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Multifunctionality of a Microbial Consortium in Phytopathogen Suppression, Plant Growth Promotion, and Yield Enhancement

Multifuncionalidade de consórcio microbiano na supressão de fitopatógenos, promoção do crescimento vegetal e incremento produtivo

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ABSTRACT
The increasing demand for sustainable agricultural production has intensified the adoption of microbial bioinputs as an alternative to conventional crop management. Beneficial microorganisms are capable of simultaneously suppressing phytopathogens, promoting plant growth, improving nutrient acquisition, and enhancing biological nitrogen fixation. This study aimed to evaluate the effects of seed-furrow application of a microbial consortium composed of *Trichoderma afroharzianum*, *Bacillus subtilis*, *Bacillus velezensis*, *Pantoea agglomerans*, and *Bradyrhizobium japonicum* on soybean performance under commercial field conditions in southwestern Paraná State, Brazil. Prior to field evaluation, the antagonistic activity of the biological agents was assessed *in vitro* against eight major soybean phytopathogens. Field experiments were conducted during the 2024/2025 growing

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season using a randomized complete block design in five commercial production areas. Agronomic evaluations included grain yield, number of pods per plant, number of seeds per pod, and thousand-grain weight. The evaluated microorganisms effectively inhibited mycelial growth of all phytopathogens under laboratory conditions, with *Trichoderma afroharzianum* exhibiting the highest inhibition rates for most pathogens. Under field conditions, the microbial consortium significantly increased soybean grain yield from 4,322.4 to 4,628.0 kg ha^{-1}, corresponding to an average increase of 305.6 kg ha^{-1} (7.1%). The increase in productivity was primarily associated with a higher number of pods per plant, whereas the number of seeds per pod and thousand-grain weight were not significantly affected. The formation of active root nodules confirmed the successful establishment of *Bradyrhizobium japonicum* symbiosis, contributing to biological nitrogen fixation and improved crop performance. These findings demonstrate that multifunctional microbial consortia represent an effective and sustainable strategy for increasing soybean productivity while reducing dependence on conventional agricultural inputs.

Keywords: Soybean; Biological control; Plant growth-promoting microorganisms; Microbial consortium; Biological nitrogen fixation; Sustainable agriculture.

RESUMO

A crescente demanda por sistemas agrícolas mais sustentáveis tem impulsionado o uso de bioinsumos microbianos como alternativa aos modelos convencionais de manejo das culturas. Microrganismos benéficos apresentam capacidade de suprimir fitopatógenos, promover o crescimento vegetal, aumentar a disponibilidade de nutrientes e potencializar a fixação biológica de nitrogênio, contribuindo para o incremento da produtividade agrícola. O presente estudo teve como objetivo avaliar o efeito da aplicação via sulco de semeadura de um consórcio microbiano composto por *Trichoderma afroharzianum*, *Bacillus subtilis*, *Bacillus velezensis*, *Pantoea agglomerans* e *Bradyrhizobium japonicum* sobre o desempenho agronômico da soja em condições comerciais de cultivo na região Sudoeste do Paraná. Inicialmente, foi avaliado *in vitro* o potencial antagonista dos microrganismos frente a oito importantes fitopatógenos da cultura da soja. Posteriormente, experimentos de campo foram conduzidos durante a safra 2024/2025 em cinco áreas comerciais, utilizando delineamento em blocos casualizados. Foram avaliados a produtividade de grãos, o número de vagens por planta, o número de grãos por vagem e a massa de mil grãos. Os microrganismos apresentaram elevada atividade antagonista contra todos os fitopatógenos avaliados, destacando-se *T. afroharzianum*, que apresentou os maiores percentuais de inibição para a maioria dos fungos. Em condições de campo, a aplicação do consórcio microbiano promoveu incremento significativo na produtividade da soja, elevando a produção de 4.322,4 para 4.628,0 kg ha^{-1}, correspondendo a um ganho médio de 305,6 kg ha^{-1} (7,1%). O aumento da produtividade esteve diretamente relacionado ao maior número de vagens por planta, enquanto o número de grãos por vagem e a massa de mil grãos não apresentaram diferenças significativas entre os tratamentos. A formação de nódulos radiculares ativos confirmou o estabelecimento da simbiose com *Bradyrhizobium japonicum*, evidenciando a contribuição da fixação biológica de nitrogênio para o desempenho da cultura. Os resultados demonstram que a aplicação de consórcios microbianos multifuncionais constitui uma estratégia eficiente e sustentável para aumentar a produtividade da soja, integrando mecanismos de promoção de crescimento, supressão de fitopatógenos e melhoria da eficiência nutricional das plantas.

Palavras-chave: *Glycine max*; bioinsumos; consórcio microbiano; controle biológico; promoção de crescimento vegetal; fixação biológica de nitrogênio.

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1. INTRODUCTION

Soybean (*Glycine max* (L.) Merr.) is one of the world's most important agricultural crops, serving as a major source of vegetable protein and oil for human consumption, animal feed, and numerous industrial applications. Since its domestication in Asia, soybean cultivation has expanded worldwide due to advances in breeding programs, mechanization, and crop management technologies. In Brazil, the crop experienced rapid expansion beginning in the 1970s, driven by the development of cultivars adapted to tropical and subtropical environments and increasing international demand, making the country the world's largest soybean producer and exporter (Batista et al., 2020; CONAB, 2021).

During the 2024/2025 growing season, Brazil cultivated approximately 47.5 million hectares of soybean, producing between 166 and 169.5 million tons, representing an increase of more than 14% compared with the previous season (CONAB, 2025; IBGE, 2025). Although remarkable genetic improvements and advances in crop management have substantially increased soybean productivity, diseases remain among the major constraints limiting yield and production stability.

Globally, plant pests and diseases are responsible for approximately 40% of agricultural yield losses, with phytopathogenic microorganisms accounting for nearly one-third of these reductions (Barbosa et al., 2023). In Brazil, more than forty diseases have been reported affecting soybean throughout its developmental cycle, many of which are capable of causing yield losses exceeding 20% under favorable environmental conditions when effective management strategies are not adopted (Moraes & Sumita, 2022). Consequently, integrated disease management has become essential for maintaining sustainable crop production while minimizing economic losses.

The effectiveness of disease management is strongly influenced by the interaction among the pathogen, the host plant, and environmental conditions, commonly described by the disease triangle. Understanding these interactions allows the implementation of integrated management strategies combining cultural practices, resistant cultivars, chemical control, and biological agents, thereby

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improving disease suppression while reducing dependence on synthetic pesticides (Camargo, 2018).

In recent years, biological inputs have emerged as an important component of sustainable agricultural production. The global biocontrol and bioinput market has shown continuous expansion, reaching an estimated value of US$ 6.06 billion in 2024, with projections exceeding US$ 10 billion by 2029, reflecting an annual growth rate above 11% (Mordor Intelligence, 2024). Brazil has become one of the fastest-growing markets worldwide, supported by regulatory advances and increasing adoption of biological technologies across major cropping systems.

Soybean represents the principal crop for biological input adoption in Brazil, accounting for approximately 62% of the treated agricultural area, followed by maize and sugarcane (Bettiol & Medeiros, 2023). Biological products based on beneficial microorganisms have gained particular attention because they simultaneously promote plant growth, enhance nutrient availability, improve biological nitrogen fixation, suppress soilborne pathogens, and stimulate plant defense mechanisms. These multifunctional characteristics have positioned microbial inoculants as strategic tools for increasing agricultural sustainability while reducing reliance on conventional chemical inputs.

Among the most widely studied beneficial microorganisms, species belonging to the genera *Trichoderma*, *Bacillus*, *Pantoea*, and *Bradyrhizobium* exhibit complementary mechanisms of action. *Trichoderma* spp. are recognized for their antagonistic activity against phytopathogens through mycoparasitism, antibiosis, competition, and induction of systemic resistance. Likewise, *Bacillus* spp. produce a broad spectrum of antimicrobial metabolites and phytohormones, contributing to disease suppression and plant growth promotion. *Pantoea* spp. have demonstrated the capacity to colonize the rhizosphere efficiently, improve nutrient acquisition, and stimulate plant development, whereas *Bradyrhizobium* spp. play a fundamental role in biological nitrogen fixation, representing one of the cornerstones of soybean production systems.

Although these microorganisms have been extensively investigated individually, information regarding their combined application directly in the seed

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furrow under commercial field conditions remains limited. Evaluating microbial consortia under large-scale production environments is particularly relevant because synergistic interactions among different beneficial microorganisms may improve crop establishment, enhance nutrient use efficiency, increase tolerance to biotic and abiotic stresses, and ultimately contribute to higher grain yield.

Therefore, the present study aimed to evaluate the effects of applying a consortium composed of *Trichoderma* spp., *Bacillus* spp., *Pantoea* spp., and *Bradyrhizobium* spp. directly into the seed furrow during soybean sowing under commercial field conditions in southwestern Paraná, Brazil. Agronomic performance was assessed through yield components and grain productivity to determine the contribution of biological inputs to soybean production under commercial farming conditions.

