ABSTRACT  *Pantoea ananatis* SGAir0210 was isolated from outdoor air collected in Singapore. The genome was assembled from long reads generated by single-molecule real-time sequencing complemented with short reads. The genome size was approximately 4.81 Mb, with 4,303 protein-coding genes, 80 tRNAs, and 22 rRNAs identified.

The Gram-negative bacterium *Pantoea ananatis* belongs to the family *Enterobacteriaceae* within the phylum *Proteobacteria*. This bacterium has been isolated from various habitats, such as plants (1), soil (2), water (3), and aviation fuel tanks (4). While there have been reports of human infection (5, 6), *P. ananatis* is known primarily as a pathogen in plant hosts, such as rice (7), maize (8), and onion (9). Recent findings, however, have also highlighted the existence of beneficial strains that live on the hosts as commensals or plant growth promoters (10–12).

Here, we present the genome of *P. ananatis* SGAir0210, isolated from tropical air by means of air sampling at an outdoor location in Singapore (1.350°N, 103.689°E) using an Andersen single-stage impactor (SKC BioStage). Air was drawn at a 28.3 liter/min flow rate and directly impacted onto marine agar (Becton, Dickinson) that was mounted on the sampler for 4 min. After incubation at 30°C, a colony was replicated in Trypticase soy agar to isolate a single organism. The pure culture was finally grown in Luria-Bertani broth (30°C) overnight before DNA extraction.

DNA was extracted using a Wizard genomic DNA purification kit (Promega) following the standard protocol. After extraction, sequencing was conducted on a Pacific Biosciences RS II platform utilizing three single-molecule real-time (SMRT) cells and a SMRTbell version 1.0 template prep kit for library preparation. In addition, 300-bp paired-end sequencing was carried out on the Illumina MiSeq platform after library preparation using a TruSeq Nano DNA kit. The SMRT sequencing yielded 35,581 subreads, whereas the MiSeq run yielded 874,001 reads.

The genome was de novo assembled using the Hierarchical Genome Assembly Process (HGAP) version 3 (13) in the PacBio SMRT Analysis version 2.3.0 package. Final polishing and error correction were performed using the MiSeq paired-end reads with Quiver and Pilon version 1.16 (14), respectively. The assembly produced two contigs with a total size of 4,808,856 bp. The chromosomal contig had a size of 4,504,557 bp (57.2-fold coverage, 53.5% G+C content), while the plasmid contig was 304,029 bp long (44.6-fold coverage, 52.0% G+C content). The chromosomal contig was unable to be circularized via Circlator (15). Species identification using average nucleotide identity analysis (ANI) performed with MiSI (Microbial Species Identifier) (16) showed a 97.2%
match to \textit{P. ananatis} strain LMG 2665. Additional analysis with Phyla-AMPHORA identified 98.4\% marker similarity to the genus \textit{Pantoea} with minimum confidence of 1.0 (17).

Genome annotation was completed with the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) version 4.2 (18). The annotation identified 4,589 genes, which consisted of 4,303 protein-coding genes, 121 RNAs (80 tRNAs, 19 noncoding RNAs, 8 subunits of the 55 rRNA, and 7 copies each of the 16S and 23S rRNAs), and 165 pseudogenes. Functional annotation with the Rapid Annotations using Subsystems Technology (RAST) server (19) identified 4,626 DNA coding sequences within 527 subsystems. Of these, 164 genes were annotated as genes related to stress response, such as heat and cold shock, which could be useful for airborne survival. Moreover, 40 genes were found to be related to phages and prophages, including proteins that are part of the phage tail and replication.

Accession number(s). The genome sequence of \textit{P. ananatis} SGAir0210 has been deposited in DDBJ/EMBL/GenBank under the accession numbers CP028033 to CP028034.

ACKNOWLEDGMENT
The work was supported by a Singapore Ministry of Education Academic Research Fund Tier 3 grant (MOE2013-T3-1-013).

