CC BY

Research Article

Plant growth-promoting bacteria from the Cerrado enhance maize development[1]

Aline Cristina Mendes Façanha[2], Wendel Gabriel Magalhães Vieira[2], Nathalia Morais Ventura[2], Leandro Coutinho Alho[2], Edmilson Júnio Medeiros Caetano[2], Carlos Augusto Cavalcante de Oliveira[3], Adriano Stephan Nascente[3]

ABSTRACT

Maize intensive cultivation with excessive fertilizer use generates environmental impacts. Plant growth-promoting bacteria offer a sustainable alternative by favoring nitrogen fixation, phosphorus solubilization, and phytohormone production. This study aimed to evaluate the effect of microorganisms previously recognized as growth promoters in rice on maize biomass and yield. The experiment was conducted under laboratory and greenhouse conditions, in a completely randomized design, with 13 treatments (12 microorganisms and one control). *Lysinibacillus boronitolerans* (BRM 71995) promoted the greatest increase in shoot dry mass (48.64 %, compared to the control), whereas *Acinetobacter* sp. (BRM 71990) stood out for root dry mass (217.12 %, compared to the control). For 100-grain weight, *Herbaspirillum seropedicae* (BRM 71996) increased values by 110.40 %, compared to *Bacillus velezensis* (BRM 71986). *H. seropedicae* (BRM 71997) was responsible for the greatest productive gains, increasing the number of grains (57.35 %, compared to the control) and yield per pot (85.14 %, compared to the control).

KEYWORDS: *Herbaspirillum seropedicae*, *Zea mays* L., multifunctional microorganisms.

RESUMO

Bactérias promotoras de crescimento vegetal do Cerrado favorecem o desenvolvimento de milho

O cultivo intensivo de milho, associado ao uso excessivo de fertilizantes, gera impactos ambientais. Bactérias promotoras do crescimento de plantas representam uma alternativa sustentável, favorecendo a fixação de nitrogênio, solubilização de fósforo e produção de fitormônios. Objetivou-se avaliar o efeito de microrganismos previamente reconhecidos como promotores de crescimento em arroz sobre a biomassa e a produtividade de milho. O experimento foi conduzido em laboratório e casa de vegetação, em delineamento inteiramente casualizado, com 13 tratamentos (12 microrganismos e um controle). *Lysinibacillus boronitolerans* (BRM 71995) promoveu o maior incremento na massa seca da parte aérea (48,64 %, em relação ao controle), enquanto *Acinetobacter* sp. (BRM 71990) destacou-se para massa seca de raízes (217,12 %, em relação ao controle). Para a massa de 100 grãos, *Herbaspirillum seropedicae* (BRM 71996) aumentou os valores em 110,40 %, em comparação a *Bacillus velezensis* (BRM 71986). *H. seropedicae* (BRM 71997) foi responsável pelos maiores ganhos produtivos, aumentando o número de grãos (57,35 %, em relação ao controle) e a produtividade por vaso (85,14 %, em relação ao controle).

PALAVRAS-CHAVE: *Herbaspirillum seropedicae*, *Zea mays* L., microrganismos multifuncionais.

INTRODUCTION

Maize (*Zea mays* L.) is one of the most widely cultivated cereals in the world, playing an essential role in both human and animal nutrition (Kerchner et al. 2024). Yield is directly related to the use of agricultural technologies, efficient management, and adaptation to climate change, being favored by practices such as no-till farming and rational use of inputs, which enhance production efficiency (Wang & Hu 2021).

However, the excessive use of fertilizers, especially nitrogen and phosphorus, has generated serious environmental impacts, such as contamination of surface and groundwater, soil acidification, nutritional imbalance, and reduction of soil biodiversity (Hu & Liu 2024). Studies indicate that reductions in fertilizer application can be

[1] Received: Mar. 19, 2026. Accepted: July 02, 2026. Published: July 13, 2026. DOI: 10.1590/1983-40632026v5685549.
[2] Universidade Federal de Goiás, Escola de Agronomia, Goiânia, GO, Brazil.
E-mail/ORCID: alinefacanha@discente.ufg.br/0000-0002-4800-4620; wendelgabriel@discente.ufg.br/0000-0002-0899-7330; nathalia_morais@discente.ufg.br/0009-0008-4140-3232; leandro.alho@ifam.edu.br/0009-0001-9786-3042; junio2@discente.ufg.br/0000-0002-4836-7640.
[3] Empresa Brasileira de Pesquisa Agropecuária (Embrapa Arroz e Feijão), Santo Antônio de Goiás, GO, Brazil.
E-mail/ORCID: carlos.cavalcante@icen.ufpa.br/0000-0003-3058-4740; adriano.nascente@embrapa.br/0000-0002-6014-3797.
Editor: Luis Carlos Cunha Junior/Data Availability Statement: Research data are only made available by authors upon request.

implemented without significantly compromising yield, promoting greater sustainability and lower environmental impact (Zou et al. 2024).

Plant growth-promoting bacteria represent a promising alternative, benefiting crops through biological nitrogen fixation, phosphorus solubilization, and phytohormone production (Lopes & Albuquerque 2018). Their use contributes to more sustainable agricultural systems, preserving soil health, reducing environmental pollution, and increasing crop resilience and yield (Ansabayeva et al. 2025). These microorganisms also improve the absorption of essential nutrients (N, P, K, Zn) and produce phytohormones such as auxins, cytokinins, and gibberellins, which stimulate root and shoot growth (Glick et al. 2021). In addition, they modulate stress-related hormones such as abscisic acid, ethylene, and jasmonate, activating specific signaling pathways in plants (Jia et al. 2025).

