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INCIDENCE OF VIRULENCE
FACTORS IN
UROPATHOGENIC
ESCHERICHIA COLI IN TWO
LEBANESE HOSPITALS AND
THE EVALUATION OF THE
CPS ID3 CHROMOGENIC
MEDIUM FOR URINE
CULTURES

by

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ABSTRACT

PREVALENCE OF VIRULENCE FACTORS IN UROPATHOGENIC ESCHERICHIA COLI IN LEBANON AND THE EVALAUTION OF THE CPS ID3 CHROMOGENIC MEDIUM FOR URINE ANALYSIS

by Majd J. Lahham

Chairperson of the Supervisory Committee:Dr. Sima Tokajian Department of Natural science division

Urinary tract infections are among the most frequent encountered infections. The vast majority of urinary tract infections are caused by Escherichia coli. The invasion and colonization of the urinary tract by uropathogenic E. coli is mediated by its virulence factors. In this study, 160 uropathogenic E. coli strains were screened for pilus associated with pyelonephritis (pap), S fimbriae (sfa), afimbriae (afa), aerobactin (aer), hemolysin (bly), and cytotoxic necrotizing factor 1 (cnf1). The prevalence of these genes among the studied isolates were

33.6, 33.1, 8.8, 45.6, 32.5, and 18.1% for pap, sfa, afa, aer, hly, and enf, respectively. Genes coding for adherence factors were present in 81% of the isolates confirming their importance role in tissue targeting and colonization of mucosal sites. Cnf gene was limited to hemolytic strains and was linked in most isolates to adhesins, while sfa was always associated with other virulence factors. Different combinations of genes were detected indicating possible synergism and/or the fact that the genes coding for these virulence factors are located on the bacterial chromosome. Detection of the virulence factors would be of a great value in understanding pathogenesis.

CPS ID3 chromogenic medium was compared to routine media for the isolation, and to API system for the identification of urinary tract pathogens. Positive predictive values were 100% for all species included in this study except Enterococcus spp. that was 66.7%. False negative results were observed in E. coli and Enterococcus spp. isolates (96% and 92.3% respectively) indicating that additional tests should be performed, particularly when white colonies are recovered. All organisms isolated from urine samples grew on this medium, but not all could be identified based on the morphological characteristics of their colonies. However, using this medium had the additional benefit of reducing the time needed for urine analysis when compared to the time needed with routine analysis. The most important advantage attributed to the use of CPS ID3 was the prompt identification of E. coli within 24 hours with no need to use additional biochemical tests. On the other hand, being expensive, having a short shelf life and not covering Staphylococcus saprophyticus were the only important drawbacks of this medium. CPS ID3 enables presumptive identification of a high proportion of urinary tract pathogens through the color of the colony, and even pathogens that were colorless were successfully isolated using this medium. The results of the present study suggest that use of chromogenic medium offers a time saving method for the reliable detection and presumptive identification of urinary tract pathogens. Moreover, it also revealed that the studying of bacterial virulence

determinants is an important aspect for the development of strategies to combat urinary tract infection.

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GLOSSARY

Glossary:

UTI: urinary tract infection.

Pap: pilus associated with pyelonephritis

Sfa: S fimbriae

Afa: A fimbriae

Cnf. cytotoxic necrotizing factor

Aer: aerobactin

Hly: hemolysin

ExPEC: extrapathogenic Escherichia coli UPEC: uropathogenic Escherichia coli

PAIs: pathogenicity islands

MRHA: mannose resistant hemagglutination MSHA: mannose sensitive hemagglutination

PCR: polymerase chain reaction

INTRODUCTION

Urinary tract infection (UTI) which is the presence of microorganisms in an otherwise sterile urinary system (Barnett and Stephens, 1997; Kunin, 1994; Zorc et al., 2005) is considered as a public health concern especially that wide range of gram-positive and gram-negative bacteria can be associated with this type of infection (Hanson et al., 1981). Escherichia coli, however, remains the most frequent isolated pathogen in UTI (Tobias et al., 2002; Stamm and Hootom, 1993; Gruneberg, 1984; Ronald, 2002), and were found to possess virulence factors that do not exist in commensal strains (Johnson, 1991; Donnenberg and Welch, 1996). Knowledge of these factors allow biologists to better understand the evolution and pathology of this organism (Usein et al., 2001), and consequently preventive therapies could be developed by targeting these virulence genes (Russo and Johnson, 2003).

Different chromogenic media can be used for the presumptive identification of UTIs' pathogens, since the enormous numbers of UTIs' cases all over the world along with the workload in medical labs acquire the necessity to design such media that can give rapid and cost effective results (Stevens, 1989; Emori and Gaynes, 1993).

Objectives of the study:

- Evaluation of the chromogenic media CPS ID3 (BioMerieux) for the identification of pathogens associated with UTIs in comparison with API (BioMerieux).
- Molecular detection of E. coli containing samples by the amplification of uspA specific gene.

3- Detection of virulence genes in *uspA* positive isolates including: *pap*, *sfa*, *afa*, *aer*, *hly*, and *cnf* using multiplex PCR.

Chapter 2

LITERATURE REVIEW

2.1 Urinary Tract Infection:

Urinary tract infection is regarded as a group of infections of different clinical severity and prognosis (Hanson et al., 1980). The etiology of UTI has been established for several years (Ronald, 2002). The members of the family Enterobacteriaceae are considered as the major causes of the urinary tract infection (UTI) which is one of the most common infectious diseases in the world (Chomarat, 2000). Many statistical studies showed that UTI was the most frequent cause of nosocomial infections, after respiratory tract infections. UTI is the second reason responsible for hospitalization and is a common cause of infection in ambulatory patients in the US (Stamm and Hootom, 1993; Emori and Gaynes; 1993; Hootom and Stamm1997). Two issues are raised when studying UTI as a public health concern: first a wide range of bacterial species can be associated with this type of infection (Hanson et al., 1981), second, as a result of antibiotic treatment; pathogens can become resistant to antimicrobial agents (Ronald, 2002). Both gramnegative bacteria (Escherichia coli, Klebsiella pneumonia, and Proteus spp.) and grampositive bacteria (Staphylococcus spp and Streptococcus spp.) can be associated with UTI. However, not all are pathogenic, with many isolates such as lactobacilli being contaminants from the surrounding area of the urethra and being non pathogenic (Barnett and Stephens, 1997).

Since a UTI definition does not specify neither the site of infection in the urinary tract nor the severity of the infection, two terms are used to diagnose such infections: pyelonephritis, infection of the upper urinary tract such as the renal pelvis or the renal parenchyma (Bergeron, 1995; Bass et al., 2003; Zorc et al., 2005), and cystitis, infection of the lower tract, such as the bladder or urethritis (Zorc et al., 2005). However, asymptomatic bacteruria is also a term

used in infections that are not associated with inflammatory symptoms (Hanson et al., 1981; Zorc et al., 2005). Moreover, uncomplicated UTI refers to infections in patients with anatomically-normal urinary tracts; while complicated UTI is used when patients have structurally or functionally abnormal urinary tracts (Bergeron, 1995; Bass et al., 2003).

Epidemiologic studies showed that all people are susceptible to UTI (Pezzlo, 1988). Host factors such as gender, age, diabetes, and catheterization were considered as important as bacterial pathogens in defining the severity of infection (Ronald, 2002). A large proportion of women, around 50%, experience UTI in their life, and 25% of this population experience another UTI within the following 6 months (Foxman, 1990), with sexual intercourse playing a major role in this incidence (Buckley et al., 1978). In infants younger than 90 days, the urinary tract is the major site exposed to infection, and according to Rushton (1997) the frequency of UTI at this age group is 1%. Abbot (1972) however, revealed that the incidence of UTI is higher in premature babies than full term infants. UTI additionally attacks elderly individuals without differentiation between males and females, which is due to functionally or structurally abnormal urinary tracts (Ackermann and Monroe, 1996). In general, over six million outpatients are infected by UTI every year (Kunin, 1996).

