



Enhancement of growth and physiological performance in maize hybrids through a dual consortium of native rhizobacterial strains

Leandris Argentele-Martínez¹ · Ofelda Peñuelas-Rubio¹ · Lorenzo Pérez López¹ · Joe Luis Arias Moscoso¹ · Francisco Cadena Cadena¹ · Jaime Garatuza-Payán² · Martha L. Vargas-Terminel² · Francisco Cervantes Ortíz³ · Jorge González Aguilera⁴ · Fábio Steiner⁴ · Alan Mario Zuffo⁵ · Estibaliz Sansinenea⁶ · Jae-Ho Shin⁷ · Ugur Azizoglu^{8,9}

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Abstract

The use of plant growth-promoting microorganisms represents a viable biotechnological solution for improving the performance of staple crops. Given the high fertilizer requirements of maize, alternative strategies such as microbial promoters are essential to enhance development, increase yields, and minimize environmental and soil degradation. In this study, a dual bacterial consortium comprising *Enterobacter cloacae* and *Priestia megaterium* isolated from the rhizosphere of *Parkinsonia aculeata* was evaluated for its effects on maize growth.

Field experiments followed a completely randomized design at the Yaqui Valley Technological Institute, using five maize hybrids. Treatments included the application of the bacterial consortium during pre-germination (T1), 15 days after emergence (T2), or no application (T3, control). Variables assessed included water absorption, germination percentage, initial and final plant height, root length and volume, maximum photosynthesis, transpiration, chlorophyll content, and NDVI, measured through the flowering stage.

The bacterial consortium did not significantly affect seed water uptake capacity or germination rates compared to the control. However, it significantly improved root volume ($p < 0.05$), chlorophyll content (20% increase), NDVI (0.83 vs. 0.78 in controls), and photosynthetic rates (25% higher in T1/T2). No differences were observed between pre-germination (T1) and post-emergence (T2) applications. Photosynthetic rates during flowering exceeded $45 \mu\text{mol CO}_2 \text{ m}^{-2} \text{ s}^{-1}$ in all hybrids, marking a 25% increase in T1 and T2, compared to the control.

These findings highlight the dual bacterial consortium as a promising eco-friendly alternative to enhance initial maize plant growth during the vegetative stages.

Keywords Rhizospheric bacteria · Root volume · Chlorophyll content · Photosynthesis · NDVI

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✉ Leandris Argentele-Martínez
oleinismora@gmail.com

✉ Ugur Azizoglu
azizoglu@erciyes.edu.tr; azizogluugur@hotmail.com;
azizoglu@kayseri.edu.tr; azizoglugur@gmail.com

Ofelda Peñuelas-Rubio
openuelas.rubio@itvy.edu.mx

¹ Tecnológico Nacional de México, Instituto Tecnológico del Valle del Yaqui, Bácum, Sonora, México

² Instituto Tecnológico de Sonora, Ciudad Obregón, Sonora, México

³ Tecnológico Nacional de México, Instituto Tecnológico de Roque, Celaya, Guanajuato, México

⁴ Department of Agronomy, Universidade Estadual de Mato Grosso do Sul (UEMS), Cassilândia 79540-000, MS, Brazil

⁵ Department of Agronomy, Universidade Estadual do Maranhão (UEMA), Balsas, MA, Brazil

⁶ Facultad de Ciencias Químicas, Benemérita Universidad Autónoma de Puebla, Puebla C.P. 72570, Pue, México

⁷ School of Applied Biosciences, College of Agriculture and Life Sciences, Kyungpook National University, Daegu 41566, Republic of Korea

⁸ Department of Crop and Animal Production, Safiye Cikrikcioglu Vocational College, Kayseri University, Kayseri, Turkey

⁹ Genome and Stem Cell Research Center, Erciyes University, Kayseri, Turkey

Introduction

The rhizosphere hosts beneficial microorganisms that enhance plant productivity through nutrient cycling and stress adaptation (Rojas-Sánchez et al. 2024). These microorganisms often exhibit significant potential as biofertilizers in agricultural applications (Argente-Martínez et al. 2025; Cangioli et al. 2024) and are critical for ecological processes such as nutrient recycling, organic matter decomposition, and mineralization (Wang et al. 2024a, b).

Certain semidesert plants harbor rhizospheric microorganisms that enhance adaptation to challenging conditions, including drought, salinity, and high temperatures typical of semiarid environments (Torres-Cruz et al. 2023). *Parkinsonia aculeata* L., a legume species native to the southern United States and northwest Mexico, exhibits remarkable adaptability to adverse conditions, likely facilitated by its associated rhizobacteria (Argente-Martínez et al. 2024a, b, c). Due to their ability to thrive under adverse conditions, numerous bacteria with growth-promoting properties have been identified (Peñuelas-Rubio 2024).

Plant growth-promoting rhizobacteria (PGPR) are classified into several groups based on their growth-promoting mechanisms: biofertilizers, biostimulants, biocontrol agents, and bioremediation agents. Currently, PGPRs are classified into biofertilizers, biostimulants, biocontrol agents, and bioremediation agents, offering sustainable solutions for soil health and crop productivity (Fadiji et al. 2024). In the context of current climate change scenarios, microbiome biotechnology is crucial for designing microbial consortia to enhance the productivity of essential crops, such as maize (Kushwaha et al. 2024).

Maize is one of the world's most important staple crops (Li et al. 2025). Maize is the most significant crop in Mexico, with yearly yields topping 26 million tons since 2020. It serves as a crucial resource for both human and animal sustenance. (Chavira 2024). However, maize yields heavily depend on high doses of chemical fertilizers due to its nutrient-intensive growth requirements (Ahmad et al. 2024a, b). Excessive fertilizer application disrupts the soil's absorptive properties and contributes to aquifers' salinization. Applying growth-promoting microorganisms to maize could provide an effective alternative for optimizing the utilization of residual soil fertilizers.

Evaluating the effects of growth-promoting microorganisms on plant physiology during the vegetative stages is a critical initial step toward assessing their potential contribution to crop agronomic performance. These assessments, incorporating multiple genetic materials under various experimental settings, provide speedy, precise, and effective judgments for implementation and validation based on correlations between physiological responses and crop

agronomic performance (Argente-Martínez et al. 2021). Furthermore, identifying microbial strains with multifunctional traits will enable the development of robust bioinoculants, paving the way for sustainable and climate-resilient agricultural practices. This study aimed to evaluate the effects of a dual bacterial consortium comprising *Enterobacter cloacae* and *Priestia megaterium*, isolated from the rhizosphere of *Parkinsonia aculeata*, on the initial maize growth, chlorophyll content, NDVI, leaf gas exchange, soil respiration using five maize hybrids as the experimental model under field conditions.

Materials and methods

Location of the experimental area

The experiment was conducted under field conditions from November 2024 to April 2025 in a 1-hectare area within the production fields of the Technological Institute of the Yaqui Valley, Sonora, Mexico (27°24'49"N, 110°07'54"W). The crop was established on gleyic vertisol soil (Almazán et al. 2023), which has been utilized for over 35 years for wheat and maize cultivation.

Soil and climate variability during the experimental period

During the experimental period, the main edaphoclimatic variables were monitored in situ. Maximum and minimum temperatures under the crop canopy, as well as relative humidity, were measured daily using a portable Aqualy sensor located in the center of the experimental site. Soil moisture was also monitored daily with an Irrometer-type device placed in representative furrows, which was recalibrated before each auxiliary irrigation. Soil moisture levels ranged from 100% immediately after irrigation to 75%, at which point new irrigation was initiated (Supplementary Fig. 1a). Supplementary Fig. 1b shows that the minimum air temperature at canopy height recorded during the crop cycle was 4.7 °C, observed in phenophase V11.

The highest air temperature at canopy height was recorded in the early stages of growth (phenophase V4, with $t=43$ °C). Because of the region's semiarid and relatively dry climate, relative humidity hovered between 46% and 51%, and rainfall was zero. The hydrothermal coefficient calculated during the five months of the evaluation was 0.

Plant material

Five commercial hybrids adapted to the soil and climatic conditions of the region were established with yields

between 12 and 18 t ha⁻¹. The final plant height of the hybrids averaged 242 cm and the biological crop cycle was 150–157 days after emergence.

