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Survey of subcutaneous fluid practices in cats with chronic kidney disease

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Chronic kidney disease (CKD) is common in elderly cats. The purpose of this study was to describe subcutaneous fluid (SQ) administration practices of owners of CKD cats to help more owners successfully give SQ fluids to their cat. An anonymous web-based survey was advertised via list serves, websites and social media. Owners of 468 cats with CKD participated. 87% of cats were 10 years or older. Cats were IRIS stage I (1%), II (20%), III (37%), IV (17%), and unknown (25%). 95% of owners said they discussed giving fluids with their veterinarian. 399 respondents stated they gave SQ fluids, 57 did not, and 12 tried but could not. Only 42% of owners were given additional educational resources. 79% said the process was ok/easy to learn. Once experienced, 15% said it was still somewhat/highly stressful on them, and 11% said it was somewhat/highly stressful for the cat. To improve tolerance 57% used food for positive reinforcement with 59% stating this improved tolerance, 60% warmed the fluids and 83% felt warming fluids increased tolerance. 74% felt that length of time it took to administer fluids affected tolerance. 82% said needle size affected tolerance. 40% of owners checked hydration status daily or twice daily and 18% of owners did not know how. 43% said they skipped/added fluids based on hydration assessment. The majority of owners were successful in administering fluids but additional education materials could be provided. Variables such as needle size, warming fluids, and length of time of administration may improve tolerance.

Resident/ Clinical Sciences

Investigating the effect of tulathromycin exposure on potential microbial community function in feedlot cattle during the early feeding period using shotgun metagenomics

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Shotgun metagenomics, facilitated by next-generation sequencing, represents a novel approach to investigate bacterial communities. The goal of this study was to use bioinformatic analysis to understand the impact of metaphylactic tulathromycin (Draxxin) exposure on the microflora of cattle in the early feeding period. Tulathromycin is a macrolide antibiotic, the most commonly used class of antibiotics in livestock production, and is commonly used to treat bovine respiratory disease. Two pens of cattle in a Texas feedlot were selected for this study. One pen was chosen to receive 800 mg of tulathromycin while the other was chosen for the control. Individual fecal samples from the rectal-anal junction were collected at arrival processing and 11 days into the feeding period. Selected fecal samples from treated (n=30) and control (n=30) animals from both sampling times were subjected to total DNA extraction for metagenomic sequencing. Sequenced reads were trimmed for poor quality nucleotides and filtered to remove bovine DNA. To evaluate the microbial community, the bioinformatic tools BWA, Humann2, and Kraken as well as various genetic databases were utilized to identify differences in the number of sequences aligning to known antimicrobial genes (resistome), metabolic functional genes, and genomes for taxonomic profiling (microbiome) respectively. Statistical comparison of community data matrices from metagenomic samples necessitates using multiple techniques such as cumulative sum scaling, Hellinger transformation, and the employment of both zero-inflated multivariate models and non-metric multidimensional scaling of Euclidean distances. Preliminary results suggest that exposure to tulathromycin during arrival processing exerts a relatively small effect on the microflora composition in treated cattle whereas the transition into the feedlot exerts a greater effect on the composition of microbial communities in all cattle. Shotgun metagenomics allows an extraordinary glimpse into complex bacterial communities, but the challenge lies in accurately interpreting the biological relevance of next-generation sequencing results.

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