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Genotyping of *Mycoplasma bovis* Isolated from Cattle Suffering from Respiratory Manifestation in Menofia Province, Egypt

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Abstract

Mycoplasma bovis in cattle may cause economic losses in cattle farms. Bovine mycoplasmosis is endemic in Egypt. The aim of the current study to determine the occurrence and molecular characterization of *M. bovis* strains recovered from cattle in Egypt. *M. bovis* was isolated by standard methods from nasal swabs, oral and conjunctival swabs of 200 diseased calves with percentages of 40, 15 and 20%, respectively. The examined *M. bovis* isolates were PCR positive to amplified fragment size 1626 bp of *uvrC* gene, 1007 bp of *gapA* gene and 797 bp of p40 pseudogene. Sequence analysis of *uvrC* gene of the field isolates showed (95.3%) similarity when compared with each other and (100%) identity with *M. bovis* reference strain (PG45) and the field strains on GenBank. Analysis of *gapA* gene of *M. bovis* isolates (Egy-8-Fa-14 and Egy-9-DK-14) showed (100%) identity between each other and (98.2%) identity with the reference strain (PG45). Our isolates showed (98.9% up to 100%) identity when compared with international field strains in GenBank. Concerning analysis of p40 pseudogene our field isolates showed (97.5%) identity when compared with each other, while (Egy-12-Fa-14) showed (99.8%) similarity with both *M. bovis* PG45 reference and field strains on GenBank. In conclusion *M. bovis* is circulating in bronchopneumonic calves in Egypt. This is the first record in Egypt to investigate some *M. bovis* genes by nucleotide sequence analysis.

Key words: Genotyping, *Mycoplasma bovis*, PCR, RespiratoryISSN 0253-8318 (PRINT)
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