Author affiliations: Shenzhen Major Infectious Disease Control Key Laboratory, Shenzhen Center for Disease Control and Prevention, Shenzhen, China (Y. Li, X. Xie, X. Shi, Y. Lin, Y. Qiu, J. Mou, Q. Chen, Y. Lu, L. Zhou, M. Jiang, H. Ma, J. Cheng, Q. Hu); Sichuan University, Chengdu, China (H. Sun); and Shenzhen University, Shenzhen (Q. Hu)

DOI: http://dx.doi.org/10.3201/eid2004.130744
The distribution of the 47 serotypes detected revealed the diversity in this surveillance were 15–39 years of age. The diarrheagenic spp., *Salmonella* coastal region of China, surpassing dominant bacterial cause of acute diarrhea in the southern coastal region. A new clonal complex, CC120, and sequence type (ST), 265, a presumed new ancestor of CC345, were identified (Table 2).

**Conclusions**

During 2007–2012, *V. parahaemolyticus* was the dominant bacterial cause of acute diarrhea in the southern coastal region of China, surpassing *Salmonella* spp., diarrheagenic *Escherichia coli*, and *Shigella* spp. (data not shown). These findings differ from those for central and northern regions of China (8,9). Most case-patients in this surveillance were 15–39 years of age. The distribution of the 47 serotypes detected revealed the diversity of *V. parahaemolyticus*, which might explain the continuing epidemic of *V. parahaemolyticus* infections in this region.

*V. parahaemolyticus* serotype O3:K6, which emerged worldwide in 1997 as a pandemic clone and spread throughout Asia and to the Americas, Europe, and Africa (1), has been dominant in Shenzhen Province. Most (68; 90.7%) O3:K6 isolates tested were new clones, defined by toxRS-targeted GS-PCR, providing evidence that pandemic O3:K6 has spread to China. Most (63; 98.5%) serotype O3:K6 strains were identified as CC3 by MLST; serotype O1:KUT, O1:K36, O4:K68, O5:K68, and O1:K25 strains were positive by GS-PCR in our study and mostly...
documented as O3:K6 serovariants (1). These results indicate the long-term evolution of O3:K6 in Asia.

*V. parahaemolyticus* serotype O4:K8 has been an epidemic strain in Asia (10, 11) and reported in Peru (12) but has been rarely seen in North America, Africa, and Europe. Serotype O4:K8 isolates from this study expressed a nonpandemic genotype. We presume that the evolution of O4:K8 was affected by local mutation and recombination rather than by a global pandemic, similar to a finding reported in Japan in 2007 (13). Notably, ST265 was predominant among strains with serotype O4:K8, whereas ST345, the previously considered founder of CC345, was not found (Table 2). Although ST265 might be a potential branch from ST345 in other regions, our findings strongly suggest that ST265 should be considered the epidemic clonal founder of CC345 in China. Overall, serotypes O3:K6 and O4:K8, stable subpopulations of the diverse *V. parahaemolyticus* population in our surveillance, have clearly been epidemic in China.

*V. parahaemolyticus* serotypes O3:K29 and O1:K56 were mainly reported in Asia, with nonpandemic groups identified in Japan (10, 14). Our study showed that prevalence of serotype O3:K29 *V. parahaemolyticus* suddenly fluctuated during 2009 and 2010 and prevalence of O1:K56 fluctuated in 2010, but no focal outbreaks were confirmed; this finding indicates that sporadic outbreaks might have occurred. In addition, serotype O3:K29 isolates were identified as ST120 and the newly determined ST480, both belonging to CC120. Limited information could be obtained from the MLST database about the O1:K56 strains, and the isolates we tested were classified as ST8.

Further, our study found *V. parahaemolyticus* serotype O1:KUT might contain ≥1 character K antigens; however, 18 isolates harbored both *tdh* and *trh* genes, a combination that is not found frequently. Therefore, an O1:KUT epidemic clone might be prevalent in this region.

