

Karakterisasi Molekuler gen *gyrA* dan *gyrB* pada Quinolone Resistance Determining Region (QRDR) *Escherichia coli* Resisten Ciprofloxacin yang Diisolasi dari Isolat Klinis Pasien Infeksi Saluran Kemih (ISK) = Molecular Characterization of *gyrA* and *gyrB* Genes on Quinolone Resistance Determining Region (QRDR) Ciprofloxacin Resistant *Escherichia coli* Isolated from Clinical Isolates of Urinary Tract Infection (UTI) Patients

Riani Agustini, author

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Abstrak

Escherichia coli bertanggung jawab atas 80-90% menyebabkan infeksi saluran kemih (ISK). Ciprofloxacin merupakan salah satu antibiotik yang berspektrum luas yang bekerja efektif terhadap *E. coli* yang biasa digunakan dalam pengobatan ISK. Namun telah banyak dilaporkan meningkatnya resistensi *E. coli* penyebab ISK terhadap Ciprofloxacin. Mutasi pada QRDR gen *gyrA* dan *gyrB* merupakan 2 gen yang banyak dilaporkan sebagai penyebab resistensi terhadap Ciprofloxacin. Di Indonesia, studi mutasi gen *gyrA* dan *gyrB* yang dikaitkan dengan resistensi *E. coli* penyebab ISK terhadap Ciprofloxacin belum dilaporkan. Oleh karena itu, dalam penelitian ini dilakukan karakterisasi daerah QRDR gen *gyrA* dan *gyrB* menggunakan metoda PCR dan DNA sekuensing yang mencakup posisi asam amino 40-110 (*gyrA*) dan posisi 407-473 (*gyrB*). Untuk gen *gyrA*, dari semua isolat (9 isolat) mengalami 2 perubahan asam amino pada posisi 83 (S83L) dan 87 (D87N) di daerah QRDR. 1 isolat mengalami 2 tambahan perubahan asam amino diluar daerah QRDR pada posisi asam amino 55 (L55V) dan posisi asam amino 66 (S66T). Adapun gen *gyrB*, dari 9 isolat semua isolat tidak mengalami perubahan asam amino di daerah QRDR. Berdasarkan analisis docking, isolat yang mengalami 4 perubahan asam amino (*gyrA*) menunjukkan pelemahan afinitas yang kuat antara DNA gyrase dan ciprofloxacin dibandingkan dengan isolat yang hanya mengalami 2 perubahan asam amino pada daerah QRDR.

.....*Escherichia coli* is responsible for 80-90% of causes of urinary tract infections (UTI). Ciprofloxacin is broad spectrum antibiotic that works effectively against *E. coli* which is commonly used in the treatment of UTI. However, there have been many reports of increasing resistance of *E. coli* that causes UTI to Ciprofloxacin. Mutations in the QRDR genes *gyrA* and *gyrB* are two genes that have been widely reported as causes of resistance to Ciprofloxacin. In Indonesia, studies of *gyrA* and *gyrB* gene mutations associated with resistance of UTI-causing *E. coli* to Ciprofloxacin have not been reported. Therefore, in this study, the QRDR region of the *gyrA* and *gyrB* genes was characterized using PCR and DNA sequencing methods covering amino acid positions 40-110 (*gyrA*) and positions 407-473 (*gyrB*). For the *gyrA* gene, all isolates (9 isolates) experienced 2 amino acid changes at positions 83 (S83L) and 87 (D87N) in the QRDR region. 1 isolate experienced 2 additional amino acid changes outside the QRDR region at amino acid position 55 (L55V) and amino acid position 66 (S66T). As for the *gyrB* gene, of the 9 isolates, all isolates did not experience amino acid changes in the QRDR region. Based on docking analysis, isolates that experienced 4 amino acid changes (*gyrA*) showed a strong weakening of the affinity between DNA gyrase and ciprofloxacin compared to isolates that only experienced 2 amino acid changes in the QRDR region.