The hybrids evaluated have an inbreeding level of S8-S9, which allows them to have a high degree of genetic stability. The Hipopótamo is the most widespread hybrid crop in northwestern Mexico and is tolerant to moderately stressful conditions such as salinity and high temperatures (Argente-Martínez et al. 2024a).

The remaining hybrids have been subject to physiological and agronomic evaluation in central and northwestern Mexico, particularly in the Yaqui Valley (Pérez-López et al. 2025), with very notable morphological characteristics among them. This variability of morphological and physiological characteristics was taken into consideration when searching for possible variations in the plant-microorganism association.

Bacterial consortium preparation

The bacterial consortium was formed by *Enterobacter cloacae* (BA1) and *Priestia megaterium* (BA7-B), which were obtained from the rhizosphere of *P. aculeata* (Peñuelas-Rubio et al. 2024). The molecular characterization and similarity percentages of these bacteria were registered in the NCBI database with accession numbers ON869243 and

ON869275, respectively. The bacterial strains were preserved at -70 °C in Luria-Bertani broth (LB) supplemented with 15% glycerol.

Biochemical characterization

A set of preliminary tests were conducted on each of the isolated strains to validate the following plant growth traits: hemolysis test, siderophore and indoleacetic acid (IAA) production, and finally, the phosphate solubilization index (Table 1). These bacteria were not hemolytic, which makes them amenable to use in agriculture, especially as they produced indoleacetic acid (IAA), were highly productive of siderophores, and could solubilize phosphate.

Hemolysis test

The hemolysis test was done according to Khalil et al. (2021), in which bacteria were cultured overnight in 5 mL of LB medium at 30 °C and 200 rpm. Circular wells of 5 mm were made on blood agar plates, to which 5 L of a bacterial suspension was added. The plates were then incubated for 24 h at 37 °C. The results were interpreted based on the length of the clear zone surrounding the wells: β -hemolysis was observed as a clear zone, demonstrating complete rupture of the red blood cells; α -hemolysis was revealed by a

Table 1 Plants' growth attributes (relative growth rate (RGR), final stem diameter (FSD), final root length (FRL), root volume, time (hh: mm) of beginning and end of the temporary wilting point (TWP), and time of wilting (Δt (min) of five maize hybrids (H, C1, C2, C3, and C4) subjected to three treatments: T1 (seed pre-germination for 24 h with a bacterial dual consortium), T2 (bacterial consortium applied 15 days after emergence), and T3 (control treatment without bacterial consortium application). Different uppercase letters in the same row and different lowercase letters in the same column indicate significant differences between treatments and hybrids, respectively, according to tukey's test for $p < 0.05$. CV: coefficients of variation for the treatments ($CV_{(Treat)}$) for the hybrids ($CV_{(Hyb)}$)

Number	Treatments	Hybrids	Plant Growth Attributes				TWT	
			RGR (cm day ⁻¹)	FSD (cm)	FRL (cm)	RV (mL ³)	Time	Δt (min)
1	T1	H	2.82a	3.80c	55.40a	755.39a	13:00–13:43	43bc
2	T2	H	2.81a	3.80c	55.30a	746.16d	13:05–13:45	40c
3	T3	H	2.63d	3.20f	46.60d	721.30k	12:00–14:00	120a
4	T1	C1	2.75ab	4.10a	54.90ab	735.80 g	13:15–14:00	45b
5	T2	C1	2.72b	4.00a	54.40b	741.40e	13:23–14:05	42c
6	T3	C1	2.47 h	3.30e	45.20d	722.30k	12:00–14:20	120a
7	T1	C2	2.68c	3.90b	54.60b	743.01e	13:00–13:30	30e
8	T2	C2	2.62d	3.90b	54.60b	739.63f	13:00–13:30	30e
9	T3	C2	2.56e	3.40e	44.80e	724.02j	11:53–13:50	117b
10	T1	C3	2.74ab	3.60d	53.80c	748.09c	13:10–13:35	35d
11	T2	C3	2.70b	3.60d	53.50c	746.18d	13:00–13:45	35d
12	T3	C3	2.66c	3.30d	44.10f	726.04i	12:00–14:20	120a
13	T1	C4	2.71b	3.70c	55.20a	750.28b	13:00–13:30	30e
14	T2	C4	2.62f	3.80bc	54.90ab	750.00b	13:00–13:30	30e
15	T3	C4	2.55 g	3.20e	44.70f	729.02 h	12:30–14:26	116b
-	CV (%)	-	6.87	3.45	8.29	15.02	-	17.81

Different uppercase letters in the same row and different lowercase letters in the same column indicate significant differences between treatments and hybrids, respectively, according to Tukey's test for $p < 0.05$. CV: coefficients of variation for the treatments ($CV_{(Treat)}$) for the hybrids ($CV_{(Hyb)}$)

slight color change surrounding the wells, indicating partial rupture of the red blood cells; and no-hemolysis (or absence of hemolysis) was indicated by the absence of any change in color or clarity of the medium surrounding the well (Misawa et al. 1995).

Siderophores

Siderophore production was determined via the O-CAS coating method (Pérez-Miranda et al. 2007) with some modifications. Colonies with yellow/orange zones were considered siderophore-producing strains after 20 min and up to 24 h.

Indolacetic acid (IAA)

IAA production was tested via the use of TSB (tryptone soy broth) agar (Becton Dickinson, USA) and incubation at 28–30 °C for 2–5 days. Approximately 1 mL of Salkowsky solution was dropped on top of the growing colonies and then incubated in the dark for 1 h. A positive result was noted by a color change to pink, indicating that these isolates were able to produce IAA (Gravel et al. 2007).

Phosphate solubilization index (SI)

This test was performed using Pikovskaya culture agar (1948). Each isolate was cultured in triplicate and incubated for 7 days at 30 °C. The formation of a clear halo in the culture medium around the colony indicates a positive reaction for that bacterium. The solubilization index (SI) was computed using the formula described by Edi-Premono et al. (1996):

$$SI\% = \frac{\text{Diameter of the colonies} + \text{Diameter of the halo}}{\text{Diameter of the colony}} \quad (1)$$

Bacterial inoculum preparation

The cryopreserved bacterial strains were subsequently grown on an LB agar medium for 24 h. To ensure strain compatibility, a cross-antagonism plate test was performed. The bacteria were inoculated linearly, in parallel, and 2 cm apart. The results indicated bacterial compatibility, hence a dual bacterial inoculum was created. The methodology proposed by Khalil et al. (2022) was followed with some modifications. A single colony was transferred to 15 mL of nutrient medium (NM) and incubated at 30 °C for 24 h at 180 rpm on an orbital shaker until a cell concentration of 1×10^7 cells/mL was reached. The culture medium was removed by centrifugation at $3000 \times g$ for 5 min at room temperature. The resulting pellet was resuspended in 1X

PBS in triplicate. Finally, the cell pellet was resuspended in 10 mL to formulate the bacterial consortium. For this purpose, a 10% solution was prepared for each bacterium, and the microbial consortium was created by mixing equal parts of both bacteria. A volume of 5 mL of this suspension was applied to each plant.

Treatments and experimental design

Two sources of variance were identified in the present study. The first consisted of the following treatments: T1 – a dual bacterial consortium used for seed pre-germination for 24 h; T2 – a dual bacterial consortium applied to the plants 15 days after emergence, with a volume of 5.0 mL per plant; and T3 – a control treatment without the application of the bacterial consortium. The second source of variation was the maize hybrids: Four regional obtained hybrids, represented by the letter C (C1, C2, C3, and C4), and one international commercial hybrid, Hipopótamo, represented by the letter H. The treatments were applied to five hybrids. The effectiveness of the treatments was validated across all five hybrids.

In total, 15 treatments were established by combining three treatment levels with five hybrid variations. The treatments were arranged in a completely randomized experimental design due to the considerable similarity in soil and climate conditions. Each experimental plot measured 12 m × 4 m, with a 1 m separation between treatments. The plots had a calculated surface area of 25 m², with a total of 306 plants per plot.

Variables evaluated

The water content absorbed by the seeds was expressed in milligrams of water. This experience was carried out under controlled conditions. After 24 h of imbibition, the seeds were carefully dried with toilet paper and reweighed to obtain the final weight. The content of absorbed water was determined by calculating the difference between the initial weight (before pre-germination) and the final weight of the seeds (24 h after pre-germination).

