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Investigation on starch and cellulose degradation, siderophore production and potassium solubilization of rhizosphere bacteria isolated from sugarcanes cultivated in Ben Cau district, Tay Ninh province, Vietnam

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Abstract

Rhizobacteria play a crucial role in enhancing plant growth through various mechanisms, including nutrient solubilization and decomposition of complex organic compounds. This study aimed to evaluate the potential of 31 rhizobacteria strains, isolated from the rhizosphere of sugarcane (*Saccharum* spp.) cultivated in Ben Cau district, Tay Ninh province, Vietnam, for starch and cellulose decomposition, siderophore synthesis, and potassium solubilization. The ability of the strains to degrade starch and cellulose was determined by agar well diffusion approach. The ability of siderophore synthesis was investigated by using the Chrome Azurol Sulfonate (CAS) assay. Potassium solubilization was quantified using the sodium tetraphenylborate method, measuring the release of soluble potassium from insoluble sources. The result showed that 74% of the strains were capable of hydrolyzing starch, with strain BC45 exhibiting the strongest activity, forming a halo zone diameter of 1.80 ± 0.20 cm. 87% of the strains showed the ability to degrade cellulose, with strains BC12 and BC49 demonstrating the highest activity, producing clearing zone diameters of 1.87 ± 0.12 cm and 1.73 ± 0.46 cm, respectively. Notably, all strains were capable of releasing soluble potassium from insoluble potassium, with BC06 showing the highest capability with K_2O concentrations of 35.23 mg/L. Additionally, 42% of the strains were able to produce siderophores. This study demonstrated that the isolated rhizobacteria possessed significant potential for starch and cellulose decomposition, potassium solubilization, and siderophore production. These findings suggest that these strains could be valuable candidates for the development of biofertilizers and biostimulants to improve sugarcane cultivation in the region.

Keywords: Rhizosphere bacteria; Starch decomposition; Cellulose decomposition; Siderophore synthesis potassium solubilization; Agar well diffusion approach

1. Introduction

The sugarcane area of Vietnam was approximately 17,484 hectares in 2023, of which the Southeast region accounts for 10,736 hectares. The sugarcane area of Tay Ninh province, a province in the Southeast region, was 7,175 hectares, the largest in the Southeast region, accounting for 41% of Vietnam's sugarcane area [1]. Ben Cau district had a sugarcane area of 342 hectares in 2023, ranking 5th among the 9 districts, a town, and a city of Tay Ninh province [2].

In Vietnam, studies have shown that sugarcane yield increases proportionally with the amount of fertilizer applied. Most of Tay Ninh province's land resources are Acrisol soils with low or imbalanced nutrient levels. Specifically, the humus content, as well as total and available nitrogen, phosphorus, and potassium are very low [3]. Therefore, in agroforestry on gray soils, attention must be paid to fertilizer investment to achieve high yields [4]. The excessive use of chemical

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fertilizers not only increases production costs but also has adverse effects on crops, ecosystems, the environment, and human health.

Towards a sustainable agricultural development, many countries around the world have been researching and applying cleaner, safer, and more environmentally friendly agricultural practices [5]. One of these methods is to exploit the beneficial relationship between plants and microorganisms in the environment. Many soil bacteria species that thrive in the plant rhizosphere soil have the ability to stimulate plant growth. These bacteria are collectively known as Plant Growth Promoting Rhizobacteria (PGPR). PGPR interact and carefully select their common partners through natural selection, creating host specificity and sensitivity to environments where there is little bacterial diversity [6].

PGPR promote plant growth by increasing the availability of nutrients to plants and producing essential metabolites without negatively impacting the environment. Furthermore, PGPR enhance the solubilization of phosphorus and other nutrients, increase iron uptake in plants through siderophore synthesis, produce antibiotics and other compounds that inhibit the growth of plant pathogens, stimulate the bioremediation of contaminated soil, help plants tolerate abiotic stresses such as extreme temperatures, salinity, and drought, and minimizes the adverse effects of various other stresses [7, 8]. The enhancement of soil nutrition and the biocontrol effects of PGPB are both facilitated by the soil-borne production of hydrolytic enzymes such as protease, cellulase, amylase, pectinase, and chitinase [9, 10].

