

ABSTRACT
THE PATTERN ANTIMICROBIAL RESISTANCE IN GUT FLORA OF CATTLE

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Introduction: Antimicrobial resistance is a serious threat to global public health worldwide. The use of antibiotics were common in human sectors, but the animal is not exception. The increasing prevalence of antimicrobial resistance (AMR) urge the researcher to explore more about AMR, to provide the data for management of infection, and preventive activity for tackling AMR. This study aimed to explore the prevalence and correlation of antibiotic usage with AMR of gut flora on cattle.

Methods: This study was a descriptive analytic. The data of antibiotic use was collected by questionair and the susceptibility pattern of gut flora was conducted by swabbing rectal specimen of cattle from 3 center of cattle faram. The dominant flora was isolated by microbiological culture as standard procedure and tested by disk diffusion method as CLSI. Total 6 antibiotics disk were used in the laboratory test. The result is analyzed with description method.

Results: Total 3 centers and 15 cattle was studied. The antibiotic use was as follow: beta-lactam antibiotic (penicillin, cloxacillin, ampicillin), tetracycline and aminoglycoside were identified among 5 cattles, tetracycline among 10 cattle and aminoglycoside among 10 cattles. Dominant gut flora of cattle showed the total 10 strains *E coli*, 3 strains *Proteus vulgaris* and 2 strains *Proteus mirabilis*. The pattern of susceptibility of gut dominant flora was as follow: sensitive against meropenem 93,3%, amoksisilin-klavulanat 86,6%, ceftazidime 86,6%, Tygecyclyne 100%, Cotrimoxazole 100%, and Amikacin 100%. The intermediate result were *Meropenem* (6.66%), *Amoxicillin-clavulanate* (12.66%), and *Ceftazidime* (12.66%). However, it is still sensitive to *Tigecyclyne*, *Trimethoprim-sulfamethoxazol*, and *Amikacin*. There not resistant straints for all isolates.

Conclusion: There was any antibiotic usage in cattle farm in East Java, such as beta-lactam antibiotic, tetracycline and aminoglycoside. Most antibiotic were susceptible against gut bacterial flora. The antibiotic with result of intermediate were identified among meropenem, amoxicillin-clavulanic acid and ceftazidime.

Keywords: Animal Gut flora, antimicrobial resistance, AMR, cattle farm