

Antimicrobial Resistance in Biofilms: Annex A References

1. O'Neill, J., Antimicrobial Resistance: Tackling a crisis for the health and wealth of nations. 2014.
2. Liu, Y.-Y., et al., Emergence of plasmid-mediated colistin resistance mechanism MCR-1 in animals and human beings in China: a microbiological and molecular biological study. *The Lancet Infectious Diseases*, 2016. 16(2): p. 161-168.
[https://doi.org/10.1016/S1473-3099\(15\)00424-7](https://doi.org/10.1016/S1473-3099(15)00424-7)
3. Hudson, J.A., et al., The agri-food chain and antimicrobial resistance: A review. *Trends in Food Science & Technology*, 2017. 69: p. 131-147.
<https://doi.org/10.1016/j.tifs.2017.09.007>
4. van Bunnik, B.A.D. and M.E.J. Woolhouse, Modelling the impact of curtailing antibiotic usage in food animals on antibiotic resistance in humans. *R Soc Open Sci*, 2017. 4(4): p. 161067.
<https://doi.org/10.1098/rsos.161067>
5. Bridier, A., et al., Biofilm-associated persistence of food-borne pathogens. *Food Microbiol*, 2015. 45(Pt B): p. 167-78.
<https://doi.org/10.1016/j.fm.2014.04.015>
6. Balcazar, J.L., J. Subirats, and C.M. Borrego, The role of biofilms as environmental reservoirs of antibiotic resistance. *Frontiers in Microbiology*, 2015. 6: p. 1216.
<https://doi.org/10.3389/fmicb.2015.01216>
7. Khan, S., T.K. Beattie, and C.W. Knapp, Relationship between antibiotic- and disinfectant-resistance profiles in bacteria harvested from tap water. *Chemosphere*, 2016. 152: p. 132-141.
<https://doi.org/10.1016/j.chemosphere.2016.02.086>
8. Li, M.Z., et al., Chronic Exposure to an Environmentally Relevant Triclosan Concentration Induces Persistent Triclosan Resistance but Reversible Antibiotic Tolerance in *Escherichia coli*. *Environmental Science & Technology*, 2019. 53(6): p. 3277-3286.
<https://doi.org/10.1021/acs.est.8b06763>
9. Molin, S. and T. Tolker-Nielsen, Gene transfer occurs with enhanced efficiency in biofilms and induces enhanced stabilisation of the biofilm structure. *Current Opinion in Biotechnology*, 2003. 14(3): p. 255-261.
[https://doi.org/10.1016/S0958-1669\(03\)00036-3](https://doi.org/10.1016/S0958-1669(03)00036-3)
10. Hutchison, M., J. Corry, and R. Madden, A Review of the Impact of Food Processing on Antimicrobial Resistant Bacteria in Secondary Processed Meats and Meat Products. 2019.
<https://doi.org/10.46756/sci.fsa.bxn990>
11. Caporaso, J.G., et al., Ultra-high-throughput microbial community analysis on the Illumina HiSeq and MiSeq platforms. *The ISME journal*, 2012. 6(8): p. 1621-1624.
<https://doi.org/10.1038/ismej.2012.8>

12. Apprill, A., et al., Minor revision to V4 region SSU rRNA 806R gene primer greatly increases detection of SAR11 bacterioplankton. *Aquatic Microbial Ecology*, 2015. 75(2): p. 129-137.
<https://doi.org/10.3354/ame01753>
13. Parada, A.E., D.M. Needham, and J.A. Fuhrman, Every base matters: assessing small subunit rRNA primers for marine microbiomes with mock communities, time series and global field samples. *Environmental microbiology*, 2016. 18(5): p. 1403-1414.
<https://doi.org/10.1111/1462-2920.13023>
14. Walters, W., et al., Improved bacterial 16S rRNA gene (V4 and V4-5) and fungal internal transcribed spacer marker gene primers for microbial community surveys. *Msystems*, 2016. 1(1): p. e00009-15.
<https://doi.org/10.1128/mSystems.00009-15>
15. Wood, D.E., J. Lu, and B. Langmead, Improved metagenomic analysis with Kraken 2. *Genome Biology*, 2019. 20(1): p. 257.
<https://doi.org/10.1186/s13059-019-1891-0>
16. Bushnell, B., BBMap. 2022.
17. Benson, D.A., et al., GenBank. *Nucleic acids research*, 2013. 41(Database issue): p. D36-D42.
<https://doi.org/10.1093/nar/gks1195>
18. Vasimuddin, M., et al. Efficient Architecture-Aware Acceleration of BWA-MEM for Multicore Systems. in 2019 IEEE International Parallel and Distributed Processing Symposium (IPDPS). 2019.
<https://doi.org/10.1109/IPDPS.2019.00041>
19. Nurk, S., et al., metaSPAdes: a new versatile metagenomic assembler. *Genome research*, 2017. 27(5): p. 824-834.
<https://doi.org/10.1101/gr.213959.116>
20. Seemann, T., Prokka: rapid prokaryotic genome annotation. *Bioinformatics*, 2014. 30(14): p. 2068-9.
<https://doi.org/10.1093/bioinformatics/btu153>
21. Wick, R.R., et al., Completing bacterial genome assemblies with multiplex MinION sequencing. *Microbial genomics*, 2017. 3(10): p. e000132-e000132.
<https://doi.org/10.1099/mgen.0.000132>
22. De Coster, W., et al., NanoPack: visualizing and processing long-read sequencing data. *Bioinformatics*, 2018. 34(15): p. 2666-2669.
<https://doi.org/10.1093/bioinformatics/bty149>
23. Kolmogorov, M., et al., metaFlye: scalable long-read metagenome assembly using repeat graphs. *Nature Methods*, 2020. 17(11): p. 1103-1110.
<https://doi.org/10.1038/s41592-020-00971-x>
24. Camacho, C., et al., BLAST+: architecture and applications. *BMC Bioinformatics*, 2009. 10: p. 421.
<https://doi.org/10.1186/1471-2105-10-421>
25. Bertrand, D., et al., Hybrid metagenomic assembly enables high-resolution analysis of resistance determinants and mobile elements in human microbiomes. *Nature Biotechnology*, 2019. 37(8): p. 937-944.
<https://doi.org/10.1038/s41587-019-0191-2>