The aims of the present study are to evaluate the potential of 31 rhizosphere bacteria, isolated from the rhizosphere of sugarcanes cultivated in Ben Cau district, Tay Ninh province, Vietnam for starch and cellulose degradation, siderophore production, and potassium solubilization. This evaluation is conducted in addition to their previously established nitrogen fixation, phosphorus solubilization, and IAA synthesis capabilities, as determined in the authors' previous study. These isolates represent a promising resource for developing biofertilizers promoting sugarcane growth, especially sugarcanes grown in Ben Cau district, Tay Ninh province, Vietnam. They achieve this by supplying N, IAA, soluble phosphorus and potassium, and siderophores to plants, enhancing soil organic matter, providing biocontrol as well as fostering a diverse rhizosphere microbiome.

2. Material and methods

2.1. Preparation of Bacteria

Thirty-one strains of root-associated bacteria were isolated from the rhizosphere of sugarcane grown in Ben Cau district, Tay Ninh province, determined their capable of nitrogen fixation and phosphate solubilization, preserved and stored in the laboratory of Saigon University were used in the study. Prior to conducting the experiments, the bacterial strains were activated on liquid LB medium, incubated for 24-48 hours at 30°C on a thermostatic shaker at 120 rpm. The cell suspension density of each strain was determined using a spectrophotometer at a wavelength of 600 nm and adjusted to a 0.5 McFarland standard, corresponding to 1.5 x 10^8 CFU/mL [11]. This standard cell density was applied to all subsequent experiments.

2.2. Investigating the organic matter degradation capability of bacterial strains

The degradative capabilities of bacterial strains towards starch and cellulose were evaluated. Starch agar and carboxymethyl cellulose (CMC) agar were employed as the respective media for assessing starch and cellulose hydrolysis. The pH of the culture media was precisely adjusted as required, and solidification was achieved using agar at a concentration of 15 g/L [12, 13, 14].

The agar well diffusion method, as previously described [15], was utilized to quantify the degradation potential of both substrates. Wells with a uniform diameter of 5 mm were aseptically created on the agar plates. Each well was subsequently inoculated with 50 µL of a bacterial suspension standardized to a cell density of 1.5 x 10^8 colony-forming units (CFU)/mL. Following incubation at 28 ± 2 ℃ for 48 hours, the formation of distinct clear zones, indicative of substrate degradation, was observed and documented.

The extent of starch and cellulose degradation was determined by measuring the diameter of these clear zones. Specifically, the clear zone diameter was calculated as the difference between the total diameter of the clear zone and the diameter of the bacterial colony [16]. A larger clear zone diameter correlated with increased substrate degradation capability.

For cellulose degradation assays, post-incubation, the agar plates were flooded with a 0.1% Congo red solution for 15 minutes, followed by rinsing with 1 M NaCl to enhance the visualization of the clear zones [17]. In the starch hydrolysis

experiments, after incubation, the agar plate surfaces were flooded with Lugol's iodine solution (prepared by dissolving 5.0 g iodine and 10 g potassium iodide in 100 mL of water) for one minute, and then the excess solution was discarded. Lugol's iodine reacts with starch, forming a dark blue complex. Areas where starch hydrolysis had occurred were characterized by clear zones, lacking the dark blue coloration, surrounding the bacterial colonies [17].

2.3. Potassium Solubilization Assay

The potassium concentration in bacterial cultures was quantified using the sodium tetraphenylborate method, in conjunction with a standard calibration curve [18]. This involved comparing the absorbance values at OD685 of the bacterial culture samples to those of standard solutions with known potassium concentrations. The potassium solubilization ability of the tested bacterial strains was then assessed by measuring the resulting K^+ concentration (mg/L) in the culture medium. A higher K^+ concentration indicated a greater degree of insoluble potassium solubilization, reflecting a superior potassium-solubilizing capability of the bacteria.

2.4. Siderophore production

Siderophore production by bacteria was able to be detected using the Chrome Azurol Sulfonate (CAS) assay, originally described by Schwyn and Neilands (1987). A color change of the CAS medium indicated the presence of siderophores. The preparation of the CAS medium followed the protocol outlined by Chaitanya et al. (2014) [19]. Growth medium for bacteria was solid or liquid Luria Bertani medium (LB). Siderophore production was assessed using the paper-disc agar diffusion method, with the CAS-Growth medium plates prepared according to the method of Srivastava et al., (2013) [20].

