SCREENING OF PATHOGENIC MICROBIOTA HARBOURING ANTIBIOTIC RESISTANCE GENES FROM HEALTHCARE WASTES IN MALAYSIA: A HIGH-THROUGHPUT AMPLICON SEQUENCING APPROACH

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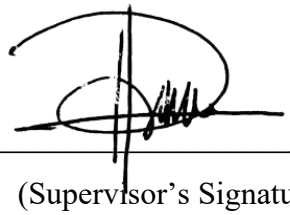

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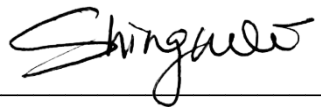

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ABSTRAK

Pembuangan sisa klinikal dari hospital tanpa pembasmian patogen dan bahan pencemar berbahaya pastinya membawa kesan negatif terhadap alam sekitar dan kesihatan awam. Pada masa kini, ujian mikrobiologi untuk sisa klinikal menggunakan pendekatan kultur yang klasik dan menyebabkan proses pengecaman bakteria terhad kepada *Bacillus* sp. dalam sampel yang dirawat. Keberkesanan gelombang mikro dalam rawatan sisa klinikal berbahaya amatlah rendah kerana kurang efektif dan tidak membunuh patogen secara berkesan. Tambahan lagi, sangat sedikit data yang dilaporkan mengenai komuniti mikrob yang lengkap dalam sisa klinikal dari hospital yang telah dirawat dengan gelombang mikro menggunakan teknologi penjujukan generasi seterusnya. Kajian ini bertujuan untuk mengenal pasti komuniti mikrob secara lengkap, bakteria yang kebal terhadap antibiotik yang masih hidup di dalam sisa klinikal setelah dirawat dengan gelombang mikro yang terdapat di tiga pengendali sisa berbeza (FC, FV, dan FA) di Semenanjung Malaysia, dan mencari gen patogenik dalam mikroorganisma terpencil. Komposisi bakteria dan kulat ditentukan melalui penjujukan amplikon dengan mensasarkan keseluruhan gen 16S rRNA dan sebahagian gen 18S rRNA dari *Internal Transcribed Spacer* (ITS) 1 dan ITS2. Kultur bakteria dilakukan untuk mengenal pasti bakteria yang hidup di dalam sisa klinikal. Bakteria yang kebal terhadap antibiotik yang diasingkan telah dianalisis menggunakan *whole genome sequencing*. Bakteria patogenik ini telah diuji kerintangan antibiotik menggunakan teknik resapan cakera. Berdasarkan hasil **objektif 1**, komposisi bakteria dalam sampel FC didominasi oleh genera *Aerococcus*, *Comamonas*, dan *Pseudomonas*, sementara FV dan FA didominasi oleh *Bacillus*, *Paenibacillus*, dan *Bacilli* yang tidak dikelaskan. Ketiga-tiga set sampel menunjukkan perbezaan yang ketara dalam kepelbagaian bakteria, dengan kepelbagaian alpha- (nilai $p = 0.048$) dan beta-diversity (nilai $p < 0.006$). Komposisi kulat berbeza secara ketara antara tiga set sampel, seperti yang dibuktikan oleh nilai alpha- ($p = 0.045$) dan kepelbagaian beta (nilai $p < 0.002$). Analisis bioinformatik mendalam mengesahkan kehadiran $bla_{\text{TEM-1}}$ dan *penP*, yang dikaitkan dengan pengeluaran jalur rintangan beta-laktamase dan beta-laktam kelas A. Berdasarkan **objektif 2**, bakteria yang hidup dikenalpasti melalui kultur adalah dari genera *Proteus*, *Stenotrophomonas*, dan *Pseudomonas*, dengan kepelbagaian beta yang ketara (nilai $p = 0.003$). Berdasarkan hasil BLASTN, bakteria kebal antibiotik yang diasingkan dari sampel VFC, VFV, dan VFA adalah *Proteus mirabilis*, *Stenotrophomonas maltophilia*, dan spesies *Pseudomonas*. Oleh kerana tidak ada spesies *Pseudomonas* tertentu yang dikenal pasti dari pangkalan data, bakteria ini berpotensi hadir sebagai bakteria baru. Untuk **objektif 3**, *P. mirabilis* dan *S. maltophilia* didapati mengandungi gen yang berkaitan dengan fungsi virulensi. Gen rintangan antibiotik $bla_{\text{OXA-10}}$ dan *sul*1 ditemui dalam *P. mirabilis* dan *S. maltophila*, mengakibatkan kekebalan terhadap beta-laktam dan kelas antagonis laluan folat antibiotik. Ujian rintangan antibiotik menunjukkan bahawa *P. mirabilis* dan *S. maltophilia* adalah bakteria perintang pelbagai dadah, menunjukkan rintangan terhadap banyak kelas antibiotik, termasuk karbapenem. Kesimpulannya, mikroorganisma dan bahan cemar berfungsi sebagai petunjuk putatif dalam penilaian rawatan sisa klinikal dari hospital, menunjukkan ketidakberkesanan pembasmian mikrob menggunakan kaedah pensterilan gelombang mikro. Penemuan kami menunjukkan bahawa mikroorganisma berkaitan klinikal, pencemar antibiotik dan gen rintangan antibiotik akan mencemarkan alam sekitar dan memudaratkan kesihatan manusia apabila dilepaskan ke tapak pelupusan melalui pemindahan gen mendatar sekiranya tidak dibendung dengan baik.

ABSTRACT

The disposal of healthcare waste without prior elimination of pathogens and hazardous contaminants has negative effects on the environment and public health. In past research the microbiological assessment of healthcare wastes employed a culture approach that resulted in the identification of *Bacillus* sp. in a sample of treated solid healthcare wastes. The effectiveness of microwave in hazardous waste treatment studied based on the survival of tested microorganisms using the culture method may overlook the presence of other pathogens after treatment. Yet, there is scarce data reported on the complete microbial community in microwave-treated healthcare waste using next-generation sequencing technology. This study aimed to profile the complete microbial community, identify viable antibiotic-resistant bacteria in microwave-treated healthcare wastes collected from three different waste operators (FC, FV, and FA) in Peninsular Malaysia, and characterize pathogenic gene markers in isolated organisms. The samples were subjected to bacterial and fungal amplicon sequencing for microbial community characterization, by targeting the full-length 16S ribosomal RNA (rRNA) gene and partial 18S rRNA gene with full-length internal transcribed spacer (ITS) 1 and ITS 2 regions, respectively. Bacterial cultivation was performed to identify viable bacteria in healthcare wastes. The isolated antibiotic-resistant bacteria were subjected to species identification and whole genome sequencing for complete genome characterization. In addition, antibiotic susceptibility testing was performed on the confirmed isolates using the disk diffusion technique to determine the antibiotic resistance patterns. Based on the results of **objective 1**, the bacterial composition in FC samples was dominated by the *Aerococcus*, *Comamonas*, and *Pseudomonas* genera, while FV and FA were dominated by *Bacillus*, *Paenibacillus*, and unclassified *Bacilli*. All three sets of samples showed significant differences in bacterial diversity, as evidenced by the alpha- (p-value = 0.048) and beta-diversity (p-value < 0.006) analyses. The fungal composition differed significantly between three groups of samples, as evidenced by the alpha- (p-value = 0.045) and beta-diversity (p-value < 0.002). The deep bioinformatic analysis confirmed the presence of $bla_{\text{TEM-1}}$ and *penP*, which are associated with the production of class A beta-lactamase and beta-lactam resistance pathways. Based on **objective 2**, the viable bacteria in VFC, VFV, and VFA samples were represented by *Proteus*, *Stenotrophomonas*, and *Pseudomonas* genera, respectively, with significant beta diversity (p-value = 0.003). Based on the BLASTN results, the primary antibiotic-resistant bacteria isolated from VFC, VFV, and VFA samples were *Proteus mirabilis*, *Stenotrophomonas maltophilia*, and *Pseudomonas* sp., respectively. As no specific *Pseudomonas* species were identified from the database, this bacterium is potentially present as a novel bacterium. For **objective 3,** *P. mirabilis* and *S. maltophilia* were discovered to contain genes associated with virulence function and transposable element expression. The antibiotic resistance genes $bla_{\text{OXA-10}}$ and *sul*1 were identified in *P. mirabilis* and *S. maltophilia*, conferring resistance to beta-lactam and folate pathway antagonist antibiotics. The antibiotic susceptibility tests revealed that *P. mirabilis* and *S. maltophilia* were multidrug-resistant bacteria, exhibiting resistance to drugs from multiple classes, including carbapenem. In conclusion, microorganisms and contaminants, which serve as putative indicators in healthcare waste treatment evaluation, revealed the limitations of the microwave sterilization method in microbial inactivation. Our findings suggested that the occurrence of clinically relevant microorganisms, antibiotic contaminants, and associated antibiotic resistance genes represents environmental and human health hazards when released into landfills *via* horizontal gene transfer.

TABLE OF CONTENT

REFERENCES

A, H. (2018). Epidemiology and Outcomes of Candidaemia among Adult Patients Admitted at Hospital Universiti Sains Malaysia (HUSM): A 5-Year Review. *IIUM Medical Journal Malaysia*, *17*(1 SE-Original Articles). https://doi.org/10.31436/imjm.v17i1.300

Aarts, M.-A. W., Brun-Buisson, C., Cook, D. J., Kumar, A., Opal, S., Rocker, G., Smith, T., Vincent, J.-L., & Marshall, J. C. (2007). Antibiotic management of suspected nosocomial ICU-acquired infection: Does prolonged empiric therapy improve outcome? *Intensive Care Medicine*, *33*(8), 1369–1378. https://doi.org/10.1007/s00134-007-0723-y

Abarenkov, K., Zirk, A., Piirmann, T., Pöhönen, R., Ivanov, F., & Nilsson, R. Henrik; Kõljalg, U. (2021). *UNITE QIIME Release for Fungi 2*. UNITE Community. https://doi.org/https://dx.doi.org/10.15156/BIO/1264763

Abd Kadir, S. A. S., Yin, C.-Y., Rosli Sulaiman, M., Chen, X., & El-Harbawi, M. (2013). Incineration of municipal solid waste in Malaysia: Salient issues, policies and waste-to-energy initiatives. *Renewable and Sustainable Energy Reviews*, *24*, 181–186. https://doi.org/10.1016/j.rser.2013.03.041

Adzitey, F., Huda, N., & Ali, G. R. R. (2013). Molecular techniques for detecting and typing of bacteria, advantages and application to foodborne pathogens isolated from ducks. *3 Biotech*, *3*(2), 97–107. https://doi.org/10.1007/s13205-012-0074-4

Agamuthu, P., & Barasarathi, J. (2021). Clinical waste management under COVID-19 scenario in Malaysia. *Waste Management & Research: The Journal for a Sustainable Circular Economy*, *39*(1_suppl), 18–26. https://doi.org/10.1177/0734242X20959701

Aguilar-Rodea, P., Estrada-Javier, E. L., Jiménez-Rojas, V., Gomez-Ramirez, U., Nolasco-Romero, C. G., Rodea, G. E., Rodríguez-Espino, B. A., Mendoza-Elizalde, S., Arellano, C., López-Marcelino, B., de la Rosa Zamboni, D., Gamiño-Arroyo, A. E., Mora-Suárez, R., Torres García, M., Franco Hernández, I., Parra-Ortega, I., Campos-Valdez, G., Velázquez-Guadarrama, N., & Rosas-Pérez, I. (2022). New Variants of Pseudomonas aeruginosa High-Risk Clone ST233 Associated with an Outbreak in a Mexican Paediatric Hospital. *Microorganisms*, *10*(8). https://doi.org/10.3390/microorganisms10081533

Ahmad, H. F., Schreiber, L., Marshall, I. P. G., Andersen, P. J., Castro-Mejía, J. L., & Nielsen, D. S. (2019). Draft Genome Sequence of Streptococcus anginosus Strain CALM001, Isolated from the Gut of an Elderly Dane. *Microbiology Resource Announcements*, *8*(24), 1–2. https://doi.org/10.1128/mra.00379-19

Al-Salem, S. M. (2018). Energy production from plastic solid waste (PSW). In *Plastics to Energy: Fuel, Chemicals, and Sustainability Implications*. Elsevier Inc. https://doi.org/10.1016/B978-0-12-813140-4.00003-0

Alanjary, M., Steinke, K., & Ziemert, N. (2019). AutoMLST: an automated web server for generating multi-locus species trees highlighting natural product potential. *Nucleic Acids Research*, *47*(W1), W276–W282. https://doi.org/10.1093/nar/gkz282

Alcaraz, E., Garcia, C., Papalia, M., Vay, C., Friedman, L., & De Rossi, B. P. (2018). Stenotrophomonas maltophilia isolated from patients exposed to invasive devices in a

university hospital in Argentina: Molecular typing, susceptibility and detection of potential virulence factors. *Journal of Medical Microbiology*, *67*(7), 992–1002. https://doi.org/10.1099/jmm.0.000764

Alotaibi, F. E., & Bukhari, E. E. (2017). Emergence of Vancomycin-resistant Enterococci at a Teaching Hospital, Saudi Arabia. *Chinese Medical Journal*, *130*(3), 340–346. https://doi.org/10.4103/0366-6999.198923

Alwabr, G. M. A., Al-Mikhlafi, A. S., Al-hakimi, S. A., & Dughish, M. A. (2016). Identification of bacteria and fungi in the solid waste generated in hospitals of Sana ' a city , Yemen. *Current Life Sciences*, *2*(3), 67–71. https://doi.org/10.5281/zenodo.57550

Amarasinghe, S. L., Su, S., Dong, X., Zappia, L., Ritchie, M. E., & Gouil, Q. (2020). Opportunities and challenges in long-read sequencing data analysis. *Genome Biology*, *21*(1), 30. https://doi.org/10.1186/s13059-020-1935-5

Anand, U., Reddy, B., Singh, V. K., Singh, A. K., Kesari, K. K., Tripathi, P., Kumar, P., Tripathi, V., & Simal-Gandara, J. (2021). Potential Environmental and Human Health Risks Caused by Antibiotic-Resistant Bacteria (ARB), Antibiotic Resistance Genes (ARGs) and Emerging Contaminants (ECs) from Municipal Solid Waste (MSW) Landfill. *Antibiotics*, *10*(4), 374. https://doi.org/10.3390/antibiotics10040374

Anju, V. T., Siddhardha, B., & Dyavaiah, M. (2020). Enterobacter Infections and Antimicrobial Drug Resistance. In B. Siddhardha, M. Dyavaiah, & A. Syed (Eds.), *Model Organisms for Microbial Pathogenesis, Biofilm Formation and Antimicrobial Drug Discovery* (pp. 175–194). Springer Singapore. https://doi.org/10.1007/978-981-15-1695-5_11

Annavajhala, M. K., Gomez-Simmonds, A., & Uhlemann, A. C. (2019). Multidrug-resistant Enterobacter cloacae complex emerging as a global, diversifying threat. *Frontiers in Microbiology*, *10*(JAN), 1–8. https://doi.org/10.3389/fmicb.2019.00044

Armbruster, C. E., Mobley, H. L. T., & Pearson, M. M. (2018). Pathogenesis of Proteus mirabilis Infection. *EcoSal Plus*, *8*(1). https://doi.org/10.1128/ecosalplus.ESP-0009-2017

ARSLAN, M., TEZCAN, E., CAMCI, H., & AVCI, M. K. (2021). Effect of DNA Concentration on Band Intensity and Resolution in Agarose Gel Elec-trophoresis. *Van Sağlık Bilimleri Dergisi*, *March*. https://doi.org/10.52976/vansaglik.969547

Ash, R. J., Mauck, B., & Morgan, M. (2002). Antibiotic Resistance of Gram-Negative Bacteria in Rivers, United States. *Emerging Infectious Diseases*, *8*(7), 713–715. https://doi.org/10.3201/eid0807.010264

Asokan, G., Ramadhan, T., Ahmed, E., & Sanad, H. (2019). WHO Global Priority Pathogens List: A Bibliometric Analysis of Medline-PubMed for Knowledge Mobilization to Infection Prevention and Control Practices in Bahrain. *Oman Medical Journal*, *34*(3), 184–193. https://doi.org/10.5001/omj.2019.37

Awodele, O., Adewoye, A. A., & Oparah, A. C. (2016). Assessment of medical waste management in seven hospitals in Lagos, Nigeria. *BMC Public Health*, *16*(1), 1–11. https://doi.org/10.1186/s12889-016-2916-1

