Epidemiological investigation of bovine tuberculosis in the wildlife-livestock interphase in the Masai Mara and Amboseli ecosystems of Kenya

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Abstract:
Bovine tuberculosis (BTB) is a chronic bacterial disease of cattle caused by Mycobacterium bovis (M bovis) that occasionally affects other species of mammals. The disease can have a major economic impact on livestock productivity with the potential of affecting entire ecosystems due to wildlife reservoirs. It is also a significant zoonosis that can spread to humans hence a disease of Public Health importance. There is substantial movement of livestock and wildlife between Kenya and Tanzania creating a potential interphase for disease transmission. Information on BTB in Kenya is very scanty hence the need for studies to ascertain the status. The overall objective of this study was to investigate the epidemiology of Mycobacterium bovis in the wildlife-livestock interphase in Kenya. The specific objectives were to determine prevalence and spatial distribution of Mycobacterium bovis in selected wildlife, and livestock species in the study areas and also assess risk factors associated with Mycobacterium bovis in the wildlife-livestock-human interphase. The study areas were Masai Mara and Amboseli ecosystems in Kenya bordering Tanzania on the South Western and South Eastern parts respectively. This was a cross sectional study involving cattle populations in the study areas and wildlife which were selected purposively. Cattle were physically restrained, ear tagged and sampled while wildlife were chemically immobilized prior to sampling. All samples were geo-referenced and maintained under cold chain for transportation to the laboratory for analysis. Blood samples from livestock and wildlife were subjected to two screening tests, Stat-Pak and Bovigam. Stat-Pak IS an immunochromatographic lateral flow technique that employs a unique cocktail of recombinant mycobacteria proteins bound to a membrane solid phase. Bovigam is an in-vitro laboratory test for diagnosis of bovine tuberculosis that detects the amount of gamma interferon produced on stimulating whole blood with purified protein derivatives (PPD). In total 346 animals (both wildlife and livestock) and 253 lymph node samples (cattle, sheep and goats) were included in this study and investigated for bovine TB. Livestock comprised 231 out of the 289 animals (79.9%) sampled in Masai Mara and 34 out of the 57 animals (59.7%) in Amboseli. Colonies from the cultures that had growth were harvested and an acid fast bacilli (AFB) staining done. The AFB positive colonies were further subjected to mycobacterium genus PCR to check for members of the mycobacterium tuberculosis complex. The prevalence on positive tuberculin test in Amboseli (6.25%) was higher than that in the Masai Mara. Using Stat-Pak, the prevalence in Masai Mara was 35.4% and this was significantly higher than the prevalence of 14.7% in the study in Amboseli, i (1) = 5.8, P = 0.018. The prevalence on using Bovigam for bovine TB among wildlife was 14.8% (12 out of 81) compared to an overall prevalence of 2.3% (6 out of 265) among the livestock. Out of the 218 bovine lymph node samples, 38 (17.4%) had Mycobacteria growth compared to 2 out of 10 (16.7%) samples obtained from goats and 6 out of 25 in sheep. On mycobacterium PCR, none of the AFB positive samples were found to be positive...
for mycobacterium tuberculosis complex. Livestock were found to play an important role in the epidemiology of BTB in the study areas. Most of the test positive wildlife were those found to be in close interaction with the livestock and those closer to the Tanzanian border in the Amboseli ecosystem appearing to be more at risk. It is recommended that some of the positive reactors should be followed to slaughter with the view of obtaining tissue samples for culture and PCR for confirmation of M bovis.