Whereas *V. parahaemolyticus* often is associated with the consumption of raw or undercooked shellfish, data from this surveillance program showed that most patients were transient residents who lived in rural areas and seldom ate seafood. However, epidemiologic data showed that *V. parahaemolyticus* infection was associated with eating outdoors and consumption of salad vegetables. Cross-contamination in food processing might be the source of infection; further epidemiologic investigation is under way.

In summary, *V. parahaemolyticus* has been prevalent for a long time in the southern coastal region of China, and diverse serotypes and multiple clones of the bacterium are circulating. On the basis of successful efforts to reduce prevalence of *V. parahaemolyticus* infections in Japan (15),

---

Table 2. Results of GS-PCR and MLST analysis of the 10 mostly commonly found serotypes of *Vibrio parahaemolyticus* isolates from patients with acute diarrhea, southern coastal region of China, 2007–2012*

| Serotype   | GS-PCR, n = 196 | MLST, n = 127 |
|------------|----------------|---------------|
|            | No. positive, n = 110 | No. negative, n = 86 | No. isolates tested | ST (no. isolates) | CC          |
| O3:K6      | 68             | 7             | 64             | ST3 (60), ST487 (1), ST489 (1), ST526 (1), ST497 (1) | CC3         |
| O4:K8      | 0              | 30            | 16             | ST265 (14), ST189 (1), ST438 (1) | CC345       |
| O3:K29     | 0              | 14            | 13             | ST120 (11), ST480 (2) | CC120       |
| O1:KUT     | 6              | 15            | 3              | ST3 (3) | CC3         |
| O1:K56     | 0              | 10            | 8              | ST8 (8) | CC8         |
| O1:K36     | 9              | 0             | 7              | ST3 (7) | CC3         |
| O4:K9      | 0              | 10            | 3              | ST332 (3) | Singleton |
| O4:K68     | 10             | 0             | 5              | ST3 (3) | CC3         |
| O5:K68     | 6              | 0             | 3              | ST3 (3) | CC3         |
| O1:K25     | 11             | 0             | 5              | ST481 (1) | Singleton |

*GS-PCR, group-specific PCR; MLST, multilocus sequence typing; ST, sequence type; CC, clonal complex.
we suggest holistic approaches involving regulations and guidance on fishery products and food hygiene to decrease the incidence of these infections in China.

Acknowledgments

We thank the personnel from 11 sentinel hospitals and participating district Centers for Disease Control and Prevention in Shenzhen for their participation in and contribution to our surveillance work.

This work was supported by China National Science and Technology Major Projects Foundation (no. 2012ZX10004215-003-005), National Natural Science Foundation of China (no. 81071433 to Q.H), and Shenzhen Public Service Platform of Pathogenic Microorganisms Repository.

Ms Li is a senior researcher in the Shenzhen Major Infectious Disease Control Key Laboratory, Shenzhen Center for Disease Control and Prevention. Her research interests include laboratory-based surveillance of foodborne pathogens and antimicrobial drug-resistant bacteria, particularly *V. parahaemolyticus* and diarrheagenic *E. coli*.

