

MOLECULAR CHARACTERIZATION, ANTIBIOGRAMS AND  
ANTIBACTERIAL ACTIVITIES OF SELECTED MEDICINAL  
PLANTS AGAINST SOME ENTERIC PATHOGENS

by

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## GENERAL SUMMARY

Infections due to *Escherichia coli* and *Salmonella* spp. are known to account for a substantial degree of morbidity and mortality in different age groups and populations worldwide. These infections may be self-limiting but in some cases antimicrobial therapy are indicated. With vaccine development still in its infancy in most cases and the increasing trend of drug resistance, the continued monitoring and assessment of antibiotics used in the treatment of these infections are paramount. In addition, there is a need to complement orthodox medicine with ethnomedicine for a lead to new drug discovery and for total primary health care coverage of the underserved populations. In this regard, medicinal plants offer great promise and studies to uncover the antimicrobial activities of medicinal plants, including structural elucidation of the active compounds and cytotoxicities of such plants are usually warranted. Furthermore, studies on the molecular landscape of the organisms, especially the various genes coding for virulence and antimicrobial resistance and the phylogenetic relatedness will illuminate knowledge on the pathogenesis and epidemiology of the pathogens.

The thesis, consisting of eight chapters, chronicles the findings on antibiogram profiles of the designated pathogens, inhibitory activities of selected medicinal plants, including their active compounds and cytotoxicity profiles as well as the molecular epidemiology of the pathogens. The first chapter gives a vivid account of the background to the study and the review of the literature.

Chapter 2 is an account of the antimicrobial resistance patterns as well as the molecular basis of resistance in *E. coli* and *Salmonella* isolates from clinical specimens. Isolates were antibiographed while PCR and sequencing were carried out to identify genes modulating antibiotic resistance. The study showed an increase in multiple-drug resistance and an emerging resistance to penem drugs, an indication of limited choice of drugs in the chemotherapy of enteric disease. An alarmingly high percentage of isolates produced extended-spectrum beta-lactamases (ESBL), with prevalent genotypes being bla<sub>CMY-2</sub>, bla<sub>SHV-1</sub>, bla<sub>TEM-20</sub> and bla<sub>TEM-1</sub>. In addition, Class I integron was significantly involved in the resistance mechanism among the isolates.

Chapter 3 was designed to investigate the pathotypes and the various virulence factors among *E. coli* and *Salmonella* isolates. Using standard diagnostic methods and molecular analysis, of the 119 *Salmonella* isolates, the results of the serovars were *S. enterica* serovar Choleraesuis (6%), *S. enterica* serovar Enteritidis (4%), *S. enterica* serovar Eppendorf (1%), *S. enterica* serovar Hadar (1%), *S. enterica* serovar Isangi (8%), *S. enterica* serovar Panama (1%), *S. enterica* serovar Typhi (52%), *S. enterica* serovar Typhimurium (25%) and untyped *Salmonella* spp. (2%). The greatest proportion of the 90 diarrhoeagenic *E. coli* were enteroaggregative *E. coli* (EAEC) 37 (41.1%), enteropathogenic *E. coli* (EPEC) 21 (23.3%) and enterohemorrhagic *E. coli* (EHEC) 21 (23.3%). Various virulence factors identified amongst the *Salmonella* strains were *fliC*-flagellin H1 (12.6%), *invA*-invasion (88.2%), *sefA*-fimbrial antigen (1.7%) while

*aggR*- transcriptional activator for EAEC aggregative adherence fimbria I expression, *eaeA-E. coli* attaching and effacing and LT- heat-labile enterotoxin were found among the *E. coli* isolates.

In chapter 4, an ethnobotanical survey of medicinal plants used in the treatment of diarrhoea and related diseases in the ORTDM in the Eastern Cape of South Africa was embarked upon. This assisted in documentation of herbal plants and the extent of usage of ethnomedicine in the district municipality with the eventual aim of assessing the efficacies of some of the plants. A total of 32 plant species belonging to 26 families were reportedly used as diarrhoea remedy in the study area. The most predominant families of medicinal plants employed and most frequently recommended were Fabaceae (16.67%), followed by Hyacinthaceae and Hydnoraceae , each accounting for 8.33%. The majority of the rural dwellers depended on ethnomedicine due to the inaccessibility to orthodox medicine. This was due to several factors such as the distance between the communities and the nearest health care centres and financial constraints.

The ethnobotanical survey led to the antibacterial screening of 12 medicinal plants: *Acacia mearnsii*, *Aloe arborescens*, *Aloe striata*, *Cyathula uncinulata*, *Eucomis autumnalis* (Mill.) Chitt., *E. comosa* (Houtt.) Wehrh. *Hermbstaedtia odorata*, *Hydnora africana*, *Hypoxis latifolia*, *Pelargonium sidoides*, *Psidium guajava* and, *Scilla natalensis* frequently recommended by the traditional healers. A qualitative phytochemical screening and bioassays of the plants' extracts was carried out. Antimicrobial screening was by broth



microdilution and bioautography. The presence of terpenoid and flavonoids in some herbs were inferred from the TLC fingerprints. Most of the tested organisms were sensitive to the crude acetone extracts with MIC values ranging from 0.078–2.5 mg/mL. Acetone and methanolic extracts of *Aloe striata*, *Cyathula uncinulata*, *E. autumnalis* and *P. guajava* were more active against enteropathogens. This preliminary study revealed the promising antibacterial activities of some of the selected herbs used in the treatment of diarrhoea and related diseases and corroborated assertions on their efficacies by traditional healers, as reflected in Chapter 5.

Chapter 6 described the separation of compounds from the bioactive ethyl acetate fractions of *C. uncinulata* by solvent-solvent fractionation. This plant was selected based on its antibacterial activity. The structure of the isolated compound was elucidated by nuclear magnetic resonance spectroscopy and mass spectroscopy methods. The NMR spectra of the isolated compound showed that the compound, with formula  $C_{22}H_{38}O_7$  and molecular weight 414.5329 had a long aliphatic chain. The isolated compound was described as Glycosylated oleanolic acid, made up of sugar with fatty acyl moiety. The MIC of fractions of extracts ranged from 0.39 to 2.5 mg/mL. The lowest MIC was observed in ethyl-acetate fraction and for the selected sub-fraction of the ethyl acetate (SSC 1) fractionation MIC was 0.63 mg/mL. The MIC of the final purified compound was 0.34 mg/mL, indicating considerable bioactivity; hence, this may serve as template for new antimicrobial formulations.

The study in chapter 7 was carried out to assess the therapeutic safety of some selected medicinal plants. The cytotoxicity of methanol extracts and fractions of six selected plants was determined using a modified tetrazolium-based colorimetric assay [3-(4, 5-dimethylthiazol)-2, 5-diphenyl tetrazolium bromide (MTT) assay]. The in vitro cytotoxicity assay on human hepatocarcinoma cell line (Huh-7) revealed that the methanol extract of *E. autumnalis* had the strongest cytotoxicity with IC<sub>50</sub> of 7.8 µg/mL. Ethyl acetate and butanol fractions of *C. uncinulata*, *H. latifolia*, *E. autumnalis* and *Lantana camara* had lower cytotoxic effects on the cancer cell lines tested with IC<sub>50</sub> values ranging from 24.8 µg/mL to 44.1 µg/mL while all the fractions of *A. arborescens* and *A. striata* had insignificant or no cytotoxic effects after 72 h of treatment. The results showed that *E. autumnalis* may serve as anticancer agent while the *Aloe* species were apparently safe within the range studied.

The general conclusions and recommendations of the various parts of the findings were captured in Chapter 8. There was increasing multi-drug resistant and emerging resistance to penem drugs among isolates particularly *Salmonella* strains. Molecular analysis showed that beta-lactamase enzymes and class 1 integron (*Int1*) genes played significant roles in antibiotic resistance among *Salmonella* spp. with diverse virulence genes identified among the *Salmonella* and *E. coli* isolates. In addition, *E. coli* strains from apparently asymptomatic subjects harboured considerable virulence genes making them potential reservoirs of factors important in the spread and acquisition of virulence and

drug resistance genes. Among the plants used in ethnomedicine in ORTDM, *A. arborescens*, *A. striata*, *C. uncinulata*, *E. autumnalis* and *P. guajava* were noted as potential plants for antibacterial agents. Further fractionation and purification of bioactive components of the ethyl acetate fraction of *C. uncinulata* yielded an isolated compound - glycosylated oleanolic acid, a sugar with fatty acyl moiety which had considerable antibacterial activities. The evaluation assay for therapeutic safety of selected medicinal plants indicated extensive cytotoxicity and selective anticancer activity of *E. autumnalis*, even though it had strong antibacterial activities.

It was recommended that measures be put in place to curtail the spread of drug resistance, particularly the ESBL-type resistance through improved and standardized laboratory practice. Proper and regular surveillance should be maintained to help guide the rational use of antibiotics in empirical treatment and measures should be in place to discourage the use of broad-spectrum antibiotics. The recognition but cautious use of medicinal plants as an alternative therapy and a probable means to mitigate the emerging resistance problem was recommended.

Overall, improved standard of hygiene both in the hospital settings and the communities is paramount to prevention of infections as 'prevention is better than cure'.

## DECLARATION

I, Mary Adejumo Bisi-Johnson Student Number 208154760, solemnly declare that this thesis entitled "Molecular characterization, antibiograms and antibacterial activities of selected medicinal plants against some enteric pathogens" constitutes the culmination of original studies undertaken by me and that the report has not been submitted to any other institution. All sources used or quoted in the study have been indicated and acknowledged by way of complete references.

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## LIST OF ABBREVIATIONS

Bla	Beta-lactamase gene
CLSI	Clinical and Laboratory Standards Institute (formerly NCCLS)
DAEC	Diffusely adherent <i>E. coli</i>
DNA	Deoxyribonucleic acid
EAEC	Enteroaggregative <i>E. coli</i>
EHEC	Enterohemorrhagic <i>E. coli</i>
EIEC	Enteroinvasive <i>E. coli</i>
EPEC	Enteropathogenic <i>E. coli</i>
ESBL	Extended-spectrum beta-lactamase
ETEC	Enterotoxigenic <i>E. coli</i>
HIV	Human immunodeficiency virus
hRf.	100fold retention factor value
IC <sub>50</sub>	50% inhibitory concentration
INT	<i>p</i> -iodonitrotetrazolium salt
<i>Int1</i>	Class 1 integron
L	Litre (s)
MDG	Millennium Development Goals
MIC	Minimum inhibitory concentration
MTT	modified tetrazolium-based colorimetric assay (3-(4, 5-dimethylthiazol)-2, 5-diphenyl tetrazolium bromide assay).
NCCLS	National Committee for Clinical Laboratory Standards (Now CLSI)

NMAHC	Nelson Mandela Academic Hospital Complex
NMEC	Neonatal meningitis <i>E. coli</i>
NMR	Nuclear magnetic resonance spectroscopy
ORTDM	Oliver R. Tambo District Municipality
PBP	Penicillin-binding protein
PCR	Polymerase chain reaction
R <sub>f</sub> value	Retention factor
S	Second (s)
TLC	Thin layer chromatography
UPEC	Uropathogenic <i>E. coli</i>
UV	Ultraviolet
WHO	World Health Organization

## LIST OF PUBLICATIONS

### Publications

Mary A Bisi-Johnson, Chikwelu L Obi, Sandeep D Vasaikar, Kamaldeen A Baba, Toshio Hattori. Molecular basis of virulence in clinical isolates of *Escherichia coli* and *Salmonella* species from a tertiary hospital in the Eastern Cape, South Africa. BMC Gut Pathogens 2011, 3:9 doi:10.1186/1757-4749-3-9.

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Mary A Bisi-Johnson, Chikwelu L Obi, Sandeep D Vasaikar, Kamaldeen A Baba, Toshio Hattori. Extended-spectrum beta-lactamases and Class 1 integron mediated resistance in clinical isolates of *Salmonella* species. Annals of Clinical Microbiology and Antimicrobials, 2011.

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2008

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2009

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## CHAPTER 1

### 1. GENERAL INTRODUCTION AND LITERATURE REVIEW

#### 1.1. Introduction

Diarrhoeal diseases remain one of the greatest health problems in many parts of the world. In some cases, the disease is mild and self-limiting; however, the symptoms may be very severe in the elderly and young children (Smith and Cheasty, 1998), as well as in immunocompromised patients such as HIV/AIDS patients. The disease is one of the hallmarks of HIV/AIDS in developing countries and is also a cardinal clinical manifestation of water borne infections (Obi *et al.*, 2007). According to a World Health Organization report (WHO, 2004), diarrhoea was rated second, after respiratory infections out of the eight deadliest diseases worldwide and was responsible for 1.8 million deaths per year. This infectious disease which can cause dehydration is primarily a symptom of gastrointestinal infection but chemical irritation of the gut or non-infectious bowel disease can also result in diarrhoea.

Studies have shown that the predominant causative agents of acute and persistent diarrhoea are Gram-negative rods such as *Escherichia coli*, *Vibrio cholerae*, *Aeromonas*, *Campylobacter*, *Salmonella species*, *Shigella species*, *Plesiomonas shigelloides* and *Yersinia enterocolitica* (Obi *et al.*, 1995, 1998, 2003; Lainson and Silva, 1999; Coker *et al.*, 2002; Oyofu *et al.*, 2002). Aside from bacterial agents of diarrhoea, other causative pathogens include protozoa

such as *Giardia lamblia* and *Cryptosporidium parvum*; viruses such as norwalkvirus and rotavirus. Although fungal agents such as *Candida* have been shown to be prevalent in children with diarrhoea (Enweani *et al.* 1994), a more recent study (Forbes *et al.*, 2001), associated higher *Candida* counts with recent antibiotic use. Faecal concentrations of *Candida* were higher in patients with diarrhoea but the study confirmed no association between faecal candida or other yeasts and diarrhoea. Norwalk viruses, calici-like viruses and rotaviruses are the major viral agents of diarrhoea. According to Parashar *et al.*, (2006), rotavirus is the leading cause of diarrhoeal hospitalization among children worldwide, causing 440,000 annual deaths in children under 5 years of age.

Production of disease by enteropathogens often involves specific serotypes of the organisms and special virulence factors. Some arsenals for pathogenicity include ability to adhere to host surfaces, production of special proteins for invasion and colonization. In addition, some pathogens are able to produce virulent factors which incapacitate the host's immune system defenses or those that poison host cells and cause tissue damage. Studies have shown that some of the pathogenic factors of enterobacteria are genetically modulated. The mechanisms of diarrhoea induction and role in the development of diarrhoeal syndrome of several genes associated with pathogenicity islands (PAIS): adhesins, hlyA, hlyB (hemolysin), sfaG (fimbria antigen type S), cnf1 (cytotoxic necrotizing factor 1), estB (heat-stable enterotoxin B), bacterial modulins, cytotoxic and cytotoxic enterotoxins, including LT, ST, Shiga-like and



cytotoxic toxins have been described (Mavzutov *et al.*, 2007; Zhrebtsova *et al.*, 2007). Virulence factors of *Salmonella* and *Shigella* species are complex and encoded both on the organism's chromosome and on large (34-120 kd) plasmids. Several *Salmonella* pathogenicity islands have been identified that mediate uptake of the bacteria into epithelial cells (type III secretion system), non-phagocytic cell invasion (*Salmonella* pathogenicity-island 1), and survival and replication within macrophages (*Salmonella* pathogenicity-island 2, *phoP/phoQ*) (Finlay, 1994; Darwin and Miller, 1999, Kato *et al.*, 2008; Charles *et al.*, 2009). *Shigella* species cause damage by two mechanisms, invasion of the colonic epithelium, which is dependent on a plasmid-mediated virulence factor (*ipa* protein, *invasin*), and production of enterotoxin (*ShET 1* and *ShET 2*), secreted by the organism. These have been shown to cause small bowel secretion and watery diarrhoea, which is not essential for colitis but enhances virulence (Wolf and Gianella, 1996; Bernasconi *et al.*, 2004). Verotoxin, which enterohemorrhagic *E coli* and *Shigella* species produce, causes systemic disorders such as seizures and hemolytic-uremic syndrome (HUS) (Trachtman and Christen, 1999).

Increasing resistance to the fluoroquinolones and the third-generation cephalosporins is of major concern among members of the Enterobacteriaceae. The susceptibility patterns of enteric bacteria to various antibiotics as reported in sub-Saharan Africa, (Sinha *et al.*, 2004; Maraki *et al.*, 2005; Yismaw *et al.*, 2006; Obi *et al.*, 2007), showed a slow decline in fluoroquinolone susceptibility. Over

90% of all the organisms isolated from a cohort study in Limpopo (Obi *et al.*, 2007), showed resistance to penicillin, cloxacillin and amoxicillin but conversely, almost all the organisms were sensitive to ciprofloxacin, gentamycin, meropenem and imipenem. On the contrary, decrease in fluoroquinolone susceptibility has been more dramatic in other areas of the world such as Latin America and Southern Europe (Jones *et al.*, 1997). Several mechanisms are involved in the antibiotic resistance of members of the Enterobacteriaceae; these include mutations involved in enzyme productions (Jones *et al.*, 1997; Jones, 2003). Enterobacteriaceae commonly express plasmid-encoded  $\beta$ -lactamases (mostly TEM-1, TEM-2, and SHV-1) that confer resistance to penicillins (Maurine *et al.*, 2002). Another type of resistance affecting third-generation cephalosporins and aztreonam (a monobactam) has been the hyperproduction of an Amp C cephalosporinase by some of the enteric strains (Jones *et al.*, 1997). The resistance to extended-spectrum cephalosporin among the Enterobacteriaceae has become a growing problem (Bradford *et al.*, 2001).

Another factor which confers antibiotic resistance to clinical isolates is class 1 integron (Leverstein-van Hall *et al.*, 2003; Segal *et al.* 2003). Most resistance integrons belong to class 1. Integrons are genetic elements composed of a gene encoding an integrase, gene cassettes and an integration site for the gene cassettes (Fluit and Schmitz, 2004). These DNA elements play important role in the spread of antibiotic-resistance genes. Recently, the discovery of larger integron structures, termed super-integrons has broadened bacterial genome

(Mazel, 2006). Integrons can be broadly divided into two: the resistance integrons and super-integrons. Several reports have linked Class 1 integrons to resistance in various Gram negative genera. This genetic element was detected and characterized in various serotypes of *Salmonella enterica* (Brown *et al.*, 2000; Guerra *et al.*, 2001); *Shigella* (Navia *et al.*, 1999; McIver *et al.*, 2002), *Escherichia* (Mazel *et al.*, 2000; Zhao *et al.*, 2001). An integron-like drug resistance region and a plasmid-borne class 1 integron was found on the transferable R-plasmid pJA8102-1 from *Aeromonas salmonicida* and an atypical *A. salmonicida* respectively (Inglis *et al.*, 1993; Barnes *et al.*, 1994). Class 2 integrons are embedded in the Tn7 family of transposons and consist of an integrase gene followed by gene cassettes (Radstrom *et al.*, 1994). Integrons belonging to class 2 have also been reported in *Salmonella* (Orman *et al.*, 2000) and *Shigella* (Gonzalez *et al.*, 1998). Class 3 integrons have been described in *Pseudomonas aeruginosa*, *Serratia marcescens*, *Alcaligenes xylosoxidans*, *P. putida* and *Klebsiella pneumoniae* isolates from Japan (Izumiya *et al.*, 2000).

With the emerging multiple antibiotic resistance saga, there has been a paradigm shift to natural products particularly medicinal plants for succor. A large proportion of the populace of developing countries employ the use of traditional medicine, alone, or in combination with Western drugs to treat a wide variety of ailments including diarrhoea (Taylor *et al.*, 2001). In South Africa, traditional medicine is well recognized and different communities use a wide variety of plants to treat gastrointestinal disorders such as diarrhea and infection

by intestinal parasites, which are particularly prevalent in rural areas (McGaw *et al.*, 2000). Many studies have documented the anti-enteric bacterial activities of some medicinal plants, *Herba pogostemonis* extracts (Liu *et al.*, 1999), *Roureopsis obliquifoliolata* and *Epinetrum villosum* (Longaga *et al.*, 2001), *Aegle Marmelos* (Correa) Linn. root extract (Mazumder *et al.*, 2006), *Zornia milneana* (Papilionoideae) (Samie *et al.*, 2007).

The importance of enteric bacteria such as *Salmonella*, *Shigella* and *E. coli* as agents of diarrhoeal disease is of great significance but, their involvements in diarrhoea cases in this local setting of Eastern Cape Province, South Africa, including associated virulence factors and genes coding for antibiotic resistance in these enteric bacterial species particularly at the molecular level have not been extensively investigated.

## 1.2. Literature survey

### 1.2.1. Diarrhoea as a Disease

Of major public health concern are diarrhoeal diseases, particularly with regards to the developing countries where they are the leading cause of childhood morbidity and mortality. Diarrhoea, most commonly caused by gastrointestinal infections occurs world-wide and causes 4% of all deaths and 5% of health loss to disability (WHO, 2000). Annually, there are approximately 4 billion cases of diarrhoea worldwide which kill around 2.2 million people, mostly children in developing countries (WHO and UNICEF, 2000). Diarrhoea goes hand

in hand with hygiene, food and water quality. It has been reported that 88% of diarrhoeal diseases are attributed to unsafe water supply, inadequate sanitation and hygiene (WHO, 2004). In the developing world, sporadic outbreaks of diarrhoea are still a common feature despite advances in health interventions.

Diarrhoea has been defined as the passage of loose, watery stools occurring more than three times in one day or the passage of loose or liquid stools more frequently than is normal for the individual (WHO, 2000). The disease may be mild and lasting a day or two and self-resolves without any special treatment. However, prolonged diarrhoea can be a sign of other problems. Diarrhoea can cause dehydration, which means the body lacks enough fluid to function properly. Dehydration is particularly dangerous in children and the elderly, and it must be treated promptly to avoid serious health problems. Likewise, diarrhoea has been associated with other infections such as malaria, measles, HIV/AIDS, pneumonia, systemic infections and meningitis (Reisinger *et al.*, 2005).

#### 1.2.2. Forms of Diarrhoea

Diarrhoea comes in different forms depending on the type of infection; it may be mucoid, watery or passed with blood.

##### 1.2.2.1. Acute Watery Diarrhoea

Acute diarrhoea is often a result of gastric flu (gastroenteritis) which is usually of viral origin. The duration of acute diarrhoea is usually less than 14 days and its associated symptoms are abdominal pain, nausea, vomiting and fever.

Gastroenteritis is caused in a few cases by bacteria and this is often times more fatal than viral diarrhea. The causative agents of acute watery diarrhea are viruses usually rotavirus in infants under 5 years (Greenberg and Estes, 2009) and norovirus in adults (Patel *et al.*, 2009). Bacterial agents of gastroenteritis include enterotoxigenic *E. coli* and *Vibrio cholerae* 01. Acute diarrhea can complicate nutritional status in children leading to malabsorption of nutrients and long-term effects of growth failure and malnutrition (Black *et al.*, 1984; Lifshitz, 1989).

#### 1.2.2.2. Acute Bloody Diarrhoea

This is often passage of loose stool with visible blood. It is termed dysentery and is an indication of invasion of bowel tissue. Complications of dysentery include intestinal damage, sepsis, malnutrition and dehydration may also occur. The main causative agents of bloody diarrhea are *Shigella* spp., *Salmonella* spp., *E. coli* 0157, *Campylobacter* spp., and *Entamoeba histolytica* (Goldsmid, 2007). Ten percent of all episodes and 15% of deaths respectively from diarrhoea in children less than 5 years of age worldwide are due to acute bloody diarrhea (Esona *et al.*, 2003).

#### 1.2.2.3. Chronic or Persistent Diarrhoea

Persistent diarrhea is associated with loose or watery stools with or without visible blood lasting more than 14 days. The main complication of this disease is malnutrition and serious non-intestinal infection; dehydration may also occur. Infective diarrhea may persist with no visible symptoms in which case an

individual becomes a carrier, often the case with *Salmonella* infection. Apart from bacterial agents chronic infective diarrhea may be caused by parasites such as *Cryptosporidium*, *Giardia lamblia*, worms and amoeba. However, some infants between the ages of 6 months to 3 years have chronic diarrhea for which no apparent medical cause can be found ([Encyclopedia of Childhood and Adolescence, n.d](#)). Chronic non infective diarrhea usually depicts more severe medical conditions mainly malabsorption in its various forms. These conditions which impede normal digestion include celiac disease, in which the wheat protein gluten is intolerable to the gut. Others are cystic fibrosis, lactose intolerance, pernicious anemia and fibrosis due to cancer therapy. Antibiotic therapy may favour proliferation of the bacterium, *Clostridium difficile*. This bacterium can produce a toxin that damages the lining of the colon and causes mild to severe diarrhea ([Encyclopedia of Childhood and Adolescence, n.d](#)).

### 1.2.3. Causes of Diarrhoea

Diarrhoea though primarily a symptom of gastrointestinal infection, chemical irritation of the gut or non-infectious bowel disease can also result in this disease. Infectious diarrhoea is caused by a host of bacterial, viral and parasitic organisms most of which can be spread as a result of poor water quality ([WHO, 2000](#)). It is more common when there is a shortage of clean water for drinking, cooking and cleaning and basic hygiene is important in prevention. Water contaminated with human faeces such as municipal sewage, septic tanks and latrines is of special concern. Food is another major source of infectious

diarrhoea when it is prepared or stored in unhygienic conditions. Food contamination by irrigation water, fish and seafood from polluted water may also contribute to diarrhea and enteric infections (CDC, 2005b; Newman, 2005; WHO, 2007). Diarrhoea can also spread from person to person, aggravated by poor personal hygiene (WHO, 2000).

#### 1.2.3.1. Non-infectious agents of diarrhea

According to Levy (1988), diarrhoea as a result of non-infectious agents includes:

- i. Carbohydrate intolerance:
  - a. Primary enzyme deficiencies (e.g. Lactose intolerance)
  - b. Glucose-galactose malabsorption (e.g. immune disorders, mucosal diseases)
- ii. Gastrointestinal allergies to Cow's milk protein, soy milk or gluten (wheat protein)
- iii. Pancreatic insufficiency: cystic fibrosis
- iv. Immune deficiencies: hypogamma globulinemia, IgA deficiency
- v. Metabolic: Abetalipoproteinemia, familial chloride diarrhoea, acid lipase deficiency.
- vi. Anatomic abnormalities: Enteric fistula, short bowel, pseudo-obstruction

#### 1.2.3.2. Infectious agents of Diarrhoea

Enteric pathogens implicated in cases of diarrhoea may be bacterial, viral, fungal, parasitic or protozoal. Another infectious agent which has been



implicated particularly in food-related infection is prion (Mead *et al*, 1999; Collinge, 2001; Smith and Bradley, 2003). Table 1 below is a slight modification of various enteric pathogens with their clinical manifestations as summarized by Goldsmid (2007). However, the scope of this study is bacterial enteric pathogens and rather than providing a general overview of infectious agents of diarrhoea, this section of the review will focus on three enteric bacterial pathogens with vast human morbidity worldwide (Buzby and Roberts, 2009):

- ❖ *Salmonella*
- ❖ *Shigella*
- ❖ *Escherichia coli*

#### I. *Salmonella*

The salmonellae are actively motile, gram-negative facultative, intracellular anaerobes which do not ferment lactose, but most form H<sub>2</sub>S or gas from carbohydrate fermentation. As with the closely related bacterium *Escherichia coli*, salmonellae are potential enteric pathogens and are leading causes of bacterial foodborne illness (Klotchko and Wallace, 2009). *Salmonella* species are also of public health significance worldwide causing a wide spectrum of disease ranging from a gastroenteritis, enteric or typhoid fever (caused by *S. enterica* serovar Typhi and *S. enterica* serovar Paratyphi serotypes), bacteremia, osteomyelitis and enterocolitis (primarily *S. enterica* serovar Typhimurium and *S. enteritidis*), to a convalescent lifetime carrier state (Owens, 2009; Klotchko and Wallace, 2009).

Table 1.1. Summary of enteric pathogens by group

PATHOGEN	COMMENTS
Bacteria	
<i>Aeromonas</i> spp.	Can be dysenteric and/or persistent
<i>Bacillus cereus</i>	Food poisoning – often associated with rice
<i>Clostridium perfringens</i> type A	Food poisoning
<i>C. perfringens</i> type C	Enteritis necroticans
<i>C. botulinum</i>	May get diarrhoea in early stages
<i>C. difficile</i>	Antibiotic associated, may be bloody in pseudomembranous colitis
Enterogaagregative <i>E. coli</i> (EAggEC)	May cause persistent diarrhoea
Enterohaemorrhagic <i>E. coli</i> (EHEC)	May cause a bloody diarrhoea; can proceed to haemolytic uraemic syndrome (especially serotype 0157:H7)
Enteroinvasive <i>E. coli</i> (EIEC)	May cause bloody diarrhoea
Enterotoxigenic <i>S. aureus</i>	Food poisoning intoxication
<i>Listeria monocytogenes</i>	Occasional cause of diarrhoea
<i>Plesiomonas shigelloides</i>	Can sometimes cause dysenteric illness
<i>Salmonella typhi</i> <i>S. paratyphi</i>	Presents initially with constipation but may develop diarrhoea later in infection
<i>Vibrio cholerae</i> 01:0139	Rare in returned travelers
Noncholera vibrios	Some associated with seafood
<i>Yersinia enterocolitica</i>	Mesenteric lymphadenitis; may cause bloody diarrhoea
Virus	
Adenovirus	Causes severe diarrhoea with dehydration
Astroviruses	Often transmitted via food than other viruses
Caliciviruses	Often transmitted via food than other viruses
Hepatitis A,  Hepatitis E	Infect the gastrointestinal or respiratory tracts causing a wide range of illness, including diarrhoea, fever, hepatitis, paralysis, meningitis and heart disease  Have the human liver as the primary target of replication and give rise to hepatitis or inflammation of the liver
Norovirus	Causes stomach flu, vomiting, diarrhea by inflammation of the stomach and intestines, and some stomach cramping
Norwalk-like viruses	Often transmitted via food than other viruses

Rotavirus	Common cause of severe viral diarrhoea in infants and young children under 5 years old
Protozoa	
<i>Balantidium coli</i>	Zoonotic – causes colitis and dysentery
<i>Blastocystis hominis</i>	If large numbers present in faecal specimen and no other cause of diarrhoea detected
<i>Crptosporidium parvum</i>	Causes enteric illness that has received much attention as an infection of immunocompromised persons
<i>Cyclospora</i>	Emerging as opportunistic pathogens associated with diarrhoea.
<i>Entamoeba histolytica</i>	Mucoid diarrhoea commonly streaked with some amount of blood.
<i>Dientamoeba fragilis</i>	Causes low-grade inflammation coupled with mucous diarrhea and gastrointestinal disturbance
<i>Giardia intestinalis/lambli</i>	Symptoms include diarrhoea (fatty, yellowish) weakness, weight loss, abdominal pain
<i>Isospora belli</i>	Watery diarrhoea in children and patients with AIDS
<i>Microsporidia</i>	Emerging as opportunistic pathogens associated with diarrhoea
<i>P. falciparum</i>	The initial presentation of complicated malaria may be diarrhoea-like illness
Helminths	
<i>Schistosoma mansoni</i>	Causes intermittent loose stools
<i>S. japonicum</i>	Causes fever, aching, cough, diarrhea, or gland enlargement
<i>Strongyloides stercoralis</i>	Especially in cases of internal autoinfection
<i>Taenia</i> spp.	Beef and pork tapeworms occasionally
<i>Trichuris trichiura</i>	With very heavy worm loads, may be bloody
<i>Trichinella</i> spp.	Diarrhoea in early infection

*Salmonella* infections may be categorized into four clinical types. Firstly, gastroenteritis (ranging from mild to fulminant diarrhoea, nausea and vomiting) typical in most individuals infected with *S. enterica* serovar Typhimurium (Honish, 2000), secondly, bacteraemia or septicaemia (high spiking fever with positive blood cultures), thirdly, enteric fever (mild fever and diarrhoea) and lastly, a carrier state in persons with previous infections. Symptoms of gastroenteritis appear 4 to 5 days after ingestion of contaminated food or water.

Diarrhoea lasts 3 to 5 days and is accompanied by fever and abdominal pain. *S. enterica* serovars Typhi, Paratyphi A and Paratyphi B can cause enteric fever without any presentation of diarrhoea and are important causes of enteric fever in underdeveloped countries.

Salmonellosis affects both humans and animals but *S. enterica* serovar Typhi is adapted to humans and does not occur in animals while non-typhoidal *Salmonella* serovars (NTS) have a broad vertebrate host range (Gordon, 2008). The dissemination of salmonellosis to various organs depends on the serotype, the size of the inoculum, and the status of the host. NTS display more severe and invasive presentation in immunocompromized individuals especially HIV carriers, including severe and progressive diseases such as chronic granulomatosis disease, blockade of IL-12/ IL-23 /IL-17 and TNF, suppurative foci and bacteremia which may be recurrent (Gordon, 2008). In the small intestine, *Salmonella* ingestion progresses to diffuse mucosal inflammation, edema, and microabscesses (Chatterjee *et al.*, 2009). Generally, most NTS do not extend beyond the lamina propria and lymphatics of the gut. Exceptions include *S. enterica* serovar Choleraesuis and *S. enterica* serovar Dublin, which can cause bacteremia with little intestinal involvement (Chiu *et al.*, 2006). *S. enterica* serovar Typhi causes intestinal necrosis which can ulcerate and result in perforation. In addition, this mucosal penetration allows uptake into the draining lymph nodes, contributing to blood stream infections and subsequent invasion of

the liver, spleen, and bone marrow. This process explains the delayed onset of symptoms in *S. enterica* serovar Typhi (Reller, 2008).

Worldwide estimates of NTS range from 200 million to 1.3 billion, with an estimated death toll of 3 million each year (Coburn *et al.*, 2007). However, typhoidal salmonellae lead to approximately 2.16 million cases of infections and 216,000 deaths worldwide (Crum *et al.*, 2004; Boyle *et al.*, 2007; Sethuraman and Kamat, 2007). In the United States, an annual estimated 1.4 million cases of salmonellosis occur among humans (Mead *et al.*, 1999). Additionally, an estimated 500 people are infected with typhoid *Salmonella* annually (Linam and Gerber, 2007). Typhoid fever is endemic in many developing areas of the world vis-à-vis Africa, Latin America and in particular five Asian countries namely: China, India, Indonesia, Pakistan, and Vietnam (Pickering *et al.*, 2005; Miller *et al.*, 2008).

The genus *Salmonella* is highly polymorphic, occurring in several distinct forms. According to Janda and Abbott (2006), two species of *Salmonella* have been recognized, *S. enterica* and *S. bongori*. Eight subgroups or subspecies have been defined using a variety of molecular methods (Janda and Abbott 1998; Brown *et al.*, 2002; Chan *et al.*, 2003). However, in 2005, all *Salmonella* species became officially recognized as a single species *S. enterica* based on their close relationship by DNA hybridization studies (Su and Chui, 2007; Reller, 2008). There are currently 2,500 serotypes (serovars) of *Salmonella* (Su and Chui, 2007). The Kauffmann-White scheme for *Salmonella* based on different

combinations of somatic O, surface Vi, and flagellar H antigens have been described (Popoff and Le Minor, 1997; Kenner *et al.*, 2000). *S. bongori* contains only a single subspecies or subgroup (subgroup V, *bongori*). *S. enterica* contains the remaining 7 subgroups, 2 of which contain the clinically relevant salmonellae. *S. enterica* serovar Typhimurium and *S. enterica* serovar Enteritidis are the most frequently isolated serovars from food-borne outbreaks throughout the world (Herikstad *et al.*, 2002) particularly from poultry products. Studies in some of the provinces of South Africa have implicated *Salmonella* spp. and other enteropathogens in diarrhoea cases linked especially to water contamination (Obi *et al.*, 2002; 2004).

Whether salmonellosis is confined to the intestinal form or progresses to systemic involvement, the ability of the organism to invade and penetrate intestinal epithelial cells is required (Altier, 2005). This invasion process is not merely a passive consequence of bacterial contact with epithelial cells, but instead requires the active participation of the bacterium, with the expression of numerous bacterial virulence genes. The process of cell invasion requires the production and transport of secreted effector proteins by a type III secretion apparatus encoded in *Salmonella* pathogenicity island I (SPI-1) (Altier, 2005). In addition, invasion is induced by several factors of the host intestinal milieu. Many invasion regulators have been described, HilA (Lostroh and Lee, 2001), HilC (Schechter *et al.*, 1999), *invA* gene, a gene associated with the invasive nature of *Salmonella* (Rahn *et al.*, 1992), *InvF* (Darwin and Miller, 1999), *PhoP/PhoQ*

(Bajaj *et al.*, 1996), HIIIE (Baxter *et al.*, 2003), H-NS (Schechter *et al.*, 2003). PhoP/PhoQ pair is essential to the expression of genes of Salmonella pathogenicity island 2 (SPI-2), which encodes a second type III secretion system. SPI-2 is required for intramacrophage survival, the cell type encountered by Salmonella immediately after the invasion of the epithelium. PhoP/PhoQ also serves to repress SPI-1 genes, a function mediated by hilA (Behlau and Miller, 1993; Bajaj *et al.*, 1996; Fahlen *et al.*, 2000). PhoP/PhoQ may thus act as a genetic switch, activating traits required for macrophage survival while repressing those not needed for invasion (Altier, 2005). Reports have shown that mutations in phoP/Q result in a marked decrease in virulence (Fields *et al.*, 1989; Miller *et al.*, 1993). Other factors involved in Salmonella virulence are the MgtC in *S. enterica* serovar Typhimurium. This is required for growth at low-Mg<sup>2+</sup> concentrations and intramacrophage survival. This gene is codified in a conserved region of the *Salmonella* pathogenicity island 3 (SPI-3), and is also present in the chromosome of other *Salmonella* serovars (Retamal *et al.*, 2009).

