

## **Abstract**

*Clostridioides difficile* infections (CDI) are generally perceived as healthcare associated infections. However, there has been recently reported an increase of CDI incidence in the community. The occurrence of *C. difficile* has been described also in animals, food and the environment water and soil. The aim of this thesis was to characterize *C. difficile* isolates derived from different sources using molecular methods.

The results were discussed with available data from Czech human *C. difficile* isolates. A total of 135 *C. difficile* isolates from the following sources were analyzed: pigs n = 57, calves n = 44, horses n = 18, water n = 15 and hedgehog. Using PCR ribotyping, 22 distinct ribotyping profiles were identified, the most frequently detected ribotypes were: 033, 011, 126, 078. Both toxigenic and non-toxigenic ribotypes were detected, including binary toxin-producing strains. The most frequently detected antimicrobial resistances were to ciprofloxacin, clindamycin, and erythromycin.

All ribotypes and sequence types identified in the *C. difficile* isolates from animals and the environment, has been found also in *C. difficile* isolates from humans which confirms the role of animals and the environment as a source for *C. difficile*. However, no epidemic ribotype 001 and 176 that dominate the current epidemiological situation in the Czech Republic, were not found in our set of *C. difficile* isolates from extra-human sources.

**Keywords:** *Clostridioides difficile*, Zoonosis, Antimicrobial resistance, Typing