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Draft genome sequence of *Staphylococcus gallinarum* BAU_KME002 strain isolated from egg surface in Bangladesh

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ABSTRACT This report describes the genome sequence of the *Staphylococcus gallinarum* BAU_KME002 strain isolated in Bangladesh in 2021 from a chicken egg surface. Our assembled genome had 50 contigs, an estimated genome length of 2,866,882 bp (with coverage of 90.0×), 36 predicted antibiotic resistance genes, and 28 predicted virulence factor genes.

Staphylococcus gallinarum is commonly found in the environment and is primarily documented in poultry (1). While *S. gallinarum* is typically not considered pathogenic in humans, it has been found in infected wounds of hospitalized individuals, the blood of a patient with chronic hepatitis B infection (2), and in cases of eye infection, specifically endophthalmitis (3).

From June 2021 to March 2022, we collected egg surface swab samples from various poultry farms and egg markets located in the Mymensingh district of Bangladesh (24.7539°N, 90.4073°E). These samples were then transported to our laboratory (24.7196°N, 90.4267°E) and subjected to overnight incubation at 37°C in nutrient broth (HiMedia, India). Following incubation, the samples were streaked onto Mannitol Salt agar (HiMedia, India) plates, and the resulting colonies underwent staining and biochemical tests to isolate *S. gallinarum* (4). The matrix-assisted laser desorption ionization time-of-flight mass spectrometry was employed to identify *S. gallinarum* (5). Finally, a *S. gallinarum* isolate was aerobically grown on a 5% bovine blood agar plate, followed by incubating at 37°C for 24 h. The Qiagen DNA Mini Kit (QIAGEN, Hilden, Germany) was then utilized to extract the genomic DNA of *S. gallinarum* BAU_KME002 from the broth culture. Next, a sequencing library was generated by employing the Nextera DNA Flex Library Prep Kit (Illumina, San Diego, CA, USA), and it was subsequently sequenced on the Illumina NextSeq2000 platform using paired-end reads (2 × 150). The Unicycler.v0.4.9 (6) tool was employed to assemble the genome, and the raw paired-end reads (*n* = 14,246,490) were trimmed using Trimmomatic.v0.39 (7). The quality of the trimmed reads was assessed using FastQC.v0.11.7 (8). Subsequently, the genome was annotated using Prokka.v1.14.6 (9), PATRIC.v3.2.76 (10), and PGAP.v3.0 (11). The presence of antibiotic resistance genes (ARGs) was determined using CARD.v3.2.4 (12), NDARO.v2023 (13), and PATRIC.v3.2.76 (10), while virulence factor genes (VFGs) were identified using VFDB (14) and Victors (15). PathogenFinder.v2.0 (16) was utilized to assess the pathogenicity index, and DrugBank.v4.0 (17) and TTD (18) were referenced for drug target genes, TCDB (19) for transporter genes, and RAST.v2.0 (20) for metabolic functional features in the assembled genome. Default parameters were used for all software unless otherwise specified.

TABLE 1 General characteristic features of the *Staphylococcus gallinarum* BAU_KME002 strain

Attributes	Values
Genome size	2,862,301 bp
Genome coverage	90.0×
G + C content	33.16
Contig L50	4
Contig N50	184,051 bp
Total genes	2,785
Coding sequences	2,762
Coding genes	2,689
Protein coding genes	2,689
RNA genes	61
tRNA genes	4
rRNAs	57
Pseudo genes	31
Hypothetical proteins	616
Proteins with functional assignments	2,146
Genes assigned to SEED subsystems	1,249
Number of subsystems	279

Our assembled *S. gallinarum* BAU_KME002 genome consisted of 50 contigs, 4 L50 contigs with an N50 value of 184,051 bp, a total length of 2,862,301 bp, an average G + C content of 33.16%, and 61 RNA genes. The general characteristics of the *S. gallinarum* BAU_KME002 are documented in Table 1.

In PathogenFinder, our genome exhibits a probability of pathogenicity index of 0.981 (98.1%) towards a human host. The *S. gallinarum* BAU_KME002 genomes harbored 38 predicted ARGs under various antibiotic categories. Our annotated genome had 15 predicted drug target genes and 17 predicted transporter genes. In addition, the current genome contained 28 predicted VFGs under different virulence determinants. Moreover, our genome harbored 279 subsystems with 32% coverage and 1,249 genes (Table 1; Fig. 1).
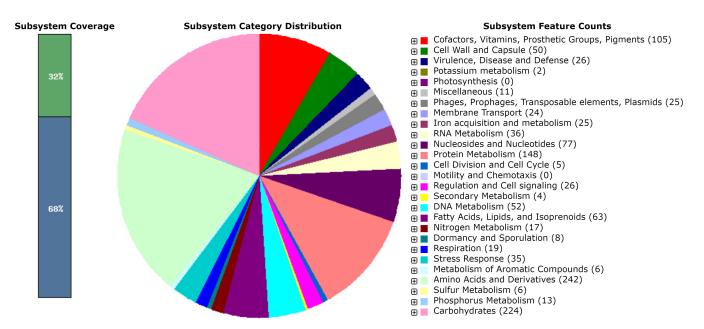