2. MATERIALS AND METHODS

2.1 In vitro evaluation of antagonistic activity

Prior to the field experiments, the antagonistic potential of the microbial products was evaluated *in vitro* against important soybean phytopathogens. The assay was conducted using disposable 8.3-cm Petri dishes containing approximately 20 mL of potato dextrose agar (PDA).

The aerial pathogens evaluated were *Septoria glycines*, *Corynespora cassiicola*, *Cercospora kikuchii*, and *Colletotrichum truncatum*, whereas the soilborne pathogens included *Macrophomina phaseolina*, *Fusarium crassistipitatum*, *Rhizoctonia solani*, and *Sclerotinia sclerotiorum*. A 7-mm mycelial plug of each pathogen was placed 1 cm from the edge of one side of the Petri dish, while 15 µL of the microbial formulations were applied to the opposite side. The evaluated products were based on *Trichoderma afroharzianum*, *Bacillus subtilis* + *Bacillus velezensis*, and *Pantoea agglomerans*, applied at the equivalent commercial field rates of 100 mL ha^{-1}, 30 g ha^{-1}, and 50 g ha^{-1}, respectively.

The plates were sealed with PVC film and incubated in a biological oxygen demand (BOD) chamber at 25 ± 1°C under a 12-h photoperiod. Radial mycelial

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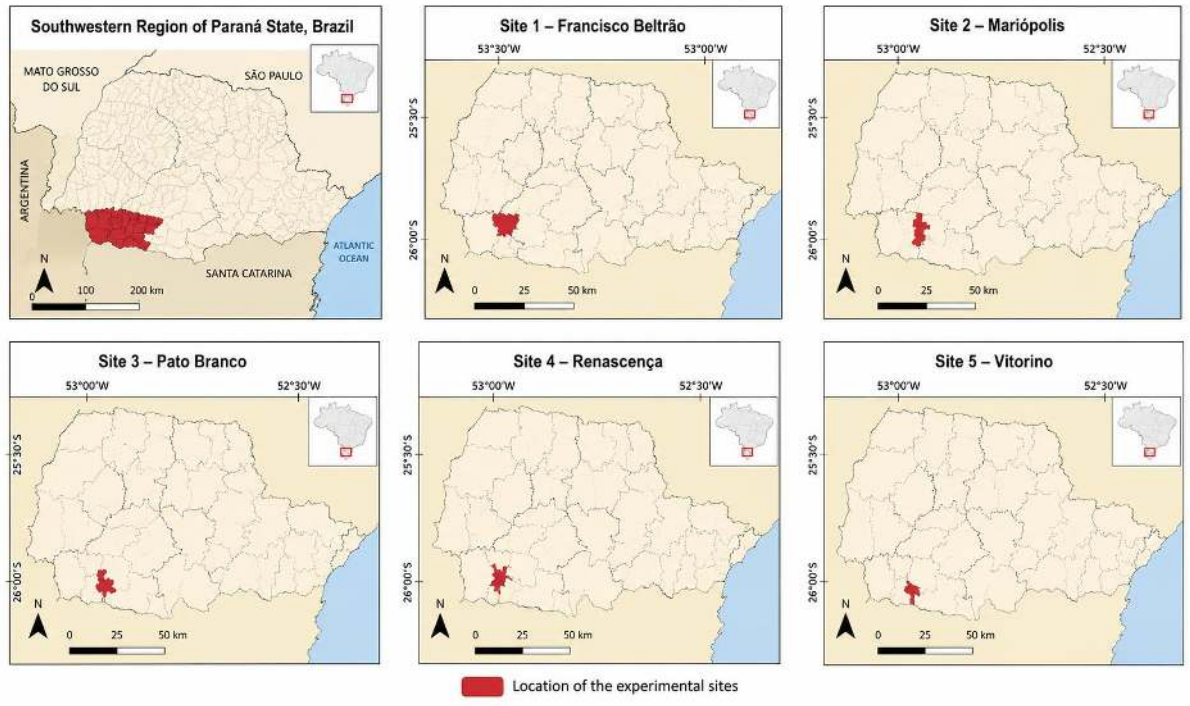
growth was measured every 24 h using a graduated ruler until the control colonies reached the edge of the plate.

The experiment followed a completely randomized design with four replicates per treatment. Data were subjected to the Shapiro–Wilk normality test followed by analysis of variance (ANOVA) using the RBio statistical package (Bhering, 2017).

2.2 Experimental sites

Field trials were conducted during the 2024/2025 growing season in five commercial soybean production areas located in the municipalities of Francisco Beltrão, Mariópolis, Pato Branco, Renascença, and Vitorino, southwestern Paraná State, Brazil (Figure 1 and Table 1).

Figure 1. Geographic location of the experimental sites in southwestern Paraná State, Brazil, highlighting the municipalities of Francisco Beltrão (Site 1), Mariópolis (Site 2), Pato Branco (Site 3), Renascença (Site 4), and Vitorino (Site 5).



Source: Adapted from Wikimedia Commons (2025).

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Table 1. Geographic characteristics of the experimental sites.

Site	Municipality	Latitude (DMS)	Longitude (DMS)	Altitude (m)
1	Francisco Beltrão	26°02′09.89″ S	53°11′00.97″ W	650
2	Mariópolis	26°16′56.88″ S	52°29′29.16″ W	850
3	Pato Branco	26°14′50.43″ S	52°35′51.32″ W	765
4	Renascença	26°05′55.41″ S	52°56′31.74″ W	700
5	Vitorino	26°12′54.72″ S	52°46′25.78″ W	779

Source: The authors.

According to the Köppen climate classification, the region is characterized as Cfa (humid subtropical), with an average annual rainfall ranging from 1,800 to 2,000 mm and elevations between 650 and 850 m. The predominant soil type is a clayey Red Latosol (*Latossolo Vermelho*), presenting favorable physical and chemical characteristics for soybean cultivation (EMBRAPA, 2006).

2.3 Experimental design and treatments

The experiment was arranged in a randomized complete block design with four replicates at each location. Two treatments were evaluated: **T1:** untreated control (without bioinput application); and **T2:** application of a microbial consortium directly into the seed furrow during sowing (Table 2).

Table 2. Experimental treatments evaluated under commercial field conditions.

Treatment	Description
T1	Untreated control (without bioinput application).
T2	Seed-furrow application of a microbial consortium composed of *Trichoderma afroharzianum* CEN 287, *Bacillus subtilis* ESALQ EpD2-5, *Bacillus velezensis* ESALQ RZ1MS9, *Pantoea agglomerans* ESALQ 33.1, and *Bradyrhizobium japonicum* strains SEMIA 5079 and SEMIA 5080.

Source: The authors.

The microbial consortium consisted of *Trichoderma afroharzianum* CEN 287 (EMBRAPA), *Bacillus subtilis* ESALQ EpD2-5, *Bacillus velezensis* ESALQ RZ1MS9, *Pantoea agglomerans* ESALQ 33.1, and *Bradyrhizobium japonicum* strains SEMIA 5079 and SEMIA 5080 (Table 3). Commercial formulations were applied according

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to the manufacturers' recommendations and registered doses approved by the Brazilian Ministry of Agriculture (MAPA) and AGROFIT database.

Table 3. Biological products applied to the seed furrow during soybean sowing.

Active ingredient	Strain	Formulation concentration	Application rate	MAPA registration
Trichoderma afroharzianum	CEN 287 (EMBRAPA)	3×10^{10} viable conidia g^{-1}	0.03 kg ha^{-1}	25422
Bacillus subtilis + *Bacillus velezensis*	ESALQ EpD2-5; ESALQ RZ1MS9	1×10^{9} viable spores mL^{-1}	0.10 L ha^{-1}	00424
Pantoea agglomerans	ESALQ 33.1	2×10^{9} CFU g^{-1}	0.05 kg ha^{-1}	SP0053139-2
Bradyrhizobium japonicum	SEMIA 5079; SEMIA 5080	6×10^{9} CFU mL^{-1}	0.18 L ha^{-1}	SP0053139-1

Source: The authors.

The consortium was selected to combine complementary biological mechanisms, including biological nitrogen fixation, plant growth promotion, nutrient mobilization, antagonism against phytopathogens, and induction of plant defense responses.

2.4 Plot establishment and bioinput application

Each experimental plot consisted of thirty soybean rows, each 150 m long and spaced 0.50 m apart, totaling approximately 2,250 m². Border rows were excluded from all evaluations.

The microbial consortium was applied directly into the seed furrow using an inoculant tank coupled to the sowing equipment (Figure 2), ensuring homogeneous distribution of the biological suspension throughout the planting operation. Application rates followed the commercial recommendations for each microbial product.