Another relevant aspect is the induction of systemic resistance, which increases tolerance to pathogens through hormonal signaling (Gui et al. 2022). The suppression of phytopathogens also occurs through mechanisms such as antibiosis, enzyme and siderophore production, as well as competition for space and nutrients (Kumar et al. 2023). At the same time, these microorganisms contribute to tolerance to abiotic stresses and efficiently colonize plant tissues through strategies such as motility, adhesion, and evasion of plant defenses (Munir et al. 2022).

Cerrado (Brazilian Savanna), recognized as a global biodiversity hotspot, presents a great potential for the prospecting of new bioinputs, given the richness of its microbiota and the diversity of ecological interactions (Bandeira et al. 2025). Despite advances in bioinput prospecting, it is still necessary to intensify the search for new strains adapted to Cerrado conditions, where studies with bacteria remain scarce.

Based on this context, the following hypotheses were formulated: seed microbiolization with Cerrado-derived bacteria increases maize biomass and yield, compared to the uninoculated control; isolates combining multiple functional traits (nitrogen fixation, phosphate solubilization, indole-3-acetic acid production, biofilm formation) promote greater agronomic gains than isolates with fewer traits; and specific strains consistently improve both vegetative growth and yield, highlighting their potential as bioinoculants for sustainable maize production.

Thus, this study evaluated the potential of multifunctional microorganisms previously characterized as growth promoters in rice on maize biomass and yield under controlled conditions, validating their effects on growth and yield variables.

MATERIAL AND METHODS

The experiment was conducted in two environments: initially at the laboratory, and subsequently in a greenhouse, at the Embrapa Arroz e Feijão, in Santo Antônio de Goiás, Goiás state, Brazil, in 2025, where the climate is classified as Aw, characteristic of Tropical Savanna (Façanha et al. 2025).

The experimental design was completely randomized, with 13 treatments [12 microorganisms – BRM 71992 (*Herbaspirillum seropedicae*); BRM 71993 (*Rhizobium* sp.); BRM 71994 (*Bacillus subtilis*); BRM 71995 (*Lysinibacillus boronitolerans*); BRM 71996 (*Herbaspirillum seropedicae*); BRM 71997 (*Herbaspirillum seropedicae*); BRM 71986 (*Bacillus velezensis*); BRM 71987 (*Pseudomonas putida*); BRM 71988 (*Acinetobacter* sp.); BRM 71989 (*Stenotrophomonas* sp.); BRM 71990 (*Acinetobacter* sp.); BRM 71991 (*Pantoea* sp.) – and one control with sterilized distilled water], each replicated four times. The bacterial isolates were previously selected under laboratory conditions and demonstrated potential for plant growth promotion, including indole-3-acetic acid (IAA) production, biological nitrogen fixation, phosphorus solubilization, and biofilm formation (Façanha et al. 2025). These isolates are preserved and deposited under their respective identifications in the multifunctional microorganism collection of the Embrapa Arroz e Feijão.

The bacterial isolates were stored in 2-mL Eppendorf® tubes. For cultivation, microorganisms were seeded in Petri dishes containing nutrient agar and incubated in a BOD chamber for 24 h, at 28 ºC. Colonies were transferred to Erlenmeyer flasks with 35 mL of nutrient broth and kept under agitation at 150 rpm and 28 ºC, for 24 h. The concentration was adjusted to optical density at 540 nm (OD540 = 0.5), equivalent to approximately 1×10^8 CFU mL^{-1}, according to spectrophotometer readings.

Seeds of the early maize hybrid FS533PWU were provided by the Embrapa Arroz e Feijão. Prior to inoculation, the seeds were surface-disinfested by immersion in 70 % ethanol for 1 min, followed

by sodium hypochlorite (NaOCl 7.5 %) for 3 min, and three successive washes in sterile distilled water (Cruz et al. 2022). Then, they were dried on absorbent paper for 24 h, inside a laminar flow chamber (Façanha et al. 2025).

Seed microbiolization followed the methodology of Cruz et al. (2022), adapted from Filippi et al. (2011), consisting of immersion in bacterial suspensions for 2 h under agitation. Additionally, the protocol of Sá et al. (2019) was adapted, with 50 seeds per replicate immersed in 10 mL of suspension. Control seeds were immersed in 10 mL of sterilized distilled water. All treatments were incubated in a shaker at 120 rpm and 26 ºC, for 2 h.

At 2 days before planting, pots (15 kg capacity) were filled with medium-textured Oxisol (Latossolo Vermelho; Santos et al. 2018), equivalent to a Typic Acrustox (USDA 2014), collected from the arable layer (0.00-0.20 m) and fertilized with 2 g of N-P_2O_5-K_2O (5-30-15). The soil chemical characteristics were: pH (H_2O) = 5.1; Ca^{2+} = 2.0 $mmol_c\ dm^{-3}$; Mg^{2+} = 0.9 $mmol_c\ dm^{-3}$; Al^{3+} = 0.0 $mmol_c\ dm^{-3}$; $H^+ + Al^{3+}$ = 2.7 $mmol_c\ dm^{-3}$; S = 5.0 mg dm^{-3}; organic carbon = 15.66 g kg^{-1}; Zn^{2+} = 1.8 mg dm^{-3}; Cu^{2+} = 1.9 mg dm^{-3}; Fe^{3+} = 53.20 mg dm^{-3}; Mn^{2+} = 28.9 mg dm^{-3}; CEC = 5.82 $mmol_c\ dm^{-3}$; base saturation (V%) = 53.65 %; $H^+ + Al^{3+}$/CEC = 46.39 %.