Subsystem Coverage

Subsystem Category Distribution

Subsystem Feature Counts
- Cofactors, Vitamins, Prosthetic Groups, Pigments (105)
- Cell Wall and Capsule (50)
- Virulence, Disease and Defense (26)
- Potassium metabolism (2)
- Photosynthesis (0)
- Miscellaneous (11)
- Phages, Prophages, Transposable elements, Plasmids (25)
- Membrane Transport (24)
- Iron acquisition and metabolism (25)
- RNA Metabolism (36)
- Nucleosides and Nucleotides (77)
- Protein Metabolism (148)
- Cell Division and Cell Cycle (5)
- Motility and Chemotaxis (0)
- Regulation and Cell signaling (26)
- Secondary Metabolism (4)
- DNA Metabolism (52)
- Fatty Acids, Lipids, and Isoprenoids (63)
- Nitrogen Metabolism (17)
- Dormancy and Sporulation (8)
- Respiration (19)
- Stress Response (35)
- Metabolism of Aromatic Compounds (6)
- Amino Acids and Derivatives (242)
- Sulfur Metabolism (6)
- Phosphorus Metabolism (13)
- Carbohydrates (224)

FIG 1 Metabolic functional features in the assembled *Staphylococcus gallinarum* BAU_KME002 genome.

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AUTHOR CONTRIBUTIONS

Fatimah Muhammad Ballah, Data curation, Formal analysis, Investigation, Methodology, Software, Writing – original draft | Md. Saiful Islam, Conceptualization, Data curation, Formal analysis, Investigation, Methodology, Software, Visualization, Writing – original draft, Writing – review and editing | Md. Liton Rana, Investigation | Mst. Minara Khatun, Writing – review and editing | Marzia Rahman, Supervision | Jayedul Hassan, Writing – review and editing | Md. Tanvir Rahman, Conceptualization, Funding acquisition, Methodology, Project administration, Resources, Supervision, Validation, Writing – review and editing

DATA AVAILABILITY

The WGS shotgun analysis of *S. gallinarum* BAU_KME002 was submitted to GenBank under the accession number JAPQEW000000000. The relevant data, including the raw reads, were deposited with BioProject accession number PRJNA907246, BioSample accession number SAMN31957329, and SRA accession number SRR22509343. In this paper, the specific version referred to is JAPQEW000000000.1.

REFERENCES

1. Shi D, Fang D, Hu X, Li A, Lv L, Guo J, Chen Y, Wu W, Guo F, Li L. 2015. Draft genome sequence of *Staphylococcus gallinarum* DSM 20610t, originally isolated from the skin of a chicken. Genome Announc 3:e00580-15. https://doi.org/10.1128/genomeA.00580-15
2. Kolawole DO, Shittu AO. 1997. Unusual recovery of animal staphylococci from septic wounds of hospital patients in Ile‐Ife, Nigeria. Lett Appl Microbiol 24:87–90. https://doi.org/10.1046/j.1472-765x.1997.00337.x
3. Yu D, Chen Y, Pan Y, Li H, McCormac MA, Tang YW. 2008. *Staphylococcus gallinarum* bacteremia in a patient with chronic hepatitis B virus infection. Ann Clin Lab Sci 38:401–404.
4. Lauková A, Marounek M. 1992. Physiological and biochemical characteristics of staphylococci isolated from the rumen of young calves and lambs. Zentralbl Mikrobiol 147:489–494.
5. Cameron M, Perry J, Middleton JR, Chaffer M, Lewis J, Keefe GP. 2018. Evaluation of MALDI-TOF mass spectrometry and a custom reference spectra expanded database for the identification of bovine-associated coagulase-negative staphylococci. J Dairy Sci 101:590–595. https://doi.org/10.3168/jds.2017-13226
6. Wick RR, Judd LM, Gorrie CL, Holt KE. 2017. Unicycler: resolving bacterial genome assemblies from short and long sequencing reads. PLoS Comput Biol 13:e1005595. https://doi.org/10.1371/journal.pcbi.1005595
7. 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
8. Andrews S. 2010. Fastqc: a quality control tool for high throughput sequence data. Online. Available from: http://www.bioinformatics.babraham.ac.uk/projects/fastqc/
9. Seemann T. 2014. Prokka: rapid prokaryotic genome annotation. Bioinformatics 30:2068–2069. https://doi.org/10.1093/bioinformatics/btu153
10. Wattam AR, Davis JJ, Assaf R, Boisvert S, Brettin T, Bun C, Conrad N, Dietrich EM, Disz T, Gabbard JL, Gerdes S, Henry CS, Kenyon RW, Machi D, Mao C, Nordberg EK, Olsen GJ, Murphy-Olson DE, Olson R, Overbeek

