

comments, and participants remained engaged throughout the session. We are planning a formal evaluation of the training tool with the field epidemiology training programs for Germany and Europe.

The exercise is a tool for building outbreak response capacities and teaches the topic in an engaging way. It can be used on its own or embedded as an ice breaker into a field epidemiology curriculum for health professionals or for school classes looking for health-related project work. Supported languages are German, English, Russian, and French. Further translations and adaptations are encouraged and will be referenced on our web page (<https://www.disease-detectives.org>).

Acknowledgments

We thank Nadine Zeitlmann, Michaela Diercke, and Hannah Lewis Winter for thoroughly reading the draft version of the manuscript and adapting the German script into an English 10-steps facilitator guide; Ariane Halm and Juliane Wunderlich for performing the same activity for the French version; and Yanina Lenz for supporting the Russian version.

About the Author

Mr. Burckhardt is a fellow supervisor and trainer at the European Programme for Intervention Epidemiology Training Alumni Network, Heidelberg, Germany. His research interests are outbreak investigations and disease surveillance. Ms. Kissling is an epidemiologist and trainer at Epiconcept, Paris, France. Her research interests are vaccine effectiveness and influenza.

References

1. Jones DS, Dicker RC, Fontaine RE, Boore AL, Omolo JO, Ashgar RJ, et al. Building global epidemiology and response capacity with field epidemiology training programs. *Emerg Infect Dis*. 2017;23. <https://doi.org/10.3201/eid2313.170509>
2. Bremer V, Bosman A, Coulombier D. New perspectives after the transition of EPIET to ECDC: the future of the programme. *Euro Surveill*. 2009;14:19374.
3. Centers for Disease Control and Prevention. Oswego: an outbreak of gastrointestinal illness following a church supper; 2003 [cited 2019 Oct 21]. <https://www.cdc.gov/eis/casestudies/xoswego.401-303.student.pdf>
4. Centers for Disease Control and Prevention. Guide to confirming an etiology in foodborne disease outbreak; 2017 [cited 2019 Oct 21]. https://www.cdc.gov/foodsafety/outbreaks/investigating-outbreaks/confirming_diagnosis.html
5. Mertens E, Kreher H, Rabsch W, Bornhofen B, Alpers K, Burckhardt F. Severe infections caused by *Salmonella* Enteritidis PT8/7 linked to a private barbecue. *Epidemiol Infect*. 2013;141:277–83. <https://doi.org/10.1017/S0950268812000726>
6. Burckhardt F, Kissling E. 'The disease detectives': a comic perspective on outbreak investigations. *Euro Surveill*. 2007;12:E071122.4.
7. World Health Organization. Immunization hand-book and facilitators' guide. South-East Asia Regional Office [cited 2019 Jan 17]. http://www.searo.who.int/india/topics/routine_immunization/Facilitators_Guide_Medical_Officers_Handbook_2010.pdf
8. Robert Koch Institute. Investigate outbreaks module [in German]. *Epidemiol Bull*. 2019; (17):143.
9. Foreign Office. The German biosecurity programme; 2017 [cited 2019 Oct 21]. <https://www.auswaertiges-amt.de/en/aussenpolitik/themen/abruestung/uebersicht-bcwaffen-node/-/239362>

Address for correspondence: Florian Burckhardt, European Programme for Intervention Epidemiology Training Alumni Network, Römerstrasse 59, 69115 Heidelberg, Germany; email: florian@burckhardt.de

Emergence of *Vibrio cholerae* O1 Sequence Type 75 in Taiwan

Yueh-Hua Tu, Bo-Han Chen, Yu-Ping Hong, Ying-Shu Liao, Yi-Syong Chen, Yen-Yi Liu, Ru-Hsiou Teng, You-Wun Wang, Chien-Shun Chiou

Author affiliations: Centers for Disease Control, Taichung, Taiwan

DOI: <https://doi.org/10.3201/eid2601.190934>

We investigated the epidemiology of cholera in Taiwan during 2002–2018. *Vibrio cholerae* sequence type (ST) 75 clone emerged in 2009 and has since become more prevalent than the ST69 clone from a previous pandemic. Closely related ST75 strains have emerged in 4 countries and may now be widespread in Asia.

Cholera, an acute diarrheal disease caused by the toxigenic *Vibrio cholerae* serogroup O1 and its derivative serogroup O139, remains a severe public health threat in some regions of the world (1). Seven cholera pandemics have occurred in the past 200 years; the most recent, caused primarily by a sequence type (ST) 69 *V. cholerae* clone, originated in Indonesia in 1961 and remains ongoing (2,3). In Taiwan, cholera appeared in 1962 and resulted in 383 cases and 24 deaths during a 3-month outbreak (4). Cholera has been rare in Taiwan since the 1962

Table. Distribution of cholera and sequence types of *Vibrio cholerae* isolates, Taiwan, 1962 and 2002–2018

Category	1962	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	Total
No. cases	383	2	1	1	2	1	0	1	3	5	3	5	7	4	10	9	2	7	63
No. isolates	4	2	1	1	2	1	0	1	3	4	3	3	6	3	8	9	2	7	56
Sequence type																			
69	4		1	1	2	1		1		1	1		2			3	1		14
75 and variants									3	3	2	3	4	3	8	6	1	7	40
723		2																	2

outbreak; however, incidence has increased in recent years. The average number of cholera cases increased from 1.5 cases/year in 1991–2008 to 5.5 cases/year in 2009–2018 (5).

