

References

1. **Kaper JB, Morris JG, Levine MM.** Cholera. *Clinical Microbiology Reviews* 1995;8:48–86.
2. **Clemens JD, Nair GB, Ahmed T, Qadri F, Holmgren J.** Cholera. *The Lancet* 2017;390:1539–1549.
3. **Centers for Disease Control and Prevention (CDC).** General information | Cholera | CDC. <https://www.cdc.gov/cholera/general/index.html> (2018, accessed 14 September 2018).
4. **Ali M, Nelson AR, Lopez AL, Sack DA.** Updated global burden of cholera in endemic countries. *PLoS Neglected Tropical Diseases* 2015;9:e0003832.
5. **Ali M, Lopez AL, You YA, Kim YE, Sah B, et al.** The global burden of cholera. *Bulletin of the World Health Organization* 2012;90:209-218A.
6. **World Health Organization.** Cholera. *Cholera*. <https://www.who.int/news-room/fact-sheets/detail/cholera> (2019, accessed 21 June 2020).
7. **Kim J-H, Mogasale V, Burgess C, Wierzba TF.** Impact of oral cholera vaccines in cholera-endemic countries: A mathematical modeling study. *Vaccine* 2016;34:2113–2120.
8. **Talavera A, Pérez EM.** Is cholera disease associated with poverty? *Journal of Infection in Developing Countries* 2009;3:408–411.
9. **World Health Organization.** Ending cholera: A global roadmap to 2030. <http://www.who.int/cholera/publications/global-roadmap.pdf> (2017, accessed 14 September 2018).
10. **Centers for Disease Control and Prevention (CDC).** Rehydration therapy | Treatment | Cholera | CDC. <https://www.cdc.gov/cholera/treatment/rehydration-therapy.html> (2018, accessed 23 March 2020).
11. **Centers for Disease Control and Prevention (CDC).** Cholera - *Vibrio cholerae* infection | Recommendations for the use of antibiotics for the treatment of cholera | Cholera | CDC. <https://www.cdc.gov/cholera/treatment/antibiotic-treatment.html> (2015, accessed 18 March 2018).

12. **Lindenbaum J, Greenough WB, Islam MR.** Antibiotic therapy of cholera in children. *Bulletin of the World Health Organization* 1967;37:529–538.
13. **World Health Organization.** *Cholera outbreak | Assessing the outbreak response and improving preparedness.* World Health Organization; 2004.
14. **Pan American Health Organisation (PAHO).** *Recommendations for clinical management of cholera.* Washington (DC); 2010.
15. **Nelson EJ, Klarman M.** *Cholera outbreak training and shigellosis program.* 2nd ed. icddr,b; 2018.
16. **Médecins Sans Frontières.** *Cholera guidelines.* 2nd ed. France; 2004.
17. **World Health Organization.** Cholera vaccines: WHO position paper - August 2017. *Weekly Epidemiological Record* 2017;92:477–500.
18. **Levine MM, Herrington D, Losonsky G, Tall B, Kaper JB, et al.** Safety, immunogenicity, and efficacy of recombinant live oral cholera vaccines, CVD 103 and CVD 103-HgR. *The Lancet* 1988;332:467–470.
19. **Ketley JM, Michalski J, Galen J, Levine MM, Kaper JB.** Construction of genetically marked *Vibrio cholerae* O1 vaccine strains. *FEMS Microbiology Letters* 1993;111:15–21.
20. **Shaikh H, Lynch J, Kim J, Excler J-L.** Current and future cholera vaccines. *Vaccine* 2020;38:A118–A126.
21. **Qadri F, Azad AK, Flora MS, Khan AI, Islam MT, et al.** Emergency deployment of oral cholera vaccine for the Rohingya in Bangladesh. *The Lancet* 2018;391:1877–1879.
22. **Hubbard TP, Billings G, Dörr T, Sit B, Warr AR, et al.** A live vaccine rapidly protects against cholera in an infant rabbit model. *Science Translational Medicine* 2018;10:eaap8423.
23. **Fakoya B, Sit B, Waldor MK.** Transient intestinal colonization by a live-attenuated oral cholera vaccine induces protective immune responses in streptomycin-treated mice. *Journal of Bacteriology.* Epub ahead of print 15 June 2020. DOI: 10.1128/JB.00232-20.

24. **Sit B, Zhang T, Fakoya B, Akter A, Biswas R, et al.** Oral immunization with a probiotic cholera vaccine induces broad protective immunity against *Vibrio cholerae* colonization and disease in mice. *PLoS Neglected Tropical Diseases* 2019;13:e0007417.
25. **Piarroux R, Barraïis R, Faucher B, Haus R, Piarroux M, et al.** Understanding the cholera epidemic, Haiti. *Emerging Infectious Diseases* 2011;17:1161–1168.
26. **Chin C-S, Sorenson J, Harris JB, Robins WP, Charles RC, et al.** The origin of the Haitian cholera outbreak strain. *New England Journal of Medicine* 2011;364:33–42.
27. **Hendriksen RS, Price LB, Schupp JM, Gillece JD, Kaas RS, et al.** Population genetics of *Vibrio cholerae* from Nepal in 2010: Evidence on the origin of the Haitian outbreak. *mBio* 2011;2:e00157-11.
28. **Camacho A, Bouhenia M, Alyusfi R, Alkohlani A, Naji MAM, et al.** Cholera epidemic in Yemen, 2016–18: An analysis of surveillance data. *The Lancet Global Health* 2018;6:e680–e690.
29. **Colwell RR.** Global climate and infectious disease: The cholera paradigm. *Science* 1996;274:2025–2031.
30. **Snow J.** *On the mode of communication of cholera.* 2nd ed. England: John Churchill; 1855.
31. **Bynum W.** In retrospect: On the mode of communication of cholera. *Nature* 2013;495:169–170.
32. **Centers for Disease Control and Prevention (CDC).** Diagnosis and detection | Cholera | CDC. <https://www.cdc.gov/cholera/diagnosis.html> (2018, accessed 25 June 2020).
33. **Howard-Jones N.** Robert Koch and the cholera vibrio: a centenary. *British Medical Journal (Clinical Research Edition)* 1984;288:379–381.
34. **Pacini F.** Osservazioni microscopiche e deduzioni patologiche sul cholera asiatico. *Gazzetta Medica Italiana* 1854;397–405.
35. **Skerman VBD, McGowan V, Sneath PHA.** Approved lists of bacterial names. *International Journal of Systematic and Evolutionary Microbiology*, 1980;30:225–420.

36. **Pollitzer R, Swaroop S, Burrows W, World Health Organization.** *Cholera*. World Health Organization. <https://apps.who.int/iris/handle/10665/41711> (1959, accessed 2 October 2019).
37. **Shimada T, Arakawa E, Itoh K, Okitsu T, Matsushima A, et al.** Extended serotyping scheme for *Vibrio cholerae*. *Current Microbiology* 1994;28:175–178.
38. **Colwell RR.** Polyphasic taxonomy of the genus *Vibrio*: Numerical taxonomy of *Vibrio cholerae*, *Vibrio parahaemolyticus*, and related *Vibrio* species. *Journal of Bacteriology* 1970;104:410–433.
39. **Davis GH, Park RW.** A taxonomic study of certain bacteria currently classified as *Vibrio* species. *Journal of General Microbiology* 1962;27:101–119.
40. **Furniss AL, Lee JV, Donovan TJ.** *The Vibrios*. London: His Majesty's Stationery Office; 1978.
41. **Gardner AD, Venkatraman KV.** The antigens of the cholera group of Vibrios. *Journal of Hygiene (London)* 1935;35:262–282.
42. **Colwell RR, Kaper J, Joseph SW.** *Vibrio cholerae*, *Vibrio parahaemolyticus*, and other vibrios: occurrence and distribution in Chesapeake Bay. *Science* 1977;198:394–396.
43. **del Refugio Castañeda Chávez M, Sedas VP, Orrantia Borunda E, Reynoso FL.** Influence of water temperature and salinity on seasonal occurrences of *Vibrio cholerae* and enteric bacteria in oyster-producing areas of Veracruz, México. *Marine Pollution Bulletin* 2005;50:1641–1648.
44. **Almagro-Moreno S, Taylor RK.** Cholera: Environmental reservoirs and impact on disease transmission. *Microbiology Spectrum* 2013;1:OH-0003-2012.
45. **Huq A, West PA, Small EB, Huq MI, Colwell RR.** Influence of water temperature, salinity, and pH on survival and growth of toxigenic *Vibrio cholerae* serovar 01 associated with live copepods in laboratory microcosms. *Applied and Environmental Microbiology* 1984;48:420–424.
46. **Singleton FL, Attwell R, Jangi S, Colwell RR.** Effects of temperature and salinity on *Vibrio cholerae* growth. *Applied and Environmental Microbiology* 1982;44:1047–1058.

47. **Meibom KL, Li XB, Nielsen AT, Wu C-Y, Roseman S, et al.** The *Vibrio cholerae* chitin utilization program. *Proceedings of the National Academy of Sciences of the United States of America* 2004;101:2524–2529.
48. **Meibom KL, Blokesch M, Dolganov NA, Wu C-Y, Schoolnik GK.** Chitin induces natural competence in *Vibrio cholerae*. *Science* 2005;310:1824–1827.
49. **Rowe-Magnus DA, Guerout A-M, Biskri L, Bouige P, Mazel D.** Comparative analysis of superintegrons: Engineering extensive genetic diversity in the Vibrionaceae. *Genome Research* 2003;13:428–442.
50. **Borgeaud S, Metzger LC, Scignari T, Blokesch M.** The type VI secretion system of *Vibrio cholerae* fosters horizontal gene transfer. *Science* 2015;347:63–67.
51. **Matthey N, Stutzmann S, Stoudmann C, Guex N, Iseli C, et al.** Neighbor predation linked to natural competence fosters the transfer of large genomic regions in *Vibrio cholerae*. *eLife* 2019;8:e48212.
52. **Waldor MK, Mekalanos JJ.** Lysogenic conversion by a filamentous phage encoding cholera toxin. *Science* 1996;272:1910–1914.
53. **Carraro N, Matteau D, Luo P, Rodrigue S, Burrus V.** The master activator of IncA/C conjugative plasmids stimulates genomic islands and multidrug resistance dissemination. *PLoS Genetics* 2014;10:pgen.1004714.
54. **Chun J, Grim CJ, Hasan NA, Lee JH, Choi SY, et al.** Comparative genomics reveals mechanism for short-term and long-term clonal transitions in pandemic *Vibrio cholerae*. *Proceedings of the National Academy of Sciences of the United States of America* 2009;106:15442–15447.
55. **Karaolis DKR, Johnson JA, Bailey CC, Boedeker EC, Kaper JB, et al.** A *Vibrio cholerae* pathogenicity island associated with epidemic and pandemic strains. *Proceedings of the National Academy of Sciences of the United States of America* 1998;95:3134–3139.

56. **Wozniak RAF, Fouts DE, Spagnoletti M, Colombo MM, Ceccarelli D, et al.** Comparative ICE genomics: Insights into the evolution of the SXT/R391 family of ICEs. *PLoS Genetics* 2009;5:e1000786.
57. **Trucksis M, Michalski J, Deng YK, Kaper JB.** The *Vibrio cholerae* genome contains two unique circular chromosomes. *Proceedings of the National Academy of Sciences of the United States of America* 1998;95:14464–14469.
58. **Val M-E, Marbouty M, de Lemos Martins F, Kennedy SP, Kemble H, et al.** A checkpoint control orchestrates the replication of the two chromosomes of *Vibrio cholerae*. *Science Advances* 2016;2:sciadv.1501914.
59. **Heidelberg JF, Eisen JA, Nelson WC, Clayton RA, Gwinn ML, et al.** DNA sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*. *Nature* 2000;406:477–483.
60. **Ramachandran R, Ciaccia PN, Filsuf TA, Jha JK, Chattoraj DK.** Chromosome 1 licenses chromosome 2 replication in *Vibrio cholerae* by doubling the *crtS* gene dosage. *PLoS Genetics* 2018;14:e1007426.
61. **Sozhamannan S, Waldminghaus T.** Exception to the exception rule: synthetic and naturally occurring single chromosome *Vibrio cholerae*. *Environmental Microbiology* Epub ahead of print 2020. DOI: 10.1111/1462-2920.15002.
62. **Johnson SL, Khiani A, Bishop-Lilly KA, Chapman C, Patel M, et al.** Complete genome assemblies for two single-chromosome *Vibrio cholerae* isolates, strains 1154-74 (serogroup O49) and 10432-62 (serogroup O27). *Genome Announcements* 2015;3:genomeA.00462-15.
63. **Bruhn M, Schindler D, Kemter FS, Wiley MR, Chase K, et al.** Functionality of two origins of replication in *Vibrio cholerae* strains with a single chromosome. *Frontiers in Microbiology* 2018;9:fmicb.2018.02932.
64. **Das B, Chattoraj DK.** Commentary: Functionality of two origins of replication in *Vibrio cholerae* strains with a single chromosome. *Frontiers in Microbiology* 2019;10:fmicb.2019.01314.