Azarfar, A., Bhattacharya, S., Siddiqui, S., & Subhani, N. (2020). Sphingobacterium Thalpophilum Bacteraemia: A Case Report. *The Internet Journal of Infectious Diseases*,

18(1), 1–4. https://doi.org/10.5580/IJID.55030

Aziz, R. K., Bartels, D., Best, A., DeJongh, M., Disz, T., Edwards, R. A., Formsma, K., Gerdes, S., Glass, E. M., Kubal, M., Meyer, F., Olsen, G. J., Olson, R., Osterman, A. L., Overbeek, R. A., McNeil, L. K., Paarmann, D., Paczian, T., Parrello, B., … 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

Babakhani, S., & Oloomi, M. (2018). Transposons: the agents of antibiotic resistance in bacteria. *Journal of Basic Microbiology*, *58*(11), 905–917. https://doi.org/10.1002/jobm.201800204

Babiker, A., Mustapha, M. M., Pacey, M. P., Shutt, K. A., Ezeonwuka, C. D., Ohm, S. L., Cooper, V. S., Marsh, J. W., Doi, Y., & Harrison, L. H. (2019). Use of online tools for antimicrobial resistance prediction by whole-genome sequencing in methicillin-resistant Staphylococcus aureus (MRSA) and vancomycin-resistant enterococci (VRE). *Journal of Global Antimicrobial Resistance*, *19*, 136–143. https://doi.org/10.1016/j.jgar.2019.04.006

Badieyan, S., Dilmaghani-Marand, A., Hajipour, M. J., Ameri, A., Razzaghi, M. R., Rafii-Tabar, H., Mahmoudi, M., & Sasanpour, P. (2018). Detection and Discrimination of Bacterial Colonies with Mueller Matrix Imaging. *Scientific Reports*, *8*(1), 10815. https://doi.org/10.1038/s41598-018-29059-5

Baghal Asghari, F., Dehghani, M. H., Dehghanzadeh, R., Farajzadeh, D., Shanehbandi, D., Mahvi, A. H., Yaghmaeian, K., & Rajabi, A. (2021). Performance evaluation of ozonation for removal of antibiotic-resistant Escherichia coli and Pseudomonas aeruginosa and genes from hospital wastewater. *Scientific Reports*, *11*(1), 24519. https://doi.org/10.1038/s41598-021-04254-z

Banana, A. A. S., Nik Norulaini, N. A., Baharom, J., Lailaatul Zuraida, M. Y., Rafatullah, M., & Kadir, M. O. A. (2013). Inactivation of pathogenic micro-organisms in hospital waste using a microwave. *Journal of Material Cycles and Waste Management*, *15*(3), 393–403. https://doi.org/10.1007/s10163-013-0130-0

Bankevich, A., Nurk, S., Antipov, D., Gurevich, A. A., Dvorkin, M., Kulikov, A. S., Lesin, V. M., Nikolenko, S. I., Pham, S., Prjibelski, A. D., Pyshkin, A. V., Sirotkin, A. V., Vyahhi, N., Tesler, G., Alekseyev, M. A., & Pevzner, P. A. (2012). SPAdes: A new genome assembly algorithm and its applications to single-cell sequencing. *Journal of Computational Biology*, *19*(5), 455–477. https://doi.org/10.1089/cmb.2012.0021

Barahona, F., & Slim, J. (2015). Sphingobacterium multivorum: Case report and literature review. *New Microbes and New Infections*, *7*, 33–36. https://doi.org/10.1016/j.nmni.2015.04.006

Barchitta, M., Maugeri, A., Clara La Rosa, M., La Mastra, C., Murolo, G., Corrao, G., & Agodi, A. (2021). Burden of healthcare-associated infections in Sicily, Italy: Estimates from the regional point prevalence surveys 2016–2018. *Antibiotics*, *10*(11). https://doi.org/10.3390/antibiotics10111360

Bassetti, M., Vena, A., Croxatto, A., Righi, E., & Guery, B. (2018). How to manage Pseudomonas aeruginosa infections. *Drugs in Context*, *7*, 1–18. https://doi.org/10.7573/dic.212527

Be'er, A., & Ariel, G. (2019). A statistical physics view of swarming bacteria. *Movement Ecology*, *7*(1), 9. https://doi.org/10.1186/s40462-019-0153-9

Behnke, M., Hansen, S., Leistner, R., Diaz, L. A. P., Gropmann, A., Sohr, D., Gastmeier, P., & Piening, B. (2013). Nosocomial infection and antibiotic use: A second national prevalence study in Germany. *Deutsches Arzteblatt International*, *110*(38), 627–633. https://doi.org/10.3238/arztebl.2013.0627

Bello-López, J. M., Cabrero-Martínez, O. A., Ibáñez-Cervantes, G., Hernández-Cortez, C., Pelcastre-Rodríguez, L. I., Gonzalez-Avila, L. U., & Castro-Escarpulli, G. (2019). Horizontal gene transfer and its association with antibiotic resistance in the genus aeromonas spp. *Microorganisms*, *7*(9), 1–11. https://doi.org/10.3390/microorganisms7090363

Besser, J., Carleton, H. A. A., Gerner-Smidt, P., Lindsey, R. L. L., & Trees, E. (2018). Next-generation sequencing technologies and their application to the study and control of bacterial infections. *Clinical Microbiology and Infection*, *24*(4), 335–341. https://doi.org/10.1016/j.cmi.2017.10.013

Blin, K., Shaw, S., Steinke, K., Villebro, R., Ziemert, N., Lee, S. Y., Medema, M. H., & Weber, T. (2019). antiSMASH 5.0: updates to the secondary metabolite genome mining pipeline. *Nucleic Acids Research*, *47*(W1), W81–W87. https://doi.org/10.1093/nar/gkz310

Bodor, A., Bounedjoum, N., Vincze, G. E., Erdeiné Kis, Á., Laczi, K., Bende, G., Szilágyi, Á., Kovács, T., Perei, K., & Rákhely, G. (2020). Challenges of unculturable bacteria: environmental perspectives. *Reviews in Environmental Science and Biotechnology*, *19*(1), 1–22. https://doi.org/10.1007/s11157-020-09522-4

Boers, S. A., Jansen, R., & Hays, J. P. (2019). Understanding and overcoming the pitfalls and biases of next-generation sequencing (NGS) methods for use in the routine clinical microbiological diagnostic laboratory. *European Journal of Clinical Microbiology and Infectious Diseases*, *38*(6), 1059–1070. https://doi.org/10.1007/s10096-019-03520-3

Bokulich, N. A., Kaehler, B. D., Rideout, J. R., Dillon, M., Bolyen, E., Knight, R., Huttley, G. A., & Gregory Caporaso, J. (2018). Optimizing taxonomic classification of marker-gene amplicon sequences with QIIME 2's q2-feature-classifier plugin. *Microbiome*, *6*(1), 1–17. https://doi.org/10.1186/s40168-018-0470-z

Bokulich, N. A., & Mills, D. A. (2013). Improved selection of internal transcribed spacer-specific primers enables quantitative, ultra-high-throughput profiling of fungal communities. *Applied and Environmental Microbiology*, *79*(8), 2519–2526. https://doi.org/10.1128/AEM.03870-12

Bolyen, E., Rideout, J. R., Dillon, M. R., Bokulich, N. A., Abnet, C. C., Al-Ghalith, G. A., Alexander, H., Alm, E. J., Arumugam, M., Asnicar, F., Bai, Y., Bisanz, J. E., Bittinger, K., Brejnrod, A., Brislawn, C. J., Brown, C. T., Callahan, B. J., Caraballo-Rodríguez, A. M., Chase, J., … Caporaso, J. G. (2019). Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. *Nature Biotechnology*, *37*(8), 852–857. https://doi.org/10.1038/s41587-019-0209-9

Borodovich, T., Shkoporov, A. N., Ross, R. P., & Hill, C. (2022). Phage-mediated horizontal gene transfer and its implications for the human gut microbiome. *Gastroenterology Report*, *10*(February), 1–12. https://doi.org/10.1093/gastro/goac012

Bortolaia, V., Kaas, R. S., Ruppe, E., Roberts, M. C., Schwarz, S., Cattoir, V., Philippon, A., Allesoe, R. L., Rebelo, A. R., Florensa, A. F., Fagelhauer, L., Chakraborty, T., Neumann, B., Werner, G., Bender, J. K., Stingl, K., Nguyen, M., Coppens, J., Xavier, B. B., … Aarestrup, F. M. (2020). ResFinder 4.0 for predictions of phenotypes from genotypes. *Journal of Antimicrobial Chemotherapy*, *75*(12), 3491–3500. https://doi.org/10.1093/jac/dkaa345

Bostanghadiri, N., Ardebili, A., Ghalavand, Z., Teymouri, S., Mirzarazi, M., Goudarzi, M., Ghasemi, E., & Hashemi, A. (2021). Antibiotic resistance, biofilm formation, and biofilm-associated genes among Stenotrophomonas maltophilia clinical isolates. *BMC Research Notes*, *14*(1), 4–9. https://doi.org/10.1186/s13104-021-05567-y

Boysen, M., Borja, M., Del Moral, C., Salazar, O., & Rubio, V. (1996). Identification at strain level of Rhizoctonia solani AG4 isolates by direct sequence of asymmetric PCR products of the ITS regions. *Current Genetics*, *29*(2), 174–181. https://doi.org/10.1007/BF02221582

Breijyeh, Z., Jubeh, B., & Karaman, R. (2020). Resistance of Gram-Negative Bacteria to Current Antibacterial Agents and Approaches to Resolve It. *Molecules*, *25*(6), 1340. https://doi.org/10.3390/molecules25061340

Bressuire-Isoard, C., Broussolle, V., & Carlin, F. (2018). Sporulation environment influences spore properties in Bacillus: evidence and insights on underlying molecular and physiological mechanisms. *FEMS Microbiology Reviews*, *42*(5), 614–626. https://doi.org/10.1093/femsre/fuy021

Brooke, J. S. (2021). Advances in the Microbiology of Stenotrophomonas maltophilia. *Clinical Microbiology Reviews*, *34*(3). https://doi.org/10.1128/CMR.00030-19

Brumfield, K. D., Huq, A., Colwell, R. R., Olds, J. L., & Leddy, M. B. (2020). Microbial resolution of whole genome shotgun and 16S amplicon metagenomic sequencing using publicly available NEON data. *PLoS ONE*, *15*(2), 1–21. https://doi.org/10.1371/journal.pone.0228899

Bucătaru, C., Săvescu, D., Repanovici, A., Blaga, L., Coman, E., & Cocuz, M.-E. (2021). The Implications and Effects of Medical Waste on Development of Sustainable Society—A Brief Review of the Literature. *Sustainability*, *13*(6), 3300. https://doi.org/10.3390/su13063300

Bukin, Y. S., Galachyants, Y. P., Morozov, I. V., Bukin, S. V., Zakharenko, A. S., & Zemskaya, T. I. (2019). The effect of 16s rRNA region choice on bacterial community metabarcoding results. *Scientific Data*, *6*, 1–14. https://doi.org/10.1038/sdata.2019.7

Burmeister, A. R. (2015). Horizontal Gene Transfer: Figure 1. *Evolution, Medicine, and Public Health*, *2015*(1), 193–194. https://doi.org/10.1093/emph/eov018

Bush, K., & Bradford, P. A. (2020). Epidemiology of β-Lactamase-Producing Pathogens. *Clinical Microbiology Reviews*, *33*(2), 1–37. https://doi.org/10.1128/CMR.00047-19

Cameron, E. S., Schmidt, P. J., Tremblay, B. J. M., Emelko, M. B., & Müller, K. M. (2021). Enhancing diversity analysis by repeatedly rarefying next generation sequencing data describing microbial communities. *Scientific Reports*, *11*(1), 1–13. https://doi.org/10.1038/s41598-021-01636-1

Camiade, M., Bodilis, J., Chaftar, N., Riah-Anglet, W., Gardères, J., Buquet, S., Ribeiro, A. F., & Pawlak, B. (2020). Antibiotic resistance patterns of Pseudomonas spp. isolated from faecal wastes in the environment and contaminated surface water. *FEMS Microbiology Ecology*, *96*(2), 1–15. https://doi.org/10.1093/femsec/fiaa008

Cason, C., D'Accolti, M., Soffritti, I., Mazzacane, S., Comar, M., & Caselli, E. (2022). Next-generation sequencing and PCR technologies in monitoring the hospital microbiome and its drug resistance. *Frontiers in Microbiology*, *13*(July), 1–10. https://doi.org/10.3389/fmicb.2022.969863

Castanheira, M., Simner, P. J., & Bradford, P. A. (2021). Extended-spectrum β -lactamases: an update on their characteristics, epidemiology and detection. *JAC-Antimicrobial Resistance*, *3*(3). https://doi.org/10.1093/jacamr/dlab092

Celandroni, F., Salvetti, S., Gueye, S. A., Mazzantini, D., Lupetti, A., Senesi, S., & Ghelardi, E. (2016). Identification and pathogenic potential of clinical Bacillus and Paenibacillus isolates. *PLoS ONE*, *11*(3), 1–13. https://doi.org/10.1371/journal.pone.0152831

Cermak, N., Datta, M. Sen, & Conwill, A. (2020). Rapid, Inexpensive Measurement of Synthetic Bacterial Community Composition by Sanger Sequencing of Amplicon Mixtures. *IScience*, *23*(3), 100915. https://doi.org/10.1016/j.isci.2020.100915

Cetinkaya, Y., Falk, P., & Mayhall, C. G. (2000). Vancomycin-Resistant Enterococci. *Clinical Microbiology Reviews*, *13*(4), 686–707. https://doi.org/10.1128/CMR.13.4.686

Chaoui, L., Mhand, R., Mellouki, F., & Rhallabi, N. (2019). Contamination of the Surfaces of a Health Care Environment by Multidrug-Resistant (MDR) Bacteria. *International Journal of Microbiology*, *2019*. https://doi.org/10.1155/2019/3236526

Checinska Sielaff, A., Urbaniak, C., Mohan, G. B. M., Stepanov, V. G., Tran, Q., Wood, J. M., Minich, J., McDonald, D., Mayer, T., Knight, R., Karouia, F., Fox, G. E., & Venkateswaran, K. (2019). Characterization of the total and viable bacterial and fungal communities associated with the International Space Station surfaces. *Microbiome*, *7*(1), 50. https://doi.org/10.1186/s40168-019-0666-x

Chen, L., Cai, Y., Zhou, G., Shi, X., Su, J., Chen, G., & Lin, K. (2014). Rapid Sanger Sequencing of the 16S rRNA Gene for Identification of Some Common Pathogens. *PLoS ONE*, *9*(2), e88886. https://doi.org/10.1371/journal.pone.0088886

Chen, S., Zhou, Y., Chen, Y., & Gu, J. (2018). Fastp: An ultra-fast all-in-one FASTQ preprocessor. *Bioinformatics*, *34*(17), i884–i890. https://doi.org/10.1093/bioinformatics/bty560

Chen, X. F., Zhang, W., Fan, X., Hou, X., Liu, X. Y., Huang, J. J., Kang, W., Zhang, G., Zhang, H., Yang, W. H., Li, Y. X., Wang, J. W., Guo, D. W., Sun, Z. Y., Chen, Z. J., Zou, L. G., Du, X. F., Pan, Y. H., Li, B., … Xu, Y. C. (2021). Antifungal Susceptibility Profiles and Resistance Mechanisms of Clinical Diutina catenulata Isolates With High MIC Values. *Frontiers in Cellular and Infection Microbiology*, *11*(October), 1–8. https://doi.org/10.3389/fcimb.2021.739496

Cheng, W., Yan, X., Xiao, J., Chen, Y., Chen, M., Jin, J., Bai, Y., Wang, Q., Liao, Z., & Chen, Q. (2020). Isolation, identification, and whole genome sequence analysis of the alginate-degrading bacterium Cobetia sp. cqz5-12. *Scientific Reports*, *10*(1), 1–10.

https://doi.org/10.1038/s41598-020-67921-7

Chong, J., Liu, P., Zhou, G., & Xia, J. (2020). Using MicrobiomeAnalyst for comprehensive statistical, functional, and meta-analysis of microbiome data. *Nature Protocols*, *15*(3), 799–821. https://doi.org/10.1038/s41596-019-0264-1

Church, D. L., Cerutti, L., Gürtler, A., Griener, T., Zelazny, A., & Emler, S. (2020). Performance and Application of 16S rRNA Gene Cycle Sequencing for Routine Identification of Bacteria in the. *American Society for Microbiology*, *33*(4), 1–74.

