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Analysis of the expression of polyamine biosynthesis genes in nodules of the garden pea (*Pisum sativum* L.) and the effect of exogenous treatment with polyamines on their development

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BACKGROUND: Polyamines are acting as signaling molecules during adaptation to stressful environment and as regulators of plant development. In plants, polyamines are represented mainly by putrescine, spermidine and spermine. The concentration of polyamines in symbiotic nodules of some legumes is 5–10 times higher than in the other organs, which indicates their important role in the formation and functioning of symbiotic nodules.

MATERIALS AND METHODS: We analyzed the expression of genes encoding polyamine biosynthesis enzymes in symbiotic nodules, as well as the effect of exogenous polyamines on the nodule number and the average nodule weight in wild-type SGE plants and symbiotic pea mutants SGEFix⁻-1 (*sym40-1*) and SGEFix⁻-2 (*sym33-3*).

RESULTS: The comparable expression level of arginine decarboxylase gene (*PsADC*) was observed in all analyzed nodules, whereas the expression level of ornithine decarboxylase gene (*PsODC*), was highly increased in nodules of SGEFix⁻-2 (*sym33-3*) mutant. Treatment of the root system with a 0.1 mM solution of polyamines mixture led to an increase in the average weight of the nodule in wild-type plants and in the SGEFix⁻-2 (*sym33-3*) mutant plants.

CONCLUSIONS: It was shown that the main pathway of putrescine synthesis in wild-type pea symbiotic nodules is the arginine pathway, while the ornithine pathway is probably associated with activation of plant defense reactions. Polyamines acting, apparently, through ethylene, affect the functioning of the nodule meristem.

Keywords: plant-microbial interactions; symbiotic nodule development; polyamines; putrescine; spermidine; spermine.

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Анализ экспрессии генов синтеза полиаминов в клубеньках гороха посевного (*Pisum sativum* L.) и влияние экзогенной обработки полиаминами на их развитие

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Введение. Концентрация полиаминов в симбиотических клубеньках некоторых бобовых в 5–10 раз превышает их концентрацию в других органах, что указывает на их важную роль в формировании и функционировании симбиотических клубеньков.

Материалы и методы. В рамках данной работы был проведен анализ экспрессии генов, кодирующих ферменты биосинтеза полиаминов, в симбиотических клубеньках, а также изучено влияние экзогенных полиаминов на клубенькообразование у растений линии дикого типа SGE и симбиотических мутантов гороха SGEFix⁻-1 (*sym40-1*) и SGEFix⁻-2 (*sym33-3*).

Результаты. Было показано, что основной путь синтеза путресцина в симбиотических клубеньках растений дикого типа — аргининовый, тогда как у мутанта SGEFix⁻-2 (*sym33-3*) активируется также орнитинный путь. Обработка корневой системы 0,1 мМ раствором смеси полиаминов приводила к увеличению среднего веса клубенька у растений дикого типа и мутанта SGEFix⁻-2 (*sym33-3*).

Заключение. Таким образом, полиамины, действуя, по-видимому, через этилен, влияют на функционирование меристемы клубеньков.

Ключевые слова: растительно-микробные взаимодействия; развитие симбиотического клубенька; полиамины; путресцин; спермидин; спермин.

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INTRODUCTION

Polyamines are low-molecular-weight organic cations present in all living organisms [1]. In plants, polyamines serve as signaling compounds for adaptation to negative environmental conditions as well as growth and development regulators. They are represented mainly by putrescine, a diamine; spermidine, a triamine, and spermine, a tetramine. They are found in the cell in the free or conjugated form associated with phenolic acids and other low-molecular-weight compounds, or with macromolecules such as proteins and nucleic acids [2].

The biosynthesis of polyamines is initiated with the formation of putrescine. In mammals and fungi, putrescine is synthesized from ornithine in a reaction catalyzed by ornithine decarboxylase. However, in plants and bacteria, there is an alternative pathway for putrescine biosynthesis, involving its synthesis from arginine in a reaction catalyzed by arginine decarboxylase.

