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PROPERTIES OF BACTERIA ISOLATED FROM ANTARCTIC VASCULAR PLANT *COLOBANTHUS QUITENSIS* AND THEIR PLANT GROWTH-PROMOTING POTENTIAL

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Background. The study of bacteria inhabiting the endosphere of Antarctic plants is relevant because it complements data on the role of microorganisms in improving plant growth and their resistance in extreme environments. The targeted use of endophytic bacteria as biofertilizers in agriculture is a promising technology for providing effective, environmentally friendly solutions, especially amid climate change. The study aimed to investigate the properties of bacteria isolated from *Colobanthus quitensis* and to determine their effects on the growth parameters of the spring wheat cultivar Tybalt in the early stages of ontogenesis and select a strain with plant growth-promoting traits for further research.

Materials and Methods. Endophytes were isolated on TSA and R2A. The ability of bacteria to fix N₂ was determined using Ashby medium. Conclusions about zinc solubilization were made based on the appearance of transparent zones around colonies after growth on medium containing ZnO. For the detection of cellulase activity, a medium with carboxymethylcellulose was used, and for amylolytic activity – starch-ammonia agar. The ability of bacteria to synthesize siderophores was determined using a medium containing hexadecyltrimethylammonium bromide and chromazurol S. The content of auxin-like compounds was determined using Salkowski reagent. The seeds were soaked in a bacterial suspension, sown into soil, and grown for 8 days at 18 ± 2 °C. Protein concentration was determined using the Bradford method. Chlorophyll *a* and *b* concentrations were determined photometrically. To assess the effect of heavy metal salts and NaCl, different amounts of these substances were added to the medium.



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Results. Some bacterial isolates obtained from the endosphere of *C. quitensis* solubilize ZnO and produce cellulases and amylases. All bacterial isolates studied produce auxin-like compounds, and most of them synthesize siderophores. Moderate and extreme halophiles are capable of growing under the influence of $\text{MnCl}_2 \cdot \text{H}_2\text{O}$, $\text{FeSO}_4 \cdot 7\text{H}_2\text{O}$, $\text{CdCl}_2 \cdot 2.5\text{H}_2\text{O}$, $\text{CoCl}_2 \cdot 6\text{H}_2\text{O}$, and $\text{K}_2\text{Cr}_2\text{O}_7$. Most of the bacterial isolates obtained from the endosphere of *C. quitensis*, despite possessing plant growth-promoting traits, had no effect on wheat growth parameters during the early stages of ontogenesis. However, bacterial isolates have also been detected that positively affect morphometric parameters and chlorophyll content in seedling leaves. Bacterial isolate R380 from the endosphere of *C. quitensis* roots, which increased chlorophyll content in the leaves of wheat after seed inoculation, was identified as *Bacillus* sp. R380 based on 16S rRNA gene sequencing.

Conclusions. As a result of screening *Colobanthus quitensis* endophytes, we isolated a promising strain, *Bacillus* sp. R380, which increases chlorophyll content in spring wheat seedlings.

Keywords: Antarctic microorganisms, *Bacillus*, *Colobanthus quitensis*, endosphere, phyllosphere, plant growth-promoting traits

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INTRODUCTION

The extremophile Antarctic dicotyledonous plant *Colobanthus quitensis* (Kunth) Bartl. (Antarctic pearlwort) is a model organism for studying the effects of abiotic stressors on plant growth and development. Populations of this plant are found along the western coast of the Antarctic Peninsula, as well as on the South Shetland and South Orkney Islands (Maritime Antarctica) (Ontivero *et al.*, 2024). The survival of *C. quitensis* in the Antarctic environment (one of the harshest regions in the world, with low temperatures, freeze-thaw cycles, intense UV radiation during the austral season, and desiccation) is explained by several physiological properties, in particular stress protein production, antioxidants, the accumulation of proline and non-structural carbohydrates, etc. Their photosynthetic system functions at temperatures close to 0 °C (Cavieres *et al.*, 2016). They reproduce sexually, but cases of asexual reproduction have been described. Reproductive strategies include self-pollination and, less commonly, cross-pollination. The presence of seeds in a state of dormancy has also been described (Ontivero *et al.*, 2024). *C. quitensis* are capable of modulating the composition of the rhizosphere and endosphere microbiome, depending on growth conditions (Znój *et al.*, 2022; Yerkhova *et al.*, 2022), which probably also ensures their survival and spread in Antarctic conditions.

Since the composition of the plant endosphere microbiome depends on the type of tissue, stage of development, and the availability of nutrients to the plant, but, above all, on environmental factors, endophytic microorganisms are being intensively studied to determine their role in plant physiology and adaptation to environmental factors, as

well as to identify promising microorganisms that promote or inhibit plant growth, and therefore may be one of the solutions for both sustainable agriculture and invasive species management (Tariq *et al.*, 2025; Grzyb & Szulc, 2024). Considering global climate change, disruption of biogeochemical cycles of elements, the increase in the scale of biological invasions, the loss of biodiversity, and the need to feed the Earth's ever-growing population, which, according to various estimates, will reach 9.8 billion people by 2050, interest in the isolation and study of endophytes of extremophile plants is justified (Searchinger *et al.*, 2019).

A multi-omic approach is used to study the plant endosphere microbiome, encompassing metataxonomy, metagenomics, metatranscriptomics, metaproteomics, and metabolomics (the term "metabolomics" was proposed to avoid the awkward term "metametabolomics") (Grzyb & Szulc, 2024). The application of these methods provides a clear understanding of the composition of the microbiome and its functional significance for the plant. However, it does not allow the isolation of microorganisms in pure culture that can be used in practice in the future.

The aim of the study was to examine the properties of bacteria isolated from *Colobanthus quitensis* and to determine their effects on the growth parameters of spring wheat cultivar Tubalt in the early stages of ontogenesis and select a strain with plant growth-promoting traits for further research.

MATERIALS AND METHODS

Isolation of endophytes of *Colobanthus quitensis*. Samples of *C. quitensis* (about 7.0 g wet weight) were collected on Deception Island (Maritime Antarctica, -62.982130°, -60.518980°) by the participants of the 27th Ukrainian Antarctic Expedition and were transferred to Ivan Franko National University of Lviv according to the Transfer Act in sterile 50-mL Falcon-type tubes.

Wet mass (0.5 g) of *C. quitensis* were washed several times with distilled water to remove soil clumps and surface sterilization was performed according to the method (Barra *et al.*, 2016; Yerkhova *et al.*, 2022), which involves rinsing the plants in the sterile distilled water (twice, 3 min), 70 % ethanol solution (2 min), and 5.6 % sodium hypochlorite solution (10 min), and again in 70 % ethanol solution (2 min). To remove residues of ethyl alcohol and sodium hypochlorite, the plants were rinsed three times with sterile distilled water for 3 min each. The water from the last rinse was poured onto tryptic soy agar (TSA) (Merck, Millipore) and R2A (Merck, Millipore) to check for sterility. Plates inoculated with water from the final plant rinse were incubated for 5–7 days at temperatures of 18 ± 2 , 28 ± 2 , and 37 ± 2 °C. Surface sterilization was considered successful if no microbial growth was observed on TSA and R2A plates incubated at different temperatures. The surface-sterilization protocol was tested three times using 0.1 g of fresh *C. quitensis* biomass in each experiment. The effectiveness of surface sterilization was also tested during the isolation of *C. quitensis* endophytes.

The shoot and the root of the plant were separated with a sterile scalpel, transferred to porcelain mortars, and ground to a homogeneous mass. The disintegrated material was mixed with 0.9 % NaCl, and 10-fold dilutions were prepared and sown on TSA (to isolate copiotrophic microorganisms) and R2A (to isolate oligotrophic microorganisms). The cultures were grown for 7–10 days at 18 ± 2 °C. Morphologically distinct colonies of microorganisms were isolated. Pure cultures were obtained by repeated streaking with a sterile loop. The purity of the culture was checked microscopically.