## II. *Shigella*

*Shigella*, the etiologic agent of bacillary dysentery or shigellosis is a facultative intracellular pathogen. This genus of Gram negative bacteria is composed of four species namely: *Shigella dysenteriae*, *Shigella flexneri*, *Shigella boydii* and *Shigella sonnei* (also designated as serogroups A to D) (Yang *et al.*, 2005). These are further subdivided into serotypes on the basis of O-specific polysaccharide of the LPS. *Shigella dysenteriae* type 1 produces severe disease

and may be associated with life-threatening complications (Niyogi, 2005). Shigellosis is endemic throughout the world where it is held responsible for some 120 million cases of severe dysentery (Weekly Epidemiological Record, 2005). The annual number of *Shigella* episodes worldwide has been estimated as 165 million, of which more than 100 million occur in the developing world with more than 1 million deaths (Kotloff *et al.*, 1999; Dupont, 2005). In developing countries, 69% of shigellosis episodes occur in children under five years of age (Kotloff *et al.*, 1999). Although *Shigella* is endemic worldwide, it affects certain populations more than others with varying species predominance in each region. Shigellae are responsible for mortality and or morbidity in high risk populations such as children under five years of age, toddlers in day-care centres, aged individuals, homosexual men and, people in war-ravaged and famine-engulfed region (Thong *et al.*, 2005). The predominant serogroup of *Shigella* circulating in a community appears to be related to the level of socioeconomic development. *S. sonnei*, which has a single serotype, is the causative agent of most shigellosis in industrialized countries where it accounts for 77% of cases (compared to 15% in developing countries), but it also has become predominant in Thailand in recent years (WHO, 2009a). However, *S. flexneri* is endemic in developing countries followed by *S. sonnei*. The frequency of occurrence of *S. dysenteriae* and *S. boydii* are equal. *S. dysenteriae* is seen most often in South Asia and sub-Saharan Africa (Kotloff *et al.*, 1999). *S. dysenteriae* type 1, also known as



Shiga bacillus, has been recognized as the major cause of epidemic dysentery for nearly 100 years ([WHO, 1999](#)).

*Shigella* spp. causes dysentery by invading the colonic mucosa and multiplying within colonic epithelial cells ultimately causing mucosal ulceration, inflammation and bleeding. This pathogen is usually transmitted by faecal-oral route via contaminated food and water or through person-to-person contact ([WHO, 2009a](#)). Shigellae are considered highly contagious due to the low numbers of infectious inoculum required to cause infection ([Dupont et al., 1989](#)). The incubation period for shigellosis is 1 to 4 days but may be up to 8 days in the case of infection due to *S. dysenteriae* ([Levine et al., 1973](#)) or last for weeks and months and result in chronic relapsing diarrhoea and a protein-losing enteropathy ([Herrington and Taylor, 1991](#)). The initial symptoms of shigellosis are fever, headache, malaise, anorexia, and occasional vomiting. *S. flexneri* and *S. dysenteriae* type 1 infections are usually characterized by frequent passage of small amounts of stool and mucus or blood. Whilst *S. sonnei* and *S. boydii* infections are less severe with watery faeces but little mucus or blood, the watery diarrhoea in *S. dysenteriae* type 1 may progress to typical dysenteric stool. Intestinal complications of shigellosis include toxic megacolon and rectal prolapse. All species of *Shigella* are known to produce varying quantities of cytotoxins which are biologically similar in properties ([Bartlett et al., 1986](#)). However, the term Shiga toxin is reserved for the highly potent protein cytotoxin produced in large quantity by *S. dysenteriae* type 1. Shiga toxin which have been

extensively studied have been shown to consist of a large A subunit and 5 smaller B subunits, a structure similar to those of cholera toxin and heat-labile enterotoxin of *E. coli* (Herrington and Taylor, 1991). Whereas the A subunit is involved in inhibition of protein synthesis, the B subunits are involved in enterotoxic effects and cytotoxicity (Jacewicz *et al.*, 1989). Shiga toxin production is not required for virulence of invasive *S. dysenteriae* strains, but may increase the severity of disease (WHO, 1999). The virulence genes responsible for the pathogenesis of shigellosis may be chromosomal or plasmid-borne. ShET1 and ShET2 are two chromosomal-borne enterotoxin genes which have been incriminated as the putative mediators of the early watery phase of shigellosis (Nataro *et al.*, 1995; Rhee *et al.*, 2001). Other genes responsible for directing epithelial cell penetration by the bacterium and for the modification of host response to infection are ial and ipaH respectively (Hale, 1991; Ménard *et al.*, 1996). Mild infections due to *Shigella* are often self-limiting in healthy individuals but complications may arise in high risk group. Shiga toxin-producing organisms can cause anemia to manifest as hemolytic uremic syndrome in children and as thrombotic thrombocytopenic purpura in adults (Koster *et al.*, 1978). Intestinal perforation is rare but has been reported in association with toxic megacolon. *Shigella* bacteremia is generally considered an unusual occurrence but has been reported among HIV-infected and other immunocompromised patients (Batchelor *et al.*, 1996) and may be difficult to eradicate.

### III. *Escherichia coli*

In contrast to the essential and beneficial role of most *Escherichia coli* isolates in the human intestine, pathogenic *E. coli* are responsible for a broad spectrum of human diseases. *E. coli* has emerged as an important cause of diarrheal related illnesses, with diverse phenotypes and pathogenic mechanisms. According to the updated report of [World Health Organization \(2009\)](#), numerous types of diarrheagenic *E. coli* have been identified worldwide namely; enteropathogenic (EPEC), enterohaemorrhagic (EHEC) or Shiga toxin-secreting (STEC), enteroinvasive (EIEC), enterotoxigenic (ETEC), diarrhoea-associated haemolytic (DHEC), entero-aggregative (EAggEC), enteroadherent *E. coli* (EAEC) and cytolethal distending toxin-secreting (CDTEC) *E. coli* and diffuse adherent *E. coli* (DAEC) strains. These have been classified on the basis of serological characteristics – O (somatic), H (flagellar), and K (capsular) surface antigen profiles and virulence properties. The prevalence and the burden of diseases of the different pathotypes are uneven ([WHO, 2009a](#)). *E. coli*, though a major facultative inhabitant of the large intestine, has become recognized as both a harmless commensal and a versatile pathogen. It is the causative agent of infections ranging from enteric infections, neonatal meningitis, pneumonia, urinary tract infections (UTI), cholecystitis, and bacteremia. Other miscellaneous *E. coli* infections include septic arthritis, endophthalmitis, suppurative thyroiditis, sinusitis, osteomyelitis, endocarditis, and skin and soft-tissue infections (especially in patients with diabetes) ([Madappa and Go, 2009](#)). *E. coli* causes 12-

50% of nosocomial infections and 4% of cases of diarrheal diseases. While EAaggEC, EAEC and EPEC cause watery *E. coli* childhood diarrhoea which is non-inflammatory and non-bloody, *E. coli* dysentery is caused by EIEC or EHEC which is characterized by fever, bloody diarrhea, and dehydration (Madappa and Go, 2009). EPEC has also been described as diarrheagenic *E. coli* which produce a characteristic histopathology known as attaching and effacing (A/E) on intestinal cells and that do not produce Shiga, Shiga-like toxins or verotoxins. However, Enterotoxigenic *E. coli* (ETEC) strains remain a major cause of infantile diarrhoea

Table 1.2. Summary of diarrheagenic *E. coli* pathotypes and clinical manifestations

E.coli Pathotype	Clinical manifestations
Enterotoxigenic <i>E. coli</i> (ETEC)	Diarrhea is watery without blood, mucous, or fecal leukocytes and ranges from mild to severe
Enterohemorrhagic <i>E. coli</i> (EHEC) or Shiga toxin-secreting (STEC)	EHEC infects the large bowel. Disease ranges from mild watery diarrhea to severe hemorrhagic colitis, often accompanied by abdominal cramping and vomiting. Diarrhea becomes bloody in 1-2 days in most patients but is usually not associated with fecal leukocytes. Fever is present in about a third of cases.
Enteroinvasive <i>E. coli</i> (EIEC)	Causes watery diarrhea, dysentery, fever, vomiting, painful abdominal cramps, and tenesmus. Stools often contain blood and leukocytes.
Enteropathogenic <i>E. coli</i> (EPEC)	EPEC infects the small intestine, causes watery diarrhea and dysentery. The resultant acute watery diarrhea may cause dehydration or become chronic and lead to failure to thrive.
Enteraggregative <i>E. coli</i> (EAEC)	Associated with persistent diarrhea (>14 days), usually watery, secretory and not accompanied by fever or vomiting
Diffusely Adherent <i>E. coli</i> (DAEC)	Majority of patients infected with this pathotype experience vomiting.

in developing countries and of travellers' diarrhoeas in visitors to these countries (WHO, 2009a). Table 1.2 shows a summary of the clinical manifestations of different pathotypes of diarrheagenic *E. coli*.

ETEC are the most frequently isolated bacterial enteropathogen in children below 5 years of age in developing countries, and account for approximately 300 million diarrhoea episodes and 380 000 deaths annually (Black, 1993; Wennerås and Erling, 2004; Steffen *et al.*, 2005). ETEC are the cause in up to 80% of cases of traveller's diarrhoea (Kass, 2005; Peny, 2005). Each year, there are an estimated 10 million cases of LT-related ETEC travellers' diarrhoea worldwide (Steffen *et al.*, 2005) with a median of 42% of travelers' diarrheal episodes in studies in Latin America, 36% in Africa, and 16% in Asia (Black, 1993). Surveillance of hospitalized cases of ETEC diarrhoea has shown that a large proportion of cases also occur in individuals over 10 years of age (WHO, 2009a). ETEC are prevalent in domestic and surface water sources in developing countries. In South Africa, Obi *et al.* (2007) reported a genetic relatedness in *E. coli* from stools of diarrhoeic HIV patients and their household drinking water. Similar result was obtained in Bangladesh by Begum and co-workers (2007) in which case there were antibiotic resistant patterns and clonal similarities between ETEC from the environment and those isolated from the stools of patient. This may explain the endemicity of the disease in these countries. Once attached to the intestinal epithelium, ETEC elaborate both the heat-labile (LT)

and the heat-stable (ST) toxins, which induce the watery diarrhoea (Freytag and Clements, 1999).

*E. coli* O157 is sorbitol non-fermenting strain of *E. coli* causing Hemorrhagic uremic syndrome (HUS). The disease symptom is characterized by severe abdominal pain and bloody stools (Griffin *et al.*, 1988; Boyce *et al.*, 1995) and can also present as non-bloody diarrhea (Rodrigue *et al.*, 1995). Of particular concern in pediatric populations estimated to occur in 8% of children, *E. coli* O157:H7 requires a relatively small inoculum for infection and spreads easily from child to child by the fecal-oral route. The incubation period of EHEC is 1-5 days, with illness duration typically 4-10 days. Chronic renal failure develops in as many as 10% of patients with HUS, and HUS kills 3-5% of affected patients (Serna and Boedeker, 2008). *E. coli* O157 is an emerging cause of food-borne illness, particularly in the northern United States and Canada where sources identified in outbreaks have included ground beef, apple juice, and alfalfa sprouts, as well as feacally contaminated drinking water and swimming pools (CDC, 2005a, 2006, 2007, 2008). In the developing countries however, drought, carriage of *E. coli* O157 by cattle, and contamination of surface water were presumed to have been important sources of infection with *E. coli* O157. In a household survey performed during a waterborne outbreak of *E. coli* O157 infections in the United States, bloody stools were reported by only 35% of those with diarrhea (Swerdlow *et al.*, 1992). The report of Effler and his co-worker (2001) provides comprehensive data on the first outbreak of *E. coli* O157

infections from the developing world. Before this outbreak, *E. coli* O157 had been isolated only once before in Southern Africa, from an elderly man undergoing surgery for lower gastrointestinal bleeding in Johannesburg in 1990 (Browning *et al.*, 1990). Thirty-one suspected *E. coli* O157 isolates obtained from clinical and environmental specimens were referred to CDC, and all were confirmed as *E. coli* O157: NM. All isolates had the *uidA* allele specific for *E. coli* O157:H7 and the genes encoding Shiga toxins 1 and 2 (Effler *et al.*, 2001). Two other outbreaks of dysentery have been attributed to *E. coli* O157 elsewhere in Africa, the first in Central African Republic in 1996, and the second in Cameroon beginning in 1997 (Cunin *et al.*, 1999; Germani *et al.*, 1997). Both of these reports have some constraints, however; in the Central African Republic, *E. coli* O157 was not isolated at the outbreak site but only implicated from molecular tests. In the Cameroon outbreak, *E. coli* O157 and *Shigella* spp were each isolated in about half of the specimens tested. Although reported outbreaks of *E. coli* O157 in Africa have been few to date, available information indicates that the pathogen has wide geographic distribution. Since the 1992 outbreak, culture-proven *E. coli* O157 diarrheal illness has been reported from several locations, including Kenya (Sang *et al.*, 1996), Nigeria (Akinyemi *et al.*, 1998), Côte d'Ivoire (Dadie *et al.*, 2000) and Central Africa Republic (Germani *et al.*, 1998). Because *E. coli* O157 is not detected by the usual methods used to isolate and identify traditional enteric bacterial pathogens, microbiology laboratories in many countries in Africa do not routinely test for this pathogen, hence *E. coli* O157

infections may go unrecognized (WHO, 1995; Wittenberg, 1999). Reports on African dysentery outbreaks attributed to *Shigella* spp. sometimes indicate that specimens were not tested until several months into the outbreak or do not describe laboratory methods that are suitable for detecting *E. coli* O157 (Aragon *et al.*, 1995; Malakooti *et al.*, 1997). The spectrum of clinical illness resulting from *Shigella* infection overlaps considerably with that of *E. coli* O157 and mixed outbreaks have been reported (Casburn-Jones and Farthing, 2004). Understanding the complex interaction of environmental and behavioral factors that enabled *E. coli* O157 to emerge so intensely in Africa is important for future diarrheal disease control efforts.

The manifestation of clinical symptomology and pathology appears to be closely associated with the possession of certain virulence gene combinations in *E. coli* (Law, 2000; Grauke *et al.*, 2002). Generally, the pathogenicity factors among *E. coli* strains include pili, k-antigen, haemolysin, adhesive factor, enterotoxins, cytotoxins, effacement factors and cytotoxic necrotic factors (Galane and Le Roux, 2001). Various genes encoding virulence markers among *Escherichia coli* were reportedly identified by Obi *et al.* (2004). These included *cnf1* and *cnf2* for necrotoxicogenic; *ST* and *LT* for enterotoxigenic; *stx1* and *stx2* for Shiga toxin producing; *bfpA* and *eaeA* for enteropathogenic, and EAEC for enteroaggregative *E. coli*. As much as the pathotypes of *E. coli* have in common various virulence gene combinations for attachment and elaboration of hemolysins and enterotoxins, there are considerable polymorphisms and



sequence variations in the molecular identities of genes that code for these virulence factors (Nagy and Fekete, 1999; Bertin *et al.*, 2001) while some factors are specific to some strains. For instance, it has been reported that adherence pili, (the bundle-forming pili, Bfp) may be involved in pathogenicity (Hacker, 1992). A PCR method has been developed for the detection of the *bfp* genes of EPEC (Gunzburg *et al.*, 1995) that showed no amplification of DNA from any other bacterial enteropathogens and was 100% specific for EPEC strains which exhibited the characteristic localized-adherence (LA) phenotype. According to Reece *et al.* (2001) variants of the outer membrane protein intimin, expressed by both pathotypes EHEC and EPEC, have been implicated as contributors to tissue tropism. EHEC and EPEC share genetic and phenotypic similarities, most notably the locus of enterocyte effacement (LEE), pathogenicity island (PAI), encoding a type III secretion system (TTSS), and the ability to form attaching and effacing (AE) intestinal lesions and intimate attachment to the host cell (Moon *et al.*, 1983; Nougayrede *et al.*, 2003; Kaper *et al.*, 2004; Caron *et al.*, 2006). The attaching and effacing (A/E) lesions on epithelial cells caused by EPEC or EHEC are mediated by binding of intimin (encoded by the *eae* gene) to its receptor (Tir) on the host cell (Hess *et al.*, 1999). Additional virulence factors in EPEC or EHEC include the expression of a plasmid (pO157)-encoded gene EHEC-*hly* (an enterohaemolysin distinct from the chromosomally encoded  $\alpha$ -haemolysin, HlyA), and a  $\beta$ -glucuronidase-encoding *uidA* gene associated with O157:H7 strains (Paton and Paton, 1998). The hair-like filamentous organelles called fimbrial

colonization factor antigens (CFAs), is known to assist ETEC strains in attachment to the small intestine (Raj, 1993). The CFA and enterotoxin genes are generally encoded on plasmids (Nataro and Kaper, 1998). Also in ETEC strains, both LT and ST genes are found and are specifically on transferable plasmids (Levine, 1987); LT is a protein that resembles cholera toxin in structure, function and mechanism of action. STs are monomeric plasmid-mediated toxins made up of an 18 to 19 amino-acid polypeptide toxin that causes diarrhoea by binding to and stimulating intestinal  $\alpha$ -bound guanylate cyclase, leading to an intracellular accumulation of cyclic GMP (Sooka *et al.*, 2004). EIEC strains are similar biochemically and in pathogenesis to *Shigella* spp. This involves epithelial cell penetration, lysis of the endocytic vacuole, intracellular multiplication (Sooka *et al.*, 2004). Ipa A-D genes are located on the large invasive plasmid of all virulent *Shigella* and EIEC organisms and the gene sequences are referred to as the invasion-associated locus (ial). IpaH sequences are present at multiple sites on both the large invasive plasmid and on the chromosomes in *Shigellae* and EIEC (Sethabutr *et al.*, 1993). EAaggEC strains produce a heat-stable enterotoxin (EAST-I) which is non-specific but has also been detected in non-aggregative and non-pathogenic *E. coli* strains. These potential virulence factors are localized on a 60-MDa plasmid common to most EAaggEC strains (Czeczulin *et al.*, 1997).

#### 1.2.4. Treatment of Diarrhoea

Enteric infections generally are self-limited conditions. However, early correction of fluid and electrolyte imbalance is the first consideration in diarrhoea

therapy. In many communities of sub-Saharan Africa, modern pharmaceutical agents are a commonly used first line of therapy for the home treatment of diarrhea or they serve as an alternative when traditional remedies fail.

Diarrhoea therapy can broadly be classified as follows: Oral rehydration treatment (ORT), intravenous fluid replacement, anti-intestinal motility (e.g. Diphenoxylate-atropine- reduces duration of diarrhoea, Loperomide), antispasmodic, antimicrobial, antisecretory and probiotics (gut flora balance). However, the WHO case management strategy for acute diarrhea as reported previously ([Richards \*et al.\*, 1993](#)) includes:

- i. early administration of appropriate fluids at home;
- ii. treatment of dehydration with WHO oral rehydration solution;
- iii. treatment of severe dehydration with intravenous electrolyte solution;
- iv. continued feeding throughout the diarrheal episode;
- v. selective use of antibiotics;
- vi. non-use of antidiarrheal drugs

Oral rehydration therapy (ORT) in the child with mild-to-moderate dehydration consists of replacement of the child's fluid deficit and ongoing losses and provision of maintenance fluid, electrolyte, and nutritional needs. In severe dehydration or where oral replacement is not possible, intravenous fluids administered in the health care setting may be needed. This should be followed after at least the initial twenty-four hours of glucose electrolyte solution therapy with slow reintroduction of sugar-free fruit drinks, bland food such as vegetables

and then regular feeds (Walker-Smith, 1990). However, there are dangers in the home use of ORT, including inappropriate preparation (electrolyte concentration) or errors of administration (usually insufficient volume) particularly in the developing countries, where literacy level is low. A study in Nigeria found that only 12.7% of people interviewed were able to correctly describe how sugar-salt solution (SSS) is prepared although almost all of them were aware of ORT (Ikpat and Young, 1992). In Zimbabwe, although nearly half the respondents were able to provide a recipe for SSS, only 12% gave the correct formulation (de Zoysa *et al.*, 1984). The home management of childhood diarrhea with ORT or SSS can be increased positively with public health education (Blum *et al.*, 1990; Touchette *et al.*, 1994).

Patients with diarrhea associated with certain bacterial and protozoal agents may benefit from therapy with an antimicrobial agent (Pickering and Cleary, 2002). In some instances, specific antimicrobial therapy may reduce morbidity and mortality associated with enteric illnesses, may prevent future complications, help to eradicate fecal shedding and to prevent transmission of enteric pathogens but antimicrobial agents should be prescribed with a consideration of their limitations (Pickering, 2003). In viral diarrhoeas for instance, hydration is the mainstay of treatment whether it be oral or parenteral, and specific pharmacologic therapy is not available. Antimotility drugs in some cases often complicate treatment. Pickering (1991) reported that antimotility medications worsen the clinical course in shigellosis and in antimicrobial-

associated colitis and have the risks attendant with overdose. Other conjectured possible side effects include toxic megacolon and colonic hemorrhage (Northrup and Flanigan, 1994) and ileus (Avery and Snyder, 1990).

*Salmonella* gastroenteritis is usually a self-limiting disease. Fluid and electrolyte replacement may be indicated in severe cases. Antibiotics are not routinely used to treat uncomplicated non-typhoidal *Salmonella* gastroenteritis because they may rather prolong illness, the length of excretion of pathogen or actually prolong the duration of convalescent carriage (Klotchko and Wallace, 2009). However, it has been suggested that infants and the elderly who are at risk for bacteremia or complications due to bacteremia deserve antimicrobial treatment (Cohen *et al.*, 1978). Fluoroquinolones such as Ciprofloxacin have been suggested as more effective than standard antibiotics for treating patients with bacteremia due to *Salmonella* (Jacobson *et al.*, 1989) and chronic suppressive therapy may be needed to prevent reoccurrence. The 4-quinolones are not only highly active *in vitro* against a broad range of enteric pathogens but generally also exhibit most of the other properties desirable for the treatment of these infections (Keusch, 1988). They are well tolerated, have good oral absorption and are more rapidly and reliably effective than earlier drugs (WHO, 2005). Nevertheless, fluoroquinolones are not recommended for use in children due to the risk of central nervous system toxicity, cardiovascular toxicity, tendon or articular toxicity, and rarely hepatic toxicity (Nelson *et al.*, 2006) even at therapeutic doses and adverse reactions may manifest during, as well as after

fluoroquinolone therapy has been completed (Saint *et al.*, 2000). Third-generation cephalosporins are widely used in children with serious infections. It has recently been suggested that the specific adverse-effect profile of quinolones must be considered when they are chosen for treatment of bacterial infections because of physiological changes in renal function (Stahlmann and Lode, 2010). The earlier drugs chloramphenicol, ampicillin and amoxicillin and trimethoprim-sulfamethoxazole are used occasionally as alternative therapy for salmonellosis. Presently, apart from the quinolones, and third-generation cephalosporins, macrolide antibiotics are preferred for empiric therapy pending sensitivities. Regrettably, sensitivity to quinolones is declining, and these are no longer fool-proof agents for typhoid fever (WHO, 2005a). A sentry antimicrobial surveillance program for North America (1997-2001) has shown that the level of susceptibility for ciprofloxacin, as the representative of other fluoroquinolones, was equal or slightly inferior to that of representative aminoglycoside (Jones, 2003). According to Ercis *et al.* (2006), nalidixic acid-resistant *Salmonella* strains are suggestive of reduced effectiveness of quinolone therapy in patients. In South Africa, the significantly increasing incidence of extended spectrum betalactamase producing *Salmonella* is set back in the use of extended-spectrum cephalosporins which are the preferred drugs for serious non-typhoidal *Salmonella* infections in children (Kruger *et al.*, 2004).

As in other diarrhoeal diseases, correction of dehydration and maintenance of fluid and electrolyte balance is the first line of therapy in

shigellosis. Antibiotics have reportedly shortened the duration of symptoms in infections due to *Shigella* (Salam and Bennish, 1991; Sack *et al.*, 2001) and can prevent relapse. Ampicillin and trimethoprim-sulfamethoxazole are good choices for sensitive strains of *Shigella*. Nalidixic acid and the newer fluoroquinolones have been shown to be effective against multiply-antibiotic resistant *Shigella* spp. (Rogerie *et al.*, 1986; Ericsson *et al.*, 1987; Pichler *et al.*, 1987). Third generation cephalosporins, such as cefixime and ceftriaxone, have also been proven through clinical trials to be better than ampicillin or TMP-SMZ and safer for use in children (Varsano *et al.*, 1991; Ashkenazi *et al.*, 1993). The WHO recent recommendations for treatment of clinically diagnosed cases of *Shigella* dysentery are ciprofloxacin as first line treatment, and pivmecillinam, ceftriaxone, or azithromycin as second line treatment (WHO 2005b). Treatment of shigellosis with antibiotics should however, be done putting regional differences in sensitivity as well as local antibiotic sensitivity patterns of *Shigella* isolates into consideration (Christopher *et al.*, 2010). In EIEC, treatment of significant symptomatic illness with fever and bloody diarrhoea should follow same course of treatment as *Shigella* diarrhoea (Herrington and Taylor, 1991). *E coli* 0157:H7 are sensitive to most antibiotics *in vitro*, antibiotics have not been shown to limit duration or ameliorate symptoms (Carter *et al.*, 1987). The illness is self limited and treatment is supportive (Herrington and Taylor, 1991). ETEC which is usually a disease of children in the developing countries is treated with ORT and intravenous fluids. Treatment of Traveller's diseases is aimed at reducing

episodes of diarrhoea and number of days of illness. Trimethoprim-sulfamethoxazole can be used both as prophylaxis and as treatment of travelers (DuPont *et al.*, 1982; Steffen *et al.*, 1988).

Manipulation of gut flora to enhance its protective and beneficial role represents a promising field of new therapeutic strategies. Probiotics are non-antibiotic formulations which are considered in diarrhoea therapy. Probiotics are live nonpathogenic microorganisms administered to improve microbial balance, particularly in the gastrointestinal tract. They are originally derived from cultured food, especially dairy products, and consist of *Saccharomyces boulardii*, a yeast, *E. coli* Nissle 1917 (a nonpathogenic *E. coli* strain), or lactic acid bacteria, such as *Lactobacillus* spp., *Lactococcus lactis* and *Bifidobacterium* spp, and are regulated as dietary supplements and foods (Damaskos and Kolios, 2008; Williams, 2010). There has been evidence for the clinical effectiveness of probiotics in the treatment of acute diarrhea, most commonly due to rotavirus, and pouchitis (Heydarian *et al.*, 2010; Williams, 2010). Probiotics appear to be a useful adjunct to rehydration therapy in treating acute, infectious diarrhoea in adults and children (Allen *et al.*, 2003). The mechanisms involved in the remediation effects of probiotics can be that of lowering intestinal pH, decreasing colonization and invasion by pathogenic organisms, or modifying the host immune response. Studies have shown that the mechanisms of action of probiotics include antimicrobial activity and suppression of bacterial growth, immunomodulation and initiation of an immune response, enhancement of



barrier activity, and suppression of human T-cell proliferation (Resta-Lenert and Barrett, 2003; Nerstedt *et al.*, 2007; Peluso *et al.*, 2007). The molecular aspects of probiotic mechanism of action have been shown experimentally, in which they have been found to induce their effect by means of their DNA (Jijon *et al.*, 2007; Rachmilewitz *et al.*, 2007). The beneficial effects of probiotics vary from one species or strain to the other.

#### 1.2.5. Some considerations on antibiotic therapy of enteric bacteria

The classifications of antibiotics are based on their mechanisms of action, chemical structure, or spectrum of activity. Antibiotics which generally may be bactericidal (lethal to bacteria) or bacteristatic (prevent bacterial growth) perform their activities mainly by targeting bacterial functions or growth processes (Calderon and Sabundayo, 2007). Bactericidal antibiotics target the bacterial cell wall while bacteriostatic antibiotics target protein synthesis (Finberg *et al.*, 2004). In terms of spectrum of activity antibiotics are also categorized either as "narrow-spectrum" based on their target specificity or "broad-spectrum" if active against a wide range of bacteria group. Table 1.3 gives a summary of some antibiotics that are used in the treatment of enteric infections by their classes and their modes of action.

Table 1.3. Some antibiotics that are used in the treatment of enteric infections and their mechanisms of action.

*CLSI Subclass	Antimicrobial Agent	Mechanism of Action
Aminoglycosides	Amikacin	Interfere with protein biosynthesis by binding to bacterial 30S ribosome subunit, inhibiting the translocation of the peptidyl-tRNA from the A-site to the P-site and also causing misreading of mRNA, leaving the bacterium unable to synthesize proteins vital to its growth.
	Gentamicin	
	Kanamycin	
Aminopenicillins	Ampicillin	Inhibit bacterial cell wall synthesis by disrupting the synthesis of the peptidoglycan layer.
$\beta$ -Lactamase inhibitor combinations	Amoxicillin-Clavulanic acid	Inhibit bacterial cell wall synthesis by disrupting the synthesis of the peptidoglycan layer.
Carbapenems	Imepenem	Inhibit bacterial cell wall synthesis
	Meropenem	
Cephalosporins (2 <sup>nd</sup> generation) Cephamycins	Cefoxitin	Inhibit bacterial cell wall synthesis by disrupting the synthesis of the peptidoglycan layer.
	Cefuroxime	
Cephalosporins (3 <sup>rd</sup> generation)	Ceftazidime	
	Ceftriaxone	
	Cefotaxime	
Folate pathway inhibitors	Trimethoprim-Sulfamethoxazole	Inhibit bacterial folic acid metabolism
Lincosamides	Clindamycin	Interfere with protein biosynthesis by binding to bacterial 50S ribosome subunit
Macrolides	Azithromycin	Interfere with protein biosynthesis irreversibly to the subunit 50S of the bacterial ribosome, thereby inhibiting translocation of peptidyl tRNA.
	Erythromycin	
Phenicol	Chloramphenicol	interfere with protein biosynthesis including 50S ribosome inhibition
Quinolones	Ciprofloxacin	Bacterial DNA gyrase or topoisomerase IV enzyme inhibitors, thereby inhibiting DNA replication and transcription.
	Nalidixic acid	
Sulfonamides	Sulfisoxazole	Inhibit bacterial folic acid metabolism

Tetracyclines	Tetracycline	Interfere with protein biosynthesis including 30S ribosome inhibition
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\*CLSI is Clinical and Laboratory Standards Institute formerly NCCLS

The choice of drugs for the treatment of enteric diseases is based on some of the following known therapeutic principles ([Keusch, 1988](#)).

- i. the agent must be active *in vitro* against the isolate,
- ii. the levels must be adequate for treating infections due to invasive pathogens both luminal and tissue,
- iii. the drugs with good enterohepatic circulation may be especially well suited for the treatment of infections due to noninvasive pathogens, and
- iv. the drugs active intracellularly may have particular value in therapy for typhoid, especially in reducing the relapse rate.

It is no gainsaying that antimicrobials have saved the lives and eased the suffering of millions of people. By helping to bring many serious infectious diseases under control, these drugs have also contributed to the major gains in life expectancy experienced during the latter part of the last century ([WHO, 2002](#)).

However, these gains seem to have been eroded as the emergence of drug resistance and multiple drug resistance (MDR) have become a threat in various nations of the world. The effectiveness of most drugs of choice has been jeopardized by many factors such as the incorporation of antibiotics into animal feeds. The authorization for the use of fluoroquinolones in food animals

enhanced the rates of fluoroquinolone-resistant *Salmonella* in animals and food, and then subsequently in human infections (FAO/OIE/WHO, 2003). The total consumption of antimicrobials has been viewed as one of the critical factors in selecting resistance even though the relationship between use and resistance is not a simple correlation (WHO, 2001) so also is under-use through lack of access, inadequate dosing, poor adherence, and substandard antimicrobials. In many developing countries particularly sub-Saharan Africa, some of the contributory factors to acquiring resistance are sources of obtaining drugs. Antimicrobial agents are readily available without a prescription hence, self-prescribing of antimicrobials is common (Dua *et al.*, 1994; Okeke *et al.*, 1999). Some of the potential sources of medications include relatives or friends with unused supplies, locally trained nurses, shopkeepers, market sales people, and unlicensed drug salesmen who buy drugs in major cities and then sell them in rural villages (Bledsoe and Goubaud, 1985; Omotade *et al.*, 1994). Other contributory factors are inadequate and inappropriate use of drugs and lack of education. "Examples of inappropriate uses of antibiotics that exert selective pressure for resistance in various bacteria are: administering them to patients who have viral upper respiratory tract infections; feeding them to farm animals to enhance their growth" (Sack *et al.*, 2001). In addition, antimicrobial agents may be of poor quality, due to degradation, counterfeiting, or lack of bioequivalence in the case of generic drugs. The use of such products results in sub-optimal serum concentrations, which promotes selection for resistance

(Okeke *et al.*, 1999). The ease of modern transport systems and frequency of international travels have also contributed greatly to the spread of resistance. Other factors in the spread of resistance are overcrowding and improper sewage disposal which according to Okeke *et al.*, (1999) promote the spread of resistant organisms among individuals and provide increased opportunities for genetic exchange among bacteria, facilitating the dissemination of antibiotic resistance determinants.

Emerging drug resistance to ciprofloxacin and second line drugs such as pivmecillinam, ceftriaxone, and azithromycin is increasingly being reported in many parts of the world, as is multiple-drug resistance (Kosek, 2008; Kuo, 2008; Pazhani, 2008). Multi-resistance in *Enterobacteriaceae* is defined as resistance to three or more of the following classes of antibiotics: cephalosporins, carbapenems, quinolones, aminoglycosides and trimethoprim/co-trimoxazole (Rodriguez-Bano *et al.*, 2004). MDR is a serious problem for the treatment of shigellosis, particularly those caused by *S. dysenteriae* type 1. Transferable MDR was first described among *Shigella* in Japan in the mid 1950s, (Watanabe, 1963), and has remained a major problem ever since. Multidrug-resistant (MDR) strains of *Salmonella* are also encountered frequently and the rates of multidrug-resistance have increased considerably (WHO, 2005a). The emergence of drug-resistant *Salmonella* is more of response to selective pressure from the use particularly in food animals. A recent global spread of a multidrug-resistant *S. enterica* serovar Typhimurium phage type DT104 in animals and humans showed

that other factors such as major shifts in the occurrence of *Salmonella* serotypes in food animal and humans do occur. In this particular case while antimicrobial usage may have facilitated the spread of DT104, international and national trade of infected animals is thought to play a major role in international spread (WHO, 2005a). MDR strains of enteric bacteria were isolated with increasing frequency from various sub-Saharan nations at various times to date. In Central Africa, MDR strains of *S. dysenteriae* type 1 were isolated during the epidemics between late 1970s and early 1980s (Frost *et al.*, 1981; Ebright *et al.*, 1984). Multiple resistance to antibiotics including trimetoprim-sulfamethazole was also reported in Zambia (Tuttle *et al.*, 1995). Data from Nigeria, Ethiopia, Senegal, Kenya, Malawi is suggestive of wide spread and increasing resistance to most commonly used drugs in the sub-Saharan African regions (Lamikanra *et al.*, 1989; Awole *et al.*, 2002; Sow *et al.*, 2007; Onyango *et al.*, 2009; Kingsley *et al.*, 2009). In South Africa, the work of Kruger *et al.* (2004) on non-typhoidal *Salmonella* isolates showed increased resistance to extended-spectrum cephalosporin. Obi *et al.* (2007) reported multiple antibiotic resistance among enteric bacteria obtained from HIV patients and their drinking water and a relationship was established between clinical and environmental strains. A very recent data from South Africa (Keddy *et al.*, 2009), showed that most commonly expressed multiple antibiotic resistance profiles among non-typhoidal *Salmonella* were ACSSuNa and ACSSuTNa, that is, resistance to a combination of 5 or 6 drugs combinations of ampicillin (A), chloramphenicol (C), streptomycin (S), sulfamethoxazole (Su),

tetracycline (T) and nalidixic acid (Na). Also, nalidixic acid-resistant with reduced susceptibility to ciprofloxacin was reported among human isolates of *Salmonella enterica* serovar Typhi from South Africa by [Smith et al., \(2010\)](#). The increasing prevalence of bacterial strains exhibiting multi-resistance to readily available and relatively cheap oral antibiotics constitutes a major obstacle to cost-effective therapy of diarrheas in sub-Saharan Africa.

