

THESIS ABSTRACT

Causative Agents of Diarrhea in Erbil Children and the Effect of Some Plant Extracts on Bacterial Isolates

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Background: In developing countries including Iraq diarrhea in children still represent a major health problem. Children diarrhea is with multiple etiology and causative agents varied geographically.

Aim: To determine the microbial causative agents of diarrhea in children in Erbil city, antibiogram and their susceptibility to plant extracts.

Materials and methods: Five hundred samples of stool were collected from children with diarrhea (infants and children under ten years of age) admitted to the Pediatric and Maternity Hospital in Erbil City from March 2007 to September 2007. The samples were cultured on different culture media and according to the colony morphology, biochemical reactions and by the use of API 20E system, the isolated organisms were determined and identified.

Results: The frequency of the isolated organisms were 35 (7%) *E.coli* I; 8 (1.6%) *E.coli* II; 17 (3.4%) *E.coli* III; 22 (4.4%) *E.coli* IV; 8 (1.6%) *Shigella dysenteriae*; 16 (3.2%) *Salmonella arizonae*; 12 (2.4%) *Salmonella typhi* and 6 (1.2%) *Vibrio cholerae*. Additionally, parasites that were isolated include *Entamoeba histolytica* 175 (35%), *Giardia lamblia* 102 (20.4%) and *Hymenolepis nana* 2 (2.4%). No infectious agents were found in 75 (15%) of the tested samples. Mixed infections were determined in 22 (4.4%) of the samples. The sensitivity of the bacterial isolates to different antibiotics was performed. There was a variation in the resistance of the isolates ranging from 2-100%, whereas other isolates were sensitive.

Most cases of diarrhea were in children less than 3 years of age and the males (64%) had more infection rates than the females (35.8%). Children from urban (77%) areas had higher infection rates than those from rural (23%) areas. Children who were bottle fed (31.4%) had higher infection rates than those who were breast fed (17.6%) or those with mixed feeding (16.6%). The most frequent signs and symptoms in diarrhea patients included fever, abdominal pain, vomiting and tenesmus. RBC's and WBC's were found in stool samples.

The MIC, MBC and inhibition zones for five plants (*Quercus infectoria* (Nutgalls), *Prosopis farcta* (pods), *Juglans regia* (leaves and exocarp of fruit) and *Prunus armeniaca* (leaves)) were determined for *E.coli* I, *E.coli* II, *E.coli* III, *E.coli* IV, *Shigella dysenteriae*, *Salmonella arizonae*, *Salmonella typhi* and *Vibrio cholerae*. The chemical composition of these extracts was determined.

The determination of the site of genes responsible for the antibiotic resistance in *E.coli* O157:H7 was performed using the genetic transformation method for *E.coli* DH5 α laboratory strain with the DNA that is absent from the highly resistant strains, *E.coli* O157:H7 4 and *E.coli* O157:H7 6. The transformation process succeeded when

using the plasmid DNA for strain 4 and failed when using strain 6. It was evident that the genes responsible for resistance to the following antibiotics were located on the plasmid DNA: amoxicillin, amoxiclav, ampicillin, cephalaxine, cefixime, cefotaxime, doxycyclin, gentamycin, nalidixic acid, nitrofurantoin, rifampicin, streptomycin and tetracycline. Whereas the genes responsible for the following antibiotic resistance were located on the chromosome: amikacin, erythromycin, chloramphenicol, ciprofloxacin, tobramycin and trimethoprim.

To reduce or remove these genes that are responsible for antibiotic resistance, the aqueous and ethanolic extracts of *Q.infectoria* were used, and by SMIC determination, the results revealed that it had a reducing effect (curing) on these genes. These results indicate that this plant's extracts were highly efficient in reducing the *E.coli* O157:H7 antibiotic resistance and this was proved using gel electrophoresis.

Conclusion: Parasitic infections was the most common (57.8%) cause of diarrhea in children, while the bacterial form 23.2% as aetiology of diarrhea in children. Resistant gene location was varied according to different antibiotics and was located either on plasmid or chromosomes. Plants extracts tested lead to reduction or removal genes responsible for microbial resistance to antibiotics and suggested the use of plant extracts as therapeutic approach for resistant bacterial strains.