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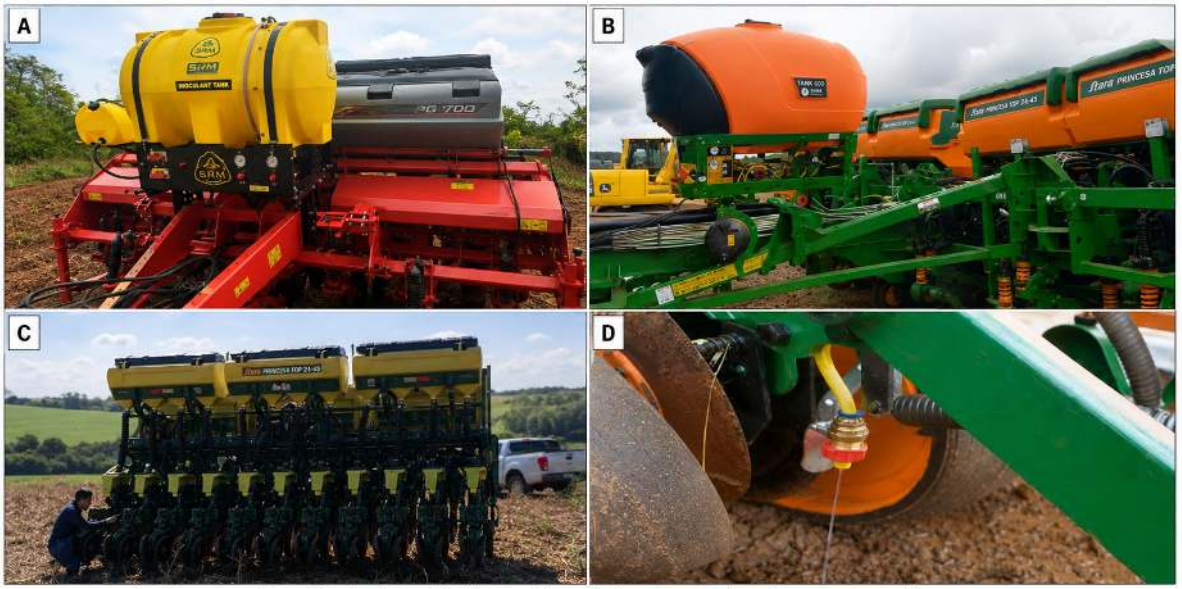
Figure 2. Seed-furrow application system used for the microbial consortium during soybean sowing. (A–B) Inoculant tank coupled to the planter; (C) calibration of the application volume; (D) directed spray into the seed furrow.



(A–B) Inoculant tank coupled to the planter; (C) calibration of the application volume; (D) directed spray into the seed furrow.
Source: The authors.

2.5 Crop management

All field experiments were established using the soybean cultivar BMX Zeus IPRO, which was sown between September 11 and 25, 2024. Crop management practices were standardized across all experimental locations according to regional technical recommendations.

Basal fertilization consisted of 250 kg ha^{-1} of the 04–20–00 ($N–P_2O_5–K_2O$) formulation, followed by a topdressing application of 150 kg ha^{-1} potassium chloride (KCl).

Weed management was performed using glyphosate (720 g kg^{-1}; 1.5 kg ha^{-1}) combined with clethodim (240 g L^{-1}; 0.5 L ha^{-1}). Insect control was carried out using beta-cyfluthrin (125 g L^{-1}; 100 mL ha^{-1}). Disease management followed the commercial production program adopted at each site, consisting of sequential fungicide applications from vegetative to reproductive growth stages using mixtures of triazoles, strobilurins, carboxamides, and multisite fungicides to ensure adequate disease control and minimize resistance selection.

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2.6 Agronomic evaluations

The effects of the treatments were assessed through the main soybean yield components (Table 4).

Table 4. Agronomic variables evaluated during the soybean growing season.

Variable	Methodology
Number of pods per plant (NPP)	Determined from ten randomly selected plants per plot.
Number of seeds per pod (NSP)	Determined from the same ten sampled plants per plot.
Thousand-grain weight (TGW)	Determined by weighing grain samples collected from each experimental unit using a precision balance.
Grain yield (kg ha^{-1})	Determined by mechanically harvesting the central rows of each experimental plot, followed by grain weighing and conversion to kilograms per hectare.

Source: The authors.

The number of pods per plant (NPP) **and** average number of seeds per pod (NSP) were determined from ten randomly selected plants per plot.

The thousand-grain weight (TGW) was determined using grain samples harvested from each experimental unit and weighed on a precision balance.

Grain yield (kg ha^{-1}) was obtained by mechanically harvesting the central rows of each plot, followed by grain weighing and conversion to kilograms per hectare.

2.7 Statistical analysis

Data were subjected to analysis of variance (ANOVA). When significant treatment effects were detected ($P \leq 0.05$), means were compared using Tukey's multiple comparison test at the 5% significance level.

Statistical analyses were performed using the **Genes** software (Version 2016). Treatment, environment (location), and treatment × environment interaction effects were included in the statistical model. Since the primary objective of the study was to compare bioinput application with the untreated control under

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commercial production conditions, treatment effects were interpreted across the evaluated environments.

3. RESULTS AND DISCUSSION

3.1 In vitro antagonistic activity against soybean phytopathogens

The *in vitro* assay demonstrated that the evaluated biological agents exhibited antagonistic activity against all soybean phytopathogens tested, although the magnitude of inhibition varied according to both the microorganism and the pathogen (Figure 3). Overall, *Trichoderma afroharzianum* showed greater inhibitory activity against most pathogens, whereas the consortium composed of *Bacillus subtilis* + *Bacillus velezensis* also promoted substantial reductions in mycelial growth, confirming its broad-spectrum antagonistic potential.

Bacillus subtilis + *B. velezensis* reduced mycelial growth by 44% for *Colletotrichum truncatum*, 41% for *Septoria glycines*, 30% for *Corynespora cassiicola*, 41% for *Cercospora kikuchii*, 49% for *Macrophomina phaseolina*, 58% for *Fusarium crassistipitatum*, 49% for *Rhizoctonia solani*, and 39% for *Sclerotinia sclerotiorum* (Figure 3). In comparison, *T. afroharzianum* inhibited mycelial growth by 57%, 67%, 51%, 37%, 69%, 43%, 53%, and 44% against the same pathogens, respectively. These results demonstrate that both biological products effectively suppressed pathogens affecting soybean, although with distinct inhibition profiles that likely reflect differences in their mechanisms of action.

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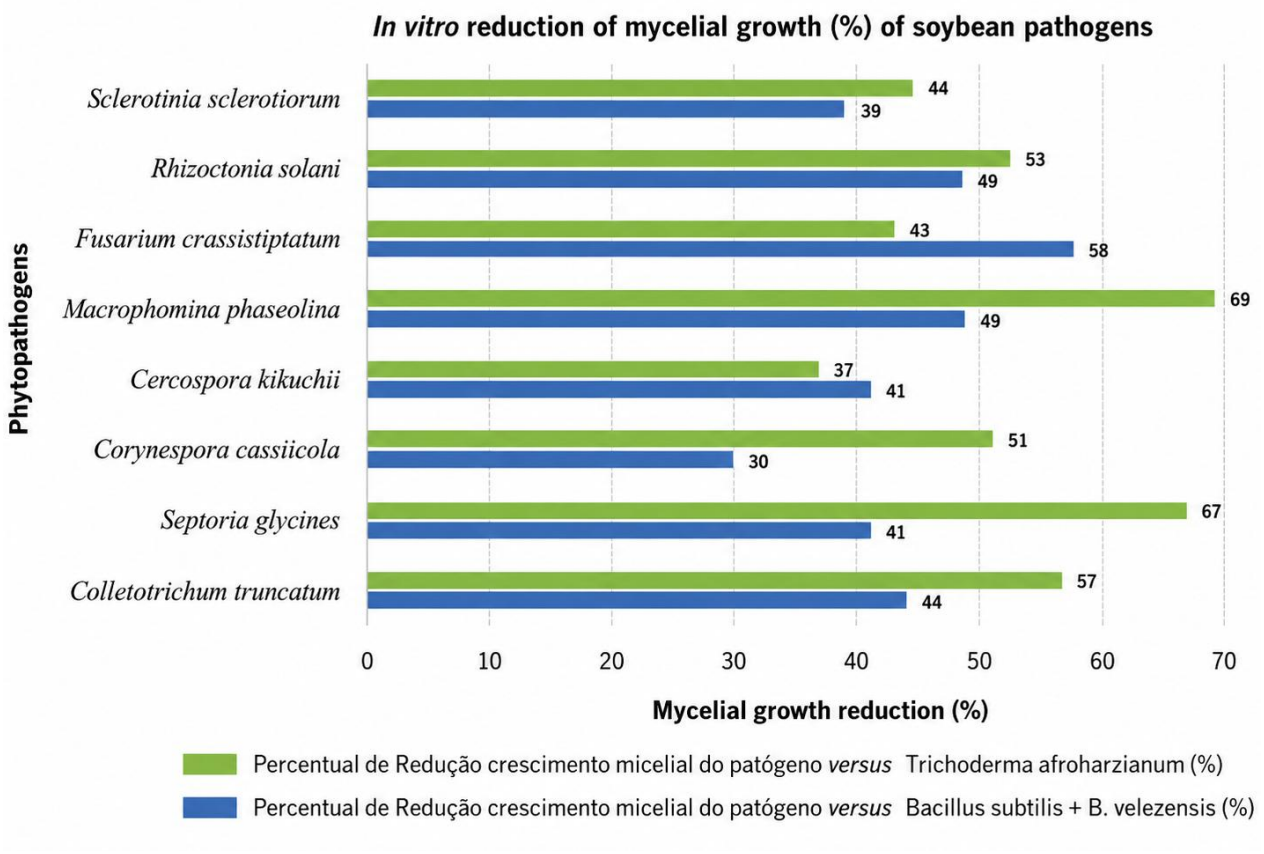
Figure 3. *In vitro* inhibition of mycelial growth (%) of major soybean phytopathogens (*Colletotrichum truncatum, Septoria glycines, Corynespora cassiicola, Cercospora kikuchii, Macrophomina phaseolina, Fusarium crassistipitatum, Rhizoctonia solani,* and *Sclerotinia sclerotiorum*) by *Bacillus subtilis* + *Bacillus velezensis* and *Trichoderma afroharzianum*.



