World Academy of Science, Engineering and Technology
International Journal of Biotechnology and Bioengineering
Vol:15, No:12, 2021

Clostridium Difficile in Western Australian Native Animals: Prevalence and Molecular Epidemiology

Authors : Karla Cautivo, Thomas Riley, Daniel Knight

Abstract : Clostridium difficile infection (CDI) is the most common cause of infectious diarrhea in hospitalised humans. C. difficile colonises the gastrointestinal tract, causes disease in a variety of animal species and can persist as a spore in diverse environments. Genetic overlap between C. difficile strains from human, animal and environmental sources suggests CDI has a zoonotic or foodborne aetiology. In Australia, C. difficile PCR ribotype RT014 (MLST clade 1) and several ST11 (MLST clade 5) RTs are found commonly in livestock. The high prevalence and diversity of ST11 strains in Australian production animals indicates Australia might be the ancestral home for this lineage. This project describes for the first time the ecology of C. difficile in Australian native animals, providing insights into the prevalence, molecular epidemiology and evolution of C. difficile in this unique environment and a possible role in CDI in humans and animals in Australia. Faecal samples were collected from wild/captive reptiles (n=37), mammals (n=104) and birds (n=102) in Western Australia in 2020/21. Anaerobic enrichment culture was performed, and C. difficile isolates were characterised by PCR ribotyping and toxin gene profiling. Seventy isolates of C. difficile were recovered (prevalence of C. difficile in faecal samples 28%, n=68/243); 27 unique RTs were identified, 5 were novel. The prevalence of C. difficile was similar for reptiles and mammals, 46% (n=17/37) and 43%(n=45/104), respectively, but significantly lower in birds (7.8%, n=8/102; $p<0.00001$ for both reptiles and mammals). Of the 57 isolates available for typing, RT237 (clade 5) and RT002 (clade 2) were the most prevalent, 15.8% (n=9/57) and 14% (n=8/57), respectively. The high prevalence of C. difficile in reptiles and mammals, particularly clade 5 strains, supported by previous studies of C. difficile in Australian soils, suggest that Australia might be the ancestral home of MLST clade 5.

Keywords : Clostridium difficile, zoonosis, molecular epidemiology, ecology and evolution
Conference Title : ICMD 2021 : International Conference on Microbial Diseases
Conference Location : Sydney, Australia
Conference Dates : December 02-03, 2021