#### 1.2.6. Mechanisms of antibacterial resistance

Various mechanisms of antimicrobials inactivation have been reported ([Neu, 1993](#); [Alekhun and Levy, 2000](#); [Fluit et al., 2001](#); [Sundsfjord et al., 2004](#)) which invariably led to the emergence of multiple drug resistance pathogens. Some of the mechanisms are:

- a) enzymatic inactivation of the antimicrobial agent,
- b) prevention of access to the target pathogen or,
- c) change or mutation in the target site,
- d) novel penicillin-binding proteins (PBPs),
- e) altered membrane permeability.

Enzymatic inactivation may result either into destruction of antimicrobial agent, such as occurs with the beta-lactamases, or lead to a major modification of the compound so that it does not bind to its target as is seen with the aminoglycosides and chloramphenicol. The second mechanism whereby access to the drug target is prevented may be by substitutions, amplifications or modifications of the drug target reducing the affinity of the drug to the target.

For example, in gram negative organisms the outer membrane proteins may be altered such that antibiotics are unable to cross the cell wall. The other mechanisms of resistance are intrinsic mechanisms not commonly specified by mobile elements such as efflux pumps that expel multiple kinds of antibiotics (Alekshun and Levy, 2007). These may lead to reduced access of the antimicrobial agents to the target by means of permeability barriers. For instance, diarrhoea causing *E. coli*, *Salmonella* and *Shigella* reportedly possessed plasmids which produce a new dihydrofolate reductase that has a low affinity for trimethoprim and sulfonamides (Nue, 1993). A very recent study on *Salmonella* spp. in South Africa by Smith and co-researchers concluded that amino-acid mutations in GyrA and ParC in combination with active efflux of antibiotic out of the bacterial cell are probable mechanisms conferring quinolone resistance (Smith *et al.*, 2010).

The genes coding for antibiotic resistance and virulence at times share common features of being located in the bacterial chromosome, as well as on plasmids. They are associated in gene clusters to form resistance or pathogenicity islands and are transferred by mobile elements (such as integrons or transposons) or phages (Villa and Carattoli, 2005).

The most appalling resistant issue among the enteric bacteria is that of the declines in susceptibility for the fluoroquinolones and the third-generation cephalosporins. While resistance to the fluoroquinolones often emerges as a result of mutations in the bacterial genome (DNA), resistance to other



antimicrobials often spread by transfer of DNA between bacterial strains (WHO, 2005a). The major mechanism of resistance to beta-lactam antibiotics among enterobacteriaceae involves production of  $\beta$ -lactamases or extended spectrum  $\beta$ -lactamases (ESBLs). ESBLs have traditionally been defined as transmissible beta-lactamases that can be inhibited by clavulanic acid, tazobactam or sulbactam. They are a group of enzymes that break down antibiotics belonging to the penicillin and cephalosporin groups and render them ineffective. The ESBLs are generally encoded by mobile genes that can be exchanged between bacteria. The prevalence of ESBL is high among some Enterobacteriaceae such as *E. coli* and *K. pneumoniae* (Winokur *et al.*, 2001). The diverse geographic distributions and remarkably variable substrate affinities of ESBLs can produce confusing susceptibility testing results (Winokur *et al.*, 2001). According to Jones (2003), the average ESBL phenotype rates for a 5 years SENTRY Program (1997-2001) showed the highest occurrence in Latin America, followed by Europe and North America. It has also been noted that when ESBL strains occur they often have co-resistances with the aminoglycosides (gentamicin), tetracyclines, and trimethoprim/ sulfamethoxazole (Winokur *et al.*, 2001).

Effective treatment of human infections has been limited by the emergence of MDR *Salmonella* strains with resistance to fluoroquinolones and third-generation cephalosporins (WHO, 2005a). Regional differences in ESBL type have also been found to reflect in the choice of therapeutic drug against ESBL strains of enteric pathogens. Jones (2003) reported that cefepime, a

fourth-generation cephalosporin, could be used against 88.0% of isolates in North America, but not for strains in the other regions. However, in all the regions of the study by Jones, only the carbapenems consistently inhibited ESBL-producing strains.

Another type of resistance affecting third-generation cephalosporins and aztreonam (a monobactam) has been the hyperproduction of an Amp C cephalosporinase an inducible enzyme by members of Enterobacteriaceae (Jones *et al.*, 1997; Coudron *et al.*, 2000). Amp C cephalosporinase is normally produced in modest amounts and does not significantly destroy the third-generation cephalosporins; however, spontaneous mutations can derepress enzyme production generating enough enzymes to hydrolyze the cephalosporins and aztreonam (Jones *et al.*, 1997). The drugs of choice against Amp C beta-lactamase producing bacteria are the carbapenems while cefepime has been reported to possess physico-chemical characteristics that enable clinical use against the ceftazidime-resistant Enterobacteriaceae (Jones and Varnam, 2002).

The role of integron in the acquisition and dissemination of resistance in enteric bacteria is very crucial. Integrons are DNA elements which contain collections of genes (gene cassettes) that are generally classified according to the sequence of the protein (integrase) that imparts the recombination function (Mazel, 2006). They have the ability to integrate stably into regions of other DNAs where they deliver, in a single exchange, multiple new genes, particularly for drug resistance (Nemergut *et al.*, 2008). Many of the gene cassettes in

resistance integrons which probably originated from super-integrons (larger integron structures with hundreds of accessory genes), encode resistance against newer antibiotics such as cephalosporins and carbapenems (Fluit and Schmitz, 2004). These genetic elements which can be carried by other mobile genetic elements such as plasmids and transposons assist in the rapid dispersion of resistance genes within bacterial species and between different species (Levesque *et al.*, 1995; Hall, 1997). Several gene cassettes and 4 distinct classes of integrons have been identified, some of which confer resistance to beta-lactams, aminoglycosides, trimethoprim, chloramphenicol, sulfonamide and quaternary ammonium compounds used as antiseptics and disinfectants (Levesque *et al.*, 1995; Hall, 1997; Mazel *et al.*, 1998). Plasmid-borne integron have been implicated in MDR *Salmonella enterica* serovar Enteritidis (Brown *et al.*, 2000). In 2008, the study by Rayamajhi and his group described a rise in trend of MDR *S. enterica* serovar Typhimurium with clinically important class 1 integron in food animal. This may have a ripple effect of resistance dissemination on the human consumers (Rayamajhi *et al.*, 2008). Recently, class 1 integrons for aminoglycoside and trimethoprim resistance were found to be widespread among members of Enterobacteriaceae in China. The study also identified class 2 integron in *Shigella* isolates and believed that these play a role in antibiotic resistance (Gu *et al.*, 2008).

#### 1.2.7. Trends in emergence and spread of antibiotic resistance

Antibiotic resistance is a rapidly growing problem in health care systems. It is a global public health concern that is impacted by both human and non-human antimicrobial use. Alexander Fleming selected and described mutants resistant to penicillin soon after he had discovered the antibiotic. In 1946, a statement was credited to Fleming which reads thus "*There is probably no chemotherapeutic drug to which in suitable circumstances the bacteria cannot react by in some way acquiring 'fastness' [resistance].*" quoted by [Alekshun and Levy \(2007\)](#). More than 6 decades after the introduction of antibiotics into clinical practice, the prescience of Fleming has come to fruition as the infectious disease community has yet to identify an antibiotic that has managed to circumvent the development of resistance ([Alekshun and Levy, 2007](#)). Resistance usually emerges to each new antibiotic used as the drug of choice for treating diarrhoeal disease soon after introduction into clinical practice. In the 1940's which marked the pre-antibiotic era, resistance to penicillin drugs among staphylococci was noted ([Barber, 1947](#)). This was mediated by the production of penicillinases in the bacterial pathogens. In the seventies, resistance to ampicillin, tetracycline and sulfonamides in Gram-negative bacteria was frequent ([Willett and Radojicic, 1976](#); [Maselle et al., 1980](#)). Resistance to trimethoprim-sulfamethazole quickly emerged soon after it became first-line drug of choice and this was soon followed by an explosion of resistance to nalidixic acid ([Jesudason and Saaya, 1997](#)). The extensive use of ampicillin, chloramphenicol and trimethoprim-sulfamethoxazole for the treatment of presumed cases of typhoid fever may

have contributed to the high prevalence of resistance to these drugs (Coovadia *et al.*, 1992; Morpeth *et al.*, 2009). Also, their use in the treatment of non-typhoidal Salmonella infections in sub-Saharan Africa is of limited value since resistance have been reported in many cases (Lepage *et al.*, 1990 ; Enwere *et al.*, 2006 ; Gordon *et al.*, 2008). In Nigeria, the prevalences of enteric bacterial strains resistant to tetracycline, ampicillin, chloramphenicol, and streptomycin among healthy individuals increased tremendously from between 9% to 35% in 1986 to 100% in 1998 (Okeke *et al.*, 2000). The increasing rate of gentamicin-resistance in Enterobacteriaceae is critical considering the importance of this drug in the treatment of bloodstream infections. Increase in gentamicin-resistance in *E. coli* was reported in Tanzania (Maselle *et al.*, 1980; Blomberg *et al.*, 2007) and Kenya (Slack and Wamola, 1977; Omari *et al.*, 1997). In Bangladesh, the isolation of vibrio strains resistant to antibiotics such as tetracycline, ampicillin, kanamycin, streptomycin and trimethoprim-sulfamethazole became noticeable from 1979 (Glass *et al.*, 1980). In South Africa, gentamicin-resistant strains which have earlier been reported (Dalsgaard *et al.*, 2001) have persisted even in environmental samples (Okoh and Igbinosa, 2010). Increasing isolation of enteric pathogens with resistance to beta-lactam drugs have been reported over the years in South Africa (Essack *et al.*, 2001; Bell *et al.*, 2002; Kruger *et al.*, 2004) and to date the status quo seems to have been maintained. Currently, isolation of gram negative bacterial strains resistant to newer cephalosporins and particularly imipenem-resistant *Pseudomonas*

*aeruginosa* are being reported (Essack *et al.*, 2001; Bell *et al.*, 2002; Kruger *et al.*, 2004). This might be an indication that we have probably entered into the post-antibiotic era, unless drastic intervention strategies are put in place to reverse the trends.

#### 1.2.8. Consequences of antibiotic resistance

Evidences have shown that adverse human health consequences due to the occurrence of resistant microorganisms are grave and may be felt harder in resource-poor settings. These main consequences of antibiotic resistance may be increased frequency of treatment failures and increased severity of infections and can have cost implications, morbidity as well as mortality repercussions.

##### 1.2.8.1. Morbidity and Mortality implications of antibiotic resistance

Whilst some underlying conditions such as old age (>65 years) and immunosuppression may constitute risk factors for colonization and infection with an MDR gram-negative bacterium (Hsu *et al.*, 2005), several studies both retrospective and prospective have shown that infections with MDR gram-negative bacteria are more frequently associated with increased morbidity and mortality than those caused by susceptible pathogens (Helms *et al.*, 2002; Travers and Barza, 2002; Varma *et al.*, 2005). Increased hospitalization and bloodstream infections have been correlated to an increased relative frequency of antimicrobial-resistant *Salmonella* (Varma *et al.*, 2005). Several studies have found similar correlation in other bacteria: ESBL-producing *E. coli* and *Klebsiella* spp., (Lautenbach *et al.*, 2001), imipenem-resistant *P. aeruginosa* (Lautenbach *et*

*al.*, 2010) and other bacteria pathogens (Angulo *et al.*, 2004). In a Canadian study, the burden of illness associated with *Salmonella enterica* serotype Typhimurium infection was identified. Infections by definitive phage type 104 (DT104) and R-type antimicrobial-resistance pattern (AK/CSSuT) were used as risk factor (Martin *et al.*, 2004). The outcome of the study was a significant estimate of hospitalization attributable to the resistance patterns of the infections. Likewise, persons with infections caused by antimicrobial-resistant *Salmonella* have been found to be more likely to have bloodstream infection or die within 90 days following specimen collection than control groups with susceptible infections. The death rate for persons with multi-drug resistant *Salmonella* infections was estimated to be 10 times higher in the two years following specimen collection than for the general population (WHO, 2005a).

#### 1.2.8.2. Cost implications of antibiotic resistance

Besides the human health impacts of resistance to first-line drugs a huge economic cost is incurred in terms of procuring newer effective antibiotics which are usually expensive and may be unavailable to local health centers. Consequentially, inavailability of effective therapy leads further to increased cost due to the length of hospitalization, the cost of the illness, in terms of treating the patient, lost wages for patient and family members and salaries of health care personnel which may be substantial (Sack *et al.*, 2001). The economic implications of drug resistant infections can be of significant value. Antibiotic-resistant infections attributably cost the U.S. healthcare system in excess of \$20

Billion annually while the medical costs per patient ranged from \$18,588 to \$29,069 (Boston and Durham, 2009). In Canada, Salmonellosis has been estimated to cause 627,200 cases of infection and cost Can\$846.2 million annually (Todd, 1989). The finding of Broughton *et al.* (2010) was substantially longer stays and higher costs associated with non-typhoidal salmonellosis that was quinolone resistant. The study gave an indication that interventions that decrease quinolone resistant prevalence will lead to significant savings for the health system in the management of hospitalized salmonellosis cases.

#### 1.2.9. Prevention of diarrhoea

The incidence of diarrhoea can be greatly reduced by proper preventive measures. The avoidance of the use of antibiotics, development and use of non-antibiotic drugs such as anti-secretory drugs has been suggested to reduce diarrhea. Some preventive measures are highlighted below.

- ❖ Breastfeeding: Exclusively breastfed babies are much less likely to get diarrhoea or to die from it than are babies who are not breastfed or are partially breastfed. Efforts should be made to improve weaning practices (Mahmood *et al.*, 1989).
- ❖ Use of safe water: The risk of diarrhoea can be reduced by using the cleanest available water, increased availability and accessibility to, and protecting domestic water from contamination (WHO, 2009b).
- ❖ Handwashing: All diarrhoeal disease agents can be spread by hands that have been contaminated by faecal materials. The risk of diarrhoea is



- substantially reduced when individuals practice regular handwashing. In addition, the risk of spread of resistant diarrhoeal pathogens, particular in the hospital setting, can greatly be reduced by handwashing of medical personnel ([Khan, 1982](#)).
- ❖ Food safety: Food contamination by diarrhoeal agents can occur at all stages in the food production chain. These include: during the growing period (by use of human fertilisers), in public places such as markets, from processing plants to kitchens and food service establishments, and when kept without refrigeration after being prepared. Evaluations of improved food handling and storage methods and practices should be done on regular basis. Health education concerning good animal husbandry, good abattoir practice and good hygiene at all stages as well as individual food safety practices should also be emphasized ([FAO/WHO, n.d](#)).
  - ❖ Control of drug resistance through food: Control of drug-resistant enteric pathogens is most efficiently achieved through the reduction of antimicrobial use. Prudent usage in food animals combined with aforementioned food safety and hygiene practices should reduce the numbers of the relevant resistant bacterial strains in food animals and lower the risk of contamination at all stages in the food production chain ([WHO, 2005a](#)). This should be complimented with proper surveillance, risk assessment and International collaborative efforts need to be increased.

- ❖ Use of latrines and safe disposal of stools: An unsanitary environment contributes to the spread of diarrhoeal agents. Because the pathogens that cause diarrhoea are excreted in the stools of an infected person or animal, proper disposal of faeces can help to interrupt the spread of infection. Faecal matter can contaminate water where children play, where mothers wash clothes, and where they collect water for home use. Every family needs access to a clean, functioning latrine. If one is not available, the family should defecate in a designated place and bury the faeces immediately. Stools of young children are especially likely to contain diarrhoeal pathogens; they should be collected soon after defecation and disposed of in a latrine or buried ([WHO, 2009b](#)).
- ❖ Immunization: Whenever new, effective vaccines become available for cholera and diseases caused by other enteric pathogens, immunization programs are vital. In 2008, two new vaccines; pneumococcal conjugate and rotavirus vaccines were made available and introduced into clinical practice in South Africa ([Harries \*et al.\*, 2009](#); [Harrison, 2009](#)) as intervention to decrease infant and child mortality from vaccine preventable causes. Measles immunization can substantially reduce the incidence and severity of diarrhoeal diseases. Every infant should be immunized against measles at the recommended age. Evaluation of the success rate of the vaccine should be carried out periodically.

- ❖ Health education: The likelihood of eradication of enteric pathogens such as *Salmonella* in domestic animals seems impossible in the foreseeable future (WHO, 2005b). There is a need to educate the general populace on the need to cook animal foods thoroughly prior to consumption so as to keep the incidence of drug-resistant pathogens in foods of animal origin to the barest minimum. Education of food handlers in the principles of safe food handling is an essential step towards reducing the incidence of food-borne diseases resulting from cross-contaminations during processing and preparation of foods (WHO, 2009a). Educating farmers and their families regarding the risks of occupationally acquired infections is also an important step in the control of human infections from food sources.

#### 1.2.10. Medicinal plants: alternative/complementary diarrhoea therapy

The unabated increasing antibiotic resistance has not only led to resistance to several antibiotic groups but has led to selection and development of multidrug-resistant bacterial strains which is a serious worldwide health menace. The need to find lasting solutions to the emerging infections which have become a global concern has necessitated the exploration of natural products in the form of medicinal plants in the treatment of various ailments, diarrhoea inclusive.

In many developing countries particularly in sub-Saharan Africa, healers use a wide variety of plants in the treatment of gastrointestinal ailments. Several studies have reported the use of herbal plants as therapeutic agents in the

treatment of diarrhoea, even though most of the herbs are used in the treatment of various other ailments (Longanga Otshudi *et al.*, 2001; Vieira *et al.*, 2001; Agunu *et al.*, 2005; Samie *et al.*, 2005; Nair and Chanda, 2007; Mbagwu and Adeyemi, 2008). Some of the plants which have been used traditionally in the treatment of diarrhoea and or stomach disorders are listed in Table 4 below.

#### 1.2.10.1. Modes of Action of Medicinal Plants

Medicinal plants generally exhibit multiple non-specific effects which are usually complementary or synergistic. More often than not, they tend to have several broad actions on a number of whole physiological systems at the same time. Investigations have described various modes of action of antidiarrhoeal herbs. These therapeutic agents can have antispasmodic effects, delay intestinal transit, suppress gut motility, inhibit intestinal motility, stimulate water adsorption or reduce electrolyte secretion (Palombo, 2006) and some of these effects have been attributed to the presence of numerous phytochemicals (such as alkaloids, tannins, flavonoids and terpenes). Tannins and flavonoids are believed to exhibit their antidiarrhoeal potentials by increasing colonic water and electrolyte re-absorption (Palombo, 2006). In an animal experimental study by Ojewole and his group, aqueous extract of *Psidium guajava* decreased the

Table 1.4. Some medicinal plants commonly used as diarrhoeal remedy in South Africa

Botanical Names	Active Ingredient	Traditional Usage	Reference

<i>Carpobrotus edulis</i> N.E. Br. (Mesembryanthemaceae)	Malic acid, citric acid, tannins	Antiseptic, anti-diarrhoeal, vasoconstrictive	Van Wyk <i>et al.</i> (1997); Wisura and Glen (1993)
<i>Elephantorrhiza elephantina</i> Benth. (Fabaceae)	Entagenic acid, tannins	Antiseptic, anti-diarrhoeal, anti-ulcerative, emetic	Van Wyk <i>et al.</i> (1997); Hutchings <i>et al.</i> (1996).
<i>Eucomis autumnalis</i> (Mill.) Chit. (family)	Homoisoflavanones, nortriterpenoids	Urinary diseases, stomach ache, diarrhoea, enema for low back pain and healing of fractures	Watt and Breyer-Brandwijk (1962); Hutchings <i>et al.</i> (1996), Van Wyk and Gericke (2000)
<i>Pelargonium sidoides</i> DC. (family)	Saponins, tannins	Tuberculosis, diarrhoea (bronchitis, infections of the upper respiratory tract)	Watt and Breyer-Brandwijk (1962); Hutchings <i>et al.</i> (1996) ; Van Wyk and Gericke (2000)
<i>Viscum capense</i> L. (Viscaceae)	Viscumside, flavonoids	Anti-diarrhoeal, anti-bronchial, uterotonic, styptic	Van Wyk and Gericke (2000)
<i>Xysmalobium undulatum</i> R. Br. (Asclepiadaceae)	Uzarin	Anti-diarrhoeal, against painful menstrual cramps	Van Wyk and Gericke (2000)

propulsive movement and transit of charcoal meal through the gastrointestinal tract (GIT) (Ojewole *et al.*, 2008). The study also showed that the aqueous extract of *P. guajava* at a dose of 50–400 mg/kg, significantly inhibited all the diarrhoeal parameters investigated: onset, frequency and severity of diarrhoea, total number of stools, number of wet stools, and weight of wet stools.

#### 1.2.10.2. Further benefits of herbal plants

Exploring the efficacy of medicinal plants in the amelioration of infectious diseases may not only be a source of succor in abating multiple antibiotic resistance infections but will also make health care affordable and available at the door-step of all. According to [Akerele \(1978\)](#) "If there is to be any real improvement in the health of the under-served populations of the world, then there will have to be full utilization of all available resources, human and material...." In Africa particularly in the rural areas, long waits for medical attention; misgivings about the effectiveness of Western medicine, and cultural dependency on traditional methods have made the people turn orthodox medicine to a last resort. In this instance, traditional medicine especially through the use of herbs has contributed immensely to the primary health care of the people. A study by the Roll Back Malaria Initiative found that in Ghana, Mali, Nigeria and Zambia, herbal medicines were the first line of home treatment for about 60% of children with high fever ([Brieger et al., 2005](#)). About 65% of the population in India regularly depends on traditional medicine. The developed countries are not spared in the use of medicinal plants and significant increase in usage over the past decade has been reported ([Pagán and Pauly, 2005](#)). In the USA and Australia 42 and 48 % of the populations respectively utilize complementary and alternative medicines ([Eisenberg et al., 1998](#)). A WHO estimate states that 70% of Canadians and 75% of people in France have tried complementary or alternative medicine, which often includes herbal remedies ([WHO, 2008](#)), and in Japan, 85% of doctors prescribe not only modern medicine

but also the traditional herbal medicine (called Kampo), which is covered by health insurance (Aschwanden, 2001). In San Francisco, London and South Africa, 75% of people living with HIV/AIDS use traditional medicine or complementary and alternative medicines.

Medicinal plants can contribute immensely to the sustainable development of the poor but naturally endowed nations. The assertion of Geldenhuys and Van Wyk (2002) was that natural resources were fundamental in the socioeconomic development of the African continent. Africa is richly endowed with a vast diversity of plants. According to Van Wyk (2008) recent data have shown that a quarter of the total number of higher plants in the world is found in sub-Saharan Africa. Also, a total of 50,136 angiosperm taxa occur in tropical Africa and Southern Africa (Klopper *et al.*, 2006). Medicinal usages in excess of 16,300 have been reported from a list of more than 5400 medicinal plant taxa on the African continent (Neuwinger, 2000). Herbal medicines are also profitable and are highly lucrative. Worldwide, they represent a market value of about US\$ 43 billion a year. According to WHO (2008) annual revenues in Western Europe reached US\$ 5 billion in 2003-2004. In China, sales of products totaled US\$ 14 billion in 2005 and herbal medicine revenue in Brazil was US\$ 160 million in 2007. In South Africa, Dold and Cocks (2002) valued annual trade in plant material at approximately R27 million.

Medicinal plants aside from being used directly as teas or in other extracted forms for their natural chemical constituents; they may serve as leads

in the discovery of new drugs. Herbs may be used as agents in the synthesis of drugs or the organic molecules and constituents may be used as models for synthetic drugs. Data have shown that a number of drugs are derived from plant materials (Newman *et al.*, 2003). Twenty-five percent of modern medicines are made from plants first used traditionally. The search for new molecules according to Gurib-Fakim (2006) has taken a slightly different route whereby the science of ethnobotany and ethnopharmacognosy are being used as guides to lead the chemist towards different sources and classes of compounds. Some examples of commonly used pharmaceutical products which are of botanical origin are aspirin from willow bark (*Salix spp.*), digitoxin, digitalin or digoxin from Common foxglove (*Digitalis purpurea*) and quinine from *Cinchona ledgerian* (El-Baz, 2007). A recent example is the endoperoxide-based antimalarial drug Artesunate that originated from artemisinin, first isolated from the Chinese herbal medicine *Artemisia annua* L (Camacho *et al.*, 2000). A number of patented products have been obtained from studies involving medicinal herbs.

#### 1.2.10.3. Safety issues in medicinal herb therapy

The issue of toxicity in natural products applies not only to herbs but also to some ordinary food substances. The constituents of many foods could be regarded as poisonous, such as the alpha gliadin produced by gluten in wheat oats and rye, the cyanogenic glycosides in many fruit seeds, the thiocyanates of the brassica vegetables, alkaloids of the *Solanaceae* and lectins of many pulses including soya and red kidney beans.



Medicinal plants have reportedly cause serious illnesses ranging from allergy to liver or kidney malfunction, to cancer, and even death. The toxicity effects of medicinal plants may be acute or long term. These effects may range from diarrhoea, hypersensitivity reactions, nausea or vomiting, to organ-targeted toxicity, immunotoxicity, embryo/fetal and prenatal toxicity, mutagenicity/genotoxicity, hepatotoxicity, nephrotoxicity, presence of epileptogenic compounds, cardiac toxins, gastrointestinal toxins to carcinogenicity (Smolinske, 2005). According to US toxicologist, Dr Lois Gold, the carcinogenicity or toxicological potentials of natural plant chemicals are comparable to those of synthetic chemicals (Ames *et al.*, 1990; Gold *et al.*, 1991). Several studies have reported varying level of cytotoxicity of medicinal plants, cytopathic defects and organ dysfunction in animal experiments. The ethanol extracts of *Athrixia phyllicoides* DC. (bush tea) which is widely used as a beverage, cough remedy and purgative were relatively toxic (McGaw *et al.*, 2006). Extract and a flavonol glycoside from *Bauhinia galpinii* were cytotoxic to Vero cells (Aderogba *et al.*, 2007; Samie *et al.*, 2010). Pyrrolizidine alkaloids which are not toxic *per se*, but can be converted to toxic metabolites in the liver are reported to be contained in several medicinal plants (Eloff and Rösemann, 2009). Examples are hepatotoxicity of pyrrolizidine-alkaloid-contained in Comfrey (*Symphytum*), *Dryopteris* (Male Fern), *Viscum* (Mistletoe) and *Corynanthe* (Yohimbe). Michellamine B one of the atropisomeric naphthylisoquinoline alkaloid dimers isolated from *Ancistrocladus korupensis* was inhibitory to several laboratory and

clinical strains of HIV-1, including the AZT resistant strain G910-6 and the pyridinone-resistant strain A17; as well as strains of HIV-2. However, the high toxicity of this compound to several human cell lines prevented its further evaluation (Boyd *et al.*, 1994). In South Africa, mutagenic effects in the *Salmonella* microsome assay have been reported in *Crinum macowanii*, *Chaetacme aristata* Planch. (Celastraceae), *Plumbago auriculata* Lam. (Plumbaginaceae), *Catharanthus roseus* (L.) G.Don. (Apocynaceae) and *Ziziphus mucronata* Willd. (Rhamnaceae) (Elgorashi *et al.*, 2003). In another study, the induction of genotoxicity on bacterial or human cells has been observed (Elgorashi *et al.*, 2002). Comfrey, Lobelia and Sassafras tea has been implicated in liver disease, vomiting, breathing problems, convulsions, cancer, and even death (Snider, 1991). Blindness has also been attributed to the use of herbal medicines. In the United Republic of Tanzania, a study by Yorston and Foster (1994) linked 25% of corneal ulcers to the use of traditional eye medicines, of which many are based on herb extracts. Another study, in Malawi found that herbal medicines were associated with 26% of childhood blindness (Courtright *et al.*, 1994).

Another safety issue is that of contamination problems. Heavy metals, pesticide residues, microbes and microbial metabolites such as aflatoxin contaminants of herbs constitute additional safety problems. Cumin seeds commonly given by Egyptians to their children to relieve coughs, aches, or itching were among five spices purchased at a local market in Egypt and

examined for toxic content. High level of the organophosphate pesticide (profenofos, 0.37g/kg) or nearly twice the residue the WHO and Codex Alimentarius Commission permit in vegetables was detected in the cumin seeds (Ahmed, 2001). According to Roy *et al.* (1988) aflatoxin contamination was detected in 14 out of the 15 common drug plants in India. Contamination of dietary and medicinal plants with exposure to fumonisin B<sub>1</sub> is widespread than expected in the Eastern Cape Province of South Africa (Sewram *et al.*, 2006). Fungal microbes and Fumonisin B<sub>1</sub> contamination of commercial traditional African medicines in South Africa have recently been reported (Katarere *et al.*, 2008). A lack of proper sterilization, along with inclusion of components such as urine, saliva, or breast milk in some of medicinal herbs used as eye remedy in Malawi, gives pathogens ample opportunity to thrive in eyes already hard hit by injury or infection (Courtright *et al.*, 1994). Perhaps the biggest problems with herbal medicines are a lack of standardization and of safety regulations. However, a very recent study conducted in Ghana suggested that rather than have heavy metal toxicity effects, the metals found in the plants of study may offer beneficial effect in case of micronutrient deficiency in herb consumers since metals are readily bioavailable (Annan *et al.*, 2010).

The foregoing literature review underlines the scale, magnitude and health associated parameters of infective diarrhea, the problems of escalating antibiotic resistance, the forays to uncover the genetic basis of antibiotic resistance and virulence of the designated bacterial pathogens, including the

potentials of the use of medicinal plants and their possible safety related issues. In spite of these challenges, comprehensive studies on updated antibiogram profiles, genetic landscape and activity of medicinal plants against enteropathogens, particularly, *Salmonella* species and *E. coli* have received little attention in South Africa.

### 1.3. Objective of the study

- i. To characterize and determine the antibiograms of *Salmonella* and diarrheogenic *E. coli* isolates from clinical samples of patients. .
- ii. To determine extended spectrum beta-lactamases (ESBL's) production and the genetic determinants among the *Salmonella* and diarrheogenic *E. coli* isolates.
- iii. To identify the gene encoding virulence factors in *Salmonella* and *E. coli* isolates.
- iv. To identify and screen various medicinal plants used by herbalists within the Oliver R. Tambo District Municipality (ORTDM) in the treatment of diarrhea and related diseases for their antimicrobial activities.
- v. To isolate pure compounds, elucidate and characterize active ingredients of selected medicinal plants and investigate their cytotoxicity effects.

### 1.4. Approach

The study involved clinical, field and laboratory studies.

- ❖ The first stage of the study was clinical-based and involved gathering demographic information about patients, history of diarrhoea, HIV status (from hospital records and surveillance data), self-medication and the usage of herbal medicine. Clinical specimens analyzed included stool and blood samples which were collected from patients through the help of qualified health care-givers, and from those deposited into the NMAHC laboratory.
- ❖ The second stage was the laboratory analysis of clinical samples obtained from the selected human subjects for the isolation of *Salmonella* and *E. coli* using standard microbiological techniques. These included the susceptibility testing of the enterobacteria using standard drugs and the identification of the resistance and virulence factors of the isolates using molecular techniques.
- ❖ The third stage of the study involved identification and selection of ethnomedical plants used in folklore practice in ORTM for diarrhea and associated diseases. This was guided by the information from the interview of traditional healers and informed elders of the communities.
- ❖ The last stage of the research involved analysis of the crude extracts of the medicinal plants for their antidiarrhoeal activities and, the isolation and characterization of the active ingredients, including cytotoxicity testing.

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## CHAPTER 2

### EXTENDED-SPECTRUM BETA-LACTAMASES AND CLASS 1 INTEGRON MEDIATED RESISTANCE IN CLINICAL ISOLATES OF *ESCHERICHIA COLI* AND *SALMONELLA*

#### 2.0. Abstract

Molecular characterization for the presence of specific antimicrobial resistance mechanisms was carried out on 119 *Salmonella* and 90 *Escherichia coli* isolates from patients with diarrhoea in the Eastern Cape Province, South Africa. PCR and sequencing were used to verify the genetic determinants responsible for extended spectrum beta-lactamases (ESBLs) phenotypes. Of the 119 *Salmonella*

isolates, 61 (51.2 %) were ESBL, positive by genotypic determination. A total of 9 (14.7 %) and 54 (88.5 %) of the 61 isolates were CMY-2 and TEM b-lactamase producers, respectively. Only 1 of the *Salmonella* spp. was CTX-M ESBL's producer. Among the *E. coli* isolates the mediators of resistance were 13 (68.4 %), 9 (47.4 %) and 2 (10.5 %) of bla<sub>SHV</sub>, bla<sub>TEM</sub> and bla<sub>CTX-M</sub> respectively. Class 1 integron (*Int1*) gene occurred significantly among the *Salmonella* species, mostly among isolates expressing TEM genes. This study reports the presence of the bla<sub>CMY-2</sub>, bla<sub>SHV-1</sub>, bla<sub>TEM-20</sub> and bla<sub>TEM-1</sub> genes and the involvement of class 1 integrons mediated resistance in *Salmonella* and *Escherichia* spp. from the Eastern Cape, South Africa. Results suggest that integrons contribute significantly to antimicrobial resistance among the enteric gram-negative bacilli studied. Molecular genotyping of pathogens is fundamental to tracking disease-associated and drug-resistant strains in various populations.

Key words: ESBLs; *Salmonella*; resistance; phenotypes, genotypes, integrons

## 2.1. Introduction

Among the agents causing gastroenteritis, *Salmonella*, *Shigella* and *Escherichia coli* are important bacterial pathogens. *Salmonellae* are regarded as ubiquitous food-borne pathogens causing widely distributed infections with the consumption of especially raw and undercooked foods of animal origin, such as beef, poultry, milk, and eggs. *Salmonellae* can be differentiated by their somatic (O) antigens, composed of lipopolysaccharides, and the flagellar (H) antigens (Kaye, 1996). More than 2,500 *Salmonella* serotypes have been identified to date (WHO,

2005). Various species of *Salmonella* cause varying types of infectious diseases. While some are host-specific some have a broad range of hosts; *S. enterica* serovar Typhi is adapted to humans and does not occur in animals while non-typhoidal *Salmonella* serovars (NTS) have a broad vertebrate host range (Gordon, 2008). *S. enterica* serovar Typhimurium and *S. enterica* serovar Enteritidis are the most frequently isolated serovars from food-borne outbreaks throughout the world (Herikstad *et al.*, 2002) and are the two most important serotypes for salmonellosis transmitted from animals to humans. *Salmonella enterica* serovar Dublin is associated with cattle while *Salmonella enterica* serovar Choleraesuis is linked with pigs (WHO, 2005).

Salmonellosis affects a significant portion of human population causing approximately 2.16 million cases of infections and 216,000 deaths worldwide (Crump *et al.*, 2004; Boyle *et al.*, 2007). Public health concerns involving *Salmonella* include sporadic outbreaks of infections due to the pathogen even in the so called developed countries despite advanced technology and infection controls (Bisi-Johnson *et al.*, 2007). In the US, a recent outbreak of *Salmonella* in ready-to eat sausages linked to spices has been reported (Gifford, 2010). Salmonellosis manifests as diarrhoea, fever, and abdominal cramps between 12 and 72 hours after eating contaminated food. The illness which usually lasts 4–7 days and is self-limiting in most people may spread in vulnerable groups, such as infants, the elderly and immuno-compromised individuals beyond the intestine to the bloodstream and cause a more severe systemic disease.

*Escherichia coli* is recognized as both a normal intestinal flora with beneficial roles and a versatile human pathogen causing a wide range of infections including diarrhoeal diseases. Based on the strain and pathogenic mechanisms, different pathotypes of diarrheagenic *E. coli* are recognized. These include Enterotoxigenic *E. coli* (ETEC) which is a cause of traveler's diarrhea, Enterohemorrhagic *E. coli* (EHEC) which cause hemorrhagic colitis or hemolytic-uremic syndrome (HUS), Enteropathogenic *E. coli* (EPEC) which cause either a watery or bloody diarrhea, Enteroinvasive *E. coli* (EIEC) a cause of *Shigella*-like dysentery, while Enteroaggregative *E. coli* (EAaggEC) is often associated with persistent diarrhoea in children in developing countries. The main reason advanced by [Chatterjee et al. \(2009\)](#) for the occurrence of many of the strains of diarrheagenic *E. coli* in the developing nations is inadequate sanitary conditions. However, the most common enteropathogen in developing countries is ETEC. This pathotype is reported to account for approximately 210 million diarrhoea episodes and approximately 380,000 deaths ([WHO, 2008](#); [Gupta et al., 2008](#)).

Antibiotics are often not recommended in the treatment of enteritis. It is believed that antibiotics prolong the carrier state of enteritis due to *Salmonella*. Nevertheless, systemic *Salmonella* infections and infections in the vulnerable groups qualify for antibiotic therapy ([DuPont, 2003](#)). Fluoroquinolones are often the drug of choice in the treatment of gastrointestinal infections in humans. Resistance to fluoroquinolones has emerged worldwide during the last decade and is associated with increased illnesses and deaths ([Helms et al., 2004](#)).



