

10-12-2017

Permanent Draft Genome Sequences for Mesorhizobium sp. Strains LCM 4576, LCM 4577, and ORS3428, Salt-Tolerant, Nitrogen-Fixing Bacteria Isolated from Senegalese Soils

Nathalie Diagne
Centre de Recherche de Bel Air

Erik Swanson
University of New Hampshire, Durham

Celine Pesce
University of New Hampshire, Durham, Celine.Pesce@unh.edu

Fatoumata Fall
Centre National de Recherches Agronomiques

Fatou Diouf
Centre National de Recherches Agronomiques

See next page for additional authors

Follow this and additional works at: https://scholars.unh.edu/mcbs_facpub

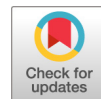
Recommended Citation

Diagne, N., E. SWANSON, C. Pesce, F. Fall, F. Diouf, N. Bakhoum, D. Fall, M. Ndigue Faye, R. OSHONE, S. Simpson, K. Morris, W. K. Thomas, L. Moulin, D. Diouf, and L. S. Tisa. 2017. Permanent Draft Genome Sequences for Mesorhizobium sp. strains LCM 4576, LCM4577, and OSR3428, Salt-Tolerant, Nitrogen-Fixing Bacteria Isolated from Senegalese Soils. GenomeA 5:e01154-17 doi: 10.1128/genomeA.01154-17

This Article is brought to you for free and open access by the Molecular, Cellular and Biomedical Sciences at University of New Hampshire Scholars' Repository. It has been accepted for inclusion in Molecular, Cellular and Biomedical Sciences Scholarship by an authorized administrator of University of New Hampshire Scholars' Repository. For more information, please contact nicole.hentz@unh.edu.

Authors

Nathalie Diagne, Erik Swanson, Celine Pesce, Fatoumata Fall, Fatou Diouf, Niokhor Bakhoun, Dioumacor Fall, Mathieu Ndigue Faye, Rediet Oshone, Stephen Simpson, Krystalynne Morris, W. Kelley Thomas, Lionel Moulin, Diegane Diouf, and Louis S. Tisa



Permanent Draft Genome Sequences for *Mesorhizobium* sp. Strains LCM 4576, LCM 4577, and ORS3428, Salt-Tolerant, Nitrogen-Fixing Bacteria Isolated from Senegalese Soils

Nathalie Diagne,^{a,b,c} Erik Swanson,^c Céline Pesce,^c Fatoumata Fall,^{b,d,g}
Fatou Diouf,^{b,d,g} Niokhor Bakhoun,^{b,d,g} Dioumacor Fall,^{b,d,e}
Mathieu Ndigue Faye,^{b,d} Rediet Oshone,^c Stephen Simpson,^c Krystalynne Morris,^c
W. Kelley Thomas,^c Lionel Moulin,^f Diegane Diouf,^{b,d,g} Louis S. Tisa^c

Centre National de Recherches Agronomiques, Institut Sénégalais de Recherches Agricoles (CNRA/ISRA), Bambey, Sénégal^a; Centre de Recherche de Bel Air, Laboratoire Mixte International Adaptation des Plantes et Microorganismes Associés aux Stress Environnementaux (LAPSE), Dakar-Bel Air, Sénégal^b; University of New Hampshire, Durham, New Hampshire, USA^c; Laboratoire Commun de Microbiologie IRD/ISRA/UCAD, Centre de Recherche de Bel Air, Route des Hydrocarbures, Dakar, Sénégal^d; Centre National de Recherches Forestières, Institut Sénégalais de Recherches Agricoles (CNRA/ISRA), Route des Pères Maristes, Dakar, Sénégal^e; IRD, Cirad, Université Montpellier, IPME, Montpellier, France^f; Département de Biologie Végétale, Université Cheikh Anta Diop (UCAD), Dakar, Sénégal^g

ABSTRACT The genus *Mesorhizobium* contains many species that are able to form nitrogen-fixing nodules on plants of the legume family. Here, we report the draft genome sequences for three *Mesorhizobium* strains. The genome sizes of strains LCM 4576, LCM 4577, and ORS3428 were 7.24, 7.02, and 6.55 Mbp, respectively.

The genus *Mesorhizobium* was proposed in 1997 and contains almost 30 species (1, 2). These bacteria are characterized by having a growth rate that is intermediate between the fast- and slow-growing rhizobia (1). *Mesorhizobium* are phylogenetically related and distinct from the large phylogenetic group that includes *Rhizobium* and *Ensifer*. Members of the genus *Mesorhizobium* can establish a nitrogen-fixing symbiosis with legume species found in many environments, including tropical, subtropical, temperate, and arctic areas (3). This large distribution suggests their adaptation to several ecoclimatic conditions (4, 5). Many different legume species have now been studied and shown to play several ecological roles which are essential to environmental sustainability. Through biological nitrogen fixation, legumes improve soil fertility by increasing the nutrient availability, acting as pioneers, and providing protection against soil erosion (6). The ability of the legume-rhizobia symbiosis to fix nitrogen significantly reduced the use of chemical fertilizers in agriculture and limited groundwater pollution by nitrates (2).