2.5. Experiment design and data analysis

Experiments were conducted using a completely randomized design with three replicates. Quantitative data were analyzed by one-way ANOVA, and mean comparisons were performed using Duncan's multiple range test at a 5% significance level, with the aid of IBM SPSS Statistics version 20.0.

3. Results and discussion

3.1. Starch degradation capability of bacterial strains

Bacterial strains being capable of starch hydrolysis form a clear zone (halo) on starch agar medium. A larger halo diameter indicates a higher starch hydrolysis ability. Out of 31 bacterial strains tested, 23 (74%) showed the ability to hydrolyze starch, while 8 (26%) did not (Table 4.2). The average halo diameter ranged from 0.17 cm to 1.7 cm. Strain BC45 exhibited the highest starch hydrolysis ability, with a halo diameter of 1.80 ± 0.20 cm. Following closely were strains BC14, BC12, and BC40, with average halo diameters of 1.70 ± 0.17 cm, 1.67 ± 0.29 cm, and 1.63 ± 0.84 cm, respectively. The eight strains that did not demonstrate starch hydrolysis ability were BC01, BC06, BC08, BC09, BC32, BC34, and BC49.

There have been reported studies of starch degradation microorganisms from different sources. PGPR is one source on those with bacterial species of starch degradation. Rhizobacteria can secrete amylases to soil to perform extracellular starch digestion and facilitate other different organic matters for plants to easily absorb and manufacture their food. Dida (2018) [21] isolated and characterized starch degrading rhizobacteria from various plants at four sites located on Jimma University Main Campus, Ethiop. Fifty-three starch degrading strains were isolated. Clear zone diameters were arranged from 0.3 cm - 1.4 cm. Zhang et al., 2024 isolated 36 bacterial strains from tobacco rhizosphere soil and leaves were capable of forming transparent zones on starch-selective culture medium. Among them, there were 19 strains with higher ability of starch hydrolysis [22]. In investigation dealing with the isolation of starch degrading rhizobacteria from soil of Mymemsingh, Bangladesh, Mawa et al., 2022 isolated 8 starch degrading bacteria strains from rhizosphere soil [17]. Dang et al., 2018 studied organic decomposition ability of 22 rhizosphere bacteria isolated from *Piper nigrum* L. Most of the isolates (21 strains) presented ability to hydrolyze starch [14]. Chouban et al., (2016) isolated 16 rhizobacteria from 08 different plant species showed ability to hydrolyze starch with diameter of clear zones arranging from 1.8 - 5.8 mm [23].

Table 1 Results of the starch degradation ability survey of 31 rhizobacteria strains

Isolate name	Halo zone diameter (cm)	Isolate name	Halo zone diameter (cm)
Control	0.00 ± 0.00^{i}	BC30	0.70 ± 0.00^{gh}
BC01	0.00 ± 0.00^{i}	BC31	0.93 ± 0.25^{defg}
BC04	1.27 ± 0.06^{bcdef}	BC32	0.00 ± 0.00^{i}
BC06	0.00 ± 0.00^{i}	BC33	0.80 ± 0.00^{efgh}
BC08	0.00 ± 0.00^{i}	BC34	0.00 ± 0.00^{i}
BC09	0.00 ± 0.00^{i}	BC36	1.37 ± 1.01^{abcd}
BC10	1.03 ± 0.00^{cdefg}	BC39	0.17 ± 0.06^{i}
BC11	0.90 ± 0.00^{defgh}	BC40	1.63 ± 0.84^{ab}
BC12	1.67 ± 0.29^{ab}	BC42	1.47 ± 0.42^{abc}
BC14	1.70 ± 0.17^{ab}	BC43	1.00 ± 0.00^{cdefg}
BC15	1.30 ± 0.00^{bcde}	BC45	1.07 ± 0.12^{cdefg}
BC16	0.43 ± 0.12^{hi}	BC46	1.80 ± 0.20^{a}
BC22	0.20 ± 0.00^{i}	BC49	0.00 ± 0.00^{i}
BC23	0.00 ± 0.00^{i}	BC53	1.10 ± 0.10^{cdefg}
BC27	0.77 ± 0.12^{fgh}	BC54	0.90 ± 0.00^{defgh}
BC28	1.27 ± 0.15^{bcdef}	BC55	0.77 ± 0.06^{fgh}

Values within the same vertical column followed by one or more identical letters indicate no statistically significant difference at an alpha significance level of 0.05 according to Duncan's test.

