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# Abstracts

## Postgraduate Student Presentations

### Cross species transmission of *Mycobacterium bovis* infection at the wildlife/ livestock interface in South Africa

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Bovine tuberculosis affects cattle in South Africa and is known to be endemic in wildlife with the African buffalo (*Syncerus caffer*) being recognized as the maintenance host. Spoligotyping and mycobacteria interspersed repetitive unit-variable number of tandem repeat (MIRU-VNTR) genotyping methods were performed to investigate the molecular characteristics of *Mycobacterium bovis* (*M. bovis*) isolates from cattle and wildlife, their distribution and transmission at the wildlife/livestock interface in northern kwa-Zulu Natal (KZN), South Africa. DNA was extracted from microbiological cultures of milk, nasal and tissue samples from bTB positive cattle and tissue samples from bTB infected wildlife. Spoligotyping and Mycobacterial Interspersed Repetitive Units-Variable Tandem Repeats (MIRU-VNTR) on 13 loci was used for molecular characterisation of the *M. bovis* isolates. SB0130 was identified as the dominant spoligotype pattern at the wildlife/livestock interface, while VNTR typing revealed a total of 29 VNTR profiles in the KZN province signifying genetic variability. The detection of 5 identical VNTR profiles in cattle and buffalo suggests *M. bovis* transmission between species. MIRU-VNTR confirmed co-infection in one cow with three strains of *M. bovis* implying introduction of infection from unrelated sources. Our findings highlight inter and intra species transmission of bovine tuberculosis at the wildlife/livestock interface and the need for the implementation of adequate bTB control measures to mitigate the spread of the pathogen.