65. **Mazel D, Dychinco B, Webb VA, Davies J.** A distinctive class of integron in the *Vibrio cholerae* genome. *Science* 1998;280:605–608.
66. **Kirkup BC, Chang L, Chang S, Gevers D, Polz MF.** *Vibrio* chromosomes share common history. *BMC Microbiology* 2010;10:137.
67. **De SN.** Enterotoxicity of bacteria-free culture-filtrate of *Vibrio cholerae*. *Nature* 1959;183:1533–1534.
68. **Kaper JB, Moseley SL, Falkow S.** Molecular characterization of environmental and nontoxicogenic strains of *Vibrio cholerae*. *Infection and Immunity* 1981;32:661–667.
69. **Moseley SL, Falkow S.** Nucleotide sequence homology between the heat-labile enterotoxin gene of *Escherichia coli* and *Vibrio cholerae* deoxyribonucleic acid. *Journal of Bacteriology* 1980;144:444–446.
70. **Sporecke I, Castro D, Mekalanos JJ.** Genetic mapping of *Vibrio cholerae* enterotoxin structural genes. *Journal of Bacteriology* 1984;157:253–261.
71. **Mekalanos JJ.** Duplication and amplification of toxin genes in *Vibrio cholerae*. *Cell* 1983;35:253–263.
72. **Zhang R-G, Scott DL, Westbrook ML, Nance S, Spangler BD, et al.** The three-dimensional crystal structure of cholera toxin. *Journal of Molecular Biology* 1995;251:563–573.
73. **Hardy SJ, Holmgren J, Johansson S, Sanchez J, Hirst TR.** Coordinated assembly of multisubunit proteins: Oligomerization of bacterial enterotoxins *in vivo* and *in vitro*. *Proceedings of the National Academy of Sciences of the United States of America* 1988;85:7109–7113.
74. **Sandkvist M, Michel LO, Hough LP, Morales VM, Bagdasarian M, et al.** General secretion pathway (*eps*) genes required for toxin secretion and outer membrane biogenesis in *Vibrio cholerae*. *Journal of Bacteriology* 1997;179:6994.
75. **Sandkvist M, Morales V, Bagdasarian M.** A protein required for secretion of cholera toxin through the outer membrane of *Vibrio cholerae*. *Gene* 1993;123:81–86.

76. **Sikora AE, Zielke RA, Lawrence DA, Andrews PC, Sandkvist M.** Proteomic analysis of the *Vibrio cholerae* type II secretome reveals new proteins, including three related serine proteases. *Journal of Biological Chemistry* 2011;286:16555–16566.
77. **Naha A, Mandal RS, Samanta P, Saha RN, Shaw S, et al.** Deciphering the possible role of *ctxB7* allele on higher production of cholera toxin by Haitian variant *Vibrio cholerae* O1. *PLoS Neglected Tropical Diseases* 2020;14:e0008128.
78. **Holmgren J, Lönnroth I, Månsson J, Svennerholm L.** Interaction of cholera toxin and membrane G_{M1} ganglioside of small intestine. *Proceedings of the National Academy of Sciences of the United States of America* 1975;72:2520–2524.
79. **Merritt EA, Sarfaty S, van den Akker F, L'Hoir C, Martial JA, et al.** Crystal structure of cholera toxin B-pentamer bound to receptor G_{M1} pentasaccharide. *Protein Science* 1994;3:166–175.
80. **Heim JB, Hodnik V, Heggelund JE, Anderluh G, Krenzel U.** Crystal structures of cholera toxin in complex with fucosylated receptors point to importance of secondary binding site. *Scientific Reports* 2019;9:12243.
81. **Heggelund JE, Burschowsky D, Bjørnstad VA, Hodnik V, Anderluh G, et al.** High-resolution crystal structures elucidate the molecular basis of cholera blood group dependence. *PLoS Pathogens* 2016;12:e1005567.
82. **Wands AM, Fujita A, McCombs JE, Cervin J, Dedic B, et al.** Fucosylation and protein glycosylation create functional receptors for cholera toxin. *eLife* 2015;4:e09545.
83. **Chinnapen DJ-F, Chinnapen H, Saslowsky D, Lencer WI.** Rafting with cholera toxin: endocytosis and trafficking from plasma membrane to ER. *FEMS Microbiology Letters* 2007;266:129–137.
84. **Wernick NLB, Chinnapen DJ-F, Cho JA, Lencer WI.** Cholera toxin: An intracellular journey into the cytosol by way of the endoplasmic reticulum. *Toxins (Basel)* 2010;2:310–325.

85. **Fujinaga Y, Wolf AA, Rodighiero C, Wheeler H, Tsai B, et al.** Gangliosides that associate with lipid rafts mediate transport of cholera and related toxins from the plasma membrane to endoplasmic reticulum. *Molecular Biology of the Cell* 2003;14:4783–4793.
86. **Tsai B, Rapoport TA.** Unfolded cholera toxin is transferred to the ER membrane and released from protein disulfide isomerase upon oxidation by Ero1. *Journal of Cell Biology* 2002;159:207–216.
87. **Cassel D, Pfeuffer T.** Mechanism of cholera toxin action: Covalent modification of the guanyl nucleotide-binding protein of the adenylate cyclase system. *Proceedings of the National Academy of Sciences of the United States of America* 1978;75:2669–2673.
88. **Gill DM, Meren R.** ADP-ribosylation of membrane proteins catalyzed by cholera toxin: basis of the activation of adenylate cyclase. *Proceedings of the National Academy of Sciences of the United States of America* 1978;75:3050–3054.
89. **Holmgren J.** Actions of cholera toxin and the prevention and treatment of cholera. *Nature* 1981;292:413–417.
90. **Gabriel SE, Brigman KN, Koller BH, Boucher RC, Stutts MJ.** Cystic fibrosis heterozygote resistance to cholera toxin in the cystic fibrosis mouse model. *Science* 1994;266:107–109.
91. **Taylor RK, Miller VL, Furlong DB, Mekalanos JJ.** Use of *phoA* gene fusions to identify a pilus colonization factor coordinately regulated with cholera toxin. *Proceedings of the National Academy of Sciences of the United States of America* 1987;84:2833–2837.
92. **Herrington DA, Hall RH, Losonsky G, Mekalanos JJ, Taylor RK, et al.** Toxin, toxin-coregulated pili, and the *toxR* regulon are essential for *Vibrio cholerae* pathogenesis in humans. *Journal of Experimental Medicine* 1988;168:1487–1492.
93. **Boyd EF, Waldor MK.** Alternative mechanism of cholera toxin acquisition by *Vibrio cholerae*: Generalized transduction of CTX Φ by bacteriophage CP-T1. *Infection and Immunity* 1999;67:5898–5905.

94. **Campos J, Martínez E, Izquierdo Y, Fando R.** VEJ ϕ , a novel filamentous phage of *Vibrio cholerae* able to transduce the cholera toxin genes. *Microbiology* 2010;156:108–115.
95. **McLeod SM, Waldor MK.** Characterization of XerC- and XerD-dependent CTX phage integration in *Vibrio cholerae*. *Molecular Microbiology* 2004;54:935–947.
96. **Huber KE, Waldor MK.** Filamentous phage integration requires the host recombinases XerC and XerD. *Nature* 2002;417:656.
97. **Feng L, Reeves PR, Lan R, Ren Y, Gao C, et al.** A recalibrated molecular clock and independent origins for the cholera pandemic clones. *PLoS ONE* 2008;3:e4053.
98. **Grim CJ, Hasan NA, Taviani E, Haley B, Chun J, et al.** Genome sequence of hybrid *Vibrio cholerae* O1 MJ-1236, B-33, and CIRS101 and comparative genomics with *V. cholerae*. *Journal of Bacteriology* 2010;192:3524–3533.
99. **McLeod SM, Kimsey HH, Davis BM, Waldor MK.** CTX ϕ and *Vibrio cholerae*: Exploring a newly recognized type of phage–host cell relationship. *Molecular Microbiology* 2005;57:347–356.
100. **Moyer KE, Kimsey HH, Waldor MK.** Evidence for a rolling-circle mechanism of phage DNA synthesis from both replicative and integrated forms of CTX ϕ . *Molecular Microbiology* 2001;41:311–323.
101. **Davis BM, Waldor MK.** CTX ϕ contains a hybrid genome derived from tandemly integrated elements. *Proceedings of the National Academy of Sciences of the United States of America* 2000;97:8572–8577.
102. **Miller V, Mekalanos J.** Synthesis of cholera toxin is positively regulated at the transcriptional level by *toxR*. *Proceedings of the National Academy of Sciences of the United States of America* 1984;81:3471–3475.
103. **Holmgren J, Svennerholm A-M.** Mechanisms of disease and immunity in cholera: A review. *Journal of Infectious Diseases* 1977;136:S105–S112.
104. **Almagro-Moreno S, Pruss K, Taylor RK.** Intestinal colonization dynamics of *Vibrio cholerae*. *PLoS Pathogens* 2015;11:e1004787.

105. **Miller VL, Taylor RK, Mekalanos JJ.** Cholera toxin transcriptional activator ToxR is a transmembrane DNA binding protein. *Cell* 1987;48:271–279.
106. **Higgins DE, Nazareno E, DiRita VJ.** The virulence gene activator ToxT from *Vibrio cholerae* is a member of the AraC family of transcriptional activators. *Journal of Bacteriology* 1992;174:6974–6980.
107. **Withey JH, DiRita VJ.** The toxbox: specific DNA sequence requirements for activation of *Vibrio cholerae* virulence genes by ToxT. *Molecular Microbiology* 2006;59:1779–1789.
108. **Miller VL, Mekalanos JJ.** Genetic analysis of the cholera toxin-positive regulatory gene *toxR*. *Journal of Bacteriology* 1985;163:580–585.
109. **DiRita VJ, Parsot C, Jander G, Mekalanos JJ.** Regulatory cascade controls virulence in *Vibrio cholerae*. *Proceedings of the National Academy of Sciences of the United States of America* 1991;88:5403–5407.
110. **Ottemann KM, Mekalanos JJ.** The ToxR protein of *Vibrio cholerae* forms homodimers and heterodimers. *Journal of Bacteriology* 1996;178:156–162.
111. **Withey JH, DiRita VJ.** Activation of both *acfA* and *acfD* transcription by *Vibrio cholerae* ToxT requires binding to two centrally located DNA sites in an inverted repeat conformation. *Molecular Microbiology* 2005;56:1062–1077.
112. **Higgins DE, DiRita VJ.** Transcriptional control of *toxT*, a regulatory gene in the ToxR regulon of *Vibrio cholerae*. *Molecular Microbiology* 1994;14:17–29.
113. **Häse CC, Mekalanos JJ.** TcpP protein is a positive regulator of virulence gene expression in *Vibrio cholerae*. *Proceedings of the National Academy of Sciences of the United States of America* 1998;95:730–734.
114. **Carroll PA, Tashima KT, Rogers MB, DiRita VJ, Calderwood SB.** Phase variation in *tcpH* modulates expression of the ToxR regulon in *Vibrio cholerae*. *Molecular Microbiology* 1997;25:1099–1111.

115. **Beck NA, Krukoni ES, DiRita VJ.** TcpH influences virulence gene expression in *Vibrio cholerae* by inhibiting degradation of the transcription activator TcpP. *Journal of Bacteriology* 2004;186:8309–8316.
116. **Skorupski K, Taylor RK.** A new level in the *Vibrio cholerae* ToxR virulence cascade: AphA is required for transcriptional activation of the *tcpPH* operon. *Molecular Microbiology* 1999;31:763–771.
117. **Behari J, Stagon L, Calderwood SB.** *pepA*, a gene mediating pH regulation of virulence genes in *Vibrio cholerae*. *Journal of Bacteriology* 2001;183:178–188.
118. **Gupta S, Chowdhury R.** Bile affects production of virulence factors and motility of *Vibrio cholerae*. *Infection and Immunity* 1997;65:1131–1134.
119. **Yang M, Liu Z, Hughes C, Stern AM, Wang H, et al.** Bile salt–induced intermolecular disulfide bond formation activates *Vibrio cholerae* virulence. *Proceedings of the National Academy of Sciences of the United States of America* 2013;110:2348–2353.
120. **Bina XR, Taylor DL, Vikram A, Ante VM, Bina JE.** *Vibrio cholerae* ToxR downregulates virulence factor production in response to cyclo(Phe-Pro). *mBio* 2013;4:e00366-13.
121. **D’Haeze W.** Three-way regulation of cholera toxin production. *Genome Biology* 2002;3:reports0056.
122. **Tischler AD, Lee SH, Camilli A.** The *Vibrio cholerae* *vieSAB* locus encodes a pathway contributing to cholera toxin production. *Journal of Bacteriology* 2002;184:4104–4113.
123. **Ayala JC, Wang H, Benitez JA, Silva AJ.** Molecular basis for the differential expression of the global regulator VieA in *Vibrio cholerae* biotypes directed by H-NS, LeuO and quorum sensing. *Molecular Microbiology* 2018;107:330–343.
124. **Conner JG, Zamorano-Sánchez D, Park JH, Sondermann H, Yildiz FH.** The ins and outs of cyclic di-GMP signaling in *Vibrio cholerae*. *Current Opinion in Microbiology* 2017;36:20–29.

