



**HAL**  
open science

## Genome-sequenced bacterial collection from sorghum aerial root mucilage

Marco Mechan-Llontop, John Mullet, Ashley Shade

### ► To cite this version:

Marco Mechan-Llontop, John Mullet, Ashley Shade. Genome-sequenced bacterial collection from sorghum aerial root mucilage. *Microbiology Resource Announcements*, In press, <10.1128/MRA.00484-23>. <hal-04277741>

**HAL Id: hal-04277741**

**<https://hal.science/hal-04277741v1>**

Submitted on 14 Nov 2023

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire HAL, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons CC BY 4.0 - Attribution - International License



AMERICAN  
SOCIETY FOR  
MICROBIOLOGY



**Microbiology**  
Resource Announcements

1  
2 **Article title**

3 Genome-sequenced bacterial collection from sorghum aerial root mucilage.

4 **Authors**

5 Marco E. Mechan-Llontop<sup>a</sup>, John Mullet<sup>a,b</sup>, and Ashley Shade<sup>c</sup>#

6 **Affiliations**

7 a. Great Lakes Bioenergy Research Center, Michigan State University, East Lansing, Michigan, USA.

8 b. Department of Biochemistry & Biophysics, Texas A&M University, College Station, Texas, USA.

9 c. Universite Claude Bernard Lyon 1; CNRS, UMR 5557 Écologie Microbienne, 16 rue Dubois 69622  
10 Villeurbanne Cedex, FRANCE

11 **Running title**

12 Bacteria from sorghum aerial root mucilage.

13 **Corresponding author's email address**

14 #Address correspondence to: Ashley Shade, [ashley.shade@cnr.fr](mailto:ashley.shade@cnr.fr)

15 **Abstract**

16 A collection of 47 bacteria isolated from the mucilage of aerial roots of energy sorghum is available at  
17 the Great Lakes Bioenergy Research Center, Michigan State University, MI, USA. We enriched bacteria  
18 with putative plant-beneficial phenotypes and include information on phenotypic diversity, taxonomy,  
19 and whole genome sequences.

20 **Announcement**

21 Plant phyllosphere exudates harbor microbial communities that can engage with the host plant, for  
22 example by supporting plant growth or resilience to various stresses (1). The heat and drought-tolerant  
23 crop bioenergy sorghum (*Sorghum bicolor* L. Moench) secretes abundant polysaccharide-rich mucilage  
24 on aerial roots (2) that selects for specialized microbiome members that are expected to have plant-

25 beneficial functions (3). As a resource for the genomic and functional diversities of bacteria associated  
26 with phyllosphere exudates, we present a collection of 47 bacterial strains isolated from sorghum aerial  
27 root mucilage. These strains represent 17 families and include 21 genera with putative plant-beneficial  
28 capabilities, including nitrogen fixation, phosphate solubilization, resistance to terpenoids, use of  
29 methanol as a carbon source, and tolerance to desiccation, based on the culture media in which the  
30 strains were originally isolated.

31 Bacterial strains were enriched from the mucilage of aerial roots of bioenergy sorghum cultivar  
32 TAM 17651 grown at the Great Lakes Bioenergy Research Center (GLBRC), as part of the Biofuel  
33 Cropping System Experiment (BCSE) in Hickory Corners, Michigan (42°23'41.6" N, 85°22'23.1" W). Aerial  
34 roots were harvested from sorghum plants grown on nitrogen-fertilized plots on September 25, 2020.  
35 We used sterile razor blades to collect between 3 to 5 aerial roots per plant into sterile 50 ml Eppendorf  
36 tubes. Within 2 hours of collection, the samples were transported to the laboratory on ice and stored at  
37 -80°C for 18 days until processing. Sorghum mucilage was first fully hydrated with sterile water,  
38 removed from roots, and then collected into sterile 1.5 ml Eppendorf tubes. Mucilage collected from  
39 different plants was pooled and serially diluted from  $10^{-1}$  to  $10^{-4}$ . To capture a diversity of bacteria from  
40 the rehydrated mucilage, we used a variety of cultivation media (Table 1). To select for anaerobic  
41 bacteria, plates were placed in anaerobic jars containing three bags of anaerobic gas generator  
42 (Mitsubishi AnaeroPack System). All plates were incubated at 25°C and 37°C for up to 14 days. Isolated  
43 colonies were transferred on new plates with the same medium as used for isolation to confirm purity.  
44 Bacteria were grown overnight on R2A broth at 28°C with shaking at 200rpm and glycerol stock (25%  
45 v/v) of pure isolates was stored at -80°C. Prior to performing whole genome sequencing, we performed  
46 full-length 16S rRNA gene sequencing, with universal primers 27F (5'- AGAGTTTGATCCTGGCTCAG-3')  
47 and 1492R (5'-TACGGTTACCTTGTTACGACTT-3') (4), of each isolate using the Sanger protocol to link

48 them to corresponding 16S rRNA gene amplicon dynamics in a field microbiome study that was  
49 executed at the same field site at Kellogg Biological Station (3).