26. Alcock, B.P., et al., CARD 2020: antibiotic resistome surveillance with the comprehensive antibiotic resistance database. *Nucleic Acids Res*, 2020. 48(D1): p. D517-d525.
27. Pimentel, H., et al., Differential analysis of RNA-seq incorporating quantification uncertainty. *Nat Methods*, 2017. 14(7): p. 687-690.
<https://doi.org/10.1038/nmeth.4324>
28. Boyer, F., et al., obitools: a unix-inspired software package for DNA metabarcoding. *Mol Ecol Resour*, 2016. 16(1): p. 176-82.
<https://doi.org/10.1111/1755-0998.12428>
29. nt Database. 2004, National Library of Medicine (US), National Center for Biotechnology Information: Bethesda (MD).
30. Leplae, R., G. Lima-Mendez, and A. Toussaint, ACLAME: a CLAssification of Mobile genetic Elements, update 2010. *Nucleic acids research*, 2010. 38(Database issue): p. D57-D61.
<https://doi.org/10.1093/nar/gkp938>
31. Beghini, F., et al., Integrating taxonomic, functional, and strain-level profiling of diverse microbial communities with bioBakery 3. *eLife*, 2021. 10: p. e65088.
<https://doi.org/10.7554/eLife.65088>
32. Guarddon, M., et al., Real-time polymerase chain reaction for the quantitative detection of tetA and tetB bacterial tetracycline resistance genes in food. *International Journal of Food Microbiology*, 2011. 146(3): p. 284-289.
<https://doi.org/10.1016/j.ijfoodmicro.2011.02.026>
33. Pei, R., et al., Effect of River Landscape on the sediment concentrations of antibiotics and corresponding antibiotic resistance genes (ARG). *Water Research*, 2006. 40(12): p. 2427-2435.
<https://doi.org/10.1016/j.watres.2006.04.017>
34. Klindworth, A., et al., Evaluation of general 16S ribosomal RNA gene PCR primers for classical and next-generation sequencing-based diversity studies. *Nucleic Acids Research*, 2012. 41(1): p. e1-e1.
<https://doi.org/10.1093/nar/gks808>
35. MRC Epidemiology Unit, U.o.C., NatCen Social Research,, National Diet and Nutrition Survey Years 1-11, 2008-2019. 2021.
36. Medical Research Council, E.a.M.C.U., NatCen Social Research, University of Newcastle upon Tyne, Institute for Ageing and Health, Human Nutrition Research Centre, Medical Research Council, Resource Centre for Human Nutrition Research,, Diet and Nutrition Survey of Infants and Young Children, 2011, E.a.M.C.U. Medical Research Council, NatCen Social Research, University of Newcastle upon Tyne, Institute for Ageing and Health, Human Nutrition Research Centre, Medical Research Council, Resource Centre for Human Nutrition Research,, Editor. 2013.
37. MRC Human Nutrition Research, Food Standards Agency Standard Recipes Database, 1992-2012. 2017.
38. McNeece, G., et al., Array based detection of antibiotic resistance genes in Gram negative bacteria isolated from retail poultry meat in the UK and Ireland. *International journal of food microbiology*, 2014. 179: p. 24-32.
<https://doi.org/10.1016/j.ijfoodmicro.2014.03.019>
39. Jaja, I.F., et al., Molecular characterisation of antibiotic-resistant *Salmonella enterica* isolates recovered from meat in South Africa. *Acta Trop*, 2019. 190: p. 129-136.

<https://doi.org/10.1016/j.actatropica.2018.11.003>

40. Wagner, E.M., et al., Identification of biofilm hotspots in a meat processing environment: Detection of spoilage bacteria in multi-species biofilms. *International Journal of Food Microbiology*, 2020. 328.

