

Isolation and Characterization of *Pseudomonas mandelii* Y02: A Novel Antarctic Strain for Herbicide Biodegradation

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Research Article

Keywords: *Pseudomonas mandelii* Y02, Herbicide degradation, Imazamox, Bioremediation, Antarctic bacteria, MLSA phylogeny

Posted Date: August 12th, 2026

DOI: <https://doi.org/10.21203/rs.3.rs-8907042/v1>

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Additional Declarations: No competing interests reported.

Abstract

Pseudomonas mandelii Y02, a psychrotolerant bacterial strain isolated from Antarctic water samples, was investigated for its herbicide-degrading potential under various environmental conditions. The strain demonstrated the ability to utilize four herbicides imazamox, pendimethalin, flurochloridone, and 2,4-D—as sole carbon sources in minimal medium. Among these, imazamox was degraded most efficiently, followed by pendimethalin, flurochloridone, and 2,4-D. Optimal degradation and growth occurred at pH 7.0 and 25°C, while extreme conditions resulted in reduced activity. Phylogenetic analysis based on 16S rRNA, *gyrB*, *rpoD*, and *rpoB* genes confirmed that strain Y02 is closely related to *P. mandelii* CPs7 and *P. cannabina*, and clusters within the *P. fluorescens*-like clade. Biochemical assays revealed distinct metabolic features compared to the reference strain *P. mandelii* CIP105273, highlighting Y02's broader substrate utilization and enzymatic profile. In a greenhouse bioassay, co-application of strain Y02 significantly reduced the phytotoxicity of imazamox on *Echinochloa crus-galli*, suggesting active biodegradation in planta. These findings underscore the bioremediation potential of *P. mandelii* Y02 for herbicide-contaminated soils, especially in cold or temperate environments.

Introduction

The rapid increase in the global population and the intensification of modern agricultural practices necessitate maximizing agricultural productivity. Therefore, using pesticides to protect crops from weeds, diseases, and pests has become crucial to ensuring high yields and abundant production (Damalas and Eleftherohorinos 2011). Chemical agents known as pesticides are generally used to prevent or control weeds, diseases, and pests to reduce crop losses and preserve high-quality products. However, overuse and uncontrolled usage of these compounds have detrimental effects on ecosystems that pose serious threats to human health and other living things. Thus, addressing the environmental and health concerns associated with pesticide usage is of paramount importance (Botías et al. 2019; Nazir et al. 2019; Sharma et al. 2019; Abubakar et al. 2020; Bhatt et al. 2021).

Herbicides are essential tools in modern agriculture, playing a crucial role in weed management to ensure crop productivity and sustainability (Sondhia 2013). Among the diverse range of herbicides, Racer (Flurochloridone), Imazamox, Pendimethalin, and 2,4-D are widely utilized for controlling a broad spectrum of weeds. Each of these herbicides belongs to a distinct chemical class, exhibiting specific modes of action to target vital physiological processes in plants. Racer (Flurochloridone) is a pre-emergence herbicide belonging to the pyrrolidinone chemical class. It primarily inhibits carotenoid biosynthesis, which causes oxidative stress and, ultimately, plant death (Schuster and Schröder 1990).

Racer is particularly effective against annual broadleaf and grass weeds in crops such as potatoes and sunflowers (Pfleeger et al. 1996). Another herbicide, Imazamox, is a member of the imidazolinone family, inhibiting acetohydroxyacid synthase (AHAS, also known as ALS). This is a key enzyme in the biosynthesis of branched-chain amino acids (Shaner et al. 1984). Due to its systemic action, Imazamox is absorbed by foliage and roots, making it effective for post-emergence weed control in soybean, maize,

and pulses (Owen et al. 2015). Pendimethalin is primarily used as a pre-emergence or early post-emergence dinitroaniline herbicide. It disrupts microtubule formation, inhibits cell division and root elongation in susceptible weed species (Senseman 2007). Pendimethalin's broad-spectrum effectiveness and residual soil activity have led to its widespread use in vegetable, legume, and cereal crop weed management (WSSA 2021). Furthermore, 2,4-D (2,4-Dichlorophenoxyacetic acid) is one of the most widely used synthetic auxin herbicides. It acts as a plant growth regulator but causes uncontrolled growth and eventual plant death (Grossmann 2010). It has been extensively applied in cereal crops and pastures for selective broadleaf weed control (Peterson et al. 2016).