The arginine pathway of biosynthesis is the main pathway in most plants. Polyamines formed from arginine are mainly involved in the processes of cell elongation and plant adaptation to abiotic stresses [3, 4]. Polyamines derived from ornithine are involved in cell proliferation in actively growing plant tissues. It is supposed, that ornithine decarboxylase is localized mainly in the cytoplasm, whereas arginine decarboxylase is localized in the thylakoid membranes of chloroplasts [5–8].

Putrescine is formed through the intermediate agmatine, which is synthesized from arginine (Fig. 1).

Putrescine is converted to spermidine and spermine by sequential transfer of aminopropyl groups from decarboxylated S-adenosylmethionine catalyzed by spermidine and spermine synthases (Fig. 1). Aminopropyl groups are formed from methionine, which is first converted to S-adenosylmethionine and then it is decarboxylated in a reaction catalyzed by S-adenosylmethionine decarboxylase (Fig. 1). S-adenosylmethionine is a precursor of both polyamines and ethylene [9].

In plants, polyamines are involved in cell division and elongation, rhizogenesis, morphogenesis, flowering, fruit ripening [10], and aging [11]. Polyamines can stabilize DNA, RNA, chromatin, and cell membranes due to their ability to bind to negatively charged molecules and inhibit lipid peroxidation [12, 13]. Treatment of plants with spermidine or spermine prevents the loss of chlorophyll, stabilizes the molecular composition of thylakoid membranes, and delays aging [14].

Cellular homeostasis of polyamines is maintained by the mutual transition of one form of polyamines to another, which are catalyzed by the enzymes polyamine oxidase and diamine oxidase. Such enzymatic reactions lead to the catabolism of polyamines as well as to the hydrogen peroxide production [15, 16]. Using Cu^{2+} and pyridoxal phosphate as cofactors, diamine oxidase catalyzes the formation of hydrogen peroxide, ammonia, and 4-aminobutanal from putrescine. Polyamine oxidase, bound by non-covalent bonds with flavin adenine dinucleotide, can oxidize spermidine and spermine to form 4-aminobutanal, (3-aminopropyl)-4-aminobutanal, 1,3-diaminopropane, and hydrogen peroxide [15, 16].

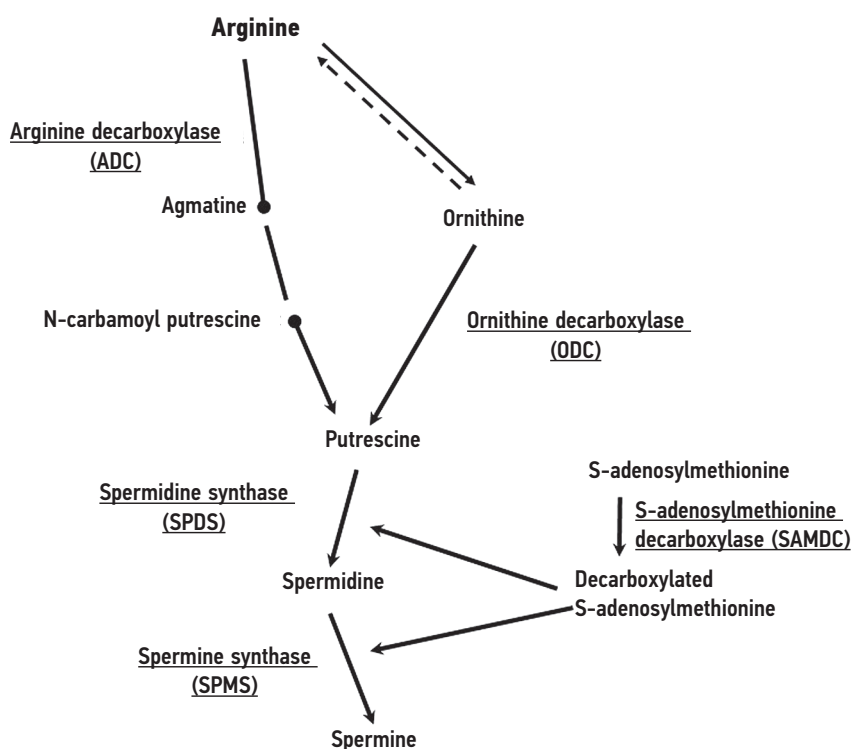


Fig. 1. Pathway of biosynthesis of polyamines in plants. The stages and enzymes are described in the main text

Polyamines also induce NO synthesis [17]. This indicates the important role of these compounds in the metabolism of reactive oxygen and nitrogen species. In addition, putrescine can enhance immune responses triggered by pathogen-associated molecular patterns, leading to an increase in plant resistance to diseases caused by bacterial pathogens [18].

