

Genome Sequence of *Rhizobacterium Serratia marcescens* Strain 90-166, Which Triggers Induced Systemic Resistance and Plant Growth Promotion

Haeyoung Jeong,^{a,b} Joseph W. Kloepper,^c Choong-Min Ryu^{a,b}

Super-Bacteria Research Center, Korea Research Institute of Bioscience and Biotechnology (KRIBB), Daejeon, Republic of Korea^a; Biosystems and Bioengineering Program, University of Science and Technology (UST), Daejeon, Republic of Korea^b; Department of Entomology and Plant Pathology, Auburn University, Auburn, Alabama, USA^c

The rhizobacterium *Serratia marcescens* strain 90-166 elicits induced systemic resistance against plant pathogens and herbivores and promotes plant growth under greenhouse and field conditions. Strain 90-166 secretes volatile compounds, siderophores, salicylic acid, and quorum-sensing autoinducers as bacterial determinants toward plant health. Herein, we present its draft genome sequence.

Received 17 May 2015 Accepted 19 May 2015 Published 18 June 2015

Citation Jeong H, Kloepper JW, Ryu C-M. 2015. Genome sequence of rhizobacterium *Serratia marcescens* strain 90-166, which triggers induced systemic resistance and plant growth promotion. *Genome Announc* 3(3):e00667-15. doi:10.1128/genomeA.00667-15.

Copyright © 2015 Jeong et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 3.0 Unported license](https://creativecommons.org/licenses/by/3.0/).

Address correspondence to Haeyoung Jeong, hyjeong@kribb.re.kr, or Choong-Min Ryu, cmryu@kribb.re.kr.

The main mechanisms of plant growth-promoting rhizobacteria (PGPR) have been ascribed to molecular plant-bacteria interactions, such as phosphate solubilization, production of antimicrobial compounds, and plant growth hormones. In addition, some PGPR strains are known to achieve biological control of plant diseases by induced systemic resistance (ISR) (1). For example, *Serratia marcescens* strain 90-166, isolated in 1990 from a field-grown plant in Alabama, USA (initially misidentified as *S. plymuthica*), and originally selected for biological control capacity against *Rhizoctonia solani* on cotton (2), can elicit ISR against cucumber mosaic virus (3), *Colletotrichum orbiculare* (4), *Erwinia tracheiphila* (5), *Pseudomonas syringae* pv. lachrymans (6), and *Fusarium oxysporum* (7). It has been suggested that *S. marcescens* 90-166 mediates ISR by a quorum-sensing-dependent mechanism (8).

The genome of strain 90-166 was sequenced using the Illumina HiSeq 2000 platform by the National Instrumentation Center for Environmental Management from Seoul National University (Seoul, Republic of Korea). From a genomic library of an average insert size of 350 bp, 31,155,434 paired reads (101 cycle, approximately 570-fold coverage) were produced. Quality trimming, filtration by length, and *de novo* assembly was carried out using the CLC Genomics Workbench 8.0 (CLC bio). The assembly consists of 63 contigs and a total length of 5,484,396 bp. The maximum contig length and N_{50} were 897,417 bp and 632,250 bp, respectively. Automatic genome annotation was carried out using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) service and the RAST server (9). Average nucleotide identity (ANI) analysis with publicly available complete genome sequences of *Serratia* genus and with the draft genome sequence of *Serratia marcescens* type strain ATCC 13880 species (10) using the JSpecies software (11) revealed that strain 90-166 is most similar to *S. marcescens* strains WW4 (ANI value, 95.6%) (12), ATCC 13880 (ANI value, 95.3%), and Db11 (ANI value, 95.3%). The closest neighbor suggested by the RAST analysis was *S. marcescens* Db11.

From the genome annotation, we identified 2,3-butanediol

dehydrogenase (EC 1.1.1.4) corresponding to production of 2,3-butanediol (8) that has been previously reported as volatile-mediated plant growth and ISR, isochorismate synthase (EC 5.4.4.2) for a siderophore, enterobactin (13), and *N*-acyl-L-homoserine lactone synthetase for secretion of a bacterial quorum-sensing signal homoserine lactone (8). More intriguingly, the genome of strain 90-166 contains genes encoding 6-methyl salicylic acid synthase for salicylic acid secretion and a LysR-family transcriptional regulator BsdA, an activator of BsdBCD in response to salicylic acid, indicating that strain 90-166 produces a plant defense hormone salicylic acid and responses salicylic acid that originates in bacteria and plants as a host of strain 90-166.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. [LCWI00000000](https://www.ncbi.nlm.nih.gov/nuccore/LCWI00000000). The version described in this paper is version LCWI01000000.

