AMERICAN SOCIETY FOR MICROBIOLOGY | Microbiology Resource Announcements

| Biotechnology | Announcement

Draft genome of *Lysinibacillus fusiformis* PwPw_T2 isolated from *Ananas comosus* revealing acetic acid producing and xenobiotic degrading enzymes

Oyetayo Olaoluwa Adefiranye,[1] Adetomiwa Ayodele Adeniji,[2] Olayide Folashade Obidi,[1] Ganiyu Oladunjoye Oyetibo,[1] Olubukola Oluranti Babalola[2]

AUTHOR AFFILIATIONS See affiliation list on p. 2.

ABSTRACT *Lysinibacillus fusiformis* PwPw_T2 isolated from deteriorating *Ananas comosus* sample collected from Lagos State, Nigeria putatively possesses genomic features like potential enzymes catalyzing acetic acid production and xenobiotic compounds degradation via various pathways as indicated by its genome sequences. These could make the organism relevant in food waste valorization and micro-biotechnology.

KEYWORDS *Lysinibacillus*, xenobiotics, acetic acid, *Ananas comosus*, genome

Lysinibacillus fusiformis PwPw_T2 was isolated from deteriorating *Ananas comosus* collected from Mushin Market, Lagos State, Nigeria (N 6° 31′ 59.9988″, E 3° 21′ 0″) as a potential vinegar producer while scavenging for acetic acid (vinegar) producers during food waste valorization. Before isolation, deteriorating *Ananas comosus* pulp was enriched on glucose, yeast extract, peptone, ethanol (GYPE) medium for 3 days followed by centrifugation at 250 rpm/2 min; pellets obtained were serially diluted. Dilutions 10^4, 10^6, and 10^8 were inoculated on YCEA medium (yeast extract, calcium carbonate, and ethanol) for 3 days at 30°C. After observing visible zone of clearing, colonies were re-inoculated on YBE medium (yeast extract, bromocresol, and ethanol) to ascertain acetic acid production (1). Interest in organism's genomic features has expanded (2–4). Hence, *L. fusiformis* PwPw_T2 genome was sequenced to further explore its genomic features and confirm presence of genes involved in acetic acid production.

Genomic DNA was extracted from fresh pure cultures on yeast extract peptone and glucose broth at 28°C–30°C for 48 hours with Quick-DNA fungal/bacterial miniprep kit (Zymo Research, Irvine, CA, USA) (5, 6). Library preparation and 2 × 150 bp paired-end sequencing were done with Nextera XT Index kit v2 (FC-131-2001 to -2004) and a NextSeq 500 system (Illumina, San Diego, CA, USA) at Quadram Institute Bioscience (Norwich, UK). Preassembly trimming was done by Trim Galore v0.6.5 (7). QUAST v5.0.2 was used to ascertain the quality of reads (8). The sequence reads were assembled into contigs with SPAdes v3.15.3 on KBase platform (9). Contigs from KBase platform were uploaded on online servers of NCBI prokaryotic Genome Automatic Annotation Pipeline (PGAAP v6.5), Bacterial and Viral Bioinformatics Resource Center (BV-BRC) (v3.30.19) (10), Rapid Annotations Subsystems Technology v2.0 (RAST), and SEED Viewer v2.0 (11, 12) for automated annotation and comparison. For all bioinformatics analyses, default settings were employed.

Details of *L. fusiformis* PwPw_T2 genome sequence are summarized in Table 1. The overview of subsystems unique to this bacteria's genome is highlighted in Fig. 1. Based on putative genome exploration on BV-BRC/Pathosystems Resource Integration Center (PATRIC) online server, *L. fusiformis* PwPw_T2 genome possesses metabolic enzymes

Editor John J. Dennehy, Department of Biology, Queens College, Queens, New York, USA

Address correspondence to Oyetayo Olaoluwa Adefiranye, oyetayooo@gmail.com, or Olubukola Oluranti Babalola, olubukola.babalola@nwu.ac.za.

The authors declare no conflict of interest.

Received 15 August 2023
Accepted 27 September 2023
Published 1 November 2023

TABLE 1 Genome annotation features of *Lysinibacillus fusiformis* PwPw_T2[a]

Parameter	Value
Genome size	4,820,104 bp
Genes (total)	4,920
Number of contigs	21
Number of scaffolds	18
tRNA, rRNA	36, 5
GC percent	37
Hypothetical proteins	1,547
CDSs (total)[b]	4,874
CDSs (with protein)	4,824
Genes (RNA)	46
Contig N50	1.5 Mb
Contig L50	2

[a]NCBI Prokaryotic Genome Automatic Annotation Pipeline (PGAAP v6.5) (https://www.ncbi.nlm.nih.gov/genome/annotation_prok/).
[b]CDSs, coding sequences.