Under field conditions, the germination percentage was calculated based on the number of germinated and emerged plants compared to the total number of seeds sowed in each treatment (306 seeds) and expressed as a percentage. The following equation was used to calculate the germination percentage (G%):

$$G\% = \frac{\text{Number of germinated seeds}}{\text{Number of total seeds}} \times 100 \quad (2)$$

This variable was measured in all treatments to assess any potential toxic effects of the bacterial consortium applied during pre-germination. Treatments T2 and T3 were also subjected to pre-germination with a similar volume of distilled water (500 mL). The final plant height (FPH, cm) was measured using a flexometer (TRUPER) at seven-day intervals from the base of the stem to the apex of the youngest visible leaf. Measurements were taken from the emergence phenophase (VE) until the flowering phenophase (VT). Based on these data, the relative growth rate (RGR) of the plants was determined as the ratio between the final height and the time elapsed until flowering. This variable was expressed in cm/day, with a sample size of $n=10$ plants per treatment.

The final stem diameter (FSD, mm) was measured at the flowering phenophase using a digital Vernier caliper (TRUPER) at the second internode of the stem, with a sample size of $n=10$ plants per treatment.

The final root length (FRL, cm) was measured using a destructive method during the flowering phenophase (VT). A total of 10 plants per treatment for each hybrid were carefully extracted using shovels, and their roots were washed before measuring their length from the base of the stem using a flexometer (TRUPER).

Root volume (RV, mL) was measured using the destructive method. The roots were washed with distilled water, and the cut roots were placed in a 1000 mL graduated cylinder containing a constant volume (300 mL) of distilled water. The increase in water level was used to determine the root volume.

The temporary wilting point (TWP, hours) was determined through visual observation when the leaves appeared wilted. This evaluation was conducted during the flowering phenophase at 76% soil humidity, one day before auxiliary irrigation. The experimental unit for this evaluation was a plot where more than 50% +1 of the plants exhibited wilting symptoms. The time at which turgor was restored was also recorded. The time difference between the onset and end of the temporary wilting point was designated as Delta t (Δt , expressed in minutes) to compare plant stress duration.

The normalized difference vegetation index (NDVI) ($1 > \text{NDVI} > -1$) was determined in the flowering phenophase (VT) using a portable Greenseeker-type device (Trimble™) (Govaerts and Verhulst 2010). Measurements were taken at 11:00 a.m., with the device positioned 0.6 m from the plant leaf area (Prakash et al. 2020).

Chlorophyll content (SPAD units) was measured only during the flowering phenophase using a portable SPAD-type device. A total of 10 measurements were taken from the central part of the leaves most exposed to sunlight at 12:00 h.

Gas exchange, including maximum photosynthesis (Amax, expressed in $\mu\text{mol CO}_2 \text{ m}^{-2} \text{ s}^{-1}$) and transpiration (E, expressed in $\mu\text{mol H}_2\text{O m}^{-2} \text{ s}^{-1}$), was measured at phenophase V4 (45 days after emergence) and during the flowering phenophase (VT). Measurements were taken between 11:00 h. and 13:00 h. using a portable PP-System under a light intensity exceeding $1,500 \mu\text{mol m}^{-2} \text{ s}^{-1}$ and a constant CO_2 concentration of $400 \mu\text{mol mol}^{-1}$ in the reference cell, with a steady flow rate of $500 \mu\text{mol s}^{-1}$. For each hybrid and treatment, 10 measurements were recorded.

Soil respiration measurements were conducted using a soil respiration chamber (LI-COR LI-7810) for all treatments during the flowering phenophase (VT). 100 mm diameter couplings were installed at a depth of 4 cm in the two central furrows of each plot to secure the chamber. Measurements were performed between 10:00 a.m. and 1:00 p.m., with each measurement lasting 5 min. Before measurement, soil humidity, and temperature were recorded to complete the equipment algorithm.

Irrigation was applied via a drip system using 5/8" tapes with drippers spaced 0.3 m. Each hybrid (five) had four irrigation lines, each 35 m long and 120 drippers. The product of the number of drippers and the volume of water released in 24 h was the total water volume in the experimental area (33.6 m^3). Irrigation intervals (II) varied (Figure S1) depending on the crop coefficient and the soil humidity sensor readings (IRROMETER), being on average an $\text{II}=24$ days. In total, five irrigation events were conducted at partial irrigation rates of 336, 345, 350, 400, and $400 \text{ m}^3 \text{ ha}^{-1}$ until the flowering phenophase (VT) was reached.

Weed control was initially performed manually and semi-mechanically, followed by the application of the selective herbicide ACRE at a dose of 1.0 L ha^{-1} . Pest control, primarily targeting *Spodoptera frugiperda*, was conducted using Palo Verde extract at a dose of 2.5 L ha^{-1} , applied at 12, 22, and 24 days after emergence (Argente-Martínez et al. 2024a, b, c).

Fertilization was carried out via fertigation for all five hybrids. The first fertilization occurred during nascent irrigation, with an application rate of 60 kg ha^{-1} nitrogen and 30 kg ha^{-1} phosphorus using a balanced N-P-0 fertilizer. The second fertilization was applied 45 days after emergence (V4 phenophase) at a rate of 32 kg ha^{-1} nitrogen (46% urea) and 25 kg ha^{-1} potassium in the form of potassium nitrate. During the flowering phenophase, Triple-18 fertilizer was applied at a rate of 15 kg ha^{-1} . Total nitrogen applied (100 kg ha^{-1}) was 20% below the regional recommendation (120 kg ha^{-1}), testing the consortium's potential to reduce fertilizer dependency.

Statistical analysis

All analyzed variables were found to comply with the theoretical assumptions of normality and variance homogeneity (de Souza et al. 2024). Each variable was then subjected to ANOVA and double-classification using a linear fixed-effects model (Fisher 1937) to identify differences between treatments and hybrids. Once significant differences between treatments were detected, TUKEY'S multiple comparison test was applied at significance levels of 5% and 1% (Tukey 1960).

Statistical indicators were determined for all analyzed variables, including the coefficient of variation (CV) and the unadjusted coefficient of determination (R^2). The unadjusted coefficient of determination was calculated as the ratio of the sum of squares of the sources of variation to the total sum of squares. Statistical analyses were conducted using the professional statistical package STATISTICA, version 10.0 for Windows (StatSoft 2014). Canonical variable analyses were performed using Rbio[®] software, version 140 for Windows (Rbio Software, UFV, Viçosa, MG, Brazil).

Table 2 Water content absorbed by the seeds and germination percentage of the five maize hybrids were evaluated under three treatments (T1: pre-germination of seeds for 24 h with a bacterial dual consortium; T2: bacterial consortium applied 15 days after emergence; and T3: control treatment without bacterial consortium application)

Number	Treatments	Hybrids	Water absorbed by seeds (g)	Germination percentage (%)
1	T1	H	1.16	100
2	T2	H	1.10	99
3	T3	H	1.12	100
4	T1	C1	1.10	100
5	T2	C1	1.10	99
6	T3	C1	1.15	100
7	T1	C2	0.99	100
8	T2	C2	1.04	99
9	T3	C2	0.99	99
10	T1	C3	1.00	100
11	T2	C3	0.98	99
12	T3	C3	1.03	99
13	T1	C4	1.10	100
14	T2	C4	1.16	100
15	T3	C4	1.10	99
CV (%)			0.93	0.56

The absence of uppercase letters in the same row and lowercase letters in the same column indicate no significant differences between treatments and hybrids, respectively, according to Tukey's test for $p < 0.05$. CV: coefficients of variation for the treatments ($CV_{(Treat)}$) for the hybrids ($CV_{(Hyb)}$)

Results and discussion

Seed water absorption and percentage of germination

Water absorption by the seeds was observed in all hybrids, as indicated by the increase in weight 24 h after the start of pre-germination. The commercial hybrid Hipopótamo exhibited the highest absorption (1.2 g), with no significant differences among treatments. The remaining hybrids showed no differences in their absorbed water content (Table 2). The lowest absorbed water content was recorded in hybrids C1, C2, and C3 in some treatments, although there were no significant differences between treatments (0.9 g).

