The increased use of antibiotics in clinical and veterinary practice provides favorable conditions for the selection, spread and persistence of antimicrobial-resistant bacteria. The expansion and intensification of intensive farming practices have raised important questions about environmental pollution and its impact on public health. Antibiotics used in animal husbandry as both growth promoters and for therapeutic purposes can reach the aquatic environment by contaminating courses of water with residual liquids from feedlot or by other confined animal husbandry. The objective of this work was to study the resistance to antibiotics of the bacterial population in the system of natural troughs that connects a feedlot of the Pampa Ondulada with Arroyo Burgos and in the micro basin of the Río El Tala. Seasonal samples were taken at the feedlot outlet (point 1), 3 km from the feedlot (point 2), at Arroyo Burgos and at Arroyo El Tala. The prevalence of Gram negative bacilli resistant to antibiotics was determined through the agar dilution method, in the Agar Violet Red Bile medium with and without antibiotics (ceftriaxone, ceftazidime, ceftiofur, oxytetracycline, and chlorotetracycline). The sensitivity to antibiotics of selected Gram negative bacteria was determined using the disk diffusion technique (CLSI). The detection of ESBL and carbapenemase was performed by phenotypic tests according to CLSI. The molecular detection of the genes was carried out by polymerase chain reaction using specific oligonucleotides. Bacteria resistant to ceftriaxone were observed in all samples. In point 2, the highest prevalences of resistant bacteria were observed. It was observed that the samples in the Arroyo Burgos microbasin presented a higher prevalence to ceftriazone followed by-ceftiofur, reaching maximum values of 100% and 30.0 and minimums of 8.6 and 7.4% respectively. On the other hand, in Arroyo El Tala there is a lower percentage of bacteria resistant to ceftiofur (0.67%) than in Arroyo Burgos. In point 2, bacteria resistant to cephalosporins of 3rd and 4th generation were isolated. Among the isolates, Escherichia coli was identified, confirming the BLEE phenotype. Can consider that intensive cattle breeding can contribute to the spread of resistant bacteria and represent a risk to public health.