Using genetic approaches, transcriptomics, and metabolomics, the key functions of various polyamines in developmental processes, from flowering to aging, as well as in the regulation of plant resistance to stress, have been identified. Recently, many studies have focused on the effects of exogenous polyamines on the growth and development of fruit and vegetable crops or model plants [19–24]. Attempts to increase the production of endogenous polyamines through genetic manipulation are becoming increasingly popular. However, the mechanisms of the regulation of the biosynthetic and catabolic pathways of polyamines at the transcriptional, translational, and post-transcriptional levels is still largely unknown. The metabolic pathway of polyamines is associated with the pathway of intermediate nitrogen metabolism and other compounds that protect against stress, hormones, and signaling molecules. Further research is required to explore the mechanism of polyamine accumulation to increase plant resistance to stress and regulate their growth. There is still little understanding of the metabolic relationships between polyamines and phytohormones during plant growth and development, especially about the relationship between polyamines and ethylene. Transgenic plants with a modified metabolism of polyamines could be an effective tool for studying the physiological functions of polyamines in higher plants [25–27].

Hydrogen peroxide produced during the catabolism of polyamines is involved in the inhibition of the *Medicago truncatula* – *Sinorhizobium meliloti* symbiotic system [28]. At the same time, legume nodules accumulate polyamines in concentrations 5–10 times higher than those in roots or leaves [29]. In the nodules of *Lotus japonicus*, the expression of genes involved in the synthesis of spermidine, spermine, and putrescine is induced at

the early stages of nodule development and decreases with age. Polyamines accumulate gradually during nodule maturation suggesting their role in division and differentiation of the nodule cells and other functions associated with nitrogen fixation [30, 31]. The role of polyamines in the early stages of infection, their effect on the regulation of nodule development and the efficiency of nitrogen fixation as well as their effect on the bacterial partner for various legumes (*L. japonicus*, *Galega orientalis*, *M. sativa*, and *M. truncatula*) are discussed in detail in reviews [32, 33].

This study is aimed to investigate the role of polyamines at the late stages of the garden pea (*Pisum sativum*) symbiotic nodule formation and functioning. For this purpose, symbiotic mutants of the garden pea are convenient models, as they allow analysis of the role of polyamines in nodule development and in the plant's defense responses during the formation of ineffective symbiosis.

MATERIALS AND METHODS
OF RESEARCH

Plant material and bacterial strain

The study used *P. sativum* mutants SGEFix⁻¹ (*sym40-1*) and SGEFix⁻² (*sym33-3*), which form white ineffective nodules [34], and the original line SGE [35] from the collection of All-Russia Research Institute for Agricultural Microbiology (Table 1). The block of nodule development in the SGEFix⁻¹ (*sym40-1*) mutant occurs after the release of bacteria into the plant cell [34]. Branched infection threads are formed in the nodules of the SGEFix⁻² (*sym33-3*) mutant, from which bacteria do not release into the cytoplasm of plant cells, but infection droplets are formed in some cells [36] and bacteria can be released [34, 37]. Plants were inoculated with the *Rhizobium leguminosarum* bv. *viciae* 3841 strain [38].

