

**ABSTRACT BOOK**



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Webinar Secretariat  TBC MON IKE | Email: [albinag@triaenatours.gr](mailto:albinag@triaenatours.gr) | Phone: 2107499309

## PHYLOGENOMIC ANALYSIS AND ANTIMICROBIAL SUSCEPTIBILITY DATA OF MYCOPLASMA BOVIS FROM DIFFERENT BELGIAN CATTLE PRODUCTION SYSTEMS

Jade Bokma<sup>1</sup>, Nick Vereecke<sup>2</sup>, Koen De Bleecker<sup>3</sup>, Jozefien Callens<sup>3</sup>, Hans Nauwynck<sup>2</sup>, Freddy Haesebrouck<sup>4</sup>, Sebastiaan Theuns<sup>2</sup>, Bart Pardon<sup>1</sup>, Filip Boyen<sup>4</sup>

<sup>1</sup>Department of Large Animal Internal Medicine, Faculty of Veterinary Medicine, Ghent University, Salisburylaan 133, 9820 Merelbeke, Belgium

<sup>2</sup>Department of Virology, Parasitology and Immunology, Faculty of Veterinary Medicine, Ghent University, Salisburylaan 133, 9820 Merelbeke, Belgium

<sup>3</sup>DGZ (Animal Health Service-Flanders), Industrielaan 29, 8820 Torhout, Belgium

<sup>4</sup>Department of Pathology, Bacteriology and Avian diseases, Faculty of Veterinary Medicine, Ghent University, Salisburylaan 133, 9820 Merelbeke, Belgium

*Mycoplasma bovis* is a leading cause of pneumonia and antimicrobial use in the different cattle sectors worldwide. Fear is that the veal calf industry harbours multi-resistant isolates because of their intensive antimicrobial use. This study compared isolates from the veal, dairy and beef sector on their antimicrobial susceptibility and genetic relatedness. MIC-values were determined (microbroth dilution) on 141 Belgian *M. bovis* isolates (2016-2019), of which 100 were whole genome sequenced (MinION Nanopore). The population was divided into wild type (WT) and non-wild type (nWT) using the epidemiological cut-off (visual eye-ball method). SNP analysis was performed to type *M. bovis* strains, and develop a phylogenetic tree (CSI Phylogeny). Logistic regression was performed on binary variables (WT=0; nWT=1). Acquired resistance was frequently observed for macrolides, and only in a few isolates also for gentamicin, florfenicol, enrofloxacin and tiamulin. No acquired resistance against oxytetracycline or doxycycline was observed. Beef isolates (64% nWT) had a three times higher odds (95%CI: 1.2-7.7) for gamithromycin resistance than dairy isolates (35%) (P=0.02), but no difference compared to veal isolates (58%). Five *M. bovis* clusters were observed, but none of them could be associated with any sector. Only *M. bovis* isolates from cluster III (85% nWT) showed a 22.7 (95%CI: 4.0-125.0) and 8.1 (95%CI: 1.6-41.7) times higher odds for gamithromycin resistance compared to clusters IV (19% nWT) and V (41% nWT) (P<0.02), respectively (Figure 1). This study could not evidence existence of sector specific *M. bovis* strains, but did show sector and strain specific gamithromycin resistance. This knowledge can contribute to better control and prevention guidelines for *M. bovis*.



Figure 1. Distribution of Belgian *M. bovis* isolates susceptible (○) or resistant (●) for gamithromycin over a SNP-based phylogenetic tree of 100 Belgian *M. bovis* isolates.