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THE ROLE OF UNIVERSAL REGULATORS OF PLANT GROWTH AND DEVELOPMENT THE DELLA PROTEINS IN THE CONTROL OF SYMBIOSIS

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❀ The regulators of the gibberellin response, the DELLA proteins, are universal participants of signaling pathways that coordinate the processes of plant growth and development. This regulation is provided by the integration of external effect, as well as internal signals, such as a level of phytohormones and secondary messengers. Since DELLA proteins are extremely sensitive to increasing or decreasing of the gibberellic acid (GA) endogenous level, their direct interaction with transcription factors modulates the activity of the latter, and, consequently, the level of expression of target genes in response to external signals causing changes in the level of GA. However, the molecular mechanisms of the effect of DELLA proteins on the development of symbiosis remain poorly understood. The review analyzes classical and modern data on the functioning of DELLA proteins in plants.

❀ **Keywords:** DELLA proteins; growth and development; symbiosis; legume-rhizobial symbiosis; transcription factors.

РОЛЬ УНИВЕРСАЛЬНЫХ РЕГУЛЯТОРОВ РОСТА И РАЗВИТИЯ РАСТЕНИЙ DELLA-БЕЛКОВ В КОНТРОЛЕ СИМБИОЗОВ

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❀ Универсальными участниками сигнальных путей, координирующими процессы роста и развития растений, являются регуляторы гиббереллинового ответа DELLA-белки. Эта регуляция обеспечивается путем интеграции внешних воздействий, а также внутренних сигналов, таких как изменение в уровне фитогормонов и вторичных мессенджеров. Поскольку DELLA-белки чрезвычайно чувствительны к повышению или же снижению эндогенного уровня гибберелловой кислоты (ГК), их прямое взаимодействие с транскрипционными факторами модулирует активность последних, а следовательно, и уровень экспрессии генов-мишеней в ответ на внешние воздействия, вызывающие изменения в уровне ГК. Одна из наиболее важных функций, которые выполняют DELLA-белки, связана с их участием в регуляции развития симбиозов растений с азотфиксирующими клубеньковыми бактериями и грибами арбускулярной микоризы. Однако молекулярные механизмы влияния DELLA-белков на развитие симбиозов остаются малоизученными. В обзоре проведен анализ классических и современных данных о функционировании DELLA-белков у растений.

❀ **Ключевые слова:** DELLA-белки; рост и развитие; бобово-ризобиальный симбиоз; транскрипционные факторы.

INTRODUCTION

Plants' ability to respond in a timely fashion to changes in external environmental conditions is critical to their survival. However, such a quick response requires the presence of universal regulators capable of rapidly perceiving and transforming the incoming information. Increasingly, data indicate that the universal participants in such signaling pathways, coordinating the processes of plant growth and development, are the negative regulators of the gibberellin response, the DELLA proteins. DELLA is one of the subfamilies of GRAS transcription factors, with the GRAS domain named after the first three open GRAS transcription factors GIBBERELLIC ACID-INSENSITIVE (GAI) REPRESSOR of *ga1–3*(RGA) and SCARECROW (SCR) in *Arabidopsis thaliana* [1]. Two of these transcription factors, namely, GAI and RGA, are DELLA proteins. Subsequently, other members of the subfamily were discovered; five DELLA proteins are known in Arabidopsis, and in addition to RGA and GAI, they also include RGALIKE1 (RGL1), RGL2 и RGL3 [2]. DELLA proteins got their name from the presence of a special amino acid sequence (aspartic acid-glutamic acid-leucine-leucine-alanine), or DELLA domain, at the N-terminus, which is conserved in all higher plants. There is also a VHYNP domain at the N-terminus, and together with the DELLA domain, it is responsible for binding to the activated receptor (GA-INSENSITIVE DWARF1, GID1) for gibberellins (GAs). At the C-terminus of the DELLA proteins, there is a GRAS domain, including several motifs conserved in the GRAS family (namely, LHRI, VHIID, LHRII, PFYRE, and SAW), and a nuclear localization signal [3, 4]. The GRAS domain is responsible for such GRAS protein functions as cell-to-cell movement and interaction with other transcription factors. In protein–protein inter-

actions, the leucine heptad repeat motifs of the GRAS domain play a crucial role.

