BMC Genomic Data

DATA NOTE

Open Access

# Complete genome sequence of *Pseudarthrobacter* sp. NIBRBAC000502770 from coal mine of Hongcheon on Republic of Korea

Min-Kyu Park[1,2,3], Yeong-Jun Park[1,2,3], Myung-Suk Kang[4], Min-Ha Kim[4], Soo-Young Kim[4] and Jae-Ho Shin[1,2,3*]

## Abstract

**Objectives** The data were collected to obtain the complete genome sequence of Pseudarthrobacter sp. NIBRBAC000502770, isolated from the rhizosphere of Sasamorpha in a heavy metal-contaminated coal mine in Hongcheon, Republic of Korea. The objective was to explore the strain's genetic potential for plant growth promotion and heavy metal resistance, particularly arsenate and copper. The aim focused on identifying microbes that enhance plant growth in metal-tolerant environments and evaluating the strain's bioremediation and agricultural uses. This study sought key genes for bioremediation and agricultural applications in contaminated soils, aiding sustainable management and biotechnology.

**Data description** We report the complete genome sequence of *Pseudarthrobacter* sp. NIBRBAC000502770, isolated from a coal mine in Hongcheon, Republic of Korea. The genome contains a chromosome (4,403,796 bp) and a plasmid (74,326 bp, named pMK-1) with 286-fold coverage. Genome annotation identified 4,209 genes, including 3,926 protein-coding genes, 51 tRNA genes, and 15 rRNA genes, with a G + C content of 66.1%. Functional analysis revealed genes related to plant growth promotion and heavy metal resistance, such as arsenate (*ars*R, *ars*C) and copper (*cop*C, *cop*D) resistance genes. Genes involved in auxin biosynthesis suggest potential agricultural applications. The genome and plasmid are available in GenBank (CP041198.1, CP014497.1), offering insights into bioremediation and plant growth in metal-contaminated environments.

**Keywords** Whole genome sequencing, *Pseudarthrobacter* sp. NIBRBAC000502770, Heavy metal resistance, De novo assembly

## Objective

*Pseudarthrobacter* sp. is a Gram-positive, aerobic bacterium predominantly found in soil. This genus was originally classified under the *Arthrobacter* genus but was reclassified following molecular phylogenetic analysis [1]. *Pseudarthrobacter* plays a crucial ecological role due to its ability to degrade organic pollutants, making it valuable in bioremediation processes [2]. The strain *Pseudarthrobacter* sp. NIBRBAC000502770 was isolated from the heavy metal-contaminated coal mine in the Hongcheon region (Republic of Korea) and screened for plant growth

*Correspondence:
Jae-Ho Shin
jhshin@knu.ac.kr
[1] Department of Applied Biosciences, College of Agriculture and Life Sciences, Kyungpook National University, Daegu 41566, Republic of Korea
[2] NGS Core Facility, Kyungpook National University, Daegu 41566, Republic of Korea
[3] Microbalance Co. Ltd, Daegu 41566, Republic of Korea
[4] National Institute of Biological Resources, Incheon 22689, Republic of Korea

promotion based on its known genetic potentiality of arsenate resistance. The goal was to identify plant-growth-promoting microorganisms in the rhizosphere of metal-contaminated area plants such as *Sasamorpha* and evaluate their bioremediation and agricultural application capability. Furthermore, its capacity to thrive in extreme environments classifies it as an extremophile, drawing significant attention for its potential applications in various conditions. Heavy metal contamination presents substantial environmental and public health hazards. Elements like lead, cadmium, mercury, and arsenic persist in soils and aquatic systems, leading to prolonged ecological toxicity [3]. These pollutants disrupt ecosystems, impairing plant growth and affecting fauna. Additionally, they bioaccumulate in the food chain, contributing to severe human health issues, including neurotoxicity, respiratory dysfunction, and developmental abnormalities [4]. Due to their environmental persistence and resistance to biodegradation, advanced remediation technologies are essential for their effective removal or neutralization [5]. Various methods exist for the removal of heavy metals from soil, but they are often costly and labor-intensive [6, 7]. From the perspective of carbon neutrality and environmental sustainability, biological control using plants has garnered significant attention [8, 9]. A biological approach for heavy metal removal is *phytoremediation*, which utilizes mechanisms such as phytovolatilization, phytoextraction, phytodegradation, and phytostimulation. However, this method has limitations, including its slow process and dependency on soil conditions and specific heavy metals [10, 11]. Due to these limitations, the application of phytoremediation in environments severely contaminated with heavy metals requires the adaptability of the plants and the use of eco-friendly supplements that can promote plant growth [11–13]. The *Pseudarthrobacter* sp. NIBRBAC000502770 strain in this study was found to produce the plant growth-promoting hormone auxin without showing any plant pathogenicity. Understanding the Plant-Growth-Promoting (PGP) mechanisms of such strains is critical for maximizing phytoremediation efficiency. Additionally, genomic resources are vital for elucidating the mechanisms involved in promoting effective heavy metal suppression, offering insights into sustainable environmental management and agricultural biotechnology applications.