Mesorhizobium strains were sampled from soils with contrasted salt concentrations in Senegal (7), illustrating a large diversity of *Mesorhizobium plurifarum* as well as new species (MSP1-3) for which several genomes have been sequenced (8). *Mesorhizobium* sp. strains LCM 4577 and LCM 4576 were isolated from rhizospheric soil surrounding a *Prosopis juliflora* plant in the Foundiougne region located in the Groundnut Basin (Senegal) in 2013 (9), while strain ORS3428 was isolated from rhizospheric soils surrounding an *Acacia senegal* tree in the Kamb region located in the sylvo-pastoral area (Senegal) in 2005 (10).

Under *in vitro* culture conditions, these strains were considered salt tolerant. Strain LCM 4577 tolerates up to 400 mM NaCl, while strains LCM 4576 and ORS3428 are

Received 13 September 2017 Accepted 18 September 2017 Published 12 October 2017

Citation Diagne N, Swanson E, Pesce C, Fall F, Diouf F, Bakhoun N, Fall D, Faye MN, Oshone R, Simpson S, Morris K, Thomas WK, Moulin L, Diouf D, Tisa LS. 2017. Permanent draft genome sequences for *Mesorhizobium* sp. strains LCM 4576, LCM 4577, and ORS3428, salt-tolerant, nitrogen-fixing bacteria isolated from Senegalese soils. *Genome Announc* 5:e01154-17. <https://doi.org/10.1128/genomeA.01154-17>.

Copyright © 2017 Diagne et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](https://creativecommons.org/licenses/by/4.0/).

Address correspondence to Louis S. Tisa, louis.tisa@unh.edu.

TABLE 1 Genome statistics

| <i>Mesorhizobium</i> strain | No. of reads | N_{50} contig size (kb) | Assembly size (Mb) | No. of contigs | Sequencing depth (×) | No. of CDSs ^a | G+C content (%) | Accession no. |
|-----------------------------|--------------|---------------------------|--------------------|----------------|----------------------|--------------------------|-----------------|---------------|
| LCM 4576 | 19,900,494 | 236 | 7.24 | 89 | 509.8 | 6,665 | 63.54 | MDDT00000000 |
| LCM 4577 | 8,750,732 | 305.7 | 7.02 | 56 | 220.3 | 6,464 | 63.74 | MDDU00000000 |
| ORS3428 | 16,898,886 | 144.6 | 6.55 | 191 | 477.7 | 5,145 | 63.12 | MDFL00000000 |

^aCDSs, coding sequences.

limited to 200 mM. Because of these properties, these strains could potentially be used in association with leguminous plants for the reforestation of saline lands. The genomes of *Mesorhizobium* sp. strains LCM 4576, LCM 4577, and ORS3428 were sequenced to provide information on their physiology and ecology and to identify molecular markers that are involved in its tolerance to salinity. Comparative genomics of the highly salt-tolerant strain LCM 4577 with the two moderately salt-tolerant strains LCM 4576 and ORS3428 may provide insight on the molecular mechanisms involved in their tolerance to salinity.

Sequencing of the draft genomes of *Mesorhizobium* sp. strains LCM 4577, LCM 4576, and ORS3428 was performed at the Hubbard Center for Genome Studies (University of New Hampshire, Durham, NH) using Illumina technology (11). A standard Illumina shotgun library was constructed and sequenced using the Illumina HiSeq 2500 platform with paired-end reads (2 × 250 bp), which generated 8,750,732 to 19,900,494 reads (Table 1). The Illumina sequence data were trimmed by Trimmomatic version 0.32 (12) and assembled using Spades version 3.5 (13) and ALLPaths-LG version r52488 (14). Data on the final draft assemblies for *Mesorhizobium* sp. strains LCM 4576, LCM 4577, and ORS3428 are presented in Table 1. The final assembled genomes of *Mesorhizobium* sp. strains LCM 4576, LCM 4577, and ORS3428 were 7,241,525, 7,019,804, and 6,552,800 bp, respectively, with an average G+C content of 64% (Table 1). These genomes were annotated via the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) and resulted in 6,665, 6,464, and 5,145 candidate protein-encoding genes, respectively.

Accession number(s). The draft genome sequences have been deposited in GenBank under the accession numbers listed in Table 1.

ACKNOWLEDGMENTS

Partial funding was provided by the New Hampshire Agricultural Experiment Station. This is scientific contribution 2752. This work was supported by the USDA National Institute of Food and Agriculture Hatch 022821 (L.S.T.), USDA Foreign Agricultural Services Borlaug Fellowship Program BF-CR-16-004 (N.D.), and the College of Life Science and Agriculture at the University of New Hampshire (Durham, NH).

Sequencing was performed on an Illumina HiSeq 2500 instrument purchased with NSF MRI grant DBI-1229361 (to W.K.T.).