Clarridge, J. E. (2004). Impact of 16S rRNA gene sequence analysis for identification of bacteria on clinical microbiology and infectious diseases. *Clinical Microbiology Reviews*, *17*(4), 840–862. https://doi.org/10.1128/CMR.17.4.840-862.2004

Codjoe, F., & Donkor, E. (2017). Carbapenem Resistance: A Review. *Medical Sciences*, *6*(1), 1. https://doi.org/10.3390/medsci6010001

Comar, M., D'Accolti, M., Cason, C., Soffritti, I., Campisciano, G., Lanzoni, L., Bisi, M., Volta, A., Mazzacane, S., & Caselli, E. (2019). Introduction of NGS in Environmental Surveillance for Healthcare-Associated Infection Control. *Microorganisms*, *7*(12), 708. https://doi.org/10.3390/microorganisms7120708

Cong, Y., Yang, S., & Rao, X. (2020). Vancomycin resistant Staphylococcus aureus infections: A review of case updating and clinical features. *Journal of Advanced Research*, *21*, 169–176. https://doi.org/10.1016/j.jare.2019.10.005

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*(10), e77302. https://doi.org/10.1371/journal.pone.0077302

Craig, L., Forest, K. T., & Maier, B. (2019). Type IV pili: dynamics, biophysics and functional consequences. *Nature Reviews Microbiology*, *17*(7), 429–440. https://doi.org/10.1038/s41579-019-0195-4

Cruz-Córdova, A., Mancilla-Rojano, J., Luna-Pineda, V. M., Escalona-Venegas, G., Cázares-Domínguez, V., Ormsby, C., Franco-Hernández, I., Zavala-Vega, S., Hernández, M. A., Medina-Pelcastre, M., Parra-Ortega, I., Rosa-Zamboni, D. D. la, Ochoa, S. A., & Xicohtencatl-Cortes, J. (2020). Molecular Epidemiology, Antibiotic Resistance, and Virulence Traits of Stenotrophomonas maltophilia Strains Associated With an Outbreak in a Mexican Tertiary Care Hospital. *Frontiers in Cellular and Infection Microbiology*, *10*(February), 1–16. https://doi.org/10.3389/fcimb.2020.00050

Cullen, C. M., Aneja, K. K., Beyhan, S., Cho, C. E., Woloszynek, S., Convertino, M., McCoy, S. J., Zhang, Y., Anderson, M. Z., Alvarez-Ponce, D., Smirnova, E., Karstens, L., Dorrestein, P. C., Li, H., Sen Gupta, A., Cheung, K., Powers, J. G., Zhao, Z., & Rosen, G. L. (2020). Emerging Priorities for Microbiome Research. *Frontiers in Microbiology*, *11*(February). https://doi.org/10.3389/fmicb.2020.00136

D'Accolti, M., Soffritti, I., Mazzacane, S., & Caselli, E. (2019). Fighting AMR in the Healthcare Environment: Microbiome-Based Sanitation Approaches and Monitoring Tools. *International Journal of Molecular Sciences*, *20*(7), 1535. https://doi.org/10.3390/ijms20071535

de Bentzmann, S., & Plésiat, P. (2011). The Pseudomonas aeruginosa opportunistic pathogen and human infections. *Environmental Microbiology*, *13*(7), 1655–1665. https://doi.org/10.1111/j.1462-2920.2011.02469.x

De Cario, R., Kura, A., Suraci, S., Magi, A., Volta, A., Marcucci, R., Gori, A. M., Pepe, G., Giusti, B., & Sticchi, E. (2020). Sanger Validation of High-Throughput Sequencing in Genetic Diagnosis: Still the Best Practice? *Frontiers in Genetics*, *11*(December), 1–8. https://doi.org/10.3389/fgene.2020.592588

De Filippis, F., Laiola, M., Blaiotta, G., & Ercolini, D. (2017). Different amplicon targets for sequencing-based studies of fungal diversity. *Applied and Environmental Microbiology*, *83*(17). https://doi.org/10.1128/AEM.00905-17

de Lima Procópio, R. E., da Silva, I. R., Martins, M. K., de Azevedo, J. L., & de Araújo, J. M. (2012). Antibiotics produced by Streptomyces. *The Brazilian Journal of Infectious Diseases*, *16*(5), 466–471. https://doi.org/10.1016/j.bjid.2012.08.014

De Maio, N., Shaw, L. P., Hubbard, A., George, S., Sanderson, N. D., Swann, J., Wick, R., Oun, M. A., Stubberfield, E., Hoosdally, S. J., Crook, D. W., Peto, T. E. A., Sheppard, A. E., Bailey, M. J., Read, D. S., Anjum, M. F., Sarah Walker, A., & Stoesser, N. (2019). Comparison of long-read sequencing technologies in the hybrid assembly of complex bacterial genomes. *Microbial Genomics*, *5*(9). https://doi.org/10.1099/mgen.0.000294

De Oliveira, D. M. P., Forde, B. M., Kidd, T. J., Harris, P. N. A., Schembri, M. A., Beatson, S. A., Paterson, D. L., & Walker, M. J. (2020). Antimicrobial Resistance in ESKAPE Pathogens. *Clinical Microbiology Reviews*, *33*(3). https://doi.org/10.1128/CMR.00181-19

De, R., Mukhopadhyay, A. K., & Dutta, S. (2020). Metagenomic analysis of gut microbiome and resistome of diarrheal fecal samples from Kolkata, India, reveals the core and variable microbiota including signatures of microbial dark matter. *Gut Pathogens*, *12*(1), 32. https://doi.org/10.1186/s13099-020-00371-8

de Siqueira, G. M. V., Pereira-dos-Santos, F. M., Silva-Rocha, R., & Guazzaroni, M.-E. (2021). Nanopore Sequencing Provides Rapid and Reliable Insight Into Microbial Profiles of Intensive Care Units. *Frontiers in Public Health*, *9*(August), 1–11. https://doi.org/10.3389/fpubh.2021.710985

Department of Environment. (2009). *Guideline On The Handling And Management Of Clinical Waste In Malaysia* (3rd ed.). Department of Environment.

Department of Statistics Malaysia. (2020). Department of Statistics Malaysia Press Release: Compendium of Environment Statistics, Malaysia 2020. *Department of Statistic, Malaysia*, *2015*(November), 1–3. https://www.dosm.gov.my/v1/index.php?r=column/pdfPrev&id=TjM1ZlFxb3VOakdmMnozVms5dUlKZz09

Department of Statistics Malaysia. (2021). Prime Minister ' S Department Department of Statistics Malaysia Press Release: Compendium of Environment Statistics, Malaysia 2021. In *Prime Minister' S Department Department of Statistics Malaysia* (Issue November).

Dhariwal, A., Chong, J., Habib, S., King, I. L., Agellon, L. B., & Xia, J. (2017). MicrobiomeAnalyst: A web-based tool for comprehensive statistical, visual and meta-analysis of microbiome data. *Nucleic Acids Research*, *45*(W1), W180–W188.

https://doi.org/10.1093/nar/gkx295

Di Marco, F., Spitaleri, A., Battaglia, S., Batignani, V., Cabibbe, A. M., & Cirillo, D. M. (2023). Advantages of long- and short-reads sequencing for the hybrid investigation of the Mycobacterium tuberculosis genome. *Frontiers in Microbiology*, *14*(February), 1–9. https://doi.org/10.3389/fmicb.2023.1104456

Diba, K., Jangi, F., Makhdoomi, K., Moshiri, N., & Mansouri, F. (2019). Aspergillus diversity in the environments of nosocomial infection cases at a university hospital. *Journal of Medicine and Life*, *12*(2), 128–132. https://doi.org/10.25122/jml-2018-0057

Domínguez-Pérez, R. A., De la Torre-Luna, R., Ahumada-Cantillano, M., Vázquez-Garcidueñas, M. S., Pérez-Serrano, R. M., Martínez-Martínez, R. E., & Guillén-Nepita, A. L. (2018). Detection of the antimicrobial resistance genes blaTEM-1, cfxA, tetQ, tetM, tetW and ermC in endodontic infections of a Mexican population. *Journal of Global Antimicrobial Resistance*, *15*, 20–24. https://doi.org/10.1016/j.jgar.2018.05.011

Drzewiecka, D. (2016). Significance and Roles of Proteus spp. Bacteria in Natural Environments. *Microbial Ecology*, *72*(4), 741–758. https://doi.org/10.1007/s00248-015-0720-6

Du, X., Huang, J., Wang, D., Zhu, Y., Lv, H., & Li, X. (2020). Whole genome sequence of an Escherichia coli ST131 strain isolated from a patient with bloodstream infection in China co-harbouring blaKPC-2, blaCTX-M-3, blaCTX-M-14, qnrS1, aac(3)-IIa and aac(6')-Ib-cr genes. *Journal of Global Antimicrobial Resistance*, *22*, 700–702. https://doi.org/10.1016/j.jgar.2020.06.027

Edgar, R. C., Haas, B. J., Clemente, J. C., Quince, C., & Knight, R. (2011). UCHIME improves sensitivity and speed of chimera detection. In *Bioinformatics* (Vol. 27, Issue 16, pp. 2194–2200). https://doi.org/10.1093/bioinformatics/btr381

Egan, S. A., Corcoran, S., McDermott, H., Fitzpatrick, M., Hoyne, A., McCormack, O., Cullen, A., Brennan, G. I., O'Connell, B., & Coleman, D. C. (2020). Hospital outbreak of linezolid-resistant and vancomycin-resistant ST80 Enterococcus faecium harbouring an optrA-encoding conjugative plasmid investigated by whole-genome sequencing. *Journal of Hospital Infection*, *105*(4), 726–735. https://doi.org/10.1016/j.jhin.2020.05.013

Egbenyah, F., Udofia, E. A., Ayivor, J., Osei, M. M., Tetteh, J., Tetteh-Quarcoo, P. B., & Sampane-Donkor, E. (2021). Disposal habits and microbial load of solid medical waste in sub-district healthcare facilities and households in Yilo-Krobo municipality, Ghana. *PLoS ONE*, *16*(12 December 2021), 1–16. https://doi.org/10.1371/journal.pone.0261211

Ekblom, R., & Wolf, J. B. W. (2014). A field guide to whole-genome sequencing, assembly and annotation. *Evolutionary Applications*, *7*(9), 1026–1042. https://doi.org/10.1111/eva.12178

Emmanuel, J., Pieper, U., Rushbrook, P., Stringer, R., Townend, W., Wilburn, S., & Zghondi, R. (2001). Safe management of wastes from health care activities. In World Health Organization (Ed.), *Bulletin of the World Health Organization* (2nd ed., Vol. 79, Issue 2). World Health Organization. https://www.who.int/publications/i/item/9789241548564

Enright, M. C., Robinson, D. A., Randle, G., Feil, E. J., Grundmann, H., & Spratt, B. G. (2002). The evolutionary history of methicillin-resistant Staphylococcus aureus (MRSA).

Proceedings of the National Academy of Sciences of the United States of America, *99*(11), 7687–7692. https://doi.org/10.1073/pnas.122108599

Erkmen, O. (2021). Practice 10 - Gram staining technique. In O. B. T.-L. P. in M. Erkmen (Ed.), *Laboratory Practices in Microbiology* (pp. 99–105). Academic Press. https://doi.org/https://doi.org/10.1016/B978-0-323-91017-0.00028-7

Esmail, G. A., Al-Dhabi, N. A., AlDawood, B., & Somily, A. M. (2021). Shotgun whole genome sequencing of drug-resistance Streptococcus anginosus strain 47S1 isolated from a patient with pharyngitis in Saudi Arabia. *Journal of Infection and Public Health*, *14*(12), 1740–1749. https://doi.org/10.1016/j.jiph.2021.11.010

Ezechukwu, I., Singal, M., & Igbinosa, O. (2019). Aerococcus Viridans: Case Report, Microbiology, and Literature Review. *American Journal of Case Reports*, *20*, 697–700. https://doi.org/10.12659/AJCR.914866

Ezraty, B., Henry, C., Hérisse, M., Denamur, E., & Barras, F. (2014). Commercial Lysogeny Broth culture media and oxidative stress: A cautious tale. *Free Radical Biology and Medicine*, *74*, 245–251. https://doi.org/10.1016/j.freeradbiomed.2014.07.010

Facciolà, A., Pellicanò, G. F., Visalli, G., Paolucci, I. A., Rullo, E. V., Ceccarelli, M., D'Aleo, F., Di Pietro, A., Squeri, R., Nunnari, G., & La Fauci, V. (2019). The role of the hospital environment in the healthcare-associated infections: A general review of the literature. *European Review for Medical and Pharmacological Sciences*, *23*(3), 1266–1278. https://doi.org/10.26355/eurrev_201902_17020

Fair, R. J., & Tor, Y. (2014). Antibiotics and Bacterial Resistance in the 21st Century. *Perspectives in Medicinal Chemistry*, *6*(6), PMC.S14459. https://doi.org/10.4137/PMC.S14459

Farooq, H., Monowar, T., Latt, S. S., Chinni, S. V, Zainol, N. H., & Sabesan, G. S. (2022). A Review of Studies on Candida Species in Peninsular Malaysia. *Advanced Biomedical Research*, *11*, 98. https://doi.org/10.4103/abr.abr_3_22

Fergestad, M. E., Touzain, F., De Vliegher, S., De Visscher, A., Thiry, D., Ngassam Tchamba, C., Mainil, J. G., L'Abee-Lund, T., Blanchard, Y., & Wasteson, Y. (2021). Whole Genome Sequencing of Staphylococci Isolated From Bovine Milk Samples. *Frontiers in Microbiology*, *12*(December), 1–20. https://doi.org/10.3389/fmicb.2021.715851

Ferronato, N., & Torretta, V. (2019). Waste mismanagement in developing countries: A review of global issues. *International Journal of Environmental Research and Public Health*, *16*(6), 1060. https://doi.org/10.3390/ijerph16061060

Finotello, F., Mastrorilli, E., & Di Camillo, B. (2016). Measuring the diversity of the human microbiota with targeted next-generation sequencing. *Briefings in Bioinformatics*, *19*(4), bbw119. https://doi.org/10.1093/bib/bbw119

Fortier, L.-C., & Sekulovic, O. (2013). Importance of prophages to evolution and virulence of bacterial pathogens. *Virulence*, *4*(5), 354–365. https://doi.org/10.4161/viru.24498

Fouhy, F., Clooney, A. G., Stanton, C., Claesson, M. J., & Cotter, P. D. (2016). 16S rRNA gene sequencing of mock microbial populations-impact of DNA extraction method, primer choice and sequencing platform. *BMC Microbiology*, *16*(1), 1–13.

https://doi.org/10.1186/s12866-016-0738-z

Franco-Duarte, R., Černáková, L., Kadam, S., Kaushik, K. S., Salehi, B., Bevilacqua, A., Corbo, M. R., Antolak, H., Dybka-Stępień, K., Leszczewicz, M., Tintino, S. R., de Souza, V. C. A., Sharifi-Rad, J., Coutinho, H. D. M., Martins, N., & Rodrigues, C. F. (2019). Advances in chemical and biological methods to identify microorganisms—from past to present. *Microorganisms*, *7*(5). https://doi.org/10.3390/microorganisms7050130

Gabashvili, E., Osepashvili, M., Koulouris, S., Ujmajuridze, L., Tskhitishvili, Z., & Kotetishvili, M. (2020). Phage Transduction is Involved in the Intergeneric Spread of Antibiotic Resistance-Associated bla CTX-M, mel, and tetM Loci in Natural Populations of Some Human and Animal Bacterial Pathogens. *Current Microbiology*, *77*(2), 185–193. https://doi.org/10.1007/s00284-019-01817-2

Gao, B., Chi, L., Zhu, Y., Shi, X., Tu, P., Li, B., Yin, J., Gao, N., Shen, W., & Schnabl, B. (2021). An introduction to next generation sequencing bioinformatic analysis in gut microbiome studies. *Biomolecules*, *11*(4), 1–22. https://doi.org/10.3390/biom11040530

García, G., Girón, J. A., Yañez, J. A., & Cedillo, M. L. (2022). Stenotrophomonas maltophilia and Its Ability to Form Biofilms. *Microbiology Research*, *14*(1), 1–20. https://doi.org/10.3390/microbiolres14010001

Gautam, V., Thapar, R., & Sharma, M. (2010). Biomedical waste management: Incineration vs. environmental safety. In *Indian Journal of Medical Microbiology* (Vol. 28, Issue 3, pp. 191–192). https://doi.org/10.4103/0255-0857.66465

