Background: Resistances to antibiotics in bacteria are an increasing threat to animal and human health. Several data suggest that use of antibiotics in livestock industry have linked to most of antibiotic-resistant human bacterial isolates. Recent studies have reported an increase in antibiotic resistance in human EHEC isolates.

Objectives: This study examined the prevalence of resistance to antibiotics, evaluated the antimicrobial resistance profiles in E. coli O26 and O111 from cattle feces, and characterized these resistant isolates.

Methods: PCR amplification. PCR assay to determine the presence of the following: genes of stx1 and stx2, eaeA, EhyA and E. coli O26 and O111 specific genes. Antimicrobial susceptibility testing. The susceptibility of the E. coli O26 and O111 isolates to the different antimicrobial agents was tested using the method standardized by the Clinical and Laboratory Standards Institute.

Results: Among 37 E. coli O26 and 25 E. coli O111 isolates from the fecal specimens obtained from cattle, 26 (70%) and 15 (60%) were resistant to at least one antibiotic, respectively. Forty (98%) of the 41 resistant isolates were resistant to 2 or more antibiotics. Ampicillin was the most common antibiotic that the isolates were resistant to, followed by tetracycline and streptomycin. None of the isolates were resistant to fluoroquinolones, such as ciprofloxacin, ofloxacin and norfloxacin, and to ceftriaxone, amikacin and imipenem. The most frequent antibiotic-resistance type was ampicillin-tetracycline-streptomycin-cephalothin-sulfisoxazole-tiacarcillin-kanamycin-minocycline-piperacillin-chloramphenicol, which accounted for 9 (22%) of the resistant isolates. PCR analysis of the EHEC virulence markers showed that 25 of the resistant E. coli O26 and O111 isolates tested positive for stx2 or both stx1 and stx2.

Conclusions: The majority of these isolates can cause serious diseases in humans and may complicate the future therapeutic options under development.