Microorganisms can effectively detoxify pesticide residues (Redmile-Gordon et al. 2014; Arora and Mishra 2016; Wu et al. 2021; Birolli et al. 2022; Wen et al. 2023). Several bacterial species are known to degrade pesticides by utilizing them as carbon and energy sources. Notable examples include *Rhodococcus* sp. (degrading metamitron) (Fang et al. 2016), *Flavobacterium* sp. (degrading chlorpyrifos), *Arthrobacter* sp. (degrading iprodione) (Campos et al. 2017), *Pseudomonas putida* (degrading diclofop-methyl) (Jilani and Khan 2004; Wang et al. 2005), *Bacillus thuringiensis* (degrading pyrethroid) (Birolli et al. 2021), and *Rhodococcus pyridinivorans* Y6 (Huang et al. 2023). Among these, pseudomonads are particularly well known for their metabolic versatility and ability to degrade a wide range of organic pollutants, including herbicides (Whyte et al. 2002; Afzal et al. 2017). Studies have reported that *Pseudomonas putida* and *Pseudomonas fluorescens* can break down 2,4-D through enzymatic pathways involving α -ketoglutarate-dependent dioxygenases, ultimately converting it into less toxic metabolites (Newcombe and Crowley 1999). *Pseudomonas* and other soil bacteria are also essential to the microbiological breakdown of pendimethalin, a dinitroaniline herbicide, which mostly occurs through nitroreduction and oxidative pathways. Similarly, imazamox degradation has been performed by soil bacteria, including *Bacillus* and *Rhodococcus* species. They utilize hydrolysis and oxidation pathways to metabolize the herbicide (Jacobsen and Hjelmsø 2014). The objective of this study was to investigate the bioremediation potential of *Pseudomonas mandelii* Y02, a bacterial strain isolated from Antarctica, for the degradation of Imazamox-contaminated soils under both *in vitro* and *in vivo* conditions.

Material and methods

Sample collection

This research was conducted under the auspices of the Presidency of the Republic of Türkiye with financial support from the Ministry of Science, Industry, and Technology. The study was coordinated by the Istanbul Technical University (ITU) Polar Research Center (PoReC). Field investigations on Ardley Island were carried out as part of the Third Turkish Antarctic Expedition (TAEIII) in 2019, during which a multidisciplinary team of 24 researchers conducted scientific studies across various disciplines. Water samples were aseptically collected from Ardley Island, Antarctica (Fig. 1) and transported to the laboratory under sterile conditions.

Selection of herbicide-degrading bacteria

To facilitate the isolation of herbicide-degrading bacteria, a chloride-free minimal medium was prepared at 10× concentration in distilled water and adjusted to pH 7.5. The basal salt composition included $\text{NaH}_2\text{PO}_4 \cdot 2\text{H}_2\text{O}$ (10.0 g/L), $\text{K}_2\text{HPO}_4 \cdot 3\text{H}_2\text{O}$ (42.5 g/L), and $(\text{NH}_4)_2\text{SO}_4$ (25.0 g/L). In addition, trace elements were added at a 10× concentration according to Hareland et al. (1975): $\text{C}_6\text{H}_9\text{NO}_6$ (1.0 g/L), MgSO_4 (2.0 g/L), $\text{FeSO}_4 \cdot 7\text{H}_2\text{O}$ (120.0 mg/L), $\text{MnSO}_4 \cdot 4\text{H}_2\text{O}$ (30.0 mg/L), $\text{ZnSO}_4 \cdot \text{H}_2\text{O}$ (30.0 mg/L), and $\text{CoCl}_2 \cdot 6\text{H}_2\text{O}$ (10.0 mg/L). The medium was sterilized by autoclaving at 121°C for 15 minutes. Following sterilization, the medium was supplemented under sterile conditions with the following herbicides at their recommended application rates, to serve as the sole carbon sources: imazamox (2.5 ml/L), pendimethalin (12.5 ml/L), flurochloridone (12.5 ml/L), and 2,4-D (10.0 ml/L). Each 50 mL Falcon tube containing the prepared medium was inoculated with bacterial suspensions that had been pre incubated at $25 \pm 2^\circ\text{C}$ for 24 hours and adjusted to an optical density (OD_{600}) of 0.1. A minimal medium without any added carbon source was used as a negative control. The tubes were incubated under shaking conditions (185 rpm) for 5 days at four different temperatures (5°C, 25°C, 30°C, and 35°C) and four pH levels (5, 7, 8, and 9) to assess bacterial growth under variable environmental conditions. Optical density (OD_{600}) values were recorded at 24-hour intervals. All experiments were performed in quadruplicate.

Physiological and biochemical characterization

The phenotypic characteristics of the bacterial isolate was examined by culturing cells on King's B medium at 25°C for 24 hours. Single colonies were used for Gram staining and motility assays using semisolid King's B medium. Catalase activity was also assessed with 3% hydrogen peroxide (v/v), while oxidase activity was determined by using a color change on the test strip (Bioanalyse Oxidase Test Kit). Furthermore, carbon source utilization was tested in M9 minimal agar medium supplemented with trace elements, 100 mM of each carbon source and 10 µL bacterial suspension ($\text{OD}_{600} = 0.1$). Biochemical characteristics and acid production from carbohydrates were analyzed using the bioMérieux API20E system.

