

DETECTION OF *Babesia* GENE AND *Coxiella burnetii* AMONG TICKS  
COLLECTED FROM CATTLE AND PASTURE IN CAVITE  
USING POLYMERASE CHAIN REACTION

THESIS

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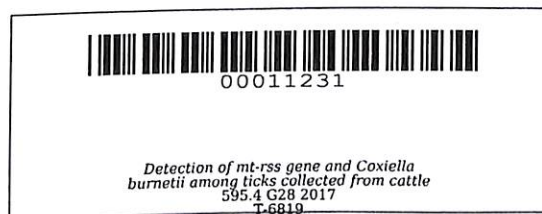
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**DETECTION OF *mt-rrs* GENE AND *Coxiella burnetii* AMONG TICKS  
COLLECTED FROM CATTLE AND PASTURE IN CAVITE  
USING POLYMERASE CHAIN REACTION**

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## ABSTRACT

**FLORANTE H. GENEROSO, DETECTION OF *mt-rrs* GENE and *Coxiella burnetii* AMONG TICKS COLLECTED FROM CATTLE AND PASTURE IN CAVITE USING POLYMERASE CHAIN REACTION**, Undergraduate Thesis. Doctor of Veterinary Medicine, Cavite State University, Indang, Cavite, May 2017, Adviser: Noemi D. Encarnacion, DVM, MVetEpi

Ticks are considered vectors of pathogens for animals and humans. They are obligate ectoparasites that feed on blood tissues of wide host range. This study aimed to determine the presence of *mt-rrs* gene and *Coxiella burnetii* among tick samples from cattle farms within the province of Cavite, Philippines using polymerase chain reaction.

A total 294 tick samples, 63 from lowland (21.42%) and 231 from central hilly (78.57%) were used in this study. All are of *Rhipicephalus microplus* species and comprises of 293 adults (99.65%) and 1 larva (0.35%). Ticks among the adult stage consist of 18 males (6.14%) and 275 females (93.85%).

Out of 294 samples, 205 tick DNA extracted using the boiling method detected 85 *mt-rrs* gene while using the BlackPREP Tick DNA/RNA kit (Life Science, Germany), out of the 89 tick DNA extracted, *mt-rrs* was detected in 80 samples. One hundred sixty-five (165) tick DNA samples were ran for pathogen detection using *Coxiella*-specific primers. Zero (0) out of 165 tick DNA samples tested positive for the presence of *Coxiella burnetii*. One (1) sample on the other hand, produced a single, clear, but having a smaller amplicon suggesting the presence of *Coxiella*-like endosymbiont in the tick population. However, phylogenetic analysis is needed to support such claim.

This study documents the detection rate of the mt-*rrs* gene using the boiling method and BlackPREP Tick DNA/RNA kit, (Life Science, Germany); and preliminary molecular survey of *Coxiella burnetii* from cattle ticks in Cavite.

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**INTRODUCTION**

Ticks are obligate blood sucking arthropods and act as vectors of pathogens with medical and veterinary relevance (Oteo *et al.*, 2015). Each tick species has preferred environmental conditions and habitats that determine their geographic distribution and, consequently, the risk areas for tick-borne diseases. The tick-borne bacterial diseases that are currently recognized are zoonoses, with the bacteria being maintained in natural cycles involving ticks and wild and / or domestic animal hosts and occasionally transmitted to people causing infections as ticks feed on them (Parola and Raoult, 2001). Pathogens can remain in different developmental stages of ticks and may be passed on to the next generation via transovarial and transtadial transmissions (Burgdorfer and Brinton, 1975 as mentioned by Wang *et al.*, 2015). Tick infestations and tick transmitted pathogens in cattle has led to significant costs and financial losses to farmers and created negative economic impacts.