

## **MOLECULAR ANALYSIS OF *M. BOVIS* STRAINS ISOLATED IN ITALY: EPIDEMIOLOGICAL INVESTIGATION IN FOUR GENETIC CLUSTERS**

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Molecular typing of isolates has become a valuable tool in the study of bovine tuberculosis (TB) epidemiology allowing investigators to achieve better knowledge of transmission and increasing incidence of infections. This statement implies the necessity to create a database containing genetic profiles of as many *M. bovis* strains as possible isolated from outbreaks occurring in our territory in recent years and to have reliable, rapid and reproducible typing techniques.

In Italy molecular typing of *M. bovis* strains isolated in herd breakdowns has been carried out on more than 1200 isolates by spoligotyping and ETRA-E analysis since 2000.

In addition we have recently selected an informative panel of 8 VNTR/MIRU markers out of 19 after having tested 100 strains characterized by spoligotype BCG-like, the most frequent in Italy.

In this work we present four interesting examples where the combination of conventional epidemiological data and molecular information allowed us to trace the sources and the modes of transmission of TB infection occurring in some field outbreaks. In particular we could confirm some hypothesis outlined by traditional epidemiological investigations such as: transmission of TB infection through common pasture; movement and trading of animals; the presence of an adjacent TB infected herd; the persistence of the same *M. bovis* strain in the herd after closure of a previous outbreak; the maintenance of TB infection in a restocked herd after cattle stamping out through infected goats kept in the herd from the previous outbreak.

Moreover the clustering of some genotypes in particular geographical areas will be shown and discussed.