Growth in a medium without a nitrogen source. Bacteria were grown for 7 days at 18 ± 2 °C in liquid Ashby's medium (Ashby, 1907; Maslovska *et al.*, 2024). The appearance of cloudiness in the medium indicated that bacteria are capable of growing in a medium without a nitrogen source. The control was a medium without inoculation.

Hydrolytic properties of bacteria. We used a medium with carboxymethylcellulose (Ahmed *et al.*, 2018) to detect cellulase activity and starch-ammonia agar (Maslovska *et al.*, 2024) to detect amylolytic activity. Bacterial cultures (2-day-old) grown on TSA were inoculated by streaking and incubated for 7 days at 18 ± 2 °C. The ability of bacteria to hydrolyze starch or cellulose was determined by adding Lugol's solution to the appropriate media (Gohel *et al.*, 2014). When polysaccharides were broken down, clear zones formed around the colonies. The enzymatic activity index (EAI) (Grata, 2020) was determined using the formula: $EAI = (A - B) / B$, where: A is the diameter of the starch/cellulose hydrolysis zone, mm; B is the diameter of the colony, mm.

Solubilization of ZnO. When microorganisms were able to solubilize ZnO after seven days of growth on a medium containing ZnO (0.1 %) (Bhakat *et al.*, 2021), transparent zones formed around the colonies. Determined the solubility index of ZnO (SI) (Choudhary *et al.*, 2024) using the formula: $SI = (A + B) / B$, where: A is the diameter of the ZnO solubilization zone, mm; B is the diameter of the bacterial colony, mm.

Content of auxin-like compounds. The bacteria were grown in a nutrient broth (Merck, Millipore) with tryptophan (0.015 %) for 3 days at a temperature of 28 ± 2 °C and aeration (160 rpm). After cultivation, the bacterial cells were centrifuged (5000 rpm, 5 min). Salkowski reagent (1.0 mL) (Gang *et al.*, 2019) was added to 1.0 mL of the supernatant. The reaction mixture was incubated in the dark for 30 min. The optical density of the reaction mixtures was determined at $\lambda = 536$ nm. The content of auxin-like compounds was determined using a calibration curve constructed using a solution of indolyl-3-acetic acid.

The ability to synthesize siderophores was examined using qualitative and quantitative methods. We used MM9 medium, which was mixed with a reaction mixture for the qualitative determination of siderophores ($0.006 \text{ g} \cdot \text{L}^{-1}$ chromazurol S, $9 \text{ mL} \cdot \text{L}^{-1}$ $10 \text{ }\mu\text{M}$ solution of $\text{FeCl}_3 \cdot 6\text{H}_2\text{O}$ in 10 mM HCl, $0.0073 \text{ g} \cdot \text{L}^{-1}$ hexadecyltrimethylammonium bromide (HDTMA) before pouring into dishes (Louden *et al.*, 2011). Bacteria were streaked and grown at 18 ± 2 °C for 5–10 days. The ability to synthesize siderophores was assessed by the formation of yellow (α -hydroxycarboxylate-type siderophores) or pink (organic acids) zones around colonies (Pandey *et al.*, 2017). Since some Gram-positive bacteria are sensitive to HDTMA (Pérez-Miranda *et al.*, 2007), the bacteria were grown on MM9 medium at 18 ± 2 °C for 5–10 days, after which the bacterial streaks were poured with a reaction mixture for the determination of siderophores in a 0.9 % agarose solution, and the formation of color around the bacterial streaks was observed.

Bacterial isolates selected during a qualitative analysis of their ability to synthesize siderophores were used to quantitatively determine the concentration of these compounds in the culture medium using the following method (Arora & Verma, 2017). A suspension ($100 \text{ }\mu\text{L}$) of a 2-day-old bacterial culture (3.0 according to McFarland) was inoculated into Luria–Bertani broth. The cultures were grown for three days at 28 ± 2 °C with aeration (160 rpm). After cultivation, the bacteria were centrifuged (5000 rpm, 5 min). To 1.0 mL of supernatant, 1.0 mL of dye solution was added (solution 1: 121.0 mg

of chromazurol S in 100 mL of distilled water; solution 2: 1 mM $\text{FeCl}_3 \cdot 6\text{H}_2\text{O}$ in 10 mM HCl, solution volume – 20.0 mL; solution 3: 729.0 mg HDTMA in 400 mL of distilled water. The three solutions were mixed and diluted 10 times with distilled water. Luria–Bertani broth was used as a control. The reaction mixture was incubated for 30 min, and the optical density was measured at $\lambda = 630$ nm. The content of siderophores was expressed in siderophore units (SU) according to the formula (Arora & Verma, 2017): $\text{SU} = [(\text{Ar} - \text{As}) / \text{Ar}] \cdot 100$, where: Ar – optical density of the control sample, As – optical density of the test sample.

Growth of bacterial isolates under the influence of heavy metals and NaCl.

TSA diluted 10 times was used, which was supplemented with $\text{MnCl}_2 \cdot 4\text{H}_2\text{O}$ (1.0–20.0 mM), $\text{FeSO}_4 \cdot 7\text{H}_2\text{O}$ (0.5–20.0 mM), $\text{CoCl}_2 \cdot 6\text{H}_2\text{O}$ (0.5–5.0 mM), $\text{CdCl}_2 \cdot 2.5\text{H}_2\text{O}$ (0.0002–0.5 mM), $\text{CuCl}_2 \cdot 2\text{H}_2\text{O}$ (1.0–6.0 mM), $\text{K}_2\text{Cr}_2\text{O}_7$ (0.1–10.0 mM) or different concentrations of NaCl (2.0–20.0 %) after sterilization. The bacteria were grown for three to five days at a temperature of 18 ± 2 °C. The medium without heavy metal compounds or without NaCl was used as a control.

Bacterization of wheat seeds. Surface sterilization of wheat seeds involved rinsing them for 15 min in tap water, followed by three rinses in sterile distilled water. After rinsing, the wheat seeds were soaked in a 5.7 % sodium hypochlorite solution containing 0.1 % Tween-20 for 10 minutes. To remove any residual sodium hypochlorite, the wheat seeds were rinsed five times with sterile distilled water. The seeds were soaked for 12 h in a bacterial suspension (3-day-old bacterial culture grown on TSA diluted in 0.9 % NaCl, final density 5.0 according to McFarland). The bacterized seeds were laid out in rows in moist soil (450 ± 20 g per sample). Every day, 50 mL of tap water was added to the soil. Wheat was grown for 8 days at 18 ± 2 °C. Wheat seed germination (State Standard of Ukraine, 2002) and pigment content in leaves were determined on the 8th day of growth. The seed bacterization was carried out in March–April 2024 (daylight duration: 11–14 hours) in accordance with the recommendations for planting spring soft wheat. The experiments were conducted in four biological replicates, each of which consisted of three technical replicates. In each technical replicate, 10 plants were randomly selected to determine morphometric parameters, and three groups were formed, each containing 5 plants, to determine pigment, protein, and dry weight content. We used Haplic Luvisols (Loamic, Aric) soil in this study. Key characteristics of the soil used in this study included pH (KCl) (State Standard of Ukraine, 2007) – 6.4 (neutral soil), hydrolytic acidity (State Standard of Ukraine, 2014) – 2.71 mg-eq/100 g soil (close to neutral), exchangeable calcium (Kyrylchuk & Bonishko, 2011) – 14.0 mg-eq/100 g soil (elevated levels), exchangeable magnesium (Kyrylchuk & Bonishko, 2011) – 2.6 mg-eq/100 g soil (a higher level), the sum of the absorbed bases (Kyrylchuk & Bonishko, 2011) – 16.8 mg-eq/100 g soil (a higher level), humus (State Standard of Ukraine, 2004) – 2.72 % (moderate level), mobile sulfur (State Standard of Ukraine, 2015) – 6.1 mg/kg soil (moderate level), easily hydrolyzable nitrogen by the Kornfield method (State Standard of Ukraine, 2015) – 126.0 mg/kg soil (low level), mobile phosphorus (P_2O_5) (State Standard of Ukraine, 2005) – 393.2 mg/kg soil (a very high level), and exchangeable potassium (K_2O) (State Standard of Ukraine, 2005) – 447.5 mg/kg soil (a very high level).