125. **Tamayo R, Schild S, Pratt JT, Camilli A.** Role of cyclic di-GMP during El Tor biotype *Vibrio cholerae* infection: Characterization of the *in vivo*-induced cyclic di-GMP phosphodiesterase CdpA. *Infection and Immunity* 2008;76:1617–1627.
126. **Sakib SN, Reddi G, Almagro-Moreno S.** Environmental role of pathogenic traits in *Vibrio cholerae*. *Journal of Bacteriology* 2018;200:e00795-17.
127. **Schild S, Tamayo R, Nelson EJ, Qadri F, Calderwood SB, et al.** Genes induced late in infection increase fitness of *Vibrio cholerae* after release into the environment. *Cell Host and Microbe* 2007;2:264–277.
128. **LaRocque RC, Harris JB, Dziejman M, Li X, Khan AI, et al.** Transcriptional profiling of *Vibrio cholerae* recovered directly from patient specimens during early and late stages of human infection. *Infection and Immunity* 2005;73:4488–4493.
129. **Bina J, Zhu J, Dziejman M, Faruque S, Calderwood S, et al.** ToxR regulon of *Vibrio cholerae* and its expression in vibrios shed by cholera patients. *Proceedings of the National Academy of Sciences of the United States of America* 2003;100:2801–2806.
130. **Kovacikova G, Skorupski K.** The alternative sigma factor σ^E plays an important role in intestinal survival and virulence in *Vibrio cholerae*. *Infection and Immunity* 2002;70:5355–5362.
131. **Merrell DS, Tischler AD, Lee SH, Camilli A.** *Vibrio cholerae* requires *rpoS* for efficient intestinal colonization. *Infection and Immunity* 2000;68:6691–6696.
132. **Silva AJ, Benitez JA.** *Vibrio cholerae* biofilms and cholera pathogenesis. *PLoS Neglected Tropical Diseases* 2016;10:e0004330.
133. **Dziejman M, Balon E, Boyd D, Fraser CM, Heidelberg JF, et al.** Comparative genomic analysis of *Vibrio cholerae*: Genes that correlate with cholera endemic and pandemic disease. *Proceedings of the National Academy of Sciences of the United States of America* 2002;99:1556–1561.
134. **Jermyn WS, Boyd EF.** Characterization of a novel *Vibrio* pathogenicity island (VPI-2) encoding neuraminidase (*nanH*) among toxigenic *Vibrio cholerae* isolates. *Microbiology* 2002;148:3681–3693.

135. **Burnet FM, Stone JD.** The receptor-destroying enzyme of *V. cholerae*. *Australian Journal of Experimental Biology and Medical Science* 1947;25:227–233.
136. **Vimr ER, Lawrisuk L, Galen J, Kaper JB.** Cloning and expression of the *Vibrio cholerae* neuraminidase gene *nanH* in *Escherichia coli*. *Journal of Bacteriology* 1988;170:1495–1504.
137. **Svennerholm L.** Chromatographic separation of human brain gangliosides. *Journal of Neurochemistry* 1963;10:613–623.
138. **Almagro-Moreno S, Boyd EF.** Sialic acid catabolism confers a competitive advantage to pathogenic *Vibrio cholerae* in the mouse intestine. *Infection and Immunity* 2009;77:3807–3816.
139. **Labbate M, Orata FD, Petty NK, Jayatilleke ND, King WL, et al.** A genomic island in *Vibrio cholerae* with VPI-1 site-specific recombination characteristics contains CRISPR-Cas and type VI secretion modules. *Scientific Reports* 2016;6:36891.
140. **Rapa RA, Islam A, Monahan LG, Mutreja A, Thomson N, et al.** A genomic island integrated into *recA* of *Vibrio cholerae* contains a divergent *recA* and provides multi-pathway protection from DNA damage. *Environmental Microbiology* 2015;17:1090–1102.
141. **Murphy RA, Boyd EF.** Three pathogenicity islands of *Vibrio cholerae* can excise from the chromosome and form circular intermediates. *Journal of Bacteriology* 2008;190:636–647.
142. **Davies BW, Bogard RW, Young TS, Mekalanos JJ.** Coordinated regulation of accessory genetic elements produces cyclic di-nucleotides for *V. cholerae* virulence. *Cell* 2012;149:358–370.
143. **Imamura D, Morita M, Sekizuka T, Mizuno T, Takemura T, et al.** Comparative genome analysis of VSP-II and SNPs reveals heterogenic variation in contemporary strains of *Vibrio cholerae* O1 isolated from cholera patients in Kolkata, India. *PLoS Neglected Tropical Diseases* 2017;11:e0005386.

144. **Blokesch M, Schoolnik GK.** Serogroup conversion of *Vibrio cholerae* in aquatic reservoirs. *PLoS Pathogens* 2007;3:e81.
145. **Bik EM, Bunschoten AE, Gouw RD, Mooi FR.** Genesis of the novel epidemic *Vibrio cholerae* O139 strain: Evidence for horizontal transfer of genes involved in polysaccharide synthesis. *The EMBO Journal* 1995;14:209–216.
146. **Albert MJ, Alam K, Ansaruzzaman M, Qadri F, Sack RB.** Lack of cross-protection against diarrhea due to *Vibrio cholerae* O139 (Bengal strain) after oral immunization of rabbits with *V. cholerae* O1 vaccine strain CVD103-HgR. *Journal of Infectious Diseases* 1994;169:230–231.
147. **Davies J, Davies D.** Origins and evolution of antibiotic resistance. *Microbiology and Molecular Biology Reviews* 2010;74:417–433.
148. **Carraro N, Rivard N, Ceccarelli D, Colwell RR, Burrus V.** IncA/C conjugative plasmids mobilize a new family of multidrug resistance islands in clinical *Vibrio cholerae* non-O1/non-O139 isolates from Haiti. *mBio* 2016;7:e00509-16.
149. **Folster JP, Katz L, McCullough A, Parsons MB, Knipe K, et al.** Multidrug-resistant IncA/C plasmid in *Vibrio cholerae* from Haiti. *Emerging Infectious Diseases* 2014;20:1951–1952.
150. **Fonseca ÉL, dos Santos Freitas F, Vieira VV, Vicente ACP.** New *qnr* gene cassettes associated with superintegron repeats in *Vibrio cholerae* O1. *Emerging Infectious Diseases* 2008;14:1129–1131.
151. **Petroni A, Melano RG, Saka HA, Garutti A, Mange L, et al.** CARB-9, a carbenicillinase encoded in the VCR region of *Vibrio cholerae* non-O1, non-O139 belongs to a family of cassette-encoded β -lactamases. *Antimicrobial Agents and Chemotherapy* 2004;48:4042–4046.
152. **Melano R, Petroni A, Garutti A, Saka HA, Mange L, et al.** New carbenicillin-hydrolyzing β -lactamase (CARB-7) from *Vibrio cholerae* non-O1, non-O139 strains encoded by the VCR region of the *V. cholerae* genome. *Antimicrobial Agents and Chemotherapy* 2002;46:2162–2168.

153. **Kim HB, Wang M, Ahmed S, Park CH, LaRocque RC, et al.** Transferable quinolone resistance in *Vibrio cholerae*. *Antimicrobial Agents and Chemotherapy* 2010;54:799–803.
154. **Fonseca ÉL da, Vicente ACP.** Spread of the *qnrVC* quinolone resistance determinant in *Vibrio cholerae*. *Antimicrobial Agents and Chemotherapy* 2011;55:457–457.
155. **Zhou Y, Yu L, Li J, Zhang L, Tong Y, et al.** Accumulation of mutations in DNA gyrase and topoisomerase IV genes contributes to fluoroquinolone resistance in *Vibrio cholerae* O139 strains. *International Journal of Antimicrobial Agents* 2013;42:72–75.
156. **Waldor MK, Tschäpe H, Mekalanos JJ.** A new type of conjugative transposon encodes resistance to sulfamethoxazole, trimethoprim, and streptomycin in *Vibrio cholerae* O139. *Journal of Bacteriology* 1996;178:4157–4165.
157. **Towner KJ, Pearson NJ, Mhalu FS, O’Grady F.** Resistance to antimicrobial agents of *Vibrio cholerae* El Tor strains isolated during the fourth cholera epidemic in the United Republic of Tanzania. *Bulletin of the World Health Organization* 1980;58:747–751.
158. **Weill F-X, Domman D, Njamkepo E, Tarr C, Rauzier J, et al.** Genomic history of the seventh pandemic of cholera in Africa. *Science* 2017;358:785–789.
159. **Kelly H.** The classical definition of a pandemic is not elusive. *Bulletin of the World Health Organization* 2011;89:540–541.
160. **Last J.** *A dictionary of epidemiology*. 4th ed. New York, NY: Oxford University Press; 2001.
161. **Barua D.** The global epidemiology of cholera in recent years. *Proceedings of the Royal Society of Medicine* 1972;65:423–428.
162. **Devault AM, Golding GB, Waglechner N, Enk JM, Kuch M, et al.** Second-pandemic strain of *Vibrio cholerae* from the Philadelphia cholera outbreak of 1849. *New England Journal of Medicine* 2014;370:334–340.
163. **Salim A, Lan R, Reeves PR.** *Vibrio cholerae* pathogenic clones. *Emerging Infectious Diseases* 2005;11:1758–1760.

164. **Cvjetanovic B, Barua D.** The seventh pandemic of cholera. *Nature* 1972;239:137–138.
165. **World Health Organization Regional Office for the Western Pacific.** *Meeting for the Exchange of Information on El Tor Vibrio Paracholera, Manila, Philippines, 16-19 April 1962 : final report.* Technical Report; Manila: WHO Regional Office for the Western Pacific. <https://iris.wpro.who.int/handle/10665.1/5806> (1962, accessed 30 June 2020).
166. **De Moor EC.** Paracholera (El Tor): Enteritis choleraeformis El Tor van Loghem. *Bulletin of the World Health Organization* 1949;2:5–17.
167. **Rebaudet S, Sudre B, Faucher B, Piarroux R.** Environmental determinants of cholera outbreaks in inland Africa: A systematic review of main transmission foci and propagation routes. *Journal of Infectious Diseases* 2013;208:S46–S54.
168. **Kumate J, Sepúlveda J, Gutiérrez G.** Cholera epidemiology in Latin America and perspectives for eradication. *Bulletin de l'Institut Pasteur* 1998;96:217–226.
169. **Barua D.** History of cholera. In: Barua D, Greenough WB (editors). *Cholera.* Boston, MA: Springer US. pp. 1–36.
170. **van de Linde PAM, Forbes GI.** Observations on the spread of cholera in Hong Kong, 1961-63. *Bulletin of the World Health Organization* 1965;32:515–530.
171. **Rebaudet S, Sudre B, Faucher B, Piarroux R.** Cholera in coastal Africa: A systematic review of its heterogeneous environmental determinants. *Journal of Infectious Diseases* 2013;208:S98–S106.
172. **Swerdlow DL, Isaäcson M.** The epidemiology of cholera in Africa. *Vibrio cholerae and Cholera* 1994;297–307.
173. **Centers for Disease Control and Prevention (CDC).** Cholera--Peru, 1991. *Morbidity and Mortality Weekly Report* 1991;40:108–110.
174. **Tauxe RV, Mintz ED, Quick RE.** Epidemic cholera in the new world: Translating field epidemiology into new prevention strategies. *Emerging Infectious Diseases* 1995;1:141–146.

175. **Guthmann JP.** Epidemic cholera in Latin America: Spread and routes of transmission. *Journal of Tropical Medicine and Hygiene* 1995;98:419–427.
176. **Centers for Disease Control and Prevention (CDC).** Cholera outbreak --- Haiti, October 2010. *Morbidity and Mortality Weekly Report* 2010;59:1411.
177. **Centers for Disease Control and Prevention (CDC).** Update on cholera --- Haiti, Dominican Republic, and Florida, 2010. *Morbidity and Mortality Weekly Report* 2010;59:1637–1641.
178. **Dowell SF, Tappero JW, Frieden TR.** Public health in Haiti — Challenges and progress. *New England Journal of Medicine* 2011;364:300–301.
179. **Guillaume Y, Ternier R, Vissieres K, Casseus A, Chery MJ, et al.** Responding to cholera in Haiti: Implications for the national plan to eliminate cholera by 2022. *Journal of Infectious Diseases* 2018;218:S167–S170.
180. **Federspiel F, Ali M.** The cholera outbreak in Yemen: Lessons learned and way forward. *BMC Public Health* 2018;18:1338.
181. **Huq A, Colwell RR, Rahman R, Ali A, Chowdhury MA, et al.** Detection of *Vibrio cholerae* O1 in the aquatic environment by fluorescent-monoclonal antibody and culture methods. *Applied and Environmental Microbiology* 1990;56:2370–2373.
182. **Colwell R, Huq A.** Marine ecosystems and cholera. *Hydrobiologia* 2001;460:141–145.
183. **Islam MS, Drasar BS, Bradley DJ.** Long-term persistence of toxigenic *Vibrio cholerae* O1 in the mucilaginous sheath of a blue-green alga, *Anabaena variabilis*. *Journal of Tropical Medicine and Hygiene* 1990;93:133–139.
184. **Alam M, Hasan NA, Sadique A, Bhuiyan NA, Ahmed KU, et al.** Seasonal cholera caused by *Vibrio cholerae* serogroups O1 and O139 in the coastal aquatic environment of Bangladesh. *Applied and Environmental Microbiology* 2006;72:4096–4104.
185. **Xu H-S, Roberts N, Singleton FL, Attwell RW, Grimes DJ, et al.** Survival and viability of nonculturable *Escherichia coli* and *Vibrio cholerae* in the estuarine and marine environment. *Microbial Ecology* 1982;8:313–323.