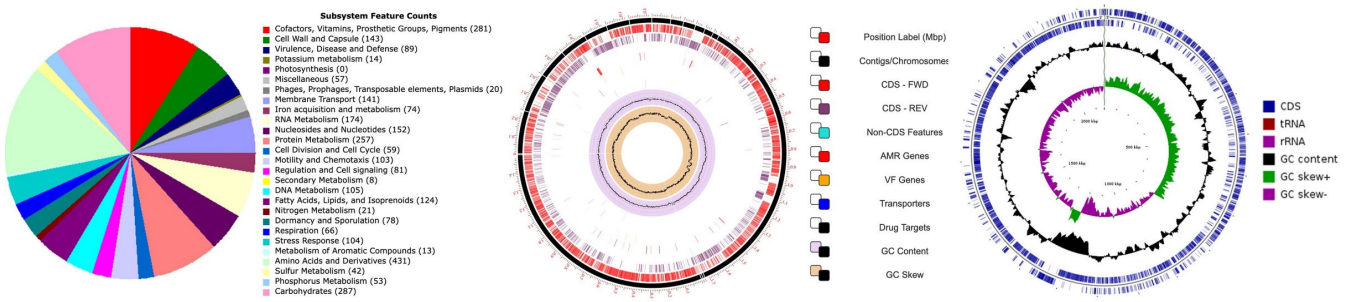

FIG 1 Overview of genome subsystems and circular views of *Lysinibacillus fusiformis* PwPw_T2 were created on RAST, Kbase, and BV-BRC online servers (9, 10, 12).

capable of degrading different types of xenobiotics via specific degradation pathway. Putatively, the isolate has potential for geraniol degradation by acetyl-CoA acetyltransferase [EC 2.3.1.9; pathway ID (PID) 00281] and fluorobenzoate degradation by N-acetylglucosamine deacetylase (EC 3.5.1; PID 00364). *L. fusiformis* PwPw_T2 also has the potential to biosynthesize alcohol dehydrogenase via glycolytic/glyconeogenetic pathway (EC 1.1.1.1; PID 00010) and aldehyde dehydrogenase via pyruvate metabolism (EC.1.2.1.3; ID 00620). Furthermore, in *L. fusiformis* PwPw_T2 genome, AntiSmash 7.0 run at default predicted biosynthetic clusters for the production of kijanimicin, beta-lactones, fengycin, petrobactin, terpenes, bacillibactin, and thiopeptides (13). The biosynthetic clusters of *L. fusiformis* PwPw_T2 make it a good candidate for further biotechnological manipulation, notably in the food manufacturing industry.

AUTHOR AFFILIATIONS

[1]Department of Microbiology, Faculty of Science, University of Lagos, Lagos, Nigeria
[2]Food Security and Safety Focus Area, Faculty of Natural and Agricultural Sciences, North-West University, Mmabatho, South Africa

AUTHOR ORCIDs

Oyetayo Olaoluwa Adefiranye http://orcid.org/0000-0002-0526-4297
Adetomiwa Ayodele Adeniji http://orcid.org/0000-0003-3417-2700
Olayide Folashade Obidi http://orcid.org/0000-0003-1932-8148
Ganiyu Oladunjoye Oyetibo http://orcid.org/0000-0002-2147-8893

Olubukola Oluranti Babalola http://orcid.org/0000-0003-4344-1909

AUTHOR CONTRIBUTIONS

Oyetayo Olaoluwa Adefiranye, Conceptualization, Data curation, Formal analysis, Writing – original draft | Adetomiwa Ayodele Adeniji, Software, Writing – review and editing | Olayide Folashade Obidi, Supervision | Ganiyu Oladunjoye Oyetibo, Supervision | Olubukola Oluranti Babalola, Supervision, Writing – review and editing

DATA AVAILABILITY

The draft whole genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession number JAUIZN000000000.1. The version described in this paper is version JAUIZN010000000. The project data are available under BioProject accession number PRJNA991757 and BioSample accession number SAMN36317136 as well as Sequence Read Archive Accession number SRR25938945.

