



Draft Genome Sequence of the Plant Growth–Promoting Rhizobacterium *Acinetobacter radioresistens* Strain SA188 Isolated from the Desert Plant *Indigofera argentea*

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ABSTRACT *Acinetobacter radioresistens* strain SA188 is a plant endophytic bacterium, isolated from root nodules of the desert plants *Indigofera* spp., collected in Jizan, Saudi Arabia. Here, we report the 3.2-Mb draft genome sequence of strain SA188, highlighting characteristic pathways for plant growth–promoting activity and environmental adaptation.

In an effort to explore the microbial diversity of desert pioneer plants, the Darwin21 project (<http://www.darwin21.net>) has been established. In the framework of the project, an extensive collection of microbial isolates from roots of different desert plants has been conducted. Preliminary results revealed a large diversity of bacterial species with a potential to promote the growth of *Arabidopsis thaliana* plants under different biotic and abiotic stresses. A selected number of these strains was sequenced and characterized as described previously (1, 2). *Acinetobacter radioresistens* strain SA188 is an endophytic bacterium isolated from surface-sterilized root nodules on roots of the pioneer plant *Indigofera argentea* Burm.f. (*Fabaceae*). Plants were collected from different regions in the Jizan area (16°56.475'N, 42°36.694'E) of the Kingdom of Saudi Arabia. Based on the 16S rRNA gene sequence, strain SA188 is closely related (with 99% genome similarity) to *A. radioresistens* strain NBRC 102413 (NR_114074.1) and to *A. radioresistens* strain FO-1 (NR_026210) (1).

The genomic DNA of strain SA188 was extracted using Qiagen's DNeasy blood and tissue kit following the manufacturer's protocol. The DNA was then sequenced using paired-end Illumina MiSeq, and the library preparation was constructed as described previously (2). Contig assembly was done with Spades assembler version 3.6 (3) with a 1-kb contig cutoff size. *De novo* assembly of MiSeq reads for *A. radioresistens* strain SA188 resulted in 38 contigs with a total length of 3,208,318 bp and a mean contig size of 84,429 bp. The N_{50} was 289,666 bp, the L50 was reached with four contigs, and the G+C content was 41.5%. MegaBLAST (4) searches of strain SA188 concatenated contigs against the NCBI reference genome database (<http://www.ncbi.nlm.nih.gov/genome>) revealed that the closest relative was *A. radioresistens* strain NBRC 102413, with top hits for three scaffolds (NZ_KB849748.1, NZ_KB849749.1, and NZ_KB849747.1) at coverages of 16%, 56%, and 14% (86% accumulative coverage) and sequence identities of 98% to 99%. The annotation of strain SA188 was carried out using the default INDIGO pipeline (5) with the exception of the open reading frame (ORF) prediction by FragGeneScan (6).

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The annotation of *A. radioresistens* strain SA188 resulted in 2,741 ORFs, seven rRNAs, 65 tRNAs, and 33 ncRNAs.

The analysis of the SA188 genome revealed the presence of multiple enzymes involved in salinity tolerance, oxidative stress, and drought tolerance. The genome encodes isochorismate synthase (EC: 5.4.4.2) (7) and trehalose phosphatase (EC: 3.1.3.12) (8), which increases salinity and drought tolerance, as well as α,α -trehalose-phosphate synthase (EC: 2.4.1.15), which confers multiple stress protection in plants (9, 10) and improvement of drought tolerance in potato (11). The genome of SA188 harbors genes encoding different enzymes allowing plants to tolerate glyphosate herbicides such as 3-phosphoshikimate 1-carboxyvinyltransferase (EC: 2.5.1.19) (12, 13) and protoporphyrinogen oxidase (EC: 1.3.3.4) (14–16). Further analysis of the SA188 genome sequence will help to elucidate the metabolic pathways involved in plant growth-promoting interaction and its molecular mechanism.

Accession number(s). The genome of *A. radioresistens* strain SA188 was deposited at DDBJ/EMBL/GenBank under the accession number [LWGP00000000](https://www.ncbi.nlm.nih.gov/nuclink/LWGP00000000). The version described in this paper is the first version, LWGP01000000.