Gazel, D., Demirbakan, H., & Erinmez, M. (2021). In vitro activity of hyperthermia on swarming motility and antimicrobial susceptibility profiles of Proteus mirabilis isolates. *International Journal of Hyperthermia*, *38*(1), 1002–1012. https://doi.org/10.1080/02656736.2021.1943546

Germain, J., Raveton, M., Binet, M.-N., & Mouhamadou, B. (2021). Potentiality of Native Ascomycete Strains in Bioremediation of Highly Polychlorinated Biphenyl Contaminated Soils. *Microorganisms*, *9*(3). https://doi.org/10.3390/microorganisms9030612

Ghasemi, M. K., & Yusuff, R. B. M. (2016). Advantages and disadvantages of healthcare waste treatment and disposal alternatives: Malaysian scenario. *Polish Journal of Environmental Studies*, *25*(1), 17–25. https://doi.org/10.15244/pjoes/59322

Girlich, D., Bonnin, R. A., Dortet, L., & Naas, T. (2020). Genetics of Acquired Antibiotic Resistance Genes in Proteus spp. *Frontiers in Microbiology*, *11*(February), 1–21. https://doi.org/10.3389/fmicb.2020.00256

Glen, K. A., & Lamont, I. L. (2021). β-lactam Resistance in Pseudomonas aeruginosa: Current Status, Future Prospects. *Pathogens*, *10*(12), 1638. https://doi.org/10.3390/pathogens10121638

Grady, E. N., MacDonald, J., Liu, L., Richman, A., & Yuan, Z.-C. (2016). Current knowledge and perspectives of Paenibacillus: a review. *Microbial Cell Factories*, *15*(1), 203. https://doi.org/10.1186/s12934-016-0603-7

Guo, Y., Song, G., Sun, M., Wang, J., & Wang, Y. (2020). Prevalence and Therapies of Antibiotic-Resistance in Staphylococcus aureus. *Frontiers in Cellular and Infection*

Microbiology, *10*(March), 1–11. https://doi.org/10.3389/fcimb.2020.00107

Gupta, R., & Gupta, N. (2021). *Competence and Sporulation in Bacillus subtilis BT - Fundamentals of Bacterial Physiology and Metabolism* (R. Gupta & N. Gupta (eds.); pp. 653–670). Springer Singapore. https://doi.org/10.1007/978-981-16-0723-3_25

Gupta, S., Mortensen, M. S., Schjørring, S., Trivedi, U., Vestergaard, G., Stokholm, J., Bisgaard, H., Krogfelt, K. A., & Sørensen, S. J. (2019). Amplicon sequencing provides more accurate microbiome information in healthy children compared to culturing. *Communications Biology*, *2*(1), 1–7. https://doi.org/10.1038/s42003-019-0540-1

Hafiz, T. A., Aldawood, E., Albloshi, A., Alghamdi, S. S., & Mubaraki, M. A. (2022). *Stenotrophomonas maltophilia Epidemiology , Resistance Characteristics , and Clinical Outcomes : Understanding of the Recent Three Years ' Trends*.

Haider, M. H., McHugh, T. D., Roulston, K., Arruda, L. B., Sadouki, Z., & Riaz, S. (2022). Detection of carbapenemases blaOXA48-blaKPC-blaNDM-blaVIM and extended-spectrum-β-lactamase blaOXA1-blaSHV-blaTEM genes in Gram-negative bacterial isolates from ICU burns patients. *Annals of Clinical Microbiology and Antimicrobials*, *21*(1), 18. https://doi.org/10.1186/s12941-022-00510-w

Haliza, A. R. (2013). Incinerator In Malaysia: Really Needs? *International Journal of Chemical, Environmental & Biological Sciences (IJCEBS)*, *1*(4), 678–681. https://citeseerx.ist.psu.edu/viewdoc/download?doi=10.1.1.1072.2264&rep=rep1&type=pdf

Hallin, M., Friedrich, A. W., & Struelens, M. J. (2009). spa typing for epidemiological surveillance of Staphylococcus aureus. *Methods in Molecular Biology (Clifton, N.J.)*, *551*, 189–202. https://doi.org/10.1007/978-1-60327-999-4_15

Handelsman, J. (2005). Metagenomics: Application of Genomics to Uncultured Microorganisms. *Microbiology and Molecular Biology Reviews*, *69*(1), 195–195. https://doi.org/10.1128/mmbr.69.1.195.2005

Hantoko, D., Li, X., Pariatamby, A., Yoshikawa, K., Horttanainen, M., & Yan, M. (2021). Challenges and practices on waste management and disposal during COVID-19 pandemic. *Journal of Environmental Management*, *286*(January), 112140. https://doi.org/10.1016/j.jenvman.2021.112140

Hao, M., Corral-Rivas, J. J., González-Elizondo, M. S., Ganeshaiah, K. N., Nava-Miranda, M. G., Zhang, C., Zhao, X., & von Gadow, K. (2019). Assessing biological dissimilarities between five forest communities. *Forest Ecosystems*, *6*(1), 30. https://doi.org/10.1186/s40663-019-0188-9

Haque, M., Sartelli, M., Mckimm, J., & Abu Bakar, M. (2018). Infection and Drug Resistance Dovepress Health care-associated infections-an overview. *Infection and Drug Resistance*, *11*(1), 2321–2333. http://dx.doi.org/10.2147/IDR.S177247

Haupt, K., Wagner, L., Häder, A., & Vylkova, S. (2020). The Fungus Among Us: Why the Treatment of Fungal Infections Is So Problematic. *Frontiers for Young Minds*, *8*(5). https://doi.org/10.3389/frym.2020.557533

Heather, J. M., & Chain, B. (2016). The sequence of sequencers: The history of sequencing

DNA. *Genomics*, *107*(1), 1–8. https://doi.org/10.1016/j.ygeno.2015.11.003

Heller, A. A., & Spence, D. M. (2019). A rapid method for post-antibiotic bacterial susceptibility testing. *PLOS ONE*, *14*(1), e0210534. https://doi.org/10.1371/journal.pone.0210534

Higgs, C., Sherry, N. L., Seemann, T., Horan, K., Walpola, H., Kinsella, P., Bond, K., Williamson, D. A., Marshall, C., Kwong, J. C., Grayson, M. L., Stinear, T. P., Gorrie, C. L., & Howden, B. P. (2022). Optimising genomic approaches for identifying vancomycin-resistant Enterococcus faecium transmission in healthcare settings. *Nature Communications*, *13*(1), 1–11. https://doi.org/10.1038/s41467-022-28156-4

Hoang, M. T. V., Irinyi, L., Hu, Y., Schwessinger, B., & Meyer, W. (2022). Long-Reads-Based Metagenomics in Clinical Diagnosis With a Special Focus on Fungal Infections. *Frontiers in Microbiology*, *12*(January). https://doi.org/10.3389/fmicb.2021.708550

Hoffman, P. N., & Hanley, M. J. (1994). Assessment of a microwave-based clinical waste decontamination unit. *Journal of Applied Bacteriology*, *77*(6), 607–612. https://doi.org/10.1111/j.1365-2672.1994.tb02808.x

Hossain, M., Rahman, N., Balakrishnan, V., Puvanesuaran, V., Sarker, M., & Kadir, M. (2013). Infectious Risk Assessment of Unsafe Handling Practices and Management of Clinical Solid Waste. *International Journal of Environmental Research and Public Health*, *10*(2), 556–567. https://doi.org/10.3390/ijerph10020556

Hossain, M. S., Santhanam, A., Nik Norulaini, N. A., & Omar, A. K. M. (2011). Clinical solid waste management practices and its impact on human health and environment – A review. *Waste Management*, *31*(4), 754–766. https://doi.org/10.1016/j.wasman.2010.11.008

Hu, S., Jiang, T., Zhou, Y., Ming, D., Gao, H., & Wang, M. (2017). Genomic analysis of the multi-drug-resistant clinical isolate Myroides odoratimimus PR63039. *Molecular Genetics and Genomics*, *292*(1), 133–144. https://doi.org/10.1007/s00438-016-1261-5

Hu, T., Chitnis, N., Monos, D., & Dinh, A. (2021). Next-generation sequencing technologies: An overview. *Human Immunology*, *82*(11), 801–811. https://doi.org/10.1016/j.humimm.2021.02.012

Hugerth, L. W., & Andersson, A. F. (2017). Analysing Microbial Community Composition through Amplicon Sequencing: From Sampling to Hypothesis Testing. *Frontiers in Microbiology*, *8*(SEP), 1–22. https://doi.org/10.3389/fmicb.2017.01561

Hurel, J., Schbath, S., Bougeard, S., Rolland, M., Petrillo, M., & Touzain, F. (2020). DUGMO: Tool for the detection of unknown genetically modified organisms with high-throughput sequencing data for pure bacterial samples. *BMC Bioinformatics*, *21*(1), 1–17. https://doi.org/10.1186/s12859-020-03611-5

Hutchings, M., Truman, A., & Wilkinson, B. (2019). Antibiotics: past, present and future. *Current Opinion in Microbiology*, *51*(Figure 1), 72–80. https://doi.org/10.1016/j.mib.2019.10.008

Hwang, S. M., Cho, H. W., Kim, T. Y., Park, J. S., Jung, J., Song, K. H., Lee, H., Kim, E. S., Kim, H. Bin, & Park, K. U. (2021). Whole-genome sequencing for investigating a health care-associated outbreak of carbapenem-resistant acinetobacter baumannii. *Diagnostics*,

11(2). https://doi.org/10.3390/diagnostics11020201

Ibrahim, S., Al-Saryi, N., Al-Kadmy, I. M. S. S., & Aziz, S. N. (2021). Multidrug-resistant Acinetobacter baumannii as an emerging concern in hospitals. *Molecular Biology Reports*, *48*(10), 6987–6998. https://doi.org/10.1007/s11033-021-06690-6

Ismail, M. A. H., Kamarudin, N., Abdul Samat, M. N., Raja Abdul Rahman, R. M. F., Saimun, S., Tan, T. L., & Neoh, H. (2021). Methicillin-Resistant Staphylococcus aureus (MRSA) Clonal Replacement in a Malaysian Teaching Hospital: Findings from an Eight-Year Interval Molecular Surveillance. *Antibiotics*, *10*(3), 320. https://doi.org/10.3390/antibiotics10030320

Jackson, B. R., & Chiller, T. (2018). *Fungal Disease Outbreaks*. *17*(12), 1–18. https://doi.org/10.1016/S1473-3099(17)30443-7.Emerging

Jafari, E., Oloomi, M., & Bouzari, S. (2021). Characterization of antimicrobial susceptibility, extended-spectrum β-lactamase genes and phylogenetic groups of Shigatoxin producing Escherichia coli isolated from patients with diarrhea in Iran. *Annals of Clinical Microbiology and Antimicrobials*, *20*(1), 1–9. https://doi.org/10.1186/s12941-021-00430-1

Jain, A., Jain, R., & Jain, S. (2020). Staining Methods – Simple Staining, Negative Staining, Gram's Staining and Acid-Fast Staining. In A. Jain, R. Jain, & S. Jain (Eds.), *Basic Techniques in Biochemistry, Microbiology and Molecular Biology: Principles and Techniques* (pp. 111–116). Springer US. https://doi.org/10.1007/978-1-4939-9861-6_31

Jalili, D., Dehghani, M., Fadaei, A., & Alimohammadi, M. (2021). Assessment of Airborne Bacterial and Fungal Communities in Shahrekord Hospitals. *Journal of Environmental and Public Health*, *2021*, 1–7. https://doi.org/10.1155/2021/8864051

Jamil, R. T., Foris, L. A., & Snowden, J. (2022). Proteus Mirabilis Infections. In *StatPearls [Internet]*. Treasure Island (FL): StatPearls Publishing [Internet]. https://www.ncbi.nlm.nih.gov/books/NBK442017/

Janda, J. M., & Abbott, S. L. (2021). The Changing Face of the Family Enterobacteriaceae (Order: " Enterobacterales "): New Members, Taxonomic Issues, Geographic Expansion, and New Diseases and Disease Syndromes. *Clinical Microbiology Reviews*, *34*(2), 1–45. https://doi.org/10.1128/CMR.00174-20

Janik-Karpinska, E., Brancaleoni, R., Niemcewicz, M., Wojtas, W., Foco, M., Podogrocki, M., & Bijak, M. (2023). Healthcare Waste—A Serious Problem for Global Health. *Healthcare*, *11*(2), 242. https://doi.org/10.3390/healthcare11020242

Jaswal, R., Pathak, A., & Chauhan, A. (2019). Metagenomic Evaluation of Bacterial and Fungal Assemblages Enriched within Diffusion Chambers and Microbial Traps Containing Uraniferous Soils. *Microorganisms*, *7*(9), 324. https://doi.org/10.3390/microorganisms7090324

Jeong, J., Yun, K., Mun, S., Chung, W. H., Choi, S. Y., Nam, Y. do, Lim, M. Y., Hong, C. P., Park, C. H., Ahn, Y., & Han, K. (2021). The effect of taxonomic classification by full-length 16S rRNA sequencing with a synthetic long-read technology. *Scientific Reports*, *11*(1), 1–12. https://doi.org/10.1038/s41598-020-80826-9

Jian, Z., Zeng, L., Xu, T., Sun, S., Yan, S., Yang, L., Huang, Y., Jia, J., & Dou, T. (2021).

Antibiotic resistance genes in bacteria: Occurrence, spread, and control. *Journal of Basic Microbiology*, *61*(12), 1049–1070. https://doi.org/10.1002/jobm.202100201

Johnson, J. S., Spakowicz, D. J., Hong, B.-Y., Petersen, L. M., Demkowicz, P., Chen, L., Leopold, S. R., Hanson, B. M., Agresta, H. O., Gerstein, M., Sodergren, E., & Weinstock, G. M. (2019). Evaluation of 16S rRNA gene sequencing for species and strain-level microbiome analysis. *Nature Communications*, *10*(1), 5029. https://doi.org/10.1038/s41467-019-13036-1

Jones, S. U., Chua, K. H., Chew, C. H., Yeo, C. C., Abdullah, F. H., Othman, N., Kee, B. P., & Puah, S. M. (2021). spa diversity of methicillin-resistant and -susceptible Staphylococcus aureus in clinical strains from Malaysia: A high prevalence of invasive European spa-type t032. *PeerJ*, *9*, 1–17. https://doi.org/10.7717/peerj.11195

Kadri, S. S. (2020). Key Takeaways From the U.S. CDC's 2019 Antibiotic Resistance Threats Report for Frontline Providers. *Critical Care Medicine*, *48*(7), 939–945. https://doi.org/10.1097/CCM.0000000000004371

Kanehisa, M., Sato, Y., Kawashima, M., Furumichi, M., & Tanabe, M. (2016). KEGG as a reference resource for gene and protein annotation. *Nucleic Acids Research*, *44*(D1), D457–D462. https://doi.org/10.1093/nar/gkv1070

Katiyar, A., Sharma, P., Dahiya, S., Singh, H., Kapil, A., & Kaur, P. (2020). Genomic profiling of antimicrobial resistance genes in clinical isolates of Salmonella Typhi from patients infected with Typhoid fever in India. *Scientific Reports*, *10*(1), 8299. https://doi.org/10.1038/s41598-020-64934-0

Kaur, D., & Chate, S. (2015). Study of antibiotic resistance pattern in methicillin resistant staphylococcus aureus with special reference to newer antibiotic. *Journal of Global Infectious Diseases*, *7*(2), 78. https://doi.org/10.4103/0974-777X.157245

Kenny, C., & Priyadarshini, A. (2021). Review of Current Healthcare Waste Management Methods and Their Effect on Global Health. *Healthcare*, *9*(3), 284. https://doi.org/10.3390/healthcare9030284

Khedher, M. Ben, Ghedira, K., Rolain, J. M., Ruimy, R., & Croce, O. (2022). Application and Challenge of 3rd Generation Sequencing for Clinical Bacterial Studies. *International Journal of Molecular Sciences*, *23*(3). https://doi.org/10.3390/ijms23031395

Kim, D.-W., & Cha, C.-J. (2021). Antibiotic resistome from the One-Health perspective: understanding and controlling antimicrobial resistance transmission. *Experimental & Molecular Medicine*, *53*(3), 301–309. https://doi.org/10.1038/s12276-021-00569-z

Kim, D. R., & Kwak, Y. S. (2021). A genome-wide analysis of antibiotic producing genes in streptomyces globisporus SP6C4. *Plant Pathology Journal*, *37*(4), 389–395. https://doi.org/10.5423/PPJ.NT.03.2021.0047