3.2. Cellulose degradation capability of bacterial strains

The cellulose-degrading ability of the tested bacterial strains was demonstrated by the appearance of clearing zones on CMC medium. Larger clearing zone sizes indicate higher cellulose-degrading ability. The results of the cellulose degradation ability survey of 31 testing bacterial strains are presented in Table 2. 27 isolates, out of 31 (87%) experimental bacterial strains showed cellulose degradation ability. The average diameter of the degradation halo rings ranged from 0.1 cm to 1.87 cm. Among these strains, BC12 and BC49 exhibited the highest cellulose degradation ability, with average degradation halo diameters of 1.87 ± 0.12 cm and 1.73 ± 0.46 cm, respectively. BC45 demonstrated the second highest cellulose degradation ability, with an average degradation halo zone diameter of approximately 1.33 ± 0.15 cm. Four out of 31 strains (13%) showed no cellulose degradation ability.

Cellulase extracellular enzymes are categorized into three major kinds, including endo- β-1,4 glucanase, exoglucanase, and β-glucosidase. These are glycoside hydrolyses that cleavage β-1,4-D glucan bonds present in cell wall components of certain fungi, bacteria, and all plants. Cellulase degrades their cell wall to produce cellobiose, glucose, and cello oligosaccharide. Cellulolytic activity has been reported as a potential biocontrol mechanism against plant pathogens such as some fungi, bacteria, and actinomycetes [24]. Several studies have reported rhizobacteria were isolated from the rhizosphere of different plants and showed cellulolytic capability [25].

When investigating rhizobacterial isolates from the apple tree rhizosphere for cellulose degradation, Jabiri et al., 2023 found that 13 of the 16 isolates tested could degrade cellulose [26]. The isolate E7-2 showed the highest cellulolytic capability. Shreshtha et al., (2025) tested 41 rhizobacteria out of 246 bacterial strains isolated from *Opuntia Ficus-Indica* cactus plant's rhizosphere for plant growth promotion characteristic analysis [27]. The result showed 40.04 % tested isolates possessed cellulase activity. Another study of 33 bacteria from the rhizosphere of date palms for cellulase activity detected that 14 % tested strains showed positive results with indexes ranging from 1.1 to 3.8 and M022 was the most efficient strain [28].

Table 2 Results of the cellulose degradation ability survey of 31 rhizobacteria strains

Isolate name	Halo zone diameter (cm)	Isolate name	Halo zone diameter (cm)
Control	0.00 ± 0.00^{g}	BC30	0.20 ± 0.00^{efg}
BC01	0.10 ± 0.00^{fg}	BC31	1.03 ± 0.45^{bc}
BC04	0.47 ± 0.25^{ef}	BC32	1.23 ± 0.55^{bc}
BC06	0.00 ± 0.00^{g}	BC33	0.40 ± 0.10^{efg}
BC08	0.10 ± 0.00^{fg}	BC34	0.27 ± 0.21^{efg}
BC09	0.00 ± 0.00^{g}	BC36	0.90 ± 0.53^{cd}
BC10	0.60 ± 0.00^{de}	BC39	0.00 ± 0.00^{g}
BC11	0.27 ± 0.06^{efg}	BC40	0.00 ± 0.00^{g}
BC12	1.87 ± 0.12^{a}	BC42	1.07 ± 0.12^{bc}
BC14	0.37 ± 0.12^{efg}	BC43	0.17 ± 0.06^{fg}
BC15	0.23 ± 0.12^{efg}	BC45	1.33 ± 0.15^{b}
BC16	1.10 ± 0.36^{bc}	BC46	0.27 ± 0.06^{efg}
BC22	0.30 ± 0.26^{efg}	BC49	1.73 ± 0.46^{a}
BC23	0.10 ± 0.00^{fg}	BC53	0.23 ± 0.23^{efg}
BC27	0.13 ± 0.06^{fg}	BC54	0.20 ± 0.00^{efg}
BC28	1.07 ± 0.06^{bc}	BC55	0.33 ± 0.12^{efg}

Values in the same vertical column followed by one or more identical letters indicate no statistically significant difference at a significance level of alpha 0.05 according to Duncan's test.