Due to the lack of DNA-binding domain in DELLA proteins, they regulate transcription in one of two ways, either through direct interaction with the DNA-binding domain of another transcription factor, inhibiting its effect on target gene expression (inhibitory effect), or through interaction, as a co-activator, with a transcription factor, which, in turn, induces transcription of the target gene (activating effect) [5]. The number of transcription factors regulated by DELLA proteins, according to some estimates, is more than 100 [6].

DELLA PROTEINS AS NEGATIVE REGULATORS OF GIBBERELLIN RESPONSE IN PLANTS

Gibberellins (GAs) are phytohormones that regulate growth and development throughout the entire life cycle of a plant, including cell division and elongation, shoot and root growth, as well as flowering, fruit development, and seed ripening [7]. Initially, DELLA proteins were considered to be plant growth repressors, but subsequently, it was revealed that they serve as negative regulators of genes, the expression of which is activated by GAs [4].

Increases in the concentrations of GAs and their binding to the soluble nuclear GID1 receptor cause degradation of DELLA proteins, as a result of the recognition by components of the F-box signaling pathway (GID2 in rice *Oryza sativa* and SLEEPY in *A. thaliana*) of DELLA proteins, which induce the assembly of DELLA proteins into the Skp, Cullin, and F-box-containing (SCF) E3 ubiquitin-ligase complex, which polyubiquitinates the DELLA proteins, targeting them for subsequent degradation by the 26S proteasome [8]. Degradation of the DELLA proteins suppresses their repressor action and, possibly, releases the GID1 receptor from the complex, so that it can interact with other DELLA protein molecules [9]. Some DELLA proteins are less sensitive to degradation under the influence of GAs than are others [10, 11].

Studies have shown that GAs are involved in the response of plants to various biotic and abiotic stresses. The endogenous concentration of GAs is apparently dependent on external signals, such as light intensity and temperature, and is also regulated by the concentrations of various phytohormones [12]. Since DELLA proteins are extremely sensitive to an increase or decrease in the endogenous GA concentration, their direct interaction with transcription factors modulates the activity of the latter and hence the level of expression of target genes controlled by these transcription factors in response to external influences which cause changes in the GA concentration.

It should also be noted that the regulation of metabolism involving GAs can be implemented, at least partially, independent of DELLA proteins [13]. For example, an increase in calcium concentration in the cytosol during GA treatment can be observed within 2 min of the treatment, whereas the significant decrease in the concentration of DELLA proteins due to their degradation occurs only after 5–10 min [14], so that the processes occurring in the cytosol in the first minutes in response to GA treatment could not have been controlled by DELLA proteins.

A comprehensive analysis of target genes for DELLA proteins has shown that, in addition to responding to a change in the GA concentration as a result of various external influences, DELLA proteins are also necessary to maintain GA homeostasis. In several studies, it was demonstrated that, in *della* mutants, the level of expression of the genes responsible for GA biosynthesis was significantly reduced [15, 16]. However, the fact that DELLA proteins do not have a DNA-binding domain and their influence on GA-biosynthesis genes is indirect, achieved by binding to transcription factors, indicates the presence of such regulators, but they are difficult to locate. Nevertheless, it has been established that SCARECROW-LIKE3 protein can be an antagonist of DELLA proteins in the control of GA biosynthesis [17].

A number of studies have shown that the GA-biosynthesis genes, *Ga20ox* and *Ga3ox*, are under the direct control of DELLA proteins [18]; moreover, in some later studies, no direct influence of DELLA proteins was demonstrated [17]. Data on the effect of DELLA proteins on the genes of the GA degradation process are also ambiguous. As a result of the analysis of *della* mutants in pea *Pisum sativum* L., a significant increase in the expression of the *GA2ox* gene, which controls GA degradation, was observed in the early stages of seedling development (6 d) [16]. However, the knockout mutant of the homologous *DELLA* gene in the related legume, *Medicago truncatula*, exhibited no significant difference in the expression level of the *GA2ox* gene compared with the wild-type plant during the plant development process [15].