Molecular analyses

Molecular identification of *Pseudomonas mandelii* Y02 was performed by sequencing of 16S rRNA, *gyrB*, *rpoD*, and *rpoB* gene regions. For this purpose, genomic DNA was extracted using a bacterial DNA extraction kit (Cat. No. 47016, Qiagen). PCR was performed in a 20 µL reaction mixture containing 6.0 µL of nuclease-free dH₂O, 10.0 µL of reaction buffer (BioMix™ Red, Bioline 25006), 1 µL of each primer (1.6 pmol), and 2 µL of template genomic DNA (2 ng/µL). The universal primers 27F and 1492R for 16S rRNA amplification were originally described by Lane (1991). Primer sequences were given in Table 1. Amplification conditions were as follows: initial denaturation at 95°C for 5 min, followed by 10 cycles of denaturation at 95°C for 1 min, annealing at 65°C–55°C for 30 s (with a 1°C decrease in each cycle), and extension at 72°C for 90 s. Subsequently, the second part of the touchdown PCR was performed with 24 cycles of denaturation at 95°C for 1 min, annealing at 55°C for 30 s (with a temperature gradient increasing from 56°C to 72°C in 90 s), extension at 72°C for 90 s, and a final extension at 72°C for 5 min.

Table 1
Primer sequences

Primer names	Sequences (5'-3')	References
16S rRNA-27F	AGAGTTTGATCMTGGCTCAG	Lane, D. J., 1991
16S rRNA-1492R	TACGGYT ACCTTGTTACGACTT	
rpoB- LAPS	TGGCCGAGAACCAGTTCCGCGT	Ait Tayeb et al., 2005
rpoB- LAPS27	CGGCTTCGTCCAGCTTGTTTCAG	
rpoD-70F	ATYGAAATCGCCAARCG	Mulet et al., 2009
rpoD-70R	AGYTTGATYGGGATGAA	
gyrB-gyrBBAUP2	GCGGAAGCGGCCNGSNATGTA	Santos and Ochman, 2004
gyrB- APru	GCNGGRTCYTTYTCYTGRCA	

PCR products and a DNA ladder (HyperLadder™, BIO-33025) were resolved via 1% agarose gel electrophoresis at 50 V for 60 min in 1× TAE buffer (90 mmol/L Tris, 20 mmol/L acetic acid, 1 mmol/L EDTA, pH 8.0). The PCR products were purified using a gel extraction kit (QIAquick, 28104) and subsequently sequenced. The obtained gene sequences were compared to those in the NCBI database using BLASTn.

Phylogenetic analysis

The gene sequences (16S rRNA, rpoB, rpoD and gyrB) of *Pseudomonas mandelii* Y02 and closely related *Pseudomonas* species were retrieved and curated for phylogenetic analysis. Sequence alignment was performed using MAFFT v7.490 (Kato and Standley, 2013) in auto mode, allowing the software to determine the optimal alignment strategy. The quality of the alignment was manually inspected, and poorly aligned regions and gaps were removed to enhance accuracy. Phylogenetic tree reconstruction was conducted using MEGA X (Kumar et al. 2018) and IQ-TREE v2.1.3 (Nguyen et al. 2015). The neighbor-joining (NJ) method was employed for tree inference under the GTR + G+I (General Time Reversible with Gamma Distribution and Invariant Sites) model which was identified as the best-fit evolutionary model using ModelFinder (Kalyaanamoorthy et al. 2017). To assess the robustness of the phylogenetic trees, bootstrap analysis was performed with 1,000 replicates. For visualization, a circular representation of the phylogenetic tree was generated using iTOL (Letunic and Bork 2021) and FigTree v1.4.4, ensuring clarity and suitability for publication.

Greenhouse bioassay for herbicide degradation

The effectiveness of a bacterial isolate in degrading the herbicide under minimal medium conditions was assessed in a pot experiment. Among the herbicides utilized in this investigation, Imazamox was chosen for this purpose since it had the maximum soil persistence. Preliminary studies under various pH and temperature conditions revealed that the bacterial isolate (*Pseudomonas mandelii* Y02) used for the

experiment had the highest potential for degradation. A weed species (*Echinochloa crus-galli*) that is susceptible to Imazamox was chosen as the target plant.

The seeds of *Echinochloa crus-galli* were pre-germinated in Petri dishes and subsequently transplanted into pots at the 2–4 leaf stage to establish the experiment. The study was designed with five different treatments, each set up consisted of four replicates to ensure statistical reliability: i. Control (Water), ii. Bacterial isolate + Herbicide + Minimal medium, iii. Imazamox (2.5 mL/L) + Water, iv. Imazamox + Minimal medium, and v. Minimal medium only.

