

INTISARI

Kajian Lintas Seksional Resistansi *Escherichia coli* O157:H7 pada Sapi Potong di Instalasi Karantina Hewan Wilayah Kerja Balai Besar Karantina Hewan, Ikan, dan Tumbuhan DKI Jakarta terhadap Beberapa Antibiotik

Escherichia coli O157:H7 (*E. coli* O157:H7) merupakan agen penyebab *foodborne disease* pada manusia yang menyebabkan penyakit *haemorrhagic colitis* (HC), *haemolytic uremic syndrome* (HUS), dan *thrombocytopenia purpura* (TPP). Sapi berperan sebagai pembawa *E. coli* O157:H7 tanpa menunjukkan gejala klinis. Kondisi ini membuat *E. coli* O157:H7 tetap berada di lingkungan dan berpotensi munculnya resistansi terhadap antibiotik. *Antimicrobial Resistance* (AMR) merupakan ancaman global bagi kesehatan masyarakat dan hewan. *E. coli* O157:H7 yang resistan terhadap antibiotik yang berada di lingkungan, dapat berpotensi menyebar ke hewan dan manusia. Penelitian ini menggunakan kajian lintas seksional dengan tujuan untuk mengetahui prevalensi *E. coli* O157:H7, resistansi terhadap antibiotik, gen resistansi dan faktor risiko yang berhubungan pada sapi potong impor asal Australia di Instalasi Karantina Hewan (IKH) Wilayah Kerja Balai Besar DKI Jakarta (BBKHIT DKI Jakarta). Penelitian ini menggunakan 680 sampel terdiri dari 650 spesimen feses sapi, 20 spesimen tanah, 5 spesimen air limbah dan 5 spesimen air minum dari 5 IKH yaitu IKH A di Kab. Cianjur, IKH B di Kab. Sukabumi, IKH C di Kab. Purwakarta, IKH D di Kab. Serang dan IKH E di Kab. Bandung Barat. Isolasi dan identifikasi *E. coli* secara konvensional. Konfirmasi *E. coli* O157:H7 dengan *Polymerase Chain Reaction* (PCR) terhadap gen *rfbO157*, *fliCH7*, *stx1* dan *stx2*. Sensitivitas terhadap antibiotik dilakukan dengan metode *Kirby Bauer* dan pemeriksaan gen resistan dengan target gen *tetA*, *blaTEM*, *strA*, *sul2*, dan *qnrS* dengan PCR. Analisis data secara deskriptif dan bivariat. Total *E. coli* sebanyak 95,44% (649/680) dan *E. coli* O157:H7 sebanyak 2,35% (16/680). *E. coli* O157:H7 yang memiliki *shiga toxin* yaitu 1,62% (11/680). *E. coli* O157:H7 resistan terhadap tetrasiklin sebanyak 31,25% (5/16) dan ampisilin sebanyak 6,25% (1/16). *E. coli* O157:H7 yang sensitif terhadap antibiotik sebanyak 69% (11/16). *E. coli* O157:H7 memiliki gen *tetA* 43,75% (7/16), *blaTEM* 12,5% (2/16), *strA* 37,5% (6/16), *sul2* 18,75% (3/16) dan *qnrS* 18,75% (3/16). Asal ternak merupakan faktor risiko kontaminasi *E. coli*. Manajemen pemeliharaan di seluruh IKH memiliki keseragaman. IKH C memiliki jumlah *E. coli* O157:H7 terbanyak dan terdapat resistansi ganda tetrasiklin dan ampisilin. Penelitian ini menunjukkan bahwa terdapat *E. coli* O157:H7 pada sapi potong asal Australia yang patogen dan telah resistan terhadap tetrasiklin dan ampisilin, sehingga perlu kewaspadaan dan penguatan pengendalian karena dapat menimbulkan risiko bagi kesehatan manusia dan hewan.

Kata kunci : Sapi impor, *E. coli* O157:H7, resistansi antibiotik, gen resistan.

ABSTRACT

Resistance Cross-Sectional Study of *Escherichia coli* O157:H7 in Beef Cattle at the Animal Quarantine Installation, Work Area of the DKI Jakarta Animal, Fish, and Plant Quarantine Center to Several Antibiotics

Escherichia coli O157:H7 (*E. coli* O157:H7) is a causative agent of foodborne disease in humans that causes hemorrhagic colitis (HC), hemolytic uremic syndrome (HUS), and thrombocytopenia purpura (TPP). Cattle act as carriers of *E. coli* O157:H7 without showing clinical symptoms. This condition allows *E. coli* O157:H7 to remain in the environment and has the potential to develop resistance to antibiotics. Antimicrobial Resistance (AMR) is a global threat to public and animal health. *E. coli* O157:H7 that is resistant to antibiotics in the environment can potentially spread to animals and humans. This study used a cross-sectional study with the aim of determining the prevalence of *E. coli* O157:H7, antibiotic resistance, resistance genes and associated risk factors in imported beef cattle from Australia at the Animal Quarantine Installation (IKH) of the DKI Jakarta Large Agency (BBKHIT DKI Jakarta). This study used 680 samples consisting of 650 cow feces specimens, 20 soil specimens, 5 wastewater specimens and 5 drinking water specimens from 5 IKH namely IKH A in Cianjur Regency, IKH B in Sukabumi Regency, IKH C in Purwakarta Regency, IKH D in Serang Regency and IKH E in West Bandung Regency. Isolation and identification of *E. coli* conventionally. Confirmation of *E. coli* O157:H7 with Polymerase Chain Reaction (PCR) against *rfbO157*, *fliCH7*, *stx1* and *stx2* genes. Sensitivity to antibiotics was carried out using the *Kirby Bauer* method and examination of resistance genes targeting the *tetA*, *blaTEM*, *strA*, *sul2*, and *qnrS* genes with PCR. Data analysis was descriptive and bivariate. Total *E. coli* was 95.44% (649/680) and *E. coli* O157:H7 was 2.35% (16/680). *E. coli* O157:H7 that has *shiga toxin* is 1.62% (11/680). *E. coli* O157:H7 is resistant to tetracycline as much as 31.25% (5/16) and ampicillin as much as 6.25% (1/16). *E. coli* O157:H7 that is sensitive to antibiotics as much as 69% (11/16). *E. coli* O157:H7 has *tetA* gene 43.75% (7/16), *blaTEM* 12.5% (2/16), *strA* 37.5% (6/16), *sul2* 18.75% (3/16) and *qnrS* 18.75% (3/16). Cattle origin is a risk factor for *E. coli* contamination. Livestock management across all IKH is consistent. IKH C has the highest number of *E. coli* O157:H7 and dual resistance to tetracycline and ampicillin. This study indicates that pathogenic *E. coli* O157:H7 is present in Australian beef cattle and is resistant to tetracycline and ampicillin, necessitating vigilance and strengthening control measures as it poses a risk to human and animal health.

Keywords: Imported cattle, *E. coli* O157:H7, antibiotic resistance, resistance gene.