## Data description

Pseudarthrobacter sp. NIBRBAC000502770, isolated from a heavy metal-rich coal mine in Hongcheon, Republic of Korea, was cultivated in tenfold diluted Luria–Bertani medium containing 370 ppm arsenate to grow heavy metal-resistant bacteria [14] The genome was sequenced using Single Molecule Real-Time (SMRT) sequencing technology, and the sequence reads were assembled de novo using the SMRT Portal version 2.3 with the HGAP protocol version 3.0 [15, 16]. The genome consists of a circular chromosome of 4,403,796 bp and a circular plasmid of 74,326 bp, named pMK-1, with an average coverage of 286-fold.

Genome annotation was conducted using the Rapid Annotation Subsystem Technology (RAST) server [17] and the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) [18], identified 4,209 total genes, including 3,926 protein-coding genes, 51 tRNA genes, and 15 rRNA genes, with a G+C content of 66.1%. The annotated genome reveals significant features related to heavy metal resistance and plant growth promotion.

Functional analysis revealed that the genome contains a complete *ars* operon (*ars*ABCRH), which includes several key genes involved in arsenic resistance, such as *ars*R (encoding the arsenical resistance operon repressor) and *ars*C (encoding arsenate reductase). These genes are essential for detoxifying arsenic, enabling the strain to survive in high arsenic environments. Additionally, the genome harbors genes associated with resistance to other heavy metals, including cadmium, and mercury, indicating a broad capacity for metal detoxification. The presence of these genes suggests that the strain has a robust system for tolerating various toxic metals, which is crucial for its survival in metal-contaminated environments and supports multiple enzymatic functions.

The presence of genes involved in auxin biosynthesis was also noted, including indole-3-glycerol phosphate synthase, which catalyzes a key step in tryptophan biosynthesis, a precursor of auxin. Furthermore, the tryptophan synthase alpha and beta subunits, essential for the final steps of the synthesis, were identified. The ability to synthesize auxin highlights the strain's potential as a plant growth-promoting bacterium, particularly in agricultural settings where heavy metal contamination is a concern.

The genome sequence of *Pseudarthrobacter* sp. NIBRBAC000502770 has been deposited in GenBank under accession number CP041198.1 and CP014497.1. A circular map of the genome was generated using the CGView server [19], providing a visual representation of the genome structure. This detailed genome data provides valuable insights into the strain's genetic makeup, particularly its mechanisms for heavy metal resistance and plant growth promotion.

In conclusion, the complete genome sequence of *Pseudarthrobacter* sp. NIBRBAC000502770 provides valuable insights into its heavy metal resistance mechanisms and plant growth-promoting potential, particularly in contaminated environments. These findings lay the

**Table 1** Overview of data files/data sets

| Label | Name of data file/data set | File types (file extension) | Data repository and identifier (DOI or accession number) |
|---|---|---|---|
| *Data file 1* | *Data file 1. Genome features of Pseudarthrobacter sp NIBRBAC000502770* | MS excel file (.xlsx) | *https://doi.org/10.6084/m9.figshare.26968357.v6* [20] |
| *Data file 2* | *Data file 2. List of heavy metal resistance gene contents of isolated Pseudarthrobacter sp. NIBR-BAC000502770* | MS excel file (.xlsx) | *https://doi.org/10.6084/m9.figshare.26968360.v2* [21] |
| *Data file 3* | *Data file 3. List of plant growth promoting activity gene contents of isolated Pseudarthrobacter sp. NIBRBAC000502770* | MS excel file (.xlsx) | *https://doi.org/10.6084/m9.figshare.26968351.v2* [22] |
| *Data file 4* | *Data file 4. Circular map of the Pseudarthrobacter sp. NIBRBAC000502770* | Portable Document Format file (.pdf) | *https://doi.org/10.6084/m9.figshare.26968354.v3* [23] |
| *Data file 5* | *Data file 5. Auxin production of Pseudarthrobacter sp. NIBRBAC000502770* | Portable Document Format file (.pdf) | *https://doi.org/10.6084/m9.figshare.27209952.v1* [24] |
| *Data set 1* | *Genome assembly of Pseudarthrobacter sp. NIBR-BAC000502770* | Fasta file (.fna) | NCBI Genome assembly *http://identifiers.org/insdc.gca:GCA_006517815* [25] |