All treatments were applied by spraying the leaves of *Echinochloa crus-galli* plants daily for five consecutive days under controlled conditions at 24–26°C. At the end of the fifth day, the number of dead plants was recorded to assess the impact of bacterial degradation on herbicide efficacy.

Statistical analysis

A two-factor repeated measures experimental design was used to analyze the data through analysis of variance (ANOVA). Levene's test indicated that the variances were homogeneous across time points ($P = 0.098$). The Shapiro-Wilk test confirmed that the data followed a normal distribution ($P = 0.120$), validating the reliability of the ANOVA results.

Results and discussion

Selection of herbicide-degrading bacteria

The herbicide degradation order of *Pseudomonas mandelii* was Imazamox>Pendimethalin>Flurochloridone > 2,4-D. The herbicides degradation capacity of *Pseudomonas mandelii* Y02's were examined under different pH and temperature conditions in a minimal medium. OD600 measurements were recorded spectrophotometrically after 24 hours of incubation. The results indicated that *P. mandelii* Y02 exhibited growth within the pH range of 5.0–8.0 and at temperatures between 5°C and 30°C. The highest bacterial growth rates were observed for all tested herbicides at pH 7.0 and 25°C. Among the tested herbicides, *P. mandelii* Y02 exhibited the highest degradation capability for Imazamox, followed by Pendimethalin, Flurochloridone, and the least for 2,4-D (Fig. 2). These growth trends align with previous findings on *Pseudomonas* species, which are known to thrive under mesophilic conditions and neutral pH (Zhang et al. 2019; Kumar et al. 2021). Similarly, under optimal physiological conditions, other *Pseudomonas* strains, such as *P. fluorescens* and *P. putida*, have been reported to degrade imidazolinone herbicides (Wang et al. 2020). In contrast, bacterial growth remained minimal at extreme pH levels (5.0 and 8.0) and temperatures (5°C and 30°C), likely due to reduced enzymatic activity (Singh et al. 2018). Notably, bacterial growth in the presence of 2,4-D was consistently lower under all conditions, suggesting that chlorinated herbicides may negatively affect enzymatic activity. This result was consistent with previous studies (Sharma et al. 2022). These findings underscores the significance of environmental factors in optimizing the bioremediation efficiency of *P.*

mandelii Y02. They highlight the need to consider appropriate pH and temperature regimes for potential applications in herbicide-contaminated soils.

Physiological and biochemical characterization

In total, 50 environmental samples were collected from soil, seawater, glacier, and lake water in the Ardley Island region of Antarctica. From these samples, 52 bacterial isolates were obtained, 8 of which exhibited growth in an herbicide-containing medium. The isolate exhibiting the most robust growth, *Pseudomonas mandelii* Y02, was selected for further analysis. On King's B medium, the colonies displayed smooth edges, a uniform surface, and fluorescence under UV light—traits consistent with typical *Pseudomonas* species (Garrrity 2005; Palleroni 2010). Both *P. mandelii* Y02 and the reference strain *P. mandelii* CIP105273 were subjected to biochemical assays to assess their metabolic capabilities. Both strains tested positive for catalase and oxidase activity, indicating the presence of enzymes essential for hydrogen peroxide breakdown and electron transport. These findings suggest efficient aerobic metabolism, characteristic of *Pseudomonas* species (Vasquez-Ponce et al. 2018) (Table 2). Nitrate reduction, a key feature for anaerobic respiration, was observed in both strains, reflecting their ability to thrive under oxygen-limited conditions. This metabolic trait aligns with the flexibility reported for *P. mandelii* strains, including *P. mandelii* CIP105273 (Vasquez-Ponce et al. 2018). In terms of carbon source utilization, *P. mandelii* Y02 was capable of utilizing glucose, fructose, trehalose, and citrate as sole carbon sources, consistent with the metabolic profile of *P. mandelii* CIP105273. However, both strains failed to ferment lactose, sucrose, maltose, galactose, ribose, L-arabinose, xylose, and sorbitol, indicating a limited ability to ferment certain sugars compared to other *Pseudomonas* species (Palleroni 2010). Similarly, amino acid utilization was also restricted. Both strains were unable to metabolize L-tyrosine, L-tryptophan, L-lysine, L-proline, and L-methionine as sole carbon and nitrogen sources. However, they were able to utilize glycine, L-serine, and pyruvate, showing similar metabolic profiles between *P. mandelii* Y02 and *P. mandelii* CIP105273 (Vasquez-Ponce et al. 2018). Notably, *P. mandelii* Y02 exhibited a more extensive metabolic capacity than the reference strain, particularly in the assimilation of several organic acids and sugars, including rhamnose and melibiose, which are absent in *P. mandelii* CIP105273. In contrast, *P. mandelii* Y02 displayed unique enzymatic activities such as arginine dihydrolase and gelatinase, which were not observed in the reference strain. These distinctive traits highlight the ecological and metabolic divergence between the two strains, despite their shared taxonomic classification.

