in vitro* growth of rice and wheat seedlings, suggesting a role for cyanobacteria-derived auxin in regulating plant growth. IAA production was observed to increase when cyanobacterial cultures of *Fisherella musicola* NDUPC001 were supplemented with L-tryptophan, a key precursor for auxin biosynthesis (Mishra *et al.*, 2019). Interestingly, when extracts obtained from L-tryptophan-treated *F. musicola* were applied to rice, significant increases in radicle length, plumule, and number of adventitious roots were observed (Mishra *et al.*, 2019).

Cytokinins play a crucial role in regulating various aspects of plant growth and development, including cell division, shoot formation, and nutrient uptake (Zhao *et al.*, 2021; Uniyal *et al.*, 2022). Cytokinins are primarily synthesized in plant tissues, but cyanobacteria also possess the ability to produce them (Hussain *et al.*, 2010, 2013). Exogenous application of cyanobacterial extracts containing cytokinin enhances plant growth, yield, and stress tolerance (Toribio *et al.*, 2020, 2021). A *Nostoc* knockout mutant in the *ipt* gene, coding for a key enzyme of cytokinin biosynthesis, showed a significant decrease in cytokinin production and plant colonization, evidencing the involvement of cyanobacterial derivatives in plant–*Nostoc* interaction (Hussain *et al.*, 2013). Salicylic acid (SA) is a plant hormone involved in various defence responses against pathogens. It plays a crucial role in activating the plant's immune system and initiating defence mechanisms. SA is also involved in regulating other plant processes, such as seed germination, root development, and flowering. The balance between cytokinins and SA is indeed crucial

during the early stages of plant development, particularly in seed germination and root elongation. Cytokinins can modulate the signalling pathways associated with SA, leading to the induction of genes involved in plant defence responses (Gilroy and Breen, 2022). Toribio *et al.* (2020) showed that different strains of cyanobacteria (*Calothrix* SAB-B797, *Nostoc* SAB-B1300, and *Nostoc* SAB-M612) are able to produce SA. Furthermore, they demonstrated an important link between germination of water-cress seeds and SA production by cyanobacteria.

Cyanobacteria and soil dynamics

Besides phytohormones, cyanobacteria also produce siderophores, low molecular weight metal chelators that function in microbial iron uptake (Årstøl and Hohmann-Marriott, 2019; Chakraborty *et al.*, 2019). In nature, hydroxamate-type siderophores are the most common, and they have been reported to be produced by *Anabaena catenula*, *A. cylindrica*, *A. variabilis*, *Aphanizomenon flos-aquae*, *Microcystis aeruginosa*, *Oscillatoria tenuis*, *O. boryana*, *Phormidium valderianum*, and *Synechocystis elongatus*, among others (Årstøl and Hohmann-Marriott, 2019). Siderophores have applications in ecological research, in agriculture, and in drug discovery as iron chelation therapy and antibiotic carriers (Kundu *et al.*, 2023). Different cyanobacterial species, which have the ability to produce siderophores for chelating Fe, have been used to promote plant growth and increase their yield by enhancing Fe uptake into plants (Toribio *et al.*, 2020). Apart from iron, cyanobacteria can also mobilize insoluble minerals making them available for plant uptake, such as P solubilization. This was demonstrated in diazotrophic cyanobacteria *Westiellopsis prolifica* and *Anabaena variabilis*, with tricalcium phosphate as the insoluble P-source (Yandigeri *et al.*, 2011). In addition to mineral solubilization, cyanobacteria also produce exopolysaccharides (EPSs), which can improve soil structure and water-holding capacity. For example, the application of capsular polysaccharides produced by *N. muscorum* to the soil, increased the amounts of water-stable aggregates (Rossi and De Philippis, 2015; Garlapati *et al.*, 2019).

Overall, the activities of PGPR cyanobacteria can promote plant growth, improve plant stress tolerance, and increase crop yield, and they should be part of the arsenal of eco-friendly and sustainable biological solutions for the agricultural industry.