Seed water absorption is primarily a physical process in which water passes through the seed coat due to a difference in osmotic potential (Riseh et al. 2024). However, in media containing solutes, the free energy of water can be affected, leading to a reduction in osmotic potential and, consequently, water potential, which may decrease absorption capacity (Ren et al. 2024). The results obtained in this study indicated that the bacterial consortium did not alter the osmotic potential of the water; therefore, it did not impact the seeds' absorption capacity. Water absorption led to germination rates over 99% for all hybrids across all conditions. Treatment T1 resulted in 100% germination for all assessed hybrids. This outcome may be attributed to seed age, storage duration, and storage conditions (Yewle et al. 2024). Importantly, the T1 treatment (pre-germination for 24 h with the dual bacterial consortium) did not cause any toxic effects on the seeds but instead promoted the highest germination percentage.

Initial and final heights of the plants

In the measurement conducted during the development phenophase, 15 days after emergence, the differences between treatments were highly significant ($F(2,135)=1975$, $p=0.00032$), with T1 showing superior results compared to T2 and T3, which did not exhibit significant differences (Fig. 1a). This result indicates that the application of the consortium during pre-germination promoted early plant development. This may be attributed to the high indoleacetic acid production capacity of *E. cloacae*, (supplementary material), where the main biochemical tests performed on the bacteria before the formation of the consortium are presented.

Highly significant differences were also observed between hybrids ($F_{(4,135)}=986.12$, $p=0.00016$) and among most hybrids, except for C2, C3, and C4, which exhibited similar plant heights under treatments T2 and T3. A highly significant interaction effect was found between treatment

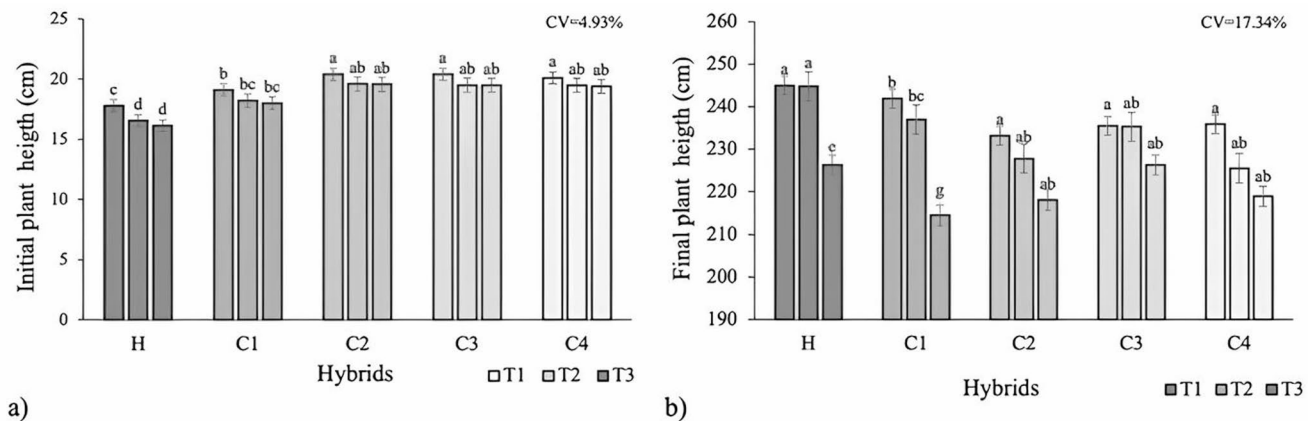


Fig. 1 Initial and final plant heights of five corn hybrids (H, C1, C2, C3, and C4) subjected to three treatments (T1: pre-germination of seeds for 24 h with a bacterial dual consortium; T2: bacterial consortium applied

15 days after emergence; and T3: control treatment without bacterial consortium application)

and hybrid type ($F_{8,135}=874, p=0.00032$). In the measurement of initial plant height, the highest percentage of variability was attributed to the treatments ($R^2 = 0.82$), while hybrids and their interaction (*Treatments* $\times$ *Hybrids*) contributed only 10% ($R^2 = 0.10$) and 7% ($R^2 = 0.07$), respectively, to the experimental error.

The measurement of final plant height during the flowering phenophase (VT) further demonstrated the effectiveness of the applied dual bacterial consortium in promoting plant development (Fig. 1b). Highly significant differences were observed among all hybrids across treatments, with T1 and T2 consistently outperforming T3. In this phenophase, the growth-promoting effect of the bacterial consortium on plant height was evident.

The hybrids with the greatest plant heights were H and C1, surpassing even the final height values provided by the varietal descriptor. No significant differences were identified between the H, C1, and C3 hybrids in the T1 and T2 treatments. There were differences compared to T3, with development increases of 7%, 12%, 34%, and 3%, respectively. The results presented here also highlight the effectiveness of evaluating the promoting effects of PGPR across various genetic materials to ensure accurate results throughout the phenology of different genetic materials. The effects of the established treatments accounted for 90% ($R^2=0.90$) of the total variability in final height throughout this development phase. The hybrids accounted for 7% ($R^2=0.07$), and the interaction explained 3% ($R^2=0.03$) of the variance. Torres et al. (2024) used *P. megaterium* ILBB592 as a bio-fertilizer and demonstrated its positive effects on most plant parameters, including nodulation and phosphorus uptake. As a result, *P. megaterium* ILBB592 is deemed an option for decreasing phosphorus fertilization while maintaining plant performance. This behavior confirms the positive effect observed in the present study.

Relative growth rate

The relative growth rate (Table 1) differed highly significantly between treatments ($F_{2,135}=10133, p=0.00012$) whereas the difference between hybrids was only significant ($F_{4,135}=27677, p=0.04713$). Additionally, there was a significant interaction effect between the two sources of variation ($F_{8,135}=6945, p=0.03810$). The highest relative growth rate was observed in hybrid H, followed by C1 and C3 in treatments T1 and T2, with no significant differences between them within any hybrid. The T3 treatment resulted in the lowest relative growth rates in hybrids C1 and C5.

The bacterial consortium increased relative growth rates in T1 and T2 by an average of 4%. Notably, in hybrid H, this value was 7% higher than in the control treatment. For this variable, the source of variation “treatments” accounted for 55% ($R^2=0.55$) of the total variability, while hybrids and their interaction contributed 30% ($R^2=0.3$) and 15% ($R^2=0.15$), respectively.

Final stem diameter

The final stem diameter also differed significantly between treatments ($F_{2,135}=5895, p=0.00317$), with this source of variation accounting for 77% of the total variability ($R^2=0.77$) (Table 1). The hybrids also showed highly significant differences ($F_{4,135}=595, p=0.00142$) but their contribution to the total variability in stem diameter was only 15% ($R^2=0.15$). The interaction effect between treatments and hybrids was significant ($F_{8,135}=119, p=0.04381$) contributing only 6% ($R^2=0.06$) to the total variability, with 1% attributed to experimental error.

Final root length

Final root length (Table 1) was one of the most variable traits among treatments ($F_{(2,135)}=1396791$, $p=0.00183$ and hybrids ($F_{(4,135)}=13578$, $p=0.01162$) with highly significant differences, as well as their interaction ($F_{(8,135)}=1104.8$, $p=0.00003$). For this variable, treatments contributed 98% ($R^2=0.98$) of the total variability, whereas hybrids accounted for only 2% ($R^2=0.02$). Although the interaction effect did not contribute to total variability, it was not entirely null. This finding implies that utilizing a single hybrid is sufficient for determining treatment effects on final root length. Nevertheless, all five hybrids were compared to enhance the accuracy of the results. Recently, Ayelo et al. (2024) used a bacterial consortium, including *Priestia*, to promote maize and cotton growth. Their findings confirmed a 25% increase in root length and a 32% increase in plant height compared to controls. These results highlight the usefulness of this bacterium, as its biochemical properties contribute to improved plant nutrition and development.

Root volume

Root volume differed highly significantly between treatments ($F_{(2,135)}=8828$, $p=0.00125$, $CV=14.6\%$, $R^2=0.81$;) and hybrids ($F_{(4,135)}=547$, $p=0.00052$, $CV=8.21\%$, $R^2=0.13$;) Additionally, a highly significant interaction was observed between these two sources of variation ($F_{(8,135)}=9.4599$, $p=0.00165$, $R^2=0.06$) (Table 1).