2.2 Escherichia coli

2.2.1 General overview of E. coli:

In 1885, Theodore Escherish isolated a new bacterial species when he was conducting studies on gastrointestinal bacterial contents. He named this species bacterium coli commune (Sussman, 1985). Between 1887 and 1902, scientists argued if this species is Bacillus typhi, which causes typhoid fever or not. Then many test including lactose fermentation showed that bacterium coli commune differs from Bacillus typhi (Ewing et al., 1981). In 1919, to honor

Theodore Escherish for his discovery, Castelani and Chalmers named this bacterium Escherichia coli (Bettelheim, 1991)

Escherichia coli —a member of the Enterobacteriaceae family- is gram-negative, a facultative anaerobic bacillus that constitutes a large part of human and warm-blooded animal flora. This species invades infants' intestines within few hours of life as a commensal organism (Drasar and Hill, 1974; Orskov and Orskov, 1985). E. coli is considered as an important member of the bacterial kingdom because of its ability to synthesize its own nutrients from single organic components and few minerals (Farmer et al., 1985; Schaechter and Neidhardt, 1987)

Although *E. coli* is a normal member of the human intestine, it can cause infections in the gastrointestinal tract and other organs in the body, including the nervous system and the urinary tracts. These infections can be attributed to the fact that this organism is an opportunistic pathogen and that it possesses virulence factors. Infection caused by *E. coli* which is considered as the leading cause of nosocomial infections (Emori and Gaynes, 1993) could be as a result of damage in the gastrointestinal barriers (Cavalieri et al., 1984; Orskov and Orskov, 1992; Nataro and Kaper, 1998; Tobias et al., 2002). Additionally, *E. coli* is a common cause of common community-onset bacteremia with the rates being higher compared to that established by *Staphylococcus aureus* or group A or group B streptococci (Jackson et al., 2005).

E. coli is classified as a commensal, intestinal and extraintestinal organism (Table 1) (Russo and Johnson, 2000), associated with enteric/diarrheal disease, urinary tract infection, and sepsis/meningitis (Nataro and Kaper, 1998). Extraintestinal E. coli infections are important causes of morbidity, mortality, and increased health-care costs (Russo and Johnson, 2003).

2.2.2 Escherichia coli and urinary tract infections:

Many studies showed that *E. coli* was the most common pathogen causing complicated and uncomplicated cases of urinary tract infections in immunocompromised and normal individuals (Table 2) (Gruneberg, 1984; Stamm and Hootom, 1993; Ronald, 2002; Tobias et al., 2002). Since the gastrointestinal tract is the habitat of this microorganism, the close proximity between urogenital sites and anus might indicate that the fecal flora was the source of urinary strains isolated in a UTI; supporting a so-called "fecal-urethral hypothesis" (Gruneberg, 1969). While Goetz et al. (1999) pointed out that extraintestinal *E. coli* was present in the normal flora without causing gastroenteritis.

E. coli isolated from patients with urinary tract infections have virulence factors that are not detected in commensal isolates. These factors allow the organism to invade and colonize the uroepithelial cells, evade the lymphatic system, and find its way into the blood stream (Johnson and Russo, 2002). Although 29 factors have been identified including adhesins, toxins, and proteases (Johnson and Stell, 2000), many pathogenic E. coli isolated from urinary tracts did not show any of the defined virulence factors. Indicating that there were many unidentified factors (Marrs et al., 2002). At the cellular level, virulence factors were classified into two categories: those found on the cell surface like adhesins, and those produced in the cell and exported to the site of action like hemolysin (Emody et al., 2003). Since such virulence factors were not unique to uropathogenic E. coli; meningitis-causing E. coli strains had these as well, this group of organisms was denoted as extraintestinal Escherichia coli (Johnson, 1991; Donnenberg and Welch, 1996; Johnson and Russo, 2002). Furthermore, Johnson et al. (2001) realized that extraintestinal E. coli belonged to the phylogenetic group B2 and to a lesser extent to the D group.

Because of its importance, Welch et al. (2002) sequenced the complete genome of an uropathogenic E. coli strain (CFT073) isolated from a woman with acute Pyelonephritis and compared it with the nonpathogenic *E. coli* strain MG1655, and the enterohemorrhagic *E. coli* strain O157:H7 (EDL933) (Table 3). Being distinctly different from each other, the difference in disease potential between O157:H7 and CFT073 was attributed to the absence of toxin-encoding genes. The CFT073 genome carried genes that encoded potential fimbrial adhesins, autotransporters, iron-sequestration systems, and phase-switch recombinases.

Table 1: Pathogenic behavior of the three main types of *E. whi*: relative participation of each *E. whi* group in the particular clinical manifestation is indicated on a semiquantitatibe scale, from – (absent) to +++ (maximal) (Russo and Johnson, 2000)

E. coli pathtoypic group	Asympotomatic intestinal colonization	Diarrhea	extraintestnal infection	
Commensal	+++		+	
Intestinal Pathogenic	1.00	+++	-	
ExPec*	+	- 2	+++	

^{*}ExPec: Extrapathogenic Escherichia coli

Table 2: Etiology of Uncomplicated Versus Complicated Urinary Tract Infection (UTI) (Ronald, 2002)

Uncomplicated UTI pathogens	Complicated UTI Pathogens
Escherichia coli	Escherichia coli
Staphylococcus saprophyticus	Klebsiella spp.
Klebsiella spp	Enterobacter cloacae
Enterococcus faecalis	Serratia marcescens
	Proteus mirabilis
	Pseudomonas aeruginosa
	Enterococcus faecalis
	Group B streptococci

Table 3: Escherichia coli CFT073: genome contents: (Welch et al., 2002)

Genome length	5,231,428 bp	
Plasmids	None	
Protein-coding genes	5,533	
rRNAs	22 genes in 7 operons	
tRNAs	89 [1 pseudo, 1 novel (Arg)	
1 extratandem (Arg), 3 phage-encoded		
Miscellaneous RNAs annotated	11	
G-C%	50.47%	
Backbone genes	3,190	
Island genes	1,827	
Backbone regions	359 (3,925,047 bp; 75.02%)	
CFT073-specific islands	247 (1,306,391 bp; 24.98%)	
Cryptic prophage	5	

2.2.3: Molecular detection of Escherichia coli:

Escherichia coli species harbor a unique protein known as the universal stress protein A (uspA), whose exact physiological role is still unknown. Since its intracellular level sharply increases under-stress conditions such as exposure to oxidants, heat, and antibodies, it could be essential for the survival of the organism when cellular growth arrests. Starvation due to the lack of nitrogen, carbon, sulfate, phosphate and amino acid, increased intracellular uspA level (Nyström and Neidhart, 1994; Gustavsson et al., 2002; Kvint et al., 2003). Mutation in uspA gene led to premature death during stasis (Nyström and Neidhart, 1993). On the other hand, over-expression of this protein kept E. coli in a growth-arrested stage (Nyström and Neidhart, 1996). The gene (434 bp) that encodes for uspA protein was found to be located on the E. coli chromosome (Nyström and Neidhart, 1992), and the protein was cytoplasmic with a molecular weight of 13.5 KDa (Freestone et al., 1997).

Chen and Griffiths (1998) took advantage of uspA specificity and developed a polymerase chain reaction to differentiate E. coli from other gram-negative bacteria using primers complementary to the flanking region of uspA gene.

2.3 Extraintestinal Escherichia coli virulence factors:

2.3.1 Extraintestinal E. coli virulence factors and Pathogenic Islands:

Hacker et al. (1990) found out that the deletion of the gene coding for the fimbriae and hemolysin in two extraintestinal *E. whi* strains resulted in loss of the other, thus linkage between these two genes was deduced and termed "Pathogenecity Island". Several studies followed showing that deletion of pathogenicity islands yielded non pathogenic *E. whi* strains (Blum et al., 1994), indicating that these islands were clusters of genes that conferred virulence to nonpathogenic strains (Groisman and Ochman, 1996). Their mobility and their high G+C content differentiated these islands from their surrounding DNA, therefore, their horizontal transfer provides nonpathogenic *E. whi* with pathogenic properties (Hacker and Kaper, 2000; Oelschlaeger et al., 2002).

2.3.2 Adherence:

Gram-negative bacilli have fimbriae that contain lectin-like domains. These domains have the ability to recognize receptors found on epitopes in cell surface glycoproteins or glycolipids (Hedlund et al., 2001). Adherence of extraintestinal *E. coli* to uroepithelial cells was considered the first step in the pathogenesis (Langermann et al., 1997; Beachey, 1981). Historically, Duguid et al. (1967) illustrated that the attachment of *E. coli* to erythrocytes was due to thin fiber-like appendages, known as fimbriae (Figure 1). Most strains of *E. coli*, isolated from urinary tracts, have such fimbriae needed for the attachment to the uroepithelial cells (Plos et al., 1995). Proteins involved in adherence were called adhesins and found on the bacterial surface. Those structures have the ability to bind glycoconjugate receptors on the epithelial cells and may or may not be associated with fimbriae (Lefflier and Svanborg Eden, 1980; Le Bouguenec, 1992). Thus, the globoseries of glycolipid receptors of certain human cells predispose them to infection. Thereby, cells that do not

have these receptors can avoid infection (Kallenius and Mollby, 1979). At the level. of E. molecular attachment coli occurred the Galα1→4βGal, found on the surface of certain cells like group P1 and P2 erythrocytes, was recognized by adhesin proteins (Lefflier and Svanborg Eden, 1980; Kallenius et al., 1980). Interestingly, these receptors have the ability to bind mannose residues, competing with some fimbriae types like type 1 pili. This type of agglutination, however, was designated as mannose sensitive hemagglutination (MSHA). This was contrary to mannose resistant hemagglutination (MRHA), where no competition occurs between other fimbriae types and mannose (Chabanon et al., 1979; Wold et al, 1988). In turn, MRHA was divided into two groups according to receptor specificity: (i) those recognizing P blood serotype (named P fimbriae) and (ii) others (named X fimbriae or X adhesins) such as S, M, F, Dr (Table 4) (Johnson, 1991)