EVOLUTION OF THE GID1 RECEPTOR–DELLA COMPLEX

The GID1 receptor-activated signaling pathway is most likely to have evolved after the separation of vascular plants from mosses. The GID1 receptor and DELLA-like proteins have been identified in mosses, but there is no evidence for either direct receptor binding to GAs or for the effect of the receptor on DELLA proteins [19]. The first functionally active DELLA proteins evolved, apparently, in clubmoss, as the active GID1–DELLA complex has been discovered in *Selaginella moellendorffii* and *Selaginella kraussiana* [19]. It is important to note that the functions of the GA-activated signaling pathway

in clubmoss are apparently different from those in higher plants, since GA treatment does not stimulate the growth of *Selaginella* spp. [20]. True DELLA proteins have been identified in gymnosperms and angiosperms [21].

The study of the angiosperm genomes revealed that in dicotyledons, unlike monocotyledons, the genes encoding DELLA proteins are often duplicated, and the functions of the resulting proteins have diversified. Based on a phylogenetic analysis, the presence of two clades of DELLA proteins in dicotyledonous plants was identified. Furthermore, the number of genes encoding these proteins is not the same for such informal plant taxonomic groups as the Asterids and the Rosids. Thus, among the Rosids, in genera such as *Populus*, *Pisum*, and *Medicago* and genera from the Brassicaceae family, representatives of two clades of DELLA proteins were found. In Asterids, on the other hand, in species such as *Solanum lycopersicum* and *Lactuca* spp., only DELLA proteins related to clade 1 were found. The absence of the known DELLA proteins related to clade 2 in the Asterids may be due to incomplete data for the analysis of genomes from these species. However, in mutants of *S. lycopersicum* (Asterids), distortions characteristic of multiple *della* mutants from a single DELLA gene in Rosids were revealed [22].

For DELLA proteins, functional redundancy is typical, and the proteins may also be interchangeable in terms of function. For example, for two DELLA proteins from Arabidopsis *RGA* and *RGL*, the possibility of functional interchangeability has been demonstrated. It had previously been established that the *RGA* gene is involved in the regulation of GA metabolism in those organs where *RGL* is not normally expressed (namely, hypocotyls, leaves, and shoots). In the *rga* mutant, a decrease in the expression of the GA-biosynthesis genes *GA20ox1*, *GA20ox2*, and *GA20x8* was noted [23]. However, when the *RGL* gene was expressed under the control of the *RGA* promoter in the *rga* mutant plants, the function of the gene was restored. These data suggest that the functional diversification of DELLA proteins is determined by their site of synthesis and the local environment, rather than by differences in biochemical activity [22].

ROLE OF DELLA PROTEINS IN INTEGRATION OF PHYTOHORMONE ACTIONS

Regulation of the growth and development of plant organs requires precise coordination of the processes of cell proliferation and differentiation. This regulation is provided by integration of external influences, as well as internal signals, such as by changing the levels of phytohormones and secondary messengers [24].

Research findings have confirmed that DELLA proteins are regulators, integrating the action of various phytohormones and coordinating the processes regulated by them. As far back as 1958, it was revealed that removal of the shoot apex from *A. thaliana* resulted in impaired root growth and caused plant insensitivity to the effects of GA [25]. However, auxin treatment of the apex removal site restored root growth, indicating that the effect of the shoot apex on root growth occurs through the regulation of the polar auxin transport, from the shoot to the roots. This suggests that the influence of these hormones (GAs and auxins) is unidirectional. The process of the degradation of DELLA proteins under the influence of GAs is probably more complicated than it seems at first glance and, apparently, can be associated with the action of auxins.

In experiments on *A. thaliana*, in the roots of which DELLA proteins of RGA were labeled with green fluorescent protein (GFP) (i. e., RGA-GFP), it was demonstrated that treatment with GAs causes the rapid disappearance of the labeled protein from the nuclei of the root cells. However, in plants in which the apex of the shoot had been removed even 4 h after treatment with GAs, RGA-GFP was still detectable, although the concentration was still lower than that in untreated control plants. If the point of apex removal was treated with the auxin indoleacetic acid (IAA), the RGA-GFP disappeared as rapidly as with the control plant. These data suggest that the probable mechanism of auxin-dependent root growth is associated with an increased effect of GAs on the degradation of DELLA proteins [26].

