Serotyping and virulence-related genes analysis of the *Vibrio parahaemolyticus* from coast cities in China

Dapeng Wang, Min Dai, Wanyi Chen, Xianming Shi

Department of Food Science and Technology and Bor Luh Food Safety Center, Shanghai Jiao Tong University, Shanghai 200240, China

Abstract:

*Vibrio parahaemolyticus* is one of the most important food-borne pathogens, which causes gastroenteritis after consuming contaminated raw or lightly cooked shellfishes. During the last decade, the pathogen becomes the leading food-borne pathogens in China.

In this study, *V. parahaemolyticus* isolates were analyzed by Polymerase Chain Reaction (PCR) for the virulence-related genes (*tdh* and *trh*) and serotyping, including 103 food-borne isolates and 158 clinical isolates. All bacteria came from three cityies, Shanghai, Zhoushan and Ningbo, which located along the east coast of China. The results demonstrated that only 4 foodborne isolates were *tdh*+ positive strains and all of them were O3:K6 serotype; however, all the clinical isolates were positive for the main virulence-related genes except 5 isolates. Six isolates were (*tdh*+/*trh*+) strains and 147 isolates were
(tdh+/trh-) strains. In addition, the strains were divided into 22 serotypes. O3:K6 isolates were the epidemic strains (107/158). The following serotypes of other isolates were O1:K6, O3:K68, O1:K25, O1:K56 and O2:K3, respectively. It suggested that the clinical strains were more diverse on serotypes of this bacterium.

The outbreak of the *V. parahaemolyticus* O3:K6 strain is decreasing in the past 10 years. Therefore, more attention should be paid in the emergence of the new serotyped *V. parahaemolyticus*, which might be the next pandemic pathogen. Changing of this pathogen should be routinely monitored in order to prevent future potential risk.

Keywords: *Vibrio parahaemolyticus*; serotyping; virulence-related genes