

## **MOLECULAR EPIDEMIOLOGICAL LINKS BETWEEN *M. BOVIS* STRAINS ISOLATED FROM CATTLE AND CERVIDS FROM EASTERN REGIONS OF PORTUGAL**

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Bovine tuberculosis (bTB) prevalence has generally been decreasing for several years in Portugal due to an ongoing UE funded eradication programme. Nevertheless, new outbreaks have been intermittently recorded in bTB free herds, especially in two Eastern regions of Portugal (Beira Interior and Portalegre District part of Alentejo region), with no evident explanation referred in official epidemiological surveys. At the same time, it has been reported that wild cervids (*Cervus elaphus*) population has been increasing in those regions. In order to study the possible role of these animals in bTB outbreaks, systematic culture, identification, spoligotyping and MIRU typing of 9 select *loci* were performed in *M. bovis* isolates from cattle and hunted deers with pathological lesions. The results indicate that cervids can harbour common spoligotypes, some of them already found in cattle of the same regions and also, in other regions of Portugal. MIRU typing further increased the discriminatory power in order to link cervids and cattle *M. bovis* isolates, reinforcing the probability of strain relatedness. These results allow us to conclude that cervids and cattle from these regions could have a common source of infection, or could transmit these strains between them. Although the direction of this possible transmission is unknown or could even function in both directions, these preliminary results should promote an increased awareness on the possible role of wild cervids on bTB maintenance in the regions studied, encouraging a systematic control of TB in deers and the implementation of confinement measures in herds neighbouring their natural habitat.