Extended-spectrum cephalosporins are important for treating persons with severe *Salmonella* infections (Hohmann, 2001). The emergence of *Salmonella* isolates resistant to oxyiminocephalosporins has become a cause for concern due to the fact that cephalosporins are the alternatives to fluoroquinolones in children because of toxicity issues (Aarestrup *et al.*, 2005). The resistant mechanism involves the production of extended-spectrum  $\beta$ -lactamases (ESBLs).

ESBL's have traditionally been defined as transmissible beta-lactamases that can be inhibited by clavulanic acid, tazobactam or sulbactam. They are a group of enzymes that break down antibiotics belonging to the penicillin and cephalosporin groups and render them ineffective. The ESBL's are generally encoded by mobile genes that can be exchanged between bacteria. The first plasmid-mediated ampicillin-hydrolyzing beta-lactamase was described in a strain of *E. coli* by Datta and Kontomichalou (1965) in Greece soon after the broad-spectrum penicillin was introduced in the 1960's and was named TEM-1 after the patient, whose name was Temoniera from whom the *E. coli* strain was isolated. This was soon followed by another common plasmid-mediated  $\beta$ -lactamase SHV-1 (for sulphhydryl variable) found in *Klebsiella pneumoniae* and *E. coli*.

The first extended-spectrum beta-lactamase (ESBL), SHV-2; capable of hydrolyzing expanded-spectrum  $\beta$ -lactam antibiotics (third-generation cephalosporins) was found in an isolate of *Klebsiella ozaenae* (Kliebe *et al.*, 1985). These enzymes have spread over various regions of the world, across

members of *Enterobacteriaceae* with almost 200 different types identified to date (Bradford, 2001). Other ESBLs are the CTX-M, VEB, PER, GES, OXA groups and the inducible chromosomal class C (AmpC) betalactamases. AmpC beta-lactamases which emerged in *Enterobacter* spp. have also migrated from chromosomal locations to plasmids and are spreading into *E. coli* and *Klebsiella* spp. Hence, it is pertinent to investigate the mechanisms of antibiotic resistance which is one of the arsenals of pathogenicity in enteric pathogens. This study was embarked upon to identify and characterize the array of ESBLs involved in drug resistance in clinical isolates of *E. coli* and *Salmonella* spp.

## 2.2. Materials and methods

### 2.2.1. Data collection and ethical approval

Written informed consents were obtained from all patients, parents or guardians as the case may be and questionnaires were administered by trained volunteer health care workers (appendices 1A-1D). The study protocol and data handling were approved by the WSU ethics committee (Protocol No. 0003/08) as well as the Department of Health, Eastern Cape, South Africa.

### 2.2.2 Bacterial isolates

One hundred and nineteen *Salmonella* spp and 90 *Escherichia coli* isolated from clinical specimens of patients attending the Nelson Mandela Academic Hospital Complex, a tertiary hospital in the Eastern Cape Province, South Africa and satellite clinics were characterized by standard microbiological procedures. Minimum inhibitory concentrations (MICs) of standard antibiotics were determined with an automated antimicrobial susceptibility system according to the manufacturer's instructions (Autoscan-4 antimicrobial susceptibility system; Siemens). Comprehensive antibiograms were determined for the isolates, using a customized antimicrobial panel of 24 antibiotics (Gram Negative combo panel NUC 45). The interpretation of susceptibility was according to the Clinical and Laboratory Standards institute (CLSI) standards for broth microdilution methods (CLSI, 2007).

### 2.2.3. Identification and characterization of resistance genes

Polymerase chain reaction (PCR) was used to confirm the presence of antibiotic resistance genes in the *E. coli* and *Salmonella* species. Testing for extended-spectrum cephalosporin-resistance mechanisms included susceptibility testing of additional  $\beta$ -lactams, such as ceftazidime and cefotaxime, and molecular characterization of  $\beta$ -lactamases and  $\beta$ -lactamase genes. Isolates were examined for the presence of ESBL enzyme  $bla_{TEM}$ ,  $bla_{SHV}$ ,  $bla_{CMY-2}$  and  $bla_{CTX-M}$

types (Arlet and Philippon, 1991; Gallego *et al.*, 1990; Gazouli *et al.*, 1988) as well as the involvement of class 1 integron *int1* genes.

#### 2.2.4. DNA extraction and primer synthesis

DNA template for PCR was obtained from pure overnight bacterial culture using Fungal/Bacterial DNA extraction kit<sup>TM</sup> (Zymo Research) following manufacturer's instructions. Eluted DNA verification and concentration measurements were carried out using NanoDrop 2000 spectrophotometer (Thermo Scientific). All primers used in amplification and sequencing reactions were synthesized by Inqaba biotechnology Industries Pty. Ltd., Pretoria, South Africa.

#### 2.2.5. DNA amplification

PCR amplifications were performed in a final volume of 25  $\mu$ L containing: 0.5 to 2  $\mu$ L of DNA template depending on concentration, 8.5 to 10  $\mu$ L of Nuclease free water, 1  $\mu$ L of each primer and 12.5  $\mu$ L Master mix (EconoTaq Green, Fermentas). Amplifications were carried out in a GeneAmp PCR System 9700 Thermocycler (Applied Biosystems). The PCR conditions were 94°C for 5 min followed by 40 cycles of: 94°C for 30 s, 59°C for 1 min, 72°C for 1 min and final 72°C for 7 min for the ESBL primer sets used and 94°C for 5 min followed by 30 cycles of: 94°C for 1 min, 55°C for 1 min, 72°C for 1 min and final 72°C for 7 min for the integron (*int1*) gene. Table 2.1 shows the primers for the target genes. Amplification products were separated by electrophoreses on 2 % agarose gel (TopVision TM, Fermentas) in 1X TBE Buffer and ethidium bromide

(5  $\mu$ L) with a 100-bp ladder (Fermentas) as molecular weight marker. Agarose gels were visualized under UV illumination (TFM-26 Ultraviolet Transilluminator, UVP, Upland, CA) and the images were captured using a digital gel documentation system (DigiDoc-It imaging system, UVP, Upland, CA).

#### 2.2.6. Sequencing reaction

PCR products were sequenced using an Applied Biosystems 3500xL Genetic analyzer (AB Biosystems). Prior to PCR products sequencing, the unincorporated dNTPs were dephosphorylated with a commercial kit from Zymo Research Corporation (Orange, CA). Subsequently, the PCR products were sequenced with the ABI PRISM BigDye terminator cycle sequencing ready reaction kit (AB Biosystems) using the same primers as employed in the PCR reactions. The products were then subjected to the following conditions: 94°C for 2 min, followed by 40 cycles of denaturation at 85°C for 1 s, annealing at 53°C for 10 s and extension at 60°C for 2 min 30 s, with a final extension at 4°C for 0 s.

Table 2.1. Primer sets for ESBLs and class I integron and the PCR conditions.

Target gene	Primer	Nucleotide Sequence (5'- 3')	Amplicon size (bp)	References
bla <sub>CMY-2</sub>	Amp3 (F)	ATGATGAAAAATCGTTATG	1,145	<a href="#">Pitout <i>et al.</i>, 1988</a>
	Amp2 (R)	CTGC TTATTGCAGCTTTTCAAGAA TGCGCCA		
bla <sub>CTX-M</sub>	CTX-MA	CGCTTTGCGATGTGCAG	550	<a href="#">Bell <i>et al.</i>, 2002</a>
	CTX-MB	ACCGCGATATCGTTGGT		

bla <sub>SHV</sub>	SHV-1 (F)	ATGCGTTATATTCGCCTGTG	846	<a href="#">Fey et al.,2000</a>
	SHV-3 (R)	GTTAGCGTTGCCAGTGCTCG		
bla <sub>TEM</sub>	TEM-1 (F)	ATGAGTATTCAACATTTCCG TG	840	<a href="#">Fey et al., 2000</a>
	TEM-4 (R)	TTACCAATGCTTAATCAGTG AG		
<i>int11</i>	INT1F	AAGGATCGGGCCTTGATGTT	471	<a href="#">Pongpech et al., 2008</a>
	INT1R	AGCGCATCAAGCGGTGAGC		

The sequencing reaction products were cleaned up using ZR-96 DNA sequencing clean-up kit<sup>TM</sup>. Thereafter, the ultra-pure products were analyzed on the sequencing machine. Sequences were aligned with known ESBL and integron sequences by a blast search of the National Center for Biotechnology Information (NCBI) data base ([www.ncbi.nlm.nih.gov/BLAST/](http://www.ncbi.nlm.nih.gov/BLAST/)) using Staden package version 1.6.0-beta4 (MRC.WTSI) and comparison and confirmation were also done with known ESBLs ([www.lahey.org/studies/](http://www.lahey.org/studies/)) compiled by [Jacoby and Bush \(n.d\)](#).

#### 2.2.7. Statistical analysis

Patients' data were analyzed using Microsoft Excel version 2003. Continuous variables were summarized as mean and standard deviation (SD). Demographic information was obtained from subjects using questionnaire.

### 2.3. Results

#### 2.3.1. Demographic features

Our subjects were predominated by male patients 165/315 (52.4%) and no age group was excluded, with the youngest patient being 3 months and the oldest 91 years. The median age  $\pm$  IQR equals  $36 \pm 22$  years where IQR (inter-quartile range) is a measure of the dispersion or how widespread out the values are. In all, there were 55 (17.5%) pediatrics patients. Information obtained from the questionnaires administered indicated that a sizeable number of our subjects depended on domestic and drinking water from unwholesome sources like rivers and streams. Prior to the clinic visit, 13 persons with diarrhea (4.1%) took some form of medicine. Three of the instances were complementary therapy with an instance of antimicrobial active against enteric gram-negative rods (GNRs) and the remaining 10 instances involved the use of concoction of medicinal plants. Most of the persons who took medicinal plants were HIV positive.

### 2.3.2. Characterization and antibiogram of isolates

Various serovars of *Salmonella* were identified with *S. enterica* serovar Typhi being the highest followed by *S. enterica* serovar Typhimurium. Resistance to 5 or more CLSI antibiotics subclasses was detected in 59/119 (49.6 %) of the *Salmonella* isolates and 18/90 (20 %) of *E. coli*. Eighty-seven (73.1 %) of the *Salmonella* isolates mostly *S. enterica* serovar Typhi were invasive strains. *Salmonella* isolates were resistant to amoxicillin, ampicillin, aztreonam, piperacillin/tazobactam, trimethoprim/ sulfamethoxazole and tetracycline with reduced susceptibility to ciprofloxacin. *E. coli* strains were also identified and showed resistance mostly to ampicillin, ampicillin/sulbactam, cephalothin,

trimethoprim/sulfamethoxazole and tetracycline. No quinolone, carbapenem or gentamicin resistant strain was found among the *E. coli* isolates. Eight out of ten *Salmonella* isolates which were resistant to the quinolone of choice (ciprofloxacin) besides being resistant to the second and third generation cephalosporins tested also exhibited resistance or intermediate resistance to at least 2 or all 3 carbapenems (ertapenem, imipenem and meropenem) drugs tested. Extended spectrum cephalosporins resistant phenotype was exhibited by 25/119 (21.0 %) of the *Salmonella* spp.

### 2.3.3. Detection of genes mediating ESBL resistance

PCR characterization and sequencing showed that the  $\beta$ -lactam resistance was mediated majorly by  $bla_{TEM}$  with the involvement of class 1 integron gene, *intI1*.  $\beta$ -lactam genes  $bla_{CMY-2}$  and  $bla_{SHV}$  were also expressed but in lower percentages. Of the 119 *Salmonella* isolates, 61 (51.2 %) were ESBL positive by genotypic determination. A total of 54 (88.5 %) and 9 (15.7 %) of the 61 isolates were TEM and CMY-2 (Amp-C) ESBL producers, respectively. Nine (11 %) isolates were positive for both  $bla_{CMY-2}$  and  $bla_{TEM}$  while only one was positive for  $bla_{CTX-M}$  genes. Of the 61 *Salmonella* isolates with one or more  $\beta$ -lactams, 45 (73.8 %) were *S. enterica* serovar Typhi; 9 (14.7 %) were *S. enterica* serovar Typhimurium; and 2 (3.3 %) were *S. enterica* serovar Isangi. Out of the 90 *Escherichia* isolates, 19 (21.1 %) were ESBL positive by genotypic determination, 13 (68.4 %), 9 (47.4 %) and 2 (10.5 %) of the 19 ESBL positive *E. coli* isolates were  $bla_{SHV}$ ,  $bla_{TEM}$  and  $bla_{CTX-M}$  genes respectively. Class I



integron genes were expressed in 83 (39.7 %) of all the isolates, 64 (77.1 %) of these were *Salmonella* spp. while 19 (22.9 %) were *E. coli*. Representative positive samples are shown in [Figures 2.1a](#) and [2.1b](#). The alignment and blast search results of representative sequenced products showed in most cases 100% correlation confirming the identity of our isolates, the ESBLs and the integron genes involved in the resistance mechanisms. Among the 4 representative isolates, sequencing for the specific bla<sub>TEM</sub> genes type revealed the presence of one bla<sub>TEM-20</sub>, two were bla<sub>TEM-1</sub> and the fourth was bla<sub>TEM-4</sub> gene. The SHV genes were of the bla<sub>SHV-1</sub> type found only in the *Escherichia* spp while the Amp-C was confirmed as bla<sub>CMY-2</sub>. The designations of the enzymes were as confirmed (<http://www.lahey.org/studies/webt.htm>). [Figure 2.2](#) shows the results of the blast search of the integron genes among the *Salmonella* isolates. The phylogenetic correlations of the integron gene sequences revealed a monophyletic clustering ([Figure 2.3](#)).

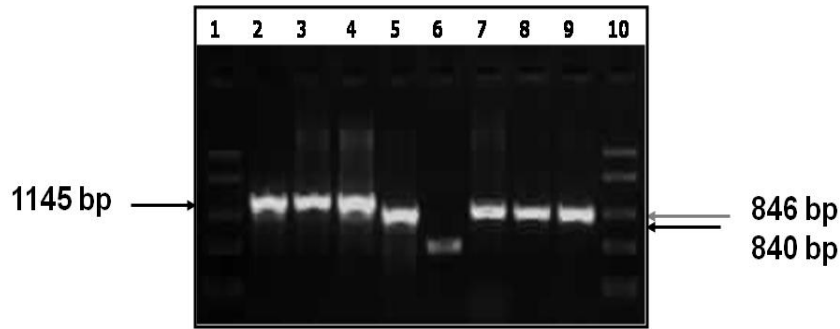


Figure 2.1A

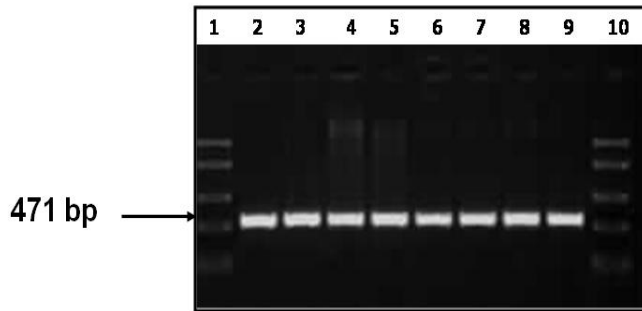


Figure 2.1B

Figure 2.1. PCR products analysis of the genomic DNA from selected *E. coli* and *Salmonella* isolates. Figure 2.1A: 100 bp molecular weight marker (lanes 1 and 10), fragment from *bla*<sub>CMY-2</sub> (lanes 2 to 4), *bla*<sub>SHV</sub> (lanes 5) and *bla*<sub>TEM</sub> (lanes 7 to 9). Figure 2.1B: 100 bp molecular weight marker (lanes 1 and 8) *Int1* (lanes 2 to 9). The relative positions in the gel of predicted size of PCR products are indicated by arrowheads on the right sides.

```

0016641.1 | XALWLP EILAPILREQLIRARAWLKDQAEORIOVALPDALERKYPRAOHWPWFVFAQHTHITOPRIGVRRHHMYDQTFQRAFKRAVEQAGITKPATPHT..LRHIFATALLRIOYDIRTVQDQLLQ...HIDVITTWIYTHVLKV
BIT | .....
21NT | .....
41NT | .....H.OTANFQHM.VNHRR.RDV.MAEQI.HQINVVTAEEQ.R.....RERVAEGV.C.QL.DACLFOYQ.EQ.L.QL.IHVMA.HDTA.WIORM.VLRKNPEP.P.PP.....ARG.....
46NT | .....
66NT | .....H.OTANFQHM.VNHRR.RDV.MAEQI.HQINVVTAEEQ.R.....RERVAEGV.C.QL.DACLFOYQ.EQ.L.QL.IHVMA.HDTA.WIORM.VLRKNPEP.P.MPOARILAAQ.RREAQRRCOPRPOIATMP.
86_INT | .....H.OTANFQHM.VNHRR.RDV.MAEQI.HQINVVTAEEQ.R.....RERVAEGV.C.QL.DACLXYO.EQ.L.QL.IHVMA.HDTA.WIORM.VLRKNPEP.P.MPOARILP.K..VQRNAAAALQLVLQPPC
169NT | .....X.....

```

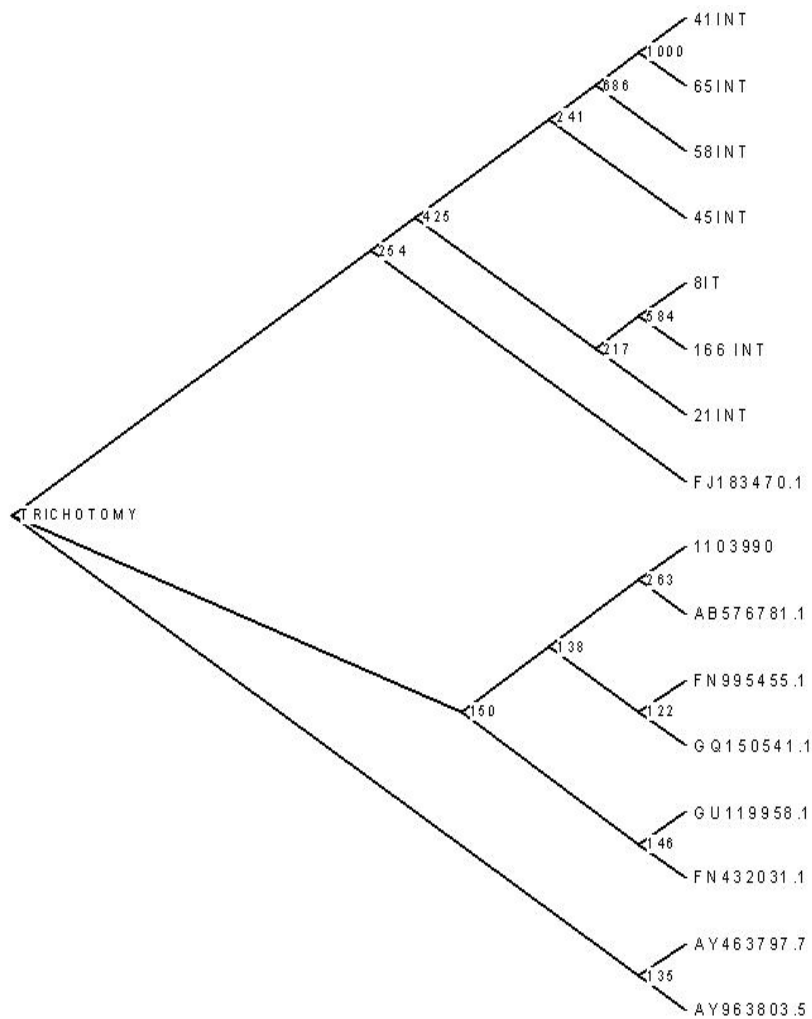
  

```

0016641.1 | QGAVR.....
BIT | .....
21NT | .....
41NT | .....
46NT | .....
66NT | HATAA.AQWVPIIRVT
86_INT | PCTRQLLAQA.....
169NT | .....P.LQC.....

```

**Figure 2.2.** Blast search result for the sequenced integron genes from selected *Salmonella* isolates.



**Figure 2.3.** A neighbour-joining phylogenetic relationship of the class 1 integron genes isolated from *Salmonella* spp.

#### 2.4. Discussion

The emergence of ESBL producing isolates has become a task which requires drastic interventions. Bacteria strains exhibiting ESBLs are often resistant to a wide variety of commonly used antibiotics. These isolates often are

not phenotypically resistant according to CLSI guidelines with the consequential avoidable treatment failures in patients who received inappropriate antibiotic therapy (Karas *et al.*, 1996; Paterson *et al.*, 1998). For this reason, ESBL producing organisms are to be reported as resistant to all extended-spectrum  $\beta$ -lactam antibiotics with the exception of the cephamycins (NCCLS, 2000; Manickam and Alfa, 2008). Apart from ESBLs, plasmid-mediated AmpC beta-lactamases are also typically associated with broad multidrug resistance (Thompson, 2001). The high frequency of resistance to drugs such as ampicillin, tetracycline and trimethoprim/sulfamethoxazole were not unexpected since, these are some of the oldest drugs used in infectious disease, and some level of resistance would have emerged over time (Salyers and Whitt, 2005).

Often time, clinically relevant ESBL-mediated resistance goes undetected in routine susceptibility tests. Molecular methods, particularly PCR have become widely used techniques for the determination and confirmation of ESBL genes. Our study investigated clinical isolates of *Salmonella* and *E. coli* for the presence of *bla*<sub>ampC</sub>, *bla*<sub>CTX-M</sub>, *bla*<sub>SHV</sub>, *bla*<sub>TEM</sub> and class 1 integron (*intI1*) by monoplex PCR. This study found that the percentage of ESBL detected phenotypically were only 21.0 % and 5.5 % for *Salmonella* and *E. coli* respectively, while the percentage detected genotypically were 51.2 % and 21.1 % respectively. AmpC type enzyme was expressed by 11 % of our isolates while *bla*<sub>SHV</sub> and *bla*<sub>TEM</sub> were noted in 6.2 % and 33.4 % of isolates, respectively. The joint occurrence of AmpC-type enzyme and ESBL in the same strain can mask the expression of ESBL (Bradford

*et al.*, 1997; Moland *et al.*, 2006). This is due to the fact that the AmpC-type beta-lactamase will not be inhibited by clavulanic acid, thus giving high MICs to both the single antimicrobial agent and the clavulanic acid combination. The result of this is that phenotypic confirmatory test may be falsely negative leading to inability to confirm the presence of ESBLs (Moland *et al.*, 2006). In a previous study conducted in South Africa, 15.6% isolates produced SHV or TEM and 1.9% produced CMY-2 ESBLs (Kruger *et al.*, 2004). Comparing this previous study with our results, an increase in the spread or expression of ESBL genes was noted, particularly the TEM and AmpC, also while the previous study failed to identify *bla*<sub>CTX-M</sub> our study observed the expression of this gene in a *Salmonella* isolate identified to be *S. choleraesuis* and 2 *E. coli* isolates. Paterson *et al.* (2003) had shown the significance of *bla*<sub>CTX-M</sub> ESBL type in *Klebsiella pneumoniae* isolates. CTX-M enzymes which predominantly hydrolyze cefotaxime over ceftazidime are reportedly increasing in recent years. Furthermore, more resistance was observed in the *Salmonella* isolates than in the *E. coli* isolates. At the onset, the recognition of  $\beta$ -lactamases conferring resistance to the extended-spectrum cephalosporins, were particularly with resistances among *Klebsiella* species and *Escherichia coli* strains, but other species of the family *Enterobacteriaceae* now also express ESBLs activities (Goldstein *et al.*, 1993; Cheng and Chen. 1994; Mariotte *et al.*, 1994; Philippon *et al.*, 1994; Morosini *et al.*, 1995). The spread of ESBL's genes have been reported to either be via epidemic bacterial strains or by plasmid dissemination between unrelated strains (Ben-Hamouda *et al.*, 2004).

Carbapenems are the drugs of choice against AmpC beta-lactamase producing bacteria (Jones, 2003; Jones and Varnam, 2002).

*Int1* genes were expressed in 83 (39.7 %) of all the isolates, 64 (77.1 %) of these were *Salmonella* spp. while 19 (22.9 %) were *E. coli*. There were simultaneous occurrence of *bla*<sub>TEM</sub>, *bla*<sub>SHV</sub> and class 1 integron in a few isolates. It was also noted that the expression of *bla*<sub>TEM</sub> and class 1 integron (*int11*) seem to co-occur in most positive isolates. Integrons are known to play a vital role in the resistance mechanisms of many pathogens. These mobile gene cassettes are carriers of one or more resistance genes and are inserted into various arrangements between 2 conserved DNA regions, generating various antimicrobial resistance genes (Levesque *et al.*, 1995). As with other mobile DNA elements, integrons assist in the rapid dispersion of resistance genes within bacterial species and between different species (Levesque *et al.*, 1995; Hall, 1997). We may hence attribute a significant role to these genes in the spread and increasing multidrug resistance isolates in our setting.

## 2.5. Conclusion

The study showed more resistance in *Salmonella* isolates than *E. coli*. The increasing rates of multi-drug resistant strains and particularly the emerging resistance to penem drugs are regrettably leading gradually to fewer options of effective antimicrobials, especially for the treatment of infants and very small children. It is pertinent to increase awareness of clinical laboratories to isolates that exhibit ESBL phenotypes and make adequate diagnostic facilities available.

This may be a serious challenge particularly in the setting of this study where like in other sub-Saharan African countries, such resources are scarce. Molecular genotyping of pathogens is fundamental to tracking disease-associated and drug-resistant strains in various populations.

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## CHAPTER 3

### MOLECULAR BASIS OF VIRULENCE IN CLINICAL ISOLATES OF *ESCHERICHIA COLI* AND *SALMONELLA SPECIES* FROM A TERTIARY HOSPITAL IN THE EASTERN CAPE, SOUTH AFRICA

#### 3.0. Abstract

This study investigated the virulence factors of *Escherichia coli* and *Salmonella* species in clinical specimens from patients with diarrhoea presenting to health care centres in Oliver R. Tambo District Municipality, Eastern Cape Province, Republic of South Africa by the use of cultural and molecular techniques. Out of a total of 315 samples screened, *Salmonella* isolates were obtained in 119 (37.8%) of cases and these comprised: *S. typhi* (52%), *S. typhimurium* (25%), *S. isangi* (8%), *S. choleraesuis* (6%), *S. enteritidis* (4%), *S. eppendorf* (1%), *S. hadar* (1%), *S. panama* (1%), and untyped *Salmonella* spp. (2%). Using molecular diagnostic methods, diarrheagenic *E. coli* were detected in 90 cases (28.6%): the greater proportion of this were enteroaggregative *E. coli* (EAEC) 37 (41.1%), enteropathogenic *E. coli* (EPEC) 21 (23.3%) and enterohemorrhagic *E. coli* (EHEC) 21 (23.3%). The virulence factors identified in the *Salmonella* strains were 105 (88.2%) *inv*, 15 (12.6%) *flic*, and 2 (1.7%) *sef* genes. The amino acid identity of the representative genes matched 95 to 100% with corresponding blast searched sequence. This study underlines the importance of understanding the virulence composition and diversity of

pathogens for enhanced clinico-epidemiological monitoring and health care delivery.

Key: *Escherichia coli*; *Salmonella*; virulence; genes; diarrhoea.

### 3.1. Introduction

Gastrointestinal infections due to pathogenic *Enterobacteriaceae* in particular *Escherichia* and *Salmonella* species are significant causes of morbidity and mortality worldwide. These infections which usually are self-limiting may be fatal in hosts with debilitating immune systems (Amar *et al.*, 2007). The fatality of infections due to these enteric pathogens depends on their serotypes, the size of the inoculum, and the status of the host (Gordon, 2008). *Escherichia* and *Salmonella* species were reported to have diverged from a common ancestor based on the evolutionary rate estimates from 5S and 16S rRNA sequence analyses while *Shigella* spp. are considered clonal lineages of *Escherichia coli* (Falkow, 1995). *Salmonella* species are mainly pathogenic, with differing host ranges; *S. enterica* serovar Typhi is adapted to humans and does not occur in animals while non-typhoidal *Salmonella* serovars (NTS) have a broad vertebrate host range (Gordon, 2008). Even though *E. coli* is generally known as commensal normal flora of the gut, some *E. coli* strains are the causative agents of neonatal meningitis, urinary tract infections, bacteremia, and infectious diarrhoea.

The major distinguishing factor between pathogenic and non-pathogenic strains of *E. coli* strains is the occurrence of virulence genes, which code for the various known strategies for pathogenicity. Analysis have shown that pathogenic *E. coli* strains from diarrhoea cases and those involved in urinary tract infections are more of a distinct subsets of *E. coli*, rather than a reflection of the random faecal flora ([Selander and Musser, 1990](#)). Some of the virulence factors of *E. coli* include ability to adhere, colonize, and invade the hosts' cells. Further to these are the secretion systems, production of cell surface molecules, transport and siderophore formation ([Finlay and Falkow, 1997](#)). According to [Kaper et al. \(2004\)](#), *E. coli* has been categorized based on the type of virulence factors present and host clinical symptoms basically into the following pathotypes: enteropathogenic *E. coli* (EPEC); enterohemorrhagic *E. coli* (EHEC); enterotoxigenic *E. coli* (ETEC); enteroaggregative *E. coli* (EAEC) and diffusely adherent *E. coli* (DAEC), a subclass of enteroaggregative *E. coli*; enteroinvasive *E. coli* (EIEC); uropathogenic *E. coli* (UPEC) and neonatal meningitis *E. coli* (NMEC).

The ability of the enteric pathogen to invade and penetrate intestinal epithelial cells is required in salmonellosis whether it is confined as the intestinal form or progresses to systemic involvement ([Altier, 2005](#)). The attribute to direct their internalization by the epithelial cells which are not normally phagocytic is a striking Salmonella-host cell interaction. According to [Galan and Curtiss \(1989\)](#) this remarkable phenotype known as invasion allowed for identification and

characterization of invasion genes. The key mechanism involves type III secretion systems which are encoded by pathogenicity island 1 (SPI-1) (McCormick, 2004). *Salmonella* also possess the ability to alter phagocytosis in order to circumvent the process. *S. enterica serovar* Typhimurium is known to delay significantly the fusion of the phagosome to the lysosome (Buchmeier and Heffron, 1991); thereby hibernating in phagocytic cells and hence adapt to resist the antimicrobial activity of the fused phagolysosome (Pizzaro-Cerda *et al.*, 1997). Bacterial survival in phagocytic cells has been observed as an alternate to invasion in accessing privileged sites in hosts. Rescigno *et al.* (2001) postulated that CD18+ expressing phagocytes are alternate route and these cells have been observed by Vasquez-Torres *et al.* (1999) as vehicles for reaching the spleen in an invasion-independent manner by *S. enterica serovar* Typhimurium.

Molecular analysis is known to give a better picture of epidemiology of infectious diseases. Studies have demonstrated the sensitivities of molecular-based methods to be greater compared to current conventional methods of analysis (Amar *et al.*, 2007). Molecular studies have led to the understanding of the genomic make-up of bacteria which generally consist of stable regions and variable regions, the flexible part that is composed of bacteriophages, plasmids, transposons as well as unstable large regions, called genomic islands. The so-called genomic islands are a gene pool required for encoding virulence factors of pathogenic bacteria and these have been designated "pathogenicity islands" (Hacker *et al.*, 2003). The concept of pathogenicity islands (Pais) was first



identified through the genetic and molecular analysis of virulence genes in uropathogenic *E. coli* and EPEC (Blum *et al.*, 1994; Morschhauser *et al.*, 1994). Pairs which are specific regions of chromosomal DNA have been described in more than 30 bacterial species (Hacker *et al.*, 2003). It is a well known concept that bacterial pathogenicity is an organized multifactorial process involving numerous chromosomal and extrachromosomal genes directed by complex regulatory circuits (Mahan *et al.*, 1996; Mellata *et al.*, 2010).

There are various shared genetic strategies for pathogenicity in enteric bacilli. Type III secretion is dedicated secretion machinery whose components are coded for by numerous homologous gene sequences shared by enteric pathogens (Falkow, 1995; Galán and Wolf-Watz, 2006). Nevertheless, there has been understanding that the similarities between EPEC virulence attributes and *Salmonella* invasion genes are more than homologous genes associated with secretion (Collazo *et al.*, 1995). Most virulence factors of pathogenic *E. coli*, *Shigella*, and *Salmonella* strains are plasmid-borne however; one or more of the essential virulence determinants are borne on an extrachromosomal element (Galan and Collmer, 1999; Madden *et al.*, 2001; Naum *et al.*, 2009). In both *E. coli* and *Salmonella* spp fimbriae might play a role in adhesion and invasion (Townsend *et al.*, 2001; Guo *et al.*, 2007). The curli fimbriae of these strains were proven to bind to several tissue-matrix proteins as well as plasminogen and its activator t-PA (Falkow, 1995).

Bacteria are emerging with new means of circumventing human efforts at curbing their nefarious schemes and various evolution patterns and innovations are certainly put in place by these pathogens. A myriad combination of virulence genes against indiscriminate genetic transfer and recombination are required for a successful emergence of pathogen (Musser, 1996; Bansal, 2008). Profiling the expression of these genes will give impetus to understanding the mechanisms by which enteric bacterial pathogens colonize, spread and at times persist in the hosts (Gonzalez-Escobedo *et al.*, 2011). This study investigated the genetic determinants of virulence in *E. coli* and *Salmonella* spp. which are significant pathogens involved in enteric diseases.

## 3.2. Materials and Methods

### 3.2.1. Specimens' collection and bacterial isolation

*Salmonella* isolates deposited at the National Institute of Communicable Diseases (NICD), Johannesburg under the surveillance study of 2005 to 2008 from this tertiary health facility were obtained. For 2009, One hundred and twenty-five fresh stool samples obtained from patients presenting with acute diarrhoea in the tertiary referral facility and surrounding clinics and 75 apparently healthy school pupils in three different schools within OR Tambo District Municipality, Eastern Cape Province, South Africa were collected in sterile stool jars or rectal swabs placed in Cary-Blair transport medium and transported on ice pack to the laboratory where analyses were done within 24 hours. Where this was not possible specimen were kept frozen. Written

informed consents were obtained from all patients, parents or guardians as the case may be and a questionnaire was administered by trained volunteer health care workers ([appendices 1A-1D](#)). The study protocol and data handling were approved by the WSU ethics committee (Protocol No. 0003/08) as well as the Department of Health, Eastern Cape, South Africa.

### 3.2.2. Bacteriological analyses

**NICD Isolates:** Bacteriological analyses of the specimens for the presence of *E. coli* and *Salmonella* using standard conventional methods and commercial anti-sera (BiowebSA), were carried out at the National Health Laboratory Services, Nelson Mandela Academic Hospital, Mthatha prior to banking at NICD from where isolates were collected for this study.

***E. coli:*** The faecal samples were cultivated on MacConkey agar. After overnight incubation at 37°C, lactose fermenting colonies (LFC) with the typical appearance of *E. coli* were selected for further analysis. Isolates were identified by biochemical assays using Microscan Gram negative combo panel NUC 45 (Siemens/ Dade Behring).

***Salmonella:*** Specimens were cultivated for the isolation of *Salmonella* species on MacConkey agar. After 24 h of incubation at 37°C, suspected colonies with typical characteristics of *Salmonella* were sub-cultured on XLD (xylose lysine deoxycholate) agar for 24 h at 37°C. Confirmation was carried out using Microscan Gram negative combo panel NUC 45 (Siemens/ Dade Behring).

### 3.2.3. DNA extraction

DNA template for PCR was obtained from pure overnight bacterial culture using Fungal/Bacterial DNA extraction kit<sup>TM</sup> (Zymo Research) and following manufacturer's instructions. The concentration of the eluted DNA was measured using NanoDrop 2000 spectrophotometer (Thermo Scientific).

### 3.2.4. DNA amplification

PCR amplifications were performed in a final volume of 25  $\mu$ L containing: 0.5  $\mu$ L to 2  $\mu$ L of DNA template depending on concentration, 8.5 to 10  $\mu$ L of Nuclease free water, 1  $\mu$ L of each primer and 12.5  $\mu$ L Master mix (EconoTaq Green, Fermentas). Amplifications were carried out in a GeneAmp PCR System 9700 Thermocycler (Applied Biosystems). All oligonucleotide primers were synthesized by Inqaba Biotechnology (Pretoria, South Africa) and the sequences are as shown in [Table 3.1](#). The PCR cycling conditions for the *E. coli* strains consisted of 95°C for 5 min while for the *Salmonella* isolates consisted of 95°C for 1 min, which were followed by 40 cycles of denaturation at 95°C for 30 s, annealing at 60°C for 30 s, and elongation at 72°C for 30 s. Amplification products were separated by electrophoreses on 2 % agarose gel (TopVision TM, Fermentas) in 1X TBE Buffer and ethidium bromide (5  $\mu$ L) with a 100-bp ladder (Fermentas) as molecular weight marker.