foundation for further studies in bioremediation and sustainable agricultural practices Table 1.

## Limitations

Recent studies increasingly highlight the issue of heavy metal contamination in various environments, particularly in mining regions where soil and groundwater are affected by lead, zinc, and cadmium. This study on *Pseudarthrobacter* sp. NIBRBAC000502770 offers valuable genomic data, but its adaptations to heavy metal-rich environments remain unverified in other contexts. Further surveys and comparative genomic studies are needed to better understand this strain's environmental significance in different contaminated areas.

### Abbreviations

PGP Plant Growth Promoting
PGPR Plant Growth Promoting Rhizobacterium
SMRT Single Molecule Real-Time
RAST Rapid Annotation using Subsystem Technology
PGAP Prokaryotic Genome Annotation Pipeline
NCBI National Center for Biotechnology Information

## Supplementary Information

The online version contains supplementary material available at https://doi.org/10.1186/s12863-025-01300-x.

Supplementary Material 1.
Supplementary Material 2.
Supplementary Material 3.
Supplementary Material 4.
Supplementary Material 5.

### Acknowledgements

We would express our appreciation and especially thank the support and cooperation of the KNU NGS Core Facility providing data analytic server. The authors acknowledge the National Institute of Biological Resources (NIBR) for providing DNA samples of Pseudarthrobacter sp. NIBRBAC000502770.

### Authors' contributions

M.-K.P., K.-M.S.: PCR confirmation and partial sequence analyses based on 16 S rRNA coding genes, whole genome sequence data analyses, preparation of the manuscript draft and revision. M.-K.P., K.-M.H., K.-S.Y., Y.-J.P., and J.-H.S.: sample collection, isolation, DNA preparation, PCR confirmation and partial sequence analyses of 16 S rRNA coding genes. J.-H.S.: experimental planning and designing, draft preparation and partial editing, and supervision. J.-H.S.: technical editing of the manuscript, and supervision.

### Funding

This work was supported by a grant from the National Institute of Biological Resources (NIBR), funded by the Ministry of Environment (NIBR202012103, NIBR202013103) and supported by the Korea Basic Science Institute (National Research Facilities and Equipment Center) grant funded by the Ministry of Education (2021R1A6C101A416), Republic of Korea.

### Data availability

The genome assembly described in this Data note can be freely and openly accessed on GenBank under accession number GCA_006517815.1.

## Declarations

### Ethics approval and consent to participate

The bacterial strain was obtained from a National Institute of Biological Resources (NIBR) with permission.

### Consent for publication

Not applicable.

### Competing interests

The authors declare no competing interests.

Received: 10 September 2024 Accepted: 13 January 2025
Published online: 17 January 2025

### References

1. Busse HJ. Review of the taxonomy of the genus Arthrobacter, emendation of the genus Arthrobacter sensu lato, proposal to reclassify selected species of the genus Arthrobacter in the novel genera Glutamicibacter gen. nov., Paeniglutamicibacter gen. nov., Pseudoglutamicibacter gen. nov., Paenarthrobacter gen. nov. and Pseudarthrobacter gen. nov., and emended description of Arthrobacter roseus. Int J Syst Evol Microbiol. 2016;66:9–37.