50 Individual isolates or the full cryopreserved collection is available. Cultures can be regrown  
51 using standard microbiological procedures to transfer a sterile inoculation loop of freezer stock onto the  
52 original isolation medium and incubation time (Table 1).

53 The high molecular weight genomic DNA of each bacterial isolate was extracted using a  
54 phenol/chloroform extraction protocol (5). The genomic DNA of each strain was submitted to the U.S.  
55 Department of Energy Joint Genome Institute (DOE-JGI), for library preparation and sequencing with the  
56 Pacific Biosciences (PacBio) platform (6). DNA was sheared to 10kb using g-TUBE columns (Covaris) and  
57 subjected to library preparation using the SMARTbell Express Template prep 2.0 kit and sequenced on  
58 the PacBio Sequel platform. Samples that failed DNA quality control required by the PacBio pipeline  
59 were instead sequenced using the NovaSeq S4 Illumina platform (7). High fidelity CCS reads >5kb were  
60 assembled with Flye 2.8.3 (8) using default settings. Raw Illumina sequences were quality-filtered using  
61 BBTools (9). Artifact filtered and normalized Illumina reads were assembled with SPAdes v3.15.3 (10) (-  
62 phred-offset 33 -cov-cutoff auto -t 16 -m 64 -careful -k 25,55,95), and contigs were discarded if the  
63 length was <1kb (BBTools reformat.sh: minlength=1000 ow=t). Genome completeness and  
64 contamination was estimated with CheckM v1.2.2 (11). The assembly was annotated using Prokka 1.14.6  
65 (12) and the phylogenetic tree was inferred using Orthofinder 2.5.5 (13) and edited with iTOLs v.6.5.8  
66 (14) (Figure 1).

## 67 **Data availability statement**

68 Raw sequencing data are available at the Joint Genome Institute's GOLD database under Study ID  
69 [Gs0157305](https://gold.jgi.doe.gov/study/Gs0157305), as well as with the National Institutes of Health Sequence Read Archive (see Table 1).

70 Genome sequencing assembly data has been deposited in the GenBank with accession numbers listed in

71 Table 1. The bacterial collection is available at The Great Lakes Bioenergy Research Center at Michigan  
72 State University, USA (glbrc@msu.edu).

## 73 **Acknowledgments**

74 This work was supported by the Great Lakes Bioenergy Research Center, U.S. Department of Energy,  
75 Office of Science, Office of Biological and Environmental Research under Award Number DE-SC0018409.  
76 Support for field research was provided by the Great Lakes Bioenergy Research Center, U.S. Department  
77 of Energy, Office of Science, Office of Biological and Environmental Research (Awards DE-SC0018409 and  
78 DE-FC02-07ER64494), by the National Science Foundation Long-term Ecological Research Program (DEB  
79 1637653) at the Kellogg Biological Station, and by Michigan State University AgBioResearch. The work  
80 conducted by the U.S. Department of Energy Joint Genome Institute, a DOE Office of Science User  
81 Facility, is supported under Contract No. DE-AC02-05CH11231.