186. **Binsztein N, Costagliola MC, Pichel M, Jurquiza V, Ramírez FC, et al.** Viable but nonculturable *Vibrio cholerae* O1 in the aquatic environment of Argentina. *Applied and Environmental Microbiology* 2004;70:7481–7486.
187. **Kaper J, Lockman H, Colwell RR, Joseph SW.** Ecology, serology, and enterotoxin production of *Vibrio cholerae* in Chesapeake Bay. *Applied and Environmental Microbiology* 1979;37:91–103.
188. **Vezzulli L, Pruzzo C, Huq A, Colwell RR.** Environmental reservoirs of *Vibrio cholerae* and their role in cholera. *Environmental Microbiology Reports* 2010;2:27–33.
189. **Domman D, Quilici ML, Dorman MJ, Njamkepo E, Mutreja A, et al.** Integrated view of *Vibrio cholerae* in the Americas. *Science* 2017;358:789–793.
190. **Shimada T, Sakazaki R.** Additional serovars and inter-O antigenic relationships of *Vibrio cholerae*. *Japanese Journal of Medical Science and Biology* 1977;30:275–277.
191. **Svennerholm AM, Holmgren J.** Synergistic protective effect in rabbits of immunization with *Vibrio cholerae* lipopolysaccharide and toxin/toxoid. *Infection and Immunity* 1976;13:735–740.
192. **Gardner AD, Venkatraman KV.** The antigens of *Vibrio cholerae*. *The Lancet* 1935;225:265.
193. **Aoki Y.** A request for unification in type and antigen designations of *Vibrio cholerae*. *Japanese Journal of Microbiology* 1962;6:79–82.
194. **Gustafsson B.** Monoclonal antibody-based enzyme-linked immunosorbent assays for identification and serotyping of *Vibrio cholerae* O1. *Journal of Clinical Microbiology* 1984;20:1180–1185.
195. **Gustafsson B, Holme T.** Immunological characterization of *Vibrio cholerae* O:1 lipopolysaccharide, O-side chain, and core with monoclonal antibodies. *Infection and Immunity* 1985;49:275–280.
196. **Lebens M, Karlsson SL, Källgård S, Blomquist M, Ekman A, et al.** Construction of novel vaccine strains of *Vibrio cholerae* co-expressing the Inaba and Ogawa serotype antigens. *Vaccine* 2011;29:7505–7513.

197. **Stroehler UH, Karageorgos LE, Morona R, Manning PA.** Serotype conversion in *Vibrio cholerae* O1. *Proceedings of the National Academy of Sciences of the United States of America* 1992;89:2566–2570.
198. **Ito T, Hiramatsu K, Ohshita Y, Yokota T.** Mutations in the *rfbT* gene are responsible for the Ogawa to Inaba serotype conversion in *Vibrio cholerae* O1. *Microbiology and Immunology* 1993;37:281–288.
199. **Chatterjee SN, Chaudhuri K.** Lipopolysaccharides of *Vibrio cholerae*. I. Physical and chemical characterization. *Biochimica et Biophysica Acta* 2003;1639:65–79.
200. **Karlsson SL, Thomson N, Mutreja A, Connor T, Sur D, et al.** Retrospective analysis of serotype switching of *Vibrio cholerae* O1 in a cholera endemic region shows it is a non-random process. *PLoS Neglected Tropical Diseases* 2016;10:e0005044.
201. **Sheehy TW, Sprinz H, Augerson WS, Formal SB.** Laboratory *Vibrio cholerae* infection in the United States. *Journal of the American Medical Association* 1966;197:321–326.
202. **Sack RB, Miller CE.** Progressive changes of *Vibrio* serotypes in germ-free mice infected with *Vibrio cholerae*. *Journal of Bacteriology* 1969;99:688–695.
203. **Khan AI, Chowdhury F, Harris JB, Larocque RC, Faruque ASG, et al.** Comparison of clinical features and immunological parameters of patients with dehydrating diarrhoea infected with Inaba or Ogawa serotypes of *Vibrio cholerae* O1. *Scandinavian Journal of Infectious Disease* 2010;42:48–56.
204. **European Medicines Agency.** Dukoral. *European Medicines Agency*. <https://www.ema.europa.eu/en/medicines/human/EPAR/dukoral> (2018, accessed 13 November 2019).
205. **Karlsson SL, Ax E, Nygren E, Källgård S, Blomquist M, et al.** Development of stable *Vibrio cholerae* O1 Hikojima type vaccine strains co-expressing the Inaba and Ogawa lipopolysaccharide antigens. *PLoS ONE* 2014;9:e108521.

206. **Centers for Disease Control and Prevention (CDC).** Chapter 6 – Laboratory identification of *Vibrio cholerae*. In: *Laboratory methods for the diagnosis of Vibrio cholerae*. Centers for Disease Control and Prevention.
207. **Alam MT, Ray SS, Chun CN, Chowdhury ZG, Rashid MH, et al.** Major shift of toxigenic *V. cholerae* O1 from Ogawa to Inaba serotype isolated from clinical and environmental samples in Haiti. *PLoS Neglected Tropical Diseases* 2016;10:e0005045.
208. **Vugia DJ, Rodriguez M, Vargas R, Ricse C, Ocampo C, et al.** Epidemic cholera in Trujillo, Peru 1992: Utility of a clinical case definition and shift in *Vibrio cholerae* O1 serotype. *The American Journal of Tropical Medicine and Hygiene* 1994;50:566–569.
209. **Hugh R.** The proposed conservation of the generic name *Vibrio* Pacini 1854 and designation of the neotype strain of *Vibrio cholerae* Pacini 1854. *International Journal of Systematic and Evolutionary Microbiology* 1964;14:87–101.
210. **Hugh R.** A comparison of *Vibrio cholerae* Pacini and *Vibrio eltor* Pribram. *International Journal of Systematic and Evolutionary Microbiology*, 1965;15:61–68.
211. **Gotschlich F.** Über cholera- und choleraähnliche Vibrionen unter den aus Mekka zurückkehrenden Pilgern. *Zeitschrift für Hygiene und Infektionskrankheiten* 1906;53:281–304.
212. **Ruffer MA.** Researches on the bacteriological diagnosis of cholera, carried out by medical officers of the sanitary, maritime and quarantine council of Egypt. *The British Medical Journal* 1907;1:735–742.
213. **Hu D, Liu B, Feng L, Ding P, Guo X, et al.** Origins of the current seventh cholera pandemic. *Proceedings of the National Academy of Sciences of the United States of America* 2016;113:E7730–E7739.
214. **Castellani A.** Paracholera. *British Medical Journal* 1916;1:448–449.
215. **Mackie TJ, Storer EJ.** Two *Vibrio* species of the “paracholera” group associated with a cholera-like outbreak. *Journal of the Royal Army Medical Corps* 1918;31:161–169.

216. **Finkelstein MH.** Problems in the bacteriology of cholera and cholera-like infections. *Transactions of the Royal Society of Tropical Medicine and Hygiene* 1931;25:29–38.
217. **Mackie TJ.** The serological relationships of the paracholera Vibrios to *Vibrio cholerae*, and the serological races of the paracholera group. *British Journal of Experimental Pathology* 1922;3:231–237.
218. **van Loghem JJ.** Über den unterschied zwischen cholera- und El Tor-Vibrionen. *Zentralblatt für Bakteriologie*;67.
219. **Alm RA, Stroehner UH, Manning PA.** Extracellular proteins of *Vibrio cholerae*: nucleotide sequence of the structural gene (*hlyA*) for the haemolysin of the haemolytic El Tor strain 017 and characterization of the *hlyA* mutation in the non-haemolytic classical strain 569B. *Molecular Microbiology* 1988;2:481–488.
220. **Manning PA, Brown MH, Heuzenroeder MW.** Cloning of the structural gene (*hly*) for the haemolysin of *Vibrio cholerae* El Tor strain 017. *Gene* 1984;31:225–231.
221. **Fan Y, Li Z, Li Z, Li X, Sun H, et al.** Nonhemolysis of epidemic El Tor biotype strains of *Vibrio cholerae* is related to multiple functional deficiencies of hemolysin A. *Gut Pathogens* 2019;11:38.
222. **Son MS, Megli CJ, Kovacicova G, Qadri F, Taylor RK.** Characterization of *Vibrio cholerae* O1 El Tor biotype variant clinical isolates from Bangladesh and Haiti, including a molecular genetic analysis of virulence genes. *Journal of Clinical Microbiology* 2011;49:3739–3749.
223. **Albert MJ.** *Vibrio cholerae* O139 Bengal. *Journal of Clinical Microbiology* 1994;32:2345–2349.
224. **Cholera Working Group for ICDDR Bangladesh, Albert MJ, Ansaruzzaman M, Bardhan PK, Faruque ASG, et al.** Large epidemic of cholera-like disease in Bangladesh caused by *Vibrio cholerae* 0139 synonym Bengal. *The Lancet* 1993;342:387–390.

225. **Ramamurthy T, Garg S, Sharma R, Bhattacharya SK, Nair GB, et al.** Emergence of novel strain of *Vibrio cholerae* with epidemic potential in southern and eastern India. *The Lancet* 1993;341:703–704.
226. **Finkelstein RA.** Cholera, *Vibrio cholerae* O1 and O139, and other pathogenic Vibrios. In: Baron S (editor). *Medical Microbiology*. Galveston (TX): University of Texas Medical Branch at Galveston. <http://www.ncbi.nlm.nih.gov/books/NBK8407/> (1996).
227. **World Health Organization.** WHO | 1998 - Cholera - *Vibrio cholerae* O139 strain. *World Health Organization*. http://www.who.int/csr/don/1998_09_22/en/ (accessed 3 January 2018).
228. **Faruque AS, Fuchs GJ, Albert MJ.** Changing epidemiology of cholera due to *Vibrio cholerae* O1 and O139 Bengal in Dhaka, Bangladesh. *Epidemiology and Infection* 1996;116:275–278.
229. **Faruque SM, Chowdhury N, Kamruzzaman M, Ahmad QS, Faruque ASG, et al.** Reemergence of epidemic *Vibrio cholerae* O139, Bangladesh. *Emerging Infectious Diseases* 2003;9:1116–1122.
230. **Faruque SM, Sack DA, Sack RB, Colwell RR, Takeda Y, et al.** Emergence and evolution of *Vibrio cholerae* O139. *Proceedings of the National Academy of Sciences of the United States of America* 2003;100:1304–1309.
231. **Berche P, Poyart C, Abachin E, Lelievre H, Vandepitte J, et al.** The novel epidemic strain O139 is closely related to the pandemic strain O1 of *Vibrio cholerae*. *Journal of Infectious Diseases* 1994;170:701–704.
232. **Calia KE, Waldor MK, Calderwood SB.** Use of representational difference analysis to identify genomic differences between pathogenic strains of *Vibrio cholerae*. *Infection and Immunity* 1998;66:849–852.
233. **Hall RH, Khambaty FM, Kothary MH, Keasler SP, Tall BD.** *Vibrio cholerae* non-O1 serogroup associated with cholera gravis genetically and physiologically resembles O1 E1 Tor cholera strains. *Infection and Immunity* 1994;62:3859–3863.

234. **Mutreja A, Kim DW, Thomson NR, Connor TR, Lee JH, et al.** Evidence for several waves of global transmission in the seventh cholera pandemic. *Nature* 2011;477:462–465.
235. **Domman D, Chowdhury F, Khan AI, Dorman MJ, Mutreja A, et al.** Defining endemic cholera at three levels of spatiotemporal resolution within Bangladesh. *Nature Genetics* 2018;50:951–955.
236. **Weintraub A, Widmalm G, Jansson P-E, Jansson M, Hultenby K, et al.** *Vibrio cholerae* O139 Bengal possesses a capsular polysaccharide which may confer increased virulence. *Microbial Pathogenesis* 1994;16:235–241.
237. **Sozhamannan S, Deng YK, Li M, Sulakvelidze A, Kaper JB, et al.** Cloning and sequencing of the genes downstream of the *wbf* gene cluster of *Vibrio cholerae* serogroup O139 and analysis of the junction genes in other serogroups. *Infection and Immunity* 1999;67:5033–5040.
238. **Stroecher UH, Parasivam G, Dredge BK, Manning PA.** Novel *Vibrio cholerae* O139 genes involved in lipopolysaccharide biosynthesis. *Journal of Bacteriology* 1997;179:2740–2747.
239. **Yamasaki S, Garg S, Nair GB, Takeda Y.** Distribution of *Vibrio cholerae* O1 antigen biosynthesis genes among O139 and other non-O1 serogroups of *Vibrio cholerae*. *FEMS Microbiology Letters* 1999;179:115–121.
240. **Waldor MK, Colwell R, Mekalanos JJ.** The *Vibrio cholerae* O139 serogroup antigen includes an O-antigen capsule and lipopolysaccharide virulence determinants. *Proceedings of the National Academy of Sciences of the United States of America* 1994;91:11388–11392.
241. **Waldor MK, Mekalanos JJ.** ToxR regulates virulence gene expression in non-O1 strains of *Vibrio cholerae* that cause epidemic cholera. *Infection and Immunity* 1994;62:72–78.
242. **Siriphap A, Leekitcharoenphon P, Kaas RS, Theethakaew C, Aarestrup FM, et al.** Characterization and genetic variation of *Vibrio cholerae* isolated from clinical and environmental sources in Thailand. *PLoS ONE* 2017;12:e0169324.

243. **Yi Y, Lu N, Liu F, Li J, Zhang R, et al.** Genome sequence and comparative analysis of a *Vibrio cholerae* O139 strain E306 isolated from a cholera case in China. *Gut Pathogens* 2014;6:3.
244. **Chowdhury F, Mather AE, Begum YA, Asaduzzaman M, Baby N, et al.** *Vibrio cholerae* serogroup O139: Isolation from cholera patients and asymptomatic household family members in Bangladesh between 2013 and 2014. *PLoS Neglected Tropical Diseases* 2015;9:e0004183.
245. **World Health Organization.** Weekly epidemiological record. *Weekly Epidemiological Record* 2004;79:281-288.
246. **World Health Organization.** Weekly epidemiological record. *Weekly Epidemiological Record* 2017;92:477-500.
247. **Saha A, Chowdhury MI, Khanam F, Bhuiyan MdS, Chowdhury F, et al.** Safety and immunogenicity study of a killed bivalent (O1 and O139) whole-cell oral cholera vaccine Shanchol, in Bangladeshi adults and children as young as 1 year of age. *Vaccine* 2011;29:8285-8292.
248. **World Health Organization.** Weekly epidemiological record. *Weekly Epidemiological Record* 1969;44:1-27.
249. **Heiberg B.** The biochemical reactions of Vibrios. *Journal of Hygiene (London)* 1936;36:114-117.
250. **Aldová E, Lázníčková K, Ātěpánková E, Lietaya J.** Isolation of nonagglutinable Vibrios from an enteritis outbreak in Czechoslovakia. *Journal of Infectious Diseases* 1968;118:25-31.
251. **Felsenfeld O, Stegherr-Barrios A, Aldová E, Holmes J, Parrott MW.** *In vitro* and *in vivo* studies of streptomycin-dependent cholera Vibrios. *Applied Microbiology* 1970;19:463-469.
252. **American Type Culture Collections.** *Vibrio cholerae* Pacini ATCC ® 25872™. https://www.lgcstandards-atcc.org/Products/All/25872.aspx?geo_country=gb#history (accessed 28 June 2020).

