

INTISARI

Kajian Epidemiologi Resistansi *Escherichia coli* O157:H7 terhadap Antibiotik pada Sapi Perah Di Daerah Istimewa Yogyakarta

Escherichia coli O157:H7 merupakan mikroorganisme patogen zoonosis yang dapat menimbulkan infeksi serius pada manusia. Penularan dari hewan ke manusia akibat kontaminasi produk asal hewan terutama susu pernah dilaporkan. Tujuan penelitian ini untuk menghitung cemaran *Escherichia coli* khususnya O157:H7, mengidentifikasi resistansi terhadap antibiotik dan gen penyandi resistansinya serta menganalisis faktor risikonya pada peternakan sapi perah di Daerah Istimewa Yogyakarta. Penelitian ini melibatkan 106 peternakan dengan sampel susu berasal dari 450 sapi perah, 106 sampel tanah, 106 sampel swab lantai kandang dan 106 sampel swab tangan pemerah. Isolasi dan identifikasi menggunakan media *MacConkey*, uji biokimia dengan media *Indole*, *Methyl Red*, *Voges-Proskauer*, *Citrate (IMVic)*, identifikasi O157 dengan media *Sorbitol MacConkey*, identifikasi O157:H7 dengan *Polymerase Chain Reaction (PCR)* dengan target gen *Stx1*, *Stx2*. Pengujian resistansi terhadap antibiotik Amoksisilin, Streptomisin, Oksitetrasiklin, Tetrasiklin dan Sulfametoksazol-Trimethoprim menggunakan metode *Kirby Bauer* dilanjutkan identifikasi gen resisten dengan target gen *strA*, *tetA* dan *sul2*. Data faktor risiko dikumpulkan melalui observasi dan wawancara pada peternak yang dianalisis secara deskriptif statistik dan regresi logistik menggunakan SPSS. Prevalensi *E. coli* pada tingkat peternakan sebesar 67,92% dan pada tingkat ternak sebesar 20,89%. Prevalensi *E. coli* O157:H7 pada tingkat peternakan sebesar 4,71% dan pada tingkat ternak sebesar 1,11%. Tingkat resistensi *E. coli* dari susu sebesar 30,9%, tanah 47,1%, kandang 18,2% dan tangan 40%, sedangkan tingkat resistansi *E. coli* O157:H7 sebesar 20% dari isolat susu. Resistansi *E. coli* terjadi pada Amoksisilin, Oksitetrasiklin, Streptomisin dan Sulfametoksazol-Trimetoprim sedangkan isolat *E. coli* O157:H7 resisten pada Sulfametoksazol-Trimetoprim. Gen penyandi resistansi antibiotik (gen *tetA*, gen *strA*, gen *sul2*) dideteksi pada *E. coli*, namun tidak ditemukan gen penyandi resisten antibiotik pada 3 gen di atas pada isolat *E. coli* O157:H7 yang diperoleh. Identifikasi faktor risiko cemaran *E. coli* menunjukkan bahwa kondisi kandang dan pengelolaan limbah yang buruk serta riwayat mastitis dan diare meningkatkan probabilitas peluang terjadinya cemaran *E. coli* sedangkan pemberian dosis antibiotik yang tidak sesuai meningkatkan probabilitas terjadinya resistansi antibiotik. Tidak dapat dilakukan analisis faktor risiko terhadap *E. coli* O157:H7. Analisis pola sebaran *E. coli* dengan metode *Average Nearest Neighbor* memiliki pola mengumpul (*clustered*) sedangkan pola *E. coli* O157:H7 dan resistensi antibiotik memiliki pola menyebar (*dispersed*). Analisis dengan metode *Standar Deviatonal Ellips* dari sampel susu dan lantai kandang yang tercemar *E. coli* menunjukkan tingkat risiko penyebaran kontaminasi yang lebih tinggi, sedangkan sebaran vertikal pada sampel tangan pemerah dan tanah menunjukkan arah dominan aliran dengan memperhatikan penanganan sanitasi yang lebih baik.

Kata kunci: *Escherichia coli* O157:H7, faktor risiko, resistansi antibiotik, sapi perah

ABSTRACT

Epidemiology Study of *Escherichia coli* O157:H7 Resistance of Antibiotics in Dairy Cattle in Yogyakarta Special Region

Escherichia coli O157:H7 is a zoonotic pathogen that can cause serious infections in humans. Transmission from animals to humans due to contamination of animal products, especially milk, has been reported. The purpose of this study was to calculate the contamination of *Escherichia coli*, particularly O157:H7, identify antibiotic resistance and resistance genes, and analyze risk factors in dairy farms in the Special Region of Yogyakarta. This study involved 106 farms with milk samples from 450 dairy cows, 106 soil samples, 106 barn floor swab samples, and 106 hand swab samples from milkers. Isolation and identification were performed using *MacConkey* medium, biochemical testing with *Indole*, *Methyl Red*, *Voges-Proskauer*, *Citrate (IMVic)* media, identification of O157 with *Sorbitol MacConkey* medium, and identification of O157:H7 with *Polymerase Chain Reaction* (PCR) targeting the *Stx1* and *Stx2* genes. Antibiotic resistance testing for Amoxicillin, Streptomycin, Oxytetracycline, Tetracycline, and Sulfamethoxazole-Trimethoprim was performed using the *Kirby Bauer* method, followed by identification of resistance genes targeting the *strA*, *tetA*, and *sul2* genes. Risk factor data were collected through observation and interviews with farmers, which were analyzed descriptively and logistically using SPSS. The prevalence of *E. coli* at the farm level was 67.92% and at the livestock level was 20.89%. The prevalence of *E. coli* O157:H7 at the farm level was 4.71% and at the livestock level was 1.11%. The prevalence of *E. coli* O157:H7 at the farm level was 4.71% and at the livestock level was 1.11%. The resistance rate of *E. coli* from milk is 30.9%, soil 47.1%, barn 18.2%, and hands 40%, while the resistance rate of *E. coli* O157:H7 is 20% from milk isolates. *E. coli* resistance occurred in Amoxicillin, Oxytetracycline, Streptomycin, and Sulfamethoxazole-Trimethoprim, while *E. coli* O157:H7 isolates were resistant to Sulfamethoxazole-Trimethoprim. Antibiotic resistance genes (*tetA*, *strA*, *sul2*) were detected in *E. coli*, but no antibiotic resistance genes were found in the above three genes in the *E. coli* O157:H7 isolates obtained. Identification of *E. coli* contamination risk factors showed that poor housing conditions and waste management, as well as a history of mastitis and diarrhea, increased the probability of *E. coli* contamination, while inappropriate antibiotic dosing increased the probability of antibiotic resistance. Risk factor analysis for *E. coli* O157:H7 could not be performed. Analysis of *E. coli* distribution patterns using the *Average Nearest Neighbor* method showed a clustered pattern, while *E. coli* O157:H and antibiotic resistance patterns showed a dispersed pattern. Analysis using the *Standard Deviation Ellips* method of milk samples and barn floors contaminated with *E. coli* showed a higher risk of contamination spread, while vertical spread in hand samples and soil samples showed a dominant flow direction that needs to be addressed with better sanitation management.

Keywords: *Escherichia coli* O157:H7, risk factors, antibiotic resistance, dairy cattle