Sowing was performed with 10 microbiolized seeds per pot. At 10 days after emergence, thinning was carried out, leaving one plant per pot. At the V2 stage, 2 g of urea per pot were applied. Bacterial suspensions were reapplied at 14 and 21 days after emergence (100 mL pot^{-1}) directly to the soil surface. Weed management was manual, irrigation was daily, and no environmental control of temperature or humidity was used.

Yield variables included number of grains per pot, 100-grain weight, and grain yield per pot. The 100-grain weight was determined by counting and weighing a sample of 100 grains, with grain moisture corrected to 13 %. The total number of grains per pot (NGP) was estimated by dividing the total grain mass per pot by the mean mass of one grain, calculated from the 100-grain sample, according to the equation: NGP = total grain mass per pot/(100-grain weight/100). Grain yield per pot was determined by weighing all grains harvested from each pot, with grain moisture corrected to 13 %.

Data were subjected to analysis of variance (Anova) at 5 % of probability. When significant differences were detected, means were compared using the LSD test at 5 %. Assumptions of normality and homoscedasticity were verified using the Shapiro-Wilk and O'Neill-Mathews tests. In cases of violation, box-cox transformation was applied. Multivariate analysis was performed by principal component analysis (PCA) using the correlation matrix, with components selected by the Kaiser criterion (eigenvalues > 1). Statistical analyses and graphs were performed in the R software (R Core Team 2023), with the packages *ExpDes.pt*, *ggplot2* and *fpp*.

RESULTS AND DISCUSSION

Significant differences were observed among treatments, indicating that the shoot dry mass was strongly influenced by the inoculated microorganisms (Figure 1). BRM 71995 (*Lysinibacillus boronitolerans*), BRM 71997 (*Herbaspirillum seropedicae*), BRM 71990 (*Acinetobacter* sp.), BRM 71989 (*Stenotrophomonas* sp.), BRM 71992 (*H. seropedicae*), and BRM 71986 (*Bacillus velezensis*) promoted increases of 48.64, 36.34, 35.43, 34.54, 30.13, and 25.54 %, respectively, when compared to the uninoculated control.

Microorganisms associated with higher shoot dry mass typically exhibit biological nitrogen fixation, converting atmospheric N_2 into ammonium (NH_4^+), which is incorporated into amino acids, proteins, and chlorophyll (Guo et al. 2023, Aasfar et al. 2024). Enhanced nitrogen assimilation increases chlorophyll content and photosynthetic efficiency, resulting in greater shoot biomass (Tong 2025). Similar responses have been reported with *Bacillus* spp. under stress conditions (Azeem et al. 2022) and with *H. seropedicae* and *Azospirillum brasilense* under low nitrogen availability (Breda et al. 2020).

Root dry mass was also significantly affected (Figure 2). BRM 71990 (*Acinetobacter* sp.), BRM 71997 (*H. seropedicae*), BRM 71996 (*H. seropedicae*), and BRM 71989 (*Stenotrophomonas* sp.) increased the root dry mass by 217.12, 194.39, 184.54, and 131.82 %, respectively, when compared to the control.

The beneficial effects observed may be partially attributed to the ability of some isolates to synthesize indole-3-acetic acid (IAA), a

phytohormone previously detected during their functional characterization (Façanha et al. 2025). However, since IAA production was not assessed under the conditions of the present study, any association between this trait and the observed plant responses should be interpreted with caution and considered a potential, rather than definitive, mechanism (Etesami & Glick 2024). Similar mechanisms have been described for *Pseudomonas* spp. (Zhang et al. 2021) and *Acinetobacter pitii*, which increased root biomass in maize seedlings (Josephine & Thomas 2022).

For 100-grain weight, no significant increases were observed relative to the control (Figure 3). In fact, BRM 71986 (*B. velezensis*) and BRM 71994 (*B. subtilis*) reduced the 100-grain weight by 38.43 and 36.71 %, respectively. Conversely, when compared to BRM 71986, BRM 71996 (*H. seropedicae*), BRM 71990 (*Acinetobacter* sp.), BRM 71993 (*Rhizobium* sp.), BRM 71997 (*H. seropedicae*), BRM 71992 (*H. seropedicae*), and BRM 71989 (*Stenotrophomonas* sp.), the 100-grain weight increased by 110.40, 78.40, 73.86, 69.26, 68.14, and 56.40 %, respectively.

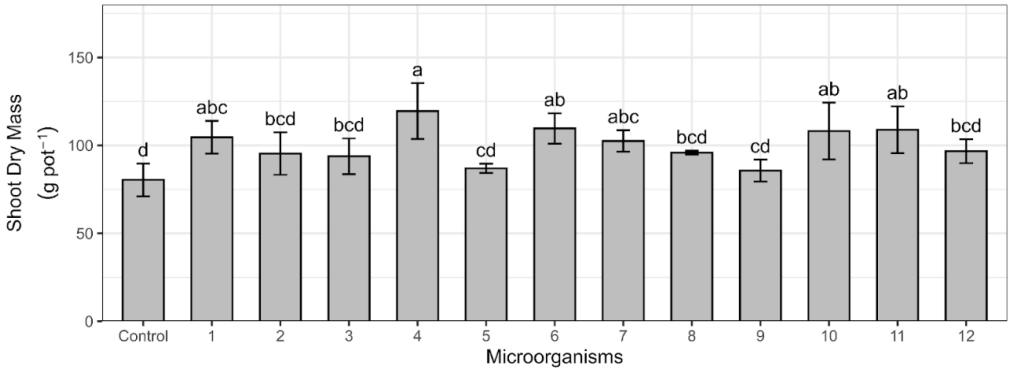

Figure 1. Shoot dry mass of maize (FS533PWU cultivar), as a function of the treatment with multifunctional microorganisms applied individually, at 102 days after sowing. Values followed by the same letter in the columns do not differ according to the LSD test. Treatments: control; 1) BRM 71992 (*Herbaspirillum seropedicae*); 2) BRM 71993 (*Rhizobium* sp.); 3) BRM 71994 (*Bacillus subtilis*); 4) BRM 71995 (*Lysinibacillus boronitolerans*); 5) BRM 71996 (*Herbaspirillum seropedicae*); 6) BRM 71997 (*Herbaspirillum seropedicae*); 7) BRM 71986 (*Bacillus velezensis*); 8) BRM 71987 (*Pseudomonas putida*); 9) BRM 71988 (*Acinetobacter* sp.); 10) BRM 71989 (*Stenotrophomonas* sp.); 11) BRM 71990 (*Acinetobacter* sp.); 12) BRM 71991 (*Pantoea* sp.).

