Foodborne Diseases due to Vibrios

Koichiro Yamamoto,* Mai Yamamoto

Department of Nutritional Sciences, Faculty of Health and Welfare Sciences, Okayama Prefectural University, Soja, Okayama 719-1197, Japan

*e-mail: yamak6212@fhw.oka-pu.ac.jp

Abstract

Vibrios are Gram-negative halophilic bacteria mainly living in sea water. Three species of vibrios are well-known to cause foodborne infectious diseases in human; namely, *Vibrio cholerae*, *V. parahaemolyticus* and *V. vulnificus*. Of them, the main symptom of *V. vulnificus* infection is not diarrhea but deadly sepsis. *V. vulnificus* is mostly infected from contaminated sea foods when taken without being cooked. The infection due to this organism proceeds rapidly and the death rate is more than 50%. Although this organism can be infected in patients whose liver is damaged like cirrhosis.

We attempted to identify pathogenic genes of *V. vulnificus* by signature-tagged transposon mutagenesis. A clinically isolated-virulent *V. vulnificus* strain was randomly inserted with signature-tagged transposon into genome DNA and about 6400 transposon insertion mutants were obtained. The mutants were inoculated into mice which were sensitized to *V. vulnificus* infection in order to screen attenuated mutants. Twelve mutants were screened by dothybridization as candidates of attenuated mutants. Lethal doses of the mutants were checked out. Lethality of the mutant was weaker than that of the parent strain, suggesting that 12 mutants might be attenuated. The DNA sequence of the flanking region to transposon insertion sites was determined. The sequence homologies to the *V. vulnificus* genome data base were found in the genes, namely, of IMP dehydrogenase, UDP-N-acetylglucosamin-2-epimerase, aspartokinase, phosphoribosylformylglycinamidine cycloligase, Na+ symporter, and hypothetical protein. Some of these genes might be necessary for *V. vulnificus* infection.

Keywords: Vibrio vulnificus, infection, foodborne, transposon