The opposite effect on DELLA proteins was observed when using ethylene instead of auxin. It is known that the phytohormone ethylene inhibits the growth of plant vegetative organs. However, as it turned out, this process may also depend, at least partially, on DELLA proteins. In the absence from the medium of 1-amino cyclopropane-1-carboxylate (ACC), the precursor of ethylene biosynthesis, the root length of the wild-type plants and the *della* mutants (*rga* and *gai*) was approximately the same. However, when grown on a medium supplemented with ACC, the roots of wild-type plants were significantly shorter than those of *rga* or *gai* mutants growing under the same conditions, indicating that the mutants were insensitive to ethylene. In a double mutant *rga gai*, lacking the two DELLA proteins RGA and GAI, the roots were even longer than in the single mutants *rga* or *gai* [27]. Studies on the treatment of plants with GAs showed that degradation of DELLA proteins, which was usually observed under these conditions, was significantly suppressed when ethylene is added. Thus, the effect of ethylene on plant growth is apparently mediated by its effect on DELLA protein concentration, by increasing the stability of these proteins [27]. When studying the mechanisms of ethylene influence, it was found that they are not associated with increased expression of the genes

encoding the DELLA proteins, but probably depend on the signal response regulator for ethylene, CTR1 (CONSTITUTIVE TRIPLE RESPONSE1). In the absence of ethylene, CTR1 inhibits the expression of ethylene-regulated genes. However, with increasing ethylene concentration, the repressor action is suppressed [28]. In the roots, where *CTR1* expression was suppressed by RNA interference following transformation with *Agrobacterium tumefaciens* containing a *CTR1*-RNAi construct, the concentration of RGA-GFP changed little in response to GA treatment, indicating that, under these conditions, the DELLA proteins were resistant to GA treatment. The existence of a link between the actions of ethylene and GA in the plant growth regulation has been shown in other studies [29, 30].

The phytohormones auxins and cytokinins play important roles in controlling the development and maintenance of the size of the apical meristem of the root. In maintaining the activity of the root apical meristem, auxins are of primary importance, as they stimulate cell division. In the proximal part of the meristem, a transition of cells from division to differentiation is noted, correlating with a decrease in the auxin gradient in this root segment. Cytokinins affect cell differentiation by suppressing the auxin-stimulatory effect on cell division. This effect results from the interaction between regulators of the cytokinin and auxin response. In particular, in *Arabidopsis*, the B-type cytokinin response regulator, the transcription factor ARR1, can induce expression of the repressor gene of Aux/IAA auxin response (*IAA3/SHY2*), which suppresses the expression of *PIN* genes encoding auxin carriers, so that auxin transport is inhibited [31, 32]. It is known that GAs, working synergistically with auxins, also play an important role in regulating the development of meristems. Recent research shows that GAs probably mediate the influence of cytokinin and auxin on one another, with this effect being mediated by the effect of GAs on DELLA proteins. GAs have been found to cause negative regulation of the cytokinin response by influencing *ARR1*. During exogenous treatment with GAs, the expression level of *ARR1* in the roots was significantly reduced. In the *rga* mutant (deficient in the DELLA protein RGA), which exhibits a constitutive effect of GA, the expression levels of *ARR1* and *SHY2* regulated by it were also reduced, suggesting that the regulation of the cytokinin–GA response is associated with the degradation of DELLA proteins [31].

DELLA proteins are also involved in direct regulation of polar auxin transport. Under conditions of GA insufficiency, the number of PIN carriers in the plasma membrane (PM) of root cells decreases, and their transfer to the vacuole increases. With an increase in GA concentration, PIN transfer to the vacuole is inhibited, and as a result, the PIN content in the PM increases [33]. The Arabidopsis mutant, in which all five known genes encoding DELLA proteins were suppressed by RNA interference, did not exhibit an increase in the concentrations of PINs in the PM following treatment with high concentrations of GAs [34]. Under those circumstances, treatment with paclobutrazol, an inhibitor of GA biosynthesis, caused a decrease in the concentration of PINs in the PM [35]. These experiments show that GA controls the transport of auxins through PIN carriers to DELLA proteins. It is known that prefoldins, regulators of tubulin assembly, the function of which is related to the regulation of the folding of cytoskeleton elements and their dynamics when interacting with DELLA proteins [36], can be involved in controlling the transfer of PINs.