Source: The authors.

The qualitative observations obtained during the dual-culture assays further supported these findings (Figure 4). Distinct antagonistic behaviors were observed according to the biological agent evaluated. The *Bacillus* formulation inhibited pathogen development primarily through competition for nutrients and ecological niches, accompanied by the production of diffusible antimicrobial metabolites, a mechanism commonly described as antibiosis. Conversely, *T. afroharzianum* displayed rapid colonization of the culture medium followed by direct contact with pathogen colonies, characteristic of competition for space and nutrients combined with mycoparasitism. In several interactions, hyphal overgrowth and coiling around pathogen hyphae were evident, indicating active parasitism of the target fungi (Figure 4).

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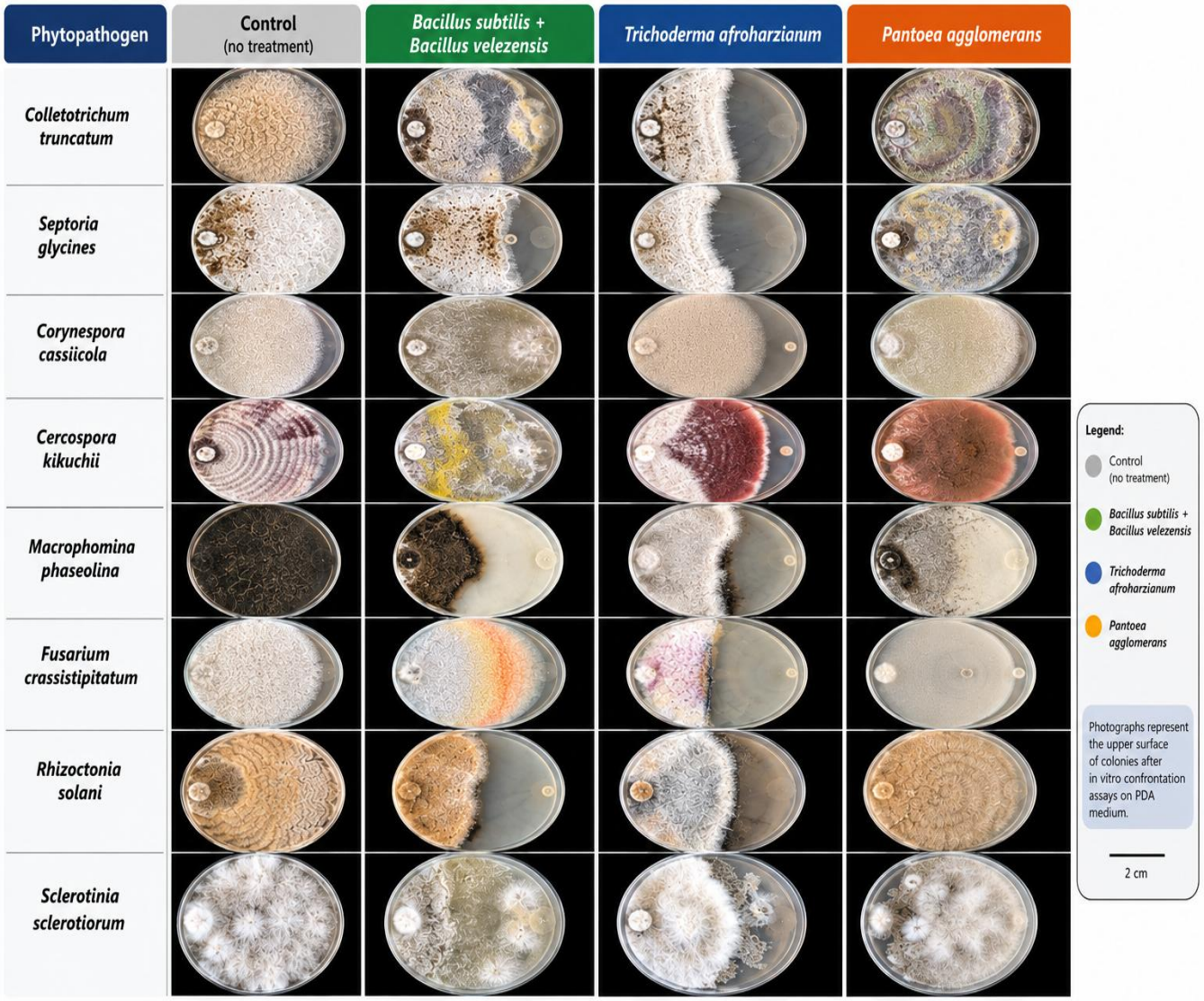
Figure 4. Representative *in vitro* antagonistic interactions between soybean phytopathogens and biological control agents. Images illustrate pathogen growth in the untreated control and in the presence of *Bacillus subtilis* + *Bacillus velezensis*, *Trichoderma afroharzianum*, and *Pantoea agglomerans*, highlighting distinct mechanisms of antagonism, including competition, antibiosis, and mycoparasitism.



Source: The authors.

The antagonistic mechanisms observed are consistent with those previously reported for these microorganisms. Species of *Trichoderma* are recognized for their ability to suppress phytopathogens through multiple complementary mechanisms, including rapid colonization of substrates, competition for nutrients, secretion of hydrolytic enzymes such as chitinases and β-1,3-glucanases, production of secondary metabolites with antifungal activity, and direct mycoparasitism. This

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multifunctional mode of action contributes to effective suppression of several soilborne and foliar pathogens while simultaneously promoting plant growth and activating induced systemic resistance.

These observations agree with previous studies describing *Trichoderma* spp. as one of the most effective biological control agents against phytopathogenic fungi due to their ability to parasitize fungal hyphae, degrade cell walls through chitinases and β-1,3-glucanases, and produce secondary metabolites with antifungal activity (Conti, 2007; Cruz, 2021). Similarly, beneficial bacteria belonging to the genus *Bacillus* produce numerous bioactive compounds capable of inhibiting fungal development while simultaneously stimulating plant growth through phytohormone production and nutrient mobilization (Cristiano Veloso, 2022).

Although *Pantoea agglomerans* exhibited less pronounced inhibition under *in vitro* conditions than *Trichoderma* and *Bacillus*, the images presented in Figure 4 indicate its capacity to restrict pathogen growth through competition and rhizosphere colonization. Previous studies have shown that *Pantoea* species contribute to disease suppression by producing antimicrobial compounds, siderophores, and plant growth-promoting substances, particularly when integrated into microbial consortia.

The complementary antagonistic responses observed among the evaluated microorganisms suggest that their combined application may provide broader pathogen suppression than individual inoculants. Because soybean production systems are simultaneously challenged by multiple soilborne and aerial pathogens, microbial consortia capable of combining antibiosis, competition, mycoparasitism, nutrient mobilization, and plant growth promotion represent an attractive strategy for sustainable disease management.

Overall, the *in vitro* results demonstrated that the evaluated biological agents effectively inhibited the mycelial growth of the principal soybean phytopathogens, supporting their subsequent evaluation under commercial field conditions. The differential inhibitory responses observed among pathogens further indicate that combining microorganisms with complementary modes of action may enhance the

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consistency and spectrum of biological control, thereby increasing the reliability of bioinput-based disease management programs.

3.2 Effect of the microbial consortium on soybean grain yield

The analysis of variance performed under a randomized complete block design revealed a significant effect of the microbial consortium on soybean grain yield ($P < 0.05$), with a coefficient of variation (CV) of 2.06%, indicating high experimental precision and excellent data reliability (Table 5).