Table 2

Biochemical differences among *P. mandelii* Y02, the Antarctic isolate *P. mandelii* CIP105273 type strain, and other *Pseudomonas* species

Characteristics	<i>P. mandelii</i> Y02	<i>P. mandelii</i> CIP105273	<i>P.</i> <i>fluorescens</i>	<i>P.</i> <i>aeruginosa</i>	<i>P.</i> <i>putida</i>
Gram Reaction	-	-	-	-	-
Catalase	+	+	+	+	+
Gelatinase	-	-	+	+	-
Oxidase	+	+	+	+	+
Arginine dihydrolase	-	-	+	+	-
Phenylalanine deaminase	-	-	-	-	-
Nitrate reduction	+	+	+	+	+
Voges-Proskauer	-	-	-	-	-
Assimilation					
Glucose	+	+	+	+	+
Lactose	-	-	-	-	-
Sucrose	-	-	-	+	-
Maltose	-	-	+	+	-
Fructose	+	+	+	+	+
Galactose	-	-	+	+	+
Ribose	-	-	+	+	+
L-Arabinose	-	-	+	+	+
Xylose	-	-	+	+	+
Sorbitol	-	-	+	+	+
Trehalose	+	+	+	+	+
Citrate	+	+	+	+	+
Malate	+	+	+	+	+
Pyruvate	+	+	+	+	+
Lactate	+	+	+	+	+
Benzoate	-	-	+	+	+

Characteristics	<i>P. mandelii</i> Y02	<i>P. mandelii</i> CIP105273	<i>P.</i> <i>fluorescens</i>	<i>P.</i> <i>aeruginosa</i>	<i>P.</i> <i>putida</i>
Phenyl Acetate	-	-	+	+	+
Glycine	+	+	+	+	+
L-Alanine	+	+	+	+	+
L-Serine	+	+	+	+	+
L-Tyrosine	-	-	+	+	+
L-Tryptophan	-	-	+	+	+
L-Lysine	-	-	-	+	+
L-Proline	-	-	+	+	+
L-Methionine	-	-	+	+	+

Pseudomonas mandelii is known for producing extracellular enzymes and bioactive secondary metabolites, which are of significant industrial interest (Li et al. 2013; Higuera-Llanten et al. 2018). In particular, carbohydrate degradation plays a crucial role in process optimization in sectors such as food, healthcare, and bioenergy (Catal et al. 2011; Shintani 2019). In this study, a novel isolate, *P. mandelii* Y02, was identified and characterized. While both *P. mandelii* Y02 and the reference strain *P. mandelii* CIP105273 shared several biochemical features such as catalase and oxidase activity, nitrate reduction, and utilization of various carbohydrates *P. mandelii* Y02 demonstrated broader metabolic versatility. This included the assimilation of additional sugars and organic acids, and distinct enzymatic activities not present in the reference strain. Previous studies have reported the ability of *P. mandelii* strains to degrade herbicide residues in contaminated environments (Kurtoglu et al. 2020), highlighting the ecological relevance of this species. The identification of *P. mandelii* Y02 in this study, particularly due to its herbicide tolerance and cold-adapted enzymatic profile, expands the known ecological and biotechnological potential of the species. These features suggest that *P. mandelii* Y02 may serve as a promising candidate for bioremediation applications in cold or herbicide-contaminated environments.

Phylogenetic analysis

Both multilocus sequence analysis (MLSA) and 16S rRNA gene sequencing confirmed that *Pseudomonas mandelii* Y02 was phylogenetically most closely related to *P. mandelii* CPs7 and *P. cannabina* across all gene regions examined. In addition, the strain exhibits strong phylogenetic affiliations with *P. tremae* and *P. antarctica*. The 16S rRNA gene-based phylogeny places *P. mandelii* Y02 within the same clade as other *Pseudomonas fluorescens*-like species, thereby reinforcing its taxonomic placement within this lineage (Fig. 3). The resulting phylogenetic trees provide insights into the evolutionary relationships of *Pseudomonas mandelii* Y02, highlighting its genetic proximity to related taxa.

Pot experiment

In the present study, a pot experiment was conducted to evaluate the capacity of *Pseudomonas mandelii* Y02 to mitigate the phytotoxic effects of Imazamox on *Echinochloa crus-galli*. Among the herbicides tested in preliminary laboratory assays, Imazamox was selected due to its high persistence in soil. The bacterial isolate *P. mandelii* Y02, previously characterized for its robust growth across variable pH and temperature conditions, was employed in combination with the herbicide under different treatment regimes. The results (Table 3) revealed significant differences in weed mortality rates among treatments ($p < 0.01$).