Research has shown the existence of interactions between signaling pathways activated by GAs, auxins, cytokinins, or ethylene. The nature of these interactions is still not completely clear, but there is growing evidence that DELLA proteins are important regulators, controlling the interactions between phytohormones.

PARTICIPATION OF DELLA PROTEINS IN THE CONTROL OF REACTIVE OXYGEN SPECIES PRODUCTION

The role of DELLA proteins in the integration of internal signals is not limited to the regulation of phytohormonal interactions but also involves control over the concentration of secondary messengers, such as reactive oxygen species (ROS). The level of ROS is significantly increased in plants when interacting with phytopathogens [37] and when under the influence of abiotic stress factors (such as increased soil salinity, drought, and temperature extremes) [38].

According to recent research, GAs may affect the level of ROS. The mechanism by which this regulation operates became more understandable after data were published, indicating that DELLA proteins are involved in this process. In a study conducted on Arabidopsis, it was shown that DELLA proteins help maintain a low level of ROS in plants under stressful conditions and thus delay the onset of cell death. This regulatory mechanism is based on the ability of DELLA proteins to induce the expression of ROS-quenching enzymes, in particular, superoxide dismutase [39].

In addition to stimulating cell death, ROS perform various essential functions in plant growth and development processes and, in particular, are important regulators of root growth and development [40]. For example, ROS play a significant role in the development of root fibrillas. A mutant defective for the gene encoding NADPH oxidase had strongly reduced root fibrillas. In a mutant for four genes (GAI, RGA, RGL1, and RGL2) encoding DELLA proteins, the root fibrillas were elongated, but

the treatment of such mutant with an NADPH oxidase inhibitor reduced the length of the root fibrillas [39].

INVOLVEMENT OF DELLA PROTEINS IN REGULATION OF SYMBIOSIS DEVELOPMENT BETWEEN LEGUMINOUS PLANTS AND NITROGEN-FIXING BACTERIA

One of the most important functions that DELLA proteins perform is associated with their participation in the regulation of the development of an endosymbiosis between leguminous plants and nitrogen-fixing nodule bacteria ("rhizobia"), which leads to the appearance of new organs, nodules, on the roots. The emergence of mutualism is initiated under the influence of Nod factor signal molecules from rhizobia, which activate two programs in parallel, namely, the development of infection and the organogenesis of nodules.

Receptor-like transmembrane kinases with LysM motifs in the extracellular domain are involved in the reception of the Nod factors [41–43]. Activation of the signaling pathway leads to periodic fluctuations in the level of calcium in the nucleus of the root cells, which contributes to the activation of calcium/calmodulin-dependent kinase (CCaMK), which, in turn, stimulates the action of several transcription factors, such as IPD3/CYCLOPS, as well as NSP1, NSP2, ERN1, and NIN, that regulate the expression of target genes [44].

Phytohormones are essential in controlling the formation and development of nodules, as they closely interact with the components of the signaling pathway activated by Nod factors. Auxins and cytokinins play an essential role in this process. The mutation leading to the constitutive activation of the cytokinin receptor CRE1/LHK1 promoted the formation of nodules in the absence of rhizobia, whereas in mutants with impaired functional activity of the receptor, a significant decrease in the number of nodules was observed. When cytokinins interact with the CRE1/LHK1 receptor, a signaling pathway is activated, the components of which can directly affect the transport or biosynthesis of auxins. In *cre1* mutants, no changes were observed in the localization of PIN proteins and polar auxin transport, which are both induced during treatment with Nod factors or during inoculation with rhizobia in wild-type plants [45, 46]. Moreover, treatment of plant roots with inhibitors of auxin transport can induce the appearance of nodule-like structures [47].

However, mechanisms for controlling the development of the endosymbiosis, involving cytokinins and auxins, require coordinated interaction with other phytohormones, primarily GAs. GAs have a significant influence on the development of symbioses, and since DELLA proteins are the main regulators that react to changes in the GA concentration, their role in symbiosis is also important.