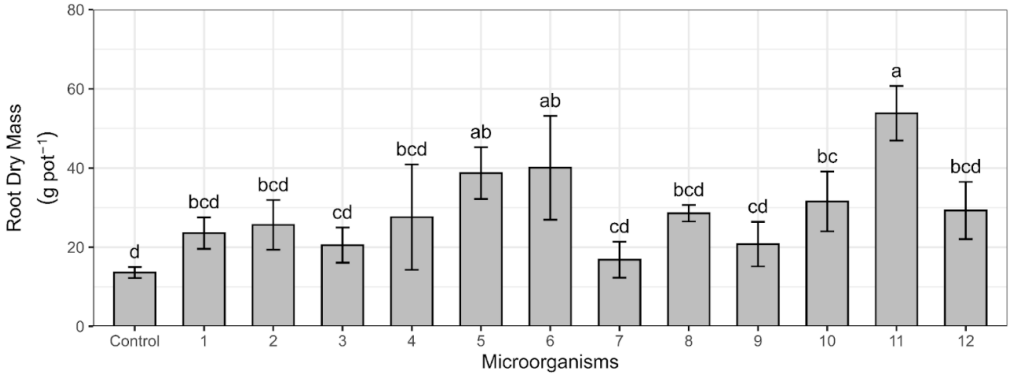

Figure 2. Root dry mass of maize (FS533PWU cultivar), as a function of treatment with multifunctional microorganisms applied individually, at 102 days after sowing. Values followed by the same letter in the columns do not differ according to the LSD test. Treatments: control; 1) BRM 71992 (*Herbaspirillum seropedicae*); 2) BRM 71993 (*Rhizobium* sp.); 3) BRM 71994 (*Bacillus subtilis*); 4) BRM 71995 (*Lysinibacillus boronitolerans*); 5) BRM 71996 (*Herbaspirillum seropedicae*); 6) BRM 71997 (*Herbaspirillum seropedicae*); 7) BRM 71986 (*Bacillus velezensis*); 8) BRM 71987 (*Pseudomonas putida*); 9) BRM 71988 (*Acinetobacter* sp.); 10) BRM 71989 (*Stenotrophomonas* sp.); 11) BRM 71990 (*Acinetobacter* sp.); 12) BRM 71991 (*Pantoea* sp.).

The reduction observed with BRM 71994 and BRM 71986 may be linked to their inability to solubilize phosphate (Façanha et al. 2025). Phosphorus is essential for ear formation and grain filling, and its deficiency reduces grain size (Kaleri et al. 2025). While *Bacillus* spp. often enhance yield (Oliveira-Paiva et al. 2024), some strains have been reported to reduce yield (Breedt et al. 2017, Ocwa et al. 2024), reinforcing the importance of strain selection.

The number of grains per pot showed significant differences (Figure 4). BRM 71997 (*H. seropedicae*), BRM 71989 (*Stenotrophomonas* sp.), and BRM 71987 (*Pseudomonas putida*) increased it by 57.35, 35.27, and 32.14 %, respectively.

The increase in the number of grains observed for some treatments may be associated with plant growth-promoting traits previously identified in the bacterial isolates, although these mechanisms were not evaluated under the conditions of the present study. BRM 71997 was previously characterized as exhibiting biological nitrogen fixation, a trait that may increase nitrogen availability to plants (Liao et al. 2024). BRM 71987 was previously shown to exhibit phosphorus solubilization, which may