ACKNOWLEDGMENTS

This work was supported by the Next-Generation BioGreen 21 Program (SSAC grant PJ009524) funded by the Rural Development Administration, BioNano Health-Guard Research Center funded by the Ministry of Science, ICT and Future Planning of Korea as a Global Frontier Project (grant H-GUARD_2013M3A6B2078953), and the KRIBB Research Initiative Program, Republic of Korea.

REFERENCES

- Kloepper JW, Tuzun S, Kuć JA. 1992. Proposed definitions related to induced disease resistance. *Biocontrol Sci Technol* 2:349–351. <http://dx.doi.org/10.1080/09583159209355251>.
- Wei G, Kloepper JW, Tuzun S. 1996. Induced systemic resistance to cucumber diseases and increased plant growth by plant growth-promoting rhizobacteria under field conditions. *Phytopathology* 86:221–224. <http://dx.doi.org/10.1094/Phyto-86-221>.
- Raupach GS, Liu L, Murphy JF, Tuzun S, Kloepper JW. 1996. Induced systemic resistance in cucumber and tomato against cucumber mosaic cucumovirus using plant growth-promoting rhizobacteria (PGPR). *Plant Dis* 80:891–894. <http://dx.doi.org/10.1094/PD-80-0891>.

4. Wei G, Kloepper JW, Tuzun S. 1991. Induction of systemic resistance of cucumber to *Colletotrichum orbiculare* by select strains of plant growth-promoting rhizobacteria. *Phytopathology* 81:1508–1512. <http://dx.doi.org/10.1094/Phyto-81-1508>.
5. Zehnder G, Kloepper J, Yao C, Wei G. 1997. Induction of systemic resistance in cucumber against cucumber beetles (Coleoptera: Chrysomelidae) by plant growth-promoting rhizobacteria. *J Econ Entomol* 90:391–396. <http://dx.doi.org/10.1093/jee/90.2.391>.
6. Liu L, Kloepper JW, Tuzun S. 1995. Induction of systemic resistance in cucumber against bacterial angular leaf spot by plant growth-promoting rhizobacteria. *Phytopathology* 85:843–847. <http://dx.doi.org/10.1094/Phyto-85-843>.
7. Liu L, Kloepper JW, Tuzun S. 1995. Induction of systemic resistance in cucumber against *Fusarium* wilt by plant growth-promoting rhizobacteria. *Phytopathology* 85:695–698. <http://dx.doi.org/10.1094/Phyto-85-695>.
8. Ryu CM, Choi HK, Lee CH, Murphy JF, Lee JK, Kloepper JW. 2013. Modulation of quorum sensing in acylhomoserine lactone-producing or -degrading tobacco plants leads to alteration of induced systemic resistance elicited by the rhizobacterium *Serratia marcescens* 90-166. *Plant Pathol J* 29:182–192.
9. Aziz RK, Bartels D, Best AA, DeJongh M, Disz T, Edwards RA, Formisano K, Gerdes S, Glass EM, Kubal M, Meyer F, Olsen GJ, Olson R, Osterman AL, Overbeek RA, McNeil LK, Paarmann D, Paczian T, Parrello B, Pusch GD, Reich C, Stevens R, Vassieva O, Vonstein V, Wilke A, Zagnitko O. 2008. The RAST server: Rapid Annotations using Subsystems Technology. *BMC Genomics* 9:75. <http://dx.doi.org/10.1186/1471-2164-9-75>.
10. Daligault HE, Davenport KW, Minogue TD, Broomall SM, Bruce DC, Chain PS, Coyne SR, Gibbons HS, Jaissle J, Rosenzweig CN, Scholz M, Teshima H, Johnson SL. 2014. Genome assembly of *Serratia marcescens* type strain ATCC 13880. *Genome Announc* 2(5):e00967-14. <http://dx.doi.org/10.1128/genomeA.00967-14>.
11. Richter M, Rosselló-Móra R. 2009. Shifting the genomic gold standard for the prokaryotic species definition. *Proc Natl Acad Sci U S A* 106:19126–19131. <http://dx.doi.org/10.1073/pnas.0906412106>.
12. Chung WC, Chen LL, Lo WS, Kuo PA, Tu J, Kuo CH. 2013. Complete genome sequence of *Serratia marcescens* WW4. *Genome Announc* 1(2):e00126-13. <http://dx.doi.org/10.1128/genomeA.00126-13>.
13. Press CM, Wilson M, Tuzun S, Kloepper JW. 1997. Salicylic acid produced by *Serratia marcescens* 90-166 is not the primary determinant of induced systemic resistance in cucumber or tobacco. *Mol Plant Microbe Interact* 10:761–768. <http://dx.doi.org/10.1094/MPMI.1997.10.6.761>.