Kim, H. S. (2020). Microbiota in Rosacea. *American Journal of Clinical Dermatology*, *21*(S1), 25–35. https://doi.org/10.1007/s40257-020-00546-8

Kisand, V., & Wikner, J. (2003). Combining Culture-Dependent and -Independent Methodologies for Estimation of Richness of Estuarine Bacterioplankton Consuming Riverine Dissolved Organic Matter. *Applied and Environmental Microbiology*, *69*(6),

3607–3616. https://doi.org/10.1128/AEM.69.6.3607-3616.2003

Klassert, T. E., Leistner, R., Zubiria-Barrera, C., Stock, M., López, M., Neubert, R., Driesch, D., Gastmeier, P., & Slevogt, H. (2021). Bacterial colonization dynamics and antibiotic resistance gene dissemination in the hospital environment after first patient occupancy: a longitudinal metagenetic study. *Microbiome*, *9*(1), 169. https://doi.org/10.1186/s40168-021-01109-7

Ko, K. K. K., Chng, K. R., & Nagarajan, N. (2022). Metagenomics-enabled microbial surveillance. *Nature Microbiology*, *7*(4), 486–496. https://doi.org/10.1038/s41564-022-01089-w

Kollu, V. K. R., Kumar, P., & Gautam, K. (2022). Comparison of microwave and autoclave treatment for biomedical waste disinfection. *Systems Microbiology and Biomanufacturing*, *2*(4), 732–742. https://doi.org/10.1007/s43393-022-00101-y

Koutsoumanis, K., Allende, A., Alvarez-Ordóñez, A., Bolton, D., Bover-Cid, S., Chemaly, M., Davies, R., De Cesare, A., Hilbert, F., Lindqvist, R., Nauta, M., Peixe, L., Ru, G., Simmons, M., Skandamis, P., Suffredini, E., Jenkins, C., Malorny, B., Ribeiro Duarte, A. S., … Herman, L. (2019). Whole genome sequencing and metagenomics for outbreak investigation, source attribution and risk assessment of food-borne microorganisms. *EFSA Journal*, *17*(12). https://doi.org/10.2903/j.efsa.2019.5898

Kunhikannan, S., Thomas, C. J., Franks, A. E., Mahadevaiah, S., Kumar, S., & Petrovski, S. (2021). Environmental hotspots for antibiotic resistance genes. *MicrobiologyOpen*, *10*(3), 1–11. https://doi.org/10.1002/mbo3.1197

Kurt, A. F., Mete, B., Houssein, F. M., Tok, Y., Kuskucu, M. A., Yucebag, E., Urkmez, S., Tabak, F., & Aygun, G. (2022). A pan-resistant Myroides odoratimimus catheter-related bacteremia in a COVID-19 patient and review of the literature. *Acta Microbiologica et Immunologica Hungarica*. https://doi.org/10.1556/030.2022.01702

Kwon, J., Yang, M.-H., Ko, H.-J., Kim, S.-G., Park, C., & Park, S.-C. (2022). Antimicrobial Resistance and Virulence Factors of Proteus mirabilis Isolated from Dog with Chronic Otitis Externa. *Pathogens*, *11*(10), 1215. https://doi.org/10.3390/pathogens11101215

Kyriakidis, I., Vasileiou, E., Pana, Z. D., & Tragiannidis, A. (2021). Acinetobacter baumannii antibiotic resistance mechanisms. *Pathogens*, *10*(3), 1–31. https://doi.org/10.3390/pathogens10030373

Lang, J., Li, Y., Yang, W., Dong, R., Liang, Y., Liu, J., Chen, L., Wang, W., Ji, B., Tian, G., Che, N., & Meng, B. (2022). Genomic and resistome analysis of Alcaligenes faecalis strain PGB1 by Nanopore MinION and Illumina Technologies. *BMC Genomics*, *23*(S1), 1–14. https://doi.org/10.1186/s12864-022-08507-7

Larsson, D. G. J., & Flach, C.-F. (2022). Antibiotic resistance in the environment. *Nature Reviews Microbiology*, *20*(5), 257–269. https://doi.org/10.1038/s41579-021-00649-x

Lee, C. R., Lee, J. H., Park, M., Park, K. S., Bae, I. K., Kim, Y. B., Cha, C. J., Jeong, B. C., & Lee, S. H. (2017). Biology of Acinetobacter baumannii: Pathogenesis, antibiotic resistance mechanisms, and prospective treatment options. *Frontiers in Cellular and Infection Microbiology*, *7*(MAR). https://doi.org/10.3389/fcimb.2017.00055

Leekha, S., Terrell, C. L., & Edson, R. S. (2011). General Principles of Antimicrobial Therapy. *Mayo Clinic Proceedings*, *86*(2), 156–167. https://doi.org/10.4065/mcp.2010.0639

Lertwattanachai, T., Montakantikul, P., Tangsujaritvijit, V., Sanguanwit, P., Sueajai, J., Auparakkitanon, S., & Dilokpattanamongkol, P. (2020). Clinical outcomes of empirical high-dose meropenem in critically ill patients with sepsis and septic shock: A randomized controlled trial. *Journal of Intensive Care*, *8*(1), 1–10. https://doi.org/10.1186/s40560-020-00442-7

Liang, Z., Yu, Y., Wang, X., Liao, W., Li, G., & An, T. (2023). The exposure risks associated with pathogens and antibiotic resistance genes in bioaerosol from municipal landfill and surrounding area. *Journal of Environmental Sciences*, *129*, 90–103. https://doi.org/https://doi.org/10.1016/j.jes.2022.09.038

Lim, S. M., & Webb, S. A. R. (2005). Nosocomial bacterial infections in intensive care units. I: Organisms and mechanisms of antibiotic resistance. *Anaesthesia*, *60*(9), 887–902. https://doi.org/10.1111/j.1365-2044.2005.04220.x

Lin, M.-F., & Lan, C.-Y. (2014). Antimicrobial resistance in Acinetobacter baumannii : From bench to bedside. *World Journal of Clinical Cases*, *2*(12), 787. https://doi.org/10.12998/wjcc.v2.i12.787

Liu, J., Li, H., Liu, Z., Meng, X., He, Y., & Zhang, Z. (2022). Study on the process of medical waste disinfection by microwave technology. *Waste Management*, *150*(December 2021), 13–19. https://doi.org/10.1016/j.wasman.2022.06.022

Liu, Liming, Wang, N., Laghari, A. A., Li, H., Wang, C., Zhao, Z., Gao, X., & Zeng, Q. (2023). A Review and Perspective of Environmental Disinfection Technology Based on Microwave Irradiation. *Current Pollution Reports*, *9*(1), 46–59. https://doi.org/10.1007/s40726-022-00247-2

Liu, Lin, Li, Y., Li, S., Hu, N., He, Y., Pong, R., Lin, D., Lu, L., & Law, M. (2012). Comparison of Next-Generation Sequencing Systems. *Journal of Biomedicine and Biotechnology*, *2012*(February), 1–11. https://doi.org/10.1155/2012/251364

Loganathan, B. G., & Masunaga, S. (2009). PCBs, Dioxins, and Furans: Human Exposure and Health Effects. In *Handbook of Toxicology of Chemical Warfare Agents* (pp. 245–253). Elsevier. https://doi.org/10.1016/B978-0-12-374484-5.00018-3

Loong, S. K., Ishak, S. N., Lim, F. S., Khoo, J. J., Tan, S. N., Freddy-Jalin, E. J., Mohdtaib, F. S., & Abubakar, S. (2018). Paenibacillus lautus, an opportunistic bacterial pathogen, isolated from Ixodes granulatus Supino (Acari: Ixodidae) collected from a Müller's giant Sunda rat (Sundamys muelleri). *Systematic and Applied Acarology*, *23*(4), 597–602. https://doi.org/10.11158/saa.23.4.2

Luplertlop, N. (2018). Pseudallescheria/Scedosporium complex species: From saprobic to pathogenic fungus. *Journal de Mycologie Médicale*, *28*(2), 249–256. https://doi.org/10.1016/j.mycmed.2018.02.015

Madoui, M. A., Engelen, S., Cruaud, C., Belser, C., Bertrand, L., Alberti, A., Lemainque, A., Wincker, P., & Aury, J. M. (2015). Genome assembly using Nanopore-guided long and error-free DNA reads. *BMC Genomics*, *16*(1), 1–11. https://doi.org/10.1186/s12864-015-1519-z

Mahdi, A. B., & Gomes, C. (2019). Effects of microwave radiation on micro-organisms in selected materials from healthcare waste. *International Journal of Environmental Science and Technology*, *16*(3), 1277–1288. https://doi.org/10.1007/s13762-018-1741-8

Malberg Tetzschner, A. M., Johnson, J. R., Johnston, B. D., Lund, O., & Scheutz, F. (2020). In Silico Genotyping of Escherichia coli Isolates for Extraintestinal Virulence Genes by Use of Whole-Genome Sequencing Data. *Journal of Clinical Microbiology*, *58*(10), 1–13. https://doi.org/10.1128/JCM.01269-20

Manzoor, M., Lommi, S., Furuholm, J., Sarkkola, C., Engberg, E., Raju, S., & Viljakainen, H. (2021). High abundance of sugar metabolisers in saliva of children with caries. *Scientific Reports*, *11*(1), 4424. https://doi.org/10.1038/s41598-021-83846-1

Martin, M. (2011). Cutadapt removes adapter sequences from high-throughput sequencing reads. *EMBnet.Journal; Vol 17, No 1: Next Generation Sequencing Data Analysis*. https://doi.org/10.14806/ej.17.1.200

Matsuo, Y., Komiya, S., Yasumizu, Y., Yasuoka, Y., Mizushima, K., Takagi, T., Kryukov, K., Fukuda, A., Morimoto, Y., Naito, Y., Okada, H., Bono, H., Nakagawa, S., & Hirota, K. (2021). Full-length 16S rRNA gene amplicon analysis of human gut microbiota using MinION™ nanopore sequencing confers species-level resolution. *BMC Microbiology*, *21*(1), 35. https://doi.org/10.1186/s12866-021-02094-5

Mawioo, P. M., Garcia, H. A., Hooijmans, C. M., Velkushanova, K., Simonič, M., Mijatović, I., & Brdjanovic, D. (2017). A pilot-scale microwave technology for sludge sanitization and drying. *Science of The Total Environment*, *601–602*, 1437–1448. https://doi.org/10.1016/j.scitotenv.2017.06.004

McCombie, W. R., McPherson, J. D., & Mardis, E. R. (2019). Next-Generation Sequencing Technologies. *Cold Spring Harbor Perspectives in Medicine*, *9*(11), a036798. https://doi.org/10.1101/cshperspect.a036798

McCutcheon, J. G., Lin, A., & Dennis, J. J. (2022). Characterization of Stenotrophomonas maltophilia phage AXL1 as a member of the genus Pamexvirus encoding resistance to trimethoprim–sulfamethoxazole. *Scientific Reports*, *12*(1), 1–18. https://doi.org/10.1038/s41598-022-14025-z

McGuinness, W. A., Malachowa, N., & DeLeo, F. R. (2017). Vancomycin Resistance in Staphylococcus aureus . *The Yale Journal of Biology and Medicine*, *90*(2), 269–281. https://doi.org/10.1201/9780849340574-15

Medema, M. H., Blin, K., Cimermancic, P., De Jager, V., Zakrzewski, P., Fischbach, M. A., Weber, T., Takano, E., & Breitling, R. (2011). AntiSMASH: Rapid identification, annotation and analysis of secondary metabolite biosynthesis gene clusters in bacterial and fungal genome sequences. *Nucleic Acids Research*, *39*(SUPPL. 2), 339–346. https://doi.org/10.1093/nar/gkr466

Mehrad, B., Clark, N. M., Zhanel, G. G., & Lynch, J. P. (2015). Antimicrobial resistance in hospital-acquired gram-negative bacterial infections. *Chest*, *147*(5), 1413–1421. https://doi.org/10.1378/chest.14-2171

Miller, A. O., Buckwalter, S. P., Henry, M. W., Wu, F., Maloney, K. F., Abraham, B. K., Hartman, B. J., Brause, B. D., Whittier, S., Walsh, T. J., & Schuetz, A. N. (2017).

Globicatella sanguinis Osteomyelitis and Bacteremia: Review of an Emerging Human Pathogen with an Expanding Spectrum of Disease. *Open Forum Infectious Diseases*, *4*(1), 1–5. https://doi.org/10.1093/ofid/ofw277

Mohan, B., Zaman, K., Anand, N., & Taneja, N. (2017). Aerococcus viridans: A rare pathogen causing urinary tract infection. *Journal of Clinical and Diagnostic Research*, *11*(1), DR01–DR03. https://doi.org/10.7860/JCDR/2017/23997.9229

Mojica, M. F., Humphries, R., Lipuma, J. J., Mathers, A. J., Rao, G. G., Shelburne, S. A., Fouts, D. E., Van Duin, D., & Bonomo, R. A. (2022). Clinical challenges treating Stenotrophomonas maltophilia infections: an update. *JAC-Antimicrobial Resistance*, *4*(3), 1–19. https://doi.org/10.1093/jacamr/dlac040

Møller, J. K., Larsen, A. R., Østergaard, C., Møller, C. H., Kristensen, M. A., & Larsen, J. (2019). International travel as source of a hospital outbreak with an unusual meticillin-resistant Staphylococcus aureus clonal complex 398, Denmark, 2016. *Eurosurveillance*, *24*(42). https://doi.org/10.2807/1560-7917.ES.2019.24.42.1800680

Morioka, H., Oka, K., Yamada, Y., Nakane, Y., Komiya, H., Murase, C., Iguchi, M., & Yagi, T. (2022). Lysinibacillus fusiformis bacteremia: Case report and literature review. *Journal of Infection and Chemotherapy*, *28*(2), 315–318. https://doi.org/10.1016/j.jiac.2021.10.030

Moriya, Y., Itoh, M., Okuda, S., Yoshizawa, A. C., & Kanehisa, M. (2007). KAAS: an automatic genome annotation and pathway reconstruction server. *Nucleic Acids Research*, *35*(Web Server), W182–W185. https://doi.org/10.1093/nar/gkm321

Muenwongtham, S., Jaturapiree, P., & Pimviriyakul, P. (2022). Effect of supplemented sugar in lysogeny broth medium on growth of Escherichia coli BL21(DE3) and recombinant protein production. *Agriculture and Natural Resources*, *56*(3), 537–546. https://doi.org/10.34044/j.anres.2022.56.3.10

Munita, J. M., & Arias, C. A. (2016). Mechanisms of Antibiotic Resistance. *Microbiology Spectrum*, *4*(2), 481–511. https://doi.org/10.1128/microbiolspec.VMBF-0016-2015

Murigneux, V., Roberts, L. W., Forde, B. M., Phan, M. D., Nhu, N. T. K., Irwin, A. D., Harris, P. N. A., Paterson, D. L., Schembri, M. A., Whiley, D. M., & Beatson, S. A. (2021). MicroPIPE: validating an end-to-end workflow for high-quality complete bacterial genome construction. *BMC Genomics*, *22*(1), 1–15. https://doi.org/10.1186/s12864-021-07767-z

Murray, C. J., Ikuta, K. S., Sharara, F., Swetschinski, L., Robles Aguilar, G., Gray, A., Han, C., Bisignano, C., Rao, P., Wool, E., Johnson, S. C., Browne, A. J., Chipeta, M. G., Fell, F., Hackett, S., Haines-Woodhouse, G., Kashef Hamadani, B. H., Kumaran, E. A. P., McManigal, B., … Naghavi, M. (2022). Global burden of bacterial antimicrobial resistance in 2019: a systematic analysis. *The Lancet*, *399*(10325), 629–655. https://doi.org/10.1016/S0140-6736(21)02724-0

Nain, Z., & Karim, M. M. (2021). Whole-genome sequence, functional annotation, and comparative genomics of the high biofilm-producing multidrug-resistant Pseudomonas aeruginosa MZ4A isolated from clinical waste. *Gene Reports*, *22*(December 2020), 100999. https://doi.org/10.1016/j.genrep.2020.100999

Nakagawa, H., & Fujita, M. (2018). Whole genome sequencing analysis for cancer genomics

and precision medicine. *Cancer Science*, *109*(3), 513–522. https://doi.org/10.1111/cas.13505

Natan, G., Worlitzer, V. M., Ariel, G., & Be'er, A. (2022). Mixed-species bacterial swarms show an interplay of mixing and segregation across scales. *Scientific Reports*, *12*(1), 16500. https://doi.org/10.1038/s41598-022-20644-3

National Center for Biotechnology Information. (2022). *Enzyme Summary for Enzyme 3.5.2.6, Beta-lactamase (EC 3.5.2.6)*. PubChem. https://pubchem.ncbi.nlm.nih.gov/protein/EC:3.5.2.6.