Table 3
Effect of treatments on the mortality rate of *Echinochloa crus-galli* in the pot experiment.

Treatment	Mortality Rate (%) $\pm$ SD*
Imazamox (2.5 ml/L) + Water	100 $\pm$ 0,000 ^a
Imazamox+ Minimal Medium	80 $\pm$ 2,34 ^b
Imazamox + Bacterial Isolate + Minimal Medium	30 $\pm$ 3,12 ^c
Minimal Medium	20 $\pm$ 4,082 ^d
Water (Control)	0 $\pm$ 0,000 ^e
*Means followed by different letters indicate statistically significant differences among treatments at $p < 0.01$.	

The highest mortality (100%) was observed in the treatment combining Imazamox at the recommended dose with water. This was followed by the Imazamox + minimal medium treatment, which induced 80 $\pm$ 2.34% mortality. Notably, when the bacterial isolate was included (Bacteria + Imazamox + minimal medium), weed mortality dropped significantly to 30 $\pm$ 3.12%. Minimal medium alone resulted in a 20 $\pm$ 4.08% mortality rate, whereas the control treatment (water only) showed no phytotoxic effect. These findings suggest that *P. mandelii* Y02 may actively degrade Imazamox, thereby reducing its bioavailability and effectiveness against *E. crus-galli*. This hypothesis is supported by previous studies demonstrating the biodegradative abilities of *Pseudomonas* spp. toward structurally similar imidazolinone herbicides (Lin et al. 2020). Members of the *P. fluorescens* group, including *P. mandelii*, are known for their enzymatic capacity to metabolize diverse xenobiotics as carbon or nitrogen sources (Singh et al. 2004; Cycon et al. 2017). Therefore, observed reduction in herbicide efficacy in this study was supported by these investigations. Furthermore, microbial interactions in the rhizosphere have been shown to influence herbicide dynamics in soil, altering both persistence and phytotoxicity (Fang et al. 2019).

Conclusion

The reduction in herbicidal activity in the presence of *P. mandelii* Y02 highlights its potential as a bioremediation agent for soils contaminated with residual herbicides. The strain's ability to reduce Imazamox toxicity without entirely eliminating weed pressure also points to a possible role in integrated weed and soil health management systems. In conclusion, the data not only affirm the biodegradation potential of *P. mandelii* Y02 but also underline its applicability in sustainable agricultural practices aimed at minimizing chemical residues in soil ecosystems.

Declarations

Conflict of interest

The authors declare no competing interests.

Ethical approval

Authors contribute to maintaining the integrity of the research and its presentation by following the rules of good scientific practice. This article does not contain any studies with human participants or animals performed by any of the authors.

Funding

This research was conducted under the auspices of the Presidency of the Republic of Türkiye and was supported by the Ministry of Industry and Technology. The study was coordinated by the Istanbul Technical University (ITU) Polar Research Center (PoIReC). Fieldwork conducted on Galindez Island formed part of the TAE III framework.

Author Contribution

The study was conceptualized by Miss Sine Kaya and Prof. Dr. Hasan Murat Aksoy, who also coordinated the data collection. Experimental work was carried out collaboratively by Miss Sine Kaya and Assist. Prof. Dr. Yilmaz Kaya. Prof. Dr. Hasan Murat Aksoy prepared the initial draft of the manuscript, which was subsequently revised for intellectual content by Prof. Dr. Sevgi Marakli.

Acknowledgements

We gratefully acknowledge the contributions of all researchers involved in the Third Turkish Antarctic Expedition (TAE III), whose efforts in sample collection and logistical support were vital to the success of this study.

Data availability

The datasets generated during and/or analyzed during the current study are available from the corresponding author on reasonable request

