

INTISARI

Latar Belakang : Infeksi yang disebabkan oleh bakteri resisten terhadap antibiotik menyebabkan tingginya angka kesakitan dan kematian yang memberikan efek serius dalam meningkatnya biaya perawatan di rumah sakit. Antibiotik selain digunakan di rumah sakit untuk pengobatan, digunakan juga dalam bidang peternakan. Makanan dan hewan ternak dianggap sebagai salah satu reservoir dari bakteri penghasil ESBL.

Tujuan Penelitian : Mengetahui prevelensi dan jenis-jenis gen pengkode ESBL pada bakteri *E. coli* yang berasal dari sampel klinis dan sampel daging ayam mentah di Jakarta dan hubungannya.

Metode : Penelitian ini adalah penelitian observasional jenis deskriptif kategorik rancangan potong lintang. Sampel daging ayam diambil dari berbagai supermarket dan pasar tradisional di Jakarta, sampel klinis diperoleh dari tiga rumah sakit RSA, RSRT dan RSH. Uji skrining ESBL menggunakan metode difusi cakram. Deteksi fenotipik bakteri ESBL menggunakan metode DDST. Deteksi gen-gen pengkode enzim β -laktamase (*bla_{SHV}*, *bla_{TEM}*, *bla_{CTX-M}*) menggunakan multiplex PCR. Sekuensing gen dilakukan oleh 1st BASE Singapura. Pohon filogenetik dibuat menggunakan MEGA 7. Analisis statistik dilakukan menggunakan uji *chi-square*.

Hasil : Prevalensi bakteri *E.coli* pada sampel daging ayam dari pasar tradisional 97,14%, lebih tinggi dibandingkan di pasar modern sebesar 78,57% ($p<0,05$). Isolat *E. coli* pada sampel klinis tiga rumah sakit RSA (17,9%), RSRT (13%) dan RSH (17,4%). Rata-rata hasil deteksi fenotip ESBL isolat *E. coli* yang berasal dari sampel ayam adalah 43,45% dan sampel klinis sebesar 37,57%. Isolat dari sampel ayam memiliki gen penyandi ESBL dominan adalah *bla_{TEM}* (56,2%) dan sampel klinis *bla_{TEM}* (52,4%). Pohon filogenetik menunjukkan bahwa isolat dari sampel ayam dan sampel klinis memiliki kekerabatan yang erat.

Kesimpulan : Terdapat kesamaan variasi gen pengkode ESBL pada isolat bakteri *E. coli* yang berasal dari sampel ayam mentah maupun sampel klinis, dimana keduanya memiliki gen dominan yang sama yaitu *bla_{TEM}*. Pohon filogenetik menunjukkan bahwa isolat dari klinis maupun sampel ayam ada yang berada pada klaster yang sama.

Kata kunci : *E. coli*, ESBL, *bla_{SHV}*, *bla_{TEM}*, *bla_{CTX-M}*

ABSTRAC

Introduction

Infections caused by antibiotic-resistant bacteria cause high rates of infection and death that have a serious effect on the rising cost of hospital care. Antibiotics in addition to being used in hospitals for treatment, are also used for livestock production. Food and farm animals are considered one of the reservoirs of ESBL-producing bacteria.

Objective : *To determine the prevalence and types of ESBL coding genes in E. coli bacteria from clinical samples and raw chicken meat samples in Jakarta and their relationship.*

Methods : *This research is an observational research with a categorical descriptive cross-sectional design. Chicken meat samples were taken from various supermarkets and traditional markets in Jakarta, clinical samples were obtained from three RSA, RSRT and RSH hospitals. The ESBL screening test uses the disc diffusion method. ESBL bacterial phenotypic detection using the DDST method. Detection of β -lactamase encoding genes (*bla_{SHV}*, *bla_{TEM}*, *bla_{CTX-M}*) using multiplex PCR. Gene sequencing was carried out by 1st BASE Singapore. Phylogenetic trees were constructed using MEGA 7. Statistical analysis was performed using the chi-square test.*

Results : *The prevalence of E.coli bacteria in chicken meat samples from traditional markets was 97.14%, higher than that in modern markets of 78.57% ($p < 0.05$). E. coli isolates in clinical samples from three hospitals RSA (17.9%), RSRT (13%) and RSH (17.4%). The average detection result for the ESBL phenotype of E. coli isolates from chicken samples was 43.45% and 37.57% for clinical samples. Isolates from chicken samples that had the dominant ESBL coding gene were *bla_{TEM}* (56.2%) and clinical samples were *bla_{TEM}* (52.4%). The phylogenetic tree shows that isolates from chicken samples and clinical samples are closely related.*

Conclusion : *There are similar variations in ESBL-coding gene in E. coli bacterial isolates derived from raw chicken samples and kilinis samples, both of which have the same dominant gen *bla_{TEM}*. Phylogenetic trees show that both clinical and chicken samples are in the same cluster.*

Keywords : *E. coli, ESBL, *bla_{SHV}*, *bla_{TEM}*, *bla_{CTX-M}**