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Assessment of Ail Gene Marker Amplicon for Molecular Characterization of Pathogenic Yersinia enterocolitica in Food Samples Collected in Iran

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Abstract:

Background: To assess the utility of the chromosomal *ail* virulence gene sequence for detection of pathogenic *Yersinia enterocolitica* in raw meet food products (beef, lamb, and chicken).

Methods: This study included 39 *Yersinia enterocolitica* positive cultures from suspicious food samples, in a working period of six months. These samples were referred to the "Food-Borne Diseases and Chronic Diarrhea Lab at Research Centre for Gastric and Liver Diseases" of the Taleghani Hospital at Shahid Beheshti University of Medical Sciences, Tehran, Iran. Isolates from 8 cultured *Y. intermedia, Y. aldovi, Y. intermedia* type O:45, *Y. kristensenii, Y. enterocolitica type* O:12/26, *Y. enterocolitica* type1/7/8, *Y. frederiksenii* type O:39, and *Y. enterocolitica* type O:8 samples were included in the study. Four non-*Yersinia* species *Salmonella typhi*, *Shigella dysenteriae*, *Shigella flexeneri*, and *Proteus mirabilis* were used for specificity testing. An established *Yersinia* type O:9 was used as positive control and for sensitivity testing. An in-house real-time PCR assay was designed in order to rapidly and specifically identifies the presence of specific *Yersinia* species.

Results: Out of 39 tested *Y. enterocolitica* samples, 6(2.3%) showed positive results for the *ail* gene PCR product, typed as O:8, and O:9, respectively. PCR products were sent for sequencing. Two sequences were registered with the National Center for Biotechnology Information (NCBI Genbank) as polymorphic *ail* gene sequences under the accession numbers of DQ157767 and DQ003329.

Conclusions: Collectively, this test is well adapted for definite confirmation of pathogenic *Y. enterocolitica* in food samples.

Keywords:

Ggenetic markers ، Real- time systems ، Molecular sequencing data

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