Determination of chlorophyll content. Alcohol extraction of pigments from wheat seedling leaves was performed after grinding the material with CaCO_3 . The concentrations of chlorophylls *a* and *b* were determined at $\lambda = 665$ nm and $\lambda = 649$ nm (the absorption maxima of chlorophyll *a* and chlorophyll *b*, respectively) (Romaniuk *et al.*, 2005).

To determine protein concentration, plant material was ground in a porcelain mortar with CaCO_3 in K,K-phosphate buffer (50 mM, pH 7.5). After steeping for 2–3 min, the extract was centrifuged (10,000 rpm, 10 min). The protein content in the supernatant was determined using the Bradford method (Bradford, 1976).

PCR amplification of the 16S rRNA gene. Genomic DNA was isolated via the soft lysis method (Green & Sambrook, 2012). The 16S rRNA gene was amplified, and the products were sequenced from universal primers 27 F and 1492R (Turner *et al.*, 1999). PCR amplification was performed using Taq polymerase (NEB M0273X) using a Mastercycler Pro thermal cyclers (Eppendorf, Germany). The sequenced fragments were analyzed via ABI Prism 3130 xl. The resulting nucleotide sequences (two for each sample corresponding to DNA readings from the 27 F and 1492R primers) were quality-checked, assembled, and trimmed. To identify strains, the 16S rRNA gene sequences were compared with the sequences in the NCBI GenBank database via BLAST search. The method of molecular identification is described in more detail in O. Maslovska *et al.* (2024). To construct a phylogenetic tree in MEGA XII, multiple sequence alignment was performed using the MUSCLE algorithm. Unaligned ends of the sequences were trimmed manually.

Nucleotide accession number. The 16S rRNA gene sequence of the identified strain has been deposited in GenBank NCBI (accession number: PZ413131).

Statistical processing of results. The experiments were conducted in four biological replicates, with three technical replicates per biological replicate. For statistical analysis of the results, Python (libraries pandas, scipy.stats, and scikit-posthocs) was used (Husak *et al.*, 2025). The normality of the data was assessed using the Shapiro–Wilk test. Since the data did not meet the assumptions of normality in most cases, non-parametric methods were prioritized. Specifically, the Kruskal–Wallis *H*-test was used to assess the statistical significance of differences between independent groups. For pairwise comparisons between groups, a post hoc analysis was performed using Dunn’s test with Holm’s adjustment. Differences were considered statistically significant at $p < 0.05$. The results in the text, tables, and figures are presented as the mean $\pm$ standard deviation. Graphs were constructed using OriginPro 8.5.

RESULTS AND DISCUSSION

The diversity and abundance of microorganisms in the endosphere of the shoots of plants are usually lower than in the endosphere of the root, rhizosphere, or soil around the rhizosphere, which is due to both the properties of microorganisms and their function for the plant, as well as the different conditions of these microenvironments (Znój *et al.*, 2022). Endophytes in the phyllosphere of Antarctic plants are directly exposed to factors such as systemic plant resistance, sharp temperature fluctuations, intense UV radiation, and the effects of free radical compounds. Microorganisms in plant roots are less intensively affected by these factors (Compant *et al.*, 2020). Obviously, the abundance and diversity of cultivated microbiota in the endosphere of the shoot of *C. quitensis* are also lower; therefore, we isolated fewer bacterial isolates from it than from the root endosphere (**Table 1**).

Depending on growing conditions, plants “recruit” microorganisms from the soil that have the properties necessary for survival. This survival strategy in Antarctic conditions has been observed in *C. quitensis*. The composition of the endosphere and rhizosphere microbiomes of *C. quitensis*, collected from sites with significantly different physico-

chemical properties on King George Island, South Shetland Islands, differed (Znój *et al.*, 2022). There are several known ways for plants to acquire the endosphere microbiome. Root endophytes mainly originate from the rhizoplane microbiome. At the same time, the endosphere of the shoot of the plant is colonized by microorganisms from the root endosphere as a result of the movement of microorganisms through the xylem, from the air through stomata or minor mechanical damage to leaves or stems, or as a result of insect bites (Lengrand *et al.*, 2024).

Table 1. Bacteria isolated from *Colobanthus quitensis*

Endosphere	Isolates of bacteria
Shoot	L302, L303, L305, L306, L311, L359, L379
Root	R308, R312, R313, R315, R317, R318, R320, R321, R323, R324, R347, R361, R362, R363, R364, R365, R366, R367, R369, R371, R372, R374, R375, R376, R377, R378, R380, R382

An important feature of endophytic bacteria is N₂ fixation (Tariq *et al.*, 2025). Among the isolated bacteria from the endosphere of the shoot of *C. quitensis*, several were able to grow in a medium without a nitrogen source (Table 2). Among the isolates of bacteria from the root endosphere, only a few were grown in Ashby's medium. During functional analysis of the microbiome composition of *C. quitensis* endosphere samples collected from various islands in the Maritime Antarctic (Znój *et al.*, 2022), a low abundance of nitrogen-fixing bacteria was also detected. The authors suggested that one way to meet the nitrogen requirements of *C. quitensis* is through the microbivory endophytes (Znój *et al.*, 2022).

All bacterial isolates from the shoot endosphere were capable of solubilizing ZnO. More than half of the bacterial isolates from the root endosphere were also capable of solubilizing ZnO. Zn is an important element for plant functioning, as its deficiency slows down nitrogen metabolism and photosynthesis, limits the synthesis of phytohormones and carbohydrates, and causes a decrease in fruit development and flowering (Sethi *et al.*, 2025). Plants absorb Zn in the form of Zn²⁺ or its chelated form, although most zinc compounds in the soil are in insoluble forms of Zn(OH)₂, ZnO, and ZnCO₃. To ensure Zn availability, plants secrete phytosiderophores and organic acids, or the rhizosphere or endosphere microbiota solubilizes zinc-containing salts (Sethi *et al.*, 2025). Among the selected isolates, the highest ZnO solubilization indices were observed for bacterial isolates R363, R364, R371, and R321 from the root endosphere of *C. quitensis*. Other isolates from the root of *C. quitensis* studied in this work formed slightly smaller zones of zinc solubilization. Among isolates from the shoot of *C. quitensis*, high solubilization indices were observed for L306 and L311 (see Table 2).

The synthesis of siderophores by symbiotic bacteria is considered in two contexts: to improve Fe availability to plants and to act as a means of biocontrol of phytopathogens by creating a local Fe-deficient environment (Kramer *et al.*, 2019). More than half of the bacterial isolates from the endosphere of *C. quitensis* synthesized siderophores (Fig. 1A). Statistically, the highest levels of siderophore content in the growth medium were found for isolate L311 from the shoot of *C. quitensis* and R381 from the root endosphere. Slightly lower siderophore content was produced by bacterial isolates L359, L303, L379, R308, R318, and R382.

