

ABSTRAK

HUBUNGAN KEBERADAAN GEN RESISTANSI ANTIMIKROBA (*Antimicrobial Resistance Gene*, ARG) GOLONGAN FLUOROKUINOLON DAN FENOTIPE RESISTANSINYA PADA *Vibrio parahaemolyticus*

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Budi daya udang vaname (*Litopenaeus vannamei*) menjadi salah satu komoditas perikanan yang berkembang pesat di Indonesia. Penggunaan beberapa antibiotik merupakan aktivitas umum guna menjaga kestabilan produktivitas udang serta mencegah infeksi bakteri patogen, seperti *V. parahaemolyticus*. Tetapi, penggunaan antibiotik yang tidak terkendali dapat memicu perkembangan resistansi antibiotik. Penelitian ini bertujuan untuk mendeteksi adanya resistansi pada bakteri *V. parahaemolyticus* secara fenotipe dan mendeteksi keberadaan gen penyandi resistansi terhadap antibiotik golongan fluorokuinolon yang berasal dari 42 isolat udang vaname budi daya. Metode pengujian yang dilakukan adalah re-identifikasi isolat bakteri *V. parahaemolyticus*, difusi cakram dan *Minimum Inhibitor Concentration* (MIC), serta deteksi gen penyandi resistansi antibiotik dengan PCR. Hasil penelitian ini menunjukkan seluruh isolat bakteri *V. parahaemolyticus* 100% sensitif terhadap antibiotik *ciprofloxacin* dan *enrofloxacin* setelah diujikan secara fenotipe. Hasil pengujian secara genotipe menunjukkan 42 isolat bakteri terdeteksi gen *gyrA* dan *gyrB*, sedangkan gen *parC* hanya terdeteksi pada 40 isolat. Berdasarkan hal tersebut, dapat disimpulkan seluruh gen terdeteksi pada isolat bakteri yang secara fenotipe menunjukkan hasil sensitif terhadap *ciprofloxacin* dan *enrofloxacin*. Ketidakdeteksian gen *parC* dapat disebabkan akibat *mismatch primer* atau adanya *silent mutation*. Oleh sebab itu, diperlukan analisis lanjutan seperti sekuensing gen untuk membuktikan ada atau tidaknya mutasi pada daerah *Quinolone Resistance Determining Region* (QRDR).

Kata Kunci: *Vibrio parahaemolyticus*, Resistansi antibiotik, Gen penyandi, *Ciprofloxacin*, *Enrofloxacin*

ABSTRACT

THE RELATIONSHIP BETWEEN THE PRESENCE OF FLUOROQUINOLONE ANTIMICROBIAL RESISTANCE GENES (ARGs) AND PHENOTYPIC RESISTANCE IN *Vibrio parahaemolyticus*

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Whiteleg shrimp (*Litopenaeus vannamei*) cultivation is one of the rapidly growing fishery commodities in Indonesia. The use of several antibiotics is a common activity to maintain stable shrimp productivity and prevent pathogenic bacterial infections, such as *V. parahaemolyticus*. However, uncontrolled antibiotic use can trigger the development of antibiotic resistance. This study aims to detect resistance in *V. parahaemolyticus* bacteria phenotypically and detect the presence of resistance-encoding genes to fluoroquinolone antibiotics derived from 42 farmed whiteleg shrimp isolates. The testing methods used were re-identification of *V. parahaemolyticus* bacterial isolates, disc diffusion and Minimum Inhibitor Concentration (MIC), as well as detection of antibiotic resistance-encoding genes by PCR. The results of this study showed that all *V. parahaemolyticus* bacterial isolates were 100% sensitive to ciprofloxacin and enrofloxacin antibiotics after being tested phenotypically. The results of genotypic testing showed that 42 bacterial isolates detected the *gyrA* and *gyrB* genes, while the *parC* gene was only detected in 40 isolates. Based on this, it can be concluded that all genes were detected in bacterial isolates that phenotypically showed sensitivity to ciprofloxacin and enrofloxacin. The undetected *parC* gene could be due to a primer mismatch or a silent mutation. Therefore, further analysis, such as gene sequencing, is required to confirm the presence or absence of mutations in the Quinolone Resistance Determining Region (QRDR).

Keywords: *Vibrio parahaemolyticus*, antimicrobial resistance, resistance genes, ciprofloxacin, enrofloxacin