Table 5. Analysis of variance (mean squares) for soybean grain yield evaluated in five commercial production areas in southwestern Paraná State, Brazil, during the 2024/2025 growing season.

Source of variation	Degrees of freedom	Grain yield
Blocks	4	126,561.4
Treatments	1	233,478.4*
Residual	4	8,535.4
Mean	–	**4,475.2**
CV (%)	–	**2.06**

Source: The authors.

Soybean plants treated with the microbial consortium produced an average grain yield of 4,628.0 kg ha^{-1}, which was significantly higher than the untreated control (4,322.4 kg ha^{-1}) according to Tukey's test (Table 6).

Table 6. Mean soybean grain yield obtained under commercial field conditions with and without seed-furrow application of the microbial consortium.

Treatment	Grain yield (kg ha^{-1})
Microbial consortium	**4,628.0 a**
Untreated control	**4,322.4 b**

Source: The authors.

Because grain yield and thousand-grain weight were determined from a single harvest at each experimental site, these variables were analyzed using a randomized complete block design, considering the five locations as blocks and treatments as the fixed factor. This statistical approach effectively accounted for environmental variability among locations while allowing robust evaluation of the average treatment effect. Conversely, the number of pods per plant and the number of seeds per pod were measured using replicated samples within each location and

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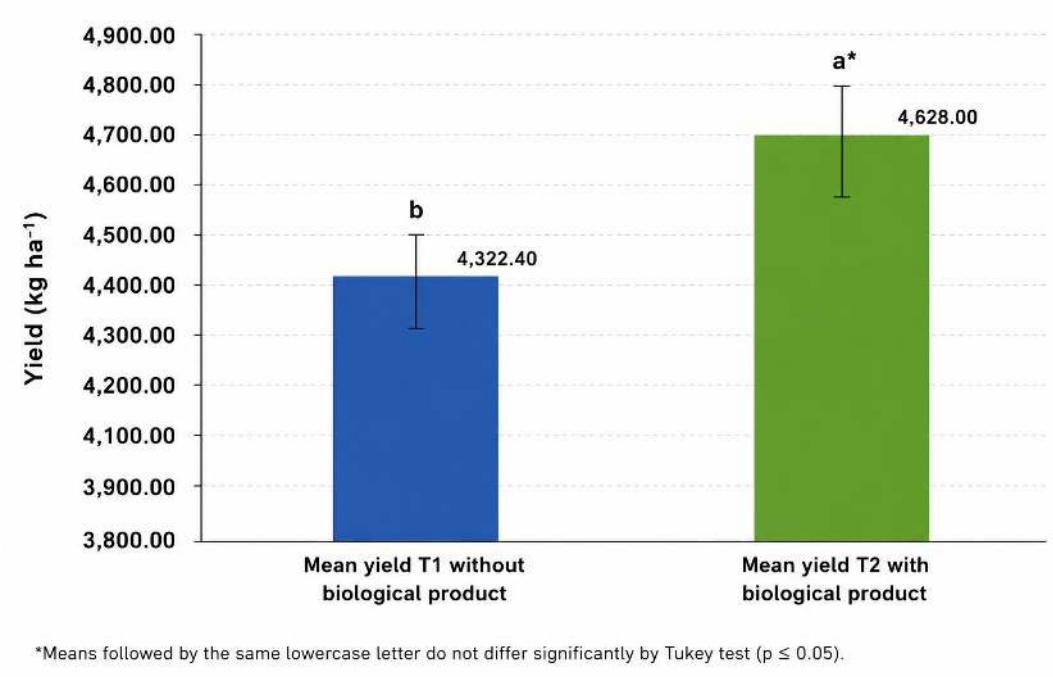
were therefore analyzed by two-way ANOVA, including the effects of treatment, environment, and treatment × environment interaction.

The microbial consortium increased soybean grain yield by an average of 305.6 kg ha^{-1}, corresponding to approximately 5.1 additional 60-kg bags ha^{-1}, representing a 7.1% increase over the untreated control (Table 6). From an agronomic perspective, this gain is highly relevant because even relatively small increases in grain yield substantially improve production profitability under commercial farming conditions. Furthermore, the consistency of the treatment response among the evaluated locations demonstrates that the beneficial effects of the biological consortium remained stable across different production environments, reinforcing the robustness of the proposed biological management strategy.

The superiority of the biological treatment is clearly illustrated in Figure 5, where soybean grain yield reached 4,628 kg ha^{-1} (77.13 bags ha^{-1}) compared with 4,322.4 kg ha^{-1} (72.04 bags ha^{-1}) in the untreated control. This increase of approximately 306 kg ha^{-1} demonstrates the capacity of beneficial microorganisms to improve crop performance under commercial production conditions.

Figure 5. Grain yield (kg ha^{-1}) of soybean under commercial field conditions with and without seed-furrow application of the microbial consortium.



*Means followed by the same lowercase letter do not differ significantly by Tukey test ($p \leq 0.05$).

Source: The authors.

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The observed increase in grain yield can be attributed to the synergistic interaction among the microorganisms composing the consortium, namely *Trichoderma afroharzianum*, *Bacillus subtilis*, *Bacillus velezensis*, *Pantoea agglomerans*, and *Bradyrhizobium japonicum*. These microorganisms are known to promote plant growth through complementary mechanisms, including biological control of phytopathogens, nutrient mobilization, phytohormone production, stimulation of root development, and enhancement of plant physiological performance (Alice, 2020).

Among the microorganisms evaluated, *Bradyrhizobium japonicum* plays a central role in soybean production due to its remarkable capacity to establish symbiosis with soybean roots and perform biological nitrogen fixation (Alice, 2020; Ferreira et al., 2019). As illustrated in Figure 6**,** treated plants developed abundant root nodules, confirming the successful establishment of the symbiotic association between *Bradyrhizobium* and soybean roots. This biological process enables the conversion of atmospheric nitrogen into ammonia through the activity of the nitrogenase enzyme, supplying nitrogen in forms readily assimilated by plants while substantially reducing the need for mineral nitrogen fertilization.

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Figure 6. Root nodulation of soybean plants inoculated with *Bradyrhizobium japonicum*, illustrating the formation of active nitrogen-fixing nodules resulting from the symbiotic association between soybean roots and rhizobial bacteria.



Source: The authors.

Root nodules constitute specialized organs in which biological nitrogen fixation takes place. Within these structures, atmospheric nitrogen (N_2) is converted into ammonia and subsequently incorporated into amino acids and proteins essential for soybean growth and grain production. Consequently, the efficiency of biological nitrogen fixation directly influences vegetative growth, reproductive development, and final grain yield (Alves et al., 2003). The extensive nodulation observed in the present study (Figure 6) therefore provides a physiological explanation for the superior agronomic performance of the treated plants.

Previous studies conducted under Brazilian field conditions have similarly reported positive effects of biological inputs on soybean productivity. Experiments performed in the Cerrado region demonstrated that the combined use of *Bradyrhizobium* spp. and *Trichoderma* spp. increased soybean grain yield by up to 17.5% compared with conventional crop management (Leão de Matos, 2022). These findings corroborate the present results and reinforce the potential of beneficial microorganisms to enhance crop performance under diverse environmental conditions.

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In addition to biological nitrogen fixation, the combined application of *Trichoderma*, *Bacillus*, *Pantoea*, and *Bradyrhizobium* likely improved nutrient availability, suppressed soilborne pathogens, and stimulated plant physiological processes, thereby creating more favorable conditions for soybean growth throughout the crop cycle. The complementary activities of these microorganisms explain the significant increase in grain yield observed in the present study and further demonstrate the effectiveness of microbial consortia as sustainable tools for modern soybean production systems (Santos et al., 2023).

The integrated evaluation of yield components (Table 7) indicates that the higher grain yield obtained with the microbial consortium resulted primarily from improvements in reproductive performance rather than changes in grain size. Consequently, a detailed analysis of the individual yield components provides valuable insight into the physiological mechanisms responsible for the productivity gains observed under commercial field conditions.

Table 7. Yield components of soybean cultivated with and without seed-furrow application of the microbial consortium, including number of pods per plant (NPP), number of seeds per pod (NSP), thousand-grain weight (TGW), grain yield (kg ha^{-1}), and grain yield (60-kg bags ha^{-1}).

Treatment	Number of pods per plant (NPP)	Number of seeds per pod (NSP)	Thousand-grain weight (kg)	Grain yield (kg ha^{-1})	Grain yield (60-kg bags ha^{-1})
Microbial consortium	44.02	2.442	0.1750	4,628.0	77.13
Untreated control	41.67	2.422	0.1740	4,322.4	72.04

Source: The authors.

3.3 Yield components

3.3.1 Number of pods per plant (NPP)

The two-way analysis of variance revealed a significant effect of the microbial consortium on the number of pods per plant (NPP) ($P < 0.05$), whereas neither the environment nor the treatment × environment interaction was significant (Table 8). These results indicate that the response to biological application was consistent

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across the five experimental locations, demonstrating the stability of the treatment under different environmental conditions. The absence of a significant interaction further suggests that the beneficial effect of the microbial consortium was maintained regardless of local environmental variability.