Table 2. Properties of bacteria isolated from *Colobanthus quitensis*

Isolates of bacteria	Growth in Ashby's medium	Synthesis of siderophores	Index of		
			ZnO solubilisation	cellulolytic activity	amylolytic activity
Isolates of bacteria from the shoot endosphere					
L302	+	+	8.1 ± 1.0 ^{bc}	–	6.1 ± 1.5 ^{bc}
L303	+	+	6.1 ± 0.9 ^c	–	10.2 ± 3.9 ^{ab}
L305	+	–	6.6 ± 1.1 ^c	–	–
L306	–	+	12.5 ± 4.1 ^{ab}	–	10.4 ± 4.1 ^{ab}
L311	–	+	12.9 ± 5.2 ^{ab}	–	13.9 ± 1.8 ^a
L359	–	+	7.8 ± 4.1 ^{bc}	2.1 ± 1.3 ^{bc}	–
L379	–	+	9.4 ± 2.4 ^{bc}	–	12.5 ± 3.4 ^a
Isolates of bacteria from the root endosphere					
R308	–	+	–	–	–
R312	–	–	–	4.8 ± 0.7 ^b	4.8 ± 1.0 ^c
R313	–	–	–	–	–
R315	–	–	–	–	–
R317	+		12.0 ± 2.6 ^{ab}	–	–
R318	+	+	8.2 ± 0.8 ^{bc}	12.0 ± 0.5 ^a	5.5 ± 0.3 ^c
R320	–	–	–	–	–
R321	–	+	13.4 ± 4.3 ^a	–	–
R323	–	+	7.0 ± 1.6 ^{bc}	–	–
R324	–	+	7.7 ± 1.3 ^{bc}	2.8 ± 0.8 ^{bc}	–
R362	–	+	10.7 ± 2.0 ^{ab}	–	5.9 ± 1.1 ^{bc}
R363	–	+	15.8 ± 1.9 ^a	0.6 ± 0.5 ^c	10.8 ± 0.8 ^{ab}
R364	–	+	15.0 ± 1.9 ^a	1.4 ± 0.5 ^c	6.2 ± 0.8 ^{bc}
R365	–	+	–	–	–
R366	–	–	–	–	–
R367	–	+	7.3 ± 1.4 ^{bc}	0.9 ± 0.1 ^c	–
R369	+	–	–	–	–
R371	–	+	13.6 ± 4.4 ^a	–	–
R372	+	–	–	–	–
R374	–	–	11.4 ± 3.7 ^{abc}	1.4 ± 0.6 ^c	–
R375	+	+	12.7 ± 1.0 ^{ab}	–	–
R376	–	+	–	–	–
R377	–	+	11.7 ± 4.2 ^{ab}	–	–
R378	–	+	–	–	–
R380	+	–	–	–	–
R381	+	+	12.4 ± 4.1 ^{ab}	–	–
R382	–	+	11.0 ± 2.5 ^{ab}	–	6.8 ± 1.7 ^{bc}

Note: «+» – feature detected, «–» – feature not detected; values of indices of ZnO solubilization, cellulolytic and amylolytic activity of bacterial isolates, denoted by the same letter, are not statistically significantly different (P > 0.05) according to Dunn's test

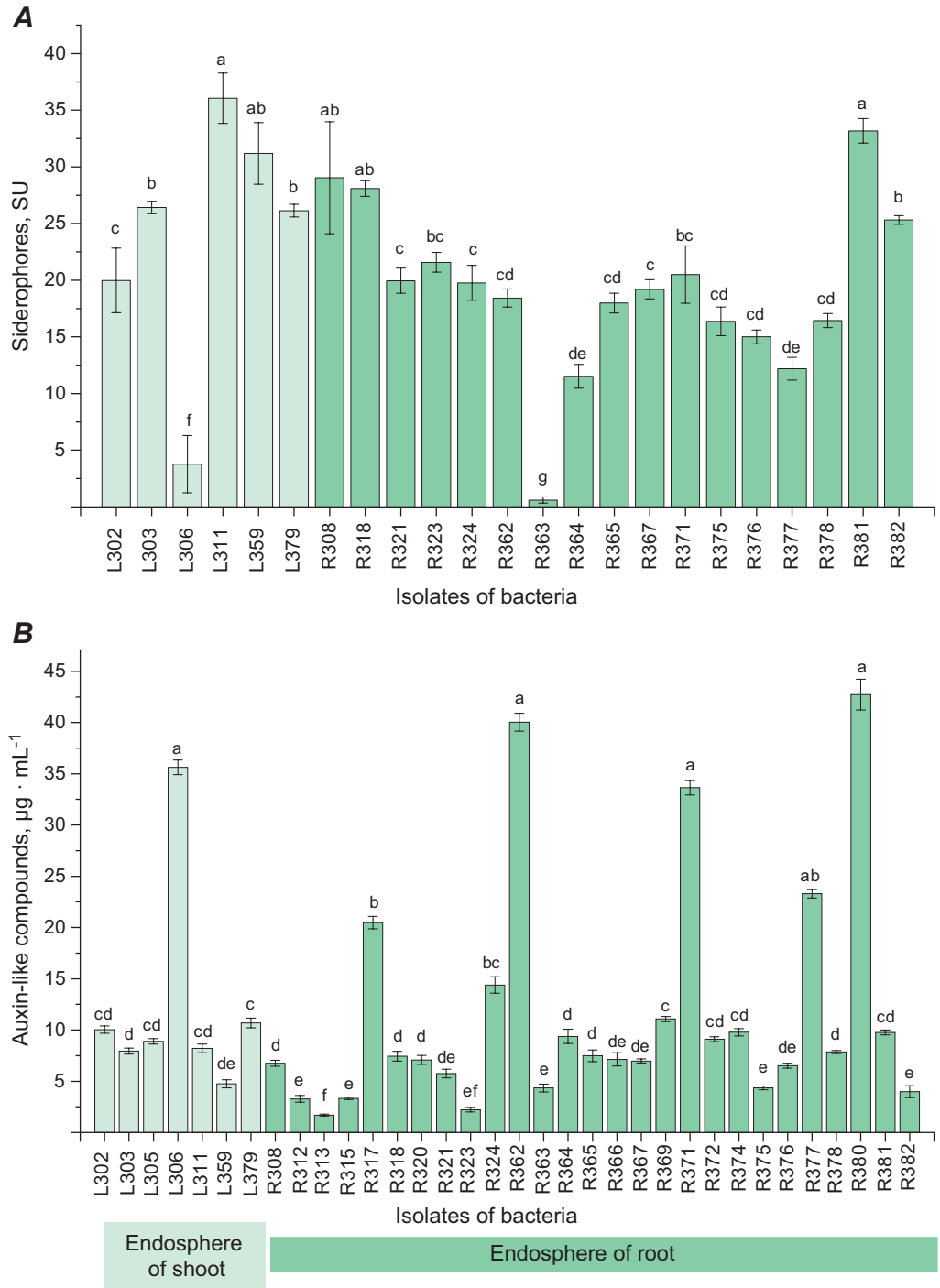


Fig. 1. The content of siderophores (**A**) and auxin-like compounds (**B**) in the culture medium of bacterial isolates from *Colobanthus quitensis* (values of content of siderophores and auxin-like compounds, denoted by the same letter, are not statistically significantly different ($P > 0.05$) according to Dunn's test)

The synthesis of hydrolytic enzymes that degrade plant cell walls, is an important prerequisite for bacterial colonization of the plant endosphere (Compant *et al.*, 2020). The movement of microorganisms in the endosphere of plants can also occur through xylem elements, without the need for enzymes that degrade plant cell walls (Grzyb & Szulc, 2024). During the determination of metabolic features of microbial communities in the rhizosphere and endosphere of *C. quitensis* (Znój *et al.*, 2022), it was found that the rhizocompartments' microbiomes most actively break down α -cyclodextrin and less intensively D-xylose and D-cellobiose. The ability of bacterial isolates from the root endosphere of *C. quitensis* to synthesize cellulases was detected in only 7 isolates. Among the shoot endophytes of *C. quitensis*, only the bacterial isolate L359 synthesized cellulase. Despite the absence of cellulase, the endophytes of the shoot of *C. quitensis* synthesized amylase. These enzymes were detected in five bacterial isolates from the shoot and in six from the root endosphere. The amylolytic activity indices of bacterial isolates L311 and L379 from the shoot of *C. quitensis* were statistically significantly higher than the amylolytic activity indices of other bacterial isolates. Bacterial isolate L359, which synthesized cellulases, did not produce amylases. Unlike cereal crops with a substantial endosperm, where amylolytic activity is critical for endophyte colonisation of the seed (Prasad *et al.*, 2025), for *C. quitensis*, which has a sparse endosperm, the role of endosphere bacterial amylases may have a different physiological basis and requires further research.

