

Molecular Evaluation of Major Virulence Genes Simultaneous with Capsular Typing of *Pasteurella multocida* Isolated From Sheep in Fars Province

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Background & Objectives: *Pasteurella multocida* causes a wide range of important diseases in domestic animals, being responsible for pneumonia in cattle and sheep. The aim of this study was to learn more about the virulence of *P. multocida* isolated from sheep.

Methods: In this purpose we designed a multiplex PCR assay for simultaneous detection of major important virulence genes including *ptfA*, *hgbA*, *toxA*, *ompH*, along with capsular typing. Thirty one isolates of *P. multocida* isolated from diseased sheep were evaluated.

Results: Capsular typing of isolates by PCR demonstrated three capsular types A, D, with prevalence of 83.8% and 9.6%, respectively. The results also showed that 30 (96.7%), 28 (90.3%), 21 (67.7%) and 24 (77.4%) of isolates were positive for presence of *toxA*, *hgbA*, *ptfA* and *ompH* genes respectively.

Conclusion: *P. multocida* capsular type A was the most common in the isolates. The remarkable high prevalence of *toxA* and *hgbA* among diseased sheep may imply to important role of these genes in epidemiology and virulence of *P. multocida*. Furthermore the high prevalence of *P. multocida* type A harbor *toxA* gene found is noticeable and attribute to its important role in respiratory infection.

Keywords: *Pasteurella Multocida*; Virulence Factor; Sheep; Fars