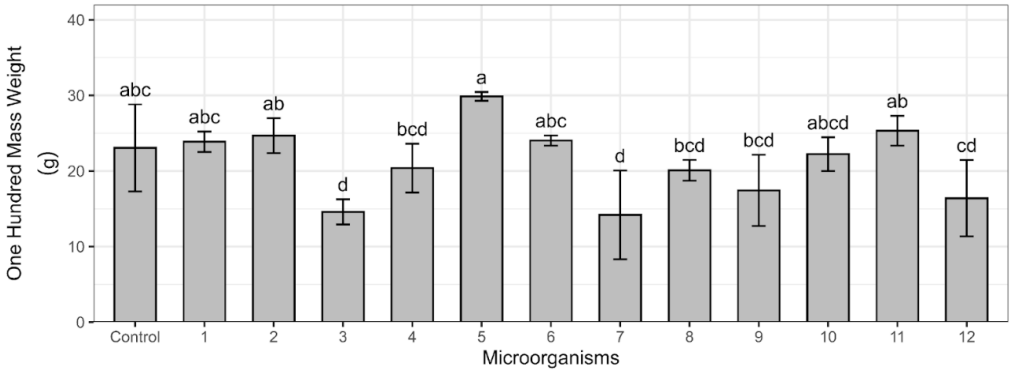

Figure 3. One hundred grain weight of maize (FS533PWU cultivar), as a function of treatment with multifunctional microorganisms applied individually, at 102 days after sowing. Values followed by the same letter in the columns do not differ according to the LSD test. Treatments: control; 1) BRM 71992 (*Herbaspirillum seropedicae*); 2) BRM 71993 (*Rhizobium* sp.); 3) BRM 71994 (*Bacillus subtilis*); 4) BRM 71995 (*Lysinibacillus boronitolerans*); 5) BRM 71996 (*Herbaspirillum seropedicae*); 6) BRM 71997 (*Herbaspirillum seropedicae*); 7) BRM 71986 (*Bacillus velezensis*); 8) BRM 71987 (*Pseudomonas putida*); 9) BRM 71988 (*Acinetobacter* sp.); 10) BRM 71989 (*Stenotrophomonas* sp.); 11) BRM 71990 (*Acinetobacter* sp.); 12) BRM 71991 (*Pantoea* sp.).

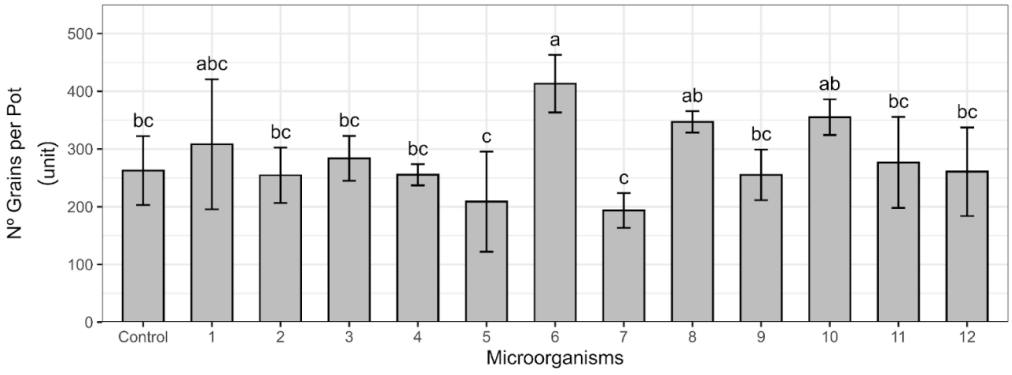

Figure 4. Number of grains per pot of maize (FS533PWU cultivar), as a function of treatment with multifunctional microorganisms applied individually, at 102 days after maize sowing. Values followed by the same letter in the columns do not differ according to the LSD test. Treatments: control; 1) BRM 71992 (*Herbaspirillum seropedicae*); 2) BRM 71993 (*Rhizobium* sp.); 3) BRM 71994 (*Bacillus subtilis*); 4) BRM 71995 (*Lysinibacillus boronitolerans*); 5) BRM 71996 (*Herbaspirillum seropedicae*); 6) BRM 71997 (*Herbaspirillum seropedicae*); 7) BRM 71986 (*Bacillus velezensis*); 8) BRM 71987 (*Pseudomonas putida*); 9) BRM 71988 (*Acinetobacter* sp.); 10) BRM 71989 (*Stenotrophomonas* sp.); 11) BRM 71990 (*Acinetobacter* sp.); 12) BRM 71991 (*Pantoea* sp.).

enhance phosphorus availability and support ATP synthesis and grain filling (Khaleeq et al. 2023). BRM 71989 was previously characterized as an indole-3-acetic acid (IAA)-producing and biofilm-forming isolate, traits that have been associated with improved root development and plant growth. However, additional biochemical analyses under the experimental conditions of the present study are required to confirm whether these mechanisms contributed to the observed responses.

Production per pot also differed significantly (Figure 5). BRM 71997 (*H. seropedicae*) increased yield by 85.14 %, when compared to the control, increasing the shoot and root dry mass, and raising the number of grains per pot, without altering the 100-grain weight.

The multivariate analysis confirmed these associations (Figure 6). The production per pot correlated strongly with number of grains per pot (r = 0.85), moderately with 100-grain weight

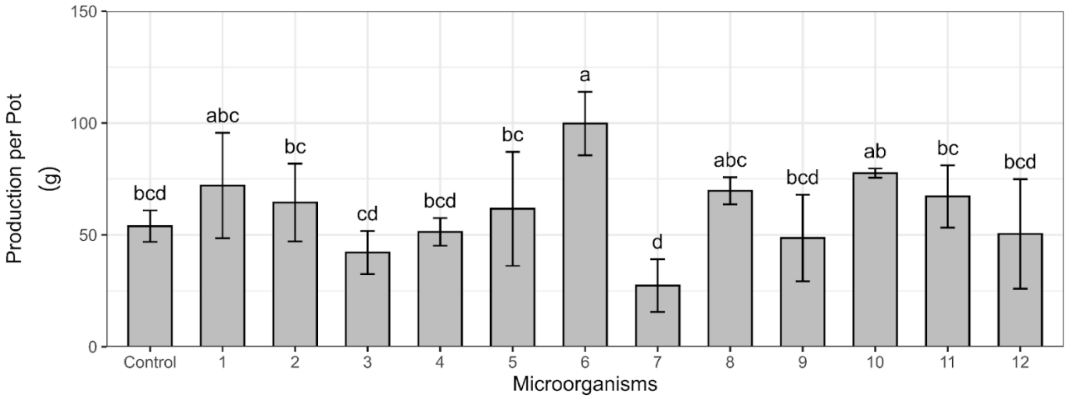

Figure 5. Production per pot of maize (FS533PWU cultivar), as a function of treatment with multifunctional microorganisms applied individually, at 102 days after sowing. Values followed by the same letter in the columns do not differ according to the LSD test. Treatments: control; 1) BRM 71992 (*Herbaspirillum seropedicae*); 2) BRM 71993 (*Rhizobium* sp.); 3) BRM 71994 (*Bacillus subtilis*); 4) BRM 71995 (*Lysinibacillus boronitolerans*); 5) BRM 71996 (*Herbaspirillum seropedicae*); 6) BRM 71997 (*Herbaspirillum seropedicae*); 7) BRM 71986 (*Bacillus velezensis*); 8) BRM 71987 (*Pseudomonas putida*); 9) BRM 71988 (*Acinetobacter* sp.); 10) BRM 71989 (*Stenotrophomonas* sp.); 11) BRM 71990 (*Acinetobacter* sp.); 12) BRM 71991 (*Pantoea* sp.).

