

Molecular Epidemiology of *Mycobacterium bovis* in Sicily: Insights from Spoligotyping for Targeted bTB Control

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INTRODUCTION & AIM

Bovine tuberculosis (bTB), caused by *Mycobacterium bovis*, is a zoonotic disease with significant implications for animal health, public health, and livestock productivity worldwide. Despite the implementation of national and regional eradication plans, Sicily remains one of the areas in Italy with the highest bTB prevalence. Several epidemiological factors contribute to this persistence, including extensive and semi-free-range farming practices, shared pastures, interspecies interactions with wildlife and local pig breeds, and the island's complex geography, which fosters ecological conditions favorable to pathogen survival and transmission.



The purpose of this work is to understand and address the specific epidemiological factors in Sicily that cause the persistent high prevalence of Bovine Tuberculosis (bTB) and hinder its eradication, but also to protect animal health, public health, and livestock productivity.

METHOD



Myocardium



Tonsil



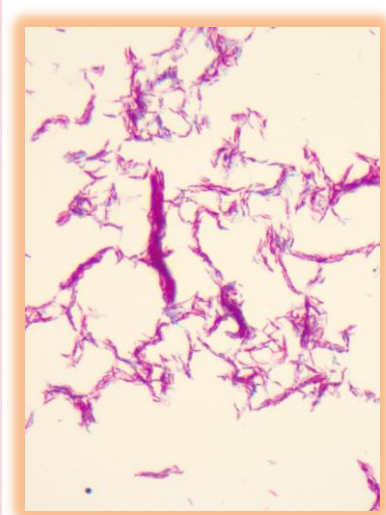
M. bovis isolates were obtained from pathological samples, such as lymph nodes and lung lesions, collected from cattle slaughtered due to suspected tuberculosis. Bacterial cultures were performed using standard solid (Löwenstein-Jensen and Stonebrink) and liquid (BACTEC MGIT 960) media. Genomic DNA from culture-positive samples was extracted and subjected to spoligotyping. This molecular technique was used to identify the genotypes circulating in the region and to assess their spatial distribution.

Stonebrink Solid media

Automated System MGIT 960 (BD) liquid media



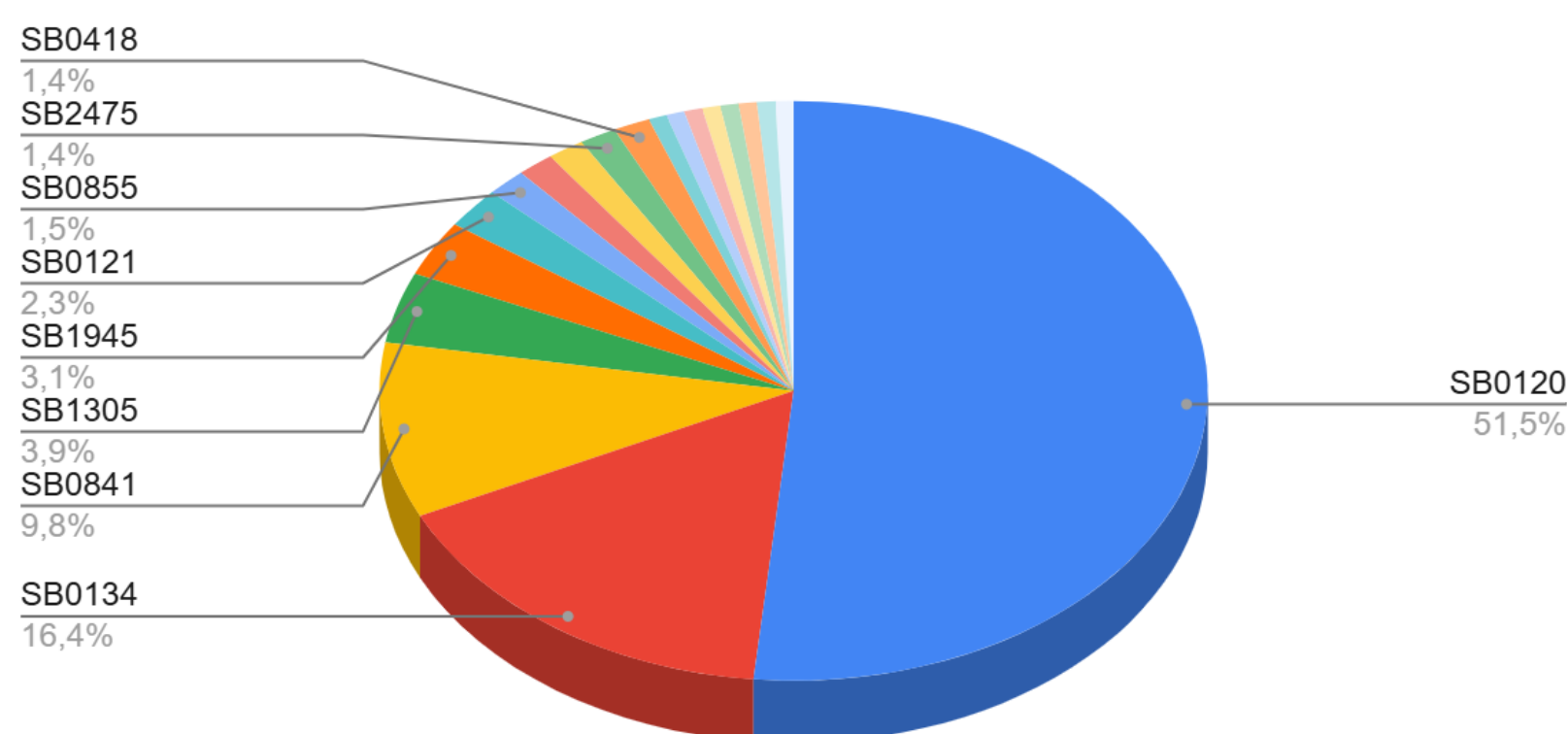
Ziehl Neelsen



RESULTS & DISCUSSION

In 2024, a total of 745 animals were analyzed, of which 213 tested positive for *Mycobacterium bovis*. Spoligotyping revealed that the genetic landscape of *M. bovis* in Sicily is characterized by a limited number of predominant genotypes, particularly SB0120, followed by others such as SB0134 and SB0841. A wider range of minor and sporadic genotypes was also detected. The distribution of genotypes varied geographically, with some provinces showing higher genetic diversity than others. These findings point to a combination of localized endemic transmission and sporadic new introductions, influenced by environmental, management, and ecological factors.

Spoligotype Prevalence in Sicily



CONCLUSION

The observed genetic heterogeneity of *M. bovis* reflects the complex epidemiology of bTB in Sicily. Molecular data such as spoligotyping provide crucial insights into strain circulation, supporting the design of more effective and geographically tailored control strategies aimed at the progressive eradication of the disease.

FUTURE WORK / REFERENCES

The primary future objective is to extend the analysis of *M. bovis* spoligotypes to a more extended period of time in order to understand the evolutionary dynamics of the dominant strains (e.g., SB0120 and SB0134) and correlate this spread with the implementation of Regional and National Eradication Plans, with the goal of identifying critical moments and strategic shortcomings for optimizing future control measures in Sicily.



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