For this study, we investigated the epidemiology of cholera in Taiwan for 2002–2018 and the source of *V. cholerae* strains in those cases. During 2002–2018, Taiwan reported 63 total cholera cases, ranging from 0 to 10 cases per year (Table). Among the patients, 62 were from Taiwan and 1 from Japan; 35 (55.6%) were male. Three (4.8%) patients were in the <14 year age range, 37 (58.7%) in the 15–64 age range, and 23 (36.5%) in the ≥65 age range. Nearly all cases, 61, were sporadic; 2 were part of a family cluster. Seven patients had traveled within the incubation period (5 days) before onset of symptoms: 2 to Indonesia, 1 to Malaysia, 1 to Thailand, 2 to the Philippines, and 1 to Vietnam.

Using pulsed-field gel electrophoresis (PFGE) and whole-genome sequencing analysis, we characterized 60 *V. cholerae* isolates: 4 recovered from patients of the 1962 cholera outbreak and 56 recovered from patients during 2002–2018. Using PFGE, the 2 most prevalent isolates we identified were VcN09.014 (n = 25) and VcN09.012 (n = 7) (Appendix Figure 1, <https://wwwnc.cdc.gov/EID/article/26/1/19-0934-App1.pdf>). We compared those PFGE patterns with those in the *Vibrio cholerae* database maintained by the US Centers for Disease Control and Prevention in 2016 and found no match for VcN09.014, but we did find 11 isolates from Guam and the Philippines that matched with VcN09.012 (identification no. KZGN11.0102).

We identified 7 ST types for the 60 isolates: ST69 (18 isolates), ST723 (2 isolates), ST75 (35 isolates), ST725 (1 isolate), ST726 (2 isolates), ST727 (1 isolates), and ST728 (1 isolate). ST725, ST726, and ST728 are single-locus variants and ST727 a double-locus variant of ST75. ST75 and its derivatives first appeared in 2009 and subsequently become the most prevalent types (Table). Among the 7 patients who had traveled abroad, we found ST69 in those returning from Thailand, the Philippines, and Malaysia; ST75 in the person returning from Vietnam; and ST723 in those

returning from Indonesia. We performed cluster analyses on whole-genome single nucleotide polymorphism profiles for the 60 isolates, which revealed 4 distinct clades (Appendix Table, Figure 2). The fact that a total of 5 isolates in clades 2 and 3 did not harbor the quinolone-resistant gene *qnrVC4* suggests that the resistance gene was introduced after the ST75 strains had emerged.

We compared core genome multilocus sequence typing profiles of the 60 isolates with 5,048 genomes in the National Center for Biotechnology Information databases as of January 19, 2019. We found that the 38 isolates in clade 2 were closely related to 10 strains from China (6), strain MS6 that was identified in Thailand in 2008 (7), and a UK strain recovered from a traveler who returned from Thailand in 2017 (8) (Appendix Figure 3). Strains from the 2 isolates in clade 3 were distantly removed from strains in clade 2 and those found near the US Gulf Coast (9,10) but more closely related to a strain recovered in 2018 and another strain from Russia. The ST75 strains from China were recovered from well water, carriers, and patients during 2005–2014 (6). One ST75 strain in clade 2 was obtained from a Taiwanese person who returned from Vietnam in 2015.

In summary, for most of recent history, cholera has been rare and primarily sporadic in Taiwan. However, the per-year rate of cholera cases has increased since 2009, concurrent with the emergence of strains of the ST75 clone. Over this time, ST75 strains have replaced ST69 as the most prevalent causative agent of cholera in Taiwan. Because closely related ST75 strains had been identified earlier in China and 2 other Southeast Asia countries, we believe our findings indicate that the ST75 clone is spreading more widely in Asia.

Acknowledgments

We sincerely thank Peter Gerner-Smidt and his colleagues at the US Centers for Disease Control and Prevention for conducting PFGE pattern similarity searching in the US PFGE National Database; Marie Anne Chattaway of Public Health England in the United Kingdom and Kazuhisa Okada of Osaka University in Japan for providing the

historical information of the *V. cholerae* ST75 strains they studied; and our colleagues in the Biobank Section of Taiwan Centers for Disease Control for providing *V. cholerae* isolates.

This study was funded by the Ministry of Health and Welfare, Taiwan (grant no. MOHW108-CDC-C-315-122129).

