Genotyping of Salmonellae Isolated from Clinical Animal Sources by Polymerase Chain Reaction (PCR)

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Background & Objectives: Salmonella is one of the most important zoonotic pathogens, with wide range of animal reservoirs and many virulence factors that plays a major role in its pathogenesis. PCR can represent an alternative to costly and time consuming culture Methods for rapid detection of pathogenic Salmonella species. Therefore, considering the importance of the spvA and invC genes in the pathogenesis of the Salmonellae, the aims of the present study were to identify the mentioned genes involving in pathogenesis of isolated Salmonella from different animal sources, evaluating their prevalence and targeting them for diagnosis of different Salmonellae.

Methods: A total of sixty five Salmonella isolates, collected fron farm animals in Shiraz and suburbs between 2004 and 2005, were evaluated for the existence of virulent genes by PCR.

Results: The results revealed that the frequency of spvA and invC genes for 65 salmonella isolates were 58.46% and 75.38%, respectively.

Conclusion: It seems that the presence of spvA gene might be used for detection of Salmonellae with virulence plasmid. Considering spvA as a plasmid gene and also because the chromosomal invC gene is associated with type III secretion system (not present in all salmonellae), it can be concluded that although detection of these genes can rely on the presence of genus salmonella, but absence of them dose not definitively reject the genus salmonella as a possible option.

Keywords: Genotyping; Salmonellae; Clinical Animal Sources