

Multidrug-resistant commensal *Escherichia coli* isolated from hospitalar and schools in the city of São Paulo.

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Overuse of antibiotics has contributed to the strength of selection in different species bacteria. Antimicrobial resistance in commensal *E. coli* and isolated from various infections have been reported worldwide. Pathogen occurrence and susceptibility profiles, however, show substantial geographic variations as well as significant differences in community and hospitalar environments. Commensal *E.coli* constitute a reservoir of resistance genes, their level of resistance is considered to be an indicator for selection pressure by antibiotic use and for resistance problems to be expected in pathogens. The aim of this study was to evaluate the susceptibility profile and the presence of *E. coli* resistance genes in children with and without antibiotic therapy. Stool samples from 30 children from schools and 31 children were collected admitted to Children's Institute, HCFM-USP. The isolation was performed on MacConkey agar and identification to the species by PCR. The determination of the minimum inhibitory concentration (MIC) were performed by broth microdilution method for drugs (Ampicillin, Ceftriaxone, Ciprofloxacin, Cefoxitin, Kanamycin, Chloramphenicol, Levofloxacin, Meropenem, Nitrofurantoin, Tetracycline and Tigecycline) and resistance genes of several classes of antibiotics: Aminoglycosides (*aac*, *ant*); β -lactam (*bla*_{CTX-M}, *bla*_{TEM}, *bla*_{KPC}, *bla*_{IMP-1} and *ampC*); chloramphenicol (*cmlA*, *cat*, *flor*); nitrofurantoin (*nfsA*, *nfsB*); quinolones (*qnrB*) and tetracycline (*tetA*, *tetB*, *tetC*) were tested by PCR. In our results of susceptibility observed high percentage of resistance among isolates (2 to 100%), mainly in the group with antibiotic therapy. In the control group was observed high resistance to nitrofurantoin (92%), ampicillin (77.7%), chloramphenicol (45%) and tetracycline (30.6%). The resistance genes showed high percentage in both groups. However, to control group showed for: *ant* (100%), *nfsA* (98%), *ampC* (83.7%), *tetA* (73.5%) and *nfsB* (59%) compared to the antibiotics group

ant (83%), *ampC* (74.5%), *tetA* (68%), *nfsA* (66%), *nfsB* (23.4%). In the control group the only gene was not detected *bla_{KPC}*, being found in all strains of group with antibiotics. The emergence and spread of *E. coli* strains resistant to several antibiotics is a major threat to the control of human / animal infections and the environment. The results of this study underscore the magnitude of the problem of bacterial resistance in strains belonging of the intestinal tract, making it a resistance reservoir, and an alert to the abuse of antibiotics.

keywords :Escherichia coli, children, bacterial resistance, susceptibility testing.