Table 4: Mannose resistant adhesins of uropathogenic E. coli (Johnson, 1991)

Adhesin type UTI	Synonym(s)	Fimbriae present	Receptor	Role in
P adhesion				
P	Gal-Gal, Pap	+	Gal (l-4)Gal	+++
F	Prs, Pap-2	+	Forssman antigen	++
ONAP	577	+	Gal(al-4)Gal	+/-
X adhesion Dr related Dr	075-X		Dr blood group antigen	++
AFA-1, AFA-II	I		Dr blood group antigen	+
S		+	NeuNAc(a2-3)Gal	+/-
М		-	M blood group antigen	+/-
G		+	GlcNAc	+/-
NFA-1, NFA-	2		2	+/-

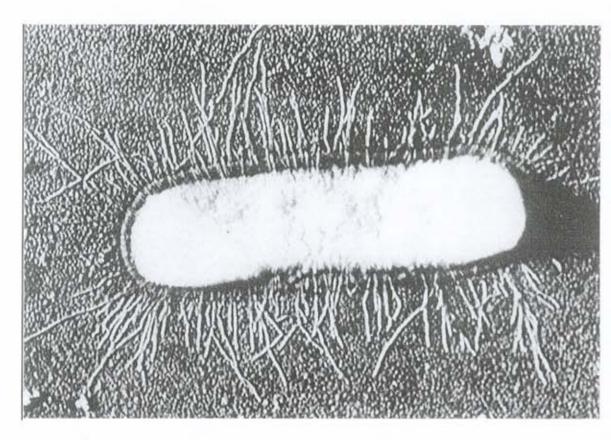


Figure 1. An early electron photomicrograph of a fimbriated *E. coli* cell, showing protoplast, cell wall, about 200 fimbriae, and no flagella. (Duguid et al., 1955)

2.3.2.1: P fimbriae: pilus associated with pyelonephritis: (pap)

P fimbriae belong to a mannose-resistant hemagglutination (MRHA) category. The P abbreviation comes from the human blood group antigen P that contains $Gal\alpha 1 \rightarrow 4\beta Gal$ moiety. This moiety was not only found on P blood group but also on certain mammalian cells like uroepithelial cells as carbohydrate components of glycosphingolipids (Marcus et al., 1981). Thus, cell lines expressing the $Gal\alpha 1 \rightarrow 4\beta Gal$ moiety, like P blood group or uroepithelial cells, were predisposed to infection by P fimbriae-containing strains (De Man et al., 1987; Kallenius et al., 1982). Pilus associated with pyeloniphritis is encoded by a cluster of genes (operon) termed pap (Figure 2), which consisted of pap A, pap F, pap G, pap E genes (Baga et al., 1984). Pap fimbriae is made of approximately 10^3 polymerized subunits with the major

subunit being pap A. Pap E, pap F, and pap G are minor subunits that existed in minute amount at the fimbrial tip (Lindberg et al., 1987). Although pap A is the major subunit of P fimbriae, it does not play any role in adherence. The ability to adhere was mainly correlated to pap G, which formed a complex with pap F. Pap F in turn was bound to pap A via pap E (Lund et al., 1987; Hoschutzky, 1989)

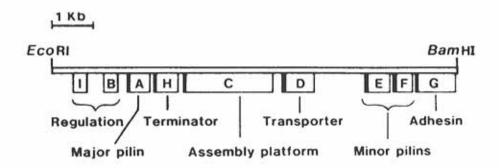


Figure 2: overview of pap operon. PapA is the major (structural) fimbrial subunit. PapH seems both to terminate fimbrial growth and to anchor the fully grown fimbriae to the cell surface. PapC is located in the outer membrane and forms the assembly platform for fimbrial growth. PapD is a periplasmic protein which forms complexes with the fimbrial subunits before assembly. PapE, PapF, and PapG are minor fimbrial components. PapG is the adhesin molecule conferring Gal(otl-4)Gal binding specificity, PapF complexes with PapG, and PapE attaches the PapF-PapG complex to fimbriae (Lindberg et al., 1987).

2.3.2.2: X Adhesion: Dr Family (Afimbriae) & S fimbriae

X adhesion belongs to the MRHA category, like P fimbriae. Two adhesins belong to this group: Dr Family (Afimbraie) and S fimbriae.

Dr family adhesins were first described by Väisänen-Rhen and Labigne-Roussel et al. (1984) who revealed that *E. voli* O75 had novel adhesins of unknown receptor specificity, and designated is as O75X. Following that, three separate groups cloned novel adhesin-encoding genes, later was found to have similar characteristics (Dr, afimbrial adhesins (afa), and F1845) (Nowicki et al., 1987; Labigne-Roussel and Falkow, 1988; Bilge et al., 1989). Nowicki et al. (1990) proved that those three adhesins and O75 X adhesin bind Dr blood group antigen. These types of adhesins structurally differ from other fimbriae in their appearance which appeared as fine mesh (Arthur et al., 1989). Dr adhesins were mostly isolated from infected pregnant women and children rather than adult men and non-pregnant women (Labigne-Roussel and Falkow, 1988). Dr Family protein was encoded by cluster of five genes. One of these genes was responsible for structural hemagglutinin (Labigne-Roussel et al., 1985).

S fimbriae were also MRHA and named S (sfa) because of its ability to bind to terminal sialyl-galactoside moiety (Parkkinen et al., 1983). Sialyl-galactoside receptors were found on uroepithelial cells of renal vascular endothelium, on the proximal and distal tubules, collecting ducts, and glomerulus (Korhonen et al., 1986). Ott et al. (1986) revealed that S-fimbriated E. whi strains were more commonly isolated from patients with bacteremia and meningitis than UTI patients, although genes that code for S fimbriae were first cloned from the uropathogenic E. whi strain O6:K15 (Korhonen et al., 1986).

2.3.3 Aerobactin:

Aerobactin (aer) is responsible for the extraction of Fe³⁺ from the ironbinding protein of the host which is then transferred through an outer membrane receptor (Carbonetti and Williams, 1984). One of the host mechanisms to fight infection is by shifting iron available in the plasma pool to intracellular storage in the form of iron-binding protein (Weinberg, 1978). E. coli strains having Aerobactin have a growth advantage over those without aerobactin in the presence of low iron concentration (Braun et al., 1984; Montgomerie, 1984). Iron taken by aerobactin is used in *E. coli* for DNA synthesis, electron transport, oxygen transport and storage, and metabolism of peroxides (Bagg and Neilands, 1987, b). Aerobactin is composed of two lysine and one citrate molecules (Neilands et al., 1985). It is encoded by an operon with five genes. One of those genes is responsible for the outer membrane protein receptor while the others are involved in synthesizing the aerobactin (Gross et al., 1985). Aerobactin operon is controlled by the concentration of iron in *E. coli*, when the iron concentration is high, transcription of the repressor gene proceeds. Conversely, when iron concentrations are low, transcription of the repressor gene is blocked (Bagg and Neilands, 1987, a).

2.3.4: Hemolysin:

Hemolysin protein (bh) lyses human erythrocyte to obtain calcium from the host cell (Short and Kurtz, 1971). Hemolysin inserts into the lipid membranes of erythrocytes and creates space channels, which are permeable mainly to calcium and other cations (Menestrina et al., 1987). Besides its ability to harm erythrocytes, hemolysin can induce tissue injury and inflammation in other host cells (Cavalieri et al., 1984). Furthermore, hemolysin induces renal tubular cells to liberate hydrogen peroxide and superoxide anion (Keane at al., 1987). Four-gene operon is responsible for producing hemolysin protein (Figure 3) (Goebel and Hedgpeth, 1982). This operon is found on the chromosome of E. coli strains isolated from humans, while it is located on a plasmid in E. coli strains isolated from animals (Welch et al., 1983). Hemolysin A is the main player in hemolytic activity and it does not need cleavage of a signal peptide or cellular lyses to be secreted. It needs activation by hemolysin C, and secretion is mediated by hemolysin B and D (Springer and Goebel, 1980).