253. **Boyd EF, Heilpern AJ, Waldor MK.** Molecular analyses of a putative CTX ϕ precursor and evidence for independent acquisition of distinct CTX ϕ s by toxigenic *Vibrio cholerae*. *Journal of Bacteriology* 2000;182:5530–5538.
254. **Sakazaki R, Tamura K, Gomez CZ, Sen R.** Serological studies on the cholera group of vibrios. *Japanese Journal of Medical Science and Biology* 1970;23:13–20.
255. **Chapman C, Henry M, Bishop-Lilly KA, Awosika J, Briska A, et al.** Scanning the landscape of genome architecture of non-O1 and non-O139 *Vibrio cholerae* by whole genome mapping reveals extensive population genetic diversity. *PLoS ONE* 2015;10:e0120311.
256. **Zinnaka Y, Carpenter CC.** An enterotoxin produced by noncholera vibrios. *Johns Hopkins Medical Journal* 1972;131:403–411.
257. **Boyd EF, Waldor MK.** Evolutionary and functional analyses of variants of the toxin-coregulated pilus protein TcpA from toxigenic *Vibrio cholerae* non-O1/non-O139 serogroup isolates. *Microbiology*, 2002;148:1655–1666.
258. **Henst CV der, Vanhove AS, Dörr NCD, Stutzmann S, Stoudmann C, et al.** Molecular insights into *Vibrio cholerae*'s intra-amoebal host-pathogen interactions. *Nature Communications* 2018;9:1–13.
259. **Bik EM, Gouw RD, Mooi FR.** DNA fingerprinting of *Vibrio cholerae* strains with a novel insertion sequence element: A tool to identify epidemic strains. *Journal of Clinical Microbiology* 1996;34:1453–1461.
260. **O'Shea YA, Reen FJ, Quirke AM, Boyd EF.** Evolutionary genetic analysis of the emergence of epidemic *Vibrio cholerae* isolates on the basis of comparative nucleotide sequence analysis and multilocus virulence gene profiles. *Journal of Clinical Microbiology* 2004;42:4657–4671.
261. **Beltrán P, Delgado G, Navarro A, Trujillo F, Selander RK, et al.** Genetic diversity and population structure of *Vibrio cholerae*. *Journal of Clinical Microbiology* 1999;37:581–590.

262. **Reen FJ, Boyd EF.** Molecular typing of epidemic and nonepidemic *Vibrio cholerae* isolates and differentiation of *V. cholerae* and *V. mimicus* isolates by PCR–single-strand conformation polymorphism analysis. *Journal of Applied Microbiology* 2005;98:544–555.
263. **Yamamoto K, Takeda Y, Miwatani T, Craig JP.** Evidence that a non-O1 *Vibrio cholerae* produces enterotoxin that is similar but not identical to cholera enterotoxin. *Infection and Immunity* 1983;41:896–901.
264. **Li M, Shimada T, Morris JG, Sulakvelidze A, Sozhamannan S.** Evidence for the emergence of non-O1 and non-O139 *Vibrio cholerae* strains with pathogenic potential by exchange of O-antigen biosynthesis regions. *Infection and Immunity* 2002;70:2441–2453.
265. **Aydanian A, Tang L, Chen Y, Morris JG, Olsen P, et al.** Genetic relatedness of selected clinical and environmental non-O1/O139 *Vibrio cholerae*. *International Journal of Infectious Diseases* 2015;37:152–158.
266. **Dziejman M, Serruto D, Tam VC, Sturtevant D, Diraphat P, et al.** Genomic characterization of non-O1, non-O139 *Vibrio cholerae* reveals genes for a type III secretion system. *Proceedings of the National Academy of Sciences of the United States of America* 2005;102:3465–3470.
267. **Chun J, Grim CJ, Hasan NA, Lee JH, Choi SY, et al.** Comparative genomics reveals mechanism for short-term and long-term clonal transitions in pandemic *Vibrio cholerae*. *Proceedings of the National Academy of Sciences of the United States of America* 2009;106:15442–15447.
268. **Farina C, Marini F, Schiaffino E, Luzzi I, Dionisi AM, et al.** A fatal *Vibrio cholerae* O37 enteritis. *Journal of Medical Microbiology*, 2010;59:1538–1540.
269. **Kaper JB, Bradford HB, Roberts NC, Falkow S.** Molecular epidemiology of *Vibrio cholerae* in the U.S. Gulf Coast. *Journal of Clinical Microbiology* 1982;16:129–134.
270. **Blake PA, Allegra DT, Snyder JD, Barrett TJ, McFarland L, et al.** Cholera — a possible endemic focus in the United States. *New England Journal of Medicine* 1980;302:305–309.

271. **Johnston JM, Martin DL, Perdue J, McFarland LM, Caraway CT, et al.** Cholera on a Gulf Coast oil rig. *New England Journal of Medicine* 1983;309:523–526.
272. **Gergatz SJ, McFarland LM.** Cholera on the Louisiana Gulf Coast: Historical notes and case report. *Journal of the Louisiana State Medical Society* 1989;141:29–34.
273. **Chen F, Evins GM, Cook WL, Almeida R, Hargrett-Bean N, et al.** Genetic diversity among toxigenic and nontoxigenic *Vibrio cholerae* O1 isolated from the Western Hemisphere. *Epidemiology and Infection* 1991;107:225–233.
274. **Cameron DN, Khambaty FM, Wachsmuth IK, Tauxe RV, Barrett TJ.** Molecular characterization of *Vibrio cholerae* O1 strains by pulsed-field gel electrophoresis. *Journal of Clinical Microbiology* 1994;32:1685–1690.
275. **Onifade TM, Hutchinson R, Zile KV, Bodager D, Baker R, et al.** Toxin producing *Vibrio cholerae* O75 outbreak, United States, March to April 2011. *Eurosurveillance* 2011;16:19870.
276. **Haley BJ, Choi SY, Grim CJ, Onifade TJ, Cinar HN, et al.** Genomic and phenotypic characterization of *Vibrio cholerae* non-O1 isolates from a US Gulf Coast cholera outbreak. *PLoS ONE* 2014;9:e86264.
277. **Centers for Disease Control and Prevention (CDC).** Non-O1 and non-O139 infections | Sources of infection & risk factors | Cholera | CDC. <https://www.cdc.gov/cholera/non-01-0139-infections.html> (accessed 18 March 2018).
278. **Chowdhury G, Joshi S, Bhattacharya S, Sekar U, Birajdar B, et al.** Extraintestinal infections caused by non-toxigenic *Vibrio cholerae* non-O1/non-O139. *Frontiers in Microbiology* 2016;7:e00144.
279. **Dalsgaard A, Forslund A, Hesselbjerg A, Bruun B.** Clinical manifestations and characterization of extra-intestinal *Vibrio cholerae* non-O1, non-O139 infections in Denmark. *Clinical Microbiology and Infection* 2000;6:625–627.
280. **Farina C, Gnechi F, Luzzi I, Vailati F.** *Vibrio cholerae* O2 as a cause of a skin lesion in a tourist returning from Tunisia. *Journal of Travel Medicine* 2000;7:92–94.

281. **Daniel D, Kumar S.** Rare strain of *Vibrio cholerae* septicemia in a patient with multiple myeloma. *Case Reports in Critical Care* 2015:596906.
282. **Kadkhoda K, Adam H, Gilmour MW, Hammond GW.** Nontoxigenic *Vibrio cholerae* septicemia in an immunocompromised patient. *Case Reports in Infectious Disease* 2012:698746.
283. **Garrine M, Mandomando I, Vubil D, Nhampossa T, Acacio S, et al.** Minimal genetic change in *Vibrio cholerae* in Mozambique over time: Multilocus variable number tandem repeat analysis and whole genome sequencing. *PLoS Neglected Tropical Diseases* 2017;11:e0005671.
284. **Sharma DP, Thomas C, Hall RH, Levine MM, Attridge SR.** Significance of toxin-coregulated pili as protective antigens of *Vibrio cholerae* in the infant mouse model. *Vaccine* 1989;7:451–456.
285. **Everiss KD, Hughes KJ, Kovach ME, Peterson KM.** The *Vibrio cholerae* *acfB* colonization determinant encodes an inner membrane protein that is related to a family of signal-transducing proteins. *Infection and Immunity* 1994;62:3289.
286. **Valiente E, Davies C, Mills DC, Getino M, Ritchie JM, et al.** *Vibrio cholerae* accessory colonisation factor AcfC: A chemotactic protein with a role in hyperinfectivity. *Scientific Reports* 2018;8:8390.
287. **Craig JP, Yamamoto K, Takeda Y, Miwatani T.** Production of cholera-like enterotoxin by a *Vibrio cholerae* non-O1 strain isolated from the environment. *Infection and Immunity* 1981;34:90–97.
288. **Ogawa A, Kato J, Watanabe H, Nair BG, Takeda T.** Cloning and nucleotide sequence of a heat-stable enterotoxin gene from *Vibrio cholerae* non-O1 isolated from a patient with traveler's diarrhea. *Infection and Immunity* 1990;58:3325–3329.
289. **Honda T, Arita M, Takeda T, Yoh M, Miwatani T.** Non-O1 *Vibrio cholerae* produces two newly identified toxins related to *Vibrio parahaemolyticus* haemolysin and *Escherichia coli* heat-stable enterotoxin. *The Lancet* 1985;2:163–164.

290. **Morris JG, Takeda T, Tall BD, Losonsky GA, Bhattacharya SK, et al.** Experimental non-O group 1 *Vibrio cholerae* gastroenteritis in humans. *Journal of Clinical Investigation* 1990;85:697–705.
291. **Dalsgaard A, Serichantalergs O, Shimada T, Sethabutr O, Echeverria P.** Prevalence of *Vibrio cholerae* with heat-stable enterotoxin (NAG-ST) and cholera toxin genes; restriction fragment length polymorphisms of NAG-ST genes among *V. cholerae* O serogroups from a major shrimp production area in Thailand. *Journal of Medical Microbiology* 1995;43:216–220.
292. **Hasan NA, Ceccarelli D, Grim CJ, Taviani E, Choi J, et al.** Distribution of virulence genes in clinical and environmental *Vibrio cholerae* strains in Bangladesh. *Applied and Environmental Microbiology* 2013;79:5782–5785.
293. **Mallard KE, Desmarchelier PM.** Detection of heat-stable enterotoxin genes among Australian *Vibrio cholerae* O1 strains. *FEMS Microbiology Letters* 1995;127:111–115.
294. **Takeda T, Peina Y, Ogawa A, Dohi S, Abe H, et al.** Detection of heat-stable enterotoxin in a cholera toxin gene-positive strain of *Vibrio cholerae* O1. *FEMS Microbiology Letters* 1991;80:23-27.
295. **Yuan P, Ogawa A, Ramamurthy T, Nair GB, Shimada T, et al.** *Vibrio mimicus* are the reservoirs of the heat-stable enterotoxin gene (*nag-st*) among species of the genus *Vibrio*. *World Journal of Microbiology and Biotechnology* 1994;10:59–63.
296. **Linhartová I, Bumba L, Mašín J, Basler M, Osička R, et al.** RTX proteins: A highly diverse family secreted by a common mechanism. *FEMS Microbiology Review* 2010;34:1076–1112.
297. **Lin W, Fullner KJ, Clayton R, Sexton JA, Rogers MB, et al.** Identification of a *Vibrio cholerae* RTX toxin gene cluster that is tightly linked to the cholera toxin prophage. *Proceedings of the National Academy of Sciences of the United States of America* 1999;96:1071–1076.
298. **Satchell KJF.** Structure and function of MARTX toxins and other large repetitive RTX proteins. *Annual Review of Microbiology* 2011;65:71–90.