Endophytes interact with the host plant by modulating the levels of phytohormones, particularly auxins, gibberellins, cytokinins, jasmonic acid, and ethylene, which directly influence root development processes such as elongation, branching, and root hair formation (Tariq *et al.*, 2025). Indole-3-acetic acid (IAA) is the principal plant auxin involved in numerous physiological processes in plants. These include intercellular signal transmission, regulation of plant development and induction of defense systems, formation of lateral and adventitious roots, influence on photosynthesis and biosynthesis of metabolites, etc. The role of IAA in regulating the synthesis of other phytohormones, in particular ethylene, was established (Orozco-Mosqueda *et al.*, 2021). All isolates of bacteria synthesized auxin-like compounds (**Fig. 1B**). The L306 bacterial isolate from the shoot of *C. quitensis* and three isolates from the root endosphere (R362, R371, R380) produced the highest amounts of auxin-like compounds. Slightly fewer auxin-like compounds were produced by isolates R377 and R317. The L306 bacterial isolate from the shoot of *C. quitensis* was among the leaders in the formation of auxin-like compounds (**Fig. 1B**), but in terms of its ability to form siderophores, it was among the isolates that produced the least.

The use of products based on plant-growth-promoting microorganisms (PGPM) is a modern approach to improving soil fertility and protecting plants from plant pathogens and adverse environmental factors. In addition to their direct effect on plants, some PGPMs also break down pesticides and detoxify heavy metal compounds. Given today's challenges, in particular, global climate change and the contamination of croplands with various pollutants resulting from human activities, there is a pressing need to identify environmentally resilient PGPM that could potentially be applied to soils that are saline or contaminated with heavy metals (Iqbal *et al.*, 2024). Antarctic substrates often contain elevated concentrations of NaCl and heavy metals due to natural mineral weathering and anthropogenic activity (Znój *et al.*, 2022), and a source of bacteria resistant to toxic substances (Romaniuk *et al.*, 2018). Among the isolates, there were bacteria resistant to the $\text{MnCl}_2 \cdot \text{H}_2\text{O}$, $\text{FeSO}_4 \cdot 7\text{H}_2\text{O}$, and $\text{K}_2\text{Cr}_2\text{O}_7$ (most bacteria grew

under the influence of 0.5 mM $K_2Cr_2O_7$; however, at higher concentrations, none of the isolates grew) (Table 3). An interesting fact was that all bacterial isolates studied in the work grew in the presence of 0.02 mM $CdCl_2 \cdot 2.5H_2O$. Cadmium is extremely toxic to living organisms (its toxicity to biota is within the range of 0.009–0.9 mM) (Yu *et al.*, 2021).

Table 3. Growth of bacterial isolates under the influence of NaCl and heavy metals

Isolate	NaCl,%				Heavy metal compounds, mM																
					MnCl ₂			FeSO ₄			CuCl ₂			CdCl ₂			CoCl ₂			K ₂ Cr ₂ O ₇	
	2.5	5.0	10.0	15.0	5.0	15.0	20.0	7.5	10.0	20.0	1.0	2.0	3.0	0.01	0.02	0.03	0.5	1.0	2.0	0.1	0.5
L302	+	-	-	-	-	-	-	+	+	-	-	-	-	+	+	-	+	+	-	+	+
L303	-	-	-	-	+	+	-	+	+	-	+	+	-	+	+	-	-	-	-	+	+
L305	+	+	-	-	-	-	-	+	+	-	-	-	-	+	+	-	+	+	+	+	+
L306	+	-	-	-	-	-	-	+	+	-	-	-	-	+	+	-	+	+	+	+	+
L311	+	+	+	+	+	+	-	+	+	-	-	-	-	+	+	-	+	+	-	+	+
L359	+	+	+	-	-	-	-	+	+	-	-	-	-	+	+	-	-	-	-	+	+
L379	+	+	-	-	+	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+
R308	+	+	+	-	-	-	-	-	-	-	-	-	-	+	+	-	-	-	-	+	+
R312	+	+	-	-	+	-	-	-	-	-	-	-	-	+	+	-	+	+	-	+	+
R313	+	+	+	-	-	-	-	-	-	-	-	-	-	+	+	-	+	-	-	+	+
R315	+	+	-	-	+	-	-	+	+	+	-	-	-	+	+	-	+	-	-	+	+
R317	+	+	-	-	+	+	-	-	-	-	-	-	-	+	+	-	+	-	-	+	+
R318	+	+	-	-	-	-	-	-	-	-	-	-	-	+	+	-	-	-	-	+	+
R320	+	+	-	-	+	+	-	+	+	-	-	-	-	+	+	-	+	-	-	+	+
R323	+	+	-	-	+	-	-	-	-	-	-	-	-	+	+	-	+	-	-	+	-
R324	+	-	-	-	+	+	+	-	-	-	-	-	-	+	+	-	+	-	-	+	-
R347	+	+	-	-	-	-	-	-	-	-	-	-	-	+	+	-	+	+	-	+	+
R361	+	+	-	-	+	+	+	-	-	-	-	-	-	+	+	-	+	+	-	+	+
R362	+	+	-	-	+	+	+	-	-	-	-	-	-	+	+	-	+	-	-	+	+
R363	+	-	-	-	-	-	-	-	-	-	-	-	-	+	+	-	+	-	-	+	+
R364	+	-	-	-	+	-	-	-	-	-	-	-	-	+	+	-	+	-	-	+	+
R366	+	+	-	-	+	+	-	-	-	-	-	-	-	+	+	-	+	-	-	+	-
R367	+	-	-	-	+	-	-	-	-	-	-	-	-	+	+	-	+	-	-	+	-
R369	+	+	-	-	-	-	-	-	-	-	-	-	-	+	+	-	+	-	-	+	+
R371	+	-	-	-	+	+	+	-	-	-	+	-	-	+	+	-	+	-	-	+	+
R372	+	+	-	-	+	-	-	-	-	-	+	-	-	+	+	-	+	-	-	+	+
R374	+	+	-	-	-	-	-	-	-	-	+	-	-	+	-	-	-	-	-	+	+
R375	-	-	-	-	-	-	-	-	-	-	+	-	-	+	+	-	+	-	-	+	+
R376	+	+	-	-	+	-	-	-	-	-	+	-	-	+	+	-	+	-	-	+	+
R377	-	-	-	-	+	-	-	-	-	-	+	-	-	+	+	-	+	-	-	+	+
R378	+	+	-	-	+	+	+	-	-	-	+	-	-	+	+	-	+	-	-	+	+
R380	+	+	-	-	-	-	-	-	-	-	+	-	-	+	+	-	+	-	-	+	-
R381	-	-	-	-	-	-	-	+	+	-	+	-	-	+	-	-	+	+	-	+	-
R382	-	-	-	-	-	-	-	-	-	-	+	-	-	+	+	-	+	-	-	+	+

Note: «+» – feature detected, «–» – feature not detected, in the work, crystal hydrates were used: $MnCl_2 \cdot 4H_2O$, $FeSO_4 \cdot 7H_2O$, $CuCl_2 \cdot 2H_2O$, $CdCl_2 \cdot 2.5H_2O$, $CoCl_2 \cdot 6H_2O$

