PHD PUBLIC DEFENCE.

DATE: ***Wednesday 22nd May 2024.***

TIME: 10:00 AM

VENUE: COVAB PRINCIPAL'S CONFERENCE ROOM

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PHD CANDIDATE.

TOPIC:

SEROPREVALENCE AND MOLECULAR EPIDEMIOLOGY OF ZOONOTIC RICKETTSIA IN ARTHROPODS AND HUMANS IN UGANDA

SUPERVISORS

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ABSTRACT

Rickettsioses are emerging, neglected infectious diseases caused by obligate intracellular Gram-negative bacteria transmitted by arthropod vectors to humans. The diseases are febrile in nature and are difficult to diagnose. Rickettsioses are underreported in sub-Saharan Africa, including Uganda. This cross-sectional study aimed at determining the epidemiology of rickettsia in arthropod vectors and humans in selected districts by molecular and serological tools. Ticks and fleas were collected from animals and environment of 360 households; identified morphologically, pooled by host, location and time of collection. The arthropods were tested for rickettsia using Real-time PCR, the amplicons were sanger-sequenced and compared for homology on NCBI GenBank. Additionally, 460 serum samples collected from febrile patients in five referral hospitals from same districts and period of vector collection were tested using IgM ELISA for SFG and TG rickettsia, Phase II IgG ELISA for Q-fever, and IFA for *Orientia* spp. Of the 471 tick pools tested, 116 (24.6%) were positive for *Rickettsia* spp. by the *gltA* primers and the variation in pool prevalence rates were not significant for the districts (χ^2=8.627, *df* =4, *p*=0.071) and host type (χ^2=2.713, *df*=2, *p*=0.258). Of 116 *gltA*-positive tick pools, 86 pools were positive for *17kDa* gene, of which 48 were successfully sequenced. The predominant *Rickettsia* spp. identified were *R. africae* in four tick species and *R. conorii* in three tick species. *Rickettsia conorii* subsp. *israelensis* was detected in one tick pool for the first time in Uganda. Of the 62 flea pools tested for *Rickettsia* spp., 29 (46.8%) were positive, of which 25 PCR amplicons were successfully sequenced for *17kDa* genes. Two (8%) sequences were identified as *R. felis* from *C. canis* and 23 (92%) were *R. asembonensis* from multiple flea species. The overall seroprevalence of SFG rickettsiosis and Q-fever were 6.3% and 7.6% respectively. Increasing age (OR-adjusted=1.4, 95%CI=1.0—1.9, p=0.026) and rural background (OR-adjusted=2.6, 95%CI=1.6—6.4, p=0.037) were both significantly associated with seropositivity for Q-fever, while only increasing age had higher odds for seropositivity for SFG rickettsia (OR-adjusted= 1.9, 95% CI= 1.4—2.6, p<0.001). One serum from Bwera hospital reacted to both SFG and Q-fever antibodies and four separate sera each were reactive for typhus group IgM and *Orientia* spp. IgM. This is the first seroprevalence finding of Q-fever, SFG and STG in febrile patients in Uganda. This study shows that multiple *Rickettsia* spp. are circulating in ticks and fleas in Uganda, including new strains previously known to occur in the Mediterranean region. Physicians should be informed about rickettsia as potential causes of acute febrile illnesses and continued surveillance to identify hotspots is essential.