References

1. Nair GB, Ramamurthy T, Bhattacharya SK, Dutta B, Takeda Y, Sack DA. Global dissemination of *Vibrio parahaemolyticus* serotype O3:K6 and its serovariants. Clin Microbiol Rev. 2007;20:39–48. http://dx.doi.org/10.1128/CMR.00025-06
2. Lin X, Ran L, Ma L, Wang Z, Feng Z. Analysis on the cases of infectious diarrhea (rather than cholera, dysentery, typhoid and paratyphoid) reported in China, 2010 [in Chinese]. Chinese Journal of Food Hygiene. 2011;23:385–9.
3. Liu X, Chen Y, Wang X, Ji R. Foodborne disease outbreaks in China from 1992 to 2001—national foodborne disease surveillance system [in Chinese]. Wei Sheng Yan Jiu. 2004;33:725–7.
4. Vongsay K, Pan Z, Zhang X, Wang S, Cheng S, Mei L, et al. Occurrence of pandemic clones of *Vibrio parahaemolyticus* isolates from seafood and clinical samples in a Chinese coastal province. Foodborne Pathog Dis. 2008;5:127–34. http://dx.doi.org/10.1089/fpd.2007.0045
5. Blackstone GM, Nordstrom JL, Vickery MC, Bowen MD, Meyer RF, DePaola A. Detection of pathogenic *Vibrio parahaemolyticus* in oyster enrichments by real time PCR. J Microbiol Methods. 2003;53:149–55. http://dx.doi.org/10.1016/S0167-7012(03)00020-4
6. Davis CR, Heller LC, Peak KK, Wingfield DL, Goldstein-Hart CL, Bodager DW, et al. Real-time PCR detection of the thermostable direct hemolysin and thermolabilehemolysin genes in a *Vibrio parahaemolyticus* cultured from mussels and mussel homogenate associated with a foodborne outbreak. J Food Prot. 2004;67:1005–8.
7. Matsumoto C, Okada J, Ishibashi M, Iwanaga M, Garg P, Ramamurthy T, et al. Pandemic spread of an O3:K6 clone of *Vibrio parahaemolyticus* and emergence of related strains evidenced by arbitrarily primed PCR and toxRS sequence analyses. J Clin Microbiol. 2000;38:578–85.
8. Qu M, Deng Y, Zhang X, Liu G, Huang Y, Lin C, et al. Etiology of acute diarrhea due to enteropathogenic bacteria in Beijing, China. J Infect. 2012;65:214–22. http://dx.doi.org/10.1016/j.jinf.2012.04.010
9. Zhu M, Cui S, Lin L, Xu B, Zhao J, Xia S, et al. Analysis of the aetiology of diarrhoea in outpatients in 2007, Henan province, China. Epidemiol Infect. 2012;7:1–910.1017/S0950268812000970.
10. Chowdhury NR, Chakraborty S, Ramamurthy T, Nishibuchi M, Yamasaki S, Takeda Y, et al. Molecular evidence of clonal *Vibrio parahaemolyticus* pandemic strains. Emerg Infect Dis. 2000;6:631–6. http://dx.doi.org/10.3201/eid0606.000612
11. Chiou CS, Hsu SY, Chiu SI, Wang TK, Chao CS. *Vibrio parahaemolyticus* serovar O3:K6 as cause of unusually high incidence of food-borne disease outbreaks in Taiwan from 1996 to 1999. J Clin Microbiol. 2000;38:4621–5.
12. Gavilan RG, Zamudio ML, Martinez-Urtaza J. Molecular epidemiology and genetic variation of pathogenic *Vibrio parahaemolyticus* in Peru. PLoS Negl Trop Dis. 2013;7:e2210. http://dx.doi.org/10.1371/journal.pntd.0002210
13. Bhoopong P, Palittapongarnpim P, Pomwised R, Kiatkittipong A, Kamruzzaman M, Nakaguchi Y, et al. Variability of properties of *Vibrio parahaemolyticus* strains isolated from individual patients. J Clin Microbiol. 2007;45:1544–50. http://dx.doi.org/10.1128/JCM.02371-06
14. Wong HC, Liu SH, Wang TK, Lee CL, Chiou CS, Liu DP, et al. Characteristics of *Vibrio parahaemolyticus* O3:K6 from Asia. Appl Environ Microbiol. 2000;66:3981–6. http://dx.doi.org/10.1128/AEM.66.9.3981-3986.2000
15. Hara-Kudo Y, Saito S, Ohsuka K, Yanasaki S, Yahiro S, Nishio T, et al. Characteristics of a sharp decrease in *Vibrio parahaemolyticus* infections and seafood contamination in Japan. Int J Food Microbiol. 2012;157:95–101. http://dx.doi.org/10.1016/j.ijfoodmicro.2012.04.019

Address for correspondence: Qinghua Hu, Shenzhen Major Infectious Disease Control Key Laboratory, Shenzhen Center for Disease Control and Prevention, 8 Longyuan Rd, Nanshan District, Shenzhen, Guangdong Province, 518055, People’s Republic of China; email: huqinghua03@163.com or cjinquan@sohu.com

Like our podcasts?
Sign up to receive email announcements when a new podcast is available.

www.cdc.gov/ncidod/eid/subscrib.htm