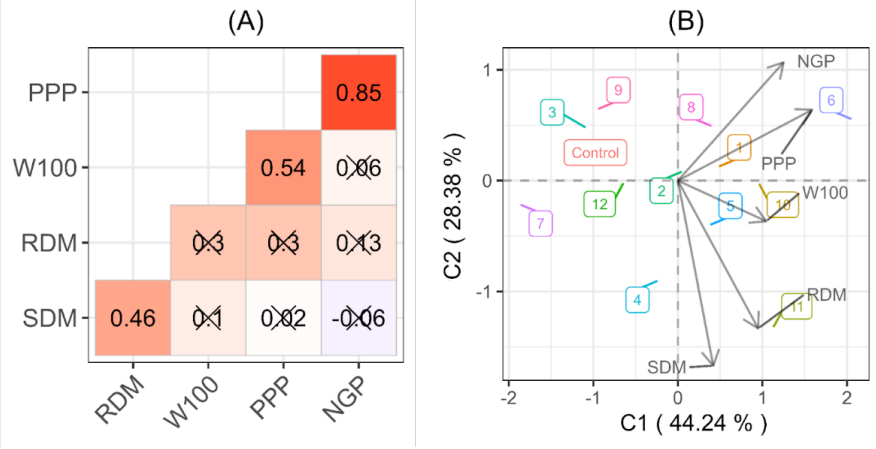

Figure 6. Correlation plot between treatments (A), and score and loading plot (B), showing correlations among variables and treatments. Variables: PPP: production per pot; NGP: number of grains per pot; W100: 100-grain weight; SDM: shoot dry mass; RDM: root dry mass. Treatments: control; 1) BRM 71992 (*Herbaspirillum seropedicae*); 2) BRM 71993 (*Rhizobium* sp.); 3) BRM 71994 (*Bacillus subtilis*); 4) BRM 71995 (*Lysinibacillus boronitolerans*); 5) BRM 71996 (*Herbaspirillum seropedicae*); 6) BRM 71997 (*Herbaspirillum seropedicae*); 7) BRM 71986 (*Bacillus velezensis*); 8) BRM 71987 (*Pseudomonas putida*); 9) BRM 71988 (*Acinetobacter* sp.); 10) BRM 71989 (*Stenotrophomonas* sp.); 11) BRM 71990 (*Acinetobacter* sp.); 12) BRM 71991 (*Pantoea* sp.).

(r = 0.54), and shoot dry mass with root dry mass (r = 0.46). BRM 71995 was associated with shoot dry mass, BRM 71990 with root dry mass, BRM 71996 and BRM 71989 with 100-grain weight, and BRM 71997 with number of grains per pot and production per pot.

In Figure 6B, the vectors indicate the contribution of each variable to the principal components: number of grains per pot and production per pot are strongly aligned with C1, reflecting their close association, whereas 100-grain weight contributes moderately to C2. This analysis highlights the isolates most related to yield components, particularly BRM 71997.

H. seropedicae possesses multiple IAA synthesis pathways, stimulating nitrogenase activity and biological nitrogen fixation (Andreozzi et al. 2019). As an endophyte, it contributes significantly to plant nitrogen accumulation (Alves et al. 2021). In greenhouse and field studies, inoculation with *H. seropedicae* increased root biomass, nutrient uptake, and grain yield (Baldotto et al. 2012, Ávila et al. 2020, Cunha et al. 2022, Silva et al. 2022).

The findings of this study highlight the potential of Cerrado-derived bacteria as sustainable bioinputs. Nevertheless, further biochemical characterization and multi-environment field trials are required to validate their agronomic efficiency and ensure a consistent performance across production systems.

CONCLUSIONS

1. Seed microbiolization with Cerrado-derived bacteria increased maize biomass and yield under controlled conditions;
2. BRM 71995 (*Lysinibacillus boronitolerans*) improved shoot dry mass, BRM 71990 (*Acinetobacter* sp.) enhanced root dry mass, and BRM 71997 (*Herbaspirillum seropedicae*) consistently increased the number of grains and yield per pot.

REFERENCES

AASFAR, A.; KADMIRI, I.; AZAROUAL, S.; LEMRISS, S.; MERNISSI, N.; BARGAZ, A.; ZEROUAL, Y.; HILALI, A. Agronomic advantage of bacterial biological nitrogen fixation on wheat plant growth under contrasting nitrogen and phosphorus regimes. *Frontiers in Plant Science*, v. 15, e1388775, 2024.

ALVES, G.; SANTOS, C.; ZILLI, J. R.; MARRIEL, I.; BREDA, F. F. A.; BODDEY, R.; REIS, V. Agronomic evaluation of *Herbaspirillum seropedicae* strain ZAE94 as an inoculant to improve maize yield in Brazil. *Pedosphere*, v. 31, n. 4, p. 583-595, 2021.

