

Isolation and Identification of *Citrobacter Freundii* from Diseased *Macrobrachium Nipponense*

Sheham Guma Ibrahim¹

¹College of Agriculture, Yangzhou University, China

Abstract

Macrobrachium nipponense one of the most freshwater in world. but face may problem in farm. Out breaks of mass mortalities occurred in *Macrobrachium nipponense* farms in Jintan county, china. The bacterial isolates from *M. nipponense* show the same phenotypic traits and biochemical characteristics, and were identified as *Citrobacter freundii* according to biochemical characteristics and molecular identification. The infection test revealed that the strain YG2 was pathogenic to *M. nipponense*, and the half lethal dose (LD50) was 3.35×10^5 CFU/mL at 7d post-infection. Detection of virulence genes indicated that YG2 was positive for *ompX*, and *LDH*, *cfa*, *ureG*, *ureF*, *ureE*, *ureD*, *viaB*. Furthermore, the results of extracellular enzyme analysis detect that the strain can produce protease, urease, amylase, lecithin, and hemolysin. Antibiotic resistance results showed that the isolate was resistant to ampicillin, cefazolin, cephalothin, cefoxitin, aboren, doxycycline, neomycin, and penicillin. This research provides a theoretical basis for a better understanding of the pathogenicity and resistance, which might contribute to the prevention of *C. freundii* in the future.

Key Words: *Citrobacter freundii*, Pathogenicity, *Macrobrachium nipponense*, Antibiotics resistance