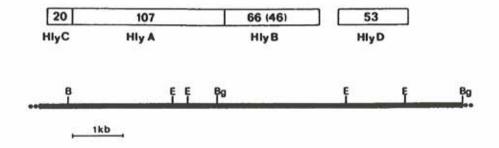


Fig 3: Overview of hly operon which consisted of hly A, hly B, hly C, and hly D (Mackman et al., 1986)

Cytotoxic necrotizing factor (enf):

The gene encoding for this protein is found in isolates having the hemolysin gene (Caprioli et al., 1987). This 110 KD protein induce dermonecrosis in rabbits, and multinucleation in the ovary of Chinese hamster through changes in cytoskeletal actin and tubulin (Caprioli et al., 1983; Fiorentini et al., 1988). Furthermore, enf promotes apoptosis in uroepithelial cells in the human bladder (Mills et al., 2000).

2.4: Detection of urinary tract pathogens:

2.4.1: Conventional methods:

Pezzlo (1988) introduced many rapid methods to detect UTI and classified them into six categories: microscopic, enzymatic, colorimetric, bioluminescence, and photometric methods. Culturing urine on agar media to enrich pathogenic bacteria is still the gold standard for UTI diagnosis (Zorc et al., 2005). Two kinds of media are routinely used: a non-selective medium, blood agar, and selective medium like MacConkey agar or Cysteine lactose electrolyte deficient medium (CLED) for gram-negative bacteria. MacConkey and CLED have lactose sugar to detect lactose fermenting

pathogens and to inhibit the swarming of Proteus spp. (Samra et al., 1998; Graham and Galloway, 2001). Urine culture is considered positive when it vields more than 105cfu/ml (Williams and Schaeffer) while 104cfu/ml is considered positive in young children (Zorc et al., 2005). Urine should be cultured before antibiotic treatment because antimicrobial agents reduce the bacterial count (Ramkrishman and Scheid, 2005). However, occasionally, 100 cfu/ml is considered a positive value in the presence of significant infection symptoms (Kunin et al., 1993). Once the bacteria are cultured and isolated, chemical tests can be applied to determine the identity of the pathogens. One of the systems used in the routine work is the API, which is a plastic strip holding microtubes containing dehydrated substrates that react with bacterial enzymes. After 18-24 hours of incubation at 37°C, the color changes on the strip are used to identify the strain (Shayegani et al., 1978). Evaluation studies showed that API system is a valuable method to routinely identify bacterial pathogens (Bulter et al., 1975; Shayegani et al., 1978). Moreover, simple tests can be additionally used to differentiate between different genera. For example, catalase test is positive for Staphylococcus spp. but not for Streptococcus spp. while the oxidase test is positive for Pseudomonas spp. but not for member of the Enterobacteriaceae family (Graham and Galloway, 2001)

2.4.2: Chromogenic media:

Rapid identification improves the ability to specify the antimicrobial treatment and reduces the incidence of antibiotic resistance (Slak, 1984; Alon et al., 1987). To help diagnose UTI, many chromogenic media develop specific colors for each bacterial species based on the reaction between bacterial specific enzyme and substrates added to the media (Scarparo et al., 2002; Samra et al., 2002). Such as the chromogenic medium CPS ID3

(BioMerieux) used in this study, which gaves burgundy color for E. coli due to the production of β -glucoronidase enzyme (Edberg and Kontnick, 1986).

2.4.3: Molecular techniques:

In the last few decades, molecular techniques have played a major role in many fields, especially in the molecular diagnosis of microorganisms. Many techniques have been used in studying bacteria including restriction fragment length polymorphism (RFLP) and the polymerase chain reaction (PCR). Those techniques facilitated the conductance of large-scale epidemiological studies and the construction of gene banks and protein banks (Tang et al., 1997). Molecular techniques have additionally helped in studying the structure and species composition of microbial communities (Muyzer et al, 1993). The PCR reaction is based on the capability of DNA polymerase isolated from thermophilic bacteria to synthesize many copies of DNA using DNA template, oligonucleotide primers, and dNTPs under specific thermal conditions (Tang et al., 1997). PCR is a very sensitive powerful method that can be applied in many fields like forensic, environmental, and genetic sciences (Tsai and Olson, 1992). The advantage of using PCR in the field of microbiology lies in the ability to detect bacteria directly from the specimen without having to culture them first, with results that can be obtained within a few hours of sample collection (Tang et al., 1997; Hinata et al., 2004). Furthermore, the high PCR's sensitivity allow for the detection of any bacterial gene even when the pathogen is present at a very low concentration or is mixed with many species as is the case with intestinal flora (Lo, 1994). When the target of the study is more than one gene, a multiplex PCR can be used where several genes can be amplified simultaneously using different primers. This method decreases the time and the cost of reaction without reducing the efficiency of the results. However, to get best results, primers used in multiplex PCR should have the same annealing temperature, and the replicons need to have different sizes to

easily separate the bands by gel electrophoresis (Henegariu et al., 1997; Singh, 2006)

.

Chapter 3

MATERIAL AND METHODS

3.1: Sample collection and reference strains:

Three hundred Mid-stream urine samples were thankfully collected By Dr. Ziad Daoud from St. George Hospital (n=232) and Dr. George Abdelnour from Notre Dame de Secoures hospital (n=68), from in and out-hospital patients. Samples with more than 100 white blood cells per mm³ were examined for the presence of bacteria using direct microscopic examination. Reference strains PM9, 2H16, and 2H25 were kindly provided by Dr. James R. Johnson (University of Minnesota).

3.2: Cultivation and enrichment of urine samples on conventional and chromogenic media:

Using 1 µl calibrated sterile loop (Himedia), urine was cultivated on CPS ID3 (Biomerieux), blood base agar (Biomerieux) with 5% Human blood, and MacConkey agar (Oxoid). Plates were incubated at 37°C overnight. After 24 hours of incubation, four criteria were examined: the color of the colonies on CPS ID3 plates, growth and hemolytic activity on blood agar plates, growth of gram-negative bacteria and lactose fermenting bacteria on MacConkey agar plates.

3.3: Reading of the chromogenic plates:

Chromogenic plates were interpreted according to the manufacturer's instructions. Pink or burgundy colonies being produced in the presence of the β -glucoronidase enzyme produced by $E.\ coli$, light to dark Brown colonies due to deaminase of *Proteeae* tribe, turquoise colonies due to β -glucosidase of Enterococci and green to brownish green colonies in KESC group (*Klebsiella*, *Enterobacter*, *Serratia*, *Citrobacter*). However, metallic grey were specific for *Pseudomonas aeruginosa* colonies, while Violet colonies were specific for *Streptococcus agalactiae*.

3.4: Identification using API system:

Well isolated bacterial colonies were suspended in 0.85% saline. The suspension was used to inoculate the API 20E strips according to manufacturer's instruction. After 24 hours of incubation at 37° C the strips were read by using the software provided by BioMerieux (APILAB PLUS Version 3.3.3). Staphylococci were identified using API Staph strips, while Streptococci using API Strep. The bacterial suspension for Streptococci prepared from organism cultivated on blood agar. The suspension was prepared according to the manufacturer's instructions. Strips were inoculated and incubated at 37°C. Results of API Strep were read after 4 hours and 24 hours according to the recommendation of the manufacturer. By using the software provided by BioMerieux (APILAB PLUS Version 3.3.3).

3.5: DNA extraction:

A loopful of each strain was suspended in 200 µl DNase free water, boiled with mixing for 15 minutes and then centrifuged at 13000 xg for 3 min at 4C.

3.6: Detection of *E. coli* containing samples:

E. coli was detected by the PCR-based amplification of the uspA gene(Chen and Griffiths, 1998). PCR was done in a total volume of 50 μl containing 5 μl of the DNA template, 0.1 mM forward (5'- CCG ATA CGC TGC CAA TCA gT -3') and reverse primers (5'- ACG CAG ACC GTA GGC CAG AT -3'), 0.2 mM of each deoxynucleotide triphosphate and 1X PCR buffer (50 mM KCl, 10 mM Tris HCl); 3mM MgCl₂, and 1U Taq polymerase (Fermantas®). The PCR was performed with a Perkin-Elmer Gene-Amp 9700 thermal cycler under the following conditions: heating at 94°C for 5 min. 30 cycles of: 94°C for 1 min, 53°C for 1 min, and 72°C for 1 min. Final extension 72° C for 5 min. DNA sample extracted from Klebsiella pneumoniae

isolate was used as a PCR negative control. The PCR amplicons (884 bp) were visualized using a UV light box after electrophoreses on 1% agarose gel containing 0.5 mg/ml ethidium bromide.

