

RINGKASAN

Tikus hutan menjadi salah satu satwa yang paling sering diburu untuk dikonsumsi oleh masyarakat Sulawesi Utara. Tikus berpotensi membawa patogen baik bakteri maupun virus melalui urin dan feses yang dapat menular ke manusia (zoonosis). Bakteri patogen pada feses tikus biasanya berasal dari kelompok bakteri Enterobacteriaceae yang infeksiya bersifat nosokomial sehingga penanganannya memerlukan antibiotik, seperti *Ceftriaxone* dari golongan β -laktam. Bakteri dapat memiliki sifat resistensi terhadap antibiotik secara alami maupun karena adanya mutasi gen. Salah satu mekanisme resistensi kelompok Enterobacteriaceae terhadap antibiotik β -laktam adalah dengan memproduksi *extended spectrum beta-lactamase* (ESBL). Oleh karena itu, tujuan dari penelitian ini adalah mengetahui keberadaan dan identitas bakteri patogen asal feses tikus hutan yang dikonsumsi yang resisten terhadap antibiotik β -laktam.

Penelitian dilakukan menggunakan metode survei dengan variabel bebas dari penelitian ini adalah jenis antibiotik dan variabel terikat adalah respon isolat bakteri asal feses tikus terhadap antibiotik. Pengambilan sampel feses tikus di pasar tradisional di Sulawesi Utara dilakukan dengan metode *purposive sampling*. Isolasi bakteri resisten antibiotik β -laktam asal feses tikus dilakukan menggunakan media *MacConkey Agar* dengan penambahan *Ceftriaxone*. Bakteri yang resisten antibiotik β -laktam dilakukan uji resistensi antibiotik atau *Antimicrobial Susceptibility Test* (AST) menggunakan metode Kirby-Bauer terhadap beberapa antibiotik, yaitu *Ceftriaxone* (CRO), *Cefoxitine* (FOX), *Amoxycillin-clavulanic Acid* (AMC), dan *Imipenem* (IPM). Isolat bakteri diidentifikasi secara fenotipik dan molekuler berdasarkan gen 16S rRNA. Gen resisten *Extended-spectrum β -lactamase*, yaitu *bla_{SHV}*, *bla_{CTX-M}*, dan *bla_{TEM}* juga diamplifikasi dari isolat bakteri yang resisten antibiotik β -laktam. Data hasil penelitian dianalisis secara deskriptif.

Hasil penelitian menunjukkan terdapat dua isolat bakteri yang resisten terhadap 3 jenis antibiotik β -laktam, yaitu isolat 1C dan 5C. Kedua isolat tersebut resisten terhadap CRO, FOX, dan AMC, serta sensitif terhadap IPM. Isolat 1C dan 5C terkonfirmasi memiliki gen resisten *bla_{TEM}* yang menyandikan *extended spectrum beta-lactamase* (ESBL) sehingga mampu resisten terhadap 3 jenis antibiotik β -laktam. Berdasarkan hasil karakterisasi fenotipik dan molekuler, kedua isolat berkerabat dekat dengan *Klebsiella aerogenes* dengan similaritas 99,85% untuk isolat 1C dan 100% untuk isolat 5C.

Kata kunci: *Ceftriaxone*, *Enterobacteriaceae*, resisten, Sulawesi Utara, tikus hutan.

SUMMARY

Forest rats are one of the most commonly hunted animals for consumption by the people of North Sulawesi. Rats have the potential to carry pathogens both bacteria and viruses through urine and feces that can be transmitted to humans (zoonosis). Pathogenic bacteria in rat feces usually come from the Enterobacteriaceae group of bacteria whose infections are nosocomial in nature so that handling requires antibiotics, such as *Ceftriaxone* from the β -lactam group. Bacteria can have resistance to antibiotics naturally or due to gene mutation. One of the resistance mechanisms of the Enterobacteriaceae group to β -lactam antibiotics is by producing *extended spectrum beta-lactamase* (ESBL). Therefore, the purpose of this study is to determine the presence and identity of pathogenic bacteria from the feces of consumed forest rats that are resistant to β -lactam antibiotics.

The research was conducted using survey method with the independent variables of this research are the type of antibiotics and the dependent variable is the response of the bacterial isolated bacteria from rat feces to antibiotics. Sampling of rat feces in traditional markets in North Sulawesi was done by purposive sampling method. Isolation of β -lactam antibiotic resistant bacteria from rat feces was conducted by using *MacConkey Agar* media with the addition of *Ceftriaxone*. Bacteria resistant to β -lactam antibiotics were tested for antibiotic resistance or *Antimicrobial Susceptibility Test* (AST) using the Kirby-Bauer method against several antibiotics, including *Ceftriaxone* (CRO), *Cefoxitine* (FOX), *Amoxycillin-clavulanic Acid* (AMC), and *Imipenem* (IPM). Bacterial isolates were identified by phenotypic, biochemical test and molecular approaches based on the 16S rRNA gene. *Extended-spectrum β -lactamase* resistant genes (*bla_{SHV}*, *bla_{CTX-M}*, and *bla_{TEM}*) were amplified from β -lactam antibiotic resistant bacterial isolates. The obtained data were analyzed by descriptive approaches.

The results showed that there were two bacterial isolates that were resistant to 3 types of β -lactam antibiotics, namely isolates 1C and 5C. Both isolates were resistant to CRO, FOX, and AMC, and sensitive to IPM. Isolates 1C and 5C are confirmed to have a resistant gene *bla_{TEM}* which encodes *extended spectrum beta-lactamase* (ESBL) so that they are resistant to 3 types of β -lactam antibiotics. Based on the results of phenotypic and molecular characterization, both isolates are closely related to *Klebsiella aerogenes* with similarity of 99.85% for isolate 1C and 100% for isolate 5C.

Keywords: *Ceftriaxone*, *Enterobacteriaceae*, *forest rat*, *resistance*, *Sulawesi Utara*.