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Complete Genome Sequence of *Pseudarthrobacter* sp. IC2-21, a Fluquinconazole-Degrading Soil Bacterium

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***Pseudarthrobacter* sp. IC2-21 is isolated from the greenhouse soil in Icheon, Gyeonggi, Korea. This strain IC2-21 is a first fluquinconazole degrading soil bacterium. We analyze the whole genome sequence of *Pseudarthrobacter* sp. IC2-21. The sequence analysis revealed that *Pseudarthrobacter* sp. IC2-21 possesses a single 4,265,009 bps circular chromosome with a DNA G+C-content of 65.4%. This chromosome contains 3,942 protein-coding sequences and 12 rRNA and 51 tRNA genes. In the result of sequence analysis, it is revealed that strain IC2-21 possessed genes coding the triazole pesticides degradation related enzymes, such as oxygenase, and fluquinconazole degradation related genes.**

Keywords: ***Pseudarthrobacter* sp. IC2-21, genome, fluquinconazole, degradation**

Triazole fungicides are effective against a diverse range of fungal pathogens in crops and have been increasingly used in agricultural practices for high yields and product quality [1]. Fluquinconazole is effective at controlling fungal diseases that cause serious damage to crops, such as the take-all disease and *Septoria tritici* blotch in wheat [2, 3]. However, triazole pesticides can cause problems if they persist in the environment [4]. Triazole pesticides are toxic to soil microorganisms. This can significantly alter the structure of soil microbial communities and decrease soil enzyme activity [5]. These changes can affect the soil health and fertility [4]. Therefore, the use of triazole pesticides should be carefully monitored. As part of the efforts to manage pesticide residues in the soil, recent research has been conducted on microorganisms that decompose pesticides [6].

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The strain IC2-21 of *Pseudarthrobacter* sp. was isolated from soil in a greenhouse and cultivated in tryptic soy broth at a temperature of 20℃ for a duration of 48 h. The conditions maintained were aerobic with a pH range between 6.0 and 10.0, with the optimal pH being 8.0. The genomic DNA was then extracted from the cultured cells of strain IC2-21 using a QIAamp DNA mini kit (Qiagen, Germany), following the guidelines provided by the manufacturer. The complete genome of the IC2-21 strain was sequenced utilizing the PacBio Sequel sequencing platform (Pacific Biosciences, USA) and the NovaSeq6000 platform (Illumina, USA) at Macrogen (Republic of Korea). The genome assembly was carried out using the Microbial Assembly Application provided (Macrogen), and the annotation was performed using the Prokaryotic Genome Annotation Pipeline from National Center for Biotechnology Information (NCBI) [7]. The complete genome sequence of strain IC2-21 was found to comprise 4,265,009 bps, with an average GC content of 65.4%. No plasmids were detected. The strain IC2-21 chromosome contained 3,942 protein-coding

Table 1. Genome features of *Pseudarthrobacter* sp. strain IC2-21.

Genome features	Chromosome
Genome size (bp)	4,265,009
G + C content (%)	65.4
Protein-coding genes (CDSs)	3,942
Number of rRNAs	12
Number of tRNAs	51
ncRNAs	3
Number of pseudogenes	28
Plasmids	0
Accession number (Genbank)	CP139145

sequences, 12 rRNA genes and 51 tRNA genes (Table 1). The OrthoANI values, calculated using the OrthoANI algorithm version v0.93.1 [8], between the genome sequences of the *P. sulfonivorans* type strain and the IC2-21 were found to be 87.33% (Fig. 1). The genome of strain IC2-21 contained genes (*pcaG* and *clcA*) associated with the synthesis of protocatechuate 3,4-dioxygenase, which catalyzes the ring cleavage step in the breakdown of aromatic compounds [9], and genes related to the 3-oxoadipate CoA-transferase subunit (*pcaI* and *pcaJ*), catechol-2,3-dioxygenase (*catE*), and the 1,2-phenylacetyl-CoA epoxidase subunit (*paaA*). Additionally, the genome of strain IC2-21 contained genes similar to those encoding flavoprotein reductase. These included *rutF*, which encodes FMN reductase (a flavin reductase domain protein that binds to FMN); *namA*, which encodes NADPH dehydrogenase (also known as NADH flavin oxidoreductase); and *fprA*, which encodes NADPH-ferredoxin reductase. Flavoprotein reductase catalyzes the addition of two molecular oxygen atoms to the adjacent carbons of the aromatic ring, facilitating ring activation and subsequent oxidation [10], thereby potentially contributing to ring opening.

Overall, sequencing analysis of the IC2-21 genome revealed that it possessed several genes involved in ring cleavage during the degradation of aromatic compounds. Therefore, this strain shows in the potential for use in bioremediation of fluquinconazole-contaminated soils.

적 요

트리아졸계 살균제인 플루퀸코나졸을 분해할 수 있는 *Pseudarthrobacter* sp. IC2-21 균주는 이천 지역의 비닐하우스 토양으로부터 분리하였다. IC2-21 균주의 전체 염기서열을 분석한 결과, 4,265,009 bps를 가진 단일 환형 염색체로서 G+C 함량은 65.4%로 구성되었다. 이 유전체는 3,884개의 단백질을 암호하는 염기서열을 가졌으며, 12개의 rRNA와 51개의 tRNA 유전자를 포함한다. 염기서열 분석 결과, IC2-21 균주는 플루퀸코나졸의 분해에 관여하는 효소인 oxygenase를 암호화하는 유전자를 가졌음을 밝혔다.