3.3. Potassium solubilization capability of bacterial strains

All tested bacterial strains (100%) exhibited the ability to solubilize insoluble potassium into soluble potassium K_2O (Table 3). The average K_2O content across measurements at 7, 14, and 21 days ranged from 9.87 mg/L to 35.23 mg/L. The five strains with the highest potassium solubilization ability were BC06, BC01, BC22, and BC34, with corresponding K_2O contents of approximately 35.23 mg/L, 32.75 mg/L, 29.63 mg/L, and 27.71 mg/L, respectively. These strains demonstrated high capability of potassium solubilization throughout the sampling period, and K_2O content increased gradually with incubation time. Several strains (BC09, BC31, BC32, BC33, BC36, BC39, BC40, BC42, BC43, BC45, BC46, BC53, and BC54) showed a gradual increase in average soluble potassium content during the first two weeks of incubation, followed by a decrease. Some strains (BC09, BC12, BC28, BC30, BC3, BC32, and BC33) exhibited an increase in average soluble potassium content during the first week, followed by a gradual decline. The remaining strains showed a gradual increase in soluble potassium content with incubation time.

Overall, the potassium solubilization capability of the bacterial strains tended to increase over time from day 7 to day 21. This suggested that the potassium solubilization process occurred continuously and became more efficient over time. Additionally, there was a significant difference in potassium solubilization capability among the tested bacterial strains. Some strains exhibited excellent solubilization ability, while others were less effective.

Potassium is an essential nutrient involved in several important plant physiological and biochemical functions for plant growth and development. Potassium forms found in the soil, namely, soil minerals, non-exchangeable, exchangeable, and water soluble. Soil minerals remaining in the structures of the minerals make up approximately 90 to 98% of soil K, that are unavailable for plant uptake. Approximately, 2–10 % of K is nonexchangeable or exchangeable and water-soluble ion [29]. Water-soluble and exchangeable potassium are readily available for plant uptake [30]. However, progressive intensification of agriculture and soil erosion have made concentration of soluble potassium usually deficient. Several investigations found that rhizobacteria are one group of potassium mineral solubilizers releasing soluble potassium form from K-bearing minerals such as illite, mica, feldspars by excreting various organic acids. These rhizobacteria were isolated from several sources: maize, oats, wheat, barley, potato, brinjal, tomato, apple, pear, walnut, and almond [29].

Table 3 Results of the potassium solubilization capability survey of 31 experimental bacterial strains

