The dairy cow contributes to the nutrition and well-being of humans by providing a variety of dairy products. It harbors a complex microbiome composed of numerous microorganisms in the reticulo-rumen and dominated by bacterial species. Little information, however, is known about the diversity of bacterial pathogens present in the rumen and cow feces of healthy cow and the subsequent effects on the performance of the host animal. The objectives of the present study were to genetically characterize the enteric bacterial pathogens found in the rumen fluid and cow feces and identify the genes responsible for antimicrobial resistance in the detected pathogens. The cow feces and rumen fluid samples were collected from lactating dairy cows reared at University of Nairobi Veterinary farm and the smallholder (Lushoto and Rungwe) farms in Tanzania. A total of 48 (6 rumen fluid and 42 fecal) samples was collected from the three study sites. Enteric bacterial pathogens detected were screened for genes associated with antimicrobial resistance using next generation sequencing techniques.

The majority of enteric bacterial pathogens characterized included Escherichia coli, Salmonella enterica, Klebsiella pneumoniae, Streptococcus agalactiae, Streptococcus pyogenes, Campylobacter coli, Campylobacter fetus, Campylobacter jejuni, Staphylococcus aureus, Staphylococcus sciuri, Enterococcus faecalis, Enterococcus faecium, Clostridium botulinum and Clostridium perfringens, among others. Those enteric bacterial pathogens were also drug resistant except only Campylobacter coli. The Campylobacter fetus was identified as the only multidrug resistant bacterial pathogen detected in the cow feces at the smallholder farms. The contigs generated following De novo assembly were blasted against the ResFinder-2.1 database in the center of Abricate to annotate the contigs into the resistant genes. The abundant resistant genes detected in the enteric bacterial pathogens in this study confer resistance to tetracycline (17 genes from 209 contigs), beta-lactam (21 genes from 67 contigs), streptomycin (6 genes from 153 contigs), sulfamethoxazole (2 genes from 72 contigs), Quinolone (3 genes from 68 contigs) and chloramphenicol (4 genes from 52 contigs) drugs.

The findings of this study may help to identify the etiology of recurrent bacterial infections in the farms. Additionally, the results of this study may help to take adequate prophylactic measures and clinical preventions in the spread of the resistant genes in the farms. Further metagenomic analysis is needed to assess the movement of antibiotic resistant bacteria and resistant genes in the dairy farms in the study sites. Such study will provide the basis for the management of drug resistant bacteria in the farms in future. Additionally, efforts should be made to stop indiscriminate use of antimicrobials in the herds and dairy farmers should be encouraged to keep treatments records for their animals.