<https://doi.org/10.1016/j.ijfoodmicro.2020.108668>

41. Beauchamp, C.S., et al., Sanitizer efficacy against *Escherichia coli* O157:H7 biofilms on inadequately cleaned meat-contact surface materials. *Food Protection Trends*, 2012. 32(4): p. 173-182.

42. Stewart, C., et al., Trends in UK meat consumption: Analysis of data from years 1-11 (2008-09 to 2018-19) of the National Diet and Nutrition Survey rolling programme. *The Lancet Planetary Health*, 2021. 5(10): p. e699-e708.

[https://doi.org/10.1016/S2542-5196\(21\)00228-X](https://doi.org/10.1016/S2542-5196(21)00228-X)

43. Fera, What is the Burden of Antimicrobial Resistance Genes in Selected Ready-to-Eat Foods? . 2021, FSA.

44. Kim, B.R., Y.M. Bae, and S.Y. Lee, Effect of environmental conditions on biofilm formation and related characteristics of *Staphylococcus aureus*. *Journal of Food Safety*, 2016. 36(3): p. 412-422.

<https://doi.org/10.1111/jfs.12263>

45. Pessi, G., et al., The global posttranscriptional regulator RsmA modulates production of virulence determinants and N-acylhomoserine lactones in *Pseudomonas aeruginosa*. *J Bacteriol*, 2001. 183(22): p. 6676-83.

<https://doi.org/10.1128/JB.183.22.6676-6683.2001>

46. Jackson, D.W., et al., Biofilm Formation and Dispersal under the Influence of the Global Regulator CsrA of *Escherichia coli*. *Journal of Bacteriology*, 2002. 184(1): p. 290-301.

<https://doi.org/10.1128/JB.184.1.290-301.2002>

47. Mulcahy, H., et al., The posttranscriptional regulator RsmA plays a role in the interaction between *Pseudomonas aeruginosa* and human airway epithelial cells by positively regulating the type III secretion system. *Infection and immunity*, 2006. 74(5): p. 3012-3015.

<https://doi.org/10.1128/IAI.74.5.3012-3015.2006>

48. Chylkova, T., et al., Susceptibility of *Salmonella* Biofilm and Planktonic Bacteria to Common Disinfectant Agents Used in Poultry Processing. *Journal of Food Protection*, 2017. 80(7): p. 1072-1079.

<https://doi.org/10.4315/0362-028X.JFP-16-393>

49. Iniguez-Moreno, M., M. Gutierrez-Lomeli, and M. Guadalupe Avila-Novoa, Kinetics of biofilm formation by pathogenic and spoilage microorganisms under conditions that mimic the poultry, meat, and egg processing industries. *International Journal of Food Microbiology*, 2019. 303: p. 32-41.

<https://doi.org/10.1016/j.ijfoodmicro.2019.04.012>

50. Kazama, H., et al., Characterization of the antiseptic-resistance gene *qacE* delta 1 isolated from clinical and environmental isolates of *Vibrio parahaemolyticus* and *Vibrio cholerae* non-O1. *FEMS Microbiol Lett*, 1999. 174(2): p. 379-84.

<https://doi.org/10.1111/j.1574-6968.1999.tb13593.x>

51. Heir, E., G. Sundheim, and A.L. Holck, The *Staphylococcus qacH* gene product: a new member of the SMR family encoding multidrug resistance. *FEMS Microbiology Letters*, 1998.

163(1): p. 49-56.

<https://doi.org/10.1111/j.1574-6968.1998.tb13025.x>

52. Slipski, C.J., et al., Characterization of Proteobacterial Plasmid Integron-Encoded *qac* Efflux Pump Sequence Diversity and Quaternary Ammonium Compound Antiseptic Selection in *Escherichia coli* Grown Planktonically and as Biofilms. *Antimicrobial Agents and Chemotherapy*, 2021. 65(10): p. e01069-21.

<https://doi.org/10.1128/AAC.01069-21>

53. Jones, I.A. and L.T. Joshi, Biocide Use in the Antimicrobial Era: A Review. *Molecules*, 2021. 26(8): p. 2276.

<https://doi.org/10.3390/molecules26082276>

54. Han, Y., et al., The impact and mechanism of quaternary ammonium compounds on the transmission of antibiotic resistance genes. *Environmental Science and Pollution Research*, 2019. 26(27): p. 28352-28360.

<https://doi.org/10.1007/s11356-019-05673-2>

55. Culotti, A. and A.I. Packman, *Pseudomonas aeruginosa* promotes *Escherichia coli* biofilm formation in nutrient-limited medium. *PloS one*, 2014. 9(9): p. e107186-e107186.

<https://doi.org/10.1371/journal.pone.0107186>

56. Charimba, G., et al., *Chryseobacterium carnipullorum* sp. nov., isolated from raw chicken. *Int J Syst Evol Microbiol*, 2013. 63(Pt 9): p. 3243-3249.

<https://doi.org/10.1099/ijs.0.049445-0>