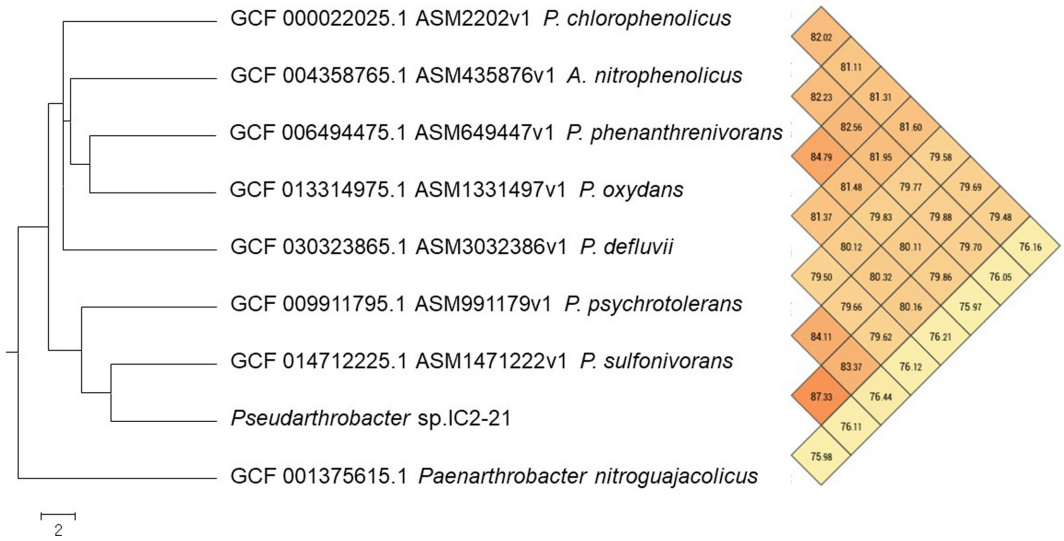

Fig. 1. Genetic similarity test of *Pseudarthrobacter* sp. IC2-21. Unweighted Pair Group Method with Arithmeti Mean (UPGMA) tree and heatmap generated with OrthoANI values calculated from Orthologous Average Identity Tool (OAT) software. The scale bar indicates 2% sequence divergence.

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Nucleotide Sequence Accession Number

The whole genome sequence of strain IC2-21 described in this study has been deposited in the NCBI database under accession number CP139145. The strain was deposited to the Korean Agricultural Culture Collection under accession number KACC 81278BP.

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Conflict of Interest

The authors have no financial conflicts of interest to declare.

References

1. Jørgensen LN, Heick TM. 2021. Azole use in agriculture, horticulture, and wood preservation – Is it indispensable? *Front. Cell. Infect. Microbial*. **11**: 730297.
2. Mavroeidi VI, Shaw MW. 2005. Sensitivity distributions and cross-resistance patterns of *Mycosphaerella graminicola* to fluquinconazole, prochloraz and azoxystrobin over a period of 9 years. *Crop Prot*. **24**: 259-266.
3. Vera Palma CA, Madariaga Burrows RP, González MG, Sepúlveda BR, Moya-Elizondo EA. 2019. Integration between *Pseudomonas protegens* strains and fluquinconazole for the control of take-all in wheat. *Crop Prot*. **121**: 163-172.
4. Roman DL, Voiculescu DI, Filip M, Ostafe V, Isvoran A. 2021. Effects of triazole fungicides on soil microbiota and on the activities of enzymes found in soil: A review. *Agriculture* **11**: 893.
5. Baćmaga M, Wyszkowska J, Kucharski J. 2016. The effect of the Falcon 460 EC fungicide on soil microbial communities, enzyme activities and plant growth. *Ecotoxicology* **25**: 1575-1587.
6. Lopes PRM, Cruz VH, de Menezes AB, Gadanhoto BP, Moreira BRdA, Mendes CR, *et al.* 2022. Microbial bioremediation of pesticides in agricultural soils: an integrative review on natural attenuation, bioaugmentation and biostimulation. *Rev. Environ. Sci. Biotechnol*. **21**: 851-876.
7. Tatusova T, DiCuccio M, Badretdin A, Chetvernin V, Nawrocki EP, Zaslavsky L, *et al.* 2016. NCBI prokaryotic genome annotation pipeline. *Nucleic Acids Res*. **44**: 6614-6624.
8. Lee I, Ouk Kim Y, Park SC, Chun J. 2016. OrthoANI: An improved algorithm and software for calculating average nucleotide identity. *Int. J. Syst. Evol. Microbiol*. **66**: 1100-1103.
9. Sim HW, Jung M, Cho YK. 2013. Erratum to: Purification and characterization of protocatechuate 3,4-dioxygenase from *Pseudomonas pseudoalcaligenes* KF707. *J. Korean Soc. Appl. Biol. Chem*. **56**: 637.
10. Yesankar PJ, Patil A, Kapley A, Qureshi A. 2023. Catalytic resilience of multicomponent aromatic ring-hydroxylating dioxygenases in *Pseudomonas* for degradation of polycyclic aromatic hydrocarbons. *World J. Microbiol. Biotechnol*. **39**:166.