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Microbiology 2018: Insights on pandemic vibrio parahaemolyticus infection

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In China, since the 1990s, V. parahaemolyticus has been a leading cause of foodborne outbreaks and bacterial infectious diarrhea, and most infections are associated with the V. parahaemolyticus O3: K6 pandemic and its serovariants. There is nevertheless a lack of a detailed description of the sero-prevalence and genetic diversity of the V. parahaemolyticus pandemic clone in China. In this study, pandemic isolates in Chinese clinical and environmental samples obtained from multiple studies were analyzed to account for this deficiency. Significant serotypic diversity was observed primarily among isolates within the ST3 pandemic, which consisted of 21 O / K antigen combinations. The O3: K6 serotype pandemic exhibited a high degree of sequence diversity, shared by eight separate STs (ST3, ST227, ST431, ST435, ST487, ST489, ST526, and ST672). Testing of susceptibility to antimicrobials revealed that most isolates shared similar profiles of susceptibility to antibiotics. They were ampicillin resistant but susceptible to most other drugs studied. In conclusion, the high rates of serotypic and genetic diversity of the pandemic clone indicate that the regions concerned are significant reservoirs for the emergence of new pandemic strains. They stress the need for routine surveillance to prevent the infection with pandemic V. parahaemolyticus, which involves tracking antimicrobial responses to avoid unnecessary antibiotic violence. We also need further investigations to delineate the specific mechanisms underlying the possible seroconversion of pandemic isolates.

Introduction

The Gram-negative bacterium Vibrio parahaemolyticus is a natural inhabitant of the estuarine and coastal environments. This pathogen is a worldwide important cause of acute gastroenteritis in humans. It is a pathogenic bacteria of multiple serotypes, and can be classified into 13 O serotypes and 71 K serotypes based on somatic (O) antigens and capsular (K) antigens. The pandemic isolates, including serotype O3: K6 and their serovariants, have spread globally through either sporadic diarrhea or food-related contaminated outbreaks since 1997.

In this study, we identified the Chinese pandemic isolates V parahaemolyticus primarily from existing literature and re-analyzed the sero-prevalence and genetic diversity of these entire pandemic isolates. In our successful diarrheal infection studies, we isolated several of these pandemic isolates, and concentrated primarily on their antimicrobial responses in this research, which was not previously demonstrated. Overall, after the advent of this clone, our goal is to produce a detailed overview of the spread of the pandemic Vibrio parahaemolyticus O3: K6 and its serovariants.

Results

According to a detailed review, an extensive map of the dissemination of the pandemic serotypes detected in China was generated. The pandemic serotypes in nine coastal provinces and two inland provinces (Beijing and Sichuan) were highly abundant and variable, with 27 clinical and four environmental pandemic serotypes identified. O3: K6 (in 11 provinces) was the most widely disseminated serotype of clinical isolates, followed by O4: K68 (in eight provinces), O1: KUT (in five provinces), O1: K25 (in four provinces), and O1: K36 (in four). They identified the four environmental serotypes in Shanghai (O1: KUT, O3: K6), Jiangsu (O3: K6, O4: K48), Zhejiang (O3: K6), and Guangdong (O4: K9).

Discussion

The pandemic V. parahaemolyticus infection has attracted much attention from scientists as an emerging public health concern. This study gave an overview of the prevalence of V. parahaemolyticus pandemic isolates in both clinical and environmental samples collected from multiple Chinese studies. We have demonstrated a high serotypic and genetic diversity of these pandemic isolates. The pandemic isolates of O3: K6 (persistent from 2002 to 2012 for 11 years) spread through 11 provinces indicates that the pandemic clone has been endemically established in China. Continued monitoring of patterns of antibiotic resistance in pandemic isolates is urgently required to prevent excessive antibiotic misuse, though most of the isolates tested in this study showed only high ampicillin resistance.

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The isolates analyzed in this study have been distributed to regions where the temperature differences and other environmental factors are vast. Therefore we suspect that in the transmission process the strains must adapt to different living environments by more frequently altering their biological properties. One of the most effective ways to accomplish this may be to make serological changes. Nevertheless, the specific serotype conversion mechanism is not yet known. Actually, the highest priority is to track the emergence of new serovariants constantly to prevent the pandemic strains from triggering coastal outbreaks and spreading to other countries and regions.

Another important aspect of this study was investigating the susceptibility of various pandemic isolates to antimicrobials. Our tests showed similar profiles of antibiotic susceptibility in ST3, ST88 and non-pandemic isolates. They concluded that the sampling location or month in which the samples were collected had no significant impact on patterns of resistance to V. parahaemolyticus, since isolates from both environmental and clinical sources shared similar profiles of resistance to antibiotics. Unsurprisingly, the majority of isolates tested in this study showed ampicillin resistance, which is very common in isolates recovered from various sources in V. parahaemolyticus.

Our findings represent a comprehensive review of the V. parahaemolyticus O3: K6 pandemic and its serovariants by thoroughly evaluating a comprehensive collection of pandemic isolates from multiple Chinese studies. The pandemic clone contains high levels of serotypic and genetic diversity, indicating that the regions involved are becoming important reservoirs for the emergence of new pandemic strains which potentially challenge the clinical management of the infection and its prevention. Thus, we emphasize the need for routine clinical and environmental monitoring to prevent infection and dissemination with pandemic V. parahaemolyticus, including monitoring antimicrobial response even though most of the current antimicrobial agents are effective in routine use. Extended research requires the process in which the isolates undergo seroconversion with pandemic genetic marks.