299. **Satchell KJF.** MARTX, multifunctional autoprocessing repeats-in-toxin toxins. *Infection and Immunity* 2007;75:5079–5084.
300. **Olivier V, Haines GK, Tan Y, Satchell KJF.** Hemolysin and the multifunctional autoprocessing RTX toxin are virulence factors during intestinal infection of mice with *Vibrio cholerae* El Tor O1 strains. *Infection and Immunity* 2007;75:5035–5042.
301. **Boardman BK, Fullner Satchell KJ.** *Vibrio cholerae* strains with mutations in an atypical type I secretion system accumulate RTX toxin intracellularly. *Journal of Bacteriology* 2004;186:8137–8143.
302. **Dolores J, Satchell KJF.** Analysis of *Vibrio cholerae* genome sequences reveals unique *rtxA* variants in environmental strains and an *rtxA*-null mutation in recent altered El Tor isolates. *mBio* 2013;4:e00624-12.
303. **Miller KA, Tomberlin KF, Dziejman M.** *Vibrio* variations on a type three theme. *Current Opinion in Microbiology* 2019;47:66–73.
304. **Mahmud J, Rashed SM, Islam T, Islam S, Watanabe H, et al.** Type three secretion system in non-toxigenic *Vibrio cholerae* O1, Mexico. *Journal of Medical Microbiology* 2014;63:1760–1762.
305. **Shin OS, Tam VC, Suzuki M, Ritchie JM, Bronson RT, et al.** Type III secretion is essential for the rapidly fatal diarrheal disease caused by non-O1, non-O139 *Vibrio cholerae*. *mBio* 2011;2:e00106-11.
306. **Garaizar J, Rementeria A, Porwollik S.** DNA microarray technology: A new tool for the epidemiological typing of bacterial pathogens? *FEMS Immunology and Medical Microbiology* 2006;47:178–189.
307. **Dutta A, Kundu JK, Chatterjee R, Chaudhuri K.** *In silico* comparative study of the genomic islands of *Vibrio cholerae* MJ1236 with those of Classical and El Tor N16961 strains of *Vibrio cholerae*. *FEMS Microbiology Letters* 2011;321:75–81.
308. **Didelot X, Pang B, Zhou Z, McCann A, Ni P, et al.** The role of China in the global spread of the current cholera pandemic. *PLoS Genetics* 2015;11:e1005072.

309. **Weill F-X, Domman D, Njamkepo E, Almesbahi AA, Naji M, et al.** Genomic insights into the 2016–2017 cholera epidemic in Yemen. *Nature* 2019;565:230–233.
310. **Hu D, Yin Z, Yuan C, Yang P, Qian C, et al.** Changing molecular epidemiology of *Vibrio cholerae* outbreaks in Shanghai, China. *mSystems* 2019;4:mSystems.00561-19.
311. **Shah MA, Mutreja A, Thomson N, Baker S, Parkhill J, et al.** Genomic epidemiology of *Vibrio cholerae* O1 associated with floods, Pakistan, 2010. *Emerging Infectious Diseases* 2014;20:13–20.
312. **Katz LS, Petkau A, Beaulaurier J, Tyler S, Antonova ES, et al.** Evolutionary dynamics of *Vibrio cholerae* O1 following a single-source introduction to Haiti. *mBio* 2013;4:mBio.00398-13.
313. **Li H, Handsaker B, Wysoker A, Fennell T, Ruan J, et al.** The sequence alignment/map format and SAMtools. *Bioinformatics* 2009;25:2078–2079.
314. **Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, et al.** SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. *Journal of Computational Biology* 2012;19:cmb.2012.0021.
315. **Page AJ, De Silva N, Hunt M, Quail MA, Parkhill J, et al.** Robust high-throughput prokaryote de novo assembly and improvement pipeline for Illumina data. *Microbial Genomics* 2016;2:e000083.
316. **Chin C-S, Alexander DH, Marks P, Klammer AA, Drake J, et al.** Nonhybrid, finished microbial genome assemblies from long-read SMRT sequencing data. *Nature Methods* 2013;10:563–569.
317. **Hunt M, Silva ND, Otto TD, Parkhill J, Keane JA, et al.** Circlator: Automated circularization of genome assemblies using long sequencing reads. *Genome Biology* 2015;16:294.
318. **Walker BJ, Abeel T, Shea T, Priest M, Abouelliel A, et al.** Pilon: An integrated tool for comprehensive microbial variant detection and genome assembly improvement. *PLoS ONE* 2014;9:e112963.

319. **Wick RR, Judd LM, Gorrie CL, Holt KE.** Unicycler: Resolving bacterial genome assemblies from short and long sequencing reads. *PLoS Computational Biology* 2017;13:e1005595.
320. **Wick RR, Schultz MB, Zobel J, Holt KE.** Bandage: Interactive visualization of *de novo* genome assemblies. *Bioinformatics* 2015;31:3350–3352.
321. **Wood DE, Salzberg SL.** Kraken: Ultrafast metagenomic sequence classification using exact alignments. *Genome Biology* 2014;15:R46.
322. **Seemann T.** Prokka: Rapid prokaryotic genome annotation. *Bioinformatics* 2014;30:2068–2069.
323. **O’Leary NA, Wright MW, Brister JR, Ciuffo S, Haddad D, et al.** Reference sequence (RefSeq) database at NCBI: Current status, taxonomic expansion, and functional annotation. *Nucleic Acids Research* 2016;44:D733–D745.
324. **Page AJ, Cummins CA, Hunt M, Wong VK, Reuter S, et al.** Roary: Rapid large-scale prokaryote pan genome analysis. *Bioinformatics* 2015;31:3691–3693.
325. **Harris SR, Feil EJ, Holden MTG, Quail MA, Nickerson EK, et al.** Evolution of MRSA during hospital transmission and intercontinental spread. *Science* 2010;327:469–474.
326. **Allué-Guardia A, Echazarreta M, Koenig SSK, Klose KE, Eppinger M.** Closed genome sequence of *Vibrio cholerae* O1 El Tor Inaba strain A1552. *Genome Announcements* 2018;6:e00098-18.
327. **Croucher NJ, Page AJ, Connor TR, Delaney AJ, Keane JA, et al.** Rapid phylogenetic analysis of large samples of recombinant bacterial whole genome sequences using Gubbins. *Nucleic Acids Research* 2015;43:e15–e15.
328. **Capella-Gutiérrez S, Silla-Martínez JM, Gabaldón T.** trimAl: A tool for automated alignment trimming in large-scale phylogenetic analyses. *Bioinformatics* 2009;25:1972–1973.

329. **Page AJ, Taylor B, Delaney AJ, Soares J, Seemann T, et al.** SNP-sites: Rapid efficient extraction of SNPs from multi-FASTA alignments. *Microbial Genomics* 2016;2:e000056.
330. **Nguyen L-T, Schmidt HA, von Haeseler A, Minh BQ.** IQ-TREE: A fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. *Molecular Biology and Evolution* 2015;32:268–274.
331. **Lewis PO.** A likelihood approach to estimating phylogeny from discrete morphological character data. *Systematic Biology* 2001;50:913–925.
332. **Guindon S, Dufayard J-F, Lefort V, Anisimova M, Hordijk W, et al.** New algorithms and methods to estimate maximum-likelihood phylogenies: Assessing the performance of PhyML 3.0. *Systematic Biology* 2010;59:307–321.
333. **Hoang DT, Chernomor O, von Haeseler A, Minh BQ, Vinh LS.** UFBoot2: Improving the ultrafast bootstrap approximation. *Molecular Biology and Evolution* 2018;35:518–522.
334. **Tonkin-Hill G, Lees JA, Bentley SD, Frost SDW, Corander J.** Fast hierarchical Bayesian analysis of population structure. *Nucleic Acids Research* 2019;47:5539–5549.
335. **Heller KA, Ghahramani Z.** Bayesian hierarchical clustering. In: *Proceedings of the 22nd International Conference on Machine Learning*. New York, NY, USA: ACM. pp. 297–304.
336. **Carver TJ, Rutherford KM, Berriman M, Rajandream M-A, Barrell BG, et al.** ACT: The Artemis comparison tool. *Bioinformatics* 2005;21:3422–3423.
337. **Sullivan MJ, Petty NK, Beatson SA.** Easyfig: A genome comparison visualizer. *Bioinformatics* 2011;27:1009–1010.
338. **Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ.** Basic local alignment search tool. *Journal of Molecular Biology* 1990;215:403–410.
339. **Carver T, Böhme U, Otto TD, Parkhill J, Berriman M.** BamView: Viewing mapped read alignment data in the context of the reference sequence. *Bioinformatics* 2010;26:676–677.

340. **Jain C, Rodriguez-R LM, Phillippy AM, Konstantinidis KT, Aluru S.** High throughput ANI analysis of 90K prokaryotic genomes reveals clear species boundaries. *Nature Communications* 2018;9:5114.
341. **Rambaut A, Lam TT, Max Carvalho L, Pybus OG.** Exploring the temporal structure of heterochronous sequences using TempEst (formerly Path-O-Gen). *Virus Evol* 2016;2:vew007.
342. **Hunt M, Mather AE, Sánchez-Busó L, Page AJ, Parkhill J, et al.** ARIBA: Rapid antimicrobial resistance genotyping directly from sequencing reads. *Microbial Genomics* 2017;3:e000131.
343. **Zankari E, Hasman H, Cosentino S, Vestergaard M, Rasmussen S, et al.** Identification of acquired antimicrobial resistance genes. *Journal of Antimicrobial Chemotherapy* 2012;67:2640–2644.
344. **Carattoli A, Zankari E, García-Fernández A, Larsen MV, Lund O, et al.** *In silico* detection and typing of plasmids using PlasmidFinder and plasmid multilocus sequence typing. *Antimicrobial Agents and Chemotherapy* 2014;58:3895–3903.
345. **Grant JR, Arantes AS, Stothard P.** Comparing thousands of circular genomes using the CGView comparison tool. *BMC Genomics* 2012;13:202.
346. **R Core Team.** *R: A language and environment for statistical computing.* <https://www.R-project.org/> (2018, accessed 20 June 2020).
347. **Sievers F, Wilm A, Dineen D, Gibson TJ, Karplus K, et al.** Fast, scalable generation of high-quality protein multiple sequence alignments using Clustal Omega. *Molecular Systems Biology* 2011;7:msb.2011.75.
348. **Gouy M, Guindon S, Gascuel O.** SeaView version 4: A multiplatform graphical user interface for sequence alignment and phylogenetic tree building. *Molecular Biology and Evolution* 2010;27:221–224.
349. **Bailey TL, Boden M, Buske FA, Frith M, Grant CE, et al.** MEME suite: Tools for motif discovery and searching. *Nucleic Acids Research* 2009;37:W202-208.

350. **McClure R, Balasubramanian D, Sun Y, Bobrovskyy M, Sumbly P, et al.** Computational analysis of bacterial RNA-Seq data. *Nucleic Acids Research* 2013;41:e140.
351. **Tjaden B.** De novo assembly of bacterial transcriptomes from RNA-seq data. *Genome Biology* 2015;16:1–10.
352. **Letunic I, Bork P.** Interactive tree of life (iTOL) v3: An online tool for the display and annotation of phylogenetic and other trees. *Nucleic Acids Research* 2016;44:W242–W245.
353. **Hadfield J, Croucher NJ, Goater RJ, Abudahab K, Aanensen DM, et al.** Phandango: An interactive viewer for bacterial population genomics. *Bioinformatics* 2018;34:292–293.
354. **Wickham H.** *ggplot2: Elegant Graphics for Data Analysis*. Springer-Verlag New York; 2016.
355. **Wickham H.** Reshaping data with the *reshape* package. *Journal of Statistical Software* 2007;21:1–20.
356. **Rutherford K, Parkhill J, Crook J, Horsnell T, Rice P, et al.** Artemis: Sequence visualization and annotation. *Bioinformatics* 2000;16:944–945.
357. **Carver T, Thomson N, Bleasby A, Berriman M, Parkhill J.** DNAPlotter: circular and linear interactive genome visualization. *Bioinformatics* 2009;25:119–120.
358. **Vella EE.** Cholera vaccines and the El Tor *Vibrio*. *British Medical Journal* 1963;1:1203–1207.
359. **Chang AC, Cohen SN.** Construction and characterization of amplifiable multicopy DNA cloning vehicles derived from the p15A cryptic miniplasmid. *Journal of Bacteriology* 1978;134:1141–1156.
360. **Norrande J, Kempe T, Messing J.** Construction of improved M13 vectors using oligodeoxynucleotide-directed mutagenesis. *Gene* 1983;26:101–106.

361. **Chowdhury F, Khan AI, Harris JB, LaRocque RC, Chowdhury MI, et al.** A comparison of clinical and immunologic features in children and older patients hospitalized with severe cholera in Bangladesh. *Pediatric Infectious Disease Journal* 2008;27:986–992.
362. **Reeves PR, Lan R.** Cholera in the 1990s. *British Medical Bulletin* 1998;54:611–623.
363. **Pan American Health Organisation (PAHO).** Cholera situation in the Americas - Update. *Epidemiological Bulletin* 1992;13:11–12.
364. **Wilson MM, Chelala C.** Cholera is walking South. *Journal of the American Medical Association* 1994;272:1226–1227.
365. **Harrison A.** Cholera takes hold in northern Argentina. *United Press International*, 2 June 1992. <https://www.upi.com/Archives/1992/02/06/Cholera-takes-hold-in-northern-Argentina/7518697352400/> (2 June 1992, accessed 12 March 2019).
366. **Petroni A, Corso A, Melano R, Cacace ML, Bru AM, et al.** Plasmidic extended-spectrum β -lactamases in *Vibrio cholerae* O1 El Tor isolates in Argentina. *Antimicrobial Agents and Chemotherapy* 2002;46:1462–1468.
367. **Pichel M, Rivas M, Chinen I, Martín F, Ibarra C, et al.** Genetic diversity of *Vibrio cholerae* O1 in Argentina and emergence of a new variant. *Journal of Clinical Microbiology* 2003;41:124–134.
368. **Castañeda NC, Pichel M, Orman B, Binsztein N, Roy PH, et al.** Genetic characterization of *Vibrio cholerae* isolates from Argentina by *V. cholerae* repeated sequences–polymerase chain reaction. *Diagnostic Microbiology and Infectious Disease* 2005;53:175–183.
369. **Pan American Health Organisation (PAHO).** Cholera situation in the Americas, 1996. *Epidemiological Bulletin* 1997;18:5–7.
370. **Pan American Health Organisation (PAHO).** Cholera in the Americas. *Epidemiological Bulletin* 1993;14:14.
371. **Pan American Health Organisation (PAHO).** Cholera situation in the Americas. *Epidemiological Bulletin* 1994;15:13–16.

