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Spreading of pandemic Vibrio parahaemolyticus O3:K6 and its serovariants in China

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n China, V. parahaemolyticus has been a leading cause of foodborne outbreaks and bacterial infectious diarrhea since the 1990s, and most infections have been associated with the pandemic *V. parahaemolyticus* clone. However, a comprehensive overview of the sero-prevalence and genetic diversity of the pandemic V. parahaemolyticus clone in China is lacking. To compensate for this deficiency, pandemic isolates in both clinical and environmental Chinese samples collected from multiple studies were analyzed here. Surprisingly, as many as 27 clinical pandemic serovariants were identified and were widely distributed across nine coastal provinces and two inland provinces. O3:K6, O4:K68 and O1:KUT represented the predominant clinical serovars. Only four environmental pandemic serovariants had previously been reported, and they were spread throughout Shanghai (O1:KUT, O3:K6), Jiangsu (O3:K6, O4:K48), Zhejiang (O3:K6) and Guangdong (O4:K9). Notably, 24 pandemic serovariants were detected within a short time frame (from 2006 to 2012). The pandemic isolates were divided into 15 sequence types (STs), ten of which fell within clonal complex (CC) 3. Only three STs (ST3, ST192 and ST305) were identified in environmental isolates. Substantial serotypic diversity was mainly observed among isolates within pandemic ST3, which comprised 21 combinations of O/K antigens. The pandemic O3:K6 serotype showed a high level of sequence diversity, which was shared by eight different STs (ST3, ST227, ST431, ST435, ST487, ST489, ST526 and ST672). Antimicrobial susceptibility testing revealed that most isolates shared similar antibiotic susceptibility profiles. They were resistant to ampicillin but sensitive to most other drugs that were tested. In conclusion, the high levels of serotypic and genetic diversity of the pandemic clone suggest that the involved regions are becoming important reservoirs for the emergence of novel pandemic strains. We underscore the need for routine monitoring to prevent pandemic V. parahaemolyticus infection, which includes monitoring antimicrobial responses to avoid excessive misuse of antibiotics.

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