Isolate name	K_2O Concentration (mg/L)			Average K_2O concentration (mg/L)
	Day 7th	Day 14th	Day 21st	
Control	0.00 ± 0.00^{l}	0.00 ± 0.00^{m}	0.00 ± 0.00^{r}	0.00
BC01	28.21 ± 9.42^{ab}	32.50 ± 11.37^{ab}	37.53 ± 8.75^{ab}	32.75
BC04	19.36 ± 3.64^{c-i}	23.82 ± 2.50^{c-h}	30.55 ± 1.10^{b-e}	24.58
BC06	29.69 ± 2.29^{a}	37.73 ± 5.10^{a}	38.26 ± 3.09^{a}	35.23
BC08	23.08 ± 0.86^{a-e}	20.93 ± 0.83^{e-k}	23.82 ± 5.04^{e-k}	22.61
BC09	17.13 ± 1.81^{d-k}	27.01 ± 2.78^{b-e}	24.45 ± 3.40^{d-j}	22.86
BC10	19.14 ± 3.31^{c-i}	24.50 ± 2.41^{b-g}	25.85 ± 2.82^{c-i}	23.16
BC11	28.23 ± 8.08^{ab}	25.36 ± 0.21^{b-f}	27.37 ± 1.47^{c-g}	26.99
BC12	20.24 ± 5.04^{c-h}	16.54 ± 2.44^{g-l}	18.49 ± 6.45^{h-n}	18.42
BC14	18.06 ± 3.45^{c-j}	14.59 ± 3.09^{i-l}	21.82 ± 4.25^{f-l}	18.16
BC15	19.53 ± 5.71^{c-i}	22.23 ± 0.38^{d-j}	28.41 ± 4.21^{c-f}	23.42
BC16	21.00 ± 1.43^{b-h}	22.14 ± 2.31^{d-i}	15.76 ± 3.24^{k-p}	19.64
BC22	25.13 ± 4.37^{abc}	31.61 ± 1.98^{abc}	32.16 ± 5.59^{a-d}	29.63
BC23	21.50 ± 4.08^{b-g}	27.41 ± 1.86^{b-e}	28.54 ± 1.77^{c-f}	25.82
BC27	14.79 ± 6.44^{f-k}	15.94 ± 13.55^{h-l}	17.62 ± 3.59^{j-o}	16.12
BC28	29.88 ± 1.65^{a}	26.80 ± 1.69^{b-e}	23.93 ± 1.21^{e-k}	26.27
BC30	11.11 ± 1.44^{jk}	9.68 ± 0.99^{l}	8.81 ± 1.18^{pq}	9.87
BC31	15.77 ± 5.03^{e-k}	23.32 ± 0.54^{c-h}	13.82 ± 8.09^{l-q}	17.64
BC32	13.67 ± 2.01^{g-k}	22.61 ± 1.30^{d-i}	19.39 ± 12.21^{g-m}	18.56
BC33	10.09 ± 0.42^{k}	21.29 ± 1.63^{d-j}	18.64 ± 3.28^{h-n}	16.67
BC34	21.69 ± 2.34^{b-f}	28.90 ± 0.44^{b-e}	32.55 ± 3.42^{abc}	27.71
BC36	23.63 ± 1.71^{a-d}	29.64 ± 0.51^{bcd}	26.55 ± 4.60^{c-h}	26.61
BC39	15.29 ± 4.47^{e-k}	26.41 ± 1.92^{b-e}	18.18 ± 2.07^{i-o}	19.96
BC40	18.98 ± 4.83^{c-i}	29.64 ± 0.80^{bcd}	8.85 ± 2.94^{pq}	19.96
BC42	12.32 ± 5.23^{ijk}	16.97 ± 1.57^{f-l}	6.52 ± 0.16^{qr}	19.15
BC43	19.64 ± 2.13^{c-i}	23.48 ± 3.28^{c-h}	19.70 ± 3.53^{g-m}	20.94
BC45	13.63 ± 2.86^{g-k}	15.99 ± 3.83^{h-l}	10.78 ± 1.00^{n-q}	13.47
BC46	21.49 ± 2.59^{b-g}	24.36 ± 3.48^{b-h}	14.61 ± 3.31^{l-q}	20.15
BC49	15.30 ± 2.12^{e-k}	12.75 ± 4.36^{kl}	10.20 ± 0.57^{opq}	12.75
BC53	13.46 ± 3.51^{h-k}	16.04 ± 7.36^{h-l}	6.80 ± 0.29^{qr}	12.10
BC54	16.65 ± 2.71 $^{d-k}$	17.89 ± 6.87^{f-l}	12.96 ± 1.59^{m-q}	15.83
BC55	13.54 ± 2.92^{h-k}	13.96 ± 5.44^{jkl}	14.32 ± 1.94^{l-q}	13.94

Values in the same vertical column followed by one or more identical letters indicate no statistically significant difference at the alpha 0.05 significance level according to Duncan's test.

Fatharan et al., (2018) isolated twenty rhizobacteria from paddy rhizosphere (*Oryza sativa* L.). Seven rhizobacterial strains had the ability of solubilization zone formation on Alexandrov agar media with feldspar. These isolates showed their capability for solubilizing potassium from mineral feldspar [31]. Similarly, 137 rhizobacterial isolates obtained from the rhizosphere soil of wheat were studied with potassium solubilization modified Aleksandrov medium plates containing mica powder by the spot test method and estimated potassium released concentration on Aleksandrov medium broth by using atomic absorption spectrometer [32]. The result showed that 20 strains had the ability to solubilize potassium from mica on the Aleksandrov medium. The potassium released concentration ranged from 15 mg to 48 mg/L.

3.4. Siderophore production of bacterial strains

Experiments were conducted to qualitatively assess the siderophore production ability of the bacterial strains. Siderophore production was indicated by the discoloration of the blue dye in the CAS reagent and the formation of a halo zone on the CAS agar medium (Figure 1). The results showed that out of the 31 tested strains, 18 strains (58%) were able to produce siderophores as determined by the CAS assay, while 13 strains (42%) did not exhibit this ability (Table 4).