About the Author

Mr. Tu is a research associate in the Centers for Disease Control, Ministry of Health and Welfare, Taiwan. His expertise includes systems biology, computational biology, and machine learning, including developing *Vibrio cholerae* core genome multilocus sequence typing profiling pipelines for the organization.

References

1. World Health Organization. Cholera Annual Report 2017. *Wkly Epidemiol Rec.* 2018;93:489–500.
2. Mutreja A, Kim DW, Thomson NR, Connor TR, Lee JH, Kariuki S, et al. Evidence for several waves of global transmission in the seventh cholera pandemic. *Nature.* 2011;477:462–5. <https://doi.org/10.1038/nature10392>
3. Lippi D, Gotuzzo E, Caini S. Cholera. *Microbiol Spectr.* 2016;4.
4. Yen CH. A recent study of cholera with reference to an outbreak in Taiwan in 1962. *Bull World Health Organ.* 1964;30:811–25. [10.1128/microbiolspec.PoH-0012-2015](https://doi.org/10.1128/microbiolspec.PoH-0012-2015)
5. Taiwan National Infectious Disease Statistics System [cited 2019 Feb 1]. <https://nidss.cdc.gov.tw>
6. Luo Y, Octavia S, Jin D, Ye J, Miao Z, Jiang T, et al. US Gulf-like toxigenic O1 *Vibrio cholerae* causing sporadic cholera outbreaks in China. *J Infect.* 2016;72:564–72. <https://doi.org/10.1016/j.jinf.2016.02.005>
7. Okada K, Na-Ubol M, Natakathung W, Roobthaisong A, Maruyama F, Nakagawa I, 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. <https://doi.org/10.1371/journal.pone.0098120>
8. Greig DR, Schaefer U, Octavia S, Hunter E, Chattaway MA, Dallman TJ, et al. Evaluation of whole-genome sequencing for identification and typing of *Vibrio cholerae*. *J Clin Microbiol.* 2018;56:e00831–18. <https://doi.org/10.1128/JCM.00831-18>
9. Watve SS, Chande AT, Rishishwar L, Mariño-Ramírez L, Jordan IK, Hammer BK. Whole-genome sequences of 26 *Vibrio cholerae* isolates. *Genome Announc.* 2016;4:e01396–16. <https://doi.org/10.1128/genomeA.01396-16>
10. Kaper JB, Bradford HB, Roberts NC, Falkow S. Molecular epidemiology of *Vibrio cholerae* in the U.S. Gulf Coast. *J Clin Microbiol.* 1982;16:129–34.

Address for correspondence: Chien-Shun Chiou, Centers for Disease Control, Central Region Laboratory, 5F, 20 Wen-Sin South 3rd Rd, Taichung City 40855, Taiwan; email: nipmcs@cdc.gov.tw

Diabetes Mellitus, Hypertension, and Death among 32 Patients with MERS-CoV Infection, Saudi Arabia

Khalid H. Alanazi, Glen R. Abedi, Claire M. Midgley, Abdulrahim Alkhamis, Taghreed Alsaqer, Abdullah Almoaddi, Abdullah Algwizani, Sameeh S. Ghazal, Abdullah M. Assiri, Hani Jokhdar, Susan I. Gerber, Hail Alabdely, John T. Watson

Author affiliations: Ministry of Health, Riyadh, Saudi Arabia (K.H. Alanazi, A. Alkhamis, T. Alsaqer, A. Almoaddi, A. Algwizani, S.S. Ghazal, A.M. Assiri, H. Jokhdar, H. Alabdely); Centers for Disease Control and Prevention, Atlanta, Georgia, USA (G.R. Abedi, C.M. Midgley, S.I. Gerber, J.T. Watson)

DOI: <https://doi.org/10.3201/eid2601.190952>

Diabetes mellitus and hypertension are recognized risk factors for severe clinical outcomes, including death, associated with Middle East respiratory syndrome coronavirus infection. Among 32 virus-infected patients in Saudi Arabia, severity of illness and frequency of death corresponded closely with presence of multiple and more severe underlying conditions.

First described in 2012, infection with Middle East respiratory syndrome coronavirus (MERS-CoV) has been reported worldwide. More than 2,200 cases have been reported to the World Health Organization, and more than one third have resulted in death (1).

Certain underlying conditions, including diabetes mellitus (DM), hypertension, chronic cardiac disease, and chronic renal disease, are recognized risk factors for illness and death caused by infection with MERS-CoV (2,3). We further explored this relationship among MERS patients admitted to a referral hospital in Riyadh, Saudi Arabia, during August 1, 2015–August 31, 2016. Enrollment criteria and data collection methods have been described (4).

We considered persons with a medical history of DM as having documented DM and persons with multiple recorded periods of hyperglycemia during hospitalization as having possible DM (4). We similarly identified patients with hypertension or chronic kidney disease (CKD) by using documentation in the medical chart. We defined cardiovascular disease as having documentation of coronary artery disease or a history of heart failure or stroke. We considered patients with cardiovascular disease or CKD to have chronic organ dam-