

Morris Animal Foundation Project Number: D07-MS 006

Title: *Escherichia coli* Resistance in Dogs and Cats: The Scope of the Problem

Statement of Research Problem Antimicrobial resistance is an emerging therapeutic challenge in dogs and cats, yet is not nationally monitored. *Escherichia coli* is a reasonable sentinel organism for monitoring: its nature facilitates resistance, and it is a common canine and feline pathogen whose effective treatment is limited by drug resistance. Previous antimicrobial therapy plays a major role in resistance. Judicious antimicrobial use guidelines could be improved with recommendations scientifically based on national monitoring of resistance and antimicrobial drug use.

Project Summary – This study will document the current and changing (3 year) patterns of antimicrobial resistance and susceptibility among pathogenic *Escherichia coli* collected from dogs or cats. Isolates will be obtained from a commercial diagnostic laboratory (IDEXX) which receives samples from all types of practices throughout the United States (US). Samples will be accompanied by minimum demographic and patient information. Minimum inhibitory concentrations (MIC) will be determined for 10 drugs (6 drug classes or subclasses, selection based on extent of veterinary use and differing mechanisms of resistance) using the Epsilon-test®. Veterinarians submitting isolates will be surveyed telephonically to collect information regarding practice demographics, and patient information, including a focus on antimicrobial exposure. Outcome measures to be determined for all isolates and within subgroups (e.g., defined by region, patient characteristics, tissue site) will include pharmacodynamic statistics (MIC range, median, etc), proportion of resistant isolates, the level of resistance (high versus low), the type of resistance (single versus multi-drug resistance), and the level of susceptibility. Comparisons will be made for outcome measures among drug or drug combinations, species, and tissues and across time (yearly). Based on questionnaire data, risk factors for the advent of resistance, with an emphasis on antimicrobial history, will be identified. For isolates that share phenotypes and risk factors, genotypes will be determined; molecular mechanisms of resistance will be described for those that are genotypically similar. This data will provide specific information to support judicious empirical antimicrobial use guidelines.

Anticipated Start Date: January 01, 2008

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