REFERENCES

1. Diba F, Alam F, Talukder AA. 2015. Screening of acetic acid producing microorganisms from decomposed fruits for vinegar production. Adv Microbiol 5:291–297. https://doi.org/10.4236/aim.2015.55028
2. Passera A, Rossato M, Oliver JS, Battelli G, Shahzad G-I-R, Cosentino E, Sage JM, Toffolatti SL, Lopatriello G, Davis JR, Kaiser MD, Delledonne M, Casati P. 2021. Characterization of *Lysinibacillus fusiformis* strain S4C11:*in vitro*, *in planta*, and *in silico* analyses reveal a plant-beneficial microbe. Microbiol Res 244:126665. https://doi.org/10.1016/j.micres.2020.126665
3. Pudova DS, Lutfullin MT, Shagimardanova EI, Hadieva GF, Shigapova L, Toymentseva AA, Kabanov DA, Mardanova AM, Vologin SG, Sharipova MR. 2018. Draft genome sequence data of *Lysinibacillus fusiformis* strain GM, isolated from potato phyllosphere as a potential probiotic. Data Brief 21:2504–2509. https://doi.org/10.1016/j.dib.2018.11.107
4. Zhao L, Bao G, Geng B, Song J, Li Y. 2015. Draft genome sequence of *Lysinibacillus fusiformis* strain SW-B9, a novel strain for biotransformation of isoeugenol to vanillin. Genome Announc 3:e00289-15. https://doi.org/10.1128/genomeA.00289-15
5. Diaz M, Kellingray L, Akinyemi N, Adefiranye OO, Olaonipekun AB, Bayili GR, Ibezim J, du Plessis AS, Houngbédji M, Kamya D, et al. 2019. Comparison of the microbial composition of African fermented foods using amplicon sequencing. Sci Rep 9:1386–1395. https://doi.org/10.1038/s41598-019-50190-4
6. Petros C, Walls D, Munger H, Wei C. 2019. An unbiased comparison of BigDye Terminator and BrilliantDye Terminator. J Biomol Tech 30:S4.
7. Krueger F. 2015. TrimGalore: a wrapper tool around Cutadapt and FastQC to consistently apply quality and adapter trimming to FastQ files. Babraham Bioinformatics 516. https://www.bioinformatics.babraham.ac.uk/projects/trim_galore.
8. Mikheenko A, Prjibelski A, Saveliev V, Antipov D, Gurevich A. 2018. Versatile genome assembly evaluation with QUAST-LG. Bioinformatics 34:i142–i150. https://doi.org/10.1093/bioinformatics/bty266
9. Arkin AP, Stevens RL, Cottingham RW, Maslov S, Henry CS, Dehal P, Ware D, Perez F, Harris NL, Canon S, et al. 2016. The DOE systems biology Knowledgebase (KBase). bioRxiv. https://doi.org/10.1101/096354
10. Olson RD, Assaf R, Brettin T, Conrad N, Cucinell C, Davis JJ, Dempsey DM, Dickerman A, Dietrich EM, Kenyon RW, et al. 2023. Introducing the bacterial and viral bioinformatics resource center (BV-BRC): a resource combining PATRIC, IRD and ViPR. Nucleic Acids Res 51:D678–D689. https://doi.org/10.1093/nar/gkac1003
11. Aziz RK, Bartels D, Best AA, DeJongh M, Disz T, Edwards RA, Formsma K, Gerdes S, Glass EM, Kubal M, et al. 2008. The RAST server: rapid annotations using subsystems technology. BMC Genomics 9:75. https://doi.org/10.1186/1471-2164-9-75
12. Overbeek R, Olson R, Pusch GD, Olsen GJ, Davis JJ, Disz T, Edwards RA, Gerdes S, Parrello B, Shukla M, Vonstein V, Wattam AR, Xia F, Stevens R. 2013. The SEED and the rapid annotation of microbial genomes using subsystems technology (RAST). Nucleic Acids Res 42:D206–D214. https://doi.org/10.1093/nar/gkt1226
13. Blin K, Shaw S, Augustijn HE, Reitz ZL, Biermann F, Alanjary M, Fetter A, Terlouw BR, Metcalf WW, Helfrich EJN, van Wezel GP, Medema MH, Weber T. 2023. antiSMASH 7.0: new and improved predictions for detection, regulation, chemical structures and visualisation. Nucleic Acids Res 51:W46–W50. https://doi.org/10.1093/nar/gkad344