Future applications: cyanobacterial-based nitrogen-fixing cereals

Global cereal production, currently estimated at 206 Mt, is projected to reach 542 Mt by 2030 (OECD-FAO, 2021). Nitrogen uptake is one of the limiting factors for crop production (Liu *et al.*, 2022), which has thus far been overcome with the large-scale, and often indiscriminate use of chemical fertilizers. This level of intensification is a major concern due to widespread pollution of water bodies by nitrate leaching into surface and

ground water (Singh and Craswell, 2021). Biological nitrogen fixation (BNF) has been proposed as a potential solution for providing an alternative source of nitrogen for cereal production (Rosenblueth *et al.*, 2018; Guo *et al.*, 2023; Jhu and Oldroyd, 2023).

Several strategies have been proposed for engineering nitrogen fixation in cereals. One of the strategies involves a synthetic biology approach to improve the associative interactions between nitrogen-fixing bacteria and cereals (Hackett *et al.*, 2022). This involves engineering novel trans-kingdom signalling between the nitrogen-fixing bacteria and the plant, and has the benefit of preventing associations with non-target plants, allowing for the customization of the bacteria–plant associations. Another strategy, drawing inspiration from rhizobia–legume symbiosis, involves the genetic engineering of nodule organogenesis for creating cereals that are capable of forming nodule-like structures to host nitrogen-fixing rhizobacteria (Guo *et al.*, 2023; Jhu and Oldroyd, 2023). The targeted expression of the nitrogenase complex in mitochondria and plastids has also been proposed. To date, attempts at expressing *nif* genes in plant mitochondria have not resulted in the successful reconstitution of a functional nitrogenase enzyme complex capable of fixing nitrogen (Allen *et al.*, 2017). One of the challenges for successful reconstitution of the nitrogenase enzyme complex in mitochondria (and possibly plastids) is the lack of knowledge of the intraorganellar levels of oxygen; the oxygen levels may be too high for nitrogenase to function even if the nitrogenase enzyme complex can be successfully reconstituted. In addition to intraorganellar expression of nitrogenase, there has been an unvalidated study reporting the successful expression of a nine-*nif* gene cluster in the cytoplasm of *A. thaliana* cells that resulted in higher biomass and chlorophyll content (Yao *et al.*, 2021, Preprint). It would be interesting to test whether this nine-*nif* gene cluster can also be used to express and reconstitute a functional nitrogenase enzyme complex for nitrogen fixation in the cytoplasm in cereals.

The various approaches outlined above have not considered the possibility of engineering nitrogen fixation from the perspective of nitrogen-fixing cyanobacteria. Nitrogen-fixing cyanobacteria are promiscuous; they can associate epiphytically and endophytically with diverse plant species, including cereals. *Nostoc* has been observed to colonize root epidermal and cortex cells intracellularly in wheat (Gantar *et al.*, 1993 and, more recently, rice (Álvarez *et al.*, 2020, 2022). These observations suggest that cereals are capable of forming intracellular symbiotic associations with nitrogen-fixing *Nostoc* cyanobacteria. The involvement of the common symbiotic signalling pathway (CSSP) in the *Nostoc*–rice endophytic association suggests potential strategies around the targeted engineering of processes relating to signal perception and transduction, more efficient intracellular infection and colonization, and heterocyst differentiation for cyanobacterial-based BNF in cereals. As nitrogen fixation is carried out in heterocysts, this can circumvent the challenges associated with expression of

nif gene clusters and subsequently reconstitution of functional oxylabile nitrogenase enzyme complexes in organelles (mitochondria and plastids) and the cytoplasm, and for the requirement for engineering nodule organogenesis to provide a low-oxygen compartment for efficient nitrogenase function.

Author contributions

VM: conceptualization; VM, CA, LJR, and AJF: investigation; VM, CA, LJR, MIP, and CKYN: writing—original draft; VM and CKYN: writing—review and editing; VM, CA, and CKYN: funding acquisition; CA, LJR, MIP, AJF, FPMH, CKYN, and VM: review and approval of the final manuscript.

Conflict of interest

No conflict of interest declared.

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