### 3.2.5. Sequencing reaction

PCR products were sequenced using an Applied Biosystems 3500xL Genetic analyzer (AB Biosystems). Prior to PCR products sequencing, the unincorporated

Table 3.1. Primer sets for the pathotypes and virulence genes for the *E. coli* and *Salmonella* spp.

Isolate species/ subgroups	Target gene	Primer	Nucleotide Sequence (5'- 3')	Amplicon size (bp)	Reference
<i>E. coli</i>					
EPEC and EHEC	<i>eaeA</i>	EAE-a	ATGCTTAGTGCTGGTTTAGG	248	Wang <i>et al.</i> , 2002
		EAE-b	GCCTTCATCATTTGCTTTTC		
EHEC	<i>stx1</i>	JMS1-F JMS1-R	GTCACAGTAACAAACCGTAACA TCGTTGACTACTTCTTATCTGGA	95	Jothikumard and Griffiths 2002
ETEC	LT	LT-1	AGCAGGTTTCCCACCGGATCACCA	132	Ito <i>et al.</i> , 1992
		LT-2	GTGCTCAGATTCTGGGTCTC		
	ST	STa-F	GCTAATGTTGGCAATTTTTATTCT GTA	190	Franck <i>et al.</i> , 1998
		STa-R	AGGATTACAACAAAGTTCACAGCAG TAA		
EAEC	<i>aggR</i>	AggRks1	GTATACACAAAAGAAGGAAGC	254	Ratchtrachai <i>et al.</i> , 1997
		aggRkas2	ACAGAATCGTCAGCATCAGC		
	<i>astA</i>	EAST-1S	GCCATCAACACAGTATATCC	106	Yatsuyanagi <i>et al.</i> , 2002
		EAST-1AS	GAGTGACGGCTTTGTAGTCC		
EIEC	<i>VirA</i>	virA-F virA-R	CTGCATTCTGGCAATCTCTTCACA TGATGAGCTAACTTCGTAAGCCCTC C	215	Villalobo and Torres 1998
<i>Salmonella</i>					
	<i>invA</i>	invA 139 invA 141	GTGAAATTATCGCCACGTTGCGGCA A TCATCGCACCGTCAAAGGAACC	284	Rahn <i>et al.</i> , 1992
	<i>sefA</i>	S1 S4	GCC GTA CAC GAG CTT ATA GA ACC TAC AGG GGC ACA ATA AC	250	Soumet <i>et al.</i> , 1997
	<i>fliC</i>	Fli15 Typ04	CGG TGT TGC CCA GGT TGG TAA T	620	Joys 1985

			ACT GGT AAA GAT GGC T		
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KEY: *flic*-flagellin H1; *invA*-invasion; *sefA*- fimbrial antigen; *aggR*- transcriptional activator for EAEC aggregative adherence fimbria I expression; *eaeA*-*E. coli* attaching and effacing; *astA*-EAEC heat-stable enterotoxin; LT- heat-labile enterotoxin; ST- heat-stable enterotoxin; *VirA*-virulence plasmid.

dNTPs were dephosphorylated with a commercial kit from Zymo Research Corporation (Orange, CA). Subsequently, the PCR products were sequenced with the ABI PRISM BigDye terminator cycle sequencing ready reaction kit (AB Biosystems) using the same primers as employed in the PCR reactions. The products were then subjected to the following conditions: 94°C for 2 min, followed by 40 cycles of denaturation at 85°C for 1 s, annealing at 53°C for 10 s and extension at 60°C for 2 min 30 s, with a final extension at 4°C for 0 s. The sequencing reaction products were cleaned up using ZR-96 DNA sequencing clean-up kit™. Thereafter, the ultra-pure products were analyzed on the sequencing machine. Sequences were aligned with known *E. coli* and *Salmonella* virulence gene sequences by a blast search of the National Center for Biotechnology Information (NCBI) data base ([www.ncbi.nlm.nih.gov/BLAST/](http://www.ncbi.nlm.nih.gov/BLAST/)) using Staden package version 1.6.0-beta4 (MRC.WTSI).

### 3.3. Results

#### 3.3.1. Bacteriological identification and molecular analysis

Results showed that *Salmonella* spp. were isolated from 119 (37.8%) of cases while diarrheagenic *E. coli* was found in 90 (28.6%) of the cases. The distributions of the different pathotypes are as shown in Figures 3.1A and 3.1B. Of the *Salmonella* isolates, 87 (74.1%) were invasive. The most common virulence factor detected among the *Salmonella* strains was *invA* found in 105 *Salmonella* spp. while *fliC* and *sef* genes were detected in 15 and 2 *Salmonella* isolates respectively. The predominant virulence gene among the diarrheagenic *E. coli* was 24 EAEC heat-stable enterotoxin *astA* genes. Table 3.2 shows the distribution of the various genes among cases and controls.

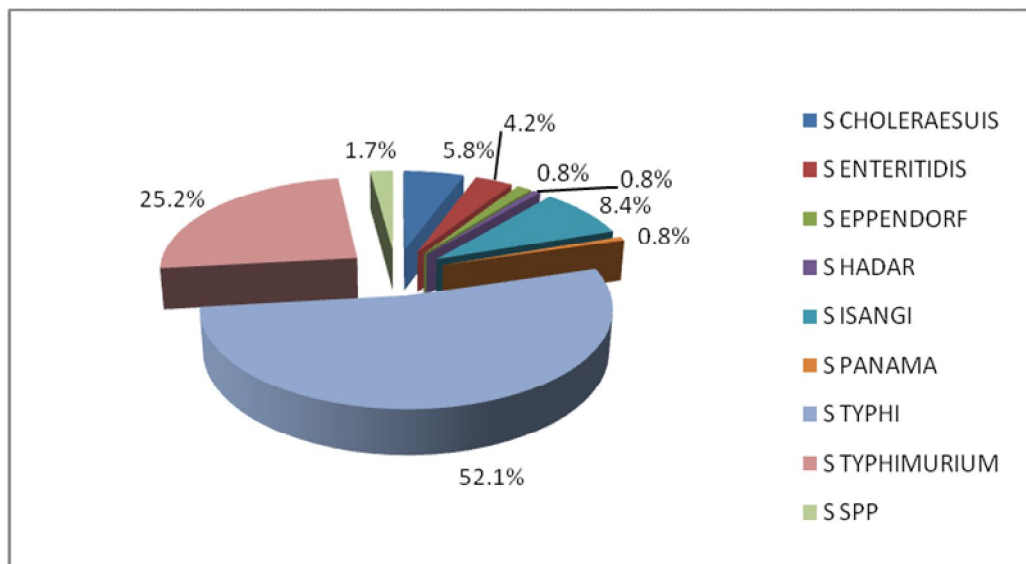


Figure 3.1A. Frequency of the various *Salmonella* isolates

Figure legend: S = *Salmonella*

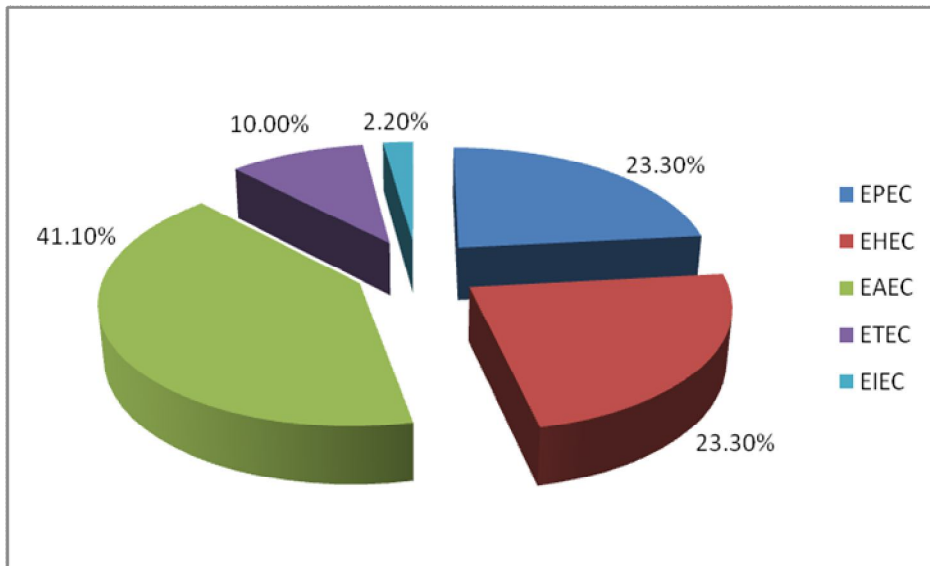


Figure 3.1B. Frequency of the diarrhoeagenic *E. coli* isolates

Figure legend: EPEC= Enteropathogenic *Escherichia coli*; EHEC= Enterohemorrhagic *E. coli*; EAEC= Enteroaggregative *E. coli*; Enterotoxigenic *E. coli*; EIEC= Enteroinvasive *E. coli*.

Table 3.2. Distribution of virulence genes among the *E. coli* and *Salmonella* spp.

Bacterial Strain	Number of isolate	Virulence genes								
		fliC	invA	sefA	aggR	eaeA	EAST	LT	ST	virA
<i>Salmonella</i> spp. (case)	119	15	105	0	ND	ND	ND	ND	ND	ND
<i>Salmonella</i> (control)	8	0	7	0	ND	ND	ND	ND	ND	ND
<i>E. coli</i> (case)	90	ND	ND	ND	13	21	24	5	0	2
<i>E. coli</i> (control)	85	ND	ND	ND	10	11	19	0	0	0

KEY: ND-Not determined.

The representative gels for PCR amplification of DNA extracted from selected *E. coli* and *Salmonella* isolates showing the presence of diverse virulence genes are indicated in [Figures 3.2A and 3.2B](#). One hundred and eighty



isolates were obtained from the 150 control subjects. *E. coli* was the predominant bacterial species being 85 (47.2%) while *Salmonella* spp. was 8 (12.1%). Other recovered bacteria species were *Proteus mirabilis* 45 (25.0%), *Klebsiella pneumoniae* 23 (12.8%) and *Enterobacter cloacae* 19 (10.5%). Sequencing analysis of the genes showed 95 to 100% conformation of the various virulence genes with corresponding blast search sequence and confirmed the strain.

#### 3.4. Discussion

Gastroenteritis is a major concern in sub-Saharan Africa as with other developing countries ([Mandeville et al., 2009](#)). South African National Burden of Disease study of the year 2000 found that diarrhoea accounted for nearly 3% of all deaths in South Africa ([Bradshaw et al., 2004](#)). According to the South African health review of 2007, death due to gastroenteritis among children was put at 15% ([Rispel et al., 2007](#)) showing increasing mortality. The developed countries are not spared in the global burden of enteric-related diarrhoea. Salmonellosis was considered a major public health problem in the United States ([Voetsch et al., 2004](#)). *E. coli* and *Salmonella* are among the bacterial pathogens implicated in gastroenteritis. These enteric pathogens have evolved different strategies for subverting normal host cellular functions ([Galán and Sansonetti, 1996](#)).

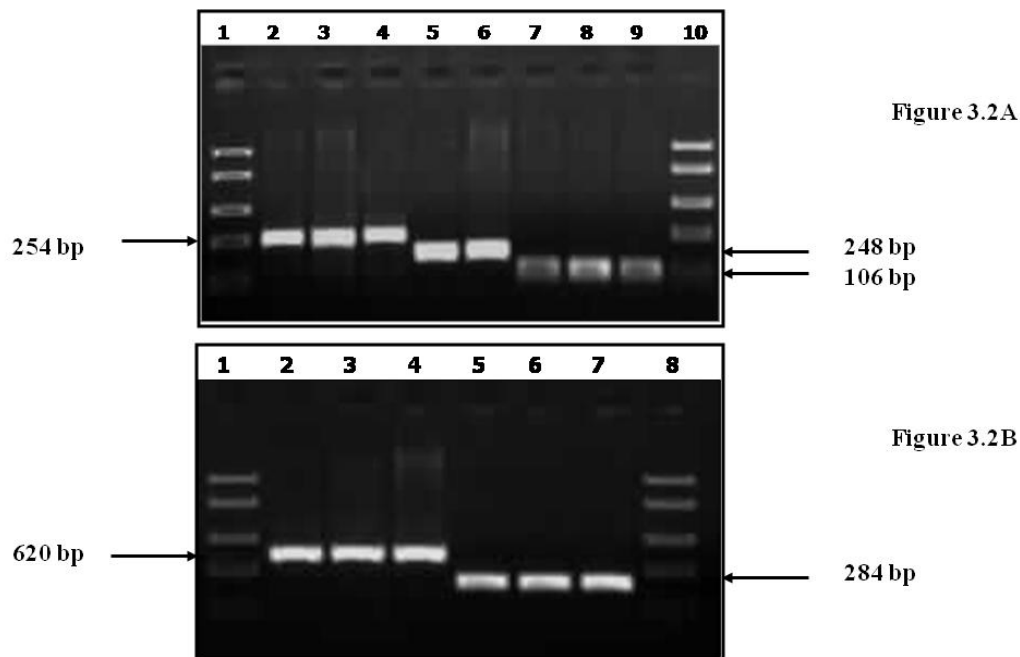


Figure 3.2. Representative gels for PCR amplification of DNA extracted from selected *E. coli* and *Salmonella* isolates showing the presence of diverse virulence genes. Figure 3.2A: 100 bp molecular weight marker (lanes 1 and 10), fragment from *aggR* (lanes 2 to 4), *eeA* (lanes 5 to 6) and *astA* (lanes 7 to 9). Figure 3.2B: 100 bp molecular weight marker (lanes 1 and 8) *fliC* (lanes 2 to 4) and *invA* (lanes 5 to 7). The relative positions in the gel of predicted size of PCR products are indicated by arrowheads on the right sides.

These pathogens cause various intestinal and extraintestinal diseases by means of virulence factors that affect a wide range of cellular processes. These virulence induced infections usually involve complex mechanisms with various specific, interdependent interactions between hosts and pathogens (Tang and Holden, 1999). The present study provides information on the pathotypes and some virulence factors associated with local isolates of *E. coli* and *Salmonella* species. *E. coli* is more than just a harmless intestinal microflora; it can also be a highly versatile, and frequently deadly, pathogen (Kaper et al., 2004). *E. coli*

strains cause diarrhoea by several distinct pathogenic mechanisms and differ in their epidemiology. Virulence genes were expressed in diarrhoeogenic *E. coli* from both cases and controls. EAEC was detected in 37 (41.1%) cases involving diarrhoeogenic *E. coli*. Studies conducted in Thailand and Brazil, reported a frequency of 12% and 11% EAEC respectively among children with acute diarrhoea (Souza *et al.*, 2001; Ratchtrachenchai *et al.*, 2004). Although the prevalence of EAEC is believed to be considerably higher in the developing countries compared to industrially developed countries, a Switzerland study, reported that EAEC was encountered in a significant proportion of diarrhoea cases among children (Pabst *et al.*, 2003). As evident in this study and previous studies, EAEC seems to be endemic within our study population and other locations in sub-Saharan Africa (Geyid *et al.*, 1998; Okeke and Nataro, 2001; Okeke *et al.*, 2003), emerging as a significant diarrheal agent worldwide with the pattern of infection changing from persistent diarrhoea to include acute diarrhoea (Scaletsky *et al.*, 2002).

The second diarrheogenic *E. coli* type detected was EHEC constituting 21 (23.3%) of all diarrheogenic *E. coli*. Enterohaemorrhagic *E. coli* (EHEC) is a subset of Shiga toxin-producing *Escherichia coli* (STEC) which is associated with severe systemic disease as haemorrhagic colitis, haemolytic-uremic syndrome (HUS) and thrombotic thrombocytopenic purpura, particularly in infants, young children and in the elderly (Nataro and Kaper, 1998; Paton and Paton, 1998). EHEC infects the large bowel and inflict damage to the colon with infectious dose

estimated to be less than 100 CFU (Griffin and Miner, 1995; Mellies *et al.*, 2007). Of the various virulence factors associated with pathogenicity in the EHEC strain, this study failed to detect both Shiga toxin 1 (*stx1*) and Shiga toxin 2 (*stx2*) but only detected intimin which is encoded by the *eaeA* gene (Dean-Nystrom *et al.*, 1997; Kang *et al.*, 2004). Intimin is known to facilitate the adherence of pathogen to intestinal villi producing attaching and effacing lesions (Holland *et al.*, 1999; Caprioli *et al.*, 2005). Previous studies have implicated EHEC in outbreaks and sporadic infections both in the United States and around the world (Waters *et al.*, 1994; Bell *et al.*, 1994; Dundas *et al.*, 2001).

Intimin (*eaeA*) gene was also detected in 21 (23.3%) of EPEC. Unlike most studies where ETEC often take the lead in bacterial enteritis due to *E. coli*, a study by Weggerhof (1987) also reported a higher incidence of EPEC from the screening of some pediatric patients with diarrhoea in Mpumalanga Province of South Africa. Another study in 1990 in Iran reported EPEC as the most frequently detected strain of diarrhoeagenic *E. coli* (Katouli *et al.*, 1990). More recent studies described the contributions of EPEC to the human disease burden as significant (Kenny, 2002; Clarke *et al.*, 2003; Kaper *et al.*, 2004; Scaletsky *et al.*, 2010). Thus EPEC plays a vital role in acute diarrhoea. EPEC is known to cause illness manifesting as watery diarrhoea with little inflammation of the intestinal mucosa (Koneman *et al.*, 1997). Virulence is initiated in EPEC by the induction of a characteristic ultrastructural lesion in which the bacteria make intimate contact with the apical plasma membrane, causing localized destruction of the intestinal

brush border and distortion of the apical enterocyte membrane (Clarke *et al.*, 2003) as is in the classical attaching and effacing (AE) lesion.

The ETEC and EIEC strains were found only in 9 (10.0%) and 2 (2.2%) of cases with diarrheagenic *E. coli* respectively. Although ETEC strains have been described as a major contributor to infantile diarrhoea in developing countries and of travellers' diarrhoea in visitors to these countries (Ako-Nai *et al.*, 1990; Sooka *et al.*, 2004; WHO, 2009a), our findings were different showing a decline in the involvement of these strains in our setting. ETEC strains cause secretory diarrhoea similar to that of *Vibrio cholerae* by forming plasmid encoded heat-labile (LT) or heat-stable (ST) enterotoxins genes (Levine, 1987; Koneman *et al.*, 1997). ETEC engage strain-specific antigenic, hair-like fimbriae in attachment to specific receptors on the surface of enterocytes in the intestinal lumen (WHO, 2009a). EIEC on the other hand produce dysentery-like diarrhoea similar to that caused by *Shigella* species by invading and multiplying within epithelial cells of the colonic mucosa, resulting in an intense inflammatory response characterized by abscesses and ulcerations that damage the integrity of the epithelial cell lining of the colon (Hale, 1998). EIEC was not a major enteric bacterial pathogen observed in this study, with prevalence similar to that reported in Mexico City by Paniagu *et al.* (2007). This pattern is not consistent with studies in other developing countries where EIEC strains were important causes of pediatric diarrhea and dysentery (Taylor *et al.*, 1986; Pacheco-Gil *et al.*, 2006).

*Salmonella* species are an important cause of varying food and water-related infections. This study detected *Salmonella* as a major cause of gastroenteritis in our setting. *Salmonella* has previously been described as one of the common causes of gastroenteritis particularly in the developing countries (Guerrant *et al.*, 1990; Galanis *et al.*, 2006). On the contrary, infectious diarrhoea in the developed world is often due to viruses (Jafari *et al.*, 2008). The most common species isolated in this study were *S. enterica* serovar Typhi (52%) and *S. enterica* serovar Typhimurium (25%). This report is consistent with other studies conducted in Iran and South Africa where *S. enterica* serovar Typhi and *S. enterica* serovar Typhimurium were described as major aetiological agents of infectious diarrhoea (Jafari *et al.*, 2008; Keddy *et al.*, 2009). *S. enterica* serovar Isangi was third in ranking of frequency of isolation. Kruger *et al.* (2004) described the increasing importance of this serotype of non-typhoidal *Salmonella* (NTS) which was a rare serotype in South Africa until 2002. Other species identified were *S. enterica* serovar Choleraesuis, *S. enterica* serovar Enteritidis, *S. enterica* serovar Eppendorf, *S. enterica* serovar Hadar, *S. enterica* serovar Panama and untyped *Salmonella* spp. The virulence factor detected among the majority (105) of the *Salmonella* spp. was *invA*. This gene which is chromosomally located aids attachment of the pathogen to the epithelial cells (Gallan and Curtiss, 1989). The other detectable virulent gene was *fliC* detected in 15 isolates. The flagellin gene, *fliC* is known to aid systemic spread of pathogen and is specific for *S. enterica* serovar Typhimurium (Soumet *et al.*,

1999). Enteric bacteria possessing *sefA* genes were not encountered in this study. The *sefA* gene which encodes the SEF14 fimbrial antigen is a virulence plasmid specific for *S. enterica* serovar Enteritidis (Doran *et al.*, 1996).

### 3.5. Conclusion

This study showed the diversity of virulence gene expression in two major enteric pathogens. It was observed among other things that some diarrhoegenic *E. coli* isolated from apparently asymptomatic subjects expressed some virulence genes at frequency as high as seen in diarrhoegenic cases. This is a pointer to the fact that asymptomatic individuals serve as reservoirs of pathogenic strains of enteric bacteria and may play a role in the spread and acquisition of virulence genes.

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## CHAPTER 4

### AN ETHNOBOTANICAL SURVEY OF INDIGENOUS PLANTS USED AS DIARRHOEA REMEDY IN O.R.TAMBO DISTRICT, EASTERN CAPE PROVINCE, SOUTH AFRICA

#### 4.0. Abstract

Indigenous health system and the use of herbal plants have been recognized as pivotal in primary health care and a system to reckon with in achieving one of the targets of the Millenial Goals on health. An ethnobotanical survey was conducted to identify indigenous herbal remedies for diarrhoea and associated stomach ailments in rural areas of O.R. Tambo district municipality in the Eastern Cape province of South Africa. The main objective of the study was to gather ethnomedical data on potentially valuable indigenous medicinal plants for the eventual development of new pharmaceuticals and also emphasize the role of ethnomedicine in primary health care. The use of herbal remedies in the treatment of diarrhoea and dysentery was investigated using interviews. The survey was conducted among traditional healers and knowledgeable local elders who use medicinal plants to treat common illnesses. Data from the survey indicated the names of plants commonly used in the treatment of diarrhoea and associated ailments, the methods of preparation, parts used and administration. A total of 32 plant species belonging to 26 families were reportedly used as diarrhoea remedy in the study area. The most predominant families of medicinal plants employed and most frequently recommended were Fabaceae 16.67%, followed by Hyacinthaceae and Hydnoraceae 8.33% each. The most commonly



utilized portions of plants for medicinal purposes included roots and leaves. Other parts were corms, bulbs, tubers, fruits and bark. The methods of preparation often employed were decoctions and infusions whilst medication was frequently administered orally or as enema. Some of the plants were used singly or mixed with other plant(s) while some edible ones are consumed as food. The survey documented a diversity of plants employed as remedy for diarrhoea. Integration of this form of health care system into western medicine is warranted but propagation of such medicinal plants is vital to sustainability of the use of medicinal plants.

Key words: Ethnobotany; Herbal remedy; Indigenous; Diarrhoea, Primary health

#### 4.1. Introduction

One of the targets on Health in the Millennium Development Goals (MDG) declared in 2000 is to provide quality and affordable health for all by the year 2015 (UN, 2000). With the MDG target date only 6 years away, this vision is bound to fail unless further concerted effort is made to improve the health of poor people. According to the World Health Organization (WHO,1978), traditional medicine has been described as one of the surest means to achieve total health care coverage of the world's population, yet this form of health care system has long been relegated to a marginal place. The importance of traditional medicine as a source of primary health care was first officially recognized by the World Health Organization in the Primary Health Care Declaration of Alma Ata (1978)

and has since been given a global attention under Traditional Medicine Programme of the health body. Recently, WHO commitment to the Millennium Declaration has been reaffirmed by its governing bodies ([WHO, 2002a, 2002b](#)) and Ministers of Health of the WHO African Region ([WHO, 2007](#)) have also made a declaration to recognize the role of traditional medicine in Primary Health Care.

In the rural and remote parts of most African countries, hospitals and clinics are often sparsely located far away from dwellers and where there is accessibility to clinics, other factors such as finance and mobility make orthodox medicine far fetched from these people. It has been estimated that up to 80% of the world's rural populations depend on plants for their primary health care, since western pharmaceuticals are often expensive, inaccessible or unsuitable ([Cunningham, 1993; WHO, 1978](#)). Considering the relative ratios of traditional practitioners and university-trained doctors in relation to the whole population in African countries, traditional healers and remedies made from plants play an important role in the health of millions of people. The people are reliant on traditional healers who usually reside among them trusting their ingenuity about the use of herbs and some other cultural and traditional beliefs. These facts thus provide a role for traditional healers among the rural dwellers' trust.

It is becoming increasingly urgent to document the medicinal use of African plants because of the rapid loss of the natural habitat for some of these plants due to anthropogenic activities. The migration factor especially among the youths to urban areas as well as the demise of most of the local practitioners

along with their wealth of knowledge are sources of threat to the future of most of the important cultures including knowledge on the use of plant species (Akerele *et al.*, 1991; Bodeker, 1994; Schlage *et al.*, 1999).

Several studies have been conducted in the Eastern Cape to identify and document biodiversity and ethnomedicinal value of the province (Van Wyk *et al.*, 1997; Grierson and Afolayan, 1999; Dold and Cocks, 2001; Van Wyk and Smith, 2001; Kambizi *et al.*, 2004; Mucina and Rutherford, 2006; Kambizi and Afolayan, 2008). Nevertheless, circumstances still warranted a survey of O.R. Tambo District Municipality (ORTDM). Why is it necessary to conduct the study in this area? What makes this district municipality peculiar? To answer these and some other questions, a grasp of what ORTDM is made up of is necessary.

#### 4.1.1. A brief description of O.R. Tambo District Municipality

O.R. Tambo District Municipality (ORTDM) is located in the east of the Eastern Cape Province along the Indian Ocean coastline of South Africa. It is situated in the former Transkei homeland area of the province which falls within the latitudes 30° 00' and 34° 15' South and longitudes 22° 45' and 30° 15' East. ORTDM is bordered by the Alfred Nzo District to the North, Ukhahlamba district to the Northwest, Chris Hani to the West and Amathole District to the Southwest (Figure 1). From the East to the West, the District measures 170 143 km, North to South 121 725 km and it measures 12857 km<sup>2</sup> in extent ([http://isrdp.dplg.gov.za/documents/IDP/ISRDP/OR\\_Tambo\\_IDP.pdf](http://isrdp.dplg.gov.za/documents/IDP/ISRDP/OR_Tambo_IDP.pdf)). It is more

than 2,700 m above sea level, and descends southward from the great interior plateau to form a relatively narrow coastal plain along the Indian Ocean.

The population of the District Municipality stands at 1.7 million persons and covers an area of 16,617 square km<sup>2</sup>. A total of 93% of the District Municipality's population reside in rural areas while an estimated 77% of the population is unemployed (STATSSA, 2001). The mother-tongue of the majority of the dwellers is *isiXhosa*, an Nguni language while the rest of the people speak Afrikaans and English.

The region is predominantly rural with large tracts of arable land, nevertheless, agriculture in ORTDM is inadequately developed and largely subsistence. Traditionally, Eastern Cape is known for rearing livestock which represents 70% of the province's gross agricultural income. Wheat, corn (maize), and sorghum are grown inland with irrigation, while oranges, pineapples, tobacco, and potatoes are cultivated along the coast (Encyclopædia Britannica, 2009). The Langeni Forest and Magwa Tea are the major contributors to the primary sector of the economy with an oncoming Mondi Forests reaching its maturity state soon.

This study area includes moderate and high rainfall areas, principally along its sub-tropical coast, but also in pockets of mountainous areas receiving an annual rainfall of above 800 mm. ORTDM has a diversity of vegetation, from grasslands and thicket to forests and bushveld including coastal and marine habitats. The district is considered to have the richest natural resources and the

most fertile areas in the country, with good soils and climatic condition ([http://isrdp.dplg.gov.za/documents/IDP/ISRDP/OR\\_Tambo\\_IDP.pdf](http://isrdp.dplg.gov.za/documents/IDP/ISRDP/OR_Tambo_IDP.pdf)). The vegetation of our study region has been previously described (Acocks 1988; Dahlgren and Van Wyk 1988; Van Wyk 1990; Hartmann 1991; Cawe *et al.*, 1994; Van Wyk 1994; Low and Rebelo, 1998; Van Wyk and Smith, 2001; Mucina and Rutherford, 2006; Clark *et al.* 2008).

This district falls within regions (namely-Maputaland, Pondoland and the Drakensberg Alpine) singled out in a world atlas of centres of plant diversity (CPD's) (Pooley, 1998). The area now classified as a Global Hotspot (Steenkamp *et al.*, 2004), a Global Hotspot being defined on the basis of irreplaceability and threat (Myers 1988). Of great significance are the coastal forests, bushveld and grassland of the Pondoland. This area has been identified as a Centre of Plant Endemism, which is floristically species-rich and contain high numbers of species endemic to them (Van Wyk and Smith 2001). It has more than 130 species of plants that occur nowhere else in the world, and including the well-known Pondoland coconut palm (ORTDM, 2009).

However, due to the rich flora of this study area coupled with the disappearing traditional knowledge on medicinally useful plants a lot of grounds still needs to be covered in the documentation of the indigenous knowledge on medicinal plants. Thus, it is critical to preserve the plants and knowledge of their uses.

Diarrhoeal diseases are often associated with low living standard, poor sanitation infrastructure and poor access to potable water sources. This in particular is a prevalent feature in the area of study owing to a high percentage of unemployment as previously reported (STATSSA, 2001). The predominantly rural Eastern Cape Province (ECP) is noted for lack of proper sanitation and piped or clean water (ECDOH, 2009). Hence, water-borne diseases are not far-fetched from ORTDM with its predominant rural dwellers depending largely on spring, pond or river water which are often shared with domestic animals. According to a previous study in South Africa (Obi *et al.*, 2007) incidence of diarrhoea could be linked to poor quality of household drinking water. A recent Eastern Cape Department of Health statistics (2009) confirm a significant number of deaths due to diarrhoea among children, with the highest number of deaths reported in the ORTDM. Of grave health consequences is cholera disease within the region. Kwa-Zulu Natal (KZN) Province of South Africa was designated as endemic for cholera (Henninger and Snell, 2002). ORTDM shares border with KZN and as indicted in figure 2, it is worthy of note that the blue arrow indicating direction of spread of cholera is towards ORTDM. A recent outbreak of cholera which ravaged Zimbabwe rapidly spread into South Africa between November 2008 and April 2009 and claimed 65 lives whilst there was >12, 000 case definition of the disease (Archer *et al.*, 2009). With the high incidence of HIV/AIDS and multidrug resistant TB in South Africa (Cohen, 2006), diarrhoea can pose a serious challenge to the public health in terms of burden of diseases.

As a result of the high incidence of diarrhoeal diseases, poor water quality and large dependence on medicinal plants due to the vast rural area, this study aimed to document information on plants commonly prescribed as diarrhoeal remedy in the ethnomedicinal practice of the indigenous people of OR Tambo District Municipality and environs.

#### 4.2. Materials and methods

Ethnobotanical survey for medicinal plants employed in the treatment of diarrhoea and associated ailments was conducted within ORTDM. Areas visited included Port St. Johns, Lusikisiki, Flagstaff, Tabankulu, Bizana, Ugie and Coffee bay from June 2008 to February 2009. The investigation was carried out using interviews among traditional healers and knowledgeable local elders who use medicinal plants to treat common illnesses. Questionnaire employed for the interview is shown in [Appendix 1C](#). The survey elicited information on the names of plants commonly used in the treatment of diarrhoea and associated ailments, the methods of preparation, parts used and administration. With the assistance of the local practitioners samples of the plant material used as diarrhoeal remedy were collected from the wild. Scientific identification of samples was aided by staff of the herbarium, Walter Sisulu University, where voucher specimens were deposited. Further characterization of plants and their usage was established by consultation of literatures and monographs ([Hutchings \*et al.\*, 1996](#); [Pooley, 1993, 1998](#); [Van Wyk \*et al.\*, 1997](#)). For data analysis, plant species were

grouped into their respective families along with local and common names. An inventory of plant species was compiled from this fieldwork.

#### 4.3. Results

Ethnobotanical information obtained from the study area on medicinal plants used in the treatment of diarrhoea has revealed 33 medicinal plants scattered in 26 families. [Table 4.1](#) shows the diverse families of the various indigenous medicinal plants. Among the families, Fabaceae provided the highest proportion of medicinal plants prescribed at 16.67% followed by Hyacinthaceae and Hydnoraceae, 8.33% each.

Most traditional healers claimed never to use cultivated plants but depend on sourcing from the wild. The frequently utilized portions of plants for medicinal decupurposes included roots, corms, leaves, and bark but roots were mostly used for the preparation of medicine in the treatment of diarrhoea, followed by the use of leaves. The methods of preparation varied considerably from one healer to the other. Plant remedies were often utilized in the form of decoctions and infusions. Extraction may be hot by boiling in water or mere soaking plant parts in cold water. Plant part may be eaten raw in some cases whilst medication is frequently administered orally or as enema. Some of these plants were used singly or mixed with other plant(s) or even with western mixtures such as salt, vinegar and in a particular instance Amsphogel (Aluminum hydroxide) was mixed with plant part by the traditional healer. The surveys also revealed that



dosage of plant extracts were not consistent. The analysis has revealed the diversity of indigenous plants used as diarrhoeal remedy in OR Tambo. These medicinal plants which are of value in the treatment of diarrhoea are also used to treat different other ailments while some edible ones are consumed as food.

#### 4.4. Discussion

Traditional medicine is the most widely used medical system in the rural setting of ORTDM. Orthodox medicine is costly and often inaccessible. Not only is ethnomedicine popular and acceptable due to their important role in primary health-care delivery systems, but also in many areas, it has been the only system available. Likewise, medicinal plants need more attention because it forms an essential component of the total well-being of humans particularly the rural dwellers whose major sources of food, shelter, energy and medicines are forest plants (Akerlele, 1988; Hamayun *et al.*, 2003). Furthermore, the emerging global problem of multidrug resistant pathogens (Alekhshun and Levy, 2007; Bisi-Johnson *et al.*, 2005; Levy 2005; Obi *et al.*, 2007) and the need for the discovery of lasting and sustainable therapy to combat diseases such as HIV/AIDs, malaria and cancer which have defied available treatments has led to a paradigm shift to natural herbal product for succor.

This study documented a diverse list of plants used as remedy for diarrhoea in ORTDM. Previous reports have also linked some of the plants encountered in the course of this survey with remedy of diarrhoea, dysentery or

stomach ailments ([Watt and Breyer-Brandwijk, 1962](#); [Bigalke, 1967](#); [Hutchings, 1989](#); [Van Wyk and Gericke, 2000](#); [Van Wyk and Wink, 2004](#);). The parts of the plants commonly used were roots and leaves. The problem of inconsistent dosaging is a critical set back which is crucial in standardization of medicinal plants. Another factor which may impact on the traditional therapy standardization is the work place hygiene and the quality of water used in preparation particularly with cold extraction. Most of the traditional healers boast of treating some ailments that have defied modern medical practice. While some of the healers embrace the idea of both western medicine and traditional medicine complementing each other, a few others do not. Some of the traditional healers tend to hide the information on plants used for different ailments largely for fear of losing patronage to the investigators or interested persons. By a way of mystifying the native trade, the vast majority of plants are collected from the wild and cultivation of the plants is often not encouraged by the traditional healers. Some participants believed that cultivated plants would have been attacked by evil spirit and hence will not be potent for use. This is similar to the findings of [Keirungi and Fabricius \(2005\)](#). Scientific evaluations of the therapeutic claims as well as toxicological data are still underprovided for many of the plant species. This study will form the basis for microbiological and phytochemical research on selected diarrhoeal medicinal plants.

An observation in the course of this study which poses a sort of concern is some of the methods used in harvesting these medicinal plants. For instance,

root excavation and bark striping of plants pose a threat to the continued existence of such plants. These two methods have been reported as most harmful harvesting methods for plants (Akerere 1991; Cunningham *et al.*, 2002). The tendency for extinction of scavenged species is obvious going by the unsustainable handling and the habit of not cultivating medicinally valuable species. For conservation to be effected, planting of designated valuable herbal plants in small gardens in the homesteads is strongly recommended. Large scale farming of commercially viable plants should be encouraged whilst scientist are implored to undertake studies on various factors affecting growth of the plants such as soil conditions, temperature, seasonal variations and disseminate best propagation methods. Conclusively, it is pertinent for scientists to urgently salvage this cheap and alternative health care system from extinction, help preserve indigenous knowledge and conserve nature.

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Figure 4.1. Map of O.R. Tambo District Municipality

(Source: [http://isrdp.dplg.gov.za/documents/IDP/ISRDP/OR\\_Tambo\\_IDP.pdf](http://isrdp.dplg.gov.za/documents/IDP/ISRDP/OR_Tambo_IDP.pdf)).