Except for hybrid C1, all hybrids had more root volume in the T1 treatment than in the T2. In some hybrids, no significant differences were observed between T1 and T2. In T3, all hybrids showed highly significant reductions in root volume compared to T1 and T2. In Hybrid H, the highest average root volumes were obtained in treatments T1 and T2 without significant differences, but in this same one (H) it was found the lowest value in T3, with a difference of 24 mL³ in average for T1 and T2. In all the remaining hybrids the average numerical difference between the values obtained in T1 and T2 for T3 was between 10 and 20 mL³. The lowest difference in root volume of the plants with (T1 and T2) and without de application of the consortium (T3) was obtained in C1. In this Hybrid, only the T2 treatment surpassed T1. For this variable, the highest percentage of variability was attributed to treatments ($R^2=0.81$), while hybrids contributed 13% ($R^2=0.13$). Although the interaction effect was highly significant, it accounted for only 6% ($R^2=0.06$) of the total variability. These findings highlight the bacterial consortium's ability to enhance variability—specifically, increased root volume—in maize crops. Root volume is one of the most critical factors influencing mineral nutrition (Lodh et al. 2024). A greater root volume ensures

adequate water uptake and improves water status (Wang et al. 2024a, b; Khan et al. 2024). A study by Lai et al. (2024) studied the effect of a bacterial consortia on plant development and observed a 35% increase in root volume compared to untreated maize crops. A larger root system supports later emergence and reduces the duration of temporary wilting. This result aligns with our findings (Table 1), which demonstrated the crop's water absorption capacity even at 78% soil moisture during the flowering phenophase (VT).

Temporary wilting point

In the T1 treatment, hybrids C2 and C4 had the shortest temporary wilting time, lasting only 30 min, with no significant difference compared to T2 (Table 1). In contrast, all hybrids in the T3 treatment exhibited a temporary wilting point of more than two hours, with hybrids C2 and C4 having the shortest wilting duration. However, hybrid C2 wilted approximately 10 min earlier than the other hybrids.

The results obtained in this study demonstrate the effectiveness of applying the dual bacterial consortium both before germination and 15 days after emergence in maintaining good water status and reducing temporary wilting time. The early onset of the temporary wilting point negatively impacts photosynthetic activity by limiting CO₂ uptake (Vennam et al. 2024).

NDVI and chlorophyll content

The NDVI significantly differ among the treatments ($F_{(2,135)}=124.16.11$, $p=0.00032$, $CV=7.44\%$, $R^2=0.92$) and also among the hybrids ($F_{(4,135)}=24.17$, $p=0.00117$, $CV=6.82\%$, $R^2=0.07$). There was also a significant interaction between treatments*Hybrids ($F_{(8,135)}=246.77$, $p=0.00011$, $R^2=0.03$). The treatment T1 showed the highest NDVI (Fig. 2a) and the major contribution to the total variability of NDVI was based on Treatment effects.

The difference identified between T3 and the two treatments (T1 and T2) illustrates the beneficial effect of the microbial community on nitrogen metabolism in plants. In both T1 and T2 treatments, the plants of all hybrids (without significant differences between them) reached NDVI values higher than 0.83 VT phenophase, indicating good nutritional status. However, in the T3 treatment, the maximum value obtained in the hybrids was 0.78 and it was found in VT phenophase. This result confirms the contribution of growth-promoting bacteria to plant development, as one of the components of the dual consortium is a producer of indoleacetic acid (IAA), which promotes better plant development.

Recently, Jyothsna et al. (2024) conducted a study on different nitrogen application management practices in

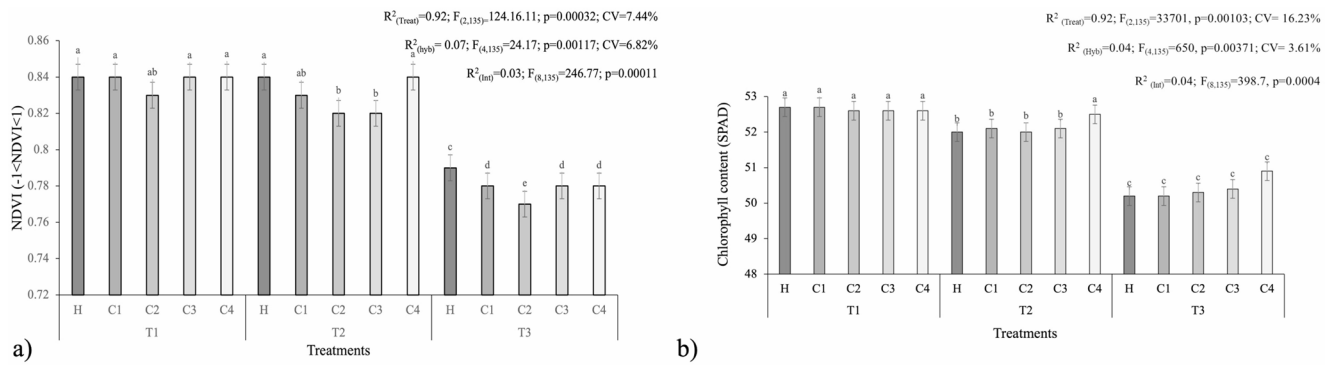


Fig. 2 Normalized Difference Vegetation Indices (NDVIs) and chlorophyll content (SPAD units) at VT phenophase (**b**) in five commercial maize hybrids (H, C1, C2, C3, and C4) under three treatments: T1 (seed pre-germination for 24 h with a bacterial dual consortium), T2 (bacterial consortium applied 15 days after emergence), and T3 (control treatment without bacterial consortium application). The rectangular bars represent the standard deviation of the mean for each treatment. $R^2(Treat)$, $R^2(Hyb)$, and $R^2(Int)$ represent the coefficients

of determination for treatments, hybrids, and their interaction, respectively. F : calculated values from Fisher's test; p : probability; CV : coefficient of variation. Different uppercase letters in the same row and different lowercase letters in the same column indicate significant differences between treatments and hybrids, respectively, according to Tukey's test for $p < 0.05$. In the columns where supercase does not appear, there were no significant differences

maize cultivation. These authors applied a recommended dose of $200 \text{ kg ha}^{-1} \text{ N}$ and 60 kg ha^{-1} phosphorus (in the form of monoammonium phosphate) and reported NDVI values of 0.8. In our study, this NDVI value was achieved in treatments T1 and T2 starting from the V8 phenophase. This value was exceeded in the V9, V10, V11, V12, and VT phenophases, with the application of only 100 kg ha^{-1} of nitrogen and 30 kg ha^{-1} of phosphorus in the form of monoammonium phosphate. These results demonstrate the contributions of *E. cloacae* and *P. megaterium*, as they have phosphate solubilization indices between 2 and 3 (Table 1). In addition, both bacteria are strong producers of siderophores, which increase the availability of micronutrients that contribute to the plants' overall physiological state, as observed through NDVI values. Moreover, their indoleacetic acid production capabilities—particularly those of *E. cloacae*—may enhance nitrogen metabolism. Sallam et al. (2024) found that utilizing *E. cloacae* in maize cultivation not only helped suppress the fungus *F. oxysporum* but also boosted plant growth by increasing chlorophyll content, which is directly related to NDVI (Gao et al. 2024).

The chlorophyll content, measured in SPAD units at VT phenophase, differed significantly between the established treatments (Fig. 2b). Likewise, the difference between hybrids was significant, though to a lesser extent. A highly significant interaction was observed between the two sources of variation. In the treatments where the bacterial consortium was applied as preemergence, all hybrids exhibited chlorophyll contents greater than 52 SPAD units without significant differences. When the bacterial consortium was applied 15 days after emergence, only the C4 hybrid showed a content greater than 52 SPAD units, also with no

significant differences compared to all the hybrids subjected to the consortium during preemergence.