82 This data was generated for JGI Proposal #508590.

83 The authors declare no conflict of interest.

## 84 **References**

- 85 1. Galloway AF, Knox P, Krause K. 2020. Sticky mucilages and exudates of  
86 plants: putative microenvironmental design elements with  
87 biotechnological value. *New Phytologist* 225:1461–1469.
- 88 2. Bennett AB, Pankievicz VCS, Ané J-M. 2020. A Model for Nitrogen Fixation  
89 in Cereal Crops. *Trends Plant Sci* 25:226–235.
- 90 3. Mehan-Llontop M, Mullet J, Shade A. 2023. Phyllosphere exudates select  
91 for distinct microbiome members in sorghum epicuticular wax and aerial  
92 root mucilage. *Phytobiomes J*
- 93 4. Miller CS, Handley KM, Wrighton KC, Frischkorn KR, Thomas BC, Banfield JF.  
94 2013. Short-Read Assembly of Full-Length 16S Amplicons Reveals Bacterial  
95 Diversity in Subsurface Sediments. *PLoS One* 8:e56018-.
- 96 5. Kutchma AJ, Roberts MA, Knaebel DB, Crawford DL. 1998. Small-Scale  
97 Isolation of Genomic DNA from *Streptomyces* Mycelia or Spores.  
98 *Biotechniques* 24:452–457.
- 99 6. Eid J, Fehr A, Gray J, Luong K, Lyle J, Otto G, Peluso P, Rank D, Baybayan P,  
100 Bettman B, Bibillo A, Bjornson K, Chaudhuri B, Christians F, Cicero R, Clark

101 S, Dalal R, deWinter A, Dixon J, Foquet M, Gaertner A, Hardenbol P, Heiner  
102 C, Hester K, Holden D, Kearns G, Kong X, Kuse R, Lacroix Y, Lin S, Lundquist  
103 P, Ma C, Marks P, Maxham M, Murphy D, Park I, Pham T, Phillips M, Roy J,  
104 Sebra R, Shen G, Sorenson J, Tomaney A, Travers K, Trulson M, Vieceli J,  
105 Wegener J, Wu D, Yang A, Zaccarin D, Zhao P, Zhong F, Korf J, Turner S.  
106 2009. Real-Time DNA Sequencing from Single Polymerase Molecules.  
107 *Science* (1979) 323:133–138.

108 7. Bennett S. 2004. Solexa Ltd. *Pharmacogenomics* 5:433–438.

109 8. Kolmogorov M, Yuan J, Lin Y, Pevzner PA. 2019. Assembly of long, error-  
110 prone reads using repeat graphs. *Nat Biotechnol* 37:540–546.

111 9. Bushnell B. BBTools software package (version 39.01). 39.01.

112 10. Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin  
113 VM, Nikolenko SI, Pham S, Prjibelski AD, Pyshkin A V, Sirotkin A V, Vyahhi  
114 N, Tesler G, Alekseyev MA, Pevzner PA. 2012. SPAdes: A New Genome  
115 Assembly Algorithm and Its Applications to Single-Cell Sequencing. *Journal*  
116 *of Computational Biology* 19:455–477.

117 11. Parks DH, Imelfort M, Skennerton CT, Hugenholtz P, Tyson GW. 2015.  
118 CheckM: assessing the quality of microbial genomes recovered from  
119 isolates, single cells, and metagenomes. *Genome Res* 1043–1055.

120 12. Seemann T. 2014. Prokka: rapid prokaryotic genome annotation.  
121 *Bioinformatics* 30:2068–2069.

122 13. Emms DM, Kelly S. 2019. OrthoFinder: phylogenetic orthology inference  
123 for comparative genomics. *Genome Biol* 20:238.

124 14. Letunic I, Bork P. 2021. Interactive Tree Of Life (iTOL) v5: an online tool for  
125 phylogenetic tree display and annotation. *Nucleic Acids Res* 49:W293–  
126 W296.

127  
128  
129  
130  
131

132 **Tables**

**TABLE 1.-** Taxonomy, colony phenotype, and genome characteristics of 49 bacterial isolates from sorghum aerial root mucilage, as described in this study. SRA is the sequence read archive of the U.S. National Institutes of Health.