ANDREOZZI, A.; PRIETO, P.; MERCADO-BLANCO, J.; MONACO, S.; ZAMPIERI, E.; ROMANO, S.; VALE, G.; DEFEZ, R.; BIANCO, C. Efficient colonization of the endophytes *Herbaspirillum huttiense* RCA24 and *Enterobacter cloacae* RCA25 influences the physiological parameters of *Oryza sativa* L. cv. Baldo rice. *Environmental Microbiology*, v. 21, n. 9, p. 3489-3504, 2019.

ANSABAYEVA, A.; MAKHAMBETOV, M.; REBOUH, N.; ABDELKADER, M.; SAUDY, H.; HASSAN, K.; NASSER, M.; ALI, M.; EBRAHIM, M. Plant growth-promoting microbes for resilient farming systems: mitigating environmental stressors and boosting crops productivity: a review. *Horticulturae*, v. 11, n. 3, e260, 2025.

ÁVILA, J.; FERREIRA, J.; SANTOS, J.; ROCHA, P.; BALDANI, V. Green manure, seed inoculation with *Herbaspirillum seropedicae* and nitrogen fertilization on maize yield. *Revista Brasileira de Engenharia Agrícola e Ambiental*, v. 24, n. 9, p. 590-595, 2020.

AZEEM, M.; HAIDER, M.; JAVED, S.; SALEEM, M.; ALATAWI, A. Drought stress amelioration in maize (*Zea mays* L.) by inoculation of *Bacillus* spp. strains under sterile soil conditions. *Agriculture*, v. 12, n. 1, e50, 2022.

BALDOTTO, M.; BALDOTTO, L.; SANTANA, R.; MARCIANO, C. Initial performance of maize in response to NPK fertilization combined with *Herbaspirillum seropedicae*. *Revista Ceres*, v. 59, n. 6, p. 841-849, 2012.

BANDEIRA, L.; FARIA, C.; CAVALCANTE, F.; MESQUITA, A.; MARTINS, C.; MARTINS, S. Metabarcoding expands knowledge on diversity and ecology of rare actinobacteria in the Brazilian Cerrado. *Folia Microbiologica*, v. 70, n. 1, p. 159-175, 2025.

BREDA, F. F. A.; ALVES, G.; LOPEZ, B.; ARAGÃO, A.; ARAÚJO, A.; REIS, V. Inoculation of diazotrophic bacteria modifies the growth rate and grain yield of maize at different levels of nitrogen supply. *Archives of Agronomy and Soil Science*, v. 66, n. 14, p. 1948-1962, 2020.

BREEDT, G.; LABUSCHAGNE, N.; COUTINHO, T. A. Seed treatment with selected plant growth-promoting rhizobacteria increases maize yield in the field. *Annals of Applied Biology*, v. 171, n. 2, p. 229-236, 2017.

CRUZ, D. R. C.; NASCENTE, A. S.; SILVA, M. A.; BARROSO NETO, J. Root and shoot development of corn seedlings as affected by rhizobacteria. *Colloquium Agrariae*, v. 18, n. 1, p. 53-63, 2022.

CUNHA, E.; PEDROLO, A.; BUENO, J.; PEREIRA, T.; SOARES, C.; ARISI, A. Inoculation of *Herbaspirillum seropedicae* strain SmR1 increases biomass in maize roots DKB 390 variety in the early stages of plant development. *Archives of Microbiology*, v. 204, n. 7, e373, 2022.

ETESAMI, H.; GLICK, B. Bacterial indole-3-acetic acid: a key regulator for plant growth, plant-microbe interactions, and agricultural adaptive resilience. *Microbiological Research*, v. 281, e127602, 2024.

FAÇANHA, A. C. M.; OLIVEIRA, C. A. C. de; CAETANO, E. J. M.; COSTA, E. I. da; NASCENTE, A. S. Bacteria from the Brazilian Savanna as growth promoters in upland rice. *Pesquisa Agropecuária Tropical*, v. 55, e83152, 2025.

FILIPPI, M. C. C.; SILVA, G. B.; SILVA-LOBO, V. L.; CORTES, M. M. C. B.; MORAES, A. J. G.; PRABHU, A. S. Leaf blast (*Magnaporthe oryzae*) suppression and growth promotion by rhizobacteria on aerobic rice in Brazil. *Biological Control*, v. 58, n. 2, p. 160-166, 2011.

GLICK, B.; SANTOS-VILLALOBOS, S.; PARRA-COTA, F.; SANTOYO, G.; GUZMÁN-GUZMÁN, P.; OROZCO-MOSQUEDA, M. Plant growth stimulation by microbial consortia. *Agronomy*, v. 11, n. 2, e219, 2021.

GUI, Y.; YU, Y.; JIANG, C.; GUO, J.; NIU, D.; LI, Z. Induced systemic resistance for improving plant immunity by beneficial microbes. *Plants*, v. 11, n. 3, e386, 2022.

GUO, K.; YANG, J.; YU, N.; LUO, L.; WANG, E. Biological nitrogen fixation in cereal crops: progress, strategies, and perspectives. *Plant Communications*, v. 4, n. 2, e100548, 2023.

HU, Y.; LIU, Y. Impact of fertilizer and pesticide reductions on land use in China based on crop-land integrated model. *Land Use Policy*, v. 141, e107155, 2024.

JIA, B.; CHEN, Y.; XU, Z.; SHI, A.; LIU, Y.; WANG, Y.; YAO, Y.; LIU, Y. Beneficial microorganisms: regulating growth and defense for plant welfare. *Plant Biotechnology Journal*, v. 23, n. 3, p. 986-998, 2025.

JOSEPHINE, C.; THOMAS, J. Plant growth ameliorating and rhizosphere competent native *Acinetobacter pittii* strain F25 from the rhizosphere of *Zea mays* L. *Indian Journal of Agricultural Research*, v. 56, n. 2, p. 186-193, 2022.