372. **Pan American Health Organisation (PAHO)**. Cholera in the Americas. *Epidemiological Bulletin* 1995;16:11–12.
373. **Eberhart-Phillips J, Besser RE, Tormey MP, Koo D, Feikin D, et al.** An outbreak of cholera from food served on an international aircraft. *Epidemiology and Infection* 1996;116:9–13.
374. **Centers for Disease Control and Prevention (CDC)**. Cholera associated with an international airline flight, 1992. *Morbidity and Mortality Weekly Report* 1992;41:134–135.
375. **Mydans S**. Cholera kills one and fells many on flight. *The New York Times*, 21 February 1992. <https://www.nytimes.com/1992/02/21/us/cholera-kills-one-and-fells-many-on-flight.html> (21 February 1992, accessed 12 March 2019).
376. **Lota L**. 5 People aboard Aerolineas Argentina flight 386 contract cholera. *Associated Press*, 20 February 1992. <https://apnews.com/94bc1d2b18b7c4dc903d17f1db8a35cb> (20 February 1992, accessed 12 March 2019).
377. **Nash NC**. Latin nations feud over cholera outbreak. *The New York Times*, 10 March 1992. <https://www.nytimes.com/1992/03/10/world/latin-nations-feud-over-cholera-outbreak.html> (10 March 1992, accessed 12 March 2019).
378. **Yildiz FH, Schoolnik GK**. Role of *rpoS* in stress survival and virulence of *Vibrio cholerae*. *Journal of Bacteriology* 1998;180:773–784.
379. **Blokesch M**. A quorum sensing-mediated switch contributes to natural transformation of *Vibrio cholerae*. *Mobile Genetic Elements* 2012;2:224–227.
380. **Mata L**. Cholera El Tor in Latin America, 1991–1993. *Annals of the New York Academy of Science* 1994;740:55–68.
381. **Wilson MM, Juliá CM, Chelala C**. How Argentina benefited from a cholera epidemic. *The Lancet* 1997;349:1375.
382. **Mouriño-Perez RR**. Oceanography and the seventh cholera pandemic. *Epidemiology* 1998;9:355–357.

383. **Mavian C, Paisie TK, Alam MT, Browne C, Rochars VMBD, et al.** Toxigenic *Vibrio cholerae* evolution and establishment of reservoirs in aquatic ecosystems. *Proceedings of the National Academy of Sciences of the United States of America*. Epub ahead of print 27 March 2020. DOI: 10.1073/pnas.1918763117.
384. **Martinez-Urtaza J, Trinanes J, Gonzalez-Escalona N, Baker-Austin C.** Is El Niño a long-distance corridor for waterborne disease? *Nature Microbiology* 2016;1:1–3.
385. **World Health Organization.** WHO | Weekly epidemiological record: cholera articles. *WHO*. <http://www.who.int/cholera/statistics/en/> (accessed 18 June 2020).
386. **Pan American Health Organisation (PAHO).** PAHO Regional Health Observatory - PHIP - Epidemic diseases - Cholera cases in the Americas since 1991. *PAHO Regional Health Observatory*. http://ais.paho.org/hip/viz/ed_colera_casesamericas.asp (accessed 18 June 2020).
387. **Rossi A, Galas M, Binztein N, Rivas M, Caffer MI, et al.** Unusual multiresistant *Vibrio cholerae* 01 El Tor in Argentina. *The Lancet* 1993;342:1172–1173.
388. **Price MN, Dehal PS, Arkin AP.** FastTree 2 – approximately maximum-likelihood trees for large alignments. *PLoS ONE* 2010;5:e9490.
389. **Fraga SG.** *Thesis*. Universidad de Buenos Aires; 2010.
390. **Matthey N, Drebes ND, Blokesch M.** Long-read-based genome sequences of pandemic and environmental *Vibrio cholerae* strains. *Microbiology Resource Announcements* 2018;7:MRA.01574-18.
391. **Eisenstark A.** Genetic diversity among offspring from archived *Salmonella enterica* ssp. *enterica* serovar Typhimurium (Demerec collection): In search of survival strategies. *Annual Review of Microbiology* 2010;64:277–292.
392. **Paul K, Ghosh A, Sengupta N, Chowdhury R.** Competitive growth advantage of nontoxigenic mutants in the stationary phase in archival cultures of pathogenic *Vibrio cholerae* strains. *Infection and Immunity* 2004;72:5478–5482.

393. **Carraro N, Sauvé M, Matteau D, Lauzon G, Rodrigue S, et al.** Development of pVCR94ΔX from *Vibrio cholerae*, a prototype for studying multidrug resistant IncA/C conjugative plasmids. *Frontiers in Microbiology* 2014;5:fmicb.2014.00044.
394. **Wang R, Liu H, Zhao X, Li J, Wan K.** IncA/C plasmids conferring high azithromycin resistance in *Vibrio cholerae*. *International Journal of Antimicrobial Agents* 2018;51:140–144.
395. **Harmer CJ, Hall RM.** The A to Z of A/C plasmids. *Plasmid* 2015;80:63–82.
396. **Wang H, Yang C, Sun Z, Zheng W, Zhang W, et al.** Genomic epidemiology of *Vibrio cholerae* reveals the regional and global spread of two epidemic non-toxigenic lineages. *PLoS Neglected Tropical Diseases* 2020;14:e0008046.
397. **Carpenter MR, Kalburge SS, Borowski JD, Peters MC, Colwell RR, et al.** CRISPR-Cas and contact-dependent secretion systems present on excisable pathogenicity islands with conserved recombination modules. *Journal of Bacteriology* 2017;199:e00842-16.
398. **Castillo D, Alvise PD, Xu R, Zhang F, Middelboe M, et al.** Comparative genome analyses of *Vibrio anguillarum* strains reveal a link with pathogenicity traits. *mSystems* 2017;2:mSystems.00001-17.
399. **Popovic T, Bopp C, Olsvik O, Wachsmuth K.** Epidemiologic application of a standardized ribotype scheme for *Vibrio cholerae* O1. *Journal of Clinical Microbiology* 1993;31:2474–2482.
400. **Wachsmuth IK, Evins GM, Fields PI, Olsvik Ø, Popovic T, et al.** The molecular epidemiology of cholera in Latin America. *Journal of Infectious Diseases* 1993;167:621–626.
401. **Pan American Health Organisation (PAHO).** Cholera in the Americas - special report: Cholera. *Bulletin of PAHO* 1991;25:267–273.
402. **Guglielmetti P, Bartoloni A, Roselli M, Gamboa H, Antunez DJ, et al.** Population movements and cholera spread in Cordillera Province, Santa Cruz Department, Bolivia. *The Lancet* 1992;340:113.

403. **Evins GM, Cameron DN, Wells JG, Greene KD, Popovic T, et al.** The emerging diversity of the electrophoretic types of *Vibrio cholerae* in the Western Hemisphere. *Journal of Infectious Diseases* 1995;172:173–179.
404. **Dalsgaard A, Skov MN, Serichantalergs O, Echeverria P, Meza R, et al.** Molecular evolution of *Vibrio cholerae* O1 strains isolated in Lima, Peru, from 1991 to 1995. *Journal of Clinical Microbiology* 1997;35:1151–1156.
405. **Pan American Health Organisation (PAHO).** Cholera situation in the Americas. An update. *Epidemiological Bulletin* 1991;12:1–4.
406. **Iqbal N, Guérout A-M, Krin E, Roux FL, Mazel D.** Comprehensive functional analysis of the 18 *Vibrio cholerae* N16961 toxin-antitoxin systems substantiates their role in stabilizing the superintegron. *Journal of Bacteriology* 2015;197:2150–2159.
407. **Chain PSG, Grafham DV, Fulton RS, FitzGerald MG, Hostetler J, et al.** Genome project standards in a new era of sequencing. *Science* 2009;326:236-237.
408. **H. M. Government.** Anti-Terrorism, Crime and Security Act 2001 (Modification) Order 2007 (2007/929). 2007.
409. **Dorman MJ, Domman D, Uddin MI, Sharmin S, Afrad MH, et al.** High quality reference genomes for toxigenic and non-toxigenic *Vibrio cholerae* serogroup O139. *Scientific Reports* 2019;9:5865.
410. **Koren S, Walenz BP, Berlin K, Miller JR, Bergman NH, et al.** Canu: Scalable and accurate long-read assembly via adaptive k-mer weighting and repeat separation. *Genome Research* 2017;gr.215087.116.
411. **Stamatakis A.** RAxML version 8: A tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics* 2014;30:1312–1313.
412. **Mukhopadhyay AK, Basu A, Garg P, Bag PK, Ghosh A, et al.** Molecular epidemiology of reemergent *Vibrio cholerae* O139 Bengal in India. *Journal of Clinical Microbiology* 1998;36:2149–2152.
413. **Kimsey HH, Nair GB, Ghosh A, Waldor MK.** Diverse CTXΦs and evolution of new pathogenic *Vibrio cholerae*. *The Lancet* 1998;352:457–458.

414. **Sharma C, Maiti S, Mukhopadhyay AK, Basu A, Basu I, et al.** Unique organization of the CTX genetic element in *Vibrio cholerae* O139 strains which reemerged in Calcutta, India, in September 1996. *Journal of Clinical Microbiology* 1997;35:3348–3350.
415. **Bhuiyan NA, Nusrin S, Alam M, Morita M, Watanabe H, et al.** Changing genotypes of cholera toxin (CT) of *Vibrio cholerae* O139 in Bangladesh and description of three new CT genotypes. *FEMS Immunology & Medical Microbiology* 2009;57:136–141.
416. **Kim EJ, Lee CH, Nair GB, Kim DW.** Whole-genome sequence comparisons reveal the evolution of *Vibrio cholerae* O1. *Trends in Microbiology* 2015;23:479–489.
417. **Davis BM, Kimsey HH, Chang W, Waldor MK.** The *Vibrio cholerae* O139 Calcutta bacteriophage CTX ϕ is infectious and encodes a novel repressor. *Journal of Bacteriology* 1999;181:6779–6787.
418. **Klinzing DC, Choi SY, Hasan NA, Matias RR, Tayag E, et al.** Hybrid *Vibrio cholerae* El Tor lacking SXT identified as the cause of a cholera outbreak in the Philippines. *mBio* 2015;6:e00047-15.
419. **Grim CJ, Choi J, Chun J, Jeon Y-S, Taviani E, et al.** Occurrence of the *Vibrio cholerae* seventh pandemic VSP-I island and a new variant. *OMICS: A Journal of Integrative Biology* 2010;14:1–7.
420. **Rowe-Magnus DA, Guerout A-M, Mazel D.** Bacterial resistance evolution by recruitment of super-integron gene cassettes. *Molecular Microbiology* 2002;43:1657–1669.
421. **Singh A.** Cholera and its prevention. *The Indian Medical Gazette* 1917;52:31–32.
422. **Bennett VB.** Cholera. *The Indian Medical Gazette* 1917;52:363.
423. **Mitchell TJ, Smith GM.** *Medical services; casualties and medical statistics of the Great War*. London. [http://hdl.handle.net/2027/uc1.\\$b744277](http://hdl.handle.net/2027/uc1.$b744277) (1931).

424. **Dorman MJ, Kane L, Domman D, Turnbull JD, Cormie C, et al.** The history, genome and biology of NCTC 30: a non-pandemic *Vibrio cholerae* isolate from World War One. *Proceedings of the Royal Society B: Biological Sciences* 2019;286:20182025.
425. **Dorman MJ, Thomson NR.** ‘Community evolution’ – laboratory strains and pedigrees in the age of genomics. *Microbiology* 2020;166:000869.
426. **Klose KE, Mekalanos JJ.** Distinct roles of an alternative sigma factor during both free-swimming and colonizing phases of the *Vibrio cholerae* pathogenic cycle. *Molecular Microbiology* 1998;28:501–520.
427. **Prouty MG, Correa NE, Klose KE.** The novel σ^{54} - and σ^{28} -dependent flagellar gene transcription hierarchy of *Vibrio cholerae*. *Molecular Microbiology* 2001;39:1595–1609.
428. **Syed KA, Beyhan S, Correa N, Queen J, Liu J, et al.** The *Vibrio cholerae* flagellar regulatory hierarchy controls expression of virulence factors. *Journal of Bacteriology* 2009;191:6555–6570.
429. **Cowan ST.** The National Collection of Type Cultures. *The Lancet* 1950;255:82–83.
430. **Correa NE, Lauriano CM, McGee R, Klose KE.** Phosphorylation of the flagellar regulatory protein FlrC is necessary for *Vibrio cholerae* motility and enhanced colonization. *Molecular Microbiology* 2000;35:743–755.
431. **Feng L, Reeves PR, Lan R, Ren Y, Gao C, et al.** A recalibrated molecular clock and independent origins for the cholera pandemic clones. *PLoS ONE* 2009;3:e4053.
432. **Institute of Medicine (US) Committee on Issues and Priorities for New Vaccine Development.** *The prospects for immunizing against Vibrio cholerae*. National Academies Press (US). <https://www.ncbi.nlm.nih.gov/books/NBK219074/> (1986, accessed 19 June 2020).
433. **Fleming A.** On the antibacterial action of cultures of a *Penicillium*, with special reference to their use in the isolation of *B. influenzae*. *British Journal of Experimental Pathology* 1929;10:226–236.
434. **World Health Organization.** WHO | Prevention and control of cholera outbreaks: WHO policy and recommendations.

http://www.who.int/cholera/prevention_control/recommendations/en/index4.html (2018, accessed 31 March 2018).