Growing conditions and harvest of material
for analysis

The seeds were sterilized with concentrated sulfuric acid for 15 min and washed with sterile water 10 times. The plants were grown in plastic jars containing 100 g

Table 1. Plant material used in the study

Genotype	Mutant allele	Nodule phenotype	References
SGE		Wild-type	[35]
SGEFix ⁻¹	<i>sym40-1</i>	Hypertrophied infection droplets, abnormal morphological differentiation of bacteroids, hydrogen peroxide accumulation and oxidative stress inside the nodule, premature degradation of symbiotic structures	[34, 39]
SGEFix ⁻²	<i>sym33-3</i>	'Locked' infection threads and the absence of bacterial release into the host-cell cytoplasm of most infected cells, 'leaky' phenotype	[34, 36, 37]

of sterile vermiculite in an MLR-352H climatic chamber (Sanyo Electric Co., Ltd., Moriguchi, Japan) at the temperature of 21°C, relative humidity of 75%, and illumination of 280 μM photons $\text{m}^{-2} \text{s}^{-1}$ under a 16/8-hour day and night regime, a nitrogen-free nutrient solution was used to water the plants [40]. To analyze gene expression, nodules (from 10 plants) were harvested 2 and 3 weeks after inoculation (WAI).

The root systems of pea seedlings were treated with a mixture of polyamines (0.1 mM putrescine, spermidine, and spermine) 40 h after inoculation. Further treatments were repeated every other day. The material for the analysis of the effect of polyamines on nodulation was collected after 2 WAIs.

Real-time PCR analysis

The nodules harvested were homogenized in liquid nitrogen. RNA was isolated according to the PureZol Isolation Reagent protocol (Bio-Rad, USA). The concentration and quality of total RNA were determined using the MultiNA microchip electrophoresis system for analysis of nucleic acids (Shimadzu Corporation, Japan). The synthesis of cDNA from 1.5 μg of total RNA treated with DNase I was performed using RevertAid Reverse Transcriptase (MBI Fermentas, Lithuania) in an automatic amplifier C1000™ Thermal Cycler (Bio-Rad, USA). Relative real-time PCR analysis was performed using iQ SYBR Green Supermix (Bio-Rad, USA) according to the protocol in the C1000™ Thermal Cycler automatic amplifier combined with a CFX96™ Real-Time System optical module (Bio-Rad, USA). The expression level was calculated by the $2^{-\Delta\Delta\text{CT}}$ method using the reference gene *PsGapC1* (L07500.1) [41]. Primer design was performed using the VectorNTI Advanced 10 software (Invitrogen, USA). The experimental results were processed statistically using the R programming environment and GraphPad Prism software. Statistically significant differences were determined using two-way ANOVA ($p \leq 0.05$).

RESULTS

Analysis of the expression of genes encoding enzymes involved in the biosynthesis of polyamines in nodules of the wild type SGE line and mutants SGEFix⁻¹ (*sym40-1*) and SGEFix⁻² (*sym33-3*)

In wild-type plants, the level of transcripts of the *PsADC* gene, encoding arginine decarboxylase, was less in three-week-old nodules than in two-week-old nodules (Fig. 2, *a*). In mutants SGEFix⁻¹ (*sym40-1*) and SGEFix⁻² (*sym33-3*), a decrease in the level of transcripts with age was also significant. Nevertheless, the level of *PsADC* transcripts in the SGEFix⁻¹ (*sym40-1*) mutant was significantly higher than that in the wild

type at all terms of the analysis, while in the SGEFix⁻² (*sym33-3*) mutant, the level of *PsADC* transcripts did not differ from that in the wild type (Fig. 2, *a*).

In wild-type plants, the level of transcripts of the *PsODC* gene, encoding ornithine decarboxylase, did not change with age, in contrast to mutant nodules, where the level of expression in three-week-old nodules was lower than in two-week-old nodules (Fig. 2, *b*). At the same time, active accumulation of *PsODC* transcripts was registered in two-week-old nodules of the SGEFix⁻² (*sym33-3*) mutants (Fig. 2, *b*).

The level of transcripts of the *PsSPDS1* gene, encoding spermidine synthase-1, did not change in three-week-old nodules as compared to two-week old nodules in all genotypes analyzed (Fig. 2, *c*), however, the expression level of this gene in mutants SGEFix⁻¹ (*sym40-1*) and SGEFix⁻² (*sym33-3*) was higher than that of the wild type at all terms of the analysis.