3.7: Detection of hly virulence gene:

PCR was performed in a total volume of 50 µl containing the following components: 5 µl of DNA template; 30 mM of hly forward (5'-AACAAGGATAAGCACTGTTCTGGCT-3') and reverse (5'-ACCATATAAGCGGTCATTCCCGTCA-3') primers; 1mM of deoxinucleotide triphosphate; 1x buffer solution, (50 mM KCl, 10 mM Tris HCl); 3 mM MgCl2, 1.5 unit of Taq DNA polymerase (Fermantas). The PCR was performed with a Perkin-Elmer Gene-Amp 9700 thermal cycler under the following conditions: heating at 94°C for 2min; followed by 30 30 cycles of denaturation at 94° C for 1 min, annealing at 60°C for 1 min, and extension at 72° C for 1.30 min; and the a final extension for 5 min at 72°C. E. coli reference strain (2h16) was used as a positive control. Sample containing water instead of DNA was used as a negative control. The PCR amplicons (1177 bp) were visualized using a UV light box after electrophoreses on 1% agarose gel containing 0.5 mg/ml ethidium bromide.

3.8: Detection of pap, sfa, cnf, aer, afa virulence genes:

Multiplex PCR was performed in a final volume of 50 μl containing the following: 5 μl of DNA template, 10 mM each of *pap* and *sfa* forward and reverse primers, 12 mM of *cnf*, *aer*, and *afa* forward and reverse primers (Table 5), 1 mM of deoxinucleotide triphosphate mixture, 1X buffer solution, 3mM MgCl2; 1.5 unit of Taq DNA polymerase (Fermantas). The PCR was performed with a Perkin-Elmer Gene-Amp 9700 thermal cycler under the specific the following conditions: heating at 94°C for 2 min; 30 cycles of denaturation at 94°C for 1 min, annealing at 60°C for 1 min, and extension at 72°C for 1 min and a final extension for 5 min at 72°C. *E. coli*

reference strain (PM9, 2h16, and 2h25) were used as positive controls. Sample containing water instead of DNA was used as a negative control. The PCR amplicons (328, 410, 498, 602, 750 bp respectivly) were visualized using a UV light box after electrophoreses on 2.5% agarose gel containing 0.5 mg/ml ethidium bromide.

Table 5: sequences of pap, sfa cnf, aer, afa, primers, adapted from Yamamoto et al. (1995).

5'-gACGGCTGTACTGCAGGGTGTGGCG-3'
5'-ATATCCTTTCTGCAGGGATGCAATA-3'
5'-CTCCGGAgAACTGGGTGCATCTTAC-3'
5'-CGGAGGAGTAATTACAAACCTGGCA-3'
5'-AAGATGGAGTTTCCTATGCAGGAG-3'
5'-CATTCAGAGTCCTGCCCTCATTATT-3'
5'-TACCGGATTGTCATATGCAGACCGT-3'
5'-AATATCTTCCTCCAGTCCGGAGAAG-3'
5'-GCTGGGCAGCAAACTGATAACTCTC-3'
5'-CATCAAGCTGTTTGTTCGTCCGCCG-3'

Chapter 4

RESULTS

4.1: Total number of each pathogen in the urine samples according to API system:

A total of 300 samples were collected from in and outpatients were donated to support this study by St. George hospital and Notre Dame de Secoure hospital, over a period of fifteen months from October 2006 to December 2007. Growth was detected in 241 samples, while 59 samples yielded no growth. Among all urinary tract pathogens, *Escherichia coli* was the most common, representing 68.85% of the studied population (n = 179), whereas *Citrobacter* and *Serratia* had the lowest percentage being 0.38% each (Table 6)

4.2: Results of CPS ID3 Chromogenic media:

The cost of the CPS ID3 was 2\$ for each plate and the shelf life was just 2 months. Colonies on chromogenic media will have a different color depending on reaction between enzymes produced by the cultivated organism and substrates available in the medium. The positive predictive value is calculated based on the specificity of the medium (Table 7). The positive predictive value of Chromogenic media was 100% for all species except for *Enterococci* (66.7%) as compared to the API system. (Figures 4, 5, 6, 7,). Sensitivity (the probability that the new test will be positive when the patient truly is infected), specificity (the probability that the new test will be negative when the patient is not infected, and the positive predictive value (true and false negative results/ true and false positive results) were calculated for each species.

Table 6: Number of pathogens recovered and Identified from positive samples and their percentage using the API system.

Species	Number	Percentage			
Escherichia coli	179	68.85%			
Klebsiella pneumonia	21	8.08%			
Klebsiella oxytoca	2	0.77%			
Pseudomonas aeruginosa	4	1.52%			
Proteus mirabilis	10	3.85%			
Proteus vulgaris	2	0.77%			
Enterobacter aerogenes	2	0.77%			
Citrobecter spp.	1	0.38%			
Serratia spp.	1	0.38%			
Staphylococcus epidermidis	5	1.92%			
Staphylococcus aureus	3	1.15%			
Staphylococcus heamolyticus	2	0.77%			
Staphylococcus auriculars	2	0.77%			
Staphylococcus sciuri	2	0.77%			
Staphylococcus saprophyticus	1	0.38%			

Species	Number	Percentage		
Staphylococcus capitis	1	0.38%		
Staphylococcus xylosus	1	0.38%		
Streptococcus faecalis	12	4.61%		
Streptococcus agalactiae	6	2.31%		
Streptococcus faecium	1	0.38%		
Streptococcus porcinus	1	0.38%		
Streptococcus cloacae	1	0.38%		
	1			

Table 7: : the sensitivity, specificity and positive predictive value of pathogens recovered on CPS ID3 chromogenic media in comparison with API system which is the reference method in this study. All KESC group, *Proteus* spp., and *streptococcus agalactia* isolates gave the expected colony color. Of 179 *E. coli* recovered in this study, 7 strains gave white colonies.

	Total number of isolates according to API system	Burgundy	Green	Brown	Turquoise	Metallic	Violet	White	Sensitivity	Specificity	Positive predictive value (PPV)
richia coli		172	-	-	-	_		7	96%	100%	100%
C group	27	-	27	-	-	-	-	-	100%	100%	100%
omonas	4	-	-	_	-	3	_	1	75%	100%	100%
v spp	12	-	-	12	_	-	-	-	100%	100%	100%
ococcus	13	-	-	-	12	-	-	1	92.3%	97.6%	66.7%
ococcus ctia	6	-	-	-	-	-	6	-	100%	100%	100%
C 90000HS	2	_	-	_	2	-	-	-	ND	ND	ND
ylococcus	17	-	-	-	4	-	-	13	ND	ND	ND .

ND: Not Determined

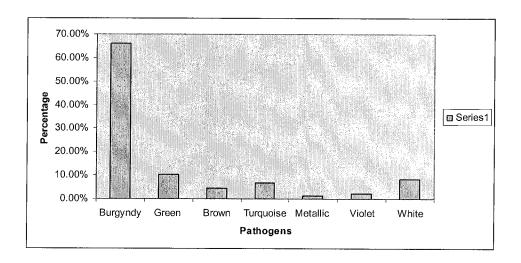


Figure 4: Number of samples that gave specific color. There were six specific colors in this medium for most prevalent isolates. The isolates that were included in this system were grown as white colonies.

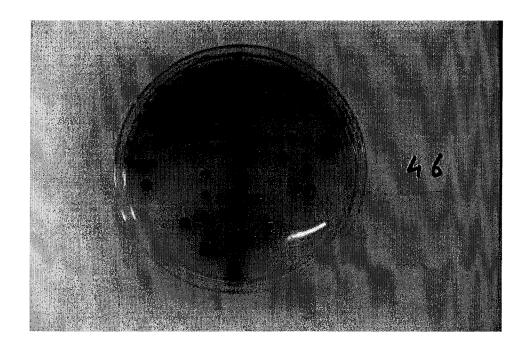


Figure 5: CPS ID 3 plate: The burgundy color in the above CPS plate indicates that the urine sample harbors *E. coli* which is the only pathogen recovered in this sample.

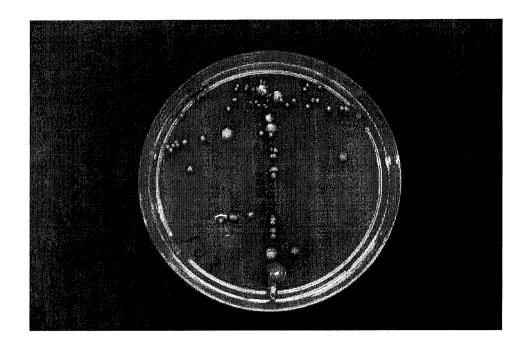


Figure 6: CPS ID 3 plate: The two colors (turquoise and white) in the above CPS plate indicated the presence of 2 pathogens: *Streptococcus* D (turquoise) and another pathogen (white) which in turn requires isolation and further testing.