In the present study, the lowest chlorophyll content (between $49 < \text{Chl} > 51$ SPAD units) was obtained in the five hybrids evaluated in the control treatment (T3). These did not present statistically significant differences among themselves. This result demonstrated the promoting effect of the dual bacterial consortium on the nutrition of maize plants. The greatest contribution to the total variability in chlorophyll content was attributed to the treatments (91%), while the hybrids and their interaction accounted for only 5% and 4%, respectively. The results obtained in the NDVI are consistent with the chlorophyll content obtained in the VT phenophase in all hybrids under treatments T1 and T2. In a study conducted by Rafique et al. (2021), indoleacetic acid (IAA) produced by *Enterobacter* was the basis of the promoting effects observed in maize phenotypes, as it stimulates cell elongation and division. Agunbiade et al. (2024) characterized a group of bacteria and evaluated their capacity to promote development in maize. One of these bacteria belonged to the *Prestia* genus. They reported a 12% plant development-promoting effect and a significant increase in chlorophyll content due to the effects of *Prestia megaterium*. The promotion of root growth by *Enterobacter cloacae* leads to improved nutrient uptake, which subsequently increases the chlorophyll content in maize (El-Ganainy et al. 2023).

Photosynthesis and transpiration

The maximum photosynthetic activity (Fig. 3a), evaluated 45 days after emergence (45 DAE), significantly differed among the established treatments ($F_{(2,135)} = 1418.11$,

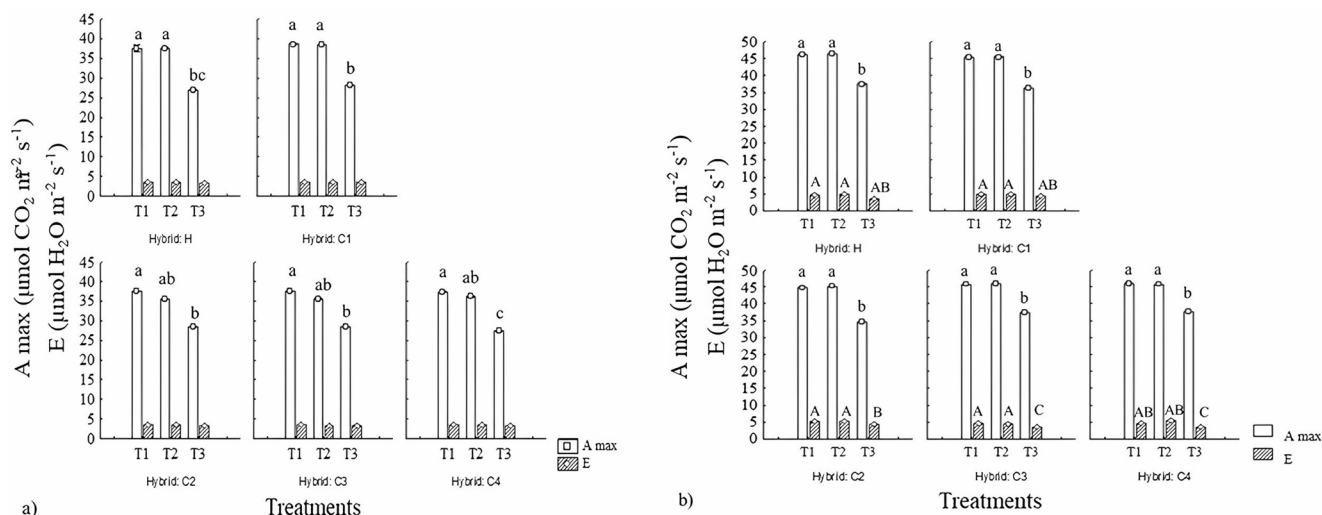


Fig. 3 Maximum photosynthesis (A max) at 45 days (a) and at 78 days (b) after emergence in five commercial hybrids of maize (H, C1, C2, C3, and C4) under three treatments (T1: pre-germination of seeds for 24 h with a bacterial dual consortium; T2: bacterial consortium applied 15 days after emergence; and T3: control treatment without bacterial consortium application). The rectangular bars represent the standard

deviation of the mean for the treatments. Different uppercase letters in the same row and different lowercase letters in the same column indicate significant differences between treatments and hybrids, respectively, according to Tukey's test for $p < 0.05$. In the columns where superscript does not appear, there were no significant differences

$p = 0.00120$, $CV = 17.23\%$, $R^2 = 0.91$), hybrids also significantly differed ($F_{(4,135)} = 7.4$, $p = 0.00020$, $CV = 7.21\%$, $R^2 = 0.12$). Moreover, highly significant interactions were detected between the treatments and the hybrids ($F_{(8,135)} = 9.45$, $p = 0.00002$, $R^2 = 0.16$). This result revealed a slight increase in photosynthesis in treatments T1 and T2 (with no differences between them) compared with that in the control treatment T3. In this growing phenophase, the contribution of the bacterial consortium in treatments T1 and T2 was an average of 30% higher than in the control (T3) (Fig. 3a). The average general variability percentage for the established treatments was $CV = 17\%$. However, the variability found in the hybrid variation source was only 8%.

At 78 days after emergence (78 DAE) (VT phenophase) (Fig. 3b), photosynthetic activity increased by an average of $10 \mu\text{mol CO}_2 \text{ m}^{-2} \text{ s}^{-1}$ compared to 45 days after emergence. This variable showed significant differences between the treatments ($F_{(2,135)} = 33863$, $p = 0.00211$, $CV = 17.11\%$, $R^2 = 0.96$) and the hybrids evaluated ($F_{(4,135)} = 485$, $p = 0.00148$, $CV = 8.15\%$, $R^2 = 0.03$). Additionally, a significant interaction effect was observed between the treatments and the hybrids ($F_{(8,135)} = 97.29$, $p = 0.02661$, $R^2 = 0.01$). Hybrids H, C1, C3, and C4, with no statistical differences between them in T1 and T2, were the most photosynthetically active, while the hybrid C2 had the lowest photosynthesis in T3. The source of variation with the greatest variability in maximum photosynthesis was the treatments (17%), while the variability generated between the hybrids was 8.15%.

Transpiration did not significantly differ between treatments ($F_{(2,135)} = 4.74$, $p = 0.01026$, $CV = 3.23\%$, $R^2 = 0.06$) when measured at 45 DAE (Fig. 3a). There were no significant differences between hybrids ($F_{(4,135)} = 0.35$, $p = 0.69938$, $CV = 0.78\%$, $R^2 = 0.01$), nor were there any significant interactions between these two sources of variation ($F_{(8,135)} = 0.94$, $p = 0.48484$, $R^2 = 0.05$). This interesting result regarding transpiration at 45 days after emergence suggests that the bacteria used in the consortium did not affect the overall rate of water loss through stomata, despite the significant increase observed in photosynthesis. Consequently, the photosynthetic water use efficiency (WUE) also remained statistically similar between the treatments. While an increase in photosynthesis generally implies increased water use efficiency, this is not always the case. In some instances, particularly under abiotic stress conditions (Argente-Martínez et al. 2024a, b, c), plants often use more water per unit of assimilated CO_2 to maintain optimal gas exchange rates, even with excessive water consumption.

In VT phenophase, transpiration showed highly significant differences between treatments ($F_{(2,135)} = 609.26$, $p = 0.00120$, $CV = 3.62\%$, $R^2 = 0.56$) and only significant differences between hybrids ($F_{(4,135)} = 65.2$, $p = 0.02013$, $CV = 1.06\%$, $R^2 = 0.15$). However, there was a highly significant interaction between these two sources of variation ($F_{(8,135)} = 38.37$, $p = 0.00162$, $R^2 = 0.21$). Regarding transpiration, the percentage of variability between hybrids was only 1%, with the lowest values found in treatment 3 for hybrids H, C1, C2, and C3, and the difference was more pronounced for C4 (Fig. 3b). The results obtained here

demonstrate the similarity of the response between hybrids and the significant contribution of the microbial consortium treatments.

All the hybrids at 78 days after emergence showed photosynthesis values higher than $43 \mu\text{mol CO}_2 \text{ m}^{-2} \text{ s}^{-1}$ in treatments T1 and T2 (Fig. 3b), which is considered high photosynthesis in maize (Alshegaihi et al. 2024). This result suggests a high capacity for carbon nutrition and, therefore, a relatively high grain yield, provided the mobilization rate of carbohydrates and proteins is also high (Asghar et al. 2024). Studies conducted by Khan et al. (2024) demonstrated the efficiency and effectiveness of using PGPR for mineral and carbon nutrition, which increased the net photosynthetic activity of maize by 27–29%. The bacteria *E. cloacae* and *P. megaterium* have not been used to promote development based on photosynthetic activity.