Néron, B., Littner, E., Haudiquet, M., Perrin, A., Cury, J., & Rocha, E. P. C. (2022). IntegronFinder 2.0: Identification and Analysis of Integrons across Bacteria, with a Focus on Antibiotic Resistance in Klebsiella. *Microorganisms*, *10*(4). https://doi.org/10.3390/microorganisms10040700

Ng, P. C., & Kirkness, E. F. (2010). Whole Genome Sequencing. In M. R. Barnes & G. Breen (Eds.), *Methods in Molecular Biology* (Vol. 628, Issue 1, pp. 215–226). Humana Press. https://doi.org/10.1007/978-1-60327-367-1_12

Nilsson, R. H., Larsson, K. H., Taylor, A. F. S., Bengtsson-Palme, J., Jeppesen, T. S., Schigel, D., Kennedy, P., Picard, K., Glöckner, F. O., Tedersoo, L., Saar, I., Kõljalg, U., & Abarenkov, K. (2019). The UNITE database for molecular identification of fungi: Handling dark taxa and parallel taxonomic classifications. *Nucleic Acids Research*, *47*(D1), D259–D264. https://doi.org/10.1093/nar/gky1022

Nirwati, H., Sinanjung, K., Fahrunissa, F., Wijaya, F., Napitupulu, S., Hati, V. P., Hakim, M. S., Meliala, A., Aman, A. T., & Nuryastuti, T. (2019). Biofilm formation and antibiotic resistance of Klebsiella pneumoniae isolated from clinical samples in a tertiary care hospital, Klaten, Indonesia. *BMC Proceedings*, *13*(Suppl 11), 1–8. https://doi.org/10.1186/s12919-019-0176-7

Niyongabo, E., Jang, Y. C., Kang, D., & Sung, K. (2019). Generation, management practices and rapid risk assessment of solid medical wastes: a case study in Burundi. *Journal of Material Cycles and Waste Management*, *21*(4), 950–961. https://doi.org/10.1007/s10163-019-00854-0

Noman, E. A., Al-Gheethi, A., Rahman, N. N. N. A., Nagao, H., & Ab. Kadir, M. (2016). Assessment of relevant fungal species in clinical solid wastes. *Environmental Science and Pollution Research*, *23*(19), 19806–19824. https://doi.org/10.1007/s11356-016-7161-8

Noone, J. C., Ferreira, F. A., & Aamot, H. V. (2021). Culture-Independent Genotyping, Virulence and Antimicrobial Resistance Gene Identification of Staphylococcus aureus from Orthopaedic Implant-Associated Infections. *Microorganisms*, *9*(4), 707. https://doi.org/10.3390/microorganisms9040707

Oberacker, P., Stepper, P., Bond, D. M., Höhn, S., Focken, J., Meyer, V., Schelle, L., Sugrue, V. J., Jeunen, G. J., Moser, T., Hore, S. R., von Meyenn, F., Hipp, K., Hore, T. A., & Jurkowski, T. P. (2019). Bio-On-Magnetic-Beads (BOMB): Open platform for high-throughput nucleic acid extraction and manipulation. *PLoS Biology*, *17*(1), 1–16. https://doi.org/10.1371/journal.pbio.3000107

Ojha, P. C., Satpathy, S. S., Ojha, A. K., Sukla, L. B., & Pradhan, D. (2022). Overcoming

challenges due to enhanced biomedical waste generation during COVID-19 pandemic. *Science of the Total Environment*, *832*(January), 155072. https://doi.org/10.1016/j.scitotenv.2022.155072

Ojha, S. C., Chankhamhaengdecha, S., Singhakaew, S., Ounjai, P., & Janvilisri, T. (2016). Inactivation of Clostridium difficile spores by microwave irradiation. *Anaerobe*, *38*, 14–20. https://doi.org/10.1016/j.anaerobe.2015.10.015

Olaniyan, O. T., Dare, A., Okoli, B., Adetunji, C. O., Ibitoye, B. O., Okotie, G. E., & Eweoya, O. (2022). Increase in SARS-CoV-2 infected biomedical waste among low middle-income countries: environmental sustainability and impact with health implications. *Journal of Basic and Clinical Physiology and Pharmacology*, *33*(1), 27–44. https://doi.org/10.1515/jbcpp-2020-0533

Olowo-okere, A., Ibrahim, Y. K. E., Olayinka, B. O., Ehinmidu, J. O., Mohammed, Y., Nabti, L. Z., Rolain, J.-M., & Diene, S. M. (2020). First whole genome sequence of Paenalcaligenes suwonensis bearing blaVIM-5 Metallo-β-lactamase: A clinical isolate responsible for acute gastroenteritis. *Infection, Genetics and Evolution*, *85*(August), 104513. https://doi.org/10.1016/j.meegid.2020.104513

Omar, D., Nazli, S. N., & Karuppannan, S. A. (2012). Clinical Waste Management in District Hospitals of Tumpat, Batu Pahat and Taiping. *Procedia - Social and Behavioral Sciences*, *68*, 134–145. https://doi.org/10.1016/j.sbspro.2012.12.213

Onywera, H., & Meiring, T. L. (2020). Comparative analyses of Ion Torrent V4 and Illumina V3-V4 16S rRNA gene metabarcoding methods for characterization of cervical microbiota: taxonomic and functional profiling. *Scientific African*, *7*, e00278. https://doi.org/10.1016/j.sciaf.2020.e00278

Padmanabhan, K. K., & Barik, D. (2019). Health Hazards of Medical Waste and its Disposal. In *Energy from Toxic Organic Waste for Heat and Power Generation* (Issue January, pp. 99–118). Elsevier. https://doi.org/10.1016/B978-0-08-102528-4.00008-0

Pang, Z., Raudonis, R., Glick, B. R., Lin, T.-J. J., & Cheng, Z. (2019). Antibiotic resistance in Pseudomonas aeruginosa: mechanisms and alternative therapeutic strategies. *Biotechnology Advances*, *37*(1), 177–192. https://doi.org/10.1016/j.biotechadv.2018.11.013

Paterson, G. K., Harrison, E. M., & Holmes, M. A. (2014). The emergence of mecC methicillin-resistant Staphylococcus aureus. *Trends in Microbiology*, *22*(1), 42–47. https://doi.org/10.1016/j.tim.2013.11.003

Paulussen, C., Hallsworth, J. E., Álvarez-Pérez, S., Nierman, W. C., Hamill, P. G., Blain, D., Rediers, H., & Lievens, B. (2017). Ecology of aspergillosis: insights into the pathogenic potency of Aspergillus fumigatus and some other Aspergillus species. *Microbial Biotechnology*, *10*(2), 296–322. https://doi.org/10.1111/1751-7915.12367

Pedro, L. P., & Chioma, Q. W. (2018). Antibiotic Susceptibility of Resistant Pseudomonas Species Generated Through the Use of Differential and Selective Media for Isolation of Pseudomonas from Environmental Samples. *South Asian Journal of Research in Microbiology*, *2*(3), 1–9. https://doi.org/10.9734/sajrm/2018/v2i329257

Peeters, J., Thas, O., Shkedy, Z., Kodalci, L., Musisi, C., Owokotomo, O. E., Dyczko, A.,

Hamad, I., Vangronsveld, J., Kleinewietfeld, M., Thijs, S., & Aerts, J. (2021). Exploring the Microbiome Analysis and Visualization Landscape. In *Frontiers in Bioinformatics* (Vol. 1). https://doi.org/https://doi.org/10.3389/fbinf.2021.774631

Pek, Z., Cabanilla, M. G., & Ahmed, S. (2021). Treatment refractory Stenotrophomonas maltophilia bacteraemia and pneumonia in a COVID-19-positive patient. *BMJ Case Reports*, *14*(6), e242670. https://doi.org/10.1136/bcr-2021-242670

Perlroth, J., Choi, B., & Spellberg, B. (2007). Nosocomial fungal infections: Epidemiology, diagnosis, and treatment. *Medical Mycology*, *45*(4), 321–346. https://doi.org/10.1080/13693780701218689

Perry-Dow, K. A., de Man, T. J. B., Halpin, A. L., Shams, A. M., Rose, L. J., & Noble-Wang, J. A. (2022). The effect of disinfectants on the microbial community on environmental healthcare surfaces using next generation sequencing. *American Journal of Infection Control*, *50*(1), 54–60. https://doi.org/10.1016/j.ajic.2021.08.027

Peters, D. L., McCutcheon, J. G., Stothard, P., & Dennis, J. J. (2019). Novel Stenotrophomonas maltophilia temperate phage DLP4 is capable of lysogenic conversion. *BMC Genomics*, *20*(1), 1–17. https://doi.org/10.1186/s12864-019-5674-5

Petersen, L. M., Martin, I. W., Moschetti, W. E., Kershaw, C. M., & Tsongalis, G. J. (2020). Third-generation sequencing in the clinical laboratory: Exploring the advantages and challenges of nanopore sequencing. In *Journal of Clinical Microbiology* (Vol. 58, Issue 1). https://doi.org/10.1128/JCM.01315-19

Peterson, E., & Kaur, P. (2018). Antibiotic resistance mechanisms in bacteria: Relationships between resistance determinants of antibiotic producers, environmental bacteria, and clinical pathogens. *Frontiers in Microbiology*, *9*(NOV), 1–21. https://doi.org/10.3389/fmicb.2018.02928

Petti, C. A., Bosshard, P.P., Brandt, M. E., Clarridge, J. E., Feldblyum, T. V., Foxall, P. A., Furtado, M. R., Pace, N. R., & Procop, G. W. (2008). Interpretive criteria for identification of bacteria and fungi by DNA target sequencing : approved guideline. *Clinical and Laboratory Standards Institute*, *28*, 71.

Pijacek, M., Bzdil, J., Bedanova, I., Danihlik, J., & Moravkova, M. (2021). The inhibiting effect of microwave radiation on Paenibacillus larvae spores suspended in water. *Veterinární Medicína*, *66*(3), 110–116. https://doi.org/10.17221/156/2020-VETMED

Pinto, C. A., Galante, D., Espinoza-Suarez, E., Gaspar, V. M., Mano, J. F., Barba, F. J., & Saraiva, J. A. (2023). Development Control and Inactivation of Byssochlamys nivea Ascospores by Hyperbaric Storage at Room Temperature. In *Foods* (Vol. 12, Issue 5). https://doi.org/10.3390/foods12050978

Piza-Buitrago, A., Rincón, V., Donato, J., Saavedra, S. Y., Duarte, C., Morero, J., Falquet, L., Reguero, M. T., & Barreto-Hernández, E. (2020). Genome-based characterization of two Colombian clinical Providencia rettgeri isolates co-harboring NDM-1, VIM-2, and other β-lactamases. *BMC Microbiology*, *20*(1), 345. https://doi.org/10.1186/s12866-020-02030-z

Poole, K. (2011). Pseudomonas Aeruginosa: Resistance to the Max. *Frontiers in Microbiology*, *2*(APR), 1–13. https://doi.org/10.3389/fmicb.2011.00065

Prestinaci, F., Pezzotti, P., & Pantosti, A. (2015). Antimicrobial resistance: a global multifaceted phenomenon. *Pathogens and Global Health*, *109*(7), 309–318. https://doi.org/10.1179/2047773215Y.0000000030

Qian, X., Gunturu, S., Guo, J., Chai, B., Cole, J. R., Gu, J., & Tiedje, J. M. (2021). Metagenomic analysis reveals the shared and distinct features of the soil resistome across tundra, temperate prairie, and tropical ecosystems. *Microbiome*, *9*(1), 108. https://doi.org/10.1186/s40168-021-01047-4

Quainoo, S., Coolen, J. P. M., van Hijum, S. A. F. T., Huynen, M. A., Melchers, W. J. G., van Schaik, W., & Wertheim, H. F. L. (2017). Whole-Genome Sequencing of Bacterial Pathogens: the Future of Nosocomial Outbreak Analysis. *Clinical Microbiology Reviews*, *30*(4), 1015–1063. https://doi.org/10.1128/CMR.00016-17

Quast, C., Pruesse, E., Yilmaz, P., Gerken, J., Schweer, T., Yarza, P., Peplies, J., & Glöckner, F. O. (2013). The SILVA ribosomal RNA gene database project: Improved data processing and web-based tools. *Nucleic Acids Research*, *41*(D1), 590–596. https://doi.org/10.1093/nar/gks1219

Rani, F. M., Rahman, N. I. A., Ismail, S., Alattraqchi, A. G., Cleary, D. W., Clarke, S. C., & Yeo, C. C. (2017). Acinetobacter spp. infections in Malaysia: A review of antimicrobial resistance trends, mechanisms and epidemiology. *Frontiers in Microbiology*, *8*(DEC), 1–13. https://doi.org/10.3389/fmicb.2017.02479

Ranjan, R., Rani, A., Metwally, A., McGee, H. S., & Perkins, D. L. (2016). Analysis of the microbiome: Advantages of whole genome shotgun versus 16S amplicon sequencing. *Biochemical and Biophysical Research Communications*, *469*(4), 967–977. https://doi.org/10.1016/j.bbrc.2015.12.083

Rast, D., Evers, K. S., Egli, A., Rudin, C., Goischke, A., & Ritz, N. (2022). Aerococcus urinae — significance of detection in the paediatric urinary tract: a case series. *European Journal of Pediatrics*, *182*(2), 749–756. https://doi.org/10.1007/s00431-022-04730-2

Raza, T., Ullah, S. R., Mehmood, K., & Andleeb, S. (2018). Vancomycin resistant Enterococci: A brief review. *Journal of the Pakistan Medical Association*, *68*(5), 768–772.

Rhoads, D. D. (2021). Stenotrophomonas maltophilia Susceptibility Testing Challenges and Strategies. *Journal of Clinical Microbiology*, *59*(9). https://doi.org/10.1128/JCM.01094-21

Richardson, L. A. (2017). Understanding and overcoming antibiotic resistance. *PLOS Biology*, *15*(8), e2003775. https://doi.org/10.1371/journal.pbio.2003775

Riley, L. W., & Blanton, R. E. (2018). Advances in Molecular Epidemiology of Infectious Diseases: Definitions, Approaches, and Scope of the Field. *Microbiology Spectrum*, *6*(6), 100–106. https://doi.org/10.1128/microbiolspec.AME-0001-2018

Rodríguez-Pérez, H., Ciuffreda, L., & Flores, C. (2020). NanoCLUST: a species-level analysis of 16S rRNA nanopore sequencing data. *Bioinformatics*, *37*(11), 1600–1601. https://doi.org/10.1093/bioinformatics/btaa900

Romero-Rodríguez, A., Ruiz-Villafán, B., Martínez-de la Peña, C. F., & Sánchez, S. (2023). Targeting the Impossible: A Review of New Strategies against Endospores. *Antibiotics*, *12*(2), 248. https://doi.org/10.3390/antibiotics12020248

Rosa Martins, P. H., Rabinovitch, L., de Orem, J. C., Silva, W. M. C., de Araujo Mesquita, F., de Magalhães, M. I. A., de Andrade Cavalcante, D., Vivoni, A. M., de Oliveira, E. J., de Lima, V. C. P., Brito, J. T., & De-Souza, M. T. (2023). Biochemical, physiological, and molecular characterisation of a large collection of aerobic endospore-forming bacteria isolated from Brazilian soils. *Neotropical Biology and Conservation*, *18*(1), 53–72. https://doi.org/10.3897/neotropical.18.e86548

Rossen, J. W. A. W. A., Friedrich, A. W. W., & Moran-Gilad, J. (2018). Practical issues in implementing whole-genome-sequencing in routine diagnostic microbiology. *Clinical Microbiology and Infection*, *24*(4), 355–360. https://doi.org/10.1016/j.cmi.2017.11.001

Roy, S., Aung, M. S., Paul, S. K., Ahmed, S., Haque, N., Khan, E. R., Barman, T. K., Islam, A., Abedin, S., Sultana, C., Paul, A., Hossain, M. A., Urushibara, N., Kawaguchiya, M., Sumi, A., & Kobayashi, N. (2020). Drug resistance determinants in clinical isolates of Enterococcus faecalis in Bangladesh: Identification of oxazolidinone resistance gene optrA in ST59 and ST902 lineages. *Microorganisms*, *8*(8), 1–16. https://doi.org/10.3390/microorganisms8081240

Rungsirivanich, P., Parlindungan, E., O'Connor, P. M., Field, D., Mahony, J., Thongwai, N., & van Sinderen, D. (2021). Simultaneous Production of Multiple Antimicrobial Compounds by Bacillus velezensis ML122-2 Isolated From Assam Tea Leaf [Camellia sinensis var. assamica (J.W.Mast.) Kitam.]. *Frontiers in Microbiology*, *12*(November), 1–14. https://doi.org/10.3389/fmicb.2021.789362

Russell, A. H., & Truman, A. W. (2020). Genome mining strategies for ribosomally synthesised and post-translationally modified peptides. *Computational and Structural Biotechnology Journal*, *18*, 1838–1851. https://doi.org/10.1016/j.csbj.2020.06.032

Russo, A., Tarantino, U., D'Ettorre, G., Della Rocca, C., Ceccarelli, G., Gasbarra, E., Venditti, M., & Iundusi, R. (2021). First report of spondylodiscitis caused by Bacillus circulans in an immunocompetent patient: Clinical case and review of the literature. *IDCases*, *23*, e01058. https://doi.org/10.1016/j.idcr.2021.e01058

Rustiati, E. L., Priyambodo, Novianasari, T., Pratiwi, D. N., Srihanto, E. A., & Angeliya, L. (2019). Comparative Study on DNA Extraction's Qualitative Analysis of Captive Sumatran Elephant in Elephant Training Center, Way Kambas National Park. *Journal of Physics: Conference Series*, *1338*(1), 012029. https://doi.org/10.1088/1742-6596/1338/1/012029

Rütschlin, S., & Böttcher, T. (2020). Inhibitors of Bacterial Swarming Behavior. *Chemistry – A European Journal*, *26*(5), 964–979. https://doi.org/https://doi.org/10.1002/chem.201901961

Sabat, A. J., Van Zanten, E., Akkerboom, V., Wisselink, G., Van Slochteren, K., De Boer, R. F., Hendrix, R., Friedrich, A. W., Rossen, J. W. A., & Kooistra-Smid, A. M. D. M. (2017). Targeted next-generation sequencing of the 16S-23S rRNA region for culture-independent bacterial identification-increased discrimination of closely related species. *Scientific Reports*, *7*(1), 1–12. https://doi.org/10.1038/s41598-017-03458-6

Saeb, A. T. M. (2018). Current Bioinformatics resources in combating infectious diseases. *Bioinformation*, *14*(01), 031–035. https://doi.org/10.6026/97320630014031

Saeb, A. T. M., Al-Rubeaan, K. A., Abouelhoda, M., Selvaraju, M., & Tayeb, H. T. (2017).

