

Typing ovine and avian *Pasteurella multocida* isolates from Iran based on LPS outer core biosynthesis loci (L1-L4)

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Abstract

Pasteurella multocida is a negative gram pathogenic bacteria that causative agent of many diseases in animals and man. Fowl cholera and ovine pasteurellosis are of the most common infection of *P. multocida* that these diseases economic damage entered into the livestock industry. Different virulence factors of *P. multocida* have been introduced that LPS have an important role in virulence of the organism. The aim of LPS typing is determination differences between *P. multocida* strains based on LPS synthesis genetics. For perform molecular typing, DNA extraction was done with the using of a boiling method of each bacterial isolate culture and genotyping done on 32 ovine isolate and 30 avian isolates by PCR with using of specific primers for LPS genotyping experiment. The amplified LPS genes by PCR, then were sequenced and compared to the sequences deposited in the GenBank database from the world. Of the 32 ovine isolates only 10 isolates were contained L3 genotype (%31.25) and of 30 avian isolates 18 isolates were contained L1 genotype (%60), 4 isolates contain L2 genotype (%13.32), 5 isolates contain L3 genotype (%16.66), 2 isolates contain all three genotypes L1, L2, L3 (%6.66), 1 isolate contain both genotype L2, L3 (%3.33). Of the 4 genotypes, ovine isolates were only contain L3 genotype in against, avian isolates were contained L1, L2, L3 genotypes that this was indicated the distribution of LPS genotypes is different based on host type. The sequencing results of Iranian isolates with GenBank isolates showed a significant difference in L3 genotype and less difference in L1, L2 genotypes.

Key words: *Pasteurella multocida*, Ovine, Avian, Lipopolysaccharid typing

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