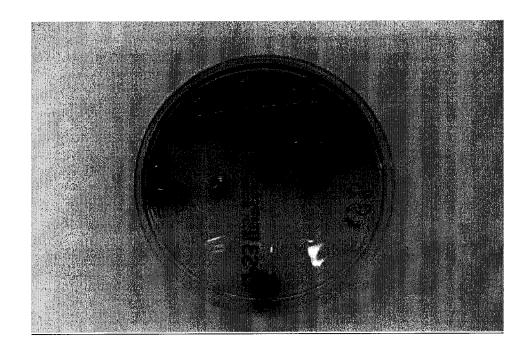


Figure 7: CPS ID 3: The three colors (burgundy and green and brown) in the above CPS plate indicated the presence of 3 pathogens: *E. coli* (burgundy), KESC group (green), and *Proteus* spp (brown).

4.3: Detection of *E. coli*-containing samples:

All 160 E. coli-containing samples (identified by API system) were further tested by PCR for the presence of the uspA gene. A gene harbored by all E. coli pathogens, hence confirming their identity (Figure 8). These were the samples that were later subjected to the PCR-detection of virulence genes according to Yamamoto et al. (1995).

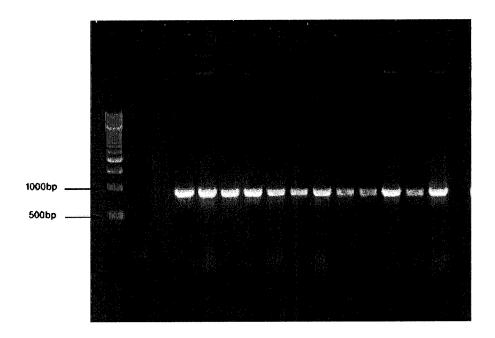


Figure 8: PCR amplification of usp A gene. Lane 1: 500 bp ladder; Lane 2: negative control containing water instead of DNA; Lane 3: negative PCR control containing DNA from Klebsiella pneumonia; Lanes 4-15: DNA extracted from uropathogenic E. coli strains recovered from urine samples collected from St. george and Notre Dame de Secures hospitals. 884 bp-amplicons confirmed the presence of Escherichia coli bacterium in those samples.

4.4: Detection of hly gene in uspA positive samples:

PCR screening for the 160 *E.coli* samples (those positive for *uspA* gene) to check the *hly* gene, indicated that 52 of them harbored this gene (Figure 9).

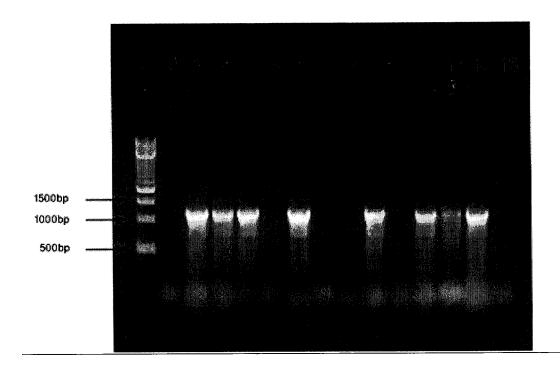


Figure 9: PCR amplification of hemolysin gene. Lane 1: 500 bp ladder. Lane 2 is negative control containing water instead of DNA. Lane 3 positive *hly* references strain 2H16 (provided by Dr. James J. Johnson, University of Minnesota). Lanes 4-15 are DNA extracted from *Escherichia coli* strains isolated from the urine of patients of St. George and Notre Dame of Secures hospitals. The 1177 bp products indicated the presence of *hly* gene in those samples.

4.5: Detection of pap, sfa, cnf, aer, afa genes using multiplex PCR:

uspA positive samples were subjected to PCR-detection of five virulence genes. The results of the PCR amplification using gene-specific primers revealed that the highest frequency (45.6%) pertains to the Aer gene and the least (8.7%) for afa gene (Table 8). Representative PCR results are presented in Figure 10.

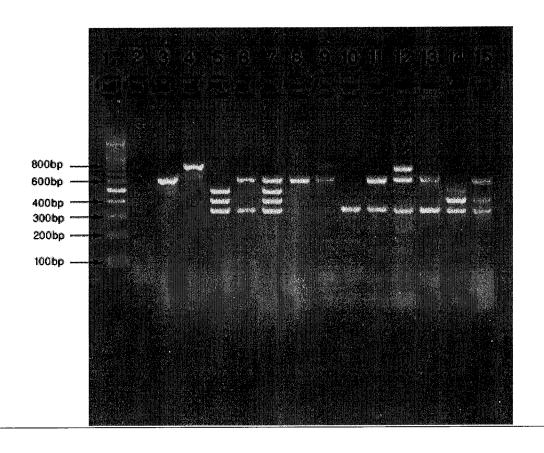


Figure 10: Multiplex PCR of pap, sfa, cnf, aer, and afa genes. Lane 1 is 100 bp ladder. Lane 2 is a negative control containing water instead of DNA. Lane 3 is E. coli reference strain PM9 that was aer gene positive. Lane 4 is E. coli reference strain 2H16 that contains afa gene. Lane 5 is E. coli reference strain 2H25 that contain pap, sfa, and cnf genes (the three E. coli reference strains PM9, 2H16, and 2H25 were provided by Dr. Johnson, University of Minnesota). Lanes 6-15 were DNA extracted from uropathogenic E. coli strains isolated from the urine of patients of St. George and Notre Dame of Secures hospitals. The 328, 410, 498, 602, and 750 bp amplicons indicated the presence of pap, sfa, cnf, aer, and afa genes respectively.

Table 8: Number of samples positive for each particular gene. The most prevalent virulence factor is aerobactin (45.625%) and the least is Afimbriae (afa) (8.75%)

Gene	pap	sfa	Cnf	Aer	Hly	afa
Number	54	53	29	73	52	14
Total						
number						
160						
percentage	33.57%	33.125%	18.125%	45.625%	32.5%	8.75%

4.6: Number of virulence factors per sample:

Of the 160 uspA-positive samples, the presence of virulence factors ranged from none to five of them per sample. Figure 11 illustrates the number of genes positive for each sample.

Of the 38 strains that gave one virulence factor, 27 strains harbored *aer* gene. As for the rest of the genes, the number of samples harboring them was generally less than five (Figure 12)

Of the 33 strains that gave two virulence factors, and among 15 possible combinations, only five patterns were significant, of which pap + aer was the most frequently detected (Figure 13).

In contrast, seven patterns were observed in the 16 strains that gave three virulence factors, while four combinations were observed with those having 4 virulence factors (Figure 14).

The 11 strains that gave 5 virulence factors had the same combination, which is pap, sfa, cnf, aer, hly (afa gene was not observed in that strains).

Of the 14 strains that gave *afa* gene, just three strains gave *afa* associated with *pap* gene. Ten strains gave *afa* gene that associated with *aer. Sfa* was associated with all factors except *afa*. Sfa was detected along with *pap* 34 times.

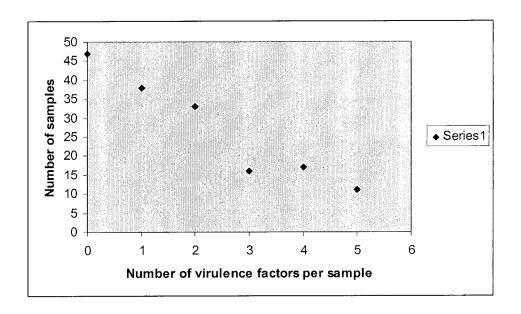


Figure 11: Number of samples VS number of virulence factors per sample.47 samples did not show any type of virulence factor whereas just 11 strains had 5 virulence factors.

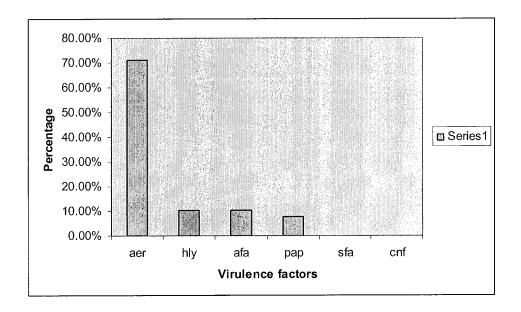


Figure 12: Number of samples that contain one virulence factor. Most of those samples had aerobactin where none of those samples had only S fimbriae or Cytotoxic necrotizing factor genes.