Isolate ID	Bacterial species	Initial isolation media	Temperature, oxygen availability	Colony phenotype	Sequencing Platform	SRA accession number	GenBank accession	Genome length (bp)	N° contigs	Coverage	GC %	Genome completeness
SORGH_AS_0335	<i>Acidovorax wautersii</i>	R2A	25 °C, anaerobic	Small, white	PacBio	<a href="#">SRP437222</a>	<a href="#">JAVIZX000000000</a>	4,571,377	1	70.4 X	68.30%	99.52%
SORGH_AS_0440	<i>Agrobacterium sp.</i>	M9 + 0.4% sucrose	25 °C, aerobic	White	PacBio	<a href="#">SRP437134</a>	<a href="#">JAVIYR000000000</a>	5,277,481	3	166.0 X	59.30%	99.04%
SORGH_AS_0745	<i>Agrobacterium sp.</i>	M9 nitrogen-free + 1% xylose	37 °C, aerobic	White, EPS production	PacBio	<a href="#">SRP437174</a>	<a href="#">JAUTBI000000000</a>	5,670,289	4	177.6 X	58.60%	99.88%
SORGH_AS_0749	<i>Agrobacterium tumefaciens</i>	M9 nitrogen-free, Carbon-free	37 °C, aerobic	White, EPS production	PacBio	<a href="#">SRP437121</a>	<a href="#">JAURJU000000000</a>	5,669,583	4	151.8 X	58.40%	99.93%
SORGH_AS_0212	<i>Arthrobacter sp.</i>	Jensen	25 °C, aerobic	White, EPS production	PacBio	<a href="#">SRP437201</a>	<a href="#">AUTAA000000000</a>	4,369,871	1	117.7 X	66.10%	99.71%
SORGH_AS_0304	<i>Atlantibacter sp.</i>	Jensen	25 °C, anaerobic	White	PacBio	<a href="#">SRP437126</a>	<a href="#">JAVLWF000000000</a>	4,876,478	2	140.5 X	56.20%	99.39%
SORGH_AS_0510	<i>Bacillus sp.</i>	R2A + 0.1% linalool	37 °C, aerobic	White	PacBio	<a href="#">SRP437241</a>	<a href="#">JAUTAU000000000</a>	4,828,420	1	171.6 X	38.90%	98.52%
SORGH_AS_0407	<i>Bacillus thuringiensis</i>	R2A + PEG6000 - 0.73MPa	25 °C, aerobic	White	PacBio	<a href="#">SRP437118</a>	<a href="#">JAURUT000000000</a>	5,894,929	5	106.5 X	35.40%	99.34%
SORGH_AS_0431	<i>Brevundimonas vesicularis</i>	M9 + 0.4% sucrose	25 °C, aerobic	pink	PacBio	<a href="#">SRP437147</a>	<a href="#">JAUTAQ000000000</a>	3,191,065	1	68.5 X	66.20%	99.05%
SORGH_AS_0447	<i>Chryseobacterium sp.</i>	TSA	25 °C, aerobic	Yellow	PacBio	<a href="#">SRP437232</a>	<a href="#">JAUTAR000000000</a>	4,374,394	1	132.6 X	39.90%	99.51%
SORGH_AS_0776	<i>Curtobacterium sp.</i>	M9 nitrogen-free + 1% xylose	37 °C, aerobic	Yellow	PacBio	<a href="#">SRP437163</a>	<a href="#">JAVIYU000000000</a>	3,877,562	1	164.5 X	71.30%	98.99%
SORGH_AS_0287	<i>Enterobacter sp.</i>	Jensen	37 °C, anaerobic	White, EPS production	PacBio	<a href="#">SRP437233</a>	<a href="#">JAVIZW000000000</a>	4,947,816	2	108.4 X	54.60%	99.97%
SORGH_AS_0622	<i>Flavobacterium sp.</i>	MMS methanol	25 °C, aerobic	Orange yellow	PacBio	<a href="#">SRP437242</a>	<a href="#">JAUTAX000000000</a>	5,243,061	1	137.1 X	33.80%	98.94%
SORGH_AS_0428	<i>Microbacterium sp.</i>	M9 + 0.4% sucrose	25 °C, aerobic	Light yellow, EPS production	PacBio	<a href="#">SRP437182</a>	<a href="#">JAVIZT000000000</a>	3,300,177	1	89.6 X	69.60%	98.23%
SORGH_AS_0445	<i>Microbacterium foliorum</i>	TSA	25 °C, aerobic	Light yellow	PacBio	<a href="#">SRP437225</a>	<a href="#">JAVIZQ000000000</a>	3,850,168	1	187.5 X	67.90%	99.14%
SORGH_AS_0209	<i>Microbacterium proteolyticum</i>	Jensen	25 °C, aerobic	White, EPS production	PacBio	<a href="#">SRP437239</a>	<a href="#">JAUSZZ000000000</a>	3,767,688	1	122.8 X	70.20%	98.48%
SORGH_AS_0344	<i>Microbacterium sp.</i>	R2A	37 °C, aerobic	Pink	PacBio	<a href="#">SRP437155</a>	<a href="#">JAUTAD000000000</a>	3,750,535	1	78.7 X	70.20%	97.98%
SORGH_AS_0421	<i>Microbacterium sp.</i>	M9 + 0.4% sucrose	25 °C, aerobic	Orange	PacBio	<a href="#">SRP437226</a>	<a href="#">JAUTAO000000000</a>	3,450,105	1	228.2 X	69.50%	97.72%