The level of *PsSPDS2* (spermidine synthase-2) transcripts decreased in three-week-old nodules compared to that in two-week-old nodules (Fig. 2, *d*) of all genotypes. As in the case of *PsSPDS1*, the level of expression of this gene in two-week-old nodules of the SGEFix⁻¹ (*sym40-1*) and SGEFix⁻² (*sym33-3*) mutants was higher than that in the wild type.

The level of transcripts of the *PsSAMDC* gene, encoding S-adenosylmethionine decarboxylase involved in the intermediate stage of spermidine synthesis, was higher in mutants than in the wild type (Fig. 2, *e*). In the SGEFix⁻¹ (*sym40-1*) mutant, the level of *PsSAMDC* gene transcripts increased with the age of the nodules, in contrast to the wild type and the SGEFix⁻² (*sym33-3*) mutant (Fig. 2, *e*).

Transcripts of the *PsSPMS* gene encoding spermine synthase were not detected at all stages in all genotypes analyzed.

Analysis of nodulation in the wild-type SGE line and mutants SGEFix⁻¹ (*sym40-1*) and SGEFix⁻² (*sym33-3*) after treatment with polyamines

In wild-type plants and in the mutant SGEFix⁻² (*sym33-3*), in contrast to the SGEFix⁻¹ (*sym40-1*) mutant, the mean weight of the nodules increased when treated with a mixture of 0.1 mM polyamines. But treatment did not affect the number of nodules formed in any of the studied genotypes (Table 2).

DISCUSSION

In the garden pea, arginine decarboxylase is responsible for the biosynthesis of putrescine in ovaries, fruits, and leaves. Arginine decarboxylase activity in the early stages of fruit development correlates with high levels of *PsADC* gene expression in fast-growing tissues [42].