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Figures

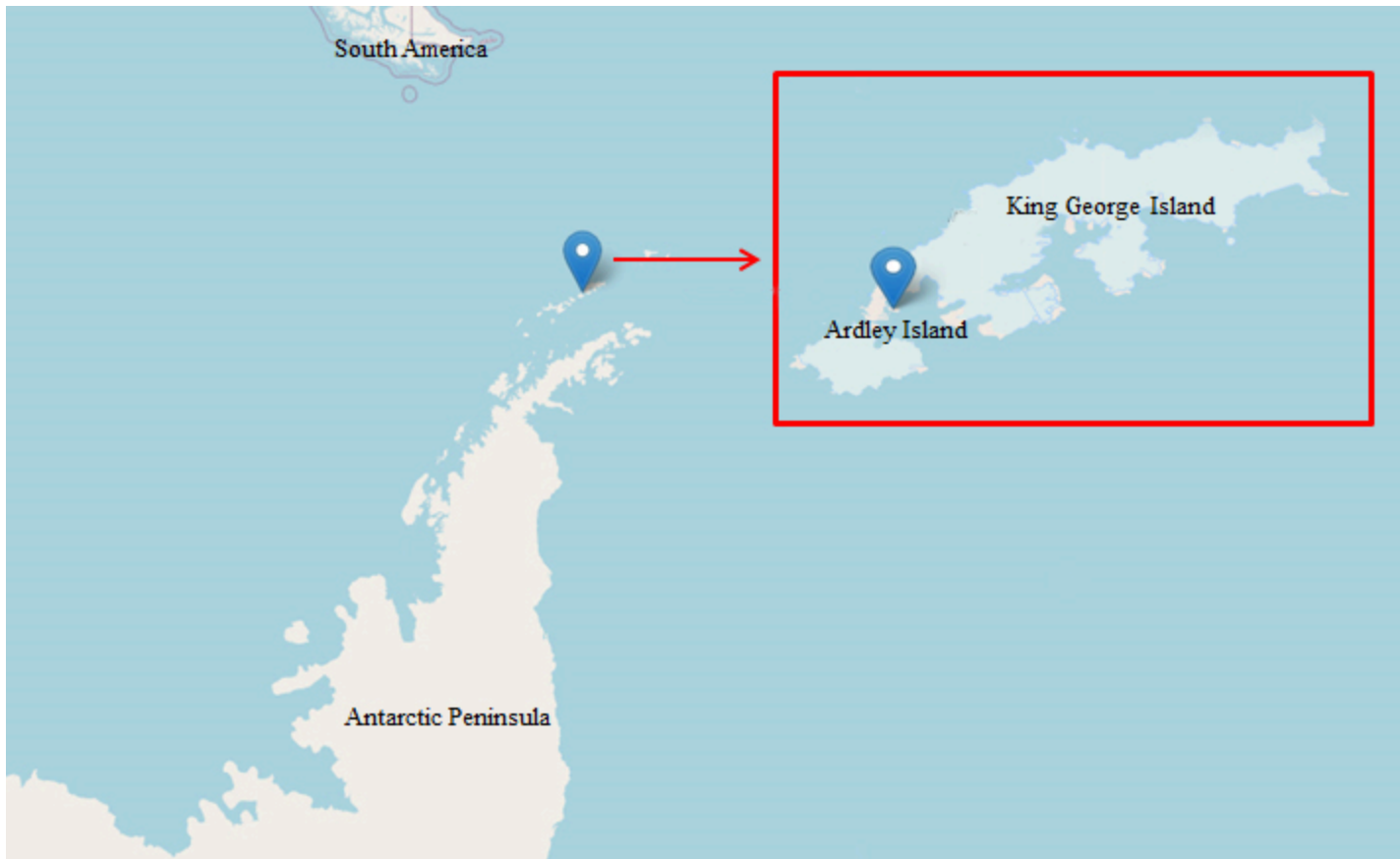
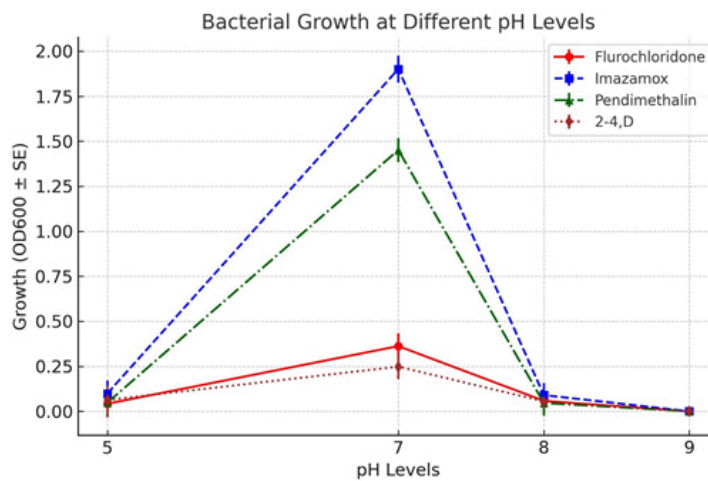
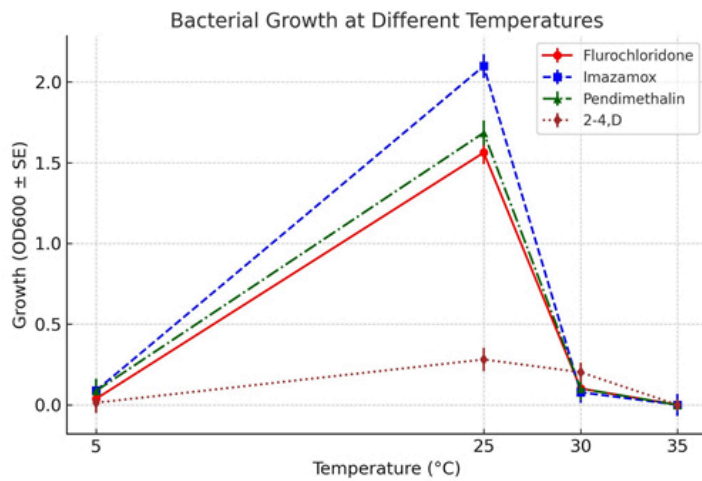


Figure 1

Sample collection site on the map (62.2139° S, 58.9333° W) at Ardley Island, Antarctica.



a



b

Figure 2

Growth of *Pseudomonas mandelii* Y02 under different pH (a) and temperature (b) conditions in the presence of herbicides.