REFERENCES

1. Jarvis BDW, Van Berkum P, Chen WX, Nour SM, Fernandez MP, Cleyet-Marel JC, Gillis M. 1997. Transfer of *Rhizobium loti*, *Rhizobium huakuii*, *Rhizobium ciceri*, *Rhizobium mediterraneum*, and *Rhizobium tianshanense* to *Mesorhizobium* gen. nov. Int J Syst Bacteriol 47:895–898. <https://doi.org/10.1099/00207713-47-3-895>.
2. Berrada H, Benbrahim KF. 2014. Taxonomy of the rhizobia: current perspectives. British Microbiol Res J 4:616–639. <https://doi.org/10.9734/BMRJ/2014/5635>.
3. Chen WM, Zhu WF, Bontemps C, Young JPW, Wei GH. 2011. *Mesorhizobium camelthorni* sp. nov., isolated from *Alhagi sparsifolia*. Int J Syst Evol Microbiol 61:574–579. <https://doi.org/10.1099/ijs.0.022947-0>.
4. Laranjo M, Alexandre A, Oliveira S. 2014. Legume growth-promoting rhizobia: an overview on the *Mesorhizobium* genus. Microbiol Res 169: 2–17. <https://doi.org/10.1016/j.micres.2013.09.012>.
5. Laranjo M, Oliveira S. 2011. Tolerance of *Mesorhizobium* type strains to different environmental stresses. Antonie Van Leeuwenhoek 99: 651–662. <https://doi.org/10.1007/s10482-010-9539-9>.
6. Cardoso D, Pennington RT, de Queiroz LP, Boatwright JS, Van Wyk B-E, Wojciechowski MF, Lavin M. 2013. Reconstructing the deep-branching relationships of the papilionoid legumes. S Afr J Bot 89:58–75. <https://doi.org/10.1016/j.sajb.2013.05.001>.
7. Diouf D, Samba-Mbaye R, Lesueur D, Ba AT, Dreyfus B, De Lajudie P, Neyra M. 2007. Genetic diversity of *Acacia seyal* del. rhizobial populations indigenous to Senegalese soils in relation to salinity and pH of the sampling sites. Microb Ecol 54:553–566. <https://doi.org/10.1007/s00248-007-9243-0>.
8. Diouf F, Diouf D, Klonowska A, Le Queré A, Bakhoun N, Fall D, Neyra M, Parrinello H, Diouf M, Ndoye I, Moulin L. 2015. Genetic and genomic diversity studies of *Acacia* symbionts in Senegal reveal new species of *Mesorhizobium* with a putative geographical pattern. PLoS One 10: e0117667. <https://doi.org/10.1371/journal.pone.0117667>.
9. Fall F. 2016. Impact de *Sporobolus robustus* Kunth sur la microflore symbiotique et l'établissement de légumineuses à usages multiples dans des sols salés du Delta du Sine-Saloum au Sénégal. PhD dissertation. Université Cheikh Anta Diop de Dakar, Dakar, Senegal.

10. Fall D, Diouf D, Ourarhi M, Faye A, Abdelmounen H, Neyra M, Sylla SN, Missbah El Idrissi M. 2008. Phenotypic and genotypic characteristics of *Acacia senegal* (L.) Willd. root-nodulating bacteria isolated from soils in the dryland part of Senegal. *Lett Appl Microbiol* 47:85–97. <https://doi.org/10.1111/j.1472-765X.2008.02389.x>.
11. Bennett S. 2004. Solexa Ltd. *Pharmacogenomics* 5:433–438. <https://doi.org/10.1517/14622416.5.4.433>.
12. Bolger AM, Lohse M, Usadel B. 2014. Trimmomatic: a flexible trimmer for Illumina sequence data. *Bioinformatics* 30:2114–2120. <https://doi.org/10.1093/bioinformatics/btu170>.
13. Nurk S, Bankevich A, Antipov D, Gurevich AA, Korobeynikov A, Lapidus A, Prjibelski AD, Pyskin A, Sirotkin A, Sirotkin Y, Stepanauskas R, Clingenpeel SR, Woyke T, McLean JS, Lasken R, Tesler G, Alekseyev MA, Pevzner PA. 2013. Assembling single-cell genomes and minimetagenomes from chimeric MDA products. *J Comput Biol* 20:714–737. <https://doi.org/10.1089/cmb.2013.0084>.
14. Gnerre S, MacCallum I, Przybylski D, Ribeiro FJ, Burton JN, Walker BJ, Sharpe T, Hall G, Shea TP, Sykes S, Berlin AM, Aird D, Costello M, Daza R, Williams L, Nicol R, Gnirke A, Nusbaum C, Lander ES, Jaffe DB. 2011. High-quality draft assemblies of mammalian genomes from massively parallel sequence data. *Proc Natl Acad Sci U S A* 108:1513–1518. <https://doi.org/10.1073/pnas.1017351108>.