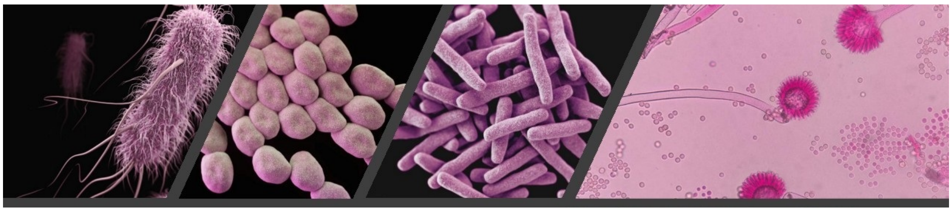

Abstract ID : **49**

Development and evaluation of a Pan-Borrelia TaqMan qPCR for detection of Borrelia spp. in ticks collected from cattle in Tanzania

Content

Bacteria of the genus Borrelia are tick-borne pathogens divided into two groups: Lyme disease (LD) group and Relapsing Fever (RF) group. Both include numerous species and new ones are still being identified. Recent studies have also reported the presence of Borrelia spp. in different hosts and across different geographical areas, highlighting the existing gaps in knowledge regarding the epidemiology of this pathogen. Continued surveys are needed to understand the prevalence and the host range of each species in order to safeguard the health of wildlife, domestic animals and humans. For this purpose, ticks collected from cattle in Tanzania in 2023, were tested for the presence of Borrelia spp. DNA. Molecular screening was performed using a new validated TaqMan real-time qPCR targeting the 16S rRNA gene able to detect all Borrelia species. A fragment of the 16SrRNA gene of the identified pathogens was sequenced and analysed for typing. One tick of 62 (1.6%) tested positive for bacteria belonging to the RF group, potentially Borrelia theileri, the main causative agent of bovine borreliosis. This species was already reported in cows in Africa, but never in Tanzania. This result confirms the importance of monitoring the spread of this pathogen in order to control the disease. Supported by EU funding within the NextGenerationEU-MUR PNRR Extended Partnership initiative on Emerging Infectious Diseases (Project no. PE00000007, INF-ACT).

Keywords

Borrelia spp., TaqMan qPCR, cattle, 16SrRNA, Tanzania, tick, Relapsing Fever group

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