Abstract

This study demonstrates that Escherichia coli isolates from human stools showed mostly higher minimum inhibitory concentrations (MICs) and significant rates of resistance (32%-67%, P<0.05) than Escherichia coli water isolates in Jordan, as follows: ampicillin (67% vs 28%), trimethoprim/sulfamethoxazole (67% vs 28%) nalidixic acid (63% vs 20%), cefuroxime (32% vs 4%), gentamicin (32% vs 17%), norfloxacin (32% vs 12%) and tetracycline (33% vs 16%). The prevalence of integron integrase genes (Intl1) in these isolates was also significantly higher in patients' stools (67%, P <0.05) than in water (36%), but the distribution of Sul 1/Sul 2 or both in association with postive Intl1 and resistance to ampicillin and sulfamethoxazole was not significantly higher (74% versus 62%, P <0.05) in isolates from stool and water. Plasmid profiles of representative multiresistant E. coli isolates from both sources indicated the presence of two common plasmids (49,25 kb) in 11/12 (91.6%), and all E. coli transconjugants were positive for class 1 integron markers (Intl 1, Sul 1 and Sul2) and mostly associated with three transferable drug-resistant determinants to ampicillin, sulfamethoxazole and tetracycline. These results indicate that class 1 integrons with conjugative R-plasmids are common and transferable among commensal antimicrobial multiresistant E. coli isolated from human feces and drinking water sources in Jordan.