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Rapid diagnosis of virulent *Pasteurella multocida* isolated from farm animals with clinical manifestation of pneumonia respiratory infection using 16SrDNA and *KMT1* genes

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ABSTRACT

The present study was conducted to characterize intra- isolates variation between clinical isolates of *P. multocida* at molecular level to check the distribution of pneumonia and hemorrhagic septicemia in some regions of Fayoum, Egypt. Also, the study is focusing on the characterizations of clinical isolates of *P. multocida* isolated from sheep, buffalo and cattle and identified by amplified 16S rDNA and KMT1 genes using their DNA as a template in PCR reaction. *P. multocida* isolates were isolated from sheep, cattle and buffalo from various locations in the Fayoum Governorate, Egypt. The results demonstrated that the five selective isolates of *P. multocida* had similar size of PCR products that generated one band of 16S rDNA having 1 471 bp and KMT1 gene having 460 bp. The phylogenetic tree and similarity of the five selective isolates of *P. multocida* which were collected from GenBank database were calculated and analyzed for the nucleotide sequence of 16S rDNA and KMT1 genes. The sequencing result of 16S rRNA gene product (1 471 bp) for the five selective isolates of *P. multocida* showed that the isolates of sheep (FUP2) shared 94.08%, 88.10% homology with the buffalo isolate (FUP8) and cattle isolate (FUP9) respectively, whereas, the buffalo isolate (FUP5) shared 98.18% and 94.40% homology with the cattle isolates (FUP12 and FUP9).

The results indicated the relationships of *P. multocida* isolated from buffalo and cattle rather than the close relationships between *P. multocida* isolated from cattle and sheep. Diagnosis of *P. multocida* by 16S rDNA and KMT1 gene sequences was important to determine the antigen that is responsible for protective cover within the same group of animals and to help for the production of new vaccines for the control of microbial infection for domestic animals.