

A Small Scale Surveillance Study on the Prevalence of Tick Population in the Tri-State Area of the Midwest and Detection of Selected Bacterial Pathogens using Molecular Methods

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ABSTRACT

Ticks are ubiquitous throughout the Midwest, and can act as vectors for different arthropod derived illnesses. The infectious nature of ticks is due to a variety of bacteria that are passed from the tick after biting its target. The goal of this research was two-fold. First to identify the species of ticks collected in the **tri-state area of Kansas, Missouri, and Oklahoma** using taxonomic ID. Secondly, molecular identification of each tick at the genus/species level by PCR amplification of cytochrome oxidase gene. This was accomplished by extracting total DNA from ticks and then performing a PCR using tick species-specific primers followed by agarose gel electrophoresis. In order to identify any bacterial DNA present in the tick, PCR was carried out to detect the eubacterial 16S rRNA gene. Specific primer sets were used to detect selected bacterial pathogens such as *Francisella tularensis* and *Rickettsia rickettsii*. The data obtained in this study would help in implementing comprehensive surveillance and management programs for ticks and tick-borne disease risk for humans and animals in this region.