MOLECULAR CHARACTERIZATION OF *Pasteurella multocida* ISOLATED FROM SOME FARM ANIMALS IN FAYOUM GOVERNORATE, EGYPT

By

Ayaat Ahmed Omer Teleb

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ABSTRACT

The present study was conducted to identify the variations among clinical isolates of *Pasteurella multocida* at molecular level to check the distribution of Pneumonia and hemorrhagic septicemia in some farm animals sheep, buffalo and cattle at Fayoum region in Egypt.

P. multocida is one of the most important gram-negative bacteria and is a commensal of the upper respiratory tract of many animals. However, under predisposing circumstances the organism is the etiological agent of a wide range of economically important diseases. Thus to understand this microbial diversity, characterization of the isolates was done by their morphological, biochemical and molecular characterization.

The five isolates chosen exhibited luxuriant growth on blood agar with translucent grayish or yellowish green colonies. However, they showed no growth on MacConkey and no hemolysis of blood, also the five isolates were positive for oxidase, catalase and H_2S production, negative of urease and can ferment glucose, fructose and glucose but can't ferment lactose. Antibiotic sensitivity showed that five isolates were sensitive to (tetracycline, clindamycin and erythromycin) but resistant to (ampicillin, trimethoprim/sulfamethoxazole and flucloxacillin). To determine the genetic diversity nine random primers OPA-01 - OPA09 were used to/which generate different profiles. The five strains of *p. multocida* showed distinct RAPD profiles and relationships among the five strains of *p. multocida*. The result of molecular characterization the showed that five strains of *p. multocida* have similar size of PCR products that generated one band of 16S rDNA and KMT1 gene that have 460 and ~1471 bp respectively. Thus the authors can recommend that diagnosis of *P. multocida* by combine of 16S rDNA and KMT1 gene, antibiotic sensitivity should be tested before curing of diseased animals. In order to reduce of use antibiotic to devoid new resistant strains of *P. multocida.*

Key words: **Antibiotic sensitivity, Morphological identification, *Pasteurella multocida*, Biochemical characterization, RAPD analysis, 16S rDNA, KMT1gene.**