Table 8. Analysis of variance (mean squares) for the number of pods per plant (NPP) and number of seeds per pod (NSP) of soybean cultivated in five commercial production areas in southwestern Paraná State, Brazil, during the 2024/2025 growing season.

Source of variation	Degrees of freedom	NPP	NSP
Treatments	1	61.2563*	0.0024ns
Environments	4	2.1641ns	0.0019ns
Treatment × Environment	4	0.1806ns	0.0009ns
Residual	30	0.9631	0.0008
Mean	–	**43.8675**	**2.4243**
CV (%)	–	**2.24**	**1.14**

Source: The authors.

Soybean plants treated with the microbial consortium produced an average of 44.02 pods per plant, whereas the untreated control averaged 41.67 pods per plant (Table 9). This increase of approximately 2.35 pods per plant represents an improvement of approximately 5.6%, demonstrating that the biological treatment significantly enhanced the formation and retention of reproductive structures. According to Tukey's multiple comparison test, the treatments differed significantly at the 5% probability level (Table 9).

Table 9. Mean number of pods per plant (NPP) of soybean cultivated with and without seed-furrow application of the microbial consortium.

Treatment	Number of pods per plant
Microbial consortium	**44.02 a**
Untreated control	**41.67 b**

Source: The authors.

The superiority of the treated plants is also evident in Figure 7, which illustrates the higher number of pods per plant obtained following seed-furrow application of the microbial consortium. Among the yield components evaluated in the present study, NPP was the most responsive variable to biological treatment, indicating that the observed increase in grain yield was primarily associated with greater pod formation rather than changes in other reproductive components.

Figure 7. Number of pods per plant (NPP) in soybean cultivated with and without seed-furrow application of the microbial consortium.

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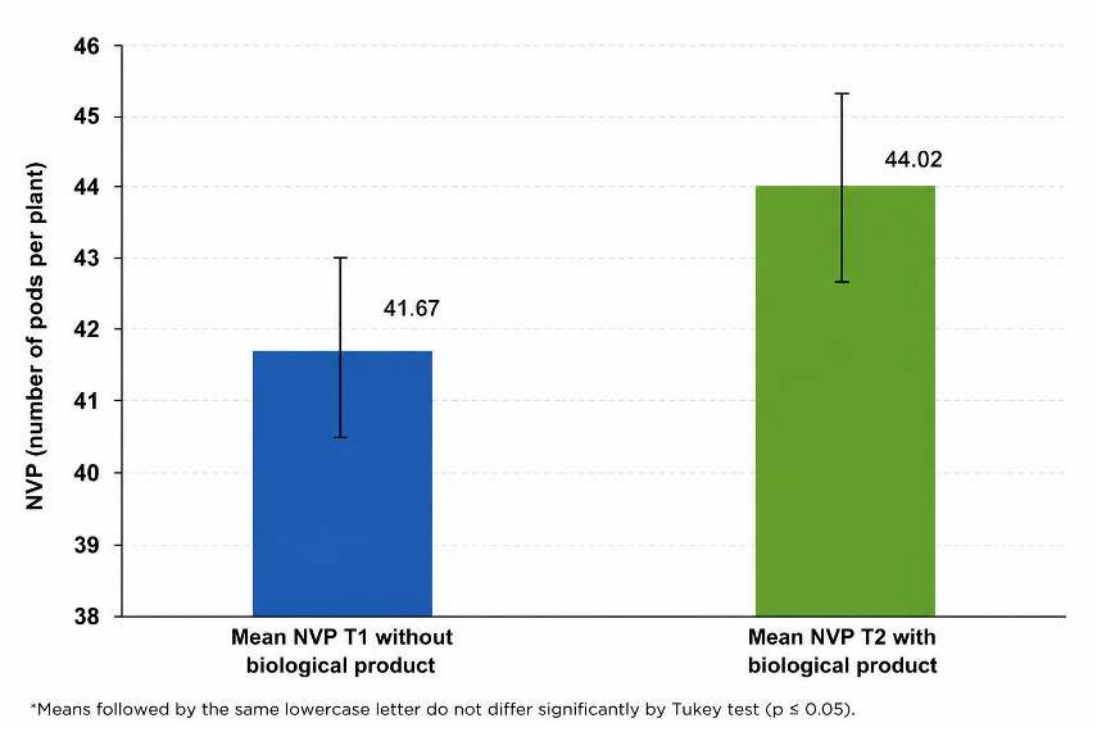

Source: The authors.

The positive effect of the microbial consortium on reproductive development is further illustrated in Figure 8, where treated plants exhibited visibly greater pod formation than untreated plants. The higher density of reproductive structures observed in the inoculated plants confirms the beneficial influence of the microbial consortium on soybean reproductive performance under commercial field conditions.

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Figure 8. Representative soybean plants illustrating the effect of microbial consortium application on pod formation. Plants treated with biological inputs exhibited greater pod production than untreated plants, demonstrating the positive influence of beneficial microorganisms on reproductive development.



Source: The authors.

The increased number of pods per plant suggests that biological treatment favored both flower retention and pod set throughout the reproductive cycle. Several physiological mechanisms may explain this response, including enhanced nutrient acquisition, improved biological nitrogen fixation, phytohormone production, and mitigation of biotic and abiotic stresses. Together, these mechanisms contribute to reducing flower and pod abortion, thereby increasing the number of pods retained until harvest.

The 5.6% increase in NPP observed in the present study agrees with previous reports demonstrating that microbial inoculation and co-inoculation primarily affect reproductive components associated with pod formation and retention. Field experiments using *Bradyrhizobium* spp. in combination with *Azospirillum brasilense* have consistently reported significant increases in grain yield accompanied by improvements in reproductive traits, particularly pod number, whereas other yield components remained comparatively stable. Costa et al. (2021) reported that co-inoculation increased agronomic efficiency mainly through

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improvements in reproductive development rather than modifications in seed characteristics, corroborating the pattern observed in the present study.

The contribution of *Trichoderma* spp. to increased pod production is likely associated with its multifunctional biological activity. Besides suppressing soilborne pathogens through mycoparasitism and antibiosis, *Trichoderma* improves nutrient uptake, modulates plant hormone balance, and stimulates root growth, resulting in greater plant vigor during reproductive development. Studies conducted under both greenhouse and field conditions have demonstrated that *Trichoderma* spp. significantly increase soybean productivity while promoting beneficial changes in rhizosphere microbial communities, ultimately favoring pod formation and retention (Wang et al., 2023).

Similarly, species of the genus *Bacillus* are widely recognized as plant growth-promoting rhizobacteria capable of enhancing root development, increasing nutrient availability, suppressing soilborne diseases, and improving tolerance to environmental stresses. These combined effects create favorable physiological conditions that reduce reproductive abortion and increase pod retention throughout the crop cycle. In soybean, treatments based on *Bacillus* spp., either alone or combined with *Trichoderma*, have consistently resulted in greater plant vigor, lower root disease incidence, and higher grain yield, supporting the increase in NPP observed in the present study (Santos et al., 2023).

Although fewer studies have specifically evaluated *Pantoea agglomerans* in soybean, this bacterium possesses several plant growth-promoting characteristics, including indole-3-acetic acid production, phosphate solubilization, biological nitrogen fixation, and efficient rhizosphere colonization. These attributes complement the activities of *Trichoderma*, *Bacillus*, and *Bradyrhizobium*, contributing to improved plant nutrition and physiological performance. Moreover, meta-analyses have demonstrated that microbial seed treatments generally enhance crop establishment, disease suppression, and grain yield across several agricultural species, supporting the inclusion of *Pantoea* within multifunctional microbial consortia (Pereira et al., 2021).

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Overall, the increase in the number of pods per plant observed in this study is consistent with the current understanding that biological inputs primarily enhance reproductive performance through the combined effects of biological control, plant growth promotion, improved nutrient acquisition, and hormonal regulation. Therefore, NPP emerged as the yield component most responsive to the microbial consortium and largely explains the significant increase in soybean grain yield obtained under commercial production conditions. These findings reinforce the potential of microbial consortia as effective and sustainable tools for improving soybean productivity across different production environments (Wang et al., 2023).

3.3.2 Number of seeds per pod (NSP)

Unlike the number of pods per plant, the average number of seeds per pod (NSP) was not significantly affected by the application of the microbial consortium. The two-way analysis of variance showed no significant effects of treatment, environment, or treatment × environment interaction (Table 8), indicating that this yield component remained stable across all evaluated locations. Mean values were 2.44 seeds per pod in the biologically treated plants and 2.42 seeds per pod in the untreated control, confirming the limited responsiveness of this variable to biological management practices.

The results presented in Figure 9 further illustrate the remarkable stability of NSP between treatments. Despite the positive effects of the microbial consortium on grain yield and pod formation, the average number of seeds per pod remained virtually unchanged. This behavior is consistent with the biological nature of this trait, which is predominantly controlled by genetic factors and generally exhibits low phenotypic plasticity in response to crop management.