Experiments with exogenous addition of GAs were able to estimate the effect of DELLA proteins on the development of infection and on the organogenesis of nodules. It has been established that GA treatment inhibits the expression of genes encoding transcription factors NSP2 and NIN which are activated under the influence of Nod factors, as well as cytokinins. Increased expression of the gene encoding the positive regulator of SLEEPY1 GA action also negatively affects the nodulation [48].

GAs have a negative impact on the formation of infection threads. In the pea mutant *na* defective in a gene for GA biosynthesis, there was a significant increase in the number of infection threads formed. In contrast, treatment of the *na* mutant with exogenous GAs reduced the number of infection threads; it was only slightly higher than the level noted in the wild type [49].

Similarly, the treatment of *M. truncatula*, another N-fixing leguminous species, with GAs significantly reduced the number of infectious threads formed, their number also being reduced in *della* mutants in which GAs act constitutively [50]. Since the site for binding with GID1 receptor in DELLA proteins is at the N-terminus, mutations at this site result in the disruption of the assembly of the GID1 complex with DELLA proteins, which, in turn, prevents degradation of the DELLA proteins induced by GAs. Synthesis of the DELLA protein form (DELLAΔ18) insensitive to the effects of GAs causes an increase in the number of infection threads in the cells of the rhizodermis, although nodules are not formed. This effect can be explained by the fact that GA treatment inhibits the development of infection threads, which occurs as a result of the effect of GAs on DELLA proteins [50].

Treating plants with high concentrations of GAs (exceeding the endogenous concentration) led to a decrease in nodulation in direct proportion to the GA concentration, whereas the addition of the GA-biosynthesis inhibitor paclobutrazol stimulated nodulation [50].

The influence of GA on the development of nodules may be different depending on its concentration. In legumes, such as peas and *Sesbania rostrata*, mutations in the genes of GA biosynthesis (causing a reduced endogenous GA concentration) cause a significant decrease in the number of nodules formed. When such mutants are treated with GA, nodulation is restored [51]. It is important to note that those rare nodules, sometimes formed in plants mutant for GA-biosynthesis genes, are characterized by altered morphology and that they are smaller than those formed in wild-type plants [51]. Nodules of a similar appearance can also arise after treatment with high concentrations of paclobutrazol [49].

These data suggest that GAs play a dual role in the development of rhizobial symbiosis, since, on the one hand,

they determine the negative regulation of infection and, on the other, they have a positive effect on the organogenesis of nodulation within a specific concentration range. It should be noted that a similar regulatory effect has also been reported for cytokinins, which have a positive effect on the initial stages of nodule organogenesis, but a negative effect on the development of infection within the rhizodermis [48]. This means that, in the symbiosis development process, the positive and negative influences of phytohormones are likely to be closely related to the time and place of their action, as well as their influence on each other. Recently, it was shown that treatment with GAs can reduce the concentrations of some forms of cytokinins in the roots, with this effect depending on DELLA proteins [52]. Thus, DELLA proteins can also influence cytokinin metabolism during nodulation.

The involvement of DELLA proteins in the control of the development of rhizobial symbiosis probably takes place at the early stages of this process. Using the yeast two-hybrid assay and bimolecular fluorescence complementation, interactions between the DELLA proteins and the transcriptional factor IPD3/CYCLOPS (regulator of the signal pathway activated by Nod factors) of *M. truncatula* were detected [50, 53]. DELLA can activate the assembly of the complex between CCaMK-IPD3 and CYCLOPSDELLA, which enhances the phosphorylation of IPD3/CYCLOPS [53].

The involvement of DELLA proteins in the formation of another complex, which plays an important role in the signal regulation of symbiosis, namely, NSP1–NSP2, has also been established [50, 53]. As in the case of IPD3/CYCLOPS, the binding of three DELLA proteins of *M. truncatula* to the transcription factor NSP2 stimulates the assembly of the complex with NSP1. In addition, through the formation of the NSP1–NSP2 complex, DELLA proteins can activate the induction of expression of the *ERN1* gene encoding a transcription factor. When the NSP1 and NSP2 transcription factors were transfected into Arabidopsis protoplasts, there was a very weak induction of the reporter gene linked to the *ERN1* promoter, but when co-transfection with DELLA took place, this induction was significantly enhanced. Analysis of expression of genes used as markers of the development of symbiosis confirmed that expression of *ERN1* and the *ENOD11* gene activated by it were reduced in *della* mutants.