2. Asimakoula S, Marinakos O, Tsagogiannis E, Koukkou A-I. Phenol Degradation by Pseudarthrobacter phenanthrenivorans Sphe3. Microorganisms. 2023;11:524–34.
3. ALLOWAY, Brian J. Heavy metals in soils: trace metals and metalloids in soils and their bioavailability. Berlin: Springer Science & Business Media; 2012.
4. Tchounwou PB, Yedjou CG, Patlolla AK, Sutton DJ. Heavy metal toxicity and the environment. Exp Suppl. 2014;101:133–64.
5. Wuana RA, Okieimen FE. Heavy metals in contaminated soils: a review of sources, chemistry, risks and best available strategies for remediation. ISRN Ecol. 2011;402647:1–20.
6. Dhaliwal SS, Singh J, Taneja PK, Mandal A. Remediation techniques for removal of heavy metals from the soil contaminated through different sources: a review. Environ Sci Pollut Res. 2019;27:1319–33.
7. Arora V, Khosla B. Conventional and contemporary techniques for removal of heavy metals from soil. Biodegradation Technology of Organic and Inorganic Pollutants. IntechOpen; 2021.
8. Salt DE, Smith RD, Raskin I. Phytoremediation. Annu Rev Plant Physiol Plant Mol Biol. 1998;49:643–68.
9. Yan A, Wang Y, Tan SN, Mohd Yusof ML, Ghosh S, Chen Z. Phytoremediation: a promising approach for revegetation of heavy metal-polluted land. Front Plant Sci. 2020;11:359.
10. Pilon-Smits E. Phytoremediation. Annu Rev Plant Biol. 2005;56:15–39.
11. Ali H, Khan E, Sajad MA. Phytoremediation of heavy metals—Concepts and applications. Chemosphere. 2013;91:869–81.
12. Khan MIR, Fatma M, Per TS, Anjum NA, Khan NA. Salicylic acid-induced abiotic stress tolerance and underlying mechanisms in plants. Front Plant Sci. 2015;6:462.
13. Beneduzi A, Ambrosini A, Passaglia LMP. Plant growth-promoting rhizobacteria (PGPR): their potential as antagonists and biocontrol agents. Genet Mol Biol. 2012;35:1044–51.
14. Abbas SZ, Riaz M, Ramzan N, Zahid MT, Shakoori FR, Rafatullah M. Isolation and characterization of arsenic resistant bacteria from wastewater. Braz J Microbiol. 2024;45:1309–15.
15. Ardui S, Ameur A, Vermeesch JR, Hestand MS. Single molecule real-time (SMRT) sequencing comes of age: applications and utilities for medical diagnostics. Nucleic Acids Res. 2018;46:2159–68.
16. Chin CS, Alexander DH, Marks P, Klammer AA, Drake J, Heiner C, et al. Nonhybrid, finished microbial genome assemblies from long-read SMRT sequencing data. Nat Methods. 2013;10:563–9.
17. Overbeek R, Olson R, Pusch GD, Olsen GJ, Davis JJ, Disz T, et al. The SEED and the Rapid Annotation of microbial genomes using Subsystems Technology (RAST). Nucleic Acids Res. 2013;42(D1):D206–14.
18. Tatusova T, DiCuccio M, Badretdin A, Chetvernin V, Nawrocki EP, Zaslavsky L, et al. NCBI prokaryotic genome annotation pipeline. Nucleic Acids Res. 2016;44:6614–24.
19. Stothard P, Wishart DS. Circular genome visualization and exploration using CGView. Bioinformatics. 2004;21:537–9.
20. Park M-K. Data file 1. Genome features of Pseudarthrobacter sp NIBRBAC000502770. 2024. https://doi.org/10.6084/m9.figshare.26968357.v6.
21. Park M-K. Data file 2. List of heavy metal resistance gene contents of isolated Pseudarthrobacter sp NIBRBAC000502770. 2024. https://doi.org/10.6084/m9.figshare.26968360.v2.
22. Park M-K. Data file 3. List of plant growth promoting activity gene contents of isolated Pseudarthrobacter sp NIBRBAC000502770. 2024. https://doi.org/10.6084/m9.figshare.26968351.v2.
23. Park M-K. Data file 4. Circular map of the Pseudarthrobacter sp. NIBRBAC000502770. 2024. https://doi.org/10.6084/m9.figshare.26968354.v3.
24. Park M-K. Data file 5. Auxin production of Pseudarthrobacter sp. NIBRBAC000502770. 2024. https://doi.org/10.6084/m9.figshare.27209952.v1.
25. Park M-K. Genome assembly of Pseudarthrobacter sp. NIBRBAC000502770. http://identifiers.org/insdc.gca:GCA_006517815.


## Publisher's Note