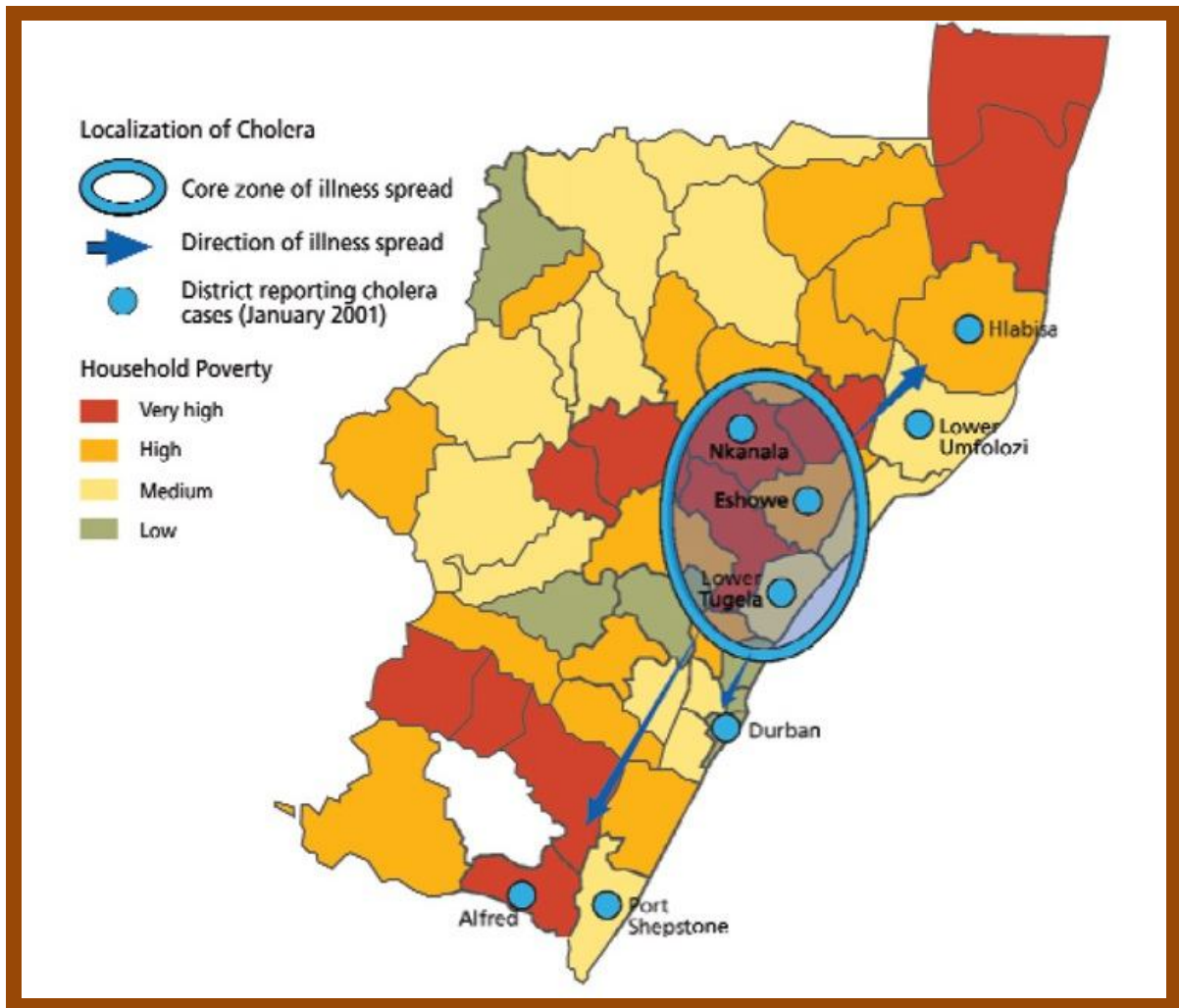


Figure 4.2. WHO Cholera endemic zone  
 (Source: [www.who.int/entity/heli/tools/en/gridmap2.jpg](http://www.who.int/entity/heli/tools/en/gridmap2.jpg); Henninger and Snell, 2002).

Table 4.1. Herbal remedies used for the treatment of diarrhoea and associated ailments.

FAMILY/SCIENTIFIC NAMES COMMON NAME	LOCAL NAMES	PLANT PART	USAGE & PREPARATION	OTHER USAGE
<p>ALLIACEAE <i>Tulbaghia alliacea</i> L.f. Wild Garlic</p>	<p>Umwelela (X) ivimba-mpunzi (X) Sikwa (Z)</p>	Bulb	Stomach ailments, bulb infusion taken orally to treat fever.	<p>Remedy for tuberculosis (TB) and influenza, as an antihypertensive or to expel intestinal worms (Watt &amp; Breyer-Brandwijk, 1962). As a medicated bath to treat paralysis, rheumatism and reduce fever temperature (Watt &amp; Breyer-Brandwijk, 1962).</p>
<p>AMARANTHACEAE <i>Hermbstaedtia odorata</i> Wild Cockscomb Rooi-aarbossie</p>	<p>Ubuphuphu (X,Z)</p>	Leaves	Leaves eaten as food and infusion for diarrhoea.	<p>Root cleansing stomach wash alone or with <i>Acaccia xanthophloea</i> and <i>Cappa</i> (Hutchings <i>et al.</i>, 1996).</p>
<p>AMARYLLIDACEAE <i>Scadoxus puniceus</i> (= <i>Hemanthus magnificus</i>, <i>H. natalensis</i>) Bloody Lily, Snake Lily</p>	<p>Umphompho – wezinja, Isiphompho, umgola (Z)</p>	Bulb & roots	Stomach ailments, diarrhoea, nausea.	<p>Bulb poisonous, use for poultices (Batten &amp; Bokelmann, 1966). Coughs (Bryant, 1966), headaches, poisoning antidote (Hutchings <i>et al.</i>, 1996).</p>

<p>ANACARDIACEAE <i>Protorhus longifolia</i> (Bernh. ex C. Krauss) Engl. Red Beech</p>	<p>Izintlwa, ikubalo, umkupati (X)</p>	<p>Bark</p>	<p>Bark dried powdered + guava + Qangazani boiled &amp; taken orally for diarrhoea and bloody stool.</p>	<p>Heart burn and stomach bleeding (<a href="#">Hutchings et al., 1996</a>).</p>
<p>APOCYNACEAE <i>Acokanthera oppositifolia</i> (Lam.) Codd= <i>A. venenata</i> Common Poison-bush</p>	<p>inHlungunyembe Intlungunyembe (X, Z)</p>	<p>Leaves</p>	<p>Leaf decoction for stomach ache, diarrhoea, antihelmintic</p>	<p>Treat snakebite (<a href="#">Gerstner, 1939</a>). Spider bite, aches, intestinal worms, cold (<a href="#">Pooley, 1993</a>). Powder from dried roots as snuff for headache (<a href="#">Bhat and Jacobs, 1995</a>).</p>
<p>ASCLEPIADACEAE <i>Xysmalobium undulatum</i> (L.) W.T.Aiton  Milkwort, Uzura</p>	<p>Ishongwe (X,Z), Itsongwe</p>	<p>Roots</p>	<p>Boil root for diarrhoea, stomach ailments or pain.</p>	<p>Dysentery, Headaches (<a href="#">Pujol, 1990</a>). Flower and seed decoction for colic, poison antidote (<a href="#">Watt &amp; Breyer-Brandwijk, 1962</a>)</p>
<p>ASPHODELACEAE <i>Aloe candelabrum</i> Berger. Candelabrum Aloe  <i>Bulbine abyssinica</i>, Bushy Bulbine,</p>	<p>Ikhalana Inkalane (X) Uphondonde (Z)  Utswelana Intelezi (X) Ibhucu (Z),</p>	<p>Leaves  Leaves, tubers</p>	<p>Leaf decoction for diarrhoea.  Boil leaves for vomiting, diarrhoea, TB.</p>	<p>Treat bilharzias, dysentery, cracked lips, skin ailments, urinary</p>

	Incelwane (X);			complaints, rheumatism, as a charm (Pooley, 1998). Tuber decoctions-antispasmodic to quell vomiting (Hutchings <i>et al.</i> , 1996).
ASTERACEAE <i>Bidens bipinnata</i> Spanish-black jack, Spanish needle	Uvelemampondweni uvelegoli	Leaves	Leaves edible, infusion for diarrhoea.	Rheumatism (Watt & Breyer-Brandwijk, 1962). Hemorrhage, reduce cancer, flu, cold and fever (Pooley, 1998).
CORNACEAE <i>Curtisia dentata</i> (Burm.f.) C.A.Sm. = <i>C. faginea</i> Assegai	Umlahleni (X,Z), Unsirayi (X), Umgxina, Umlahleni (Sefile), Uzintlwa	Bark, Root	Diarrhoea, stomach ailments.	Stomach ailments including diarrhoea, blood strengthener, aphrodisiac (Pajol, 1990).
EUPHORBIACEAE <i>Euphorbia cooperi</i> N.E.Br. ex. Berger Euphorbia or Milkweed, Spurge, Transvaal Candelabra Tree	Umhlonhlo (X)	Bark of root	Bark of root ground dry boiled, then mix with a sachet epsom salt, cool & add 2 spoons vinegar for diarrhoea, stomach disorders. For infants, mix equal portion of decoction with Amsphojel to flavour milk.	

<p>FABACEAE subfamily MIMOSACEAE <i>Acacia mearnsii</i> De Wild Blackwood, Black Wattle</p> <p>FABACEAE (LEGUMINOSAE) <i>Elephantorrhiza elephantina</i> (Burch.) Skeels Elephant's Root</p>	<p>Ublekwana (X) Udywabasi (X, Z) Indywabasi</p> <p>Intolwane (X,Z)</p>	<p>Bark</p> <p>Root, stem</p>	<p>Bark infusion taken orally for diarrhoea, dysentery</p> <p>Boil equal part plant + <i>Acokanthera oblongifolia</i> for diarrhoea, stomach ailment. Infusion of ground stem alone for diarrhoea and menstrual disorder.</p>	<p>Sore throat, coughs, children fever, tooth ache (<a href="#">Hutchings et al., 1996</a>).</p> <p>Syphilis, stop bleeding (<a href="#">Jacot Guillardmod, 1971</a>), chest complaints, heart conditions (<a href="#">Watt &amp; Breyer-Brandwijk, 1962</a>). Fever, ulcers, dysentery, diarrhoea, dysmenorrhoea (<a href="#">Bryant, 1966</a>).</p>
<p>GERANIACEAE <i>Pelargonium sidoides</i> Rose-scented Pelargonium</p> <p><i>P. luridum</i> Wild geranium</p>	<p>Umsongelo (X)</p> <p>Umsongelo, ishwaqa</p>	<p>Leaves, roots</p> <p>Leaves</p>	<p>Infusion of leaves or root enema for diarrhoea, dysentery and vomiting.</p> <p>Eaten raw as vegetable, treat dysentery, nausea, vomiting, fever</p>	<p>Bruised leaves soothes skin rashes, in tea to treat kidney &amp; bladder ailments, nausea, gonorrhoea, root decoction severe diarrhoea in Transkei (<a href="#">Hutchings et al., 1996</a>). Leaf paste for wound, powdered root mixed with food for dysentery (<a href="#">Watt &amp; Breyer-Brandwijk, 1962</a>).</p>

<p>HYACINTHACEAE <i>Eucomis autumnalis</i> (Mill.) Chitt. Common Pineapple Flower</p> <p><i>Scilla nervosa</i> (Burch.) Jessop White Scilla</p> <p><i>Scilla</i> sp.</p>	<p>Ubuhlungu becanti Isithithibala (X) Umathinga (Z)</p> <p>Umagaqana, magaqana (X), Imbizankulu ingema (Z) Umasixabane (X)</p>	<p>Bulb</p> <p>Bulb</p> <p>Root</p>	<p>Boil bulb for abdominal problems.</p> <p>All purpose herb. For diarrhoea, TB, various diseases, cleans blood.</p> <p>Infusion of ground tuber + <i>H. africana</i> + <i>Curtisia dentate</i> for diarrhoea</p>	<p>Decoctions of bulb and roots for coli, flatulence (Cunningham, 1993). Syphilis (Watt &amp; Breyer-Brandwijk, 1962). Treat urinary &amp; pulmonary ailments, fever (Hutchings et al., 1996; Roberts, 1990).</p> <p>Purgative, sprain, fracture, cancers (Watt &amp; Breyer-Brandwijk, 1962). Rheumatic fever, dysentery (Rood, 1994; Silayo et al., 1999).</p>
<p>HYDNORACEAE <i>Hydnora africana</i> Warty Jackal Food, Jakkalskos Kanip</p>	<p>Ubuklunga (X) Umavumbuka(Z), Umafumbuka (X)</p>	<p>Fruits, tuber, leaves</p>	<p>Boil handful of ground dried tubers + blackwood + peach for diarrhea</p>	<p>Parasitic on <i>Euphorbia</i> roots. Fruit pulp like potato eaten by people birds jackal, plant dried ground raw for dysentery, amenorrhoea. Swollen glands or inflamed throat (Watt &amp; Breyer-Brandwijk, 1962).</p>
<p>HYPOXIDACEAE</p>				

<i>Hypoxis latifolia</i> Hook. African potato (Eng.) Small Yellow star-flower	Inongwe Ilabateka (X)	Tuber	Boil ground dried tuber for diarrhoea.	Treat benign prostrate ( <a href="#">van Staden, 1981</a> ). Headaches, dizziness, mental disorders, inflammation, HIV ( <a href="#">Singh, 1999</a> ; <a href="#">van Wyk, 2000</a> ).
<i>H. hemerocallidea</i> = <i>H. rooperi</i> Star-flower	Inongwe Ilabateka (X)			
IRIDACEAE <i>Gladiolus sericeo-villosus</i> Hook.f. <i>forma sericeo-villosus</i> Natal Lily, parrot's beak gladiolus	Umnunge (X)	Corm	Corm's decoction for cold and dysentery, TB (use with care)	Corms for dysentery oral and enema ( <a href="#">Hutchings et al., 1996</a> ). Impotence ( <a href="#">Watt &amp; Breyer-Brandwijk, 1962</a> ). Menstrual pain ( <a href="#">Bryant, 1966</a> ).
MESEMBRYANTHEMACEAE <i>Carprobatus edulis</i> Hottentot's fig, ghaukum, rankvy	Ikhambi-lamabulawo, umgongozi, Igcuthuma Unomatyumtyum, igcukuma	Leaves	Various diseases, diarrhoea	Allergies, diabetes, sore throats ( <a href="#">Hutchings et al., 1996</a> ). Juice from pounded leaves as gargle for sore throats, thrush, diphtheria, treat digestive troubles, diarrhea & dysentery ( <a href="#">Watt &amp; Breyer- Brandwijk, 1962</a> ).
MYRTACEAE <i>Psidium guajava</i> L. Guava	Ugwava (X,Z)	Leaves	Leaves boiled for alone or mixed with other plants for diarrhea.	Infusion of leaves for bloody diarrhea ( <a href="#">Hutchings et al., 1996</a> ). Roots for venereal disease by Vhavenda ( <a href="#">Mabogo,</a>



				1990) The Ethnobotany of the Vhavenda. Unpublished Master of Science Thesis, University of Pretoria).
OLEACEAE <i>Olea europaea</i> subsp. <i>Africana</i> Wild Olive	Uzintlwa (X)	Fruit	Infusion for diarrhoea and bloody Stool	Leaves for urinary and bladder infections (Roberts, 1983; Pooley, 1993). Immature fruits as astringents against diarrhea (Iwu, 1993).
POLYGONACEAE <i>Rumex obtusifolius</i> Dock	Idololenkonyane (X,Z)	Leaves	Leaf extract for diarrhea	Infertility in women (Watt & Breyer-Brandwijk, 1962). Leaf decoction for worms (Watt & Breyer-Brandwijk, 1962). Scabies, powdered root as gargle for laryngitis
ROSACEAE <i>Prunus africana</i> (Hook.f.) Kalkman Red Stinkwood, Bitter Almond, Peach	Umkhakhazi (X), Umkakase (X)	Roots	Root of peach + bark of blackwood + leaves of guava + roots of umswaninge for diarrhoea, abdominal ailments.	The bark extracts have become popular in Europe for the treatment of benign prostate hypertrophy (Van Wyk et al. 1997)
RUBIACEAE <i>Pentanisia prunelloides</i>	Icishamlilo, Icimamilo	Roots, leaves,	Boil grated dried bulb,	A range of ailments, root

(Klotzsch ex Eckl. & Zeyh) Walp Broad-leaved Pentanisia	(X,Z)	bulb	a spoon taken orally to stop vomiting, diarrhoea in children. For adult, a wine shot 3 times daily. Expose face to steam from boiling herb for pimples. Rub leaves to soothe swollen body. For diarrhoea and vomiting.	as enema for stomach pain ( <a href="#">Hutchings et al., 1996</a> ). Hemorrhoids, snakebite, rheumatism ( <a href="#">Bryant, 1966</a> ; <a href="#">Gerstner, 1941</a> ).
RUBICEAE Pavetta – Bride’s Bush <i>Psychotria capensis</i> (Eckl.) Vatke Black Bird-berry	Isithitibala (Z), UmGono-gono (X)	Fruits		Unspecified part for tuberculosis ( <a href="#">Batten &amp; Bokelmann, 1966</a> ). Leave paste for wound. For gastric complaints and root infusions are taken to cause vomiting ( <a href="#">Hutchings et al., 1996</a> ).
SAPINDACEAE Atalaya – Krantz Ashes <i>Hippobromus pauciflorus</i> (L.f.) Radilk. False Horsewood	Ulwathile (X)	Bark, root, leaves	Diarrhoea, dysentery	Coughs, catarrh related headaches ( <a href="#">Bryant, 1966</a> ). Eye problems ( <a href="#">Watt &amp; Breyer-Brandwijk, 1962</a> ).
SCOPHULARIACEAE <i>Physalis peruviana</i> Cape gooseberry	Igquzu (X)	Leaves	Leaf edible, stomach disorders.	Leaf infusion as enema to relieve abdominal ailment in children ( <a href="#">Watt &amp; Breyer-Brandwijk, 1962</a> ). Treat high blood pressure,

				diabetes (Watt & Breyer-Brandwijk, 1962).
SOLANACEAE <i>Solanum aculeastrum</i> Dun Apple of Sodom, poison apple, Goat apple	Umthuma (X,Z)	Fruits, roots, leaves.	Fruit decoction orally for haemorrhoids & dysentery, fruit as enema for diarrhoea.	Fruit pulp as enema. Rheumatism, ringworm in cattle (Pooley, 1993). Root & leaves for coughs, fever, sore throats, colic, indigestion, abdominal pain, venereal diseases (Watt & Breyer-Brandwijk, 1962; Kokwaro, 1976).
VERBENACEAE <i>Clerodendrum glabrum</i> E.mey = <i>C. rehmannii</i> Cat's Whiskers or Verbena Tree or Tinderwood	Umqangazani Uqangazana (X), iNunkisiqaqa(X) Umqangazane	Leaves	Bloody stool, chest infections.	Snakebite (Roberts, 1990). Leaf infusion for intestinal parasites (Watt & Breyer-Brandwijk, 1962). Leaf + root of <i>Cymbopogon marginata</i> (Steud.) for roundworms, threadworms, cough, fevers (Hutchings <i>et al.</i> , 1996).

KEY: X = Xhosa; Z = Zulu.

## CHAPTER 5

### PHYTOCHEMICAL ANALYSIS AND ANTIBACTERIAL SCREENING OF CRUDE EXTRACTS OF SOME HERBAL PLANTS OF THE EASTERN CAPE PROVINCE, SOUTH AFRICA

#### 5.0. Abstract

This study was conducted to identify and evaluate the antibacterial activity of indigenous herbal remedies for diarrhoea and associated stomach ailments in rural areas of O.R. Tambo district municipality in the Eastern Cape Province, South Africa. The crude aqueous, methanolic and acetone extracts of twelve selected medicinal plants were screened against clinical isolates of *Salmonella isangi*, *S. typhi*, *S. Typhimurium*, *Shigella flexneri* type 1b and *Sh. sonnei* phase II. The herbs which were selected based on high frequency of prescriptions by the traditional healers were *Acacia mearnsii*, *Aloe arborescens*, *Aloe striata*, *Cyathula uncinulata*, *Eucomis autumnalis* (Mill.) Chitt., *E. comosa* (Houtt.) Wehrh. *Hermbstaedtia odorata*, *Hydnora africana*, *Hypoxis latifolia*, *Pelargonium sidoides*, *Psidium guajava*, *Scilla natalensis*. A qualitative phytochemical screening of the plants extracts was by thin layer chromatography. Plants extracts were screened for antibacterial activity using two types of bioassays: serial dilution microplate technique and bioautography. The preliminary screening revealed that most of the tested organisms were sensitive to the crude acetone extracts with MIC values ranging from 0.078–2.5 mg/mL. Acetone and methanolic extracts of *Aloe striata*, *Cyathula uncinulata*, *E. autumnalis* and *P. guajava* were more active against enteropathogens matching up to gentamicin in

terms of the MIC. Water extracts showed minimal or no activity in most cases. The presence of terpenoid and flavonoids in some herbs were inferred from the TLC fingerprint. The bioautograms revealed different fractions of the extract mainly responsible for the antibacterial activity. *S. enteric serovar Typhi* was the most sensitive of the tested organisms to the crude extracts. This preliminary study has revealed the antibacterial activities of some of the selected herbs used in the treatment of diarrhoea and related diseases and corroborates assertions by traditional healers on their efficacies.

Key words: Herbal remedy; Indigenous; Diarrhoea; Antibacterial

### 5.1. Introduction

Diarrhoea is a disease which remains a problem worldwide, leading to nearly 19% of the 10 million under-5 deaths that occurred in the world in 2004 ([World Health Statistics, 2006](#)). Studies have shown that diarrhoea, HIV/AIDS, water and food-borne diseases account for a high percentage of morbidity and mortality in different age groups but mostly in children 0-5 years ([WHO, 2003](#); [Bryce et al., 2005](#)). Every individual has at least an episode or more of diarrhoea in a lifetime. Children may have up to 10 episodes before their fifth birthday. Alarmingly, a child dies every 15 seconds from diarrhoea, caused largely by unsafe water and inadequate sanitation ([WHO, 2005](#)). Despite advancement in technology in the industrialized nations, diarrhoea continues to be an important cause of morbidity and incurs substantial health-care costs ([World](#)

[Gastroenterology Organisation, 2008](#)). The greatest burden of the disease however, is in sub-Saharan Africa and Asia ([Morris et al., 2003](#)).

Treatment failures of enteric diseases, particularly, the emerging multidrug resistant enteric bacteria is a big challenge. Multiple antibiotic resistances is on the increase among clinical isolates of bacteria ([Bisi-Johnson et al., 2005](#); [Obi et al., 2007](#)) and the emergence of resistance to the 3<sup>rd</sup> and 4<sup>th</sup> generation beta-lactam drugs has made therapy more complicated. The burden of resistance to extended-spectrum cephalosporin and other beta-lactam drugs among the *Enterobacteriaceae* is enormous both in the hospital and community ([Bradford, 2001](#)). Pharmaceutical industries have produced a number of new drugs in the last three decades. Currently, an estimated 122 drugs from 94 plant species have been discovered through ethnobotanical leads ([Fabricant and Farnsworth, 2001](#)). Some of these include Ephedrine (bronchodilator) derived from *Ephedra sinica*, Quinine (antimalarial) from *Cinchona ledgerian* ([El-Baz, 2007](#)) and recently is the antimalarial compound Artemisin, derived from *Artemisia annua* L ([Camacho et al., 2000](#)). Despite these big strides, resistance to antimicrobials by microorganisms is still on the increase due mainly to the remarkable genetic plasticity of the microorganisms ([Kunin, 2009](#)), inappropriate use: high selective pressures of use or under use through inaccessibility, poor quality drugs, inadequate dosing, poor adherence, and the increased mobility of the world population ([Okeke et al., 2007](#)). In addition, the incorporation of antimicrobials as growth promoting additives in animal feed is also a contributory

factor to the emergence of drug-resistant bacteria (WHO, 2005; Foley and Lynne, 2007). The sub-therapeutic use leads to bacterial exposure to sublethal concentration of drugs over a period of time leading to selection of resistance strains (Burt and Reinders, 2003). The rate at which new drugs are developed is way behind compared to the changing virulence and drug resistant patterns of microbes. According to Kunin (2009) review of the book by Owen and Lautenbach (2008), antimicrobial resistance is the inevitable result of Darwinian evolution — natural selection and survival of the fittest. While there is a continuous modification of strategies by microbes in the 'no victor no vanquish' fight for survival, drug resistance and development according to Ridley (2001) takes 10 to 15 years and hence the quest for new drugs should be a continuous process (Hostettmann *et al.*, 2000).

Medicinal plants have been acknowledged as potential sources of new compounds of therapeutic value and as sources of lead compounds for drug design and development (Newman *et al.*, 2003). The use of traditional herbs in the treatment of various ailments has been as long as the history of man even though the mechanisms of actions of many herbs are unknown. The Fossil date of plant use as medicines is put at approximately 60, 000 years ago (Fabricant and Farnsworth, 2001). Traditional medicine has been reaffirmed by the WHO (2007) as one of the surest means to achieve total health care coverage of the world's population. Various studies have documented the use of medicinal plants in various parts of the world including developed countries (Van Wyk *et al.* 1997;

Aschwanden, 2001; WHO, 2008) and more than 80% of the populace are reportedly dependent on traditional remedies (WHO, 1978). In South Africa, a sizeable number of both the rural and urban dwellers rely on traditional medicine for their primary health care (Fennell *et al.*, 2004). In most cases, a plant is often used for a variety of ailments which may then suggest a concerted or wholesome therapy. This postulation is corroborated by the review of Gurib-Fakim (2006) where medicinal plants are said to be made of mixture of chemical components which may act individually, additively or synergistically. Some of the documented use of plants in stomach related ailments includes that of Iwu (1993) in which immature fruits of *Olea europaea* subsp. *Africana* (Wild Olive), was reported to be used as astringents against diarrhoea. *Pentanisia prunelloides* (Klotzsch ex Eckl. & Zeyh) Walp is being used for a range of ailments and the root serves as enema for stomach pain (Hutchings *et al.*, 1996). However, many herbs are yet to be explored scientifically and moreover, the need to find a lasting solution to the problem of infectious diseases with lingering treatment failures necessitated further exploration of natural products to uncover new grounds in drug production. This study screened and evaluated the antibacterial activity of selected medicinal plants used in ethnomedicine in the Oliver R. Tambo municipality of Eastern Cape South Africa against some enteropathogenic bacteria.



## 5.2. Materials and Methods

All reagents and chemical used in this study were of technical grade and were obtained from Merck Pty Ltd, and Biorad Pty Ltd, South Africa except otherwise stated. Standard aseptic techniques were observed in all cases.

### 5.2.1. Plant material

Various plant parts used in the treatment of diarrhoea and related diseases in Oliver R. Tambo District municipality in the Eastern Cape province of South Africa were collected over a period of 12 months (June 2008 to July 2009). These were corms, bulb, tuber, leaves and bark of *Acacia mearnsii*, *Aloe arborescens*, *Aloe striata*, *Cyathula uncinulata*, *Eucomis autumnalis* (Mill.) Chitt., *E. comosa* (Houtt.) Wehrh. *Hermbstaedtia odorata*, *Hydnora africana*, *Hypoxis latifolia*, *Pelargonium sidoides*, *Psidium guajava*, *Scilla natalensis*. The common names and ethnomedical usage of the selected plants are listed in [Table 5.1](#).

#### 5.2.2.1. Preparation and extraction

Plant parts were washed with distilled water, air-dried and milled into a fine powder with a Jankel and künkel Model A10 mill. Fifty gram portion of ground dried material macerated in 500 ml of each of acetone, methanol and water on an orbital shaker for 2-3 h. The samples were suction-filtered through a Whatman No 1 filter paper. The filtrate was concentrated at 45°C using a Rotavapor (Eyela N-1100, Rikakikai, China). The reduced extract was transferred to a pre-weighed glass vial and sunction-dried at room temperature with a vacuum pump (ULVAC KIKO, Tokyo). Working stock solutions of extracts were

Table 5.1. Names, plant parts and Traditional usage of herbs investigated

Plant Name	Common name	Plant part	Traditional usage	References
<i>Acacia mearnsii</i> De Wild. Family: Fabaceae	Blackwood Black Wattle	Bark	Diarrhoea, dysentery, sore throat, coughs, children fever, tooth ache	Hutchings <i>et al.</i> , 1996
<i>Aloe arborescens</i> Family: Asphodelaceae	Aloe	Leaves	Vomiting, Skin ailments, diarrhoea, urinary complaints, rheumatism, tuberculosis	Castleman, 1991; Hutchings <i>et al.</i> , 1996.
<i>Aloe striata</i> Family: Asphodelaceae	Aloe	Leaves	Treatment of constipation	Haller, 1990
<i>Cyathula uncinulata</i> (Schrad.) Schinz Family: Amaranthaceae	NA	Leaves	Antidiarrhoea, philter or medicine for love	Tomani <i>et al.</i> , 2008; Yamada, 1999.
<i>Eucomis autumnalis</i> (Mill.) Chitt. Family:Hyacinthaceae	Common Pineapple Flower	Bulb	Decoctions of bulb and roots for colic, flatulence	Cunningham, 1993.
<i>Eucomis comosa</i> (Houtt.) Wehrh. Family:Hyacinthaceae	Pineapple lily	Bulb	Help teething in children and to treat rheumatism	Watt and Breyer-Brandwijk ,1962
<i>Hermbstaedtia odorata</i> Wild Cockscomb Family: Amaranthaceae	Rooi-aarbossie	Leaves	Cleansing stomach wash alone or with <i>Acaccia xanthophloea</i> and <i>Cappa</i>	Hutchings <i>et al.</i> , 1996
<i>Hydnora africana</i> Thunb. Family: Hydnoraceae	Warty Jackal Food, Jakkalskos Kanip	Tuber	Diarrhoea, plant dried ground raw for dysentery, amenorrhoea, swollen glands	Watt and Breyer-Brandwijk ,1962

<i>Hypoxis latifolia</i> Hook. Family: Hypoxidaceae	African potato	Tuber	Headaches, dizziness, mental disorders, to treat cancers, inflammation, HIV, diarrhoea	<a href="#">Singh, 1999;</a> <a href="#">van Wyk, 2000</a>
<i>Pelargonium sidoides</i> Family: Geraniaceae	Rose- scented Pelargonium	Root	Gonorrhoea, diarrhoea, dysentery, root decoction severe diarrhoea, stomach ailment in children	<a href="#">Hutchings et al., 1996</a>
<i>Psidium guajava</i> Family: Myrtaceae	Guava	Leaves	Leaves used for diarrohea, Infusion of leaves for bloody diarrhoea, infusion as enema for severe diarrhoea	<a href="#">Hutchings et al., 1996</a>
<i>Scilla nervosa</i> (Burch.) Jessop Family:Hyacinthaceae	White Scilla	Corms	Rheumatic fever, dysentery. All purpose herb.	<a href="#">Rood, 1994;</a> <a href="#">Silayo et al., 1999</a>

Key: NA= Not available

obtained by re-dissolving in acetone or methanol as the case may be to yield 10 mg/ml solutions. Plant materials were kept in air-tight containers while extracts were kept at 4°C in the dark.

### 5.2.3. TLC analysis of extracts

Thin layer chromatography (TLC) was used to determine the composition of extracts. The TLC plates were prepared in duplicate and developed in different solvent systems according to [Eloff \(1998\)](#): Benzene: ethanol: ammonium hydroxide (BEA) (36:4:0.4); Ethylacetate: methanol: water (EMW) (40:5.4:4);

Chloroform: ethylacetate: formic acid (CEF) (20:16:4). An aliquot of 10 µl of extract was separated by TLC (Merck, Kieselgel 60 F<sub>254</sub>) in a closed, saturated TLC tank. Chromatograms were visualized under visible and ultraviolet light (254 nm and 360 nm, Camac Universal UV lamp TL-600). One TLC plate per solvent system was then sprayed with Vanillin-sulphuric acid (0.1 g vanillin, 28 ml methanol, 1 ml sulphuric acid) for the detection of higher alcohols, phenols, steroids and essential oils (Stahl, 1988). The plates were heated at 105°C until the colours of chromatograms were completely developed.

For the qualitative evaluation of a given substance, the R<sub>f</sub> value (retention factor) on TLC was used as the parameter for comparison. R<sub>f</sub> values of substances = ratio of distance start – substance zone to distance start – solvent front and specific chemical reactions. An hypothetical TLC plate showing this is seen in figure 5.1.

R<sub>f</sub> values of substances =  $\frac{\text{distance starting line} - \text{middle of spot}}{\text{distance starting line} - \text{solvent front}} = \frac{b}{a}$   
A further qualitative assignment is by the visualisation of native fluorescence of separated substances which is excited by UV (Ultraviolet) light at 254 nm and 366 nm but mostly long-wave UV.

#### 5.2.4. Determination of minimum inhibitory concentration

The minimum inhibitory concentration (MIC) values of plant extracts against the enteric pathogens were determined in 96 well microtiter plates (Eloff, 1998). The test organisms used were *Escherichia coli*, *Enterococcus faecalis*, *Pseudomonas aeruginosa*, *Staphylococcus aureus*, *S. typhi*, *S. enterica* serovar

Typhimurium, *Shigella flexneri* type 1b and *Sh. sonnei* phase II. A McFarland No1 standard suspension of bacteria inoculum was prepared in Mueller-Hinton Broth. After filling each well with 100  $\mu$ L sterile distilled water and a series of two-fold dilutions of extract (10 mg/mL), 100  $\mu$ L of the inoculum was added to the well to make a final volume of 300  $\mu$ L. Plates were incubated at 37°C for 18 h. An hour before the end of incubation, 40  $\mu$ L of 0.2 mg/mL INT (*p*-iodonitrotetrazolium salt) solution was added to each well. The lowest concentration where growth was inhibited was recorded as the minimum inhibitory concentration (MIC). This was indicated by a clear well after incubation with INT as against pink colouration.

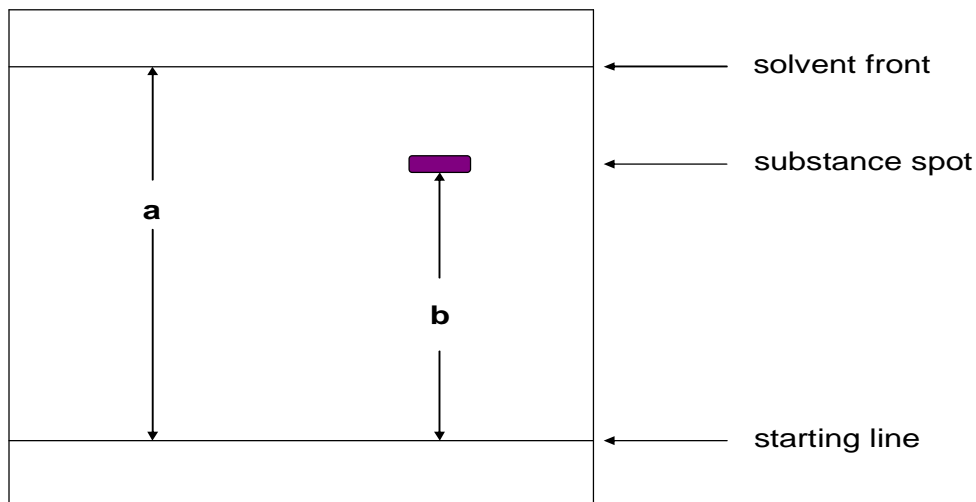


Figure 5.1. A hypothetical TLC plate showing parameters for  $R_f$  value

#### 5.2.5. Bioautographic assay

##### 5.2.5.1. Preparation of TLC plates for bioautography

The bioautography procedure as described by Begue and Kline (1972) was used to identify bioactive chromatograms of plant extracts. The duplicate of TLC

plates prepared in section 2.3 were dried overnight under a stream of air to remove residual TLC solvents which may be harmful to bacteria.

#### 5.2.5.2. Preparation of bacteria

A 10 ml of overnight broth culture of test bacteria in Mueller Hinton broth (Merck) was centrifuged at 5300 x g for 20 minutes. The supernatant was discarded and the pellet was re-suspended in 2– 4 ml of fresh broth.