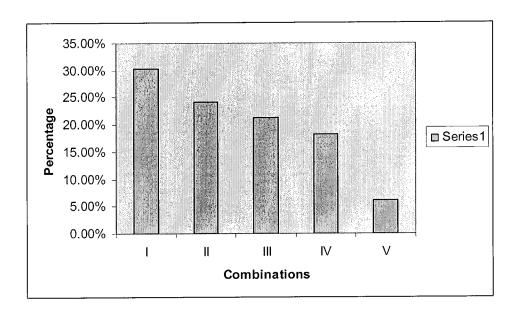


Figure 13: Number of samples that contain two virulence factors. Of the 160 uropahtogenic *E. voli* strains included in this study, 33 strains harbored 2 virulence factors. (I:pap+aer, II: sfa+aer, III: sfa+hly, IV:aer+afa, V: pap+sfa)

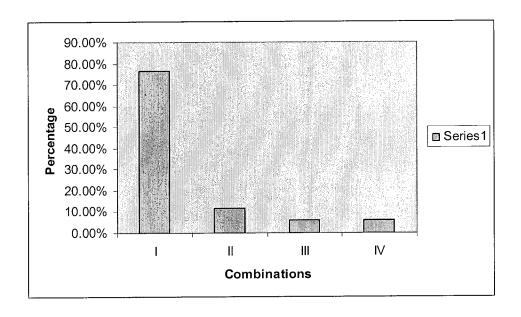


Figure 14: Number of samples that contain 4 virulence factors. The combination pap+sfa+cnf+hly was the most prevalent among other

combination. (I: pap+ sfa+ cnf+hly. II: pap+sfa+ aer+ hly, III: pap+ cnf+ aer+hly, IV: sfa+cnf+aer+hly)

Chapter 5

Discussion

In this study, CPS ID3 was evaluated as a direct isolation medium for urine samples. The enormous advantage of this medium was the ability to identify microorganisms growing within a mixed population according to colony color, as well as the ability to perform anti-microbial susceptibility tests without the need for further isolation. Bacteria that gave small colonies such as *Enterococcus* spp. were more frequently recovered on CPS ID3 medium than from conventional media because the specific colony color characterizing these pathogens facilitated the detection especially when growing along with other gram-negative bacteria. Furthermore, when two organisms have the same colonial morphology like *E. coli* and *Klebsiella pneumonia* they could be distinguished depending on their colony color on chormogenic media. Another advantage of CPS ID3 was that it did not require any additional equipment to read the culture results and the test was easy to perform.

Our study agreed with many other (Samra et al., 1998; Scarparo et al., 2002) showing that chromogenic media could support the growth of all UTI pathogens. However, Aspevall et al. (2002) reported that chromogenic media did not consistently support the growth of gram-positive bacteria and blood agar was recommended to detect these pathogens. In this study, around 15% of the recovered isolates were gram-positive.

CPS ID3 had similar to some other Chromogenic media, inhibited the swarming of many organisms such as *Proteus* spp. (Samra et al., 1998; Chaux et al., 2002; Hengstler et al., 1997; Milles and Wren, 2005); a property not seen with blood agar (Hengstler et al., 1997); Thus allowing the detection of other isolates within a mixed population. On the other hand, CPS ID3 could not be used to differentiate between *Proteus mirabilis* and other *Proteus*

spp., and accordingly Indole test is recommended for the specific identification of *P. mirabilis* which was indole negative where other *proteus* spp. are indole positive. Moreover, *Klebsiella pneumonia*, *Enterobacter spp.*, *Serratia spp.* and *Citrobacter spp.* could not be differentiated from each other, since all these bacteria gave similar colonies, and accordingly additional biochemical test should be performed. This was in harmony with the findings of Scarparo et al. (2002).

Hengstler et al. (1997), on the other hand, using BBL CHROMagar Orientation found that the fastidious strains of *Streptococcus agalactia* may not grow or grow as tiny colonies on CLED agar (cycteine lactose electrolyte deficient) or MacConkey agar. *Streptococcus agalactia* strains can be easily differentiated on CPS ID3 by their violet color.

Studies that evaluated CPS ID2 showed that about 95 to 98% of E. coli strains produced β -glucoronidase enzyme which was used in CPS ID media to identify E. coli (Mazoyer et al., 1995; Nunez et al., 1995; Orenga et al., 1993). The majority of E. coli strains (96%) isolated in this study produced this enzyme. Although Salmonella and Shigella were also β -glucoronidase positive (Le Minor et al., 1978), these organisms were rarely isolated from urine (Kilian and Bulow, 1979). Hansen and Yourassowsky (1984) indicated that Shigella was never isolated from urine samples, while Scarparo et al. (2002) recommended that indole test should be done on all positive β glucoronidase colonies, since Salmonella and Shigella spp. were indole negative. However, and according to the results of this study, where Salmonella nor Shigella spp. were detected, we do not recommend doing the indole test especially that it is time consuming. The biggest advantage of using Chromogenic media was the ability to identify E. coli strains within 24 hours without the need to do any additional biochemical tests. However, indole test should be conducted in the case of gram -negative bacteria appearing white colonies to avoid false negative results with E. coli.

Hengestler et al. (1997) revealed that Citrobacter spp. on ChromAgar Orientation and CPS ID2 plates gave false positive results as it appeared on the form of pink to red colonies similar to E. coli. Moreover, in this study also indicated that Proteus spp. and Enterobacter spp. appeared again as red to pink colonies which additionally interfered with proper E. coli identification. On the other hand, using Oxoid UTI medium Fallon et al. (2003) showed that out of 18 Citrobacter strains, 11 appeared as purple colonies similar to E. coli, while only one Citrobacter was misidentified using CPS ID2 medium. Accordingly, it was recommended that all strains that gave pink to red colonies should be subjected to the indole test to rule out E. coli isolates. In this study, none of these organisms gave a burgundy colonies which was specific for E. coli, and thus indole test was not needed using this medium. However, the absence of false positive results in our study could be possibly attributed to the low number of Enterobacter (n=2), Citrobacter (n=1), and Proteus (n=12) recovered. In addition, CPS ID3 and contrary to CPS ID2 could be used for the identification of Citrobacter spp. which reduced the error of misidentifying Citrobacter as E. coli. Moreover, in CPS ID2, Streptococcus aglactia could appear as blue colonies like Enterococcus spp., while in CPS ID3 Streptococcus aglactia gave violet colonies, which was easily distinguishable from *Enterococcus* colonies appearing as turquoise colonies. Ciragil et al. (2006) showed that CPS ID3 medium helped in the detection of all S. agalactia, enterococci, staphylococci that grew on blood agar. However, these results revealed that *Staphylococcus* spp. appeared as colorless colonies, and additional chemical tests were needed to confirm the isolation Both Enterococcus faecalis and faecium had colonial of staphylococci. morphology, and therefore could not be distinguished at the species level. This was in harmony with studies based on the use of chromogenic media (Merlino et al., 1995; Willinger and Manfi, 1995; Hengstler et al., 1997; Scarparo et al., 2002).

The positive predictive value of CPS ID3 with *Enterococcus* spp. was low (PPV=66.7%), which was possibly due to the fact that 4 *Staphylococcus* spp.

and 2 *Streptococcus* spp gave also turquoise colonies. Perry et al. (2003) using the *S. aureus* ID chromogenic medium, found that some *Staphylococcus* species might occasionally produce colored colonies as a results of the hydrolysis of a chromogenic β-glucosidase substrate. Ahmet et al., (1995) showed that *Streptococcus milleri* could be identified by the testing for β-glucosidase enzyme.

On CPS ID 3 medium, *E. coli* usually appeared as pink to burgundy colonies. Two *E. coli* variants were detected in this study in one of the urine specimens. Those two variants were distinguished as the first appeared as a pink colony and the second variant as burgundy. This was a situation where more biochemical tests were recommended to determine whether these two variants corresponded to two different infecting strains so as to determine the suitable antibiotic treatment. Similar results were reported by Carricajo et al. (1999) and by Scarparo et al. (2002), where also two *E. coli* variants were recovered from on urine in sample and were distinguishable based on their colony colors on Chromogenic media.

One of the disadvantages of CPS ID3 was that Staphylococcus saprophyticus is not included in the system although it is considered as one of the common pathogens that colonized the urinary tracts (Barnett and Stephens, 1997). Furthermore, oxidase test was recommended to differentiate between Pseudomonas spp. (oxidase positive) and Enterobacteriaceae family (oxidase negative). The sensitivity of CPS ID3 to Pseudomonas spp. was 75%. The low sensitivity of the medium might be due to the low number of strains recovered from the urine samples (n=4). The catalase test was recommended to differentiate between Staphylococcus spp. (catalase positive) and Streptococcus spp. (catalase negative), especially that in this study 4 Staphylococcus spp. appeared as turquoise colonies, which was specific for Enterococcus spp. Results of oxidase and catalase test could be obtained in few minutes.

CPS ID3 reduced 50% of the time needed for the identification (24 hours instead of 48 hours) of isolates without the need for any additional tests. In our study, 72 % of isolated strains were directly identified using this medium, and it reduced the time needed when working with mixed cultures.