Most isolates from the endosphere of the shoot and root of *C. quitensis* grew under the influence of NaCl at a concentration of 2.5 %. Fourteen bacterial isolates were resistant to the influence of NaCl at a concentration of 5 %. Four bacterial isolates (two from the endosphere of the shoot and two from the endosphere of the root of *C. quitensis*) grew under the influence of 10 % NaCl. The bacterial isolate L311, isolated from the shoot endosphere of *C. quitensis*, proved to be an extreme halophile, capable of growing in the presence of 15 % NaCl in the environment. In addition to tolerance to NaCl, this bacterial isolate was also resistant to $\text{MnCl}_2 \cdot 4\text{H}_2\text{O}$ (15.0 mM), $\text{FeSO}_4 \cdot 7\text{H}_2\text{O}$ (10.0 mM), $\text{CuCl}_2 \cdot 2\text{H}_2\text{O}$ (0.02 mM), $\text{CoCl}_2 \cdot 6\text{H}_2\text{O}$ (1.0 mM), and $\text{K}_2\text{Cr}_2\text{O}_7$ (0.5 mM). The bacterial isolate L379 was isolated from the endosphere of the shoot of *C. quitensis*. It grew in the presence of 5.0 % NaCl in the medium and was also resistant to the effects of $\text{MnCl}_2 \cdot 4\text{H}_2\text{O}$ (20.0 mM), $\text{FeSO}_4 \cdot 7\text{H}_2\text{O}$ (20.0 mM), $\text{CdCl}_2 \cdot 2.5\text{H}_2\text{O}$ (0.02 mM), $\text{CoCl}_2 \cdot 6\text{H}_2\text{O}$ (2.0 mM), and $\text{K}_2\text{Cr}_2\text{O}_7$ (0.5 mM). This is the only isolate of bacteria from the selected sample that was able to grow under the influence of 3.0 mM CuCl_2 . The importance of endophytes for plants is often explained by their role in ensuring survival under a range of stressful conditions, including low / high temperatures, drought, salinity, and heavy metals. For this purpose, endophytes implement multiple strategies to improve plant survival, in particular by changing morphological characteristics, such as root system architecture, modulating nitrogen and other element metabolism, synthesizing phytohormones, osmolytes, exopolysaccharides, etc. One of the effects of heavy metal compounds is the generation of free radical compounds, which cause oxidative stress. To counteract this, bacteria synthesise low-molecular antioxidants and antioxidant defence enzymes (Tariq *et al.*, 2025).

The effect of bacterial isolates on the growth parameters of spring wheat in the early stages of ontogenesis. One of the stages of research into endophytic microorganisms is the re-inoculation of plants of the same species from which they were isolated (Lengrand *et al.*, 2024). It is known that microorganisms from the rhizosphere or endosphere of Antarctic plants also promote the growth of agricultural plants (Maslovska *et al.*, 2024). Model plants for the study of PGPM are *Arabidopsis thaliana* (Bianco, 2024), *Medicago truncatula* (Stanton-Geddes *et al.*, 2013), and *Lotus japonicus* (Gómez-Repollés *et al.*, 2025). Among agricultural crops are corn, *Zea mays* (Vidotti *et al.*, 2019), rice, *Oryza sativa* (Ríos-Ruiz *et al.*, 2025), tomato, *Solanum lycopersicum* (Liu *et al.*, 2022), etc. Wheat is one of the most widely grown crops in the world, as one-third of the world's population depends on it for their diet. This crop can thrive in a variety of environmental conditions and farming systems, and the search for ways to stimulate its growth and improve yields remains a pressing issue (Lamlom *et al.*, 2023). This crop was selected to determine the plant growth-promoting potential of the isolated endophytes of *C. quitensis*. To study the effect of bacterial isolates from the endosphere of *C. quitensis* on wheat growth indicators in the early stages of ontogenesis, bacterial isolates that synthesised siderophores, auxin-like compounds, and hydrolytic enzymes were selected. These bacteria were also halotolerant and resistant to heavy metal salts (see **Table 3**). No statistically significant difference was found in the germination of wheat seeds treated with bacterial isolates L306, L379, R318, R320, R362, R371, and 0.9 % NaCl on the third day of cultivation (**Table 4**). However, the germination of wheat seeds treated with bacterial isolates L311 ($p = 0.041$), L359 ($p = 0.027$), and R380 ($p = 0.015$) was slightly lower compared to the germination of wheat seeds treated with the bacterial isolate L305 on the third day of growth. On the eighth day, the germination rate of

wheat seeds treated with all bacterial isolates did not differ from the control. Treatment of wheat seeds with isolates from the endosphere of *C. quitensis* did not cause changes in moisture content and dry weight of leaves of 8-day-old seedlings either.

Table 4. Seed germination, moisture content, and dry weight of leaves of spring wheat cultivar Tybalt treated with *Colobanthus quitensis* endophytes

Bacterial isolates	Seed germination, %		Moisture, %	Dry mass, %
	3 day	8 day		
Control	43.5 ± 10.0 ^{ab}	90.0 ± 4.3 ^a	88.22 ± 0.98 ^a	11.77 ± 0.98 ^a
Isolates of bacteria from the shoot endosphere				
L305	50.5 ± 3.4 ^a	95.0 ± 2.6 ^a	88.90 ± 0.33 ^a	11.09 ± 0.33 ^a
L306	42.0 ± 2.8 ^{ab}	91.5 ± 5.3 ^a	89.70 ± 0.77 ^a	10.30 ± 0.77 ^a
L311	28.5 ± 3.4 ^b	97.0 ± 2.0 ^a	87.62 ± 0.27 ^a	12.37 ± 0.27 ^a
L359	27.0 ± 5.0 ^b	94.0 ± 3.3 ^a	88.23 ± 0.67 ^a	11.77 ± 0.67 ^a
L379	44.5 ± 6.2 ^{ab}	96.0 ± 1.6 ^a	88.77 ± 0.43 ^a	11.22 ± 0.43 ^a
Isolates of bacteria from the root endosphere				
R318	34.5 ± 3.4 ^{ab}	89.5 ± 3.4 ^a	88.34 ± 0.53 ^a	11.65 ± 0.53 ^a
R320	30.5 ± 4.7 ^{ab}	92.5 ± 3.4 ^a	87.69 ± 0.24 ^a	12.31 ± 0.24 ^a
R362	34.0 ± 3.3 ^{ab}	98.0 ± 1.6 ^a	88.53 ± 0.53 ^a	11.46 ± 0.53 ^a
R371	30.0 ± 5.9 ^{ab}	91.5 ± 3.8 ^a	88.99 ± 1.28 ^a	11.01 ± 1.28 ^a
R380	27.0 ± 2.6 ^b	88.5 ± 2.5 ^a	88.28 ± 0.70 ^a	11.72 ± 0.70 ^a

Note: control – wheat seeds were treated with 0.9 % NaCl before sowing; values of wheat seed germination, moisture content, and dry weight of seedlings after seed inoculation with bacterial isolates and in the control, denoted by the same letter, are not statistically significantly different ($P > 0.05$) according to Dunn's test

Seed inoculation with bacterial isolates from the endosphere of the shoot of *C. quitensis* had a positive effect on wheat root length. After inoculation of wheat seeds with isolate L306, a significant increase ($p < 0.001$) in root length of 8-day-old seedlings was observed compared to the control. The roots of wheat seedlings treated with L379 isolate were also longer ($p = 0.023$) than those in the control group (**Table 5**). The L306 bacterial isolate was among the leaders in auxin-like compound production and ZnO solubilization among the bacterial isolates studied. This isolate also produced a small amount of siderophores. The L379 bacterial isolate produced moderate amounts of auxin-like compounds and siderophores and showed moderate ZnO solubilization index values (see **Table 2, Fig. 1**). Bacterization of wheat seeds with isolates from the root endosphere of *C. quitensis* did not cause significant changes in root length, except for bacterial isolates R318 and R380. The length of wheat roots, whose seeds were bacterized with isolates R318 ($p < 0.001$) and R380 ($p = 0.013$), was shorter compared to the control. After inoculation of wheat seeds with these bacterial isolates, the length of wheat seedling shoots also decreased (R318 ($p = 0.022$), R380 ($p < 0.001$)). A reduction in the length of wheat seedling shoots was observed after wheat seeds were inoculated with isolate R362 ($p < 0.001$). It is known that auxins in low concentrations stimulate root formation and play an extremely important role in the survival of plants under stress

conditions. However, in excessive concentrations, they induce the synthesis of ethylene (a stress and aging hormone), which inhibits the elongation of the main root and shoot, while stimulating the formation of a large number of root hairs or lateral roots, disrupting growth balance and inhibiting shoot development (Kurepa & Smalle, 2022). It is likely that isolates R362 and R380 produce auxin levels toxic to young wheat seedlings, leading to the development of young wheat seedling retardation.