R, Parrello B, Pusch GD, Shukla M, Vonstein V, Warren A, Xia F, Yoo H, Stevens RL. 2017. Improvements to PATRIC, the all-bacterial bioinformatics database and analysis resource center. Nucleic Acids Res. 45:D535–D542. https://doi.org/10.1093/nar/gkw1017

11. Tatusova T, DiCuccio M, Badretdin A, Chetvernin V, Nawrocki EP, Zaslavsky L, Lomsadze A, Pruitt KD, Borodovsky M, Ostell J. 2016. NCBI prokaryotic genome annotation pipeline. Nucleic Acids Res. 44:6614–6624. https://doi.org/10.1093/nar/gkw569

12. Alcock BP, Huynh W, Chalil R, Smith KW, Raphenya AR, Wlodarski MA, Edalatmand A, Petkau A, Syed SA, Tsang KK, Baker SJC, Dave M, McCarthy MC, Mukiri KM, Nasir JA, Golbon B, Imtiaz H, Jiang X, Kaur K, Kwong M, Liang ZC, Niu KC, Shan P, Yang JYJ, Gray KL, Hoad GR, Jia B, Bhando T, Carfrae LA, Farha MA, French S, Gordzevich R, Rachwalski K, Tu MM, Bordeleau E, Dooley D, Griffiths E, Zubyk HL, Brown ED, Maguire F, Beiko RG, Hsiao WWL, Brinkman FSL, Van Domselaar G, McArthur AG. 2023. CARD 2023: expanded curation, support for machine learning, and resistome prediction at the comprehensive antibiotic resistance database. Nucleic Acids Res. 51:D690–D699. https://doi.org/10.1093/nar/gkac920

13. National database of antibiotic resistant organisms (NDARO). National center for biotechnology information. Available from: https://www.ncbi.nlm.nih.gov/pathogens/antimicrobial-resistance/. . Accessed June 20, 2023

14. Liu B, Zheng D, Zhou S, Chen L, Yang J. 2022. VFDB 2022: a general classification scheme for bacterial virulence factors. Nucleic Acids Res. 50:D912–D917. https://doi.org/10.1093/nar/gkab1107

15. Sayers S, Li L, Ong E, Deng S, Fu G, Lin Y, Yang B, Zhang S, Fa Z, Zhao B, Xiang Z, Li Y, Zhao X-M, Olszewski MA, Chen L, He Y. 2019. Victors: a web-based knowledge base of virulence factors in human and animal pathogens. Nucleic Acids Res. 47:D693–D700. https://doi.org/10.1093/nar/gky999

16. Cosentino S, Voldby Larsen M, Møller Aarestrup F, Lund O. 2013. Pathogenfinder-distinguishing friend from foe using bacterial whole genome sequence data. PLoS One 8:e77302. https://doi.org/10.1371/journal.pone.0077302

17. Law V, Knox C, Djoumbou Y, Jewison T, Guo AC, Liu Y, Maciejewski A, Arndt D, Wilson M, Neveu V, Tang A, Gabriel G, Ly C, Adamjee S, Dame ZT, Han B, Zhou Y, Wishart DS. 2014. Drugbank 4.0: shedding new light on drug metabolism. Nucleic Acids Res. 42:D1091–7. https://doi.org/10.1093/nar/gkt1068

18. Zhou Y, Zhang Y, Lian X, Li F, Wang C, Zhu F, Qiu Y, Chen Y. 2022. Therapeutic target database update 2022: facilitating drug discovery with enriched comparative data of targeted agents. Nucleic Acids Res. 50:D1398–D1407. https://doi.org/10.1093/nar/gkab953

19. Saier MH Jr, Reddy VS, Tsu BV, Ahmed MS, Li C, Moreno-Hagelsieb G. 2016. The transporter classification database (TCDB): recent advances. Nucleic Acids Res. 44:D372–D379. https://doi.org/10.1093/nar/gkv1103

20. Aziz RK, Bartels D, Best AA, DeJongh M, Disz T, Edwards RA, Formsma 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 9:1–15. https://doi.org/10.1186/1471-2164-9-75