435. **Miller VL, DiRita VJ, Mekalanos JJ.** Identification of *toxS*, a regulatory gene whose product enhances *toxR*-mediated activation of the cholera toxin promoter. *Journal of Bacteriology* 1989;171:1288–1293.
436. **Bhattacharya MK, Bhattacharya SK, Garg S, Saha PradipK, Dutta D, et al.** Outbreak of *Vibrio cholerae* non-01 in India and Bangladesh. *The Lancet* 1993;341:1346–1347.
437. **Hammer BK, Bassler BL.** Regulatory small RNAs circumvent the conventional quorum sensing pathway in pandemic *Vibrio cholerae*. *Proceedings of the National Academy of Sciences of the United States of America* 2007;104:11145–11149.
438. **Joelsson A, Liu Z, Zhu J.** Genetic and phenotypic diversity of quorum-sensing systems in clinical and environmental isolates of *Vibrio cholerae*. *Infection and Immunity* 2006;74:1141–1147.
439. **Greig DR, Schaefer U, Octavia S, Hunter E, Chattaway MA, et al.** Evaluation of whole-genome sequencing for identification and typing of *Vibrio cholerae*. *Journal of Clinical Microbiology* 2018;56: e00831-18.
440. **Okada K, Na-Ubol M, Natakuathung W, Roobthaisong A, Maruyama F, et al.** Comparative genomic characterization of a Thailand-Myanmar isolate, MS6, of *Vibrio cholerae* O1 El Tor, which is phylogenetically related to a ‘US Gulf Coast’ clone. *PLoS ONE* 2014;9:e98120.
441. **Nonaka L, Suzuki S.** New Mg²⁺-dependent oxytetracycline resistance determinant *tet34* in *Vibrio* isolates from marine fish intestinal contents. *Antimicrobial Agents and Chemotherapy* 2002;46:1550–1552.
442. **Burnet FM.** The initiation of cellular infection by influenza and related viruses. *The Lancet* 1948;251:7–11.
443. **Judicial Commission of the International Committee on Bacteriological Nomenclature.** Opinion 31. Conservation of *Vibrio* Pacini 1854 as a bacterial generic

name, conservation of *Vibrio cholerae* Pacini 1854 as the nomenclatural type species of the bacterial genus *Vibrio*, and designation of neotype strain of *Vibrio cholerae* Pacini. *International Journal of Systematic and Evolutionary Microbiology*, 1965;15:185–186.

444. **Hugh R.** A comparison of the proposed neotype strain and 258 isolates of *Vibrio cholerae* Pacini. *International Journal of Systematic and Evolutionary Microbiology*, 1965;15:13–24.
445. **Burrows W, Mather AN, Elliott ME, Wagner SM.** Studies on immunity to Asiatic cholera I. Introduction. *Journal of Infectious Diseases* 1946;79:159–167.
446. **Mukherjee B, De SN.** Observations on some newer differential features of the El Tor vibrio and *Vibrio cholerae*. *The Journal of Pathology and Bacteriology* 1966;91:256–263.
447. **Doorenbos W, Kop J.** El Tor Vibrio in chloramphenicol estimation. *The Lancet* 1951;257:691.
448. **Zhang R, Wang Y, Leung PC, Gu J-D.** pVC, a small cryptic plasmid from the environmental isolate of *Vibrio cholerae* MP-1. *The Journal of Microbiology* 2007;45:193–198.
449. **Lilly J, Camps M.** Mechanisms of theta plasmid replication. *Microbiology Spectrum* 2015;3: PLAS-0029-2014.
450. **Newland JW, Voll MJ, McNicol LA.** Serology and plasmid carriage in *Vibrio cholerae*. *Canadian Journal of Microbiology* 1984;30:1149–1156.
451. **McDevitt S.** Methyl red and Voges-Proskauer test protocols. *ASMScience Laboratory Protocols*. <https://www.asmscience.org/content/education/protocol/protocol.3204> (2009, accessed 25 May 2020).
452. **Yoon SS, Mekalanos JJ.** 2,3-Butanediol synthesis and the emergence of the *Vibrio cholerae* El Tor biotype. *Infection and Immunity* 2006;74:6547–6556.
453. **Kovacikova G, Lin W, Skorupski K.** Dual regulation of genes involved in acetoin biosynthesis and motility/biofilm formation by the virulence activator AphA and the

- acetate-responsive LysR-type regulator AlsR in *Vibrio cholerae*. *Molecular Microbiology* 2005;57:420–433.
454. **Oh YT, Lee K-M, Bari W, Raskin DM, Yoon SS.** (p)ppGpp, a small nucleotide regulator, directs the metabolic fate of glucose in *Vibrio cholerae*. *Journal of Biological Chemistry* 2015;290:13178–13190.
455. **Kovacikova G, Skorupski K.** Regulation of virulence gene expression in *Vibrio cholerae* by quorum sensing: HapR functions at the *aphA* promoter. *Molecular Microbiology* 2002;46:1135–1147.
456. **Iwanaga M, Yamamoto K.** New medium for the production of cholera toxin by *Vibrio cholerae* O1 biotype El Tor. *Journal of Clinical Microbiology* 1985;22:405–408.
457. **Iwanaga M, Yamamoto K, Naomi H, Ichinose Y, Nakasone N, et al.** Culture conditions for stimulating cholera toxin production by *Vibrio cholerae* O1 El Tor. *Microbiology and Immunology* 1986;30:1075–1083.
458. **Kovacikova G, Skorupski K.** A *Vibrio cholerae* LysR homolog, AphB, cooperates with AphA at the *tcpPH* promoter to activate expression of the ToxR virulence cascade. *Journal of Bacteriology* 1999;181:4250–4256.
459. **Kovacikova G, Skorupski K.** Binding site requirements of the virulence gene regulator AphB: differential affinities for the *Vibrio cholerae* classical and El Tor *tcpPH* promoters. *Molecular Microbiology* 2002;44:533–547.
460. **Kovacikova G, Skorupski K.** Differential activation of the *tcpPH* Promoter by AphB determines biotype specificity of virulence gene expression in *Vibrio cholerae*. *Journal of Bacteriology* 2000;182:3228–3238.
461. **Hankins JV, Madsen JA, Giles DK, Brodbelt JS, Trent MS.** Amino acid addition to *Vibrio cholerae* LPS establishes a link between surface remodeling in Gram-positive and Gram-negative bacteria. *Proceedings of the National Academy of Sciences of the United States of America* 2012;109:8722–8727.
462. **Hall RH, Drasar BS.** *Vibrio cholerae* HlyA hemolysin is processed by proteolysis. *Infection and Immunity* 1990;58:3375–3379.

463. **Yamamoto K, Ichinose Y, Shinagawa H, Makino K, Nakata A, et al.** Two-step processing for activation of the cytolysin/hemolysin of *Vibrio cholerae* O1 biotype El Tor: Nucleotide sequence of the structural gene (*hlyA*) and characterization of the processed products. *Infection and Immunity* 1990;58:4106–4116.
464. **Alm RA, Mayrhofer G, Kotlarski I, Manning PA.** Amino-terminal domain of the El Tor haemolysin of *Vibrio cholerae* O1 is expressed in classical strains and is cytotoxic. *Vaccine* 1991;9:588–594.
465. **Herrera CM, Crofts AA, Henderson JC, Pingali SC, Davies BW, et al.** The *Vibrio cholerae* VprA-VprB two-component system controls virulence through endotoxin modification. *mBio* 2014;5:e02283-14.
466. **Lee D, Kim EJ, Baek Y, Lee J, Yoon Y, et al.** Alterations in glucose metabolism in *Vibrio cholerae* serogroup O1 El Tor biotype strains. *Scientific Reports* 2020;10:308.
467. **Liang K, Islam MT, Hussain N, Winkjer NS, Im MS, et al.** Draft genome sequences of eight *Vibrio* sp. clinical isolates from across the United States that form a basal sister clade to *Vibrio cholerae*. *Microbiology Resource Announcements* 2019;8:MRA.01473-18.
468. **Xu Q, Dziejman M, Mekalanos JJ.** Determination of the transcriptome of *Vibrio cholerae* during intrainestinal growth and midexponential phase *in vitro*. *Proceedings of the National Academy of Sciences of the United States of America* 2003;100:1286–1291.
469. **Merrell DS, Butler SM, Qadri F, Dolganov NA, Alam A, et al.** Host-induced epidemic spread of the cholera bacterium. *Nature* 2002;417:642–645.
470. **Beyhan S, Tischler AD, Camilli A, Yildiz FH.** Differences in gene expression between the Classical and El Tor biotypes of *Vibrio cholerae* O1. *Infection and Immunity* 2006;74:3633–3642.
471. **Mandlik A, Livny J, Robins WP, Ritchie JM, Mekalanos JJ, et al.** RNA-seq-based monitoring of infection-linked changes in *Vibrio cholerae* gene expression. *Cell Host and Microbe* 2011;10:165–174.

472. **Krin E, Pierlé SA, Sismeiro O, Jagla B, Dillies M-A, et al.** Expansion of the SOS regulon of *Vibrio cholerae* through extensive transcriptome analysis and experimental validation. *BMC Genomics* 2018;19:373.
473. **Zhang Z, Chen G, Hu J, Hussain W, Fan F, et al.** Mr.Vc: A database of microarray and RNA-seq of *Vibrio cholerae*. *Database* 2019;2019:baz069.
474. **DuPai CD, Wilke CO, Davies BW.** A comprehensive coexpression network analysis in *Vibrio cholerae*. *mSystems*;5. Epub ahead of print 25 August 2020. DOI: 10.1128/mSystems.00550-20.
475. **Papenfort K, Förstner KU, Cong J-P, Sharma CM, Bassler BL.** Differential RNA-seq of *Vibrio cholerae* identifies the VqmR small RNA as a regulator of biofilm formation. *Proceedings of the National Academy of Sciences of the United States of America* 2015;112:E766–E775.
476. **Miller VL, Mekalanos JJ.** A novel suicide vector and its use in construction of insertion mutations: Osmoregulation of outer membrane proteins and virulence determinants in *Vibrio cholerae* requires *toxR*. *Journal of Bacteriology* 1988;170:2575–2583.
477. **Peterson KM, Mekalanos JJ.** Characterization of the *Vibrio cholerae* ToxR regulon: Identification of novel genes involved in intestinal colonization. *Infection and Immunity* 1988;56:2822–2829.
478. **Skorupski K, Taylor RK.** Cyclic AMP and its receptor protein negatively regulate the coordinate expression of cholera toxin and toxin-coregulated pilus in *Vibrio cholerae*. *Proceedings of the National Academy of Sciences of the United States of America* 1997;94:265–270.
479. **Rashid M, Rashed SM, Islam T, Johura F-T, Watanabe H, et al.** CtxB1 outcompetes CtxB7 in *Vibrio cholerae* O1, Bangladesh. *Journal of Medical Microbiology* 2016;65:101–103.
480. **Basler M, Pilhofer M, Henderson GP, Jensen GJ, Mekalanos JJ.** Type VI secretion requires a dynamic contractile phage tail-like structure. *Nature* 2012;483:182–186.

481. **Basler M, Ho BT, Mekalanos JJ.** Tit-for-tat: Type VI secretion system counterattack during bacterial cell-cell interactions. *Cell* 2013;152:884–894.
482. **Peng Y, Wang X, Shou J, Zong B, Zhang Y, et al.** Roles of Hcp family proteins in the pathogenesis of the porcine extraintestinal pathogenic *Escherichia coli* type VI secretion system. *Scientific Reports* 2016;6:26816.
483. **Silverman JM, Agnello DM, Zheng H, Andrews BT, Li M, et al.** Haemolysin coregulated protein is an exported receptor and chaperone of type VI secretion substrates. *Molecular Cell* 2013;51:584–593.
484. **Metzger LC, Stutzmann S, Scignari T, Van der Henst C, Matthey N, et al.** Independent regulation of type VI secretion in *Vibrio cholerae* by TfoX and TfoY. *Cell Reports* 2016;15:951–958.
485. **Dong TG, Mekalanos JJ.** Characterization of the RpoN regulon reveals differential regulation of T6SS and new flagellar operons in *Vibrio cholerae* O37 strain V52. *Nucleic Acids Research* 2012;40:7766–7775.
486. **Pukatzki S, Ma AT, Sturtevant D, Krastins B, Sarracino D, et al.** Identification of a conserved bacterial protein secretion system in *Vibrio cholerae* using the *Dictyostelium* host model system. *Proceedings of the National Academy of Sciences of the United States of America* 2006;103:1528–1533.
487. **Kitaoka M, Miyata ST, Brooks TM, Unterweger D, Pukatzki S.** VasH is a transcriptional regulator of the type VI secretion system functional in endemic and pandemic *Vibrio cholerae*. *Journal of Bacteriology* 2011;193:6471–6482.
488. **Unterweger D, Kitaoka M, Miyata ST, Bachmann V, Brooks TM, et al.** Constitutive type VI secretion system expression gives *Vibrio cholerae* intra- and interspecific competitive advantages. *PLoS ONE* 2012;7:e48320.
489. **Miyata ST, Kitaoka M, Wieteska L, Frech C, Chen N, et al.** The *Vibrio cholerae* type VI secretion system: Evaluating its role in the human disease cholera. *Frontiers in Microbiology* 2010;1:fmicb.2010.00117.

490. **Hersch SJ, Watanabe N, Stietz MS, Manera K, Kamal F, *et al.*** Envelope stress responses defend against type six secretion system attacks independently of immunity proteins. *Nature Microbiology* 2020;5:706–714.