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**Poster Session III**

**Tuberculosis: clinical observations**

**MYCOBACTERIUM BOVIS IN BURKINA FASO, EPIDEMIOLOGIC AND GENETIC LINKS BETWEEN HUMANS AND CATTLE ISOLATES**

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**Objectives:** In sub-Saharan Africa, bovine tuberculosis (bTB) is a serious problem for livestock production but also a risk for humans. The main goal of this study is to better understand the circulation of *M. bovis* in Burkina Faso within and between cattle and humans by a genetic approach.

**Methods:** We characterised 33 isolates of *M. bovis*, using mycobacterial interspersed repetitive-unit-variable-number tandem-repeat (MIRU-VNTR) typing, and spoligotyping, and RDAf1 deletion typing. Twenty six *M. bovis* isolates were isolated from 102 carcasses with TB lesions out of 1499 slaughtered cattle and 7 from patients presenting pulmonary tuberculosis (TB) out of 576.

**Results:** Spoligotyping confirmed *M. bovis* identification and 12 patterns were detected among the 33 isolates. Five spoligotypes were already described in Mbovis.org ([www.Mbovis.org](http://www.Mbovis.org)) database, while 7 were new. The combination of spoligotyping and MIRU-VNTR typing provided exactly the same distribution than the MIRU-VNTR patterns alone. Seven clusters were detected, grouping together either isolates from cattle (n=5), or from humans (n=1) or from human and cattle (n=1). Two clonal complexes of *M. bovis*, Af1 (81.8%) and Af5 (18.2%), clearly separated in the phylogenetic tree based on spoligotyping and MIRU-VNTR data, have been identified in cattle and human population in Burkina Faso.

**Discussion/Conclusion:** The 6.8% (TB lesions detected in 102 carcasses out of 1499) prevalence of bTB in cattle recorded in the present study was close to other published results from Sahalian countries. The low rate of human pulmonary TB caused by *M. bovis* in our study (compared to other studies in Africa) could be explained by different factors: (i) a high number of *M. bovis* infections are responsible for extrapulmonary TB cases linked to ingestion of unpasteurized infected milk and in our study the TB cases were exclusively pulmonary (ii) pulmonary TB due to *M. bovis* must be more frequent in cattle breeders or slaughterhouse workers because of the close contact with animals and in this study, our research was not specifically focused on these exposed populations. On a genetic point of view, we obtained the same population organization than in Mali concerning the proportion of clonal complexes, Af1 and Af5. The transhumance activities and the transit of Malian livestock by Burkina Faso can explain the share of genotypes between Burkina Faso and Mali. The genetic analyses suggest that in Burkina Faso *M. bovis* is circulating also not only between cattle but also between humans and between humans and cattle. These results confirm that bTB represents a potential health hazard both for animals and humans in this region where cattle transmission seems imperfectly controlled.