

The epidemiology of non-tuberculous mycobacteria and the associated risks in Mubende District

1,3 Muwonge A, 1,3 Kankya C, 1 Skjerve E, 3 Opuda-Asibo J and 2 Djønne B

1 Norwegian School of Veterinary Science, Oslo, Norway,

2 National Veterinary Institute, Oslo, Norway,

3 Makerere University, Kampala, Uganda

Environmental mycobacteria represent an emerging group of pathogens especially with the era of HIV/AIDS mycobacteria associated infection. They cause opportunistic infection in immuno-compromised hosts, as well as cervical lymphadenitis in children(1). As this group of bacteria has been found in drinking water and soil (2), the environment has then been considered a likely source of infection. However, the observed genetic diversity of strains recovered from AIDS patients and their occurrence of *M. avium* in animals and various environmental samples suggest the existence of additional reservoirs. *Mycobacterium avium* (MAC) is known to cause lymphadenitis with local granulomatous lesions in pigs and can also cause similar infections in humans (3). Studies using restriction fragment length polymorphism (RFLP), have shown that pigs and humans share a high degree of IS1245-based polymorphism, indicating that pigs may be an important vehicle for *M. avium* infections in humans. Studies have also shown a genetic homology of food and clinical isolates (4).

The study involves a cross-sectional multi-stage sampling of pigs from thirteen sub-counties of Mubende district in Uganda. A total of 1000 lymph nodes collected from slaughterhouses between August 2008 and January 2009 will be used to establish infection prevalence. Pigs were thoroughly examined at slaughter and cases with positive signs were sampled for mycobacteriological examination at the National Veterinary Institute, Oslo. Individual variables such as age, sex and management factors such as herd size housing, feeding, watering, veterinary care and herding style were recorded and will be used to establish associations with MAC infection. Furthermore, soils and water were collected from the sources in the study areas in order to establish the genetic relatedness between the environmental and pig isolates. The metrological picture as well as topography and vegetation cover of Mubende district was collected to establish a more complete epidemiological picture. Microbiology 125, 175-181.