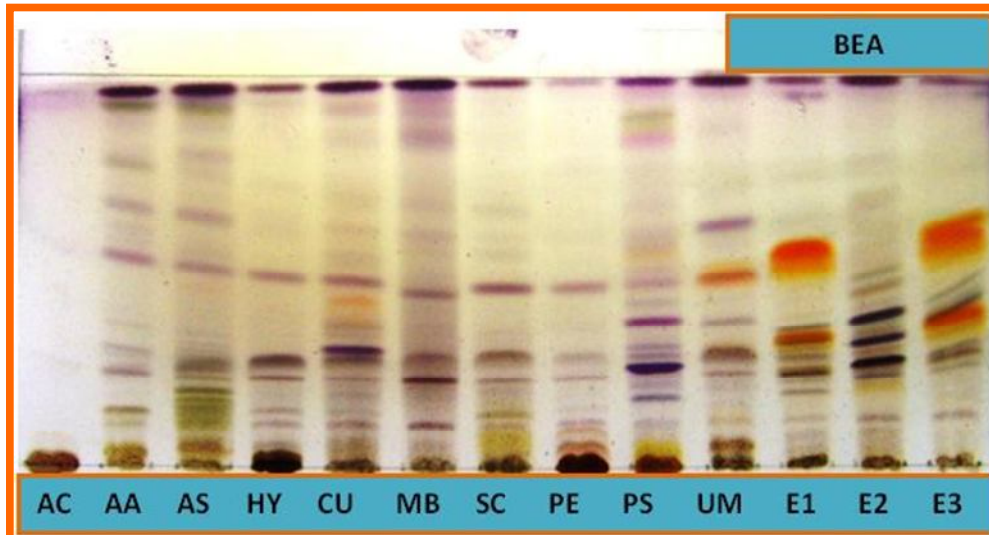
#### 5.2.5.3. Bioassay method

The dried chromatographic plates were sprayed with the test bacteria until they were completely wet. The plates were incubated overnight at 37°C in a clean chamber at 100% relative humidity. After overnight incubation, plates were sprayed with a 2 mg/mL solution of INT (*p*-iodonitrotetrazolium violet, Sigma Chemicals). Plates were returned into incubator and monitored for colour development. Inhibition of growth was indicated by clear or yellow zones on chromatogram.

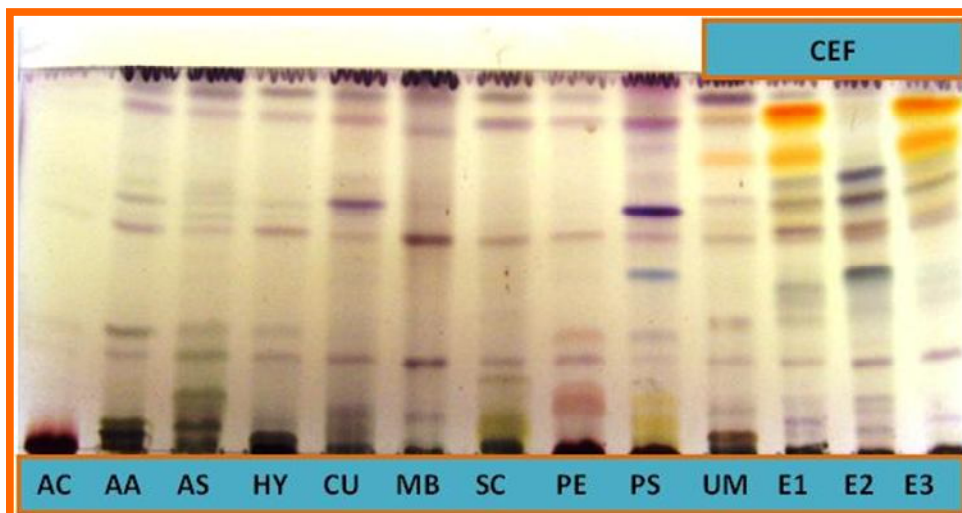
### 5.3. Results

Acetone and methanol extracts of plants yielded upon separation more compounds than the aqueous extracts; hence, water was not a good eluting solvent. This is similar to the observation of [Eloff \*et al.\* \(2005\)](#). The chromatograms of most extracts were best eluted by the medium polar (CEF) and polar extractants (EMW) separating compounds in extracts into bands based

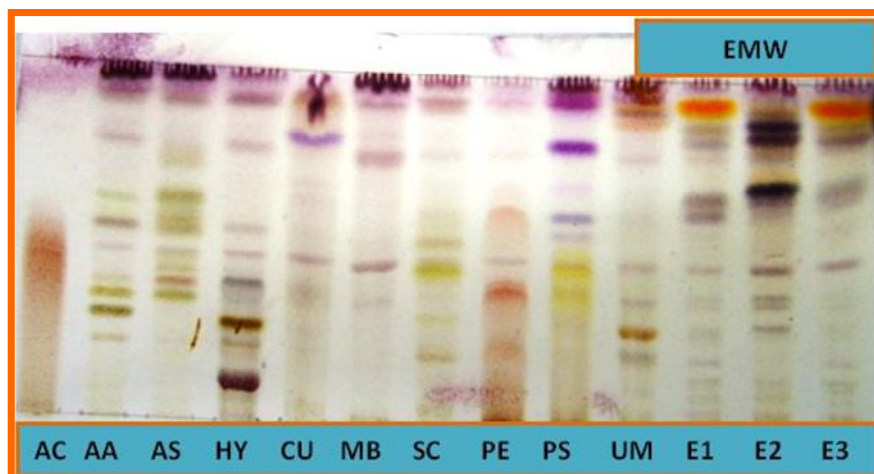
on polarities. The TLC fingerprints of the different chromatograms with the various solvent systems are shown in figures 5.2, 5.3, 5.4



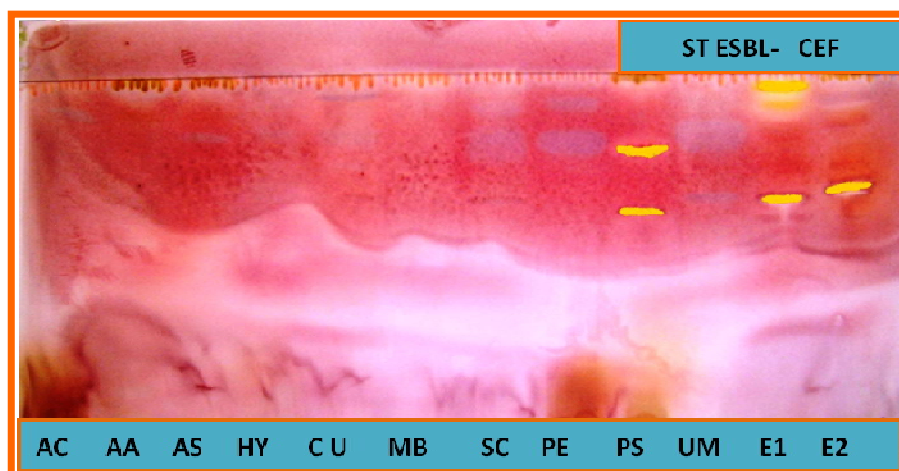
**Figure 5. 2.** TLC separation of components of the different plant extracts with BEA as eluent and vanillin-sulphuric acid spray reagent. For name of extracts lanes from left to right see list of abbreviations.



**Figure 5. 3.** TLC separation of components of the different plant extracts with CEF as eluent and vanillin-sulphuric acid spray reagent. For name of extracts lanes from left to right see list of abbreviations.



**Figure 5. 4.** TLC separation of components of the different plant extracts with EMW as eluent and vanillin-sulphuric acid spray reagent. For name of extracts lanes from left to right see list of abbreviations.

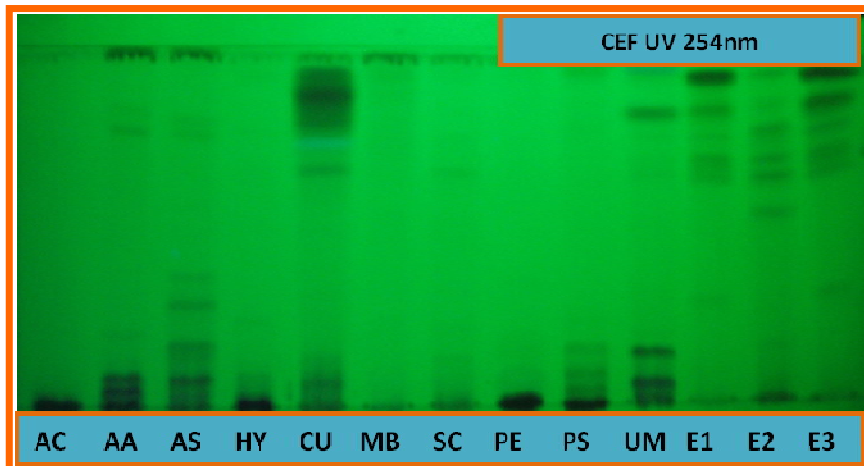


**Figure 5.5.** Bioautograms of components of the different plant extracts with CEF as eluent sprayed with *S. Typhimurium*. For name of extracts lanes from left to right see list of abbreviations.

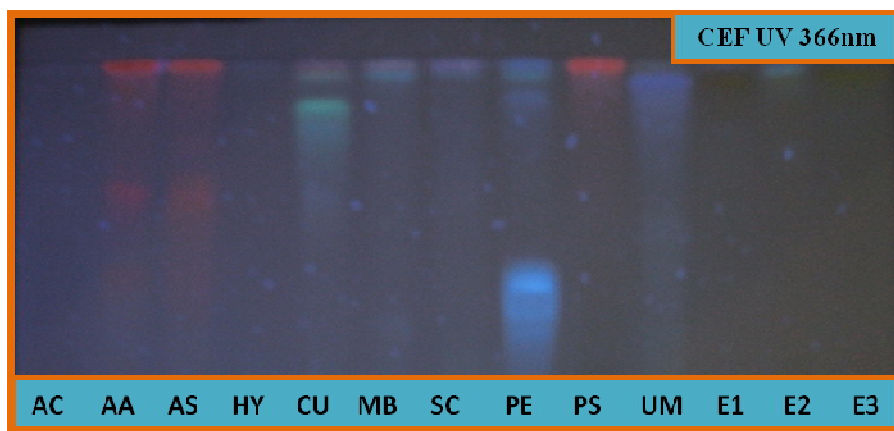
The TLC plates as captured under short and long-wave UV were as shown in figures 5.6A and 5.6B respectively. The characteristic green and blue fluorescence in lanes 5 to 8 and 10 under long-wave UV light (366 nm)



presumptively indicated presence of flavonoids according to the TLC evaluation scheme of Wagner and Bladt (1996), whereas spots of quenching of the TLC



**Figure 5. 6A.** TLC separation of components of the different plant extracts with CEF as eluent viewed under UV 254 nm before vanillin-sulphuric acid reagent spray and heat treatment. Lanes from left to right: AC-*Acacia mearnsii*, AA, AS, HY, CU, MB, SC, PE, PS, UM, E1, E2, E3.



**Figure 5. 6B.** TLC separation of components of the different plant extracts with CEF as eluent viewed under UV 366 nm before vanillin-sulphuric acid reagent spray and heat treatment. Lanes from left to right: AC-*Acacia mearnsii*, AA, AS, HY, CU, MB, SC, PE, PS, UM, E1, E2, E3.

fluorophor appeared as dark zones against light green fluorescent background with short-wavelength UV light (254 nm). These evaluation methods were further augmented with the non-specific post-chromatographic charring

detection technique (spraying with vanillin-sulphuric acid and heat treatment) (Jork *et al.*, 1989). Based on the chosen visualization spray reagent, most solvents extracted at least seven compounds with the exception of extract of *Acacia mearnsii*. The  $R_f$  values of major compounds eluted with CEF (Figure 5.3) were AA (0.59, 0.67, 0.89), AS (0.57, 0.89), HY (0.59, 0.88), CU (0.26, 0.65, 0.86), MB (0.18, 0.48, 0.84), SC (0.18, 0.24, 0.48, 0.86), PE (0.26, 0.30, 0.57, 0.88), PS (0.18, 0.47, 0.57, 0.64, 0.88), UM (0.18, 0.56, 0.77, 0.84, 0.88), E1 and E3 (0.24, 0.59, 0.65, 0.71, 0.79, 0.89), E2 (0.26, 0.50, 0.60, 0.68, 0.71).

The bioautography results revealed different fractions of the extracts which were responsible for the antibacterial activity. EA, EC and *P. guajava* gave one or two major bands of bioactive compounds (Figure 5.5). There were two major antibacterial compounds from PG with  $R_f$  values of 0.64 and 0.79, two from EA with  $R_f$  values of 0.65 and 0.88, and one from EC with  $R_f$  values of 0.68 which inhibited the growth of *S. enterica* serovar Typhimurium with CEF used as the solvent system. Active antibacterial compound was shown as clear or yellowish spot of inhibition of the growth of test organism by bioautogram. The pinkish contrasting area of bacterial growth was indicative of non-cleavage of the tetrazolium salt to yield the pinkish or purplish formazan product seen in the background (Begue and Kline, 1972). Little or no correlation existed between the MIC values and bioautography of some plant extracts because many of the components extracted did not show area of antibacterial activity, even though there were several chromatograms shown with the chemical detection. For

instance *A. arborescens* and *A. striata* had impressive MIC values but no bioactive bioautogram was shown for these plant species. This observation may be attributable to volatility, decomposition or instability of bioactive components during the course of the bioassay. For the extracts showing bioactive compounds (PS, E1 and E2) the antibacterial activity resided mostly in non-polar compounds.

The MIC values of the plants extracts ranged from 0.039 mg/mL and 2.5 mg/mL after 24 h of incubation. The average MIC values vary for the different bacterial species with the lowest in *S. typhi* (Table 5.2.). Of all the crude plant extracts evaluated, *A. arborescence*, *C. uncinulata*, *E. autumnalis* and *P. guajava* showed considerable antibacterial activities having minimal MIC between 0.039 mg/mL and 0.078 mg/mL (red highlights, Table 5.2.) which were comparable to that of the reference antibiotic (gentamicin).

#### 5.4. Discussion

It is a known fact that non polar bioactive compounds may not be extracted with water, however in traditional practice, water is used as extractant in most preparations hence water was also included as extraction solvent for the selected plants. However, water was not a good eluting solvent compared with acetone or methanol which yielded upon separation more compounds than the aqueous extracts. This is similar to the observation of Eloff *et al.* (2005). Acetone and methanol extract of these plants also possessed better bioactivity than the aqueous extracts. The very limited activity of the aqueous extracts agreed with

Table 5.2. Average MIC values of plant extracts at 2 h and 24 h

BACTERIA		PLANT EXTRACTS AND ANTIBIOTIC CODES											
CODES	AC	AA	AS	E1	E2	HY	IQ	MB	SC	PE	PS	UM	
EC 2H	1.25	2.5	2.5	0.625	2.5	2.5	2.5	2.5	2.5	1.25	0.156	2.5	0.039
EC 24H	1.25	0.625	0.625	0.312	0.625	2.5	1.25	2.5	2.5	1.25	0.312	1.25	0.078
EF 2H	0.625	1.25	2.5	0.312	2.5	2.5	1.25	2.5	2.5	0.312	0.078	2.5	0.625
EF 24H	0.625	0.039	0.039	0.156	0.078	2.5	0.625	2.5	0.312	0.625	0.156	0.312	0.625
PA 2H	0.312	1.25	1.25	0.312	0.312	2.5	0.312	1.25	0.078	0.078	0.039	0.078	2.5
PA 24H	1.25	0.312	0.625	0.312	0.625	1.25	1.25	2.5	0.078	1.25	0.312	1.25	2.5
SA 2H	0.312	2.5	2.5	0.078	0.312	1.25	0.625	2.5	2.5	0.156	0.078	2.5	0.078
SA 24H	0.312	0.018	0.018	0.312	0.156	0.312	0.156	0.078	0.156	0.312	0.156	0.078	0.078
SI 2H	1.25	0.156	0.312	0.156	0.312	2.5	0.625	1.25	1.25	1.25	0.312	1.25	0.625
SI 24H	1.25	1.25	0.625	1.25	2.5	2.5	2.5	2.5	2.5	2.5	2.5	2.5	2.5
St 2H	0.039	0.078	0.312	0.078	0.078	0.625	0.625	1.25	0.312	0.312	0.156	0.625	0.156
St 24H	0.312	0.156	1.25	0.625	0.312	2.5	1.25	2.5	1.25	0.312	0.312	1.25	1.25
STE- 2H	1.25	2.5	2.5	0.156	0.625	2.5	1.25	2.5	1.25	1.25	0.312	1.25	2.5
STE- 24H	1.25	0.078	0.078	0.156	0.625	1.25	1.25	2.5	0.625	1.25	0.312	0.625	2.5
STE+ 2H	1.25	1.25	2.5	0.156	0.312	2.5	0.625	1.25	1.25	1.25	0.078	1.25	0.078
STE+ 24H	1.25	0.078	0.312	0.312	0.625	2.5	1.25	2.5	1.25	1.25	0.312	0.625	0.156
SHF 2H	0.312	0.078	0.156	0.625	0.625	0.312	0.625	1.25	1.25	0.625	0.078	1.25	0.078
SHF 24H	0.625	0.018	0.078	0.078	0.312	1.25	1.25	2.5	0.625	0.625	0.312	0.312	0.078
SHS 2H	0.625	0.156	0.312	0.312	1.25	2.5	0.625	1.25	2.5	1.25	0.156	2.5	0.156
SHS 24H	0.625	0.039	0.039	0.039	0.312	1.25	0.312	1.25	0.625	0.625	0.312	0.312	0.156

Legend 1

EC 2H	<i>Escherichia coli</i> at 2h
EC 24H	<i>E. coli</i> at 24h
EF 2H	<i>Enterococcus faecalis</i> at 2h
EF 24H	<i>E. faecalis</i> at 24h
PA 2H	<i>P. aeruginosa</i> at 2h
PA 24H	<i>P. aeruginosa</i> at 24h
SA 2H	<i>Staphylococcus aureus</i> at 2h
SA 24H	<i>S. aureus</i> at 24h
SI 2H	<i>Sahnonella isangi</i> at 2h
SI 24H	<i>S. isangi</i> at 24h
St 2H	<i>S. typhi</i> at 2h
St 24H	<i>S. typhi</i> at 24h
STE- 2H	<i>S. Typhimurium</i> ESBL-ve at 2h
STE- 24H	<i>S. Typhimurium</i> ESBL-ve at 24h
STE+ 2H	<i>S. Typhimurium</i> ESBL+ve at 2h
STE+ 24H	<i>S. Typhimurium</i> ESBL+ve at 24h
SHF 2H	<i>Shigella flexneri</i> at 2h
SHF 24H	<i>Sh. flexneri</i> at 24h
SHS 2H	<i>Sh. sonnei</i> at 2h
SHS 24H	<i>Sh. sonnei</i> at 24h

Legend 2

AC	Extract of <i>Acacia mearnsii</i>
AA	Extract of <i>Aloe arborescence</i>
AS	Extract of <i>Aloe striata</i>
CU	Extract of <i>Cyathula uncinilata</i>
E1	Extract of <i>Eucomis autumnalis</i> (A)
E2	Extract of <i>Eucomis comosa</i>
E3	Extract of <i>Eucomis autumnalis</i> (B)
HY	Extract of <i>Hypoxis latifolia</i>
MB	Extract of <i>Hernbstaedtia odorata</i>
SC	Extract of <i>Scilla nervosa</i>
PE	Extract of <i>Pelargonium sidoides</i>
PS	Extract of <i>Psidium guajava</i>
UM	Extract of <i>Hydnora Africana</i>
GENT	Gentamycin

the findings of [Alanis et al. \(2005\)](#) where aqueous extracts activity was minimal compared with other extracts. The separation and qualitative analysis of crude extracts of plants were based on the microanalytical separation TLC method. The principle of TLC as an analytical tool is known for more than 100 years now and was enhanced by the pioneering work of [Egon Stahl \(1988\)](#). For the qualitative evaluation by TLC, the parameter used is not only the the  $R_f$  value (retention factor) but also the 100fold value  $hR_f$ . The  $R_f$  values are between 0 and 1 but best between 0.1 and 0.8 (i.e. 10 – 80 for  $hR_f$ ). The  $R_f$  values of most of the separated compounds ranged between 0.18 and 0.8 except for a few compounds, hence these values were within the stipulated best  $R_f$  value range ([Nagel, n.d.](#)).

The presence of compounds such as flavonoids and triterpenoids as indicated by the TLC plates are in accordance with some other previous studies ([Heller and Tamm, 1981](#); [Della Loggia et al., 1989](#); [Amschler et al., 1996](#); [Koorbanally et al., 2006](#)). A total of seven homoisoflavonoids of varying sub-classes including a novel benzylidene type and two spirocyclic nortriterpenoids were isolated from three species of *Eucomis* by [Koorbanally et al., \(2006\)](#). The occurrence of homoisoflavonoids (homoisoflavanones or 3-benzyl-4-chromanones) is said to be restricted largely to the Hyacinthaceae. Several reports on the biological activity of homoisoflavonoids indicated their anti-inflammatory, antibacterial, antihistaminic, antimutagenic and angioprotective qualities, and value as potent phosphodiesterase inhibitors ([Heller and Tamm,](#)

1981; Della Loggia *et al.*, 1989; Amschler *et al.*, 1996). *Aloe* species are known to elaborate various phenolic compounds, including anthrone-C-glycosides, phenylpyrone derivatives and chromones (Reynolds, 1985). Of the root samples of 172 species of *Aloe*, aloesaponarin I, aloesaponarin II and laccaic acid o-methyl ester, together with their corresponding pre-antraquinones were detected in 129 species (van wyk *et al.*, 1985). Furthermore, the study revealed that 1,8 - Dihydroxyanthraquinones (chrysophanol and asphodelin) were in all the tested species except three. *A. striata* Haw was positive for the presence of chrysophanol and asphodelin while *A. arborescens* Mill was positive for the presence of chrysophanol, asphodelin, laccaic acid D-methyl ester and aloesaponol 1 (van wyk *et al.*, 1985). The laxative effects of Aloe are said to be due primarily to the 1, 8-dihydroxyanthracene glycosides, aloin A and B (formerly known as barbaloin) (Tyler *et al.*, 1988; Tyler, 1994). Aloe emodin, chrysophanol and aloin have been reported from *Aloe ferox* (Kambizi *et al.*, (2004) and these compounds were shown to possess antibacterial activities.

In most cases plant extracts were reportedly more active against Gram-positive (GP) pathogens (Vlietinck *et al.*, 1995), a similar observation was found in this study but in addition, most of the extracts had substantial activity against the selected Gram-negative (GN) enteric bacteria. *P. sidoides* gave a moderate antibacterial activity in particular against *E. faecalis*, *S. aureus* and *Shigella* species. Similarly, anti-infective properties of the commercially important *Pelargonium* have been investigated (Lalli *et al.*, 2008). *H. latifolia* did not show

good antibacterial activity against most of the tested bacteria and this is in harmony with the findings on *H. decumbens* (Chiappeta *et al.*, 1984). Even though the sterols in *Hypoxis* spp. had been reported to reduce plasma viral loads and stabilized CD4 cell counts in HIV positive patients (Bouic *et al.*, 1999), while an aqueous extract of *Hypoxis hemerocallidea* (*H. rooperi*) (62.5 µg/ml) inhibited some microorganisms, the inhibitory concentration was less potent than ciprofloxacin, the reference antibiotic (Steenkamp *et al.*, 2006).

#### 5.5. Conclusion

This preliminary screening showed that the crude extracts of some of the herbs used in traditional medicine in our area of study have potentials as antibacterial agents. *A. arborescens*, *A. striata*, *C. uncinulata*, *E. autumnalis* and *P. guajava* are particularly promising in the context of this study since the activities of the crude extracts compared reasonably with gentamicin. This gives scientific credence to the use of these plants. Further studies on the active compounds and evaluation of the safety of the plants and or their components are warranted. The need for continued screening of indigenous plants is inevitable because of the dynamic nature of infectious agents and their continued development of resistance over time.

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## CHAPTER 6

### ISOLATION, CHARACTERIZATION AND STRUCTURAL ELUCIDATION OF BIOACTIVE FRACTIONS OF *CYATHULA UNCINULATA* (Schrad.) Schinz

#### 6.0. Abstract

*Cyathula uncinulata* (Schrad.) Schinz is used in ethnomedicine in various parts of the world. This study isolated and characterized bioactive compounds from *C. uncinulata* (Schrad.) Schinz based on its antibacterial activities from the previous plant screening. Separation of compounds from the bioactive ethyl acetate fractions of the plant was by solvent-solvent fractionation. The structure of the compounds was elucidated by nuclear magnetic resonance spectroscopy and mass spectroscopy methods. The NMR and EI-MS spectra of the isolated compound showed that the compound with formula  $C_{22}H_{38}O_7$  and molecular weight 414.5329, has a long aliphatic chain and is said to be made up of sugar and fatty acyl moiety. The MIC of fractions of extracts ranged from 0.39 mg/mL to 2.5 mg/mL, with the lowest MIC observed in ethyl-acetate fraction. The MIC of the selected sub-fraction of the ethyl acetate fractionation (SSC 1) was 0.63 mg/mL. The MIC of the final purified compound was 0.34 mg/mL, indicating considerable bioactivity. This study isolated a glycosylated oleanolic acid from *C. uncinulata* (Schrad.) Schinz. The compound possessed considerable bioactivity in comparison with the crude extract and the control antibiotic. This is an indication that this plant may be a candidate template for new antimicrobial.

Key words: *Cyathula uncinulata*, extract, fraction, MIC, bioactive, compound

## 6.1. Introduction

*Cyathula uncinulata* (Schrad.) Schinz is a large genus of sub-shrubs of about 27 species distributed in Asia, Pacific Islands, Africa, and North and South America belonging to the family *Amaranthaceae*. The stems are erect or ascending and leaves are opposite, petiolate with entire margin. Flowers clustered in cymose partial inflorescences, 1-3 in each cluster, hermaphroditic and partly accompanied by sterile ones. The flowers are bracts ovate, membranous and often spiny. The seeds of *C. uncinulata* are oblong or ellipsoid.

In South Africa, *C. uncinulata* (CU) was recently described as one of the flora of 1195 species of the botanically least known regions, the Sneeuberg mountain complex (Eastern Cape). This region where the plant is referred to locally as *Isinama* (Dold and Cocks, 1999); comprises one of the most prominent sections of the Great Escarpment in Southern Africa (Clark *et al.*, 2009). Previous studies on CU have reported its ethnobotanical study (Jeruto *et al.*, 2008a), antidiarrheal activity and phytochemical screening (Tomani *et al.*, 2008). In the Eastern part of former Zaire, CU is used by men as a philter or medicine for love (Yamada, 1999). Furthermore, an Ethiopian study reported a considerable consensus among traditional healers in the treatment of *Rissaa* (an ailment) by drinking a mixture of CU and leaves of *Croton macrostachyus* crushed fresh and mixed with water (Yineger *et al.*, 2008).

Various reports on the ethnomedicine and ethnobiology of the genus *Cyathula* exist. A phylogenetic analysis found that *Cyathula*, some other members of the families *Amaranthaceae* and *Chenopodiaceae* constituted a monophyletic group and hence supported the call for *Chenopodiaceae* to be merged with *Amaranthaceae* (Ogundipe and Chase, 2009). *Cyathula officinalis* Kuan (COK) was shown to contain polysaccharides which could increase mouse red cell immunity function by strengthening red cell immune adherence and cleanup of circulating immune complex (Li *et al.*, 1999). COK whose root is a commonly-used traditional Chinese herbal medicine with a wide range of pharmacological activities (Pharmacopoeia Commission of People's Republic of China, 2000) has also demonstrated anti-tumor activity. Components of COK were able to suppress the growth of mouse S180 tumor, H22 liver cancer cells (Chen and Liu, 2001). In an antiviral experiment, sulfated derivative of RCP, a kind of polysaccharide extracted from COK was adjudged to express comparable antiviral activity with the commonly used antiviral drug ACV (0.5 mg/mL) at concentrations of 2.0 mg/mL and 4.0 mg/mL.

In their bid to reinvestigate phytoecdysteroids of the *Cyathula* species, Okuzumi and co-investigators (2005) isolated two cyasterone stereoisomers and a known cyasterone reported to possess antitumor-promoting activity (Takasaki *et al.*, 1999). Several C<sub>29</sub>-phytoecdysteroids such as cyasterone (Takemoto *et al.*, 1967; Slama *et al.*, 1993), capitasterone (Takemoto *et al.*, 1968) and makisterone C (Imai *et al.*, 1968) possess potent insect molting

hormone activity. In a clinical experiment, a traditional Chinese medicine: concentrated herbal extracts of cooked *Cyathula* and concoction of 9 other ingredients restored ovarian function effectively and promptly in a patient with premature ovarian failure (POF) and 8-year secondary amenorrhea, thus the combination may offer another option for treating infertility in patients with POF (Chao *et al.*, 2003). *Cyathula* is a component of some Chinese formulations acclaimed to be therapeutic against endometriosis and have severe blood stasis effects (Dharmananda, 2002).

The shoots of *C. prostrata* (L.) Bl. was reported to be used in India ethnotherapy of dysentery, skin diseases and as an appetizer (Kala 2005). In Kenya, the leaves and roots of *C. schimperiana* non Moq are used as decoction (internal) for malaria, as antidiarrhoea, against fungal infections while the root of *C. cylindrica* Moq roots is used as decoction (internal) for malaria, purgative and as emetic (Jeruto *et al.*, 2008b). Among the native Ecuadorian, the Quichua people apply the flowers and shredded leaves of *C. achyranthoides* to dog bites (Lescure *et al.*, 1987) while the Shuar eat the raw young leaves to relieve headaches (Russo, 1992).

Previous studies have isolated bioactive compounds from some members of this Genus. Glycoside and oleanic acids were isolated and tested for their inhibitory activities by Zhou and his co-worker (2005). Fructans which exist as a wide range of oligo- and polysaccharides in many species of bacteria, fungi, and plants were isolated from COK by Chen and Tian (2003). Bioassays showed that



the graminans-type fructan that is comprised of a  $\beta$ -D-fructofuranosyl backbone could inhibit growth of Lewis pulmonary carcinoma implanted in mice (Chen and Tian, 2003). Recently, a new heterocyclic compound, named 5, 5'-diisobutoxy-2, 2'-bifuran was isolated for the first time from COK (Liu *et al.* 2010). From our preliminary screening, *C. uncinulata* was among the plants which gave promising MIC values. However, based on the literature, studies on bioactive compounds from this plant species are very rare. This study explores the active components of *C. uncinulata* and their biological effects.

## 6.2. Materials and methods

### 6.2.1. Plant collection

The leaves of *C. uncinulata* were collected in the Eastern Cape province of South Africa. *C. uncinulata* was identified by the Kei Herbarium curator, Dr. Immelman in the Department of Botany, Walter Sisulu University, South Africa where voucher specimen has been deposited. South Africa. The photographic images of CU are shown in Figure 6.1. The plant materials were air-dried at room temperature. Dried plant materials were ground to powder and stored in the dark at room temperature for further analysis.

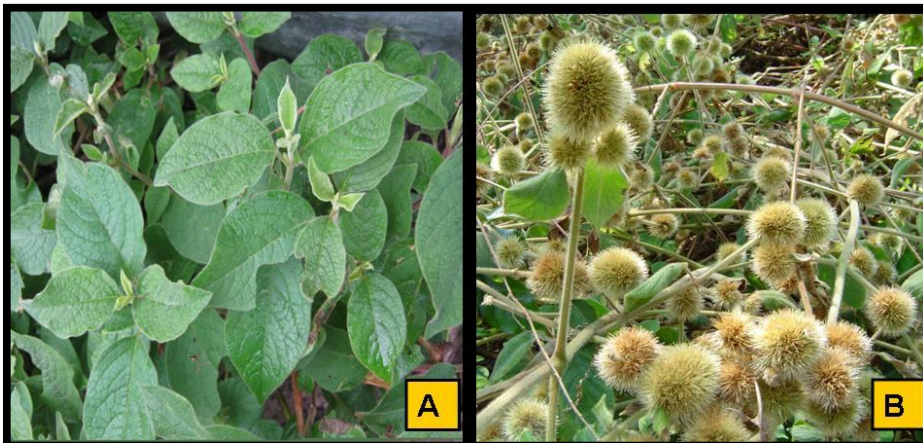


Figure 6.1A. Leaves of *C. uncinilata* plant (Picture taken from source garden at Flagstaff, Eastern Cape, South Africa). Figure 6.1B. *C. uncinilata* showing the plant flowering. Source [http://www.metafro.be/prelude/view\\_symptom?si=V\(027\)](http://www.metafro.be/prelude/view_symptom?si=V(027))

#### 6.2.2 Extraction of plant material

Powdered plant materials were exhaustively extracted with methanol (MeOH). The supernatant was filtered through cotton wool and Whatman No. 1 filter paper using a Buchner funnel. The extract was concentrated at 45 °C using a Rotavapor (Eyela N-1100, Rikakikai, China). The reduced extract was transferred to a pre-weighed glass vial and sunction-dried at room temperature with a vacuum pump (ULVAC KIKO, Tokyo). The quantity extracted was then determined to be 2g.

#### 6.2.3. Solvent-solvent fractionation of dried plant extract

The dried methanol extract of *Cyathula* leaves was subjected to solvent-solvent fractionation as previously described by Oshima *et al.* (1986). The MeOH extract was partitioned sequentially in ethyl acetate (EtoAc), *n*-butanol and water. The EtoAc fraction (1 g) was subjected to column chromatography over 100 g silica gel 60 (70- 230 mesh) eluting with *n*-hexane–ethyl acetate (10:1 →

4:1 → 1:1 → 1:4, v/v) and ethyl acetate–MeOH (10:0 → 9:1 → 4:1 → 1:1, v/v) to yield fractions designated as SSC1-1 to SSC1-8. Fraction SSC1-5 (20 mg) denoted SSC2 was further subjected to column chromatography over a lipophilic Sephadex (bead size 25-100 μL; Sigma-Aldrich) eluting sequentially with Chloroform and Chloroform-MeOH (20:1 → 9:1). The sub-fractions obtained were combined based on their TLC fingerprint pattern to yield 4 sub-fractions SSC2-1-2, SSC2-3 (3.6 mg); SSC2-4-6 (14.3 mg) and SSC2-7-10 (1.1 mg). A final column chromatography was performed with sub-fraction SSC2-4-6 now denoted as SSC3 using a finer silica gel 60 (40 – 50 μm Cica-Reagent, Kantochemical, Japan). The solvent flow of eluent was n-hexane- acetone (8:1 → 4:1 → 2:1) and acetone only. The flow through with similar  $R_f$  values from the TLC fingerprint were pooled together to yield four sub-fractions designated SSC3-1-8; SSC3-9-10; SSC3-11-14 and SSC3-15. A schematic pictograph of the steps involved in the fractionation of extract and fractions is shown in [figure 6.2](#).

#### 6.2.4. TLC fingerprinting of fractions

The dried fractions were dissolved to a concentration of 10 mg/mL in methanol and TLC fingerprinting was done as described previously ([Stahl, 1988](#)). Several mobile systems were used. For the TLC of SSC1 fractions the mobile systems were H: E 4:1, H: E 1:1, C: M 20:1, C: M 8:1, C: M 2:1 and C: M: W: A 1:1:0.1:0.05. For the TLC of SSC2, the mobile systems were H: A 2:1 and C: M 20:1. Finally for the TLC of SSC3, the mobile system was C: M 20:1. The detecting agent for chromatograms was anisaldehyde.