SORGH_AS_0454	<i>Microbacterium sp.</i>	TSA	25 °C, aerobic	Orange	PacBio	<a href="#">SRP437164</a>	<a href="#">JAVIYS000000000</a>	3,569,378	1	197.0 X	69.60%	97.98%
SORGH_AS_0505	<i>Microbacterium sp.</i>	M9 nitrogen-free +	25 °C, aerobic	Orange, EPS production	PacBio	<a href="#">SRP437119</a>	<a href="#">JAUTAT000000000</a>	2,952,848	1	139.1 X	69.60%	97.79%
SORGH_AS_0426	<i>Microbacterium testaceum</i>	M9 + 0.4% sucrose	25 °C, aerobic	Orange	PacBio	<a href="#">SRP437123</a>	<a href="#">JAUTAP000000000</a>	3,569,373	1	202.9 X	69.80%	97.31%
SORGH_AS_0594	<i>Microbacterium testaceum</i>	Jensen	37 °C, aerobic	Orange, EPS production	PacBio	<a href="#">SRP437144</a>	<a href="#">JAUTAW000000000</a>	3,750,737	1	192.6 X	70.20%	97.98%
SORGH_AS_0422	<i>Mucilaginibacter terrae</i>	M9 + 0.4% sucrose	25 °C, aerobic	Pink, EPS production	PacBio	<a href="#">SRP437139</a>	<a href="#">JAVLVU000000000</a>	5,485,925	1	173.4 X	43.00%	97.62%
SORGH_AS_0306	<i>Paenibacillus sp.</i>	Jensen	25 °C, anaerobic	White, EPS production	PacBio	<a href="#">SRP437208</a>	<a href="#">JAUTBP000000000</a>	5,288,478	1	208.8 X	39.20%	99.45%
SORGH_AS_0338	<i>Paenibacillus sp.</i>	R2A	25 °C, anaerobic	Pink, EPS production	PacBio	<a href="#">SRP437186</a>	<a href="#">JAVIYQ000000000</a>	5,288,506	1	244.2 X	39.20%	99.36%
SORGH_AS_0197	<i>Pantoea ananatis</i>	Pirovskaya	25 °C, aerobic	Yellow	PacBio	<a href="#">SRP437179</a>	<a href="#">JAUTBM000000000</a>	5,000,175	5	197.6 X	53.40%	99.34%
SORGH_AS_0213	<i>Pantoea ananatis</i>	Jensen	25 °C, aerobic	Yellow, EPS production	Illumina	<a href="#">SRP437485</a>	<a href="#">JAVIZK000000000</a>	4,919,493	39	310.9 X	56.50%	100%
SORGH_AS_0797	<i>Pantoea anthophila</i>	M9 nitrogen-free + 1% arabinose	37 °C, aerobic	White, EPS production	PacBio	<a href="#">SRP437125</a>	<a href="#">JAUTBH000000000</a>	4,704,313	5	127.5 X	56.60%	100%
SORGH_AS_0585	<i>Pedobacter agri</i>	Jensen	25 °C, aerobic	Pink	PacBio	<a href="#">SRP437169</a>	<a href="#">JAUTAV000000000</a>	5,055,982	1	181.8 X	38.00%	97.61%
SORGH_AS_0191	<i>Pseudomonas fluorescens</i>	KB	25 °C, aerobic	White, fluorescens, EPS production	PacBio	<a href="#">SRP437154</a>	<a href="#">JAVIZU000000000</a>	6,080,362	1	43.2 X	60.10%	99.52%
SORGH_AS_0201	<i>Pseudomonas psychrotolerans</i>	Pirovskaya	25 °C, aerobic	Yellow	PacBio	<a href="#">SRP437137</a>	<a href="#">JAVJAF000000000</a>	5,262,371	1	156.0 X	64.70%	98.47%
SORGH_AS_0199	<i>Pseudomonas sp.</i>	Pirovskaya	25 °C, aerobic	Yellow	PacBio	<a href="#">SRP437202</a>	<a href="#">JAVJAE000000000</a>	5,020,881	1	146.4 X	65.90%	99.77%
SORGH_AS_0211	<i>Pseudomonas sp.</i>	Jensen	25 °C, aerobic	Yellow	PacBio	<a href="#">SRP437120</a>	<a href="#">JAVIZV000000000</a>	4,840,922	1	62.3 X	66.10%	99.87%
SORGH_AS_0260	<i>Rhizobium sp.</i>	M9 + 0.4% sucrose	37 °C, anaerobic	White	PacBio	<a href="#">SRP437152</a>	<a href="#">JAURUW000000000</a>	5,274,802	3	126.6 X	59.30%	99.62%
SORGH_AS_0285	<i>Rhizobium sp.</i>	Jensen	25 °C, aerobic	Yellow	PacBio	<a href="#">SRP437128</a>	<a href="#">JAURUX000000000</a>	5,277,463	3	136.4 X	59.30%	99.36%
SORGH_AS_0755	<i>Rhizobium sp.</i>	M9 nitrogen-free, Carbon-free	37 °C, aerobic	White, EPS production	PacBio	<a href="#">SRP437200</a>	<a href="#">JAURUV000000000</a>	5,423,623	3	122.8 X	59.40%	99.84%
SORGH_AS_0787	<i>Rhizobium sp.</i>	M9 nitrogen-free + 1% arabinose	25 °C, aerobic	White, EPS production	PacBio	<a href="#">SRP437131</a>	<a href="#">JAUTBG000000000</a>	5,400,756	3	141.4 X	58.20%	98.19%
SORGH_AS_0301	<i>Rhodococcus sp.</i>	Jensen	25 °C, aerobic	Pink, EPS production	PacBio	<a href="#">SRP437130</a>	<a href="#">JAUTAC000000000</a>	4,603,776	2	55.1 X	68.60%	97.93%
SORGH_AS_0303	<i>Rhodococcus sp.</i>	Jensen	25 °C, aerobic	Pink, EPS	PacBio	<a href="#">SRP437177</a>	<a href="#">JAUTBO000000000</a>	4,508,481	1	162.5 X	68.50%	98.78%