Protein biosynthesis in plant cells is highly dependent on the availability of nitrogen sources, the intensity of photosynthesis, and other factors (Mokhele *et al.*, 2012). No statistically significant changes were observed in the protein content of wheat seedling leaves whose seeds had been treated with bacterial isolates from the endosphere of *C. quitensis*, with the exception of bacterial isolate L359. After inoculating wheat seeds with strain L359, a decrease in protein content was observed, calculated on a dry weight basis of the wheat leaves ($p = 0.012$) (Fig. 2).

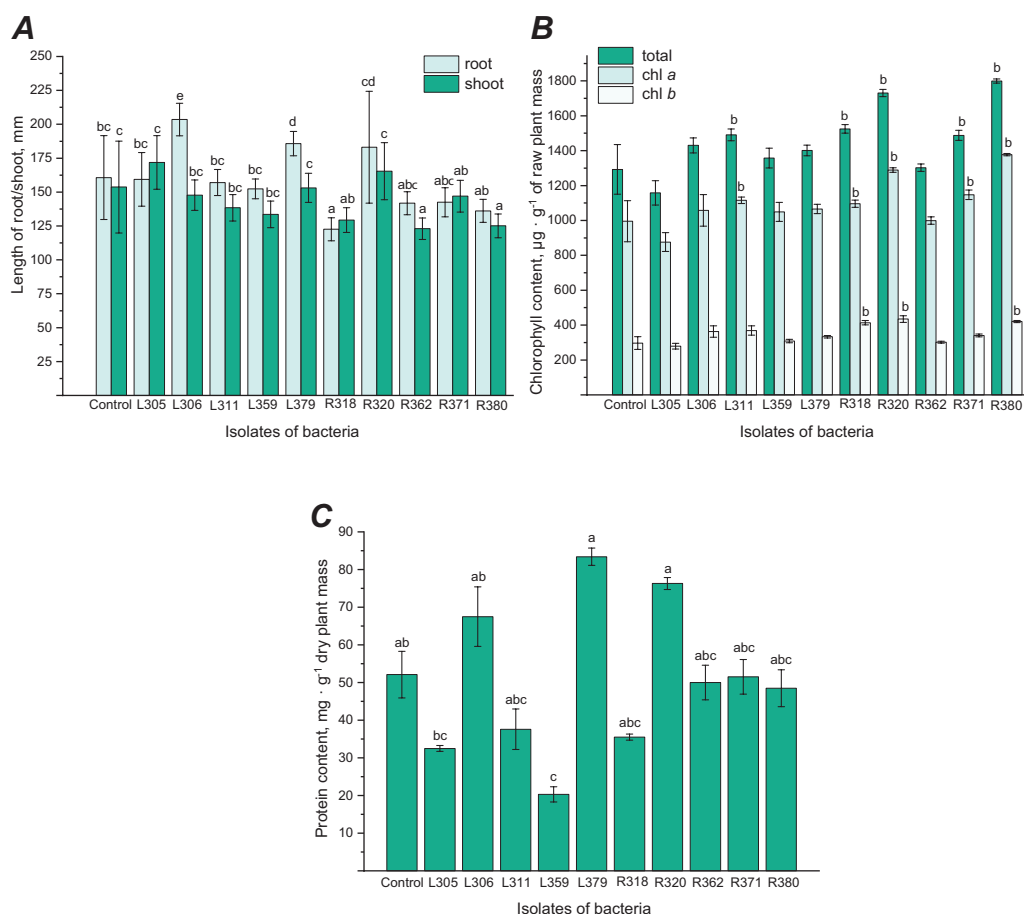


Fig. 2. Root and shoot length (**A**), pigment (**B**) and protein (**C**) content in leaves of *Triticum aestivum* cultivar Tybalt treated with isolates from *Colobanthus quitensis* (control – wheat seeds were treated with 0.9 % NaCl before sowing; identical letters indicate no significant differences in root and shoot length, chlorophyll, and protein content in seedling leaves after seed inoculation with bacterial isolates and in the control, as determined by the Dann's test ($p < 0.05$; $M \pm \text{SD}$; $n = 4$))

Increased chlorophyll content (total, *a*, and *b*) in the leaves of 8-day-old wheat seedlings was observed after bacterization of wheat seeds with isolates R320 ($p = 0.009$) and R380 ($p < 0.001$) from the endosphere of the root of *C. quitensis*. The effects of these isolates on wheat seedlings differ: inoculating wheat seeds with isolate R380 increased chlorophyll content in seedling leaves but decreased root and shoot length compared to the control, whereas treating wheat seeds with the R320 isolate resulted in an increase in chlorophyll content in the leaves without any statistically significant changes in root or shoot length. The 39 % increase in chlorophyll content in wheat shoots whose seeds were inoculated with isolate R380 compared to the control group likely indicates that the R380 bacterial isolate directly or indirectly affects plant metabolism. However, the plant's energy is limited, and it can allocate it either to linear growth (cell elongation) or to qualitative changes (pigment synthesis). We assume that, as a result of inoculating wheat seeds with the R380 bacterial isolate, wheat development shifted from "rapid growth" to "preparation for stress", which is beneficial in Antarctic conditions but appears to be suppressed in comfortable laboratory conditions. The possibility of acting as biopriming agents is described for representatives of the genera *Rhizobium*, *Azospirillum*, *Pseudomonas*, *Bacillus*, *Trichoderma*, and *Gliocladium* (Sahoo *et al.*, 2025). Based on the nucleotide sequence of the 16S rRNA gene, this isolate was identified as *Bacillus* sp. R380 (Fig. 3). According to phylogenetic analysis, the 16S rRNA gene sequence of *Bacillus* sp. R380 belongs to the *Bacillus subtilis* clade.

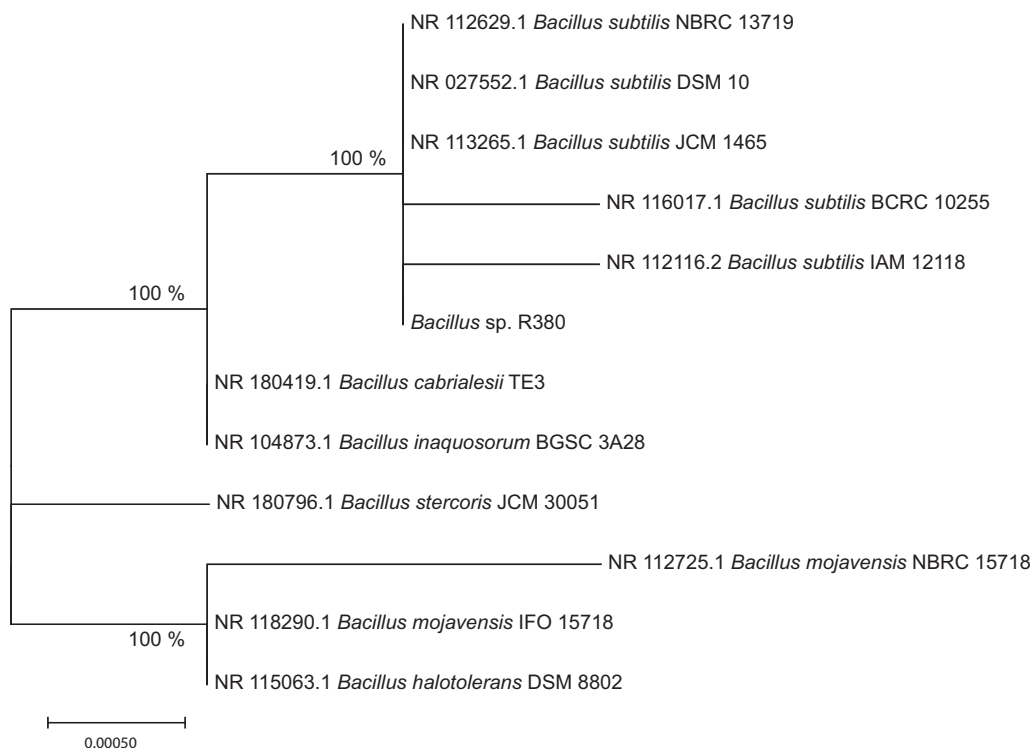


Fig. 3. Phylogenetic reconstruction of the 16S rRNA gene of the R380 and its next relatives according to the Hasegawa–Kishino–Yano model. Near the branches are the percentages from 1000 bootstrap replications. Phylogenetic analysis was conducted using MEGA XII

Treatment of wheat seeds with isolate R320 resulted in an increase in chlorophyll content in leaves without statistically significant changes in root or shoot length. Changes in protein content in wheat leaves were detected after bacterization of wheat seeds with isolate L359 ($p = 0.012$).