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REFERENCES

- Lafi FF, Bokhari A, Alam I, Bajic VB, Hirt H, Saad MM. 2016. Draft genome sequence of the plant growth-promoting *Cupriavidus gilardii* strain JZ4 isolated from the desert plant *Tribulus terrestris*. *Genome Announc* 4(4): e00678-16. <https://doi.org/10.1128/genomeA.00678-16>.
- Lafi FF, Ramirez-Prado JS, Alam I, Bajic VB, Hirt H, Saad MM. 2016. Draft genome sequence of *Halomonas elongata* strain K4, an endophytic growth-promoting bacterium enhancing salinity tolerance in *planta*. *Genome Announc* 4(6):e01214-16. <https://doi.org/10.1128/genomeA.01214-16>.
- Rainey FA, Lang E, Stackebrandt E. 1994. The phylogenetic structure of the genus *Acinetobacter*. *FEMS Microbiol Lett* 124:349–353. <https://doi.org/10.1111/j.1574-6968.1994.tb07307.x>.
- Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. *J Comput Biol* 19:455–477. <https://doi.org/10.1089/cmb.2012.0021>.
- Camacho C, Coulouris G, Avagyan V, Ma N, Papadopoulos J, Bealer K, Madden TL. 2009. BLAST plus: architecture and applications. *BMC Bioinformatics* 10:421. <https://doi.org/10.1186/1471-2105-10-421>.
- Alam I, Antunes A, Kamau AA, Ba Alawi WB, Kalkatawi M, Stingl U, Bajic VB. 2013. INDIGO—integrated data warehouse of microbial genomes with examples from the Red Sea extremophiles. *PLoS One* 8:e82210. <https://doi.org/10.1371/journal.pone.0082210>.
- Rho MN, Tang HX, Ye YZ. 2010. FragGeneScan: predicting genes in short and error-prone reads. *Nucleic Acids Res* 38:e191. <https://doi.org/10.1093/nar/gkq747>.
- Sadeghi M, Dehghan S, Fischer R, Wenzel U, Vilcinskas A, Kavousi HR, Rahnamaeian M. 2013. Isolation and characterization of isochorismate synthase and cinnamate 4-hydroxylase during salinity stress, wounding, and salicylic acid treatment in *Carthamus tinctorius*. *Plant Signal Behav* 8:e27335. <https://doi.org/10.4161/psb.27335>.
- Ge LF, Chao DY, Shi M, Zhu MZ, Gao JP, Lin HX. 2008. Overexpression of the trehalose-6-phosphate phosphatase gene *OstPP1* confers stress tolerance in rice and results in the activation of stress responsive genes. *Planta* 228:191–201. <https://doi.org/10.1007/s00425-008-0729-x>.
- Miranda JA, Avonce N, Suárez R, Thevelein JM, Van Dijck P, Iturriaga G. 2007. A bifunctional TPS-TPP enzyme from yeast confers tolerance to multiple and extreme abiotic-stress conditions in transgenic *Arabidopsis*. *Planta* 226:1411–1421. <https://doi.org/10.1007/s00425-007-0579-y>.
- Suárez R, Wong A, Ramírez M, Barraza A, Orozco Mdel C, Cevallos MA, Lara M, Hernández G, Iturriaga G. 2008. Improvement of drought tolerance and grain yield in common bean by overexpressing trehalose-6-phosphate synthase in rhizobia. *Mol Plant Microbe Interact* 21:958–966. <https://doi.org/10.1094/MPMI-21-7-0958>.
- Stiller I, Dulai S, Kondrák M, Tarnai R, Szabó L, Toldi O, Bánfalvi Z. 2008. Effects of drought on water content and photosynthetic parameters in potato plants expressing the trehalose-6-phosphate synthase gene of *Saccharomyces cerevisiae*. *Planta* 227:299–308. <https://doi.org/10.1007/s00425-007-0617-9>.
- Tian YS, Xu J, Han J, Zhao W, Fu XY, Peng RH, Yao QH. 2013. Complementary screening, identification and application of a novel class II 5-enopyruvylshikimate-3-phosphate synthase from *Bacillus cereus*. *World J Microbiol Biotechnol* 29:549–557. <https://doi.org/10.1007/s11274-012-1209-9>.
- Jiang LL, Zuo Y, Wang ZF, Tan Y, Wu QY, Xi Z, Yang GF. 2011. Design and syntheses of novel *N*-(benzothiazol-5-yl)-4,5,6,7-tetrahydro-1*H*-isindole-1,3(2*H*)-dione and *N*-(benzothiazol-5-yl)isindoline-1,3-dione as potent protoporphyrinogen oxidase inhibitors. *J Agric Food Chem* 59:6172–6179. <https://doi.org/10.1021/jf200616y>.
- Luo YP, Jiang LL, Wang GD, Chen Q, Yang GF. 2008. Syntheses and herbicidal activities of novel triazolinone derivatives. *J Agric Food Chem* 56:2118–2124. <https://doi.org/10.1021/jf703654g>.
- Zuo Y, Yang SG, Luo YP, Tan Y, Hao GF, Wu QY, Xi Z, Yang GF. 2013. Design and synthesis of 1-(benzothiazol-5-yl)-1*H*-1,2,4-triazol-5-ones as protoporphyrinogen oxidase inhibitors. *Bioorg Med Chem* 21: 3245–3255. <https://doi.org/10.1016/j.bmc.2013.03.056>.