A systematic review and meta-analysis on the global prevalence of cattle microsporidiosis with focus on Enterocytozoon bieneusi: An emerging zoonotic pathogen

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Abstract:

Microsporidiosis, caused by the zoonotic eukaryote microsporidia spp. have serious health threat in high-risk groups, including immunocompromised individuals. Cattle plays a major role as reservoirs of microsporidia among the animals because of close-contact with humans. Hence, we aimed to evaluate the prevalence and genetic diversity of cattle microsporidiosis at a global scale through systematic review and meta-analysis approach. A comprehensive literature searches of published articles related to the molecular distribution of microsporidiosis in cattle was conducted between 1 January 1990 and 20 December 2020. The confidence intervals (95 %) and point estimates were calculated using the random-effects model. A total of 1809 was retrieved from the initial search, after exclusion of irrelevant articles 37 articles met inclusion criteria to be included for final analysis. The estimated pooled prevalence of cattle microsporidiosis was 14 % (CI: 11.5–17 %) worldwide. Accordingly, the calves had the highest prevalence 20 % (CI: 14.8–26.5 %). According to internal transcribed spacer (ITS) gene, Enterocytozoon bieneusi with genotypes BEB4 (22 studies), J (21 studies), and I (17 studies) were the highest reported genotypes. The present results highlight the role of cattle as reservoir hosts for human-infecting microsporidia. Strategies for control and prevention of these pathogens should be designed to mitigate the risk of cattle to human transmission.