Figure 4 presents the results of a canonical variable analysis based on experimental data from five hybrids, three bacterial consortia, and nine variables. The analysis accounts for 99.3% of the total variability in the data. The representation indicates that combinations of hybrids with the control treatment (absence of bacterial consortium) did not affect any of the evaluated variables. However, the combinations involving the two bacterial consortia (T1 and T2), regardless of the hybrid used, had a positive impact on the

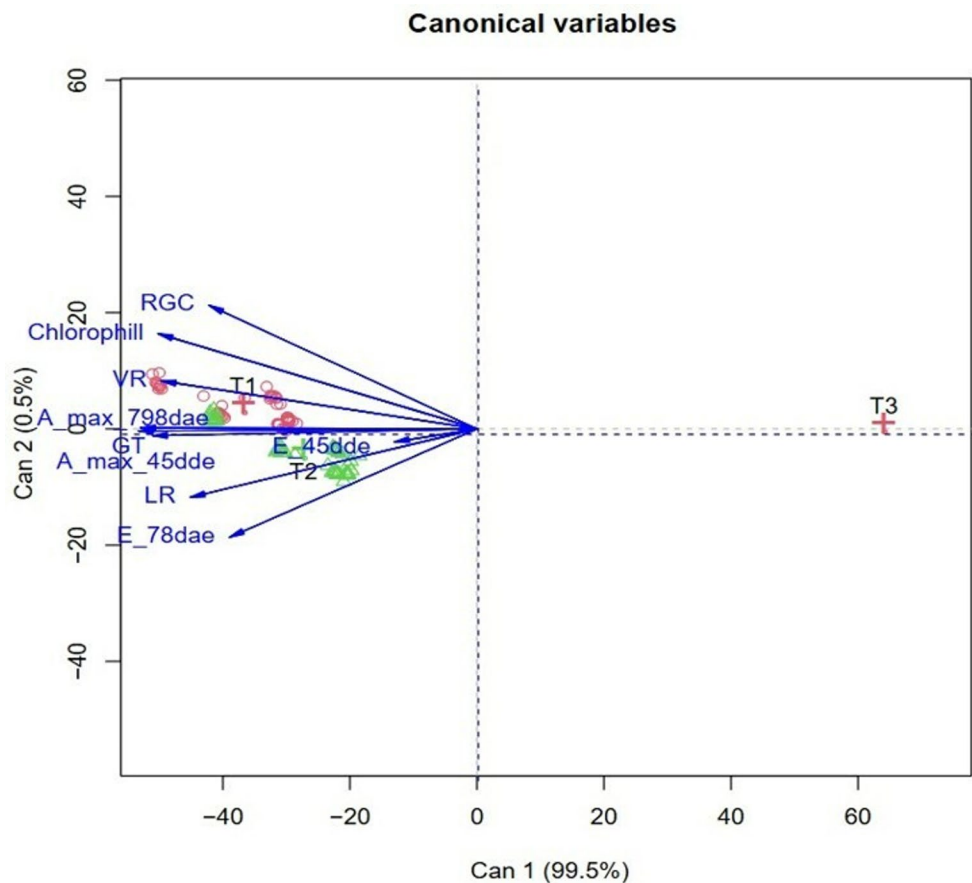
performance of all measured variables, as evidenced by the proximity of the treatments and variables shown in Fig. 4.

Multivariate analyses are crucial tools for better understanding experimental results that involve a large number of variables (Ratke et al. 2024; Zuffo et al. 2024). Graphical representations help interpret the results and the associations between treatments and variables, highlighting the importance of this approach (Aguilera et al. 2023). The clear associations between bacterial consortium treatments and their effects on various maize hybrids are shown in Fig. 4.

Mowafy et al. (2021) reported that treating plants with *Enterobacter cloacae* significantly increased the content of chlorophylls and other pigments, which were not evaluated here. This finding, which aligns with the results obtained in this study regarding development promotion, is consistent with the high photosynthetic activity observed.

The results demonstrated that, compared to the non-inoculated control, inoculation with *P. megaterium* considerably increased plant dry weight by 26.96% and 8.79%, respectively, and the number of grains per plant by 48.97% and 35.29% (Srihaworn et al. 2023). In general, the bacterial consortium promoted all the morphological and physiological variables across all five maize hybrids evaluated. This outcome can be attributed to the fact that the siderophores produced by this bacterium provide not only iron but also

Fig. 4 Canonical analysis for five commercial maize hybrids (H, C1, C2, C3, and C4) under three treatments (T1: pregermination of seeds for 24 h with a bacterial dual consortium; T2: bacterial consortium applied 15 days after emergence; and T3: control treatment without bacterial consortium application), evaluated from emergence (VE) until VT phenophase. The rectangular bars represent the standard deviation of the mean for each treatment. A_max_45dde: Maximum photosynthesis 45 days after emergence; E_45dde: transpiration 45 days after emergence; Chlorophyll: chlorophyll content (SPAD units); A_max_798dae: maximum photosynthesis 78 days after emergence (VT phenophase); E_78dae: transpiration 78 days after emergence (VT phenophase); RGC: relative growth rate; LR: final root length; GT: final stem diameter; VR: root volume



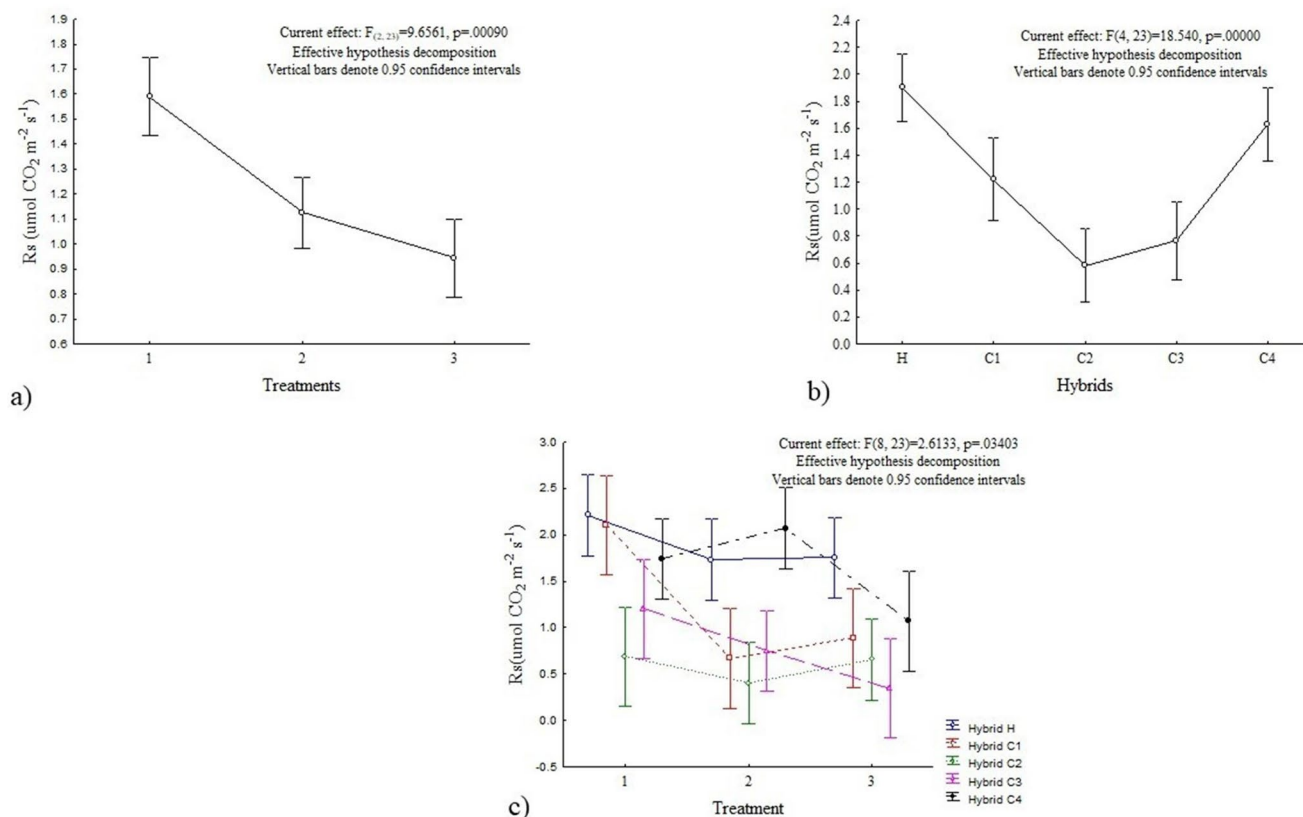


Fig. 5 Analysis of the isolated factors (Treatments **a**); Hybrids **b**) and the interaction (Treatments*Hybrids **c**)) for five commercial maize hybrids (H, C1, C2, C3, and C4) under three treatments (T1: pre-germination of seeds for 24 h with a bacterial dual consortium; T2:

bacterial consortium applied 15 days after emergence; and T3: control treatment without bacterial consortium application), evaluated from emergence (VE) until the VT phenophase. The rectangular bars represent the standard deviation of the mean for each treatment

other micronutrients that support growth, as reported by Bendaha et al. (2019). Additionally, the ability of *E. cloacae* to solubilize phosphate allows plants to access more phosphates, which are essential for all metabolic processes.