KALERI, A.; ANJUM, E.; AHMED, J.; RAJPER, S.; WAGAN, G.; SHAH, T.; DIN, Z.; SHUJRA, H.; MANZOOR, D.; KALERI, G. Interactive effects of nitrogen and phosphorus on maize growth, development, and yield performance. *Planta Animalia*, v. 4, n. 4, p. 59-64, 2025.

KERCHNER, A.; MADRUGA, F.; RODRIGUES, H.; SILVA, A.; POHL, S.; HARTER, L.; MUNARI, J.; TUNES, L.; SILVA, A. Corn culture: from the first records to harvesting and storage. *Colloquium Agrariae*, v. 20, e244826, 2024.

KHALEEQ, K.; NAZIR, R.; HEMMAT, N.; SIRAT, W.; SAMIM, M. Response of maize (*Zea mays* L.) to the soil application of phosphorus fertilizer. *Journal of Agriculture and Ecology*, v. 17, n. 1, p. 90-93, 2023.

KUMAR, S.; DIKSHA; SINDHU, S. S.; KUMAR, R.; KUMARI, A.; PANWAR, A. Harnessing phyllosphere microbiome for improving soil fertility, crop production, and environmental sustainability. *Journal of Soil Science and Plant Nutrition*, v. 23, n. 4, p. 4719-4764, 2023.

LIAO, Z.; ZHANG, C.; ZHANG, Y.; YU, S.; YAN, S.; ZHANG, S.; LI, Z.; FAN, J. Nitrogen application and soil mulching improve grain yield of rainfed maize by optimizing source-sink relationship and grain filling process on the Loess Plateau of China. *European Journal of Agronomy*, v. 153, e127060, 2024.

LOPES, C. V. A.; ALBUQUERQUE, G. S. C. Agrotóxicos e seus impactos na saúde humana e ambiental: uma revisão sistemática. *Saúde em Debate*, v. 42, n. 117, p. 518-534, 2018.

MUNIR, N.; HANIF, M.; ABIDEEN, Z.; SOHAIL, M.; EL-KEBLAWY, A.; RADICETTI, E.; HAIDER, G. Mechanisms and strategies of plant microbiome interactions to mitigate abiotic stresses. *Agronomy*, v. 12, n. 9, e2069, 2022.

OCWA, A.; SSEMUGENZE, B.; HARSÁNYI, E. Seed treatment with *Bacillus* bacteria improves maize production: a narrative review. *Acta Agraria Debreceniensis*, n. 1, p. 105-111, 2024.

OLIVEIRA-PAIVA, C.; BINI, D.; SOUSA, S.; RIBEIRO, V.; SANTOS, F.; LANA, U.; SOUZA, F.; GOMES, E.; MARRIEL, I. Inoculation with *Bacillus megaterium* CNPMS B119 and *Bacillus subtilis* CNPMS B2084 improve P-acquisition and maize yield in Brazil. *Frontiers in Microbiology*, v. 15, e1426166, 2024.

R CORE TEAM. *R*: a language and environment for statistical computing. Vienna: R Foundation for Statistical Computing, 2023.

SÁ, M. N. F.; LIMA, J. S.; JESUS, F. N.; PEREZ, J. O. Microbiolização na qualidade de sementes e crescimento inicial de plantas de *Vigna unguiculata* L. Walp. *Acta Brasiliensis*, v. 3, n. 3, p. 111-115, 2019.

SANTOS, H. G. dos; JACOMINE, P. K. T.; ANJOS, L. H. C. dos; OLIVEIRA, V. À. de; LUMBRERAS, F. F.; COELHO, M. R.; ALMEIDA, J. A. de; ARAÚJO FILHO, J. C. de; OLIVEIRA, J. B. de; CUNHA, T. J. F. *Sistema brasileiro de classificação de solos*. 5. ed. Brasília, DF: Embrapa, 2018.

SILVA, I. L.; SOARES, C.; SOARES, T.; ALMEIDA, F.; ALMEIDA-SILVA, F.; GAZARA, R.; MENESES, C.; CANELLAS, L.; SILVEIRA, V.; VENANCIO, T.; OLIVARES, F. Multiomic approaches reveal hormonal modulation and nitrogen uptake and assimilation in the initial growth of maize inoculated with *Herbaspirillum seropedicae*. *Plants*, v. 12, n. 1, e48, 2022.

TONG, J. Silicon nanoparticles alter soybean physiology and improve nitrogen fixation potential under atmospheric carbon dioxide (CO_2). *Plants*, v. 14, n. 13, e2009, 2025.

UNITED STATES DEPARTMENT OF AGRICULTURE (USDA). Natural Resources Conservation Service. *Keys to soil taxonomy*. 12. ed. Washington, DC: USDA, 2014.

WANG, J.; HU, X. Research on corn production efficiency and influencing factors of typical farms: based on data from 12 corn-producing countries from 2012 to 2019. *PLoS One*, v. 16, n. 7, e0254423, 2021.

ZHANG, B.; LI, P.; WANG, Y.; WANG, J.; LIU, X.; WANG, X.; HU, X. Characterization and synthesis of indole-3-acetic acid in plant growth promoting *Enterobacter* sp. *RSC Advances*, v. 11, n. 50, p. 31601-31607, 2021.

ZOU, Y.; LI, L.; WANG, Y.; DUAN, R.; DONG, H.; ZHANG, Y.; DU, Z.; CHEN, F. Growth and yield of maize in response to reduced fertilizer application and its impacts on population dynamics and community biodiversity of insects and soil microbes. *Frontiers in Plant Science*, v. 15, e1362905, 2024.