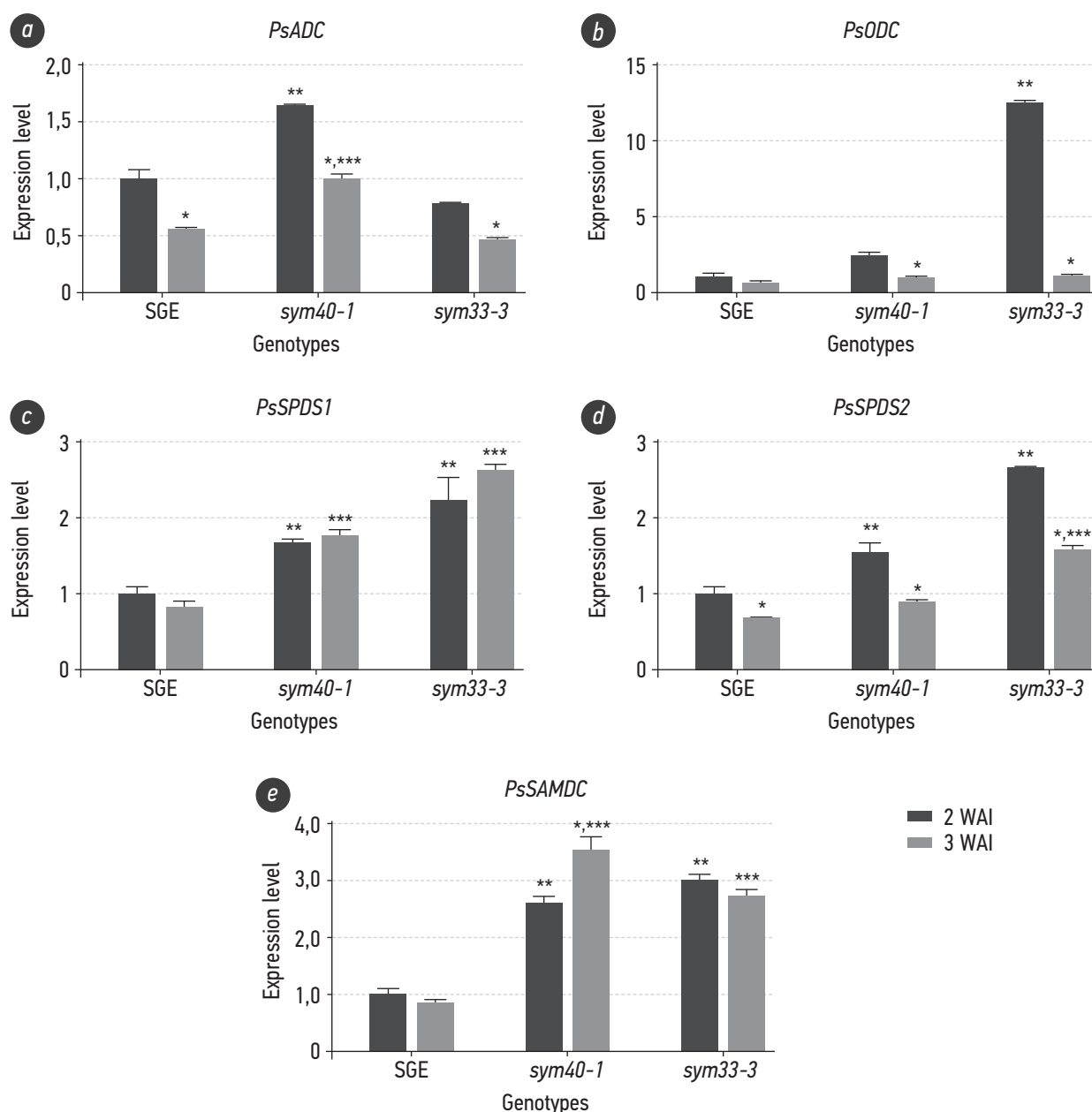


Fig. 2. Level of relative expression of polyamine biosynthesis genes: *a* – *PsADC* gene encoding arginine decarboxylase; *b* – *PsODC* gene encoding ornithine decarboxylase; *c* – *PsSPDS1* gene encoding spermidine synthase-1; *d* – *PsSPDS2* gene encoding spermidine synthase-2; *e* – *PsSAMDC* gene encoding S-adenosylmethionine decarboxylase in two- and three-week old nodules of wild-type garden pea SGE and mutants SGEFix⁻¹ (*sym40-1*) and SGEFix⁻² (*sym33-3*). * – within the genotype when compared with two-week old nodules; ** – from the wild-type SGE line at week 2 after inoculation (2 WAI); *** – from the wild-type SGE line at week 3 after inoculation (3 WAI); p ≤ 0.05

The high level of *PsADC* gene transcripts (Fig. 2, *a*), observed in this study in two-week-old wild-type pea nodules, may be associated with active processes of differentiation of infected cells, accompanied by an increase in cell size [43]. In *L. japonicus*, the level of *LjADC* and *LjODC* transcripts was maximal in young 10-day-old nodules and it was decreased with increasing age of the nodules [30]. At the same time, a correlation was observed between the expression of the *LjODC* and *LjADC* genes with the expression of *LjCycD3* encoding the D-type cyclin. In plants, D-type cyclins are involved in the control of the cell cycle, as well as in other plant

development programs [44]. Polyamines are more likely to participate in the development of *L. japonicus* nodules than in the process of nitrogen fixation since the transcripts of the gene encoding nitrogenase are found at high levels only after 2 WAI [30].

An increase in the *PsADC* gene expression in the SGEFix⁻¹ (*sym40-1*) mutant (Fig. 2, *a*) may be associated with the accumulation of hydrogen peroxide and oxidative stress in these nodules [39]. The catabolism of polyamines leads to the formation of hydrogen peroxide and acrolein, which can potentially cause cell damage under stress conditions [15, 16, 45]. However, hydrogen

Table 2. Influence of treatment with 0.1 mM polyamines mixture on the nodulation parameters in the different pea genotypes