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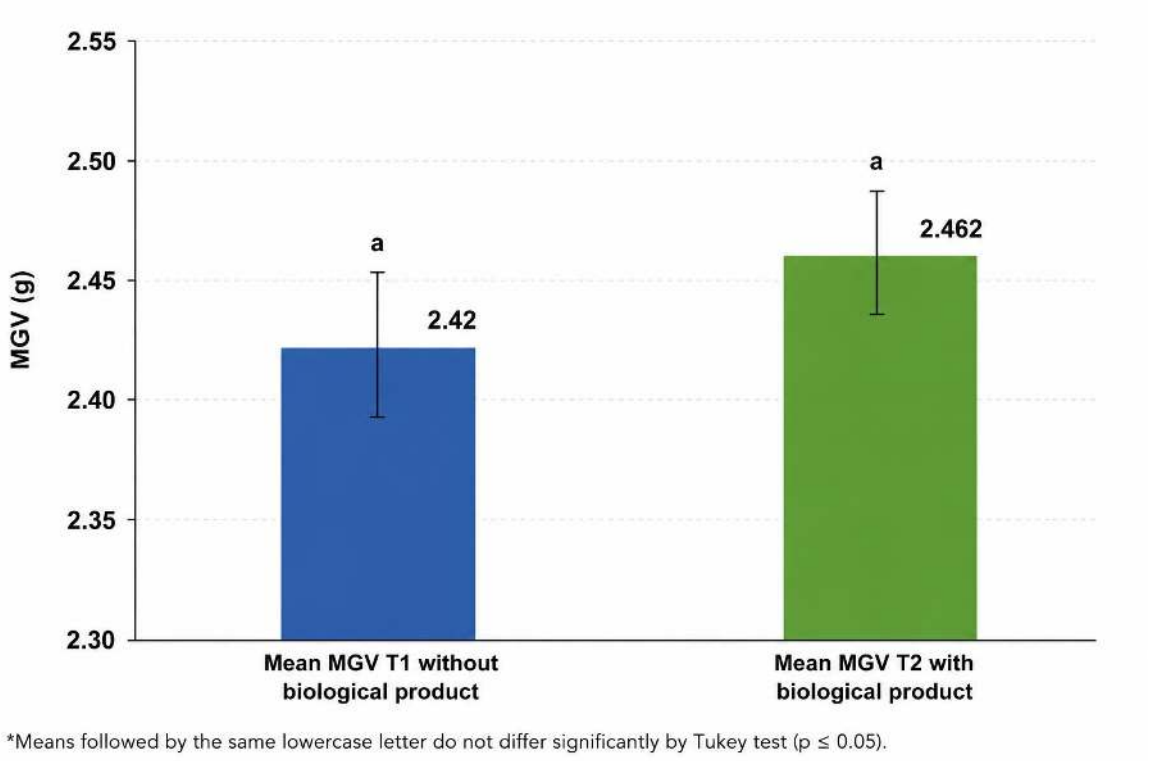
Figure 9. Mean number of seeds per pod (NSP) in soybean cultivated with and without seed-furrow application of the microbial consortium.



Source: The authors.

Previous genetic studies have demonstrated that the number of seeds per pod is largely regulated by specific genomic regions, including loci such as **Ln/JAG1**, and therefore tends to be considerably less responsive to environmental conditions or agronomic practices than other yield components, such as pod number, branching, or node production. Consequently, management strategies capable of substantially increasing grain yield frequently do so without significantly altering the number of seeds produced per pod (Wang et al., 2024).

This interpretation is consistent with reports evaluating microbial inoculation in soybean. Several field studies involving co-inoculation with *Bradyrhizobium* spp. and *Azospirillum brasilense* have reported significant increases in grain yield and improvements in reproductive development while observing no statistical changes in the number of seeds per pod (Silva et al., 2020; Tormena, 2021; Costa et al., 2020). These findings indicate that beneficial microorganisms generally exert a greater

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influence on reproductive processes associated with flower retention, pod set, and pod maintenance than on the internal development of individual pods.

From a physiological perspective, microorganisms such as *Trichoderma* spp. and *Bacillus* spp. promote plant growth by improving nutrient availability, stimulating phytohormone production, enhancing root development, and increasing tolerance to biotic and abiotic stresses. These mechanisms primarily favor the establishment and maintenance of reproductive structures, thereby increasing the total number of pods per plant rather than modifying the number of seeds contained within each pod. Therefore, the stability of NSP observed in the present study is biologically plausible and agrees with previous reports demonstrating that microbial inoculation mainly affects reproductive efficiency without altering genetically controlled yield components (Zhang et al., 2024).

Overall, the absence of significant differences in NSP indicates that the increase in soybean productivity observed in the present study was not associated with changes in seed number per pod but rather with improvements in other yield components, particularly the greater number of pods retained per plant.

3.3.3 Thousand-grain weight (TGW)

The thousand-grain weight (TGW), analyzed using a randomized complete block design with the experimental locations considered as blocks, was not significantly affected by the application of the microbial consortium. This result indicates that biological treatment did not directly influence individual grain weight and that the observed increase in grain yield cannot be attributed to changes in this yield component. Nevertheless, the treated plants exhibited a slight numerical increase in TGW (0.1750 kg) compared with the untreated control (0.1740 kg), as shown in Figure 10**.**

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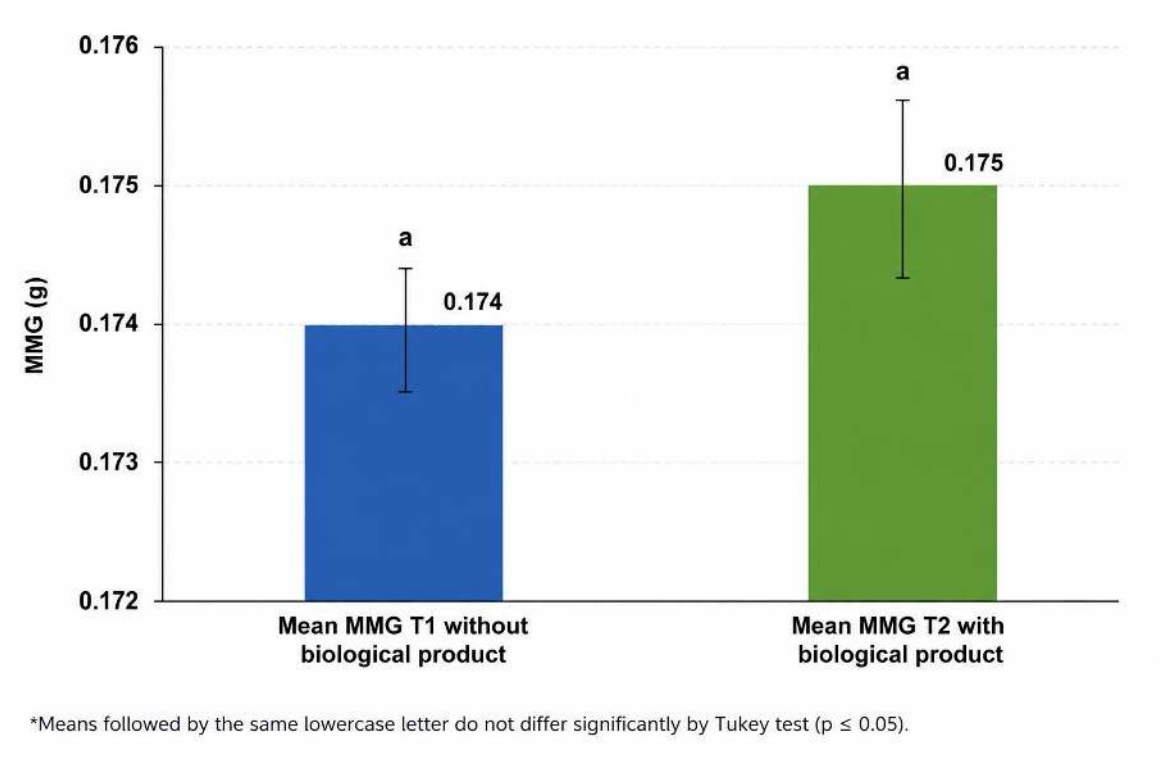
Figure 10. Thousand-grain weight (TGW/MMG) of soybean cultivated with and without seed-furrow application of the microbial consortium.



Source: The authors.

Although modest, this numerical increase may indicate a slight improvement in grain filling associated with better physiological balance and nutrient acquisition promoted by the interaction between beneficial microorganisms in the rhizosphere. However, the magnitude of this difference was insufficient to produce statistical significance under the experimental conditions evaluated.