REFERENCES
1. Coutinho TA, Venter SN. 2009. \textit{Pantoea ananatis}: an unconventional plant pathogen. Mol Plant Pathol 10:325–335. https://doi.org/10.1111/j.1364-3703.2009.00542.x.
2. Gasser F, Cardinale M, Schildberger B, Berg G. 2012. Biocontrol of \textit{Botrytis cinerea} by successful introduction of \textit{Pantoea ananatis} in the grapevine phyllosphere. Int J Wine Res 4:53–63. https://doi.org/10.2147/IJWR.S31339.
3. Pieleggi M, Pieleggi SAV, Olchanheski LR, da Silva PAG, Munoz Gonzalez AM, Koskinen WC, Barber B, Sadowsky MJ. 2012. Isolation of mesotrione-degrading bacteria from aquatic environment in Brazil. Chemosphere 86:1127–1132. https://doi.org/10.1016/j.chemosphere.2011.12.041.
4. Rauch ME, Graef HW, Rozenzhak SW, Jones SE, Bleckmann CA, Kruger RL, Naik RR, Stone MO. 2006. Characterization of microbial contamination in United States Air Force aviation fuel tanks. J Ind Microbiol Biotechnol 33:29–36. https://doi.org/10.1007/s10029-005-0023-x.
5. De Baere T, Verhelst R, Labit C, Verschraegen G, Wauters G, Claeys G, Vaneechoutte M. 2004. Bacteremic infection with \textit{Pantoea ananatis}. J Clin Microbiol 42:4393–4395. https://doi.org/10.1128/JCM.42.9.4393–4395.2004.
6. De Maayer P, Chan WY, Rezzonico F, Bühlimann A, Venter SN, Blom J, Goessmann A, Frey EJ, Smits THM, Duffy B, Coutinho TA. 2012. Complete genome sequence of clinical isolate \textit{Pantoea ananatis} LMG S342. J Bacteriol 194:1615–1616. https://doi.org/10.1128/JB.06715-11.
7. Wu LW, Liu RF, Niu YF, Lin HY, Ye WJ, Guo LB, Hu XM. 2016. Whole genome sequence of \textit{Pantoea ananatis} R100, an antagonistic bacterium isolated from rice seed. J Biotechnol 225:1–2. https://doi.org/10.1016/j.jbiotec.2016.03.007.
8. Lana UGDP, Gomes EA, Silva DD, Costa RV, Cota LV, Parreira DF, Souza IRP, Guimarães CT. 2012. Detection and molecular diversity of \textit{Pantoea ananatis} associated with white spot disease in maize, sorghum, and crabgrass in Brazil. J Phytopathol 160:441–448. https://doi.org/10.1111/j.1439-0434.2012.01924.x.
9. Weller-Stuart T, Chan WY, Coutinho TA, Venter SN, Smits THM, Duffy B, Gozczynska T, Cowan DA, de Maayer P. 2014. Draft genome sequences of the onion center rot pathogen \textit{Pantoea ananatis} PA4 and maize brown stalk rot pathogen \textit{P. ananatis} BD442. Genome Announc 2(4):e00750-14. https://doi.org/10.1128/GNA.00750-14.
10. Meglas E, dos Reis Junior FB, Ribeiro RA, Ollero FJ, Meglas M, Hungria M. 2018. Draft genome sequence of \textit{Pantoea ananatis} strain 1.3B, a bacterium isolated from the rhizosphere of \textit{Oryza sativa} var. Puntal that shows biotechnology potential as an inoculant. Genome Announc 6(4):e01547-17. https://doi.org/10.1128/genomeA.01547-17.
11. Weller-Stuart T, de Maayer P, Coutinho TA. 2017. \textit{Pantoea ananatis}: genomic insights into a versatile pathogen. Mol Plant Pathol 18:1191–1198. https://doi.org/10.1111/mpp.12517.
12. Sheibani-Tezerji R, Naveed M, Jelh M-A, Sesitsch A, Rattie T, Mitter B. 2015. The genomes of closely related \textit{Pantoea ananatis} maize seed endophytes having different effects on the host plant differ in secretion system genes and mobile genetic elements. Front Microbiol 6:440. https://doi.org/10.3389/fmicb.2015.00440.
13. Chin C-S, Alexander DH, Marks P, Klammer AA, Drake J, Heiner C, Clum A, Copeland A, Huddleston J, Eichler EE, Turner SW, Korlach J. 2013. Nonhybrid, finished microbial genome assemblies from long-read SMRT sequencing data. Nat Methods 10:563–569. https://doi.org/10.1038/nmeth.2474.
14. Walker BJ, Abeel T, Shea M, Priest M, Abouelliel A, Sakthikumar S, Cuomo CA, Zeng Q, Wortman J, Young SK, Earl AM. 2014. Pilon: an integrated tool for comprehensive microbial variant detection and genome assembly improvement. PLoS One 9:e112963. https://doi.org/10.1371/journal.pone.0112963.
15. Hunt M, De Silva N, Otto TD, Parkhill J, Keane JA, Harris SR. 2015. Circulator: automated circularization of genome assemblies using long sequencing reads. Genome Biol 16:294. https://doi.org/10.1186/s13059-015-0849-0.
16. Varghese NJ, Mukherjee S, Ivanova N, Konstantinidis KT, Mavrommatis K, Kyprides NC, Pati A. 2015. Microbial species delineation using whole genome sequences. Nucleic Acids Res 43:6761–6771. https://doi.org/10.1093/nar/gkv657.
17. Wang Z, Wu M. 2013. A phyllum-level bacterial phylogenetic marker database. Mol Biol Evol 30:1258–1262. https://doi.org/10.1093/molbev/msr059.
18. Tatusova T, DiCuccio M, Badretdin A, Chetvernin V, Nawrocki EP, Zaslavsky T, DiCuccio M, Badretdin A, Chetvernin V, Nawrocki EP, Zaslavsky T.