				production								
SORGH_AS_0500	<i>Siphonobacter sp.</i>	M9 nitrogen-free +	25 °C, aerobic	Orange, EPS production	PacBio	<a href="#">SRP437204</a>	<a href="#">JAVIYT000000000</a>	6,158,200	9	119.3 X	44.10%	99.70%
SORGH_AS_0438	<i>Sphingomonas sp.</i>	M9 + 0.4% sucrose	25 °C, aerobic	Orange	PacBio	<a href="#">SRP437229</a>	<a href="#">JAVIZS000000000</a>	4,040,749	4	165.8 X	67.80%	98.99%
SORGH_AS_0742	<i>Sphingomonas sp.</i>	M9 nitrogen-free + 1% xylose	37 °C, aerobic	Yellow	PacBio	<a href="#">SRP437158</a>	<a href="#">JAVIZP000000000</a>	4,247,105	2	30.2 X	67.10%	99.25%
SORGH_AS_0789	<i>Sphingomonas sp.</i>	M9 nitrogen-free + 1% arabinose	37 °C, aerobic	Yellow	PacBio	<a href="#">SRP437240</a>	<a href="#">JAVIYV000000000</a>	4,247,089	2	13.5 X	67.10%	99.42%
SORGH_AS_0802	<i>Sphingomonas sp.</i>	M9 nitrogen-free + 1% galactose	25 °C, aerobic	Orange	Illumina	<a href="#">SRP437478</a>	<a href="#">JAVIZL000000000</a>	3,943,888	20	398.6 X	67.10%	99.55%
SORGH_AS_0457	<i>Stenotrophomonas rhizophila</i>	TSA	25 °C, aerobic	White	PacBio	<a href="#">SRP437136</a>	<a href="#">JAUTAS000000000</a>	4,160,543	1	107.6 X	66.70%	99.71%
SORGH_AS_0321	<i>Stenotrophomonas sp.</i>	Jensen	25 °C, anaerobic	Yellow	PacBio	<a href="#">SRP437127</a>	<a href="#">JAVIZG000000000</a>	4,110,757	1	159.9 X	66.70%	99.20%
SORGH_AS_0282	<i>Stenotrophomonas sp.</i>	Jensen	37 °C, aerobic	Yellow	PacBio	<a href="#">SRP437122</a>	<a href="#">JAUTAB000000000</a>	4,172,479	1	166.1 X	66.70%	99.77%

133

134

135

136

137

138

139

140

141

142

143

144

145