Genome sequencing and analysis of the first spontaneous Nanosilver resistant bacterium Proteus mirabilis strain SCDR1. *Antimicrobial Resistance & Infection Control*, *6*(1), 119. https://doi.org/10.1186/s13756-017-0277-x

Sáez-Nieto, J. A., Medina-Pascual, M. J., Carrasco, G., Garrido, N., Fernandez-Torres, M. A., Villalón, P., & Valdezate, S. (2017). Paenibacillus spp. isolated from human and environmental samples in Spain: detection of 11 new species. *New Microbes and New Infections*, *19*, 19–27. https://doi.org/10.1016/j.nmni.2017.05.006

Saito, K., Koido, S., Odamaki, T., Kajihara, M., Kato, K., Horiuchi, S., Adachi, S., Arakawa, H., Yoshida, S., Akasu, T., Ito, Z., Uchiyama, K., Saruta, M., Xiao, J., Sato, N., & Ohkusa, T. (2019). Metagenomic analyses of the gut microbiota associated with colorectal adenoma. *PLOS ONE*, *14*(2), e0212406. https://doi.org/10.1371/journal.pone.0212406

Salipante, S. J., SenGupta, D. J., Cummings, L. A., Land, T. A., Hoogestraat, D. R., & Cookson, B. T. (2015). Application of Whole-Genome Sequencing for Bacterial Strain Typing in Molecular Epidemiology. *Journal of Clinical Microbiology*, *53*(4), 1072–1079. https://doi.org/10.1128/JCM.03385-14

Salverda, M. L. M., De Visser, J. A. G. M., & Barlow, M. (2010). Natural evolution of TEM-1 β-lactamase: experimental reconstruction and clinical relevance. *FEMS Microbiology Reviews*, *34*(6), 1015–1036. https://doi.org/10.1111/j.1574-6976.2010.00222.x

Sandhu, S. S., Pourang, A., & Sivamani, R. K. (2019). A review of next generation sequencing technologies used in the evaluation of the skin microbiome: What a time to be alive. *Dermatology Online Journal*, *25*(7). https://doi.org/10.5070/d3257044797

Sandle, T. (2020). Assessing Gram-stain error rates within the pharmaceutical microbiology laboratory. *EJPPS EUROPEAN JOURNAL OF PARENTERAL AND PHARMACEUTICAL SCIENCES*, *25*(1). https://doi.org/10.37521/ejpps/25102

Sarzynski, S. H., Warner, S., Sun, J., Matsouaka, R., Dekker, J. P., Babiker, A., Li, W., Lai, Y. L., Danner, R. L., Fowler, V. G., & Kadri, S. S. (2022). Trimethoprim-Sulfamethoxazole Versus Levofloxacin for Stenotrophomonas maltophilia Infections: A Retrospective Comparative Effectiveness Study of Electronic Health Records from 154 US Hospitals. *Open Forum Infectious Diseases*, *9*(2). https://doi.org/10.1093/ofid/ofab644

Saxena, A. K., Kumar, M., Chakdar, H., Anuroopa, N., & Bagyaraj, D. J. (2020). Bacillus species in soil as a natural resource for plant health and nutrition. *Journal of Applied Microbiology*, *128*(6), 1583–1594. https://doi.org/10.1111/jam.14506

Schaffer, J. N., & Pearson, M. M. (2016). Proteus mirabilis and Urinary Tract Infections. *Microbiology Spectrum*, *3*(5), 100–106. https://doi.org/10.1128/microbiolspec.UTI-0017-2013

Scheffler, R. J., Bratton, B. P., & Gitai, Z. (2022). Pseudomonas aeruginosa clinical blood isolates display significant phenotypic variability. *PLOS ONE*, *17*(7), e0270576. https://doi.org/10.1371/journal.pone.0270576

Schoch, C. L., Seifert, K. A., Huhndorf, S., Robert, V., Spouge, J. L., Levesque, C. A., Chen, W., Bolchacova, E., Voigt, K., Crous, P. W., Miller, A. N., Wingfield, M. J., Aime, M. C., An, K. D., Bai, F. Y., Barreto, R. W., Begerow, D., Bergeron, M. J., Blackwell, M., … Schindel, D. (2012). Nuclear ribosomal internal transcribed spacer (ITS) region as a

universal DNA barcode marker for Fungi. *Proceedings of the National Academy of Sciences of the United States of America*, *109*(16), 6241–6246. https://doi.org/10.1073/pnas.1117018109

Scientific, F. (2017). *Agar Powder*. *24*, 32317. https://www.flinnsci.com/api/library/Download/97b649b8158e4e3caab34d2ee9264417

Shaw, P., Kumar, N., Mumtaz, S., Lim, J. S., Jang, J. H., Kim, D., Sahu, B. D., Bogaerts, A., & Choi, E. H. (2021). Evaluation of non-thermal effect of microwave radiation and its mode of action in bacterial cell inactivation. *Scientific Reports*, *11*(1), 14003. https://doi.org/10.1038/s41598-021-93274-w

Sheu, C.-C., Chang, Y.-T., Lin, S.-Y., Chen, Y.-H., & Hsueh, P.-R. (2019). Infections Caused by Carbapenem-Resistant Enterobacteriaceae: An Update on Therapeutic Options. *Frontiers in Microbiology*, *10*(JAN). https://doi.org/10.3389/fmicb.2019.00080

Singh, N. S., Singhal, N., & Virdi, J. S. (2018). Genetic Environment of blaTEM-1, blaCTX-M-15, blaCMY-42 and Characterization of Integrons of Escherichia coli Isolated From an Indian Urban Aquatic Environment. *Frontiers in Microbiology*, *9*(MAR), 1–8. https://doi.org/10.3389/fmicb.2018.00382

Siracusa, G., Yuan, Q., Chicca, I., Bardi, A., Spennati, F., Becarelli, S., Levin, D. B., Munz, G., Petroni, G., & Di Gregorio, S. (2020). Mycoremediation of Old and Intermediate Landfill Leachates with an Ascomycete Fungal Isolate, Lambertella sp. In *Water* (Vol. 12, Issue 3). https://doi.org/10.3390/w12030800

Sousa, A. M., Machado, I., Nicolau, A., & Pereira, M. O. (2013). Improvements on colony morphology identification towards bacterial profiling. *Journal of Microbiological Methods*, *95*(3), 327–335. https://doi.org/10.1016/j.mimet.2013.09.020

Spagnolo, A. M., Sartini, M., & Cristina, M. L. (2021). Pseudomonas aeruginosa in the healthcare facility setting. *Reviews in Medical Microbiology*, *32*(3), 169–175. https://doi.org/10.1097/mrm.0000000000000271

Srivastava, S., & Singhvi, R. (2015). Impact of Solid Waste on Health and the Environment. *International Journal of Science and Research (IJSR)*, *4*(9), 1770–1773. http://irnet.sg/irnet_journal/IJSDGE/IJSDGE_doc/IJSDGE_V2I1,2_papers/31.pdf

Steinmann, J., Mamat, U., Abda, E. M., Kirchhoff, L., Streit, W. R., Schaible, U. E., Niemann, S., & Kohl, T. A. (2018). Analysis of phylogenetic variation of Stenotrophomonas maltophilia reveals human-specific branches. *Frontiers in Microbiology*, *9*(APR), 1–10. https://doi.org/10.3389/fmicb.2018.00806

Sulaiman, M. R., Kadir, S. A. S. A., Ibrahim, R., & Husin, M. (2007). A Study on the Problems of the Usage of Incinerators in Malaysia. In *Scientific Research Journal* (1st ed., Vol. 4, Issue 1, pp. 1–12). https://doi.org/10.1016/S1474-4422(07)70211-9

Sullivan, M. J., Altman, D. R., Chacko, K. I., Ciferri, B., Webster, E., Pak, T. R., Deikus, G., Lewis-Sandari, M., Khan, Z., Beckford, C., Rendo, A., Samaroo, F., Sebra, R., Karam-Howlin, R., Dingle, T., Hamula, C., Bashir, A., Schadt, E., Patel, G., … van Bakel, H. (2019). A Complete Genome Screening Program of Clinical Methicillin-Resistant Staphylococcus aureus Isolates Identifies the Origin and Progression of a Neonatal Intensive Care Unit Outbreak. *Journal of Clinical Microbiology*, *57*(12).

https://doi.org/10.1128/JCM.01261-19

Tagini, F., & Greub, G. (2017). Bacterial genome sequencing in clinical microbiology: a pathogen-oriented review. *European Journal of Clinical Microbiology & Infectious Diseases*, *36*(11), 2007–2020. https://doi.org/10.1007/s10096-017-3024-6

Talapko, J., Juzbašić, M., Matijević, T., Pustijanac, E., Bekić, S., Kotris, I., & Škrlec, I. (2021). Candida albicans—The Virulence Factors and Clinical Manifestations of Infection. In *Journal of Fungi* (Vol. 7, Issue 2). https://doi.org/10.3390/jof7020079

Tay, D.D., Siew, S. W., Shamzir Kamal, S., Razali, M. N., & Ahmad, H. F. (2022). ITS1 amplicon sequencing of feline gut mycobiome of Malaysian local breeds using Nanopore Flongle. *Archives of Microbiology*, *204*(6). https://doi.org/10.1007/s00203-022-02929-3

Tay, D. D., Siew, S. W., Razali, M. N., & Ahmad, H. F. (2021). Metadata Analysis For Gut Microbiota between Indoor and Street Cats of Malaysia. *Current Science and Technology*, *1*(1), 56–65. https://doi.org/10.15282/cst.v1i1.6443

Tedersoo, L., Anslan, S., Bahram, M., Põlme, S., Riit, T., Liiv, I., Kõljalg, U., Kisand, V., Nilsson, R. H., Hildebrand, F., Bork, P., & Abarenkov, K. (2015). Shotgun metagenomes and multiple primer pair-barcode combinations of amplicons reveal biases in metabarcoding analyses of fungi. *MycoKeys*, *10*(May), 1–43. https://doi.org/10.3897/mycokeys.10.4852

Tedersoo, L., Tooming-Klunderud, A., & Anslan, S. (2018). PacBio metabarcoding of Fungi and other eukaryotes: errors, biases and perspectives. *New Phytologist*, *217*(3), 1370–1385. https://doi.org/10.1111/nph.14776

Thien, C. Y., & Jusoh, M. N. H. (2021). Overview of Clinical Waste Management in Malaysia. *Frontiers in Water and Environment*, *1*(1), 47–57. https://www.akademiabaru.com/submit/index.php/fwe/article/view/3810

Tolera, M., Abate, D., Dheresa, M., & Marami, D. (2018). Bacterial Nosocomial Infections and Antimicrobial Susceptibility Pattern among Patients Admitted at Hiwot Fana Specialized University Hospital, Eastern Ethiopia. *Advances in Medicine*, *2018*, 1–7. https://doi.org/10.1155/2018/2127814

Tripathi, N., & Sapra, A. (2023). Gram Staining. In *StatPearls [Internet]*. StatPearls Publishing. https://www.ncbi.nlm.nih.gov/books/NBK562156/

Tripathi, V., & Tripathi, P. (2017). Antibiotic Resistance Genes: An Emerging Environmental Pollutant. In *Environmental Science and Engineering (Subseries: Environmental Science)* (Issue 9783319462479, pp. 183–201). https://doi.org/10.1007/978-3-319-46248-6_9

Tronnolone, H., Tam, A., Szenczi, Z., Green, J. E. F., Balasuriya, S., Tek, E. L., Gardner, J. M., Sundstrom, J. F., Jiranek, V., Oliver, S. G., & Binder, B. J. (2018). Diffusion-Limited Growth of Microbial Colonies. *Scientific Reports*, *8*(1), 5992. https://doi.org/10.1038/s41598-018-23649-z

Tsui, C., Kong, E. F., & Jabra-Rizk, M. A. (2016). Pathogenesis of Candida albicans biofilm. *Pathogens and Disease*, *74*(4), ftw018. https://doi.org/10.1093/femspd/ftw018

Turner, J., Muraoka, A., Bedenbaugh, M., Childress, B., Pernot, L., Wiencek, M., & Peterson,

Y. K. (2022). The Chemical Relationship Among Beta-Lactam Antibiotics and Potential Impacts on Reactivity and Decomposition. *Frontiers in Microbiology*, *13*(March), 1–18. https://doi.org/10.3389/fmicb.2022.807955

Turner, S. A., & Butler, G. (2014). The Candida Pathogenic Species Complex. *Cold Spring Harbor Perspectives in Medicine*, *4*(9), a019778–a019778. https://doi.org/10.1101/cshperspect.a019778

Uddin, T. M., Chakraborty, A. J., Khusro, A., Zidan, B. R. M., Mitra, S., Emran, T. Bin, Dhama, K., Ripon, M. K. H., Gajdács, M., Sahibzada, M. U. K., Hossain, M. J., & Koirala, N. (2021). Antibiotic resistance in microbes: History, mechanisms, therapeutic strategies and future prospects. *Journal of Infection and Public Health*, *14*(12), 1750–1766. https://doi.org/10.1016/j.jiph.2021.10.020

Umar, Z., Ashfaq, S., Parikh, A., Ilyas, U., Foster, A., Bhangal, R., Khan, J., & Nassar, M. (2022). Stenotrophomonas Maltophilia and Urinary Tract Infections: A Systematic Review. *Cureus*, *14*(6), 1–5. https://doi.org/10.7759/cureus.26184

Underhill, D. M., & Iliev, I. D. (2014). The mycobiota: interactions between commensal fungi and the host immune system. *Nat Rev Immunol*, *14*(6), 405–416.