Genotype	Average nodule weight, mg		Nodule number	
	Control	Treatment	Control	Treatment
SGE	0.143 ± 0.025	0.192 ± 0.010 *	81.5 ± 10.7	76 ± 10.5
SGEFix ⁻¹ (<i>sym40-1</i>)	0.037 ± 0.003	0.034 ± 0.001	94 ± 12	100.8 ± 13.5
SGEFix ⁻² (<i>sym33-3</i>)	0.088 ± 0.007	0.172 ± 0.008 **	14.2 ± 1.3	15.1 ± 1.0

*, ** – statistically significant difference of the average nodule dry weight in plants treated with a mixture of polyamines compare with control plants (* $p < 0.05$, ** $p < 0.0001$; Sidak's test).

peroxide is also a signaling molecule that can activate the antioxidant defense system of plants [46]. Indeed, *Zea mays* leaves pretreated with spermine and putrescine showed increased resistance to oxidative stress caused by paraquat [47]. Treatment with exogenous spermidine increased significantly the content of spermidine and spermine and decreased the level of putrescine in the roots of *Cucumis sativus* seedlings under conditions of hypoxic stress. These changes were associated with increased activity of antioxidant enzymes and lower peroxidation of membrane lipids, which ultimately resulted in an increase in plant resistance to hypoxia [48, 49]. Thus, it is likely that polyamines are regulators of redox homeostasis and play a dual role in the oxidative stress of plants [50, 51].

It should also be noted that polyamines are involved in plant protection against pathogenic microorganisms. It has been revealed that treatment with exogenous putrescine of *Arabidopsis thaliana* seedlings induces defense reactions such as callose deposition and an increase in the expression of several marker genes of pattern-activated immunity. These responses are dependent on hydrogen peroxide and NADPH oxidases, thus suggesting that reactive oxygen species mediate signaling triggered by putrescine. Putrescine enhances the responses of pattern-activated immunity due to the production of reactive oxygen species, which leads to an increase in plant resistance to bacterial pathogens [18].

The increased expression level of the *PsSPDS1* and *PsSPDS2* genes (Fig. 2, c, d) in the nodules of the mutant lines SGEFix⁻¹ (*sym40-1*) and SGEFix⁻² (*sym33-3*) may be associated with the participation of polyamines (namely, spermidine) in modulation of defense reactions activated in these nodules [41].

The accumulation of *PsODC* gene transcripts in the SGEFix⁻² (*sym33-3*) mutant in two-week-old nodules (Fig. 2, b) may be associated with a strong activation of specific defense reactions in the nodules of this mutant [41, 52] as a result of activation of the ornithine pathway of putrescine biosynthesis besides with arginine pathway.

Treatment with exogenous polyamines did not affect the number of nodules, however it led to an increase

in the average nodule weight in the wild-type SGE line and the SGEFix⁻² (*sym33-3*) mutant, but not in the SGEFix⁻¹ (*sym40-1*) mutant (Table 2). In previous studies, treatment of *Glycine max* leaf disks with a 1 mM solution of spermidine and spermine increased ethylene production [53]. An increase in ethylene production was also observed when *Oryza sativa* segments were treated with polyamines [54]. At the same time, it was previously demonstrated that exogenous ethylene (added in the form of ethephon) causes an increase in the average nodule weight both in the wild-type SGE line and in the SGEFix⁻² (*sym33-3*) mutant [55]. This suggests that the effect of polyamines on nodule weight is mediated by the action of ethylene. The absence of such effect for the nodules of the SGEFix⁻¹ (*sym40-1*) mutant can probably be due to the early cessation of the meristem functioning in such nodules [56], which is manifested in their small size. The high signal level detected during immunolocalization of 1-aminocyclopropane 1-carboxylic acid in the meristematic cells of nodules confirms the importance of ethylene for the meristem functioning [57].

The findings of this study reveal that in the garden pea, the main pathway of putrescine synthesis in effective symbiotic nodules is the arginine pathway. Additionally, in ineffective nodules of the SGEFix⁻² (*sym33-3*) mutant, the ornithine pathway is activated, possibly leading to the activation of strong defense reactions in the ineffective nodules of this mutant. Furthermore, polyamines, indirectly through ethylene, seem to affect the nodule meristem functioning.

ADDITIONAL INFORMATION

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