Soil respiration

Soil respiration is the primary pathway through which carbon dioxide (CO₂) fixed by plants is released into the atmosphere. The rates of soil respiration are primarily influenced by the amount and composition of decomposable organic matter, soil temperature and moisture, root biomass, and microbial activity (Lewczuk et al. 2024). The analysis of soil respiration, evaluated only during the flowering phenophase (VT), confirmed the presence of the bacterial consortium in the rhizosphere of the hybrids studied (Fig. 5).

When analyzing the effect of individual factors and their interaction (Fig. 5), it was found that the treatments contributed 14.06% of the total variance, with a statistically significant effect ($F_{(2,23)}=9.6561, p=0.000903$). In general, treatments T1 and T2 resulted in a significant increase compared to T3 (control). The hybrid factor accounted

for 53.98% of the total variance, indicating a strong effect ($F_{(4,23)}=18.5396, p=0.000001$). The interaction between Treatment and Hybrid explained 15.22% of the variance, showing a significant interaction ($F_{(8,23)}=2.6133, p=0.034033$) (Fig. 5).

The significant interaction result shows that even within the same plant species, there is variability in response due to the living and metabolically active nature of the organisms involved. Further measurements at the end of the crop cycle will be needed to conduct a more comprehensive analysis and verify these findings. The residual error accounted for 16.74% of the variance, suggesting that there is room for improvement in the model.

We found that the R_s rates measured during the sampling campaign contrast and are comparable with seasonally dry natural ecosystems, agrosystems, and cultivars. For example, during the dry season for a tropical dry forest, Vargas-Terminel et al. (2022) reported a mean R_s rate of $1.29 \pm 0.09 \mu\text{mol CO}_2 \text{ m}^{-2} \text{ s}^{-1}$ while, for xeric shrubland was $0.404 \mu\text{mol CO}_2 \text{ m}^{-2} \text{ s}^{-1}$ and $1.24 \mu\text{mol CO}_2 \text{ m}^{-2} \text{ s}^{-1}$ during the dry and wet season, respectively (Guillen-Cruz et al., 2023). In agrosystems, Zhang et al. (2025) reported R_s variations

for winter and summer rotational crops from $1.50 \pm 0.41 \mu\text{mol CO}_2 \text{ m}^{-2} \text{ s}^{-1}$ to $5.83 \pm 0.27 \mu\text{mol CO}_2 \text{ m}^{-2} \text{ s}^{-1}$ and Han et al. (2007) observed a mean R_s rate of $3.16 \mu\text{mol CO}_2 \text{ m}^{-2} \text{ s}^{-1}$ during the growing season in a spring maize crop. Meanwhile, Du et al. (2021) found in maize under tillage practices a mean R_s rate of $4.90 \pm 0.44 \mu\text{mol CO}_2 \text{ m}^{-2} \text{ s}^{-1}$ during two-growing cycles (June–October) and Lai et al. (2012) found mean RS values of $2.11 \mu\text{mol CO}_2 \text{ m}^{-2} \text{ s}^{-1}$ and $2.77 \mu\text{mol CO}_2 \text{ m}^{-2} \text{ s}^{-1}$ in *Elaeagnus angustifolia* and *Triticum aestivum* crop systems, respectively and, in semi-arid agricultural sites with different soil and crop management showed a mean of $1.82 \mu\text{mol CO}_2 \text{ m}^{-2} \text{ s}^{-1}$ during the dry season and $3.05 \mu\text{mol CO}_2 \text{ m}^{-2} \text{ s}^{-1}$ in the wet season (Guillen-Cruz et al. 2023). According to research examining a variety of block treatments, Ollio et al. (2025) found that the mean RS for potato crops under a multiple fertilization scope was $0.1648 \mu\text{mol CO}_2 \text{ m}^{-2} \text{ s}^{-1}$ in treatments that included microbial inoculants.

The ranking of homogeneous groups was clarified. For example, the lowest CO_2 flux was observed in C3-Treatment 3 ($0.35 \mu\text{mol CO}_2 \text{ m}^{-2} \text{ s}^{-1}$), while the highest was observed in H-Treatment 1 ($2.21 \mu\text{mol CO}_2 \text{ m}^{-2} \text{ s}^{-1}$). Some redundancies in groups (e.g., multiple C2 values) should be verified to ensure no input errors.

The increased results in the T1 and T2 treatments confirm the presence of microorganisms associated with the rhizosphere of plants from the majority of the hybrids tested. Furthermore, these findings demonstrate that the degree of interaction or association is highly dependent on the genetic material used. Also, these findings are further reinforced by soil respiration analyses, which confirm the sustained presence and activity of the bacterial consortium in treated rhizospheres. Notably, the increased soil respiration in consortium-treated plots reflects an elevated microbial metabolic activity, contributing to improved soil health and nutrient cycling.

The significant contribution of the treatments to the total variability in all the morphological and physiological variables evaluated confirms their growth-promoting effect on maize. Additionally, the considerable similarity in the responses of the hybrids, despite their distinct development patterns, demonstrates that the treatments are effective in promoting good growth and physiological performance. These findings will be further validated once their correlation with agronomic performance variables is established. In all variables evaluated in the interaction, it was shown that *E. cloacae* and *P. megaterium* contribute to plant development, even with fertilization doses lower than the typical application standards used in the Yaqui Valley. These results help reduce the contaminant load caused by excessive nitrogen application to the soil.

Since rhizobacteria thrive in highly saline environments with limited nutrient availability and temperatures typical of semiarid climates, they are likely associated with plant species that grow in similar conditions. Subsequent analyses can concentrate on integrating particular metrics that could further confirm the bacterial consortium.

Conclusion

The present study provides compelling evidence that the application of a dual bacterial consortium comprising *E. cloacae* and *P. megaterium* significantly enhances maize physiological performance and growth metrics. Our findings demonstrate that these plant growth-promoting rhizobacteria (PGPR) do not adversely affect seed water absorption or germination rates. Instead, they exert profound positive effects on root volume, chlorophyll content, photosynthetic efficiency, and soil respiration, as evidence of improved soil health. The application of the consortium, whether during pre-germination or 15 days of post-emergence, generates the same promoting effect with increased root biomass and a substantial reduction in wilting time, indicating superior water regime and efficiency. The integration of *E. cloacae* and *P. megaterium* into maize cultivation represents a transformative step toward reducing chemical input dependency while maintaining or even enhancing crop productivity. By leveraging microbial biotechnology, this study not only advances the understanding of PGPR-mediated plant enhancement but also provides a scalable solution to promote environmentally responsible and resilient agricultural practices for global food security challenges.

The dual bacterial consortium addresses major issues related to excessive nitrogen and phosphorus applications and offers a practical and environmentally beneficial substitute for traditional chemical fertilizers from an agronomic standpoint. The ability of *E. cloacae* and *P. megaterium* to solubilize phosphate and produce siderophores enhances nutrient bioavailability, which translates into superior plant vigor and metabolic efficiency. Moreover, their significant role in modulating root architecture suggests their utility in sustainable agricultural practices aimed at mitigating abiotic stressors such as drought and soil degradation.

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Data availability The datasets used and/or analyzed during the current study are available from the corresponding author on reasonable request.

Declarations

Ethics approval and consent to participate Not applicable.

Consent for publication Not applicable.

Competing interests The authors declare no competing interests.

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