Van Heel, A. J., De Jong, A., Song, C., Viel, J. H., Kok, J., & Kuipers, O. P. (2018). BAGEL4: A user-friendly web server to thoroughly mine RiPPs and bacteriocins. *Nucleic Acids Research*, *46*(W1), W278–W281. https://doi.org/10.1093/nar/gky383

van Rhijn, N., & Bromley, M. (2021). The Consequences of Our Changing Environment on Life Threatening and Debilitating Fungal Diseases in Humans. *Journal of Fungi*, *7*(5), 367. https://doi.org/10.3390/jof7050367

Vassallo, A., Kett, S., Purchase, D., & Marvasi, M. (2021). Antibiotic-Resistant Genes and Bacteria as Evolving Contaminants of Emerging Concerns (e-CEC): Is It Time to Include Evolution in Risk Assessment? *Antibiotics*, *10*(9), 1066. https://doi.org/10.3390/antibiotics10091066

Vasudevan, K., Devanga Ragupathi, N. K., Jacob, J. J., & Veeraraghavan, B. (2020). Highly accurate-single chromosomal complete genomes using IonTorrent and MinION sequencing of clinical pathogens. *Genomics*, *112*(1), 545–551. https://doi.org/10.1016/j.ygeno.2019.04.006

Virolle, C., Goldlust, K., Djermoun, S., Bigot, S., & Lesterlin, C. (2020). Plasmid Transfer by Conjugation in Gram-Negative Bacteria: From the Cellular to the Community Level. *Genes*, *11*(11), 1239. https://doi.org/10.3390/genes11111239

Wang, J., Shen, J., Ye, D., Yan, X., Zhang, Y., Yang, W., Li, X., Wang, J., Zhang, L., & Pan, L. (2020). Disinfection technology of hospital wastes and wastewater: Suggestions for disinfection strategy during coronavirus Disease 2019 (COVID-19) pandemic in China. *Environmental Pollution*, *262*(January), 114665. https://doi.org/10.1016/j.envpol.2020.114665

Wang, N., Tang, C., & Wang, L. (2022). Risk Factors for Acquired Stenotrophomonas maltophilia Pneumonia in Intensive Care Unit: A Systematic Review and Meta-Analysis. *Frontiers in Medicine*, *8*(January), 1–9. https://doi.org/10.3389/fmed.2021.808391

Wang, Y., Yu, Z., Ding, P., Lu, J., Klümper, U., Murray, A. K., Gaze, W. H., & Guo, J. (2022). Non-antibiotic pharmaceuticals promote conjugative plasmid transfer at a community-wide level. *Microbiome*, *10*(1), 124. https://doi.org/10.1186/s40168-022-01314-y

Wang, Z., Wu, J., Song, J., & Bai, J. (2023). Effect of Different Excipients on Fungal Flora during Aerobic Fermentation of Thermal Hydrolyzed Kitchen Waste. *Journal of Physics: Conference Series*, *2468*(1), 12134. https://doi.org/10.1088/1742-6596/2468/1/012134

Weber, D. J., Rutala, W. A., Miller, M. B., Huslage, K., & Sickbert-Bennett, E. (2010). Role of hospital surfaces in the transmission of emerging health care-associated pathogens: Norovirus, Clostridium difficile, and Acinetobacter species. *American Journal of Infection Control*, *38*(5 SUPPL.), S25–S33. https://doi.org/10.1016/j.ajic.2010.04.196

Weber, T., Blin, K., & Shaw, S. (2019). *antiSMASH 5 USER MANUAL antiSMASH 5 antiSMASH database MANUAL*.

Wenzler, E., Kamboj, K., & Balada-Llasat, J. M. (2015). Severe Sepsis Secondary to Persistent Lysinibacillus sphaericus, Lysinibacillus fusiformis and Paenibacillus amylolyticus Bacteremia. *International Journal of Infectious Diseases*, *35*, e93–e95. https://doi.org/10.1016/j.ijid.2015.04.016

Wick, R. R., Judd, L. M., Gorrie, C. L., & Holt, K. E. (2017). Unicycler: Resolving bacterial genome assemblies from short and long sequencing reads. *PLOS Computational Biology*, *13*(6), e1005595. https://doi.org/10.1371/journal.pcbi.1005595

Wijayawardene, N. N., Bahram, M., Sánchez-Castro, I., Dai, D.-Q., Ariyawansa, K. G. S. U., Jayalal, U., Suwannarach, N., & Tedersoo, L. (2021). Current Insight into Culture-Dependent and Culture-Independent Methods in Discovering Ascomycetous Taxa. *Journal of Fungi*, *7*(9), 703. https://doi.org/10.3390/jof7090703

Willis, A. D. (2019). Rarefaction, Alpha Diversity, and Statistics. *Frontiers in Microbiology*, *10*(OCT). https://doi.org/10.3389/fmicb.2019.02407

Winand, R., Bogaerts, B., Hoffman, S., Lefevre, L., Delvoye, M., Van Braekel, J., Fu, Q., Roosens, N. H. C., De Keersmaecker, S. C. J., & Vanneste, K. (2020). Targeting the 16s rRNA gene for bacterial identification in complex mixed samples: Comparative evaluation of second (illumina) and third (oxford nanopore technologies) generation sequencing technologies. *International Journal of Molecular Sciences*, *21*(1), 1–22. https://doi.org/10.3390/ijms21010298

World Health Organization. (2002). 3 Best practices for incineration. *World Health Organisation*, 12–24. https://www.who.int/water_sanitation_health/medicalwaste/en/smincinerators3.pdf

World Health Organization. (2017). *WHO publishes list of bacteria for which new antibiotics are urgently needed*. https://www.who.int/news/item/27-02-2017-who-publishes-list-of-bacteria-for-which-new-antibiotics-are-urgently-needed

World Health Organization. (2021). 2021 Antibacterial Agents in Clinical and Preclinical Development. In *World Health Organization*. https://www.who.int/publications/i/item/9789240021303

Wu, X., Spencer, S., Gushgari-Doyle, S., Yee, M. O., Voriskova, J., Li, Y., Alm, E. J., &

Chakraborty, R. (2020). Culturing of "Unculturable" Subsurface Microbes: Natural Organic Carbon Source Fuels the Growth of Diverse and Distinct Bacteria From Groundwater. *Frontiers in Microbiology*, *11*(December). https://doi.org/10.3389/fmicb.2020.610001

Wu, Y., & Yao, M. (2010). Inactivation of bacteria and fungus aerosols using microwave irradiation. *Journal of Aerosol Science*, *41*(7), 682–693. https://doi.org/10.1016/j.jaerosci.2010.04.004

Xia, J., Gao, J., & Tang, W. (2016). Nosocomial infection and its molecular mechanisms of antibiotic resistance. *BioScience Trends*, *10*(1), 14–21. https://doi.org/10.5582/bst.2016.01020

Xiao, M., Pang, L., Chen, S. C. A., Fan, X., Zhang, L., Li, H.-X., Hou, X., Cheng, J.-W., Kong, F., Zhao, Y.-P., & Xu, Y.-C. (2016). Accurate Identification of Common Pathogenic Nocardia Species: Evaluation of a Multilocus Sequence Analysis Platform and Matrix-Assisted Laser Desorption Ionization-Time of Flight Mass Spectrometry. *PLOS ONE*, *11*(1), e0147487. https://doi.org/10.1371/journal.pone.0147487

Xiao, T., & Zhou, W. (2020). The third generation sequencing: The advanced approach to genetic diseases. *Translational Pediatrics*, *9*(2), 163–173. https://doi.org/10.21037/TP.2020.03.06

Yabes, J. M., Perdikis, S., Graham, D. B., & Markelz, A. (2018). A rare case of Aerococcus urinae infective endocarditis in an atypically young male: case report and review of the literature. *BMC Infectious Diseases*, *18*(1), 522. https://doi.org/10.1186/s12879-018-3414-0

Yahya, E., Almashgab, A. M., Abdulsamad, M. A., Allaq, A. A., Alqadhi, A. M., Garatem, F. M., & Aljundi, S. S. (2021). Evaluation the Effect of Microwave Radiation on Gram Positive and Negative Bacteria. *Journal of Chemistry and Nutritional Biochemistry*, *2*(1), 39–45. https://doi.org/10.48185/jcnb.v1i1.136

Yamin, D., Husin, A., & Harun, A. (2020). Distribution of candidemia in Malaysian tertiary care hospital revealed predominance of Candida parapsilosis. *Tropical Biomedicine*, *37*(4), 903–910. https://doi.org/10.47665/tb.37.4.903

Yang, R.-H., Su, J.-H., Shang, J.-J., Wu, Y.-Y., Li, Y., Bao, D.-P., & Yao, Y.-J. (2018). Evaluation of the ribosomal DNA internal transcribed spacer (ITS), specifically ITS1 and ITS2, for the analysis of fungal diversity by deep sequencing. *PLOS ONE*, *13*(10), e0206428. https://doi.org/10.1371/journal.pone.0206428

Yang, Y., Jiang, X., Chai, B., Ma, L., Li, B., Zhang, A., Cole, J. R., Tiedje, J. M., & Zhang, T. (2016). ARGs-OAP: online analysis pipeline for antibiotic resistance genes detection from metagenomic data using an integrated structured ARG-database. *Bioinformatics*, *32*(15), 2346–2351. https://doi.org/10.1093/bioinformatics/btw136

Yee, Y. C., Yong, A. G., Fong, N. Y., Keng, T. K., Wai-Fong, Y., & Kok-Gan, C. (2016). Genome Sequences of Two Multidrug-Resistant Proteus mirabilis Strains Harboring CTX-M-65 Isolated from Malaysia. *Genome Announcements*, *4*(6), 10.1128/genomea.01301-16. https://doi.org/10.1128/genomea.01301-16

Yin, X., Jiang, X. T., Chai, B., Li, L., Yang, Y., Cole, J. R., Tiedje, J. M., & Zhang, T. (2018).

ARGs-OAP v2.0 with an expanded SARG database and Hidden Markov Models for enhancement characterization and quantification of antibiotic resistance genes in environmental metagenomes. *Bioinformatics*, *34*(13), 2263–2270. https://doi.org/10.1093/bioinformatics/bty053

Yoon, E. J., & Jeong, S. H. (2021). Mobile Carbapenemase Genes in Pseudomonas aeruginosa. *Frontiers in Microbiology*, *12*(February). https://doi.org/10.3389/fmicb.2021.614058

Yoon, Y. K., Lee, M. J., Ju, Y., Lee, S. E., Yang, K. S., Sohn, J. W., & Kim, M. J. (2019). Determining the clinical significance of co-colonization of vancomycin-resistant enterococci and methicillin-resistant Staphylococcus aureus in the intestinal tracts of patients in intensive care units: a case–control study. *Annals of Clinical Microbiology and Antimicrobials*, *18*(1), 28. https://doi.org/10.1186/s12941-019-0327-8

Yu, X., Jiang, W., Shi, Y., Ye, H., & Lin, J. (2019). Applications of sequencing technology in clinical microbial infection. *Journal of Cellular and Molecular Medicine*, *23*(11), 7143–7150. https://doi.org/10.1111/jcmm.14624

Yu, Z., Gunn, L., Brennan, E., Reid, R., Wall, P. G., Gaora, P., Hurley, D., Bolton, D., & Fanning, S. (2016). Complete genome sequence of Clostridium estertheticum DSM 8809, a microbe identified in spoiled vacuum packed beef. *Frontiers in Microbiology*, *7*(NOV), 1–10. https://doi.org/10.3389/fmicb.2016.01764

Zahornacký, O., Porubčin, Š., Rovňáková, A., & Jarčuška, P. (2022). Gram-Negative Rods on Inanimate Surfaces of Selected Hospital Facilities and Their Nosocomial Significance. *International Journal of Environmental Research and Public Health*, *19*(10), 6039. https://doi.org/10.3390/ijerph19106039

Zainulabid, U. A., Kamarudin, N., Rus, R. M., Soffian, S. N., Yassim, A. S. M., How, S. H., & Ahmad, H. F. (2022). Hybrid de novo Whole-Genome Assembly and Annotation of SARS-CoV-2 Virus from Nosocomial Infection in Pahang, Malaysia. *International Journal of Infectious Diseases*, *116*, S19. https://doi.org/10.1016/j.ijid.2021.12.046

Zainulabid, U. A., Wei, S., Kamarudin, N., Periyasamy, P., & Ahmad, H. F. (2023). TAPPING THE PATHOGENIC BACTERIA FROM HOSPITAL WATER TAP SYSTEM IN MALAYSIA USING FLONGLE NANOPORE. *International Journal of Infectious Diseases*, *134*, S6. https://doi.org/https://doi.org/10.1016/j.ijid.2023.05.032

Zhang, R.-M., Liu, X., Wang, S.-L., Fang, L.-X., Sun, J., Liu, Y.-H., & Liao, X.-P. (2021). Distribution patterns of antibiotic resistance genes and their bacterial hosts in pig farm wastewater treatment systems and soil fertilized with pig manure. *Science of The Total Environment*, *758*, 143654. https://doi.org/10.1016/j.scitotenv.2020.143654

Zhang, W., Mo, G., Yang, J., Hu, X., Huang, H., Zhu, J., Zhang, P., Xia, H., & Xie, L. (2021). Community structure of environmental microorganisms associated with COVID-19 affected patients. *Aerobiologia*, *37*(3), 575–583. https://doi.org/10.1007/s10453-021-09708-5

Zhang, X.-H., Ahmad, W., Zhu, X.-Y., Chen, J., & Austin, B. (2021). Viable but nonculturable bacteria and their resuscitation: implications for cultivating uncultured marine microorganisms. *Marine Life Science & Technology*, *3*(2), 189–203. https://doi.org/10.1007/s42995-020-00041-3

Zhao, H., Liu, H., Wei, G., Zhang, N., Qiao, H., Gong, Y., Yu, X., Zhou, J., & Wu, Y. (2022). A review on emergency disposal and management of medical waste during the COVID-19 pandemic in China. *Science of the Total Environment*, *810*, 152302. https://doi.org/10.1016/j.scitotenv.2021.152302

Zhou, J., Wu, L., Deng, Y., Zhi, X., Jiang, Y. H., Tu, Q., Xie, J., Van Nostrand, J. D., He, Z., & Yang, Y. (2011). Reproducibility and quantitation of amplicon sequencing-based detection. *ISME Journal*, *5*(8), 1303–1313. https://doi.org/10.1038/ismej.2011.11

Zhou, K., Tao, Y., Han, L., Ni, Y., & Sun, J. (2019). Piperacillin-Tazobactam (TZP) Resistance in Escherichia coli Due to Hyperproduction of TEM-1 β-Lactamase Mediated by the Promoter Pa/Pb. *Frontiers in Microbiology*, *10*(APR), 1–6. https://doi.org/10.3389/fmicb.2019.00833

Zhou, Y. H., Ma, H. X., Dong, Z. Y., & Shen, M. H. (2018). Comamonas kerstersii bacteremia in a patient with acute perforated appendicitis. *Medicine (United States)*, *97*(13), 5–7. https://doi.org/10.1097/MD.0000000000009296

Zhou, Z. C., Feng, W. Q., Han, Y., Zheng, J., Chen, T., Wei, Y. Y., Gillings, M., Zhu, Y. G., & Chen, H. (2018). Prevalence and transmission of antibiotic resistance and microbiota between humans and water environments. *Environment International*, *121*(September 2018), 1155–1161. https://doi.org/10.1016/j.envint.2018.10.032

Zhu, Y., Huang, W. E., & Yang, Q. (2022). Clinical Perspective of Antimicrobial Resistance in Bacteria. *Infection and Drug Resistance*, *Volume 15*(January), 735–746. https://doi.org/10.2147/IDR.S345574

Zhu, Z., Xu, J., & He, F. (2021). Genomic and phylogenetic analysis of multidrug-resistant Achromobacter xylosoxidans ST273 strain MTYH1 co-carrying blaOXA-114g and blaCARB-2 recovered from a wound infection in China. *Journal of Global Antimicrobial Resistance*, *25*, 110–113. https://doi.org/10.1016/j.jgar.2021.03.008

Ziesemer, K. A., Mann, A. E., Sankaranarayanan, K., Schroeder, H., Ozga, A. T., Brandt, B. W., Zaura, E., Waters-Rist, A., Hoogland, M., Salazar-García, D. C., Aldenderfer, M., Speller, C., Hendy, J., Weston, D. A., MacDonald, S. J., Thomas, G. H., Collins, M. J., Lewis, C. M., Hofman, C., & Warinner, C. (2015). Intrinsic challenges in ancient microbiome reconstruction using 16S rRNA gene amplification. *Scientific Reports*, *5*(1), 16498. https://doi.org/10.1038/srep16498

Zimmermann, K. (2017). Microwave as an emerging technology for the treatment of biohazardous waste: A mini-review. *Waste Management and Research*, *35*(5), 471–479. https://doi.org/10.1177/0734242X16684385

Zimmermann, K. (2018). Microwave technologies: An emerging tool for inactivation of biohazardous material in developing countries. *Recycling*, *3*(3). https://doi.org/10.3390/recycling3030034