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**Title:** Integration of different resistance gene cassettes in variable region of class 1 and 2 integrons of Shigella spp.

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**Abstract:** Background and Objective: Shigella spp. is one of the major causative agents of diarrhea in both developing and developed countries. It causes gastroenteritis especially in children which is annually reported in Iran. The aim of this study was to confirm the identity of Shigella spp. by a species-specific PCR and to detect the diversity and resistance gene content of class 1 and 2 integrons among Shigella spp.

**Material and Methods:** Shigella strains were isolated from stool samples in summer 2010 and characterized by serotyping, biochemical tests and species-specific PCR of ipaH gene. Class 1 integron was detected by amplification of class-specific integrase gene and their resistance gene content was identified by amplification and sequencing of their variable resistance region.

**Results:** Among the total 37 strains (identified as ipaH+) S. sonnei was the most frequent serogroup (56.7%), followed by S. flexneri (32.4%), S. boydii (8.1%) and S. dysenteriae (2.7%). Twelve strains (34%) harbored class 1 integrons. Three types of class 1 integrants were identified in this study including 750, 1500 and 1600 bp gene cassettes among 8.1, 2.7, and 18.9% of isolates which correspond to dihydropholate reductase (dfrA7), aminoglycoside adenyl transferase (aadB)/chloramphenicol acetyltransferase (catB3) and dihydropholate reductase (dfrA17)/ aminoglycoside adenyltransferase (aadA5), respectively, as identified by sequence analysis of the variable region of class 1 integron. Two types of class 2 integrons were identified harboring dfrA1 and sat1 (1500 bp) in 43.2% (including S. sonnei, S. flexneri and S. boydii ) and dfrA1, sat1 and aadA1 (2300 bp) in 24.3% (only S. sonnei) of isolates.

**Conclusion:** The predominance of dfr and aad family gene cassettes reflects the stability and persistence of this group of resistance gene cassettes in class 1 integron. This finding, together with the absence of relative diversity in arrangement and organization of gene cassettes, suggests the transferability of the entire integron structure rather than individual gene cassettes.

**class1 & 2 integrons , aad ,dfr**

**Presentation:** Poster