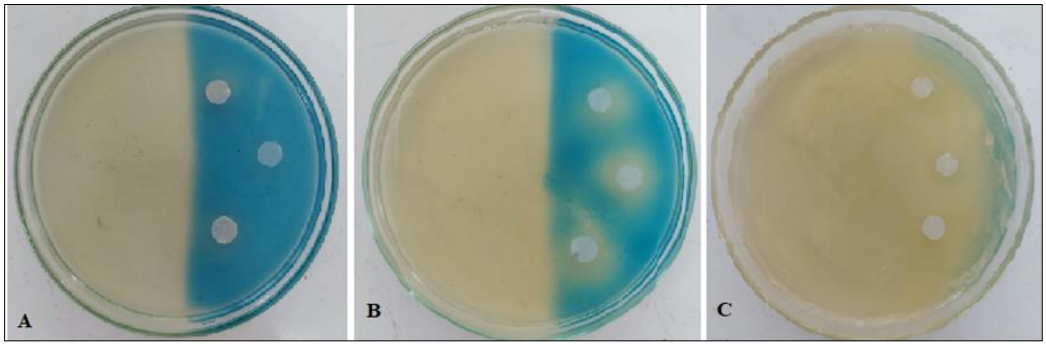

Figure 1 Siderophore production by selected bacterial strains: (A) BC22, (B) BC40, and (C) BC23

Table 4 Siderophore production ability of 31 experimental bacterial strains

Isolate name	Siderophore production	Isolate name	Siderophore production
Control		BC30	✓
BC01		BC31	✓
BC04		BC32	✓
BC06	✓	BC33	✓
BC08	✓	BC34	✓
BC09	✓	BC36	
BC10	✓	BC39	
BC11		BC40	✓
BC12	✓	BC42	
BC14	✓	BC43	
BC15		BC45	
BC16	✓	BC46	
BC22		BC49	✓
BC23	✓	BC53	✓
BC27		BC54	✓
BC28	✓	BC55	✓

To survive, rhizobacteria need iron. Their primary method of iron acquisition is through the production and utilization of siderophores. These siderophores allow the bacteria to compete with harmful soil fungi for iron. This iron competition is a key way to control fungal diseases in agriculture. Research has shown that rhizobacteria protect plants from root pathogens like *Fusarium oxysporum* and *Rhizoctonia solani* by producing not only siderophores, but also other defensive compounds called secondary metabolites, and enzymes that break down fungal cell walls (lytic enzymes) [33]. Siderophore producing rhizobacteria were isolated from different plant rhizospheres. Paharia et al., (2017) isolated four siderophore producing rhizobacteria out of 31 bacterial isolates from rice plants on CAS agar plates [34]. Total of 49 bacterial strains were isolated from three samples of sugarcane rhizosphere soil (*S. spontaneum* L.), 14 rhizobacterial isolates produced siderophores [35]. Another study of biocontrol activity of sugarcane rhizobacteria against red rot pathogen *C. falcatum* isolated a total of 226 sugarcane rhizobacteria strains from the six different cultivars. 26 bacterial strains were selected for characterizing plant-growth-promoting activity, antifungal potential. Eleven rhizobacteria had the capability to produce siderophore [36]

4. Conclusion

The study investigated capability of starch, cellulose decomposition, siderophore synthesis and potassium solubilization of 31 rhizobacterial strains isolated from rhizosphere of sugarcanes (*Saccharum spp*.) cultivated in Ben Cau district, Tay Ninh province, Vietnam. The result showed that 74% strains exhibited their activity to hydrolyze starch, of which BC45 formed a halo zone with the largest diameter of 1,80 ± 0,20 cm. 87% of the experimental bacterial strains showed cellulose-degrading ability. The average radii of the clearing zones ranged from 0.1 cm to 1.87 cm. Among them, the two strains with the highest cellulose-degrading ability were BC12 and BC49, with average clearing zone radii of 1.87 ± 0.12 cm and 1.73 ± 0.46 cm, respectively. All strains were able to release soluble potassium from insoluble potassium. Average concentration of K_2O after the experiment period was 9.87 mg/L – 35.23 mg/L. Among them, BC06 showed the highest capability with K_2O concentrations of 35,23 mg/L. 42% strain showed the ability to produce siderophore. These results collectively indicate that the isolated rhizobacteria possess a range of beneficial traits that could contribute to improved sugarcane growth and soil health. Future research should focus on evaluating the efficacy of these strains in field trials and exploring their potential for application as biofertilizers or biostimulants in sustainable agriculture.

Compliance with ethical standards

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Disclosure of conflict of interest

There is no conflict of interest.

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