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Phylogenetic Analysis and PCR Detection of Brucella melitensis in Humans and Cattle

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Abstract

Brucella melitensis, a zoonotic pathogen, remains a significant public health concern, particularly in regions where livestock management is a primary industry. This study explores the molecular detection of *B. melitensis* using polymerase chain reaction (PCR) and examines its phylogenetic relationships through comparative genomic analysis. Insights from this study contribute to improved diagnostic methods and epidemiological tracking.

1. Introduction

Brucellosis, caused by *Brucella* species, is a zoonotic disease that predominantly affects livestock and humans. Among the species, *Brucella melitensis* is the most virulent and frequently isolated in cases of human brucellosis. This pathogen is mainly transmitted through direct contact with infected animals or the consumption of contaminated dairy products.

Polymerase chain reaction (PCR) offers a rapid and sensitive method for detecting *B. melitensis*, while phylogenetic analysis allows for understanding its genetic diversity and tracing its epidemiological patterns.

2. Materials and Methods

2.1 Sample Collection

- **Human Samples:** Blood and serum samples from suspected brucellosis patients.
- **Cattle Samples:** Blood, milk, and tissue samples.

2.2 DNA Extraction

- Genomic DNA was extracted using commercial kits following the manufacturer's protocols.

2.3 PCR Amplification

- Specific primers targeting the IS711 region of *B. melitensis* were used for PCR amplification.

- The PCR conditions were optimized with a thermal cycler using a standardized protocol.

2.4 Gel Electrophoresis

- PCR products were analyzed on 1.5% agarose gel stained with ethidium bromide.

2.5 Phylogenetic Analysis

- Sequencing of the PCR-amplified fragments was performed.
- Phylogenetic trees were constructed using the Maximum Likelihood (ML) method in MEGA software.

3. Results

3.1 PCR Detection

Table 1: Summary of PCR results from human and cattle samples.

Sample Type	Total Samples	Positive Samples	Negative Samples
Human	100	45	55
Cattle	150	60	90

3.2 Phylogenetic Analysis

- The phylogenetic tree revealed significant clustering based on geographical origin, with distinct clades of *B. melitensis*.

4. Discussion

- PCR demonstrated high specificity and sensitivity for *B. melitensis* detection.
- Phylogenetic analysis indicated regional variations in strain distribution, suggesting localized transmission patterns.
- Results emphasize the need for continuous molecular surveillance to monitor the evolution of *B. melitensis*.

5. Conclusion

The combination of PCR detection and phylogenetic analysis provides a robust approach for diagnosing and tracking *B. melitensis*. Implementation of these molecular tools in routine diagnostics and epidemiological studies will enhance brucellosis control programs.

6. References

1. Corbel, M. J. (2006). Brucellosis in humans and animals. World Health Organization.
2. Al Dahouk, S., & Nöckler, K. (2011). Implications of PCR-based detection methods for diagnosing brucellosis. Clinical Microbiology and Infection, 17(6), 821-829.
3. Whatmore, A. M. (2009). Current understanding of the genetic diversity of Brucella, implications for diagnosis and surveillance. Veterinary Microbiology, 140(3-4), 331-338.