Based on an analysis of the characteristics of eight-day-old seedlings, we have observed the initial responses of wheat seedlings following seed inoculation. This approach is well-suited for screening studies and for detecting microorganisms with plant growth-promoting potential under laboratory conditions.

The early stages of plant ontogenesis (seed germination, seedling establishment, spatial organization of the root and aboveground parts) form the basis of plant life and agricultural productivity and have a decisive influence on resource uptake, stress tolerance, and reproductive potential under various agroecological conditions. Optimizing early plant development is viewed as the central focus of strategies for creating next-generation crop ideotypes that are resilient to climate change and enhance growth and yield stability in the face of increasing environmental variability. These strategies are based on combining knowledge from genomics, phenomics, and predictive systems biology with cutting-edge technologies, for example, to modulate dormancy, stress tolerance, and root system development using CRISPR/Cas technology, microbiome engineering to improve seed germination and root-soil interactions, and the application of nanotechnology to enhance seed viability and seedling stress tolerance (Al-Sawa'eer *et al.*, 2026).

CONCLUSION

Some bacterial isolates obtained from the endosphere of *C. quitensis* solubilize ZnO and produce cellulases and amylases. All the isolates studied produce auxin-like compounds, and most synthesize siderophores. Moderate and extreme halophiles are capable of growing under the influence of $\text{MnCl}_2 \cdot 4\text{H}_2\text{O}$, $\text{FeSO}_4 \cdot 7\text{H}_2\text{O}$, $\text{CdCl}_2 \cdot 2.5\text{H}_2\text{O}$, $\text{CoCl}_2 \cdot 6\text{H}_2\text{O}$, and $\text{K}_2\text{Cr}_2\text{O}_7$. Most of these isolates from the endosphere of *C. quitensis*, despite their plant growth-promoting traits, had no effect on wheat growth parameters during the early stages of development. However, bacterial isolates have also been identified that have a positive effect on the morphometric parameters or chlorophyll content in the leaves of seedlings. Isolate R380 from the endosphere of *C. quitensis* roots was capable of growing in a medium containing 5.0 % NaCl, 1.0 mM $\text{CuCl}_2 \cdot 2\text{H}_2\text{O}$, 0.02 mM $\text{CdCl}_2 \cdot 2.5\text{H}_2\text{O}$, 0.5 mM $\text{CoCl}_2 \cdot 6\text{H}_2\text{O}$ or 0.1 mM $\text{K}_2\text{Cr}_2\text{O}_7$. Inoculation of wheat seeds with this isolate led to an increased chlorophyll content in leaves of 8-day-old seedlings. Isolate R380 was identified as *Bacillus* sp. R380, based on 16S rRNA gene sequencing, and was selected for further study.

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COMPLIANCE WITH ETHICAL STANDARDS

Conflict of Interest. The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

AUTHOR CONTRIBUTIONS

Conceptualization [S.H.; O.M.; S.K.; O.M.]; methodology [S.H.; O.M.; S.K.]; data analysis [S.H.; O.M.; S.K.]; investigation [S.H.; O.M.; S.K.; V.H., O.T.]; resources [S.H.; O.M.; S.K.; O.M.]; writing – original draft preparation [S.H.; O.M.; S.K.; V.H.; O.M.]; writing – review and editing [S.H.; O.M.; S.K.; O.M.]; visualization [S.H.; O.M.; S.K.; V.H.].

All authors have read and agreed to the published version of the manuscript.

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ВЛАСТИВОСТІ БАКТЕРІЙ, ВИДІЛЕНИХ З АНТАРКТИЧНОЇ СУДИННОЇ РОСЛИНИ *COLOBANTHUS QUITENSIS*, І ЇХНІЙ ФІТОСТИМУЛЮВАЛЬНИЙ ПОТЕНЦІАЛ

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Обґрунтування. Дослідження бактерій, що заселяють ендосферу рослин Антарктики, є актуальними, оскільки доповнюють дані про участь мікроорганізмів у покращенні росту рослин і їхньої стійкості в екстремальних умовах існування. Цілеспрямоване використання бактерій ендofітів як біодобрих у сільському господарстві є перспективною технологією для забезпечення ефективних і екологічних рішень, особливо в період зміни клімату. Метою роботи було дослідити властивості бактерій, виділених з *Colobanthus quitensis*, визначити їхній вплив на показники росту ярої пшениці сорту Тубалт на ранніх етапах онтогенезу та відібрати штам, який виявляє фітостимулювальні властивості, для подальших досліджень.

Матеріали та методи. Ендосфіти виділяли на ТСА і R2A. Здатність бактерій до фіксації N_2 визначали з використанням середовища Ешбі. Висновки про солюбілізацію цинку робили за появою прозорих зон навколо колоній після росту на середовищі з ZnO . Для виявлення целюлазної активності використовували середовище з карбоксиметилцелюлозою, амілолітичної активності – крохмально-аміачний агар. Здатність бактерій синтезувати сидерофори було з'ясовано з використанням середовища з гексадецилтриметиламоній бромідом і хромазуолом S. Вміст ауксиноподібних сполук визначали з використанням реактиву Сальковського. Насіння замочували у суспензії бактерій і висівали у ґрунт, вирощували впродовж 8 діб за температури $+18 \pm 2$ °C. Концентрацію білка визначали за методом Бредфорда. Концентрацію хлорофілів *a* та *b* визначали фотометрично. Для визначення впливу солей важких металів і NaCl у середовище вносили їхні різні кількості.

Результати. Деякі ізоляти бактерій, виділені з ендосфери *C. quitensis*, солюбілізують ZnO , синтезують целюлази й амілази. Усі досліджувані ізоляти бактерій продукують ауксиноподібні сполуки, більшість – синтезують сидерофори. Помірні й екстремальні галофіли здатні рости за впливу $MnCl_2 \cdot 4H_2O$, $FeSO_4 \cdot 7H_2O$, $CdCl_2 \cdot 2.5H_2O$, $CoCl_2 \cdot 6H_2O$, $K_2Cr_2O_7$. Більшість виділених з ендосфери *C. quitensis* ізолятів бактерій, попри наявність фітостимулювальних властивостей, не виявляли жодного впливу на показники росту пшениці на ранніх етапах онтогенезу. Однак також виявлено ізоляти бактерій, які позитивно впливають на морфометричні показники або вміст хлорофілу в листках паростків. Ізолят бактерій R380 з ендосфери кореня *C. quitensis*, який забезпечував зростання вмісту хлорофілу в листках пшениці після бактеризації насіння, за послідовністю гена 16S rPHK було ідентифіковано як *Bacillus* sp. R380.

Висновки. Унаслідок скринінгу ендосфітів *Colobanthus quitensis* ми виділили перспективний штам *Bacillus* sp. R380, який підвищує вміст хлорофілу в паростках ярої пшениці.

Ключові слова: антарктичні мікроорганізми, *Bacillus*, *Colobanthus quitensis*, ендосфера, філосфера, фітостимулювальні властивості