Using co-immunoprecipitation, it was revealed that DELLA proteins can serve as a link between IPD3 and NSP2, since their precipitation was noted only in the presence of DELLA. In addition, DELLA proteins interact with another participant in the signaling pathway, namely, the transcription factor NF-YA1 [50].

Interestingly, the expression level of the genes encoding NSP1 and NSP2 transcription factors may differ in the double *della1 della2* and single *della1* mutants of *M. truncatula*. In the double mutant, the expression levels of both *NSP1* and *NSP2* were significantly decreased compared with the wild type. These data are consistent with the finding that exogenous treatment with GAs also reduced the expression level of these genes and, consequently, that this decrease is mediated by the degradation of DELLA proteins under the influence of GAs [15]. In the single mutant, there was no significant difference in the expression of *NSP1* and *NSP2* compared with the wild type, which probably indicates that DELLA proteins can partially compensate for the functions of one another [50].

DELLA PROTEINS AS COMMON COMPONENTS OF THE SIGNALING PATHWAY THAT CONTROLS THE DEVELOPMENT OF THE LEGUME/ RHIZOBIAL SYMBIOSIS AND THE ARBUSCULAR MYCORRHIZA FUNGAL SYMBIOSIS

Under the influence of signaling molecules secreted by arbuscular mycorrhiza (AM) fungi, plants activate processes that promote the growth and distribution of fungal threads in root tissues and the formation of intercellular mycelia. At further stages, the threads are developed in the cells of the cortex, and specialized structures are formed, called arbuscules [54]. Phosphorus and nitrogen enter the root through the arbuscules, and fungi receive carbohydrates from the plant [55]. The development of symbiosis with AM fungi is regulated in accordance with the phosphate, nitrogen, and photosynthetic status of the plant.

It has been found that many components of the signaling cascade activated during the development of symbioses are common for both the nitrogen-fixing symbiosis and symbiosis with AM fungi. They include CCaMK and transcription factors IPD3/CYCLOPS, NSP1, and NSP2 [56, 57]. Relatively recently, it was reported that DELLA proteins are also necessary for the development of symbiosis with AM fungi and that they serve as “common” regulators in the development of the two types of symbiosis [15, 53].

It has been demonstrated, using the model leguminous plant *M. truncatula*, that, in plants under conditions of phosphorus deficiency, the expression level of the genes encoding DELLA proteins increases significantly and remains high during the development of the symbiosis, but decreases when phosphorus is added to the environment. When analyzing *della* mutants, it was shown that, after inoculation of single mutants, such as *della1* and *della2*, with AM fungi, the development of mycorrhiza was the same as in the wild type; in the double mutant, however, the formation of arbuscules was reduced by 85%. Transcription of the *MtPT4* and *MtLEC5* genes, which are markers of the development of arbuscules in cells of inoculated plants [58], was significantly reduced in the double

mutant, as was the expression level of the marker for the development of the fungus *Diversispora epigaea* (formerly *Glomus versiforme*), the alpha tubulin gene [15].

Synthesis in the *M. truncatula* root cells of the DELLA1Δ18 protein (developed using transformation with a *Della1Δ18* construct), which is insensitive to the action of GAs, induced the expression of some marker genes for the development of symbiosis with AM fungi, namely, *MtBCP1* and *MtSCP1*, *MtSbtM1*, and *MtVapyrin*, in the absence of fungal inoculation. Similarly, the synthesis of the DELLA1Δ18 protein in *Lotus japonicus* root cells induced the expression of the *NSP1* and *NSP2* genes, as well as that of the *DWARF27* gene activated by these transcription factors, which is involved in the biosynthesis of strigolactones. Moreover, such expression was sufficient to restore the ability to form arbuscules in the mutant *nsp1 nsp2* [59].

Thus, analysis of data from studies of the roles of DELLA proteins in the development of two types of symbiosis confirms their role as universal participants in signaling pathways that enable the plants to rapidly activate intracellular regulators under the influence of external signals.

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