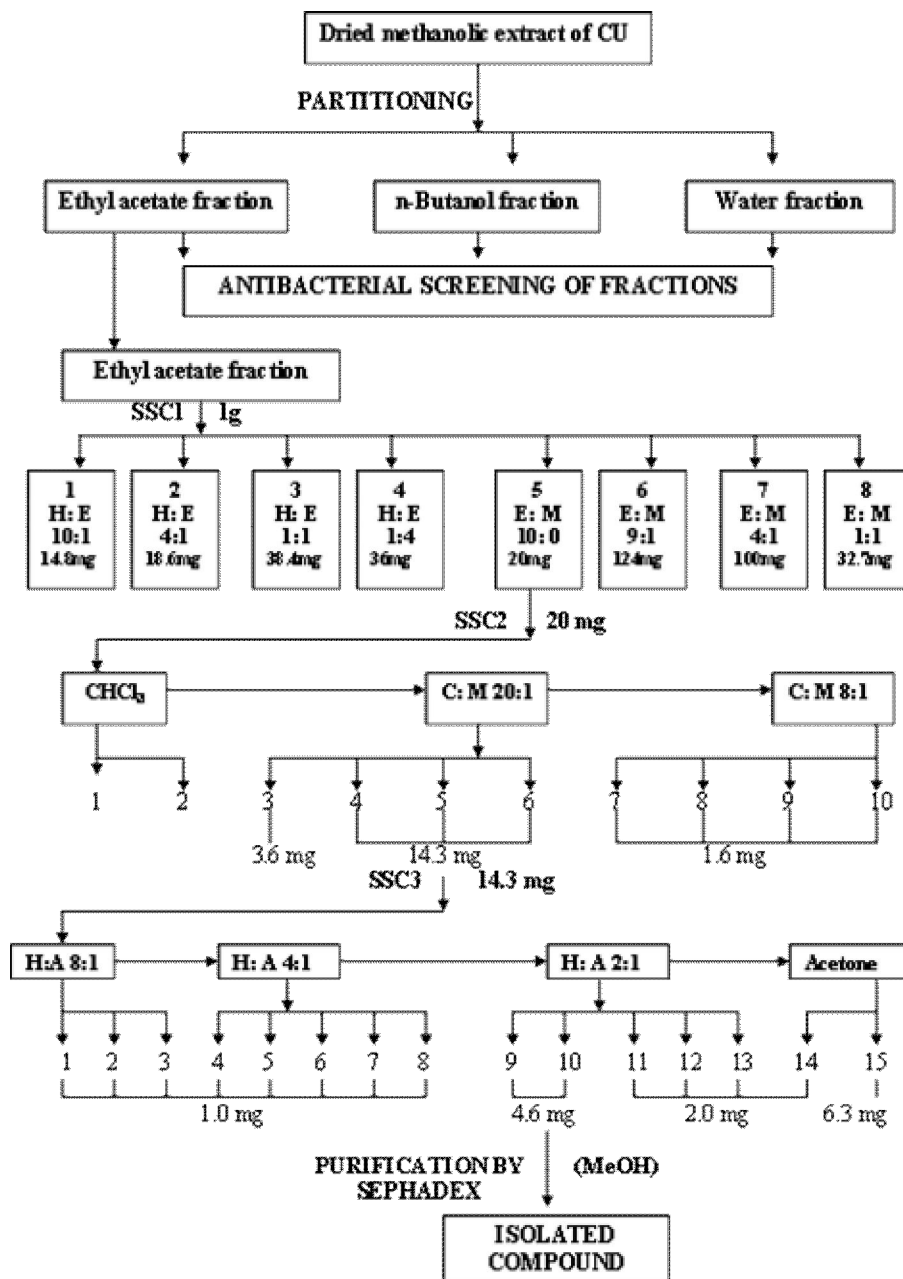


Figure 6.2. Schematic diagram of Solvent-Solvent fractionation of *C. uncinulata*

### 6.2.5. Antimicrobial assay of fractions

The microplate dilution assay as previously described (Eloff, 1998) was used to determine the minimum inhibitory concentration (MIC) values of

fractions of *C. uncinulata* extracts against a kanamycin sensitive *Escherichia coli* HB101 strain (Lacks and Greenberg, 1977).

#### 6.2.6. Isolation of pure compounds

Based on TLC analysis and the bioassay-guided fractionation, sub-fraction SSC3-9-10 (Figure 6.2) was selected for purification and further characterization. SSC3-9-10 was purified by a lipophilic Sephadex LH-20 (bead size 25-100  $\mu\text{l}$ ; Sigma-Aldrich) using MeOH (Oshima *et al.*, 1995). The final pure compound was then subjected to NMR analysis and EI-MS.

#### 6.2.7. Preparation of pure compound for NMR and MS analysis

NMR analysis was as previously described (Oshima *et al.*, 1995). The vacuumed concentrated isolated pure compound was added to an NMR capillary tube and was dissolved by adding Chloroform-d for NMR (ACROS ORGANICS) and 99.8+% D, stab. with silver foil, 0.03 v/v % TMS (Merck) to a depth of 4 cm. The NMR capillary tube was then fitted in place for the  $^{13}\text{C}$  and  $^1\text{H}$  NMR analysis in a JEOL-AL 400 FT NMR system 400 MHz (JEOL FT NMR System AL400). Electro impact mass spectra (EI-MS) were recorded on a JMS DX-303 mass spectrometer (Guo *et al.*, 2006).

### 6.3. Results

#### 6.3.1. Solvent-solvent fractionation yield

The solvent-solvent fractionation yielded four fractions. The result of fraction yield is tabulated below (Table 6.1). The highest quantity of plant

material remained in the water fraction; the quantity of plant material extracted in ethyl- acetate fraction was 300.7 mg while the lowest quantity was obtained in the methanol extract.

<b>Table 6.1</b> Quantity of the fractions extracted from solvent-solvent fractionation of methanolic extract of <i>Cyathula uncinulata</i> leaves		<b>Table 6.2</b> Average MIC values of the fractions of <i>Cyathula uncinulata</i> leaf extracts tested against <i>E. coli</i>	
<b>Fractions</b>	<b>Quantity extracted (mg)</b>	<b>Fractions</b>	<b>MIC of fractions against <i>E. coli</i> (mg/ml)</b>
Methanol	100.1	Methanol	1.09
Ethyl acetate	300.7	Ethyl acetate	0.39
n-butanol	100.7	n-butanol	2.34
Water	739.9	Water	2.50
Total of extract fractions	1242.4	Kanamycin	0.19

In total, 1242.4 mg (approximately 1.2 g) was extracted from the 2 g starting methanol extract of *C. uncinulata* giving a 60 % yield.

### 6.3.2. TLC fingerprints

The TLC fingerprints of *C. uncinulata* after bulk extraction are shown below (Figure. 6.3). The solvent systems were Hexane and Ethyl acetate ratio one to one with 4 times capillary application of extract on TLC (H:E 1:1x 4); Hexane and Ethyl acetate ratio one to one with one capillary application of extract on TLC (H:E 1:1x1); Hexane and Ethyl acetate ratio four to one with 4 times capillary application on TLC (H:E 4:1x 4); Hexane and Ethyl acetate ratio

four to one with one capillary application of extract on TLC (H:E 4:1x1); Chloroform and Methanol ratio two to one with 4 capillary application of extract on TLC (C : M 2:1x 4); Chloroform and Methanol ratio eight to one with one capillary application of extract on TLC (C:M 8:1x1); Chloroform and Methanol ratio twenty to one with one capillary application of extract on TLC = C:M 20:1x1);

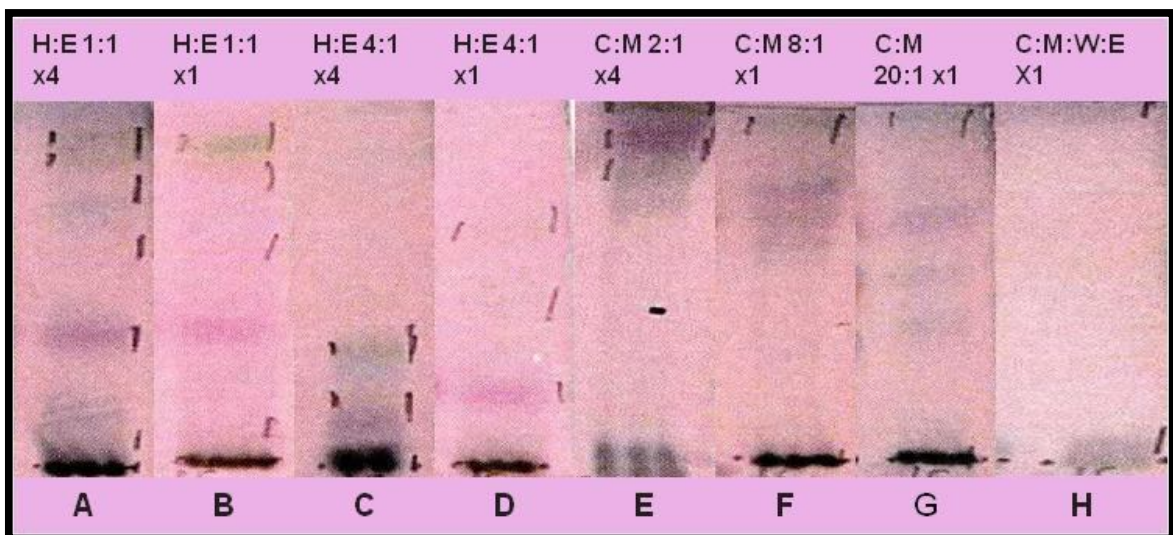
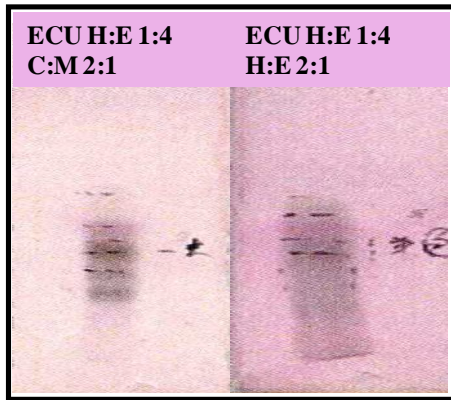


Figure. 6.3. TLC fingerprints of *C. uncinulata* after bulk extraction

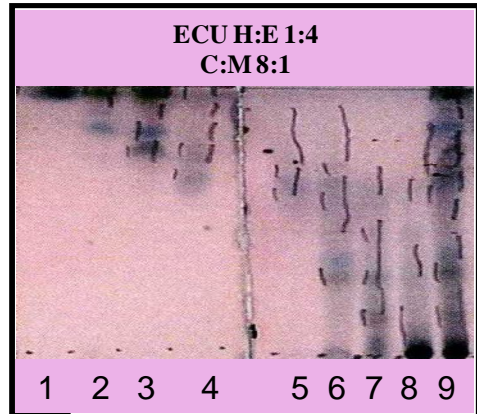
Chloroform, Methanol, water and Ethyl acetate with one capillary application of extract on TLC (C:M:W:A 1:1:0.1:0.05). A better separation of plant extract components was obtained with the hexane-ethyl acetate combinations compared to chloroform-methanol. The TLC plates of the further sequential fractions developed in anisaldehyde are shown in figures 6.4A to 6.4G. Lanes having



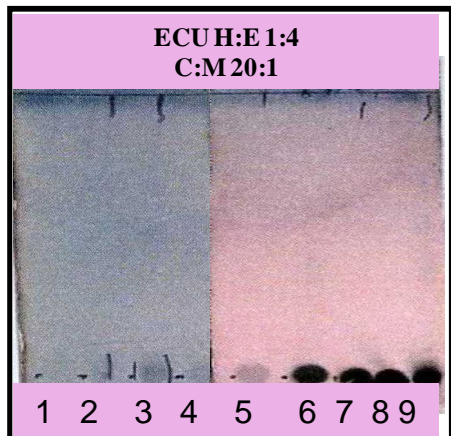
compounds with the same  $R_f$  values were pooled together. These pooling together of fractions in lanes 9 and 10 (Figure 6.4G) led finally to the isolation of a pure compound with  $R_f$  of 0.38.



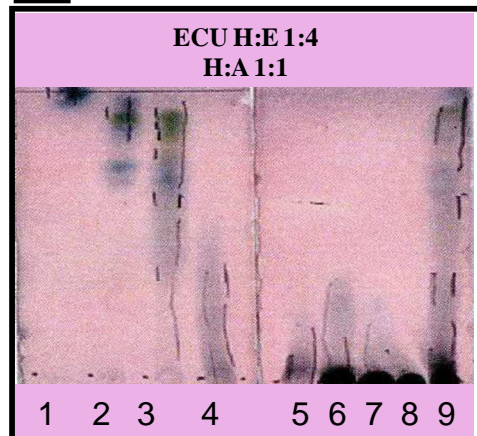
**A**



**B**

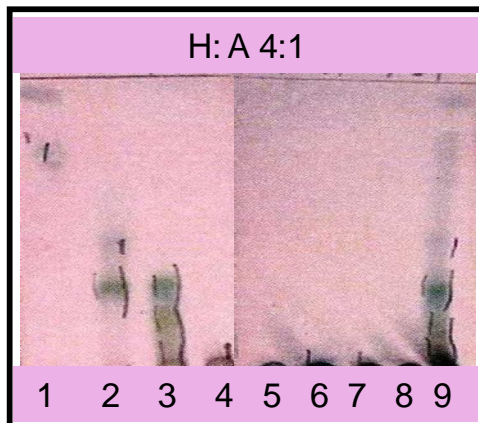


**C**

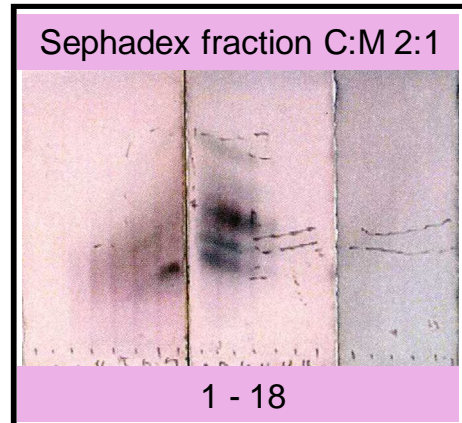


**D**

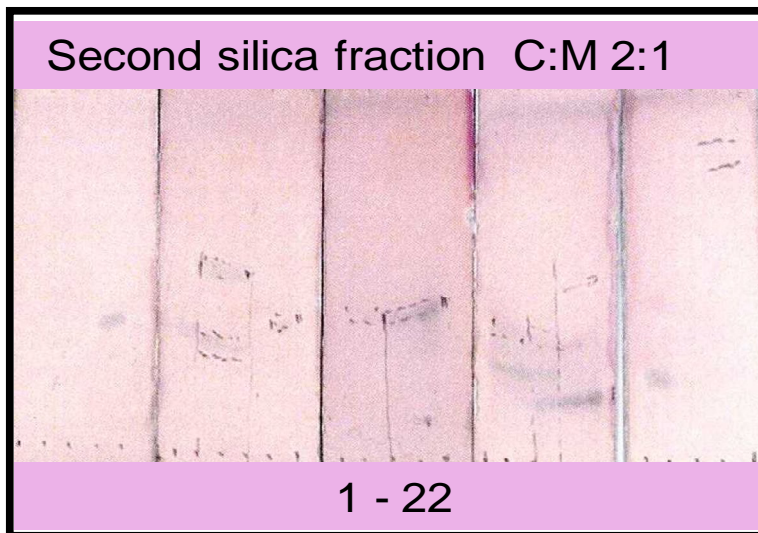




**E**



**F**



**G**

Figure 6.4. TLC chromatogram showing fractions obtained from open column chromatography of ethyl acetate fraction of the methanol extract of *C. uncinulata* leaves. A- TLC for SSC1; the mobile systems were H: E 2:1 and C: M 20:1. B, C, D, E-TLC for SSC2; the mobile systems were C: M 8:1, C: M 20:1, H: A 1:1, H: A 1: 4 respectively. F, G- TLC for SSC3; mobile system was C: M 2:1. All TLC plates were detected with anisaldehyde. (A= Acetone; H=Hexane; E=Ethyl acetate; C=Chloroform and M= Methanol).

### 6.3.3. Minimum inhibitory concentrations of the fractions

The MICs of the fractions of *C. uncinulata* against *E. coli* are provided in [Table 6.2](#). The MIC ranged from 0.39 mg/mL to 2.5 mg/mL whereas the MIC of Kanamycin, the positive control was 0.19 mg/mL. The lowest MIC was observed in ethyl-acetate fraction while the highest MIC values were recorded in n-butanol and water fractions. The MIC of the selected sub-fraction of the ethyl acetate (SSC 1) fractionation was 0.63 mg/mL while for the final purified compound; the MIC was 0.34 mg/mL

### 6.3.4. Identification and elucidation of structure of the isolated compound

The NMR and the EI MS spectra of the isolated compound are as shown in [appendices 4A to 4C](#). The NMR spectra of the isolated compound showed that the compound has a long aliphatic chain. The proposed structure for the isolated compound as determined by <sup>1</sup>H NMR spectrum is shown in [appendix 4D](#). The formula of the compound is C<sub>22</sub>H<sub>38</sub>O<sub>7</sub> while the molecular weight is 414.5329.

## 6.4. Discussion

Solvent-solvent fractionation and column chromatography were employed to isolate the pure compound. The structure of this compound was elucidated predominantly by nuclear magnetic resonance (NMR) spectroscopy and mass spectroscopy methods. NMR essentially provides a means of determining the structure of an organic compound by measuring the magnetic moments of its hydrogen atoms. In most compounds, hydrogen atoms are attached to different

groups (as  $-CH_2$ ,  $-$ ,  $-CH_3$ -,  $-CHO$ ,  $-NH_2$ -,  $-CHOH$ -, etc.) and the NMR spectrum provides a record of the number of hydrogen or carbon atoms in the different locations. The NMR proton and EI MS spectra of the fraction yielding the pure compound are shown in [Appendix 4A-C](#). The isolated compound shown in [appendix 4D](#) is made up of sugar and fatty acyl moiety composed of hydrocarbon tails. A new glycoside, 3-O-[ $\alpha$ -L-rhamnopyranosyl-(1 $\rightarrow$ 3)-(n-butyl- $\beta$ -D-glucopyranosiduronate)]-28-O- $\beta$ -D-glucopyranosyloleanolic acid together with several other glycosides were isolated from the roots of *C. officinalis* by [Zhou and co-workers \(2005a\)](#). Glycosides of fatty acids or glycolipids are found in bacteria, yeasts and fungi but also in several plants. The functions and potential applications of this compound have been reviewed by [Kitamoto and co-worker \(2002\)](#). Sugar-based esters of fatty acids are nonionic surfactants of great potential applications. They are nontoxic, odourless, tasteless and biodegradable and because of their multi-functional properties and safety, this group of compounds has attracted attention from cosmetics, pharmaceutical, surfactant and nutrition scientists ([Kitamoto et al., 2002](#)).

The aqueous fraction of the extract of *C. uncinulata* yielded the highest quantity of plant components while the ethyl acetate fraction extracted the least ([Table 6.1](#)). However, the least antibacterial activity was recorded in this fraction as opposed to the ethyl acetate fraction which had the least MIC values of 0.39 mg/ml ([Table 6.2](#)) hence the choice of ethyl acetate fraction for further fractionation and isolation of bioactive compound. The final compound had an

average MIC of 0.34 mg/mL which was very close to 0.19 mg/mL of kanamycin, the positive control, hence possessing a considerable antibacterial activity.

Researchers have reported the isolation and biological activities of various compounds from members of the genus *Cyathula*. Four new compounds 4-[(1-ethoxy-2-hydroxy) ethyl]phenol (1), 2,3-isopropylidene cyasterone (2), 24-hydroxycyasterone (3) and 2,3-isopropylidene isocyasterone (4), together with fourteen known compounds were isolated from the *C. Officinalis* Kuan ([Zhou et al., 2005b](#)). *C officinalis* Kuan seems to be the most widely studied of the genus whereas reports on isolation of bioactive compounds from *C. uncinulata* are scarce. Other studies on the genus *Cyathula* reported mainly on biological activities and cytotoxicity effect of extracts of *C. achyranthoides* and *C. prostata* ([Sowemimo et al., 2009](#)). This study is a report on a bioactive compound from *C. uncinulata*. Further work will be required to confirm the nomenclature of this compound but going by literature ([Zhou et al., 2005a](#)), this bioactive compound may be described as a glycosylated oleanolic acid.

## 6.5. Conclusion

This study isolated a glycosylated oleanolic acid from *C. uncinulata* (Schrad.) Schinz. The compound possessed considerable bioactivity in comparison with the crude extract and the control antibiotic. This is an indication that this plant may be a candidate or serve as template for new antimicrobial. The main focus of several studies are the isolation and identification of bioactive

compounds from plants, nonetheless, it is imperative to recognize the complexity of plants and that a single compound may not be responsible for the observed activity but rather a combination of compounds acting by synergism or as complements. This may further explain why bioactivity is lost in some cases in the course of isolation of active components.

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## CHAPTER 7

### CYTOTOXICITY OF SELECTED PLANTS USED IN ETHNOMEDICINE IN THE EASTERN CAPE PROVINCE OF SOUTH AFRICA



## 7.0. Abstract

Several herbs are traditionally used in the treatment of various ailments particularly in the rural areas of South Africa where herbal medicine is often the only source of health care system. Many of these herbs have not been assessed for safety or toxicity to tissues or organs of the mammalian recipients. This study evaluated the safety of some medicinal plants used inter alia in the treatment of diarrhoea, and stomach disorders. The cytotoxicity of methanol extracts and fractions of six selected plants was determined by using a modified tetrazolium-based colorimetric assay (3-(4, 5-dimethylthiazol)-2,5-diphenyl tetrazolium bromide (MTT) assay). The in vitro cytotoxicity assay on human hepatocarcinoma cell line (Huh-7) revealed that the methanol extract of *Eucomis autumnalis* had the strongest cytotoxicity with  $IC_{50}$  of 7.8  $\mu\text{g/mL}$ . Ethyl acetate and butanol fractions of *Cyathula uncinulata*, *Hypoxis latifolia*, *E. autumnalis* and *Lantana camara* had lower cytotoxic effects on the cancer cell lines tested with  $IC_{50}$  values ranging from 24.8  $\mu\text{g/mL}$  to 44.1  $\mu\text{g/mL}$  while all the fractions of *Aloe arborescens* and *A. striata* had insignificant or no cytotoxic effects after 72 h of treatment. Our results indicate that the methanol fraction of *E. autumnalis* had a profound cytotoxic effect which puts a query on its safety and hence a call for caution in its usage.

Key words: Herbs; extracts; fractions; safety; cytotoxicity; profile; treatment

## 7.1. Introduction

Various plants are used in the ethnomedicine of enteric diseases. Several studies have documented reports on some herbs used in ethnotherapy of diarrhea, dysentery, vomiting, stomach cramps and other associated ailments (McGaw *et al.*, 2000; Vieira *et al.*, 2001; Samie *et al.*, 2005). Contrary to the belief of a large proportion of the populace that anything natural is safe, many commonly used herbs cause acute toxic effects and in the long term may be toxic. The toxic effects may range from diarrhoea, hypersensitivity reactions, nausea or vomiting, to organ-targeted toxicity; immunotoxicity, embryo/foetal and prenatal toxicity, mutagenicity/genotoxicity, hepatotoxicity, nephrotoxicity, presence of epileptogenic compounds, cardiac toxins, gastrointestinal toxins to carcinogenicity (Smolinske, 2005). Other adverse effects of herbal medicines may include cardiovascular, hepatic, renal, neurological and dermatologic toxic effects. In the review by Luyckx and Naicker (2008), it was stated that 'drug-induced nephrotoxicity reportedly contributes to up to 26% of cases of hospital-acquired acute kidney injury (AKI) and 18% of cases of community-acquired AKI globally, and folk remedies account for up to 35% of cases of AKI in the developing world.'

Many of the plants widely acclaimed to be of therapeutic values have not enjoyed vigorous assessment of their safety profiles. A number of complications arising after the administration of medicinal herbs have been reported. Foyaca-Sibat *et al.* (2001) described case reports of two patients with neuromyotonia not linked to malignancies. The patients were reported to have developed acute

renal failure while under treatment with herbal medications by their traditional healer in the former Transkei region of South Africa.

Other researchers have also identified medicinal plants with potential toxicity such as the extracts of *Athrixia phyllicoides* DC. (Bush tea) (McGaw *et al.*, 2006); extracts and a flavonol glycoside from *Bauhinia galpinii* (Aderogba *et al.*, 2007). Genotoxicity and mutagenic effects in the *Salmonella* microsome assay respectively have been reported in *Crinum macowanii*, *Chaetacme aristata* Planch. (Celastraceae), *Plumbago auriculata* Lam. (Plumbaginaceae), *Catharanthus roseus* (L.) G.Don. (Apocynaceae) and *Ziziphus mucronata* Willd. (Rhamnaceae) (Elgorashi *et al.*, 2003). Additionally, Michellamine B-an alkaloid dimers isolated from *Ancistrocladus korupensis* was inhibitory to several laboratory and clinical strains of HIV-1, including the AZT resistant strain G910-6 and the pyridinone-resistant strain A17; as well as strains of HIV-2. However, the high toxicity of this compound to several human cell lines prevented its further evaluation (Boyd *et al.*, 1994). Data on the cytotoxic assessments of herbs are very few compared with the huge number of plants acclaimed to have therapeutic values (Oshima *et al.*, 1986; Neuwinger, 2000). This study investigated the cytotoxic effects of *Aloe arborescens*, *A. striata*, *Cyathula uncinulata*, *Eucomis autumnalis*, *Hypoxis latifolia* and *Lantana camara* commonly used in the treatment of gastrointestinal infections in the Oliver R. Tambo District Municipality (ORTDM), Eastern Cape Province, South Africa.

## 7.2. Materials and methods

### 7.2.1. Plant material, extraction and fractionation

Fresh plant parts were collected in ORTDM, Eastern Cape Province, South Africa between July 2008 and February 2010. The plants were identified in the Kei herbarium, Walter Sisulu University, South Africa where voucher specimens have been deposited. Information on the selected herbs is presented in [Table 7.1](#) ([van Staden, 1981](#); [Cunningham, 1993](#); [Pooley, 1993](#); [Inada \*et al.\* 1995](#); [Dold and Cocks, 2000](#); [Van Wyk and Gericke, 2000](#); [Abdulla \*et al.\*, 2009](#); [Bisi-Johnson \*et al.\*, 2010](#)). The air-dried plant parts were extracted three times with methanol (Merck, Japan) and filtered using a Buchner funnel and Whatman No. 1 filter paper. The extracts were concentrated under reduced pressure at a temperature of 40°C using a rotating evaporator to yield methanol extract. The methanol extract was then suspended in deionised water and partitioned sequentially with Ethyl acetate and n-butanol. The fractions were concentrated under reduced pressure to yield the corresponding fractions and the remaining water fraction.

### 7.2.2. Antibacterial assay

The antibacterial assays involved the determination of the minimum inhibitory concentrations (MICs) of plant extracts against test organisms. The broth dilution method was carried out in 96-well microtitre plates using ampicillin-resistant and

Table 7.1. Selected plants investigated and their usage

Herb	Local name	Plant part	Uses and Refences
<i>Aloe arborescens</i> Mill	Ikhala Inkalane	Leaves	Leaf decoction for diarrhoea ( <a href="#">Bisi-Johnson <i>et al.</i> 2009</a> ), effective

ASHODELACEAE	encane (Z)		burn treatment (Pooley, 1993)
<i>Aloe striata</i> Ham ASHODELACEAE	Inkalana (X) Intelezi (Ng)	Leaves	Leaf decoction for diarrhoea ((Bisi-Johnson <i>et al.</i> 2009), purgative, expels worms)
<i>Cyathula uncinulata</i> AMARANTHACEAE	Isinama (X)	Leaves	Leaf decoction for HIV treatment (Bisi-Johnson <i>et al.</i> 2009), stomach ailment
<i>Eucomis autumnalis</i> HYACINTHACEAE	Ubhulungu becanti (X) Umathunga (Z)	Root	Decoctions of bulb and roots for coli, flatulence (Cunningham, 1993)
<i>Hypoxis latifolia</i> HYPOXIDACEAE	Ilabatheka (X,Z)	Root	Treat benign prostrate (van Staden , 1981); Headaches, dizziness, mental disorders, HIV inflammation (Singh, 1999; van Wyk, 2000); Boil ground dried tuber for diarrhoea.
<i>Lantana camara</i> VERBENACEAE	Ubuhobe besikhiwa (N) Mbarapati (S) Iqunube, utywala bentaka (X)	Leaves Flower	Leaf decoction for HIV treatment (this study); antiviral (Inada <i>et al.</i> 1995); rheumatism, sexually transmitted diseases (Dold and Cocks, 2000); treatment of wound (Abdulla <i>et al.</i> 2009)

Key: N – Ndebele; Ng – Nguni; S – Shona; X – Xhosa; Z – Zulu

kanamycin-resistant strains of *Escherichia coli* as the test organisms. A McFarland No1 standard suspension of bacteria inoculum was prepared in sterile Mueller Hinton Broth (MHB). Triplicate tests were performed in a series of two-fold dilutions of extract (10 mg/mL) as previously described (Eloff, 1998). Kanamycin was used as the positive control for ampicillin-resistant *E. coli* strain while ampicillin was used in the case of kanamycin-resistant *E. coli* strain. Plates were incubated at 37°C for 18 h and an hour before the end of incubation, 40 µL of 0.2 mg/mL INT (*p*-iodonitrotetrazolium salt) solution was added to each well.

The lowest concentration indicating inhibition of growth was recorded as the MIC. This was indicated by the clear well after further incubation with INT as opposed to the pinkish colouration in growth wells.

### 7.2.3. Cytotoxicity assays

The *in vitro* cytotoxicities of the selected herbs and solvent-solvent fractions on a human hepatoma cell line, (Huh-7), which was established from a hepatocellular carcinoma were examined using a modified MTT assay (Plumb *et al.*, 1989). The Huh-7 was maintained at – 80°C in Dulbecco's Modified Eagle Medium (DMEM) and recovered from preservative by centrifugation. The pellet was re-suspended in fresh DMEM and cultured in a humidified atmosphere at 37°C using RPMI 1640 supplemented with 10% foetal bovine serum, 100 U/mL penicillin G and 100ug/mL streptomycin and L-glutamine (Gibco BRL) in 5% CO<sub>2</sub> incubator (Thermo Fischer Scientific, Wakenyaku Co. Ltd, Japan). Cells were sub-cultured every 2 days after confluent growth was observed.

The MTT assay was carried out as follows. Briefly, the cells at a density of  $1 \times 10^4$  per cell were seeded in each well of a flat bottom 96-well plate containing 100 µL of the growth medium. Cells were permitted to adhere for 24 h, and then treated with various fractions at concentrations 0, 1, 10 and 100 µg/mL for 72 h. After that, 20 µL of 5 mg/mL MTT in phosphate buffered saline (PBS) was added to each well and the plate was incubated for an additional 2 h. The medium was discarded and the formazan blue, which formed in the cells, were dissolved with 100 µL MTT stop solution (Triton-X100-20 mL; Isopropyl alcohol-500 mL; HCl-2

mL). After incubation at 37°C for 10min, the absorbance of the dissolved solutions was detected at 490 nm on a microplate ELISA reader (Thermo Labsystems, Japan). Cytotoxicity was expressed as the concentration of extract or fraction inhibiting cell growth by 50% (IC<sub>50</sub>) and was analysed using MS Excel 2007. All tests and analyses were run in triplicate.

### 7.3. Results

#### 7.3.1. Antibacterial activities

The average MIC values of the plant extracts ranged from 0.27 mg/mL and 2.5 mg/mL after 24 h of incubation (Figure 7.1). The Ethyl acetate fraction of each type of plant was the most active fraction against the test bacteria. *E. autumnalis* had the least MIC (0.27 mg/mL) followed by *C. uncinulata* (0.39 mg/mL) and thus demonstrated good antibacterial activities. The methanol extract of *H. latifolia*, water fraction of *A. arborescens*, *C. uncinulata*, *E. autumnalis*, and *L. camara* had the highest value of MIC (2.5 mg/mL).

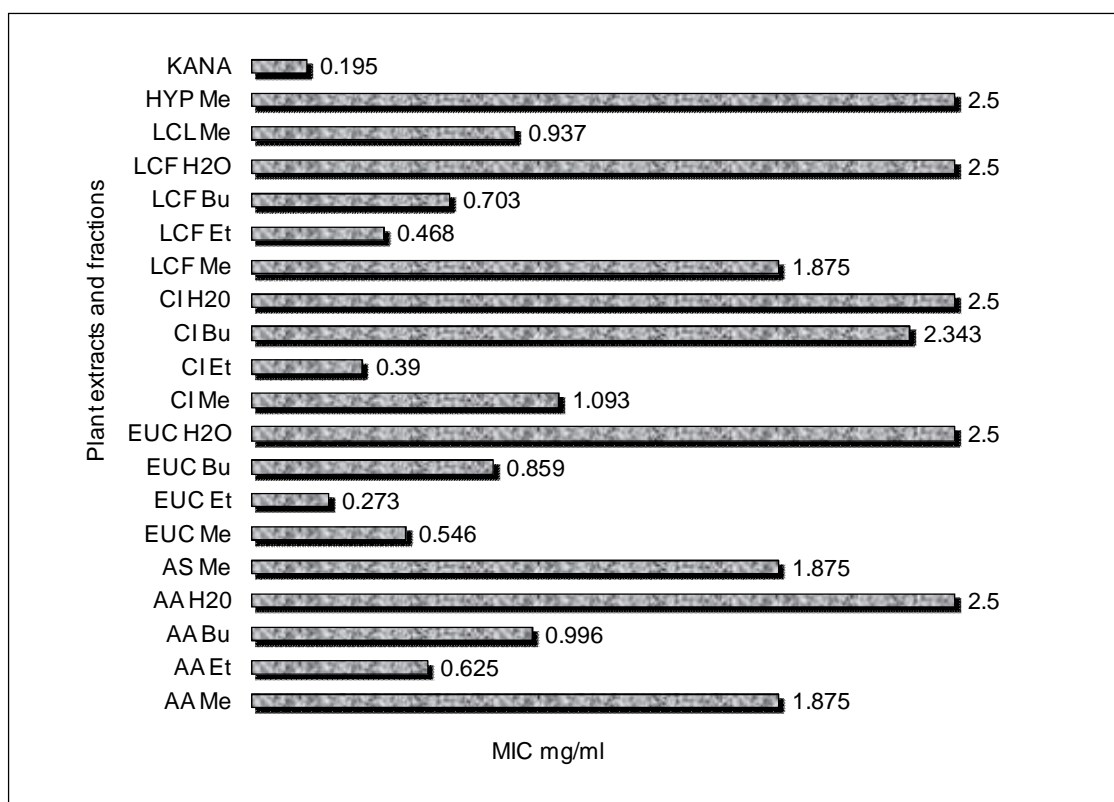


Figure 7.1. Minimum inhibitory concentrations of plant extracts and fractions

Figure legend:

AA Me = Methanol fraction of *A. arborescens* (AA); AA Et = Ethyl acetate fraction of AA; AA Bu = n-Butanol fraction of AA; AA H<sub>2</sub>O = Water fraction of AA; AS Me = Methanol fraction of *A. striata* (AS); EUC Me = Methanol fraction of *E. autumnalis* (EA); EUC Et = Ethyl acetate fraction of EA; EUC Bu = n-Butanol fraction of EA; EUC H<sub>2</sub>O = Water fraction of EA; CI Me = Methanol fraction of *C. uncinulata* (CU); Et = Ethyl acetate fraction of CU; CI Bu = n-Butanol fraction of CU; CI H<sub>2</sub>O = Water fraction of CU; LCF Me = Methanol fraction of *L. camara* fruit/flower (LCF); LCF Et = Ethyl acetate fraction of LCF ; LCF Bu = n-Butanol fraction of LCF; LCF H<sub>2</sub>O = LCF Water fraction of LCF; LCL Me = Methanol fraction of *L. camara* leaves; HYP Me = Methanol fraction of *Hypoxis latifolia*.

### 7.3.2. Cytotoxicities of methanol extracts and fractions.

The results of cytotoxicities of the extracts and fractions of the investigated plants on human hepatic cell line (Huh-7) are shown in [Table 7.2](#).

The methanol extract of *E. autumnalis* (IC<sub>50</sub> 7.8 µg/mL) was more cytotoxic than



the control toxic substance, berberine (IC<sub>50</sub> 9.8 µg/mL), other plant extracts and solvent fractions.

Table 7.2. Inhibitory concentration, IC<sub>50</sub> (ug/ml) of selected herbs

Code S/No	Sample code	Extract fractions	IC <sub>50</sub> (ug/ml)
1	BUB Me	AA Methanol fraction	>1000
2	BUB Et	AA Ethyl Acetate fraction	>1000
3	BUB Bu	AA n-Butanol fraction	>1000
4	BUB H <sub>2</sub> O	AA Water fraction	>1000
5	BUS Me	AS Methanol fraction	1000
6	EUC Me	EA Methanol fraction	7.8
7	EUC Et	EA Ethyl Acetate fraction	28.5
8	EUC Bu	EA n-Butanol fraction	39.3
9	EUC H <sub>2</sub> O	EA Water fraction	379.0
10	IS Me	CU Methanol fraction	24.8
11	IS Et	CU Ethyl Acetate fraction	36.3
12	IS Bu	CU n-Butanol fraction	30.0
13	IS H <sub>2</sub> O	CU Water fraction	714.0
14	LCF Me	LCF Methanol fraction	169.0
15	LCF Et	LCF Ethyl Acetate fraction	44.1
16	LCF Bu	LCF n-Butanol fraction	150.0
17	LCF H <sub>2</sub> O	LCF Water fraction	1000
18	LCL Me	LCL Methanol fraction	161.0
19	HYP Me	HYP Methanol fraction	24.4
PC	Positive control	Berberine	9.8

Key: AA – *Aloe arborescens*; AS – *Aloe striata*; EA – *Eucomis autumnalis*; CI – *Cyathula uncinulata*; LCF – *Lantana camara* (flower/fruits); LCL – *Lantana camara* (leaves); HYP – *Hypoxis latifolia*.

Of the solvent fractions, the Ethyl acetate and butanol fractions of *C. uncinulata*, *H. latifolia*, *E. autumnalis* and *L. camara* had moderate cytotoxic effects on the cancer cell lines tested with IC<sub>50</sub> values ranging from 24.8 µg/mL to 44.1 µg/mL while all the fractions of *A. arborescens* and *A. striata* had insignificant or no cytotoxic effects after 72 h of treatment (IC<sub>50</sub> 1000 to >1000 µg/mL).

#### 7.4. Discussion

This study evaluated the cytotoxicity and antibacterial activities of methanol extracts and solvent fractions of *A. arborescens*, *A. striata*, *C. uncinulata*, *E. autumnalis*, *H. latifolia* and *L. camara