



Intraspecific variation in 16S rRNA gene of *Mycoplasma synoviae* determined by DNA sequencing

Marcos R. Buim^a, Melissa Buzinhani^a, Maurício Yamaguti^a,
Rosângela C. Oliveira^a, Elena Mettifogo^a, Jorge Timenetsky^a,
Antonio J. Piantino Ferreira^{b,*}

^a Departamento de Microbiologia, Instituto de Ciências Biomédicas II,
Universidade de São Paulo, São Paulo, SP, Brazil

^b Departamento de Patologia, Faculdade de Medicina Veterinária e Zootecnia,
Universidade de São Paulo, Av. Prof. Dr. Orlando M. Paiva, 87,
CEP: 05508-270, São Paulo, SP, Brazil

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Abstract

Mycoplasma synoviae (MS) is an important avian pathogen may cause both respiratory disease and joint inflammation synovitis in poultry, causing economic losses to the Brazilian poultry industry. The genotypic variation in 16S rRNA gene is unknown. Partial sequences of 16S rRNA gene of 19 strains of *M. synoviae* were sequenced and analyzed in order to obtain molecular characterization and evaluation of the genetic variability of strains from distinct Brazilian areas of poultry production. Different polymorphic patterns were observed. The number of polymorphic alterations in the studied strains ranged from 0 to 6. The nucleotide variations, including deletion, insertion and substitutions, ranged from 3 to 5. The genotypic diversity observed in this study may be explained by spontaneous mutations that may occur when a lineage remains in the same flock for long periods. The culling and reposition in poultry flocks may be responsible for the entry of new strains in different areas.

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Keywords: *Mycoplasma synoviae*; Genotypic variation; Poultry; 16S rRNA gene

* Corresponding author. Tel.: +55 11 3091 1352; fax: +55 11 3091 7354.
E-mail address: af.piantino@fmvz.usp.br (A.J.P. Ferreira).

Résumé

Mycoplasma synoviae (MS) est un important agent pathogène aviaire qui peut causer des maladies respiratoires ou des problèmes articulaires comme des synovites, en provoquant des pertes économiques pour l'industrie aviaire brésilienne. La variation génotypique dans le gène 16S est méconnue. La séquence partielle du gène rRNA 16S de 19 échantillons de *Mycoplasma synoviae* a été séquencée et analysée pour obtenir la caractérisation moléculaire et l'analyse de la variabilité génétique des échantillons de différentes régions brésiliennes de production aviaire. Des différentes séquences pléomorphiques ont été observées. Le nombre de modifications pléomorphiques dans les échantillons étudiés a varié de zéro (0) à six (6). Les variations de nucléotides, y compris délétion, insertion et substitutions, ont varié de trois (03) à cinq (05). La diversité génotypique observée dans cette étude peut être expliquée par les mutations spontanées qui peuvent se produire quand l'ascendance se maintient dans le même environnement par une longue période. La sélection et le remplacement dans les lots d'oiseaux peuvent être responsables de l'entrée de nouveaux échantillons dans différents secteurs de production aviaire.

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Mots clés : *Mycoplasma synoviae* ; variation génotypique ; volaille ; gene rRNA 16S

1. Introduction

Mycoplasmas belong to the class mollicutes and are the smallest self-replicating wall-less prokaryotes. Their small genome size is a result of the degenerative evolution and as a result they lack various genetic mechanisms and metabolic routes, with some nutritional requirements being met by scavenging from their host. This reduced genome has resulted in the loss of several DNA repair enzyme, leading to a higher mutation rate than many other bacteria [1]. Due to their dependence on the host for many nutrients, mycoplasmas are usually found intimately adhered to epithelial host cells in which the nutritional requirements are better obtained [2].

Mycoplasmas contain a reduced number of ribosomal genes with only one or two operons in a different organization [3]. The phylogeny of the Mollicute group has been established by analysis of 16S RNA gene. However, the Mollicutes 16S rRNA may show inter and intraspecific variations and conserved regions in their nucleotide sequences [4].

Mycoplasma synoviae is pathogenic specie for commercial poultry having been found in other birds. Intraspecies variability among mycoplasma strains and their ability to interact with other diseases-production factor may help to explain the wide variability of clinical manifestation, difficulties in diagnosis and their ability to persist within the host for long periods of time, and difficulties involved in control and eradication programs [5].

The DNA sequencing is an important technique in the identification and localization of inter and intraspecific variations of genes. The 16S gene are suitable for distinguishing between such closely related species [6]. In the present report, partial sequences of 16S rRNA of 19 strains of MS were sequenced and analyzed in order to obtain molecular characterization and evaluation of the genetic variability of samples from distinct Brazilian areas.

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