

分枝桿菌分子鑑定方法之研究

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摘要

分枝桿菌(*Mycobacterium* spp.)為一種抗酸性細菌，依照傳統鑑定方法及近年基因之研究可以細分成百種以上。其中又分為好幾個子群(如 *Mycobacterium tuberculosis* complex、*Mycobacterium avium* complex 等)，但僅部分對獸醫研究上有重要性，包括常見的 *M. bovis* (牛型分枝桿菌)、*M. paratuberculosis* (副結核分枝桿菌)及 *M. marinum* 等，在分子鑑定方法研究方面主要是特定基因序列比對(包括 16S rRNA、ITS 1 及 *hsp65*)，本研究目的是以 *hsp65* 基因序列比對及其衍伸之 HaeIII/BstEII-PRA (PCR Restriction Enzyme Analysis) 分析實驗室內已知分枝桿菌並用於鑑定未知之種類。

Study of mycobacterial molecular identification methods

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Abstract

Mycobacterium spp. are acid-fast bacteria, which can be identified into more than hundred species according to traditional biochemical characterizations and recent genomic analyses. Mycobacteria include several groups, e.g. *Mycobacterium tuberculosis* complex、*Mycobacterium avium* complex. Only a few species are important in veterinary medicine, such as *M. bovis*, *M. paratuberculosis*, *M. marinum* etc. Molecular identification for mycobacteria focus on sequence analysis of specific genes, for example: 16S rRNA, ITS 1, *hsp65*, etc. In this study, *hsp65* gene sequencing and HaeIII/BstEII-PRA (PCR restriction enzyme analysis) of *hsp65* gene were used to confirm reference strains and identify unknown isolates.