Multi-host tuberculosis: Molecular perspective of epidemiological processes

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Animal tuberculosis (TB), caused by *Mycobacterium bovis* (*M. bovis*) and, less frequently, by *Mycobacterium caprae* (*M. caprae*), is a worldwide distributed disease that affects livestock and several wildlife species. In Portugal, both pathogens are maintained in a multi-host system with cattle (*Bos taurus*) and goat (*Capra aegagrus*) acting as main host species for *M. bovis* and *M. caprae*, respectively. A national eradication program is currently implemented in the cattle population and an epidemiological risk area for TB in red deer (*Cervus elaphus*) and wild boar (*Sus scrofa*) is also established since 2011. However, the epidemiological situation for most regions is still far from the officially TB-free status, with TB herd prevalence reaching 0.29% in 2016.

Red deer and wild boar are described as *M. bovis* reservoirs in the Iberian Peninsula, however the specific role exerted by each of these species in transmission cascades is still under scrutiny.

To better understand the transmission dynamics of *M. bovis* and *M. caprae* in a multi-host scenario in Portugal, knowledge of pathogen population diversity and structure, as well as of the underlying genotypic evolution through space and time, has to be refined. A collection of *M. bovis* (*n*=948) and *M. caprae* (*n*=55) isolates from long-term surveillance (2002-2016) in Portugal, isolated from livestock (cattle, goat and sheep) and wildlife (red deer and wild boar) has thus been characterized based on specific genomic regions, using spoligotyping and MIRU-VNTR analysis as hierarchical genotyping techniques. The uniformity of genotypic profiles shared by livestock and wildlife within the same spatiotemporal context highlight epidemiological connections and suggests intra- and interspecies transmission events. Evolutionary relationships between *M. bovis* isolates have also been explored by MST (Minimum Spanning Tree) analysis and by a Bayesian clustering algorithm, suggesting sympatry of different phylogenetic groups.

The data obtained thus far reinforce the complexity of *M. bovis* and *M. caprae* epidemiology. To understand the persistence and biogeographic specificities of certain strains that were capable of crossing the species barrier whole genome sequencing of both pathogens is underway. Phylogeographic reconstruction will contribute to a deeper knowledge of transmission cascades and resilience dynamics, which are crucial to inform new control choices.

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FCUL (Building C2), 12h00-13h00, room 2.2.14