Concerning cost effective studies, Scarparo et al. (2002) showed that the price of CPS ID is 0.44\$/plate. We have estimated our cost at 2\$/plate. This variation in price was attributed to delivery charges. It is not wise to determine cost effectiveness based only on the price of a chromogenic media and a conventional media, as we should also be taking into consideration the additional biochemical tests that should be done.

Finally, CPS ID3 enables presumptive identification of a high proportion of urinary tract pathogens through the color of the colony, and even pathogens that were colorless were successfully isolated using this medium. Time and biochemical tests can be sharply reduced enabling the clinician to recommend the appropriate therapy immediately after growth. The false positive results within the *Enterobacteriaceae* were very low (high specificity), allowing technicians in the clinical labs to be confident enough to report results without doing any further tests. However, the conventional biochemical tests should be applied whenever white colonies are recovered. White colored colonies are an indicator either to false negative results or are due to organisms not included in the system such as *Staphylococcus* spp. Finally, as the CPS ID3 and according to our results can be used for the identification of the members of the *Enterobacteriaceae* family, the use of other media such as MacConkey agar was not recommended anymore.

In this study, virulence factors in uropathogenic *E. coli* were detected using a multiplex PCR assay. Blanco et al. (1997) revealed that there was a correlation between results obtained using PCR assay and those obtained by phenotypic methods. Additionally, PCR-based detection was found to be quicker easier and inexpensive, facilitating detection of virulence related

genes in *E. coli*. Time required to obtain results using PCR assay was much less than time needed with colony hybridization test (Le Bouguenec et al., 1992), with Yamamoto et al.(1995a) revealing that multiplex PCR was a useful method for the rapid detection of *E. coli* virulence factors.

Of the 17 strains that were positive for four tested virulence genes, 14 strains were positive for the combination of pap^+ , sfa^+ , cnf^+ , and bly^+ which was in accordance with Yamamoto et al (1995 b), who reported that this combination was the most dominant among isolates associated with cystitis in Japan. There was a genetic linkage between those genes as shown by Hacker et al. (1990) who showed that deletion of gene coding for fimbriae or hemolysin resulted in the loss of the other.

On the other hand, and regarding the hemolysin (h/y) gene and the cytotoxic necrotizing factor (cnf), the results of this study agreed with many others and showed that presence of cnf was limited to hemolytic strains (Caprioli et al., 1987; Caprioli et al., 1989; Ruiz et al., 2002). However, not all E. coli strains that produced hly were cnf producing. It is noteworthy that in this study none of the tested strains had only these two genes, but rather these were associated with other virulence factors. In contrast, hly gene was detected as the only virulence factor in four of the tested strains. However, although cnf was limited to hemolytic strains, it required other adhesion gene to be virulent. Blanco et al. (1997) showed that there was a direct chromosomal link between cnf, hly and pap operons, which partly was in harmony with our results where we detected in three strains the presence of the hly and cnf genes in the absence of the pap. Hacker et al. (2002) reported that different pathogenicity islands had different combinations of genes.

Johnson et al. (1991) indicated that uropathogenic *E. coli* strains usually had adhesin genes, while in this study and in 19% of the tested isolates, we were not able to detect any adhesin. Most of these samples (87%) not having adhesin factors were aerobactin positive. There could be two explanations

for this co- occurrence of virulence genes: strains that contain aer gene do not require adhesin proteins to colonize urinary tracts, or aer were linked to classes of adhesins that were not undertaken in this study such as type 1 fimbriae, which was mannose sensitive hemaaglutination. Since type1 fimbria was found to be consistently associated with extraintestinal E. coli strains (O'Hanley et al., 1985; Usein et al., 2001), it was excluded form this study. Sfa adhesin was detected in 33% of the strains and this was an obvious indication that uropathogenic E. coli strains examined in this study had this type of adhesin. Ott et al. (1986), studied the sfa adhesins and reported that S-fimbriated strains were mainly associated with meningitis rather than with urinary tract infection.

Of the 11 strains that were positive for 5 virulence factors (amongst 6 tested), afa gene was not detected and this was in accordance with the finding of Usein et al. (2001). Usein et al. also screened for the same six virulence factors and found that the afa and sfa genes were not detected together in any of the tested strains, which was again in harmony with our results. Moreover, results of this study also agreed with those of Usein et al. (2001) with respect to the association between the afa and aer genes.

In this study, 32.5 and 45% of the strains were found to be positive for *hly* and *aer* respectively, while Santo et al. (2006) reported that 96 and 76% of the strains were positive for *hly* and *aer*, respectively. The difference between both studies might be attributed to the methods used in the evaluation, where Santo et al. (2006) relied basically on phenotypic methods, or alternatively it could be simply due to differences correlated to geographical factors (Lebanon versus Brazil).

Johnson et al. (1991) reported that Mannose resistant hemagglutination (MRHA) were common among hemolytic strains. Our results agreed with this observation were only around 8% of the tested strains did not have of the known adhesins. Johnson et al. (1991) suggested that there was a

synergism between MRHA adhesins and other virulence factors. Further studies are recommended to elucidate the presence of any functional correlation between MRHA adhesins and *bly*.

Aer gene occurred with all types of adhesins, whereas Jacobson et al. (1998) reported that aer was commonly found with pap. Johnson et al. (1988) revealed that aer locus could be either chromosomal or plasmid gene, with the chromosomal being associated with pap gene. Since the extraction method undertaken in this study recovered both chromosomal and plasmid DNA we could not have any conclusion with this respect especially the aer gene was detected with all other studied virulence factors.

S fimbriae adhesin (sfa) was not observed alone among the samples included in this study. No one of articles published concerning this type of adhesin reported about this observation. Furthermore, sfa was not limited to any type of the studied genes like the case of hly and enf suggesting that sfa played a role in adherence but it could not play a major role in pathogenecity without the presence of the other studied genes.

Hly gene was not amplified in the multiplex PCR assay where the primers for hlyA were designed to amplify a fragment with a size of 1177bp. It is usually difficult to amplify such a big fragment using a multiplex PCR reaction. Therefore, hly gene was detected separately in a simplex PCR assay.

Future work:

Blood agar medium is routinely used to determine bacterial counts in urine samples. It would be of great interest if the CPS ID3 could be used instead of blood agar for the above purpose.

E. coli isolation was confirmed through the amplification of the uspA gene. A multiplex PCR designed to detect virulence genes should also be standardized to include primers that can simultaneously detect the uspA gene.

It is recommended to screen the same samples for the O: K: H serotypes to find out if there is any correlation between E. coli serotypes and the prevalence of the studied genes. Furthermore, determination of the antibiogram for the isolates having adhesin specific genes is another aspect that needs to be studied.

Chapter 6

Conclusion

- The use of CPS ID3 helped in differentiating between different organisms in mixed populations and supported the growth of all types of organisms frequently involved in UTI.
- Chromogenic media inhibited swarming of *Proteus* spp.
- CPS ID3 could be used routinely in clinical laboratories since it saved 50% of the time compared to routine analysis.
- The positive predictive values were 100% for all organisms included in this study except *Enterococcus* which was 66.7%.
- CPS ID 3 could differentiate between *E. coli* and other members of the *Enterobacteriaceae* family based on the differences in the morphology of the colonies.
- Additional biochemical tests should be performed with white colonies recovered on CPS ID3 medium.
- Non of the isolates included in this study had the morphological characteristics as that of *E. coli*. Hence, false positive results were not encountered (specificity of *E. coli* 100%).
- Staphylococcus saprophyticus, which is considered as one of the pathogens that cause urinary tract infection, did not give any specific color on CPS ID3 medium.

- CPS ID3 had the disadvantage of being expensive and having a short shelf life.
- The prevalence of the studied virulence factors among 160 strains of *E. coli* were 33.6, 33.1, 8.8, 45.6, 32.5, and 18.1% for *pap, sfa, afa, aer, bly,* and *cnf,* respectively.
- Most strains possessed adherence factors confirming the importance of these proteins in mediating the colonization of the urinary tracts.
- This study revealed, like many others, that *cnf* was limited to hemolytic strains and most hemolytic strains were linked to genes coding for adhesins genes.
- None of the samples had only *sfa* gene, which existed in combination with other genes. Neither *sfa* nor the *afa* genes were detected in any of the tested strains.
- In many isolates, the *aer* gene was not associated with genes encoding for adhesins. This could indicate that such isolates either do not require adherence factors to colonize the urinary tract, or that the *aer* gene was linked to other factors not undertaken in this study.
- Sfa was detected in 33% of the isolates although it was a gene mainly detected in E. coli associated with meningitis.
- Of the 17 strains that were positive for four tested virulence genes, the combination pap^+ , sfa^+ , cnf^+ , and hly^+ was observed in 14 of these isolates.
- Within the 11 isolates that were positive for five of the studied virulence factors, none had the *afa* gene.

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