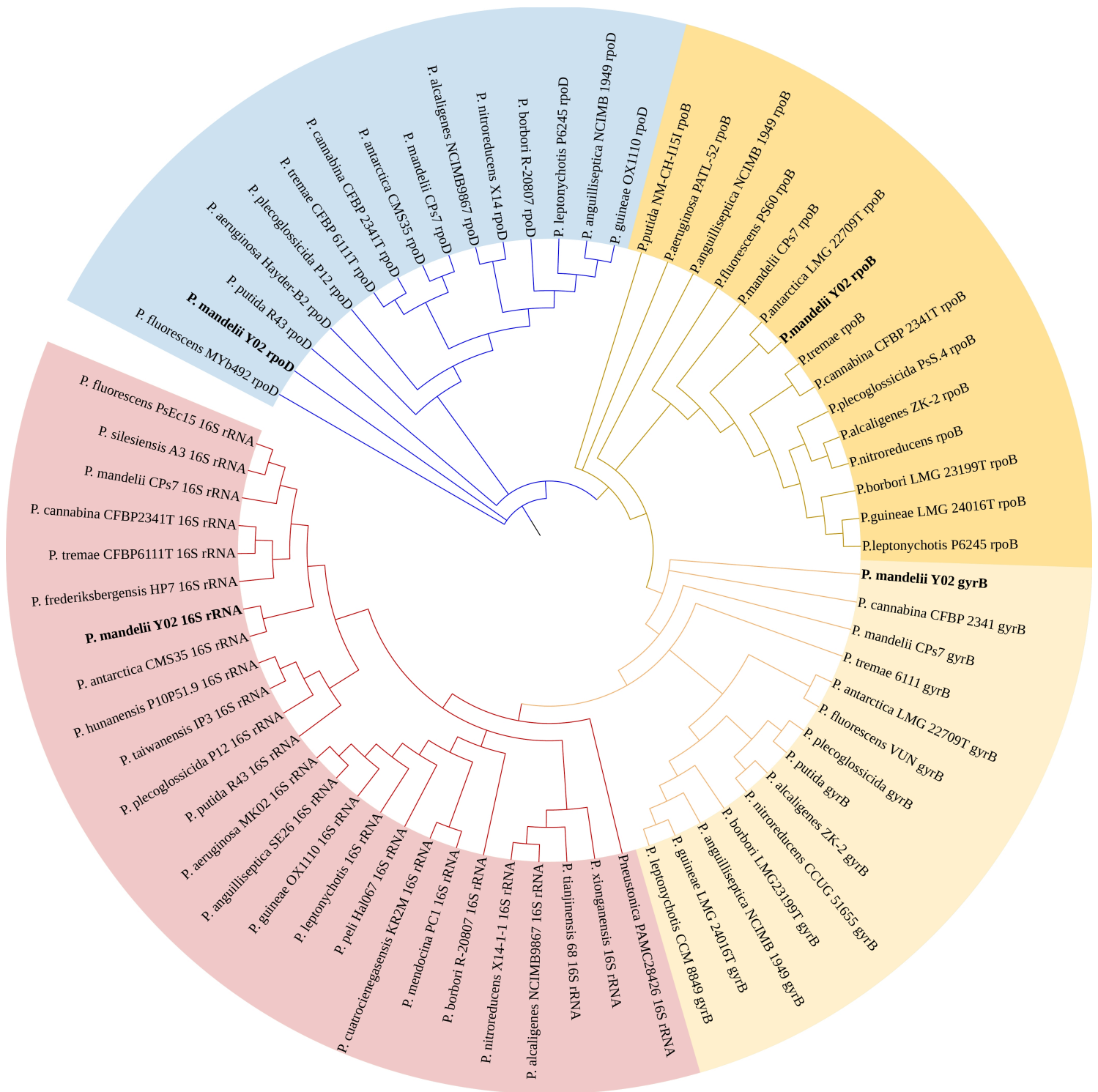


Figure 3

Phylogenetic relationships of *Pseudomonas mandelii* Y02 based on MLSA of the 16S rRNA, *rpoB*, *rpoD*, and *gyrB* gene regions. Bootstrap values (expressed as percentages of 1,000 replicates) are indicated at branch nodes. The scale bar represents sequence divergence.