Thousand-grain weight is recognized as a trait strongly influenced by genotype, although moderate phenotypic plasticity may occur depending on environmental conditions during grain filling. Factors such as water availability, plant nutrition, population density, and photosynthetic efficiency may indirectly affect final grain weight. Likewise, beneficial microorganisms capable of improving phosphorus solubilization, biological nitrogen fixation, and nutrient uptake may contribute to grain filling by increasing the availability of assimilates during reproductive development. In the present study, however, these effects were not sufficient to significantly modify TGW.

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Despite the absence of statistical significance, the slight increase observed in TGW may still have contributed to the higher grain yield when considered together with the substantial increase in pod number. Previous studies have reported that relatively small improvements in thousand-grain weight can contribute to overall yield gains when associated with favorable changes in other yield components. Silva et al. (2019), for example, observed that increases of less than 1% in TGW contributed to significant improvements in soybean productivity when combined with a greater number of pods per plant following the application of biological inputs.

Taken together, the results demonstrate that the superior grain yield obtained with the microbial consortium was primarily associated with enhanced reproductive performance, particularly the increased number of pods per plant, whereas the number of seeds per pod and thousand-grain weight remained essentially unchanged. These findings indicate that the beneficial microorganisms evaluated in the present study predominantly influenced reproductive establishment and pod retention rather than seed formation or grain filling, providing a physiological explanation for the productivity gains observed under commercial soybean production conditions.

4. CONCLUSION

The present study demonstrated that the seed-furrow application of a microbial consortium composed of *Trichoderma afroharzianum*, *Bacillus subtilis*, *Bacillus velezensis*, *Pantoea agglomerans*, and *Bradyrhizobium japonicum* represents an effective biological strategy for improving soybean performance under commercial field conditions.

Under laboratory conditions, the evaluated microorganisms exhibited broad-spectrum antagonistic activity against the major soybean phytopathogens, confirming their potential for biological disease suppression through complementary mechanisms, including competition, antibiosis, and mycoparasitism.

Under field conditions, the microbial consortium significantly increased soybean grain yield by approximately 306 kg ha^{-1} (5.1 bags ha^{-1}), corresponding to a 7.1% increase compared with the untreated control. This positive response was

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consistent across the five experimental locations, demonstrating the stability and reliability of the biological treatment under different production environments.

The increase in grain yield was primarily associated with a significant improvement in the number of pods per plant, whereas the number of seeds per pod and thousand-grain weight were not significantly affected. These findings indicate that the microbial consortium predominantly enhanced reproductive establishment and pod retention rather than seed formation or grain filling.

Overall, the integration of beneficial microorganisms with complementary biological functions promoted simultaneous improvements in plant nutrition, biological nitrogen fixation, rhizosphere competence, and pathogen suppression, resulting in greater crop productivity. Therefore, the evaluated microbial consortium represents a promising and sustainable alternative for soybean production, contributing to higher productivity while supporting strategies aimed at reducing dependence on conventional chemical inputs and improving the sustainability of modern agricultural systems.

Finally, further studies should investigate the long-term performance of these microbial consortia under different edaphoclimatic conditions, soybean genotypes, and management systems, as well as their interactions with indigenous soil microbiota, in order to optimize their agronomic efficiency and broaden their application in commercial soybean production.

REFERENCES

AGROFIT: SISTEMA DE AGROTÓXICOS FITOSSANITÁRIOS. Ministério da Agricultura, Pecuária e Abastecimento – MAPA. Disponível em: https://agrofit.agricultura.gov.br/agrofit_cons/principal_agrofit_cons. Acesso em: 5 set. 2025.

AGROPLANNING. Bioinsumos: tendências e perspectivas de adoção no Brasil. São Paulo, 2025.

ALICE, A. Bioinsumos e aumento de produtividade em soja: efeitos sinérgicos de microrganismos. Revista Brasileira de Ciência Agrária, v. 15, n. 2, p. 45–56, 2020.

ALVES, B. J. R.; BODDEY, R. M.; URQUIAGA, S. Fixação biológica de nitrogênio em leguminosas cultivadas no Brasil. Pesquisa Agropecuária Brasileira, v. 38, n. 3, p. 313–323, 2003.

REMUNOM
ISSN 2178-6925

Received: 13/03/2026 - **Accepted:** 30/07/2026
Vol: 13.07
DOI: 10.66104/r2jqvk41
Pages: 1-31

BARBOSA, P.; RODRIGUES, R.; CABRAL, A. Impacto de pragas e patógenos na agricultura: desafios para a sustentabilidade. Revista Brasileira de Fitopatologia, Brasília, v. 48, n. 2, p. 101–118, 2023.

BATISTA, M. A. et al. Soja: produção e mercado mundial. Informações Econômicas, São Paulo, v. 50, n. 6, p. 5–12, 2020.

BHERING, L. L. Rbio: a tool for biometric and statistical analysis using the R platform. Crop Breeding and Applied Biotechnology, v. 17, n. 2, p. 187-190, 2017.

BETTIOL, W.; MEDEIROS, F. C. L. Bioinsumos na agricultura brasileira: situação atual e perspectivas. Cadernos de Ciência & Tecnologia, Brasília, v. 40, p. 1–22, 2023.

BRASIL. Decreto nº 4.074, de 4 de janeiro de 2002. Regulamenta a Lei nº 7.802, de 11 de julho de 1989. Diário Oficial da União, Brasília, 8 jan. 2002.

BRASIL. Lei nº 7.802, de 11 de julho de 1989. Dispõe sobre agrotóxicos e seus componentes. Diário Oficial da União, Brasília, 12 jul. 1989.

CAMARGO, L. E. A. Genética e resistência de plantas a patógenos. Piracicaba: ESALQ/USP, 2018.

CONAB. Acompanhamento da safra brasileira de grãos: safra 2020/21. Brasília: Companhia Nacional de Abastecimento, 2021.

CONAB. Acompanhamento da safra brasileira de grãos 2024/25 – 12º levantamento. Brasília: Companhia Nacional de Abastecimento, 2025.

COSTA, M.; SILVA, R.; PEREIRA, L. Coinoculação de Bradyrhizobium e Azospirillum: efeitos sobre rendimento e componentes da soja. Revista Brasileira de Ciência do Solo, v. 44, n. 1, p. 101–112, 2020.

EMBRAPA. CENTRO NACIONAL DE PESQUISA DE SOLOS. Sistema brasileiro de classificação de solos. 2. ed. Rio de Janeiro: Embrapa Solos, 2006.

EMBRAPA. EMPRESA BRASILEIRA DE PESQUISA AGROPECUÁRIA. Tecnologias de produção de soja: região central do Brasil 2014. Londrina: Embrapa Soja, 2013.

FARIA, J. A.; OLIVEIRA, L. F. Interações entre bioinoculantes e fungicidas em soja: efeitos sobre nodulação e produtividade. Revista Brasileira de Agrociência, v. 27, n. 2, p. 123–134, 2021.

PEREIRA, R. T.; MENDES, F.; COSTA, L. Efeito de bioinsumos sobre número de vagens e grãos por planta em soja. Journal of Plant Production, v. 13, n. 1, p. 25–36, 2021.

REMUNOM
ISSN 2178-6925

Received: 13/03/2026 - **Accepted:** 30/07/2026
Vol: 13.07
DOI: 10.66104/r2jqvk41
Pages: 1-31

SANTOS, J. P.; ALMEIDA, R. C.; COSTA, L. F. Sinergia de microrganismos na promoção do crescimento de soja: estudo de caso. Journal of Agricultural Microbiology, v. 9, n. 1, p. 33–47, 2023.

SANTOS, P.; ALVES, R.; COSTA, M. Bacillus e Trichoderma aplicados em consórcio: impacto sobre vigor, sanidade radicular e rendimento em soja. Journal of Applied Agricultural Science, v. 19, n. 2, p. 145–159, 2023.

SILVA, T.; OLIVEIRA, F.; PEREIRA, R. Componentes de rendimento em soja: estabilidade do número de grãos por vagem frente a manejo biológico. Journal of Plant Production, v. 12, n. 4, p. 321–332, 2020.

TORMENA, C. A. Efeitos da coinoculação de microrganismos promotores de crescimento em soja: avaliação de componentes de rendimento. Scientia Agricola, v. 78, n. 5, p. 401–412, 2021.

WANG, Y.; LI, X.; ZHANG, J. Trichoderma and Pantoea spp. for enhanced reproductive performance and yield in soybean. Crop Protection, v. 162, p. 105–116, 2023.

Wang, Q.; Zhang, W.; Xu, W.; Zhang, H.; Liu, X.; Chen, X.; Chen, H. Genome-Wide Association Study and Identification of Candidate Genes Associated with Seed Number per Pod in Soybean. International Journal of Molecular Sciences, v. 25, n. 5, artigo 2536, 2024. DOI: 10.3390/ijms25052536

ZHANG, L.; CHEN, H.; LIU, X. Influência de bioinoculantes sobre pegamento floral e estabilidade de grãos por vagem em soja. Frontiers in Plant Science, v. 15, p. 1124–1135, 2024.