

Summary

Pathogenic *Escherichia coli* (*E.coli*) strains are known to cause intestinal and extraintestinal infections in human. A wide variety of infectious diseases could be caused by *E. coli* strains, including urinary tract infection, septicemia, newborn meningitis, central nervous system and respiratory system infections. Several bacterial agents can cause diarrheal and urinary tract infections, among these *E.coli* strains are detected a one of the important cause of morbidity and mortality of diarrhoea and UTI throughout the world.

The aims of this study were to identification and genotyping of *Escherichia coli* isolated from clinical specimens (Burns,wounds , urinary tract infections , diarrhea , and vaginal swabs) and hospitals environments in relation to virulence properties and antimicrobial susceptibility.

A total of 318 samples were collected during the period from September 2012 to march 2013 .All specimens were screened for the presence of *E. coli* by cultured on MacConkey agar and Eosin-methylene blue agar then identified by biochemical tests and confirmed by API 20E system which revealed that:90/318(28.33%) gave positive growth for *E.coli* as following : 1/42(2.38%)was obtained from burns,7/25(28%)from high vaginal swabs , 11/41 (26.82%) from wounds infections,18/33(54.54%)from diarrheal infections and 38/67(56.71 %)from urinary tract infections, while 15/110 (13.63%) from environmental isolates. The isolated were subjected to molecular identification as *E.coli* by used the intergenic spacer region primer(*ITS*). The confirmed isolates were examined to detect the phylogenetic group based on triplex PCR by using a combination of two genes (*chuA* and *yjaA*) and an anonymous DNA fragment (*TSP*) .

Universal primers (*ITS*) indicated that all isolates 90(100%) gave positive results .The phylogenetic analysis revealed that 90 (*E.coli*) isolates belonged to three phylogenetic groups A &D 36(40%)for each, while B2 18 (20%) and no one

LIST OF CONTENTS

isolates belong to B1 phylogenetic types . Among 50 tested bacteria, (100%) isolates had at least two of the virulence genes , *Pap* and *VT1* was the most prevalent gene(100%).While only one isolates were positive for *VT2* gene.

Out of the 16 of antibiotics used, 87(92.22%) isolates were multidrug resistance .All isolates have been found resistant to at least one β -lactam antibiotics.

List of Figures	VIII
List of Abbreviations	XI
Chapter one	
1-1-Introduction	
Chapter two	
2-1-Structure Review	4
2-1-1 Genus <i>Escherichia</i>	4
2-1-1-1 <i>Escherichia coli</i>	4
2-1-1-1-1 Classification	4
2-1-1-1-2 General Characterization	4
2-1-1-1-3 Typing Methods	12
2-1-1-1-4 Conventional typing methods- serotyping	15
2-1-1-1-5 <i>E. coli</i> phylotype	15
2-1-1-1-6 Intestinal pathogenic <i>E. coli</i>	17
2-1-1-1-6-1 Enteropathogenic <i>E. coli</i>	17
2-1-1-1-6-2 Enterohemorrhagic <i>E. coli</i>	18
2-1-1-1-6-3 Enterotoxigenic <i>E. coli</i>	20
2-1-1-1-6-4 Enteroinvasive <i>E. coli</i>	21
2-1-1-1-6-5 Enteropneumogenic EPEC and Shiga-like spp	22
2-1-1-1-6-6 Diffusely adherent <i>E. coli</i>	23
2-1-1-1-6-7 Extraintestinal pathogenic <i>E. coli</i> (ExPEC)	24
2-1-1-1-6-8 Virulence factors of <i>E. coli</i>	26
2-1-1-1-6-8-1 Pathogenicity Islands	26
2-1-1-1-6-8-2 Adhesins	27
2-1-1-1-6-8-3 Aggregation factors antigen (AFA)	28
2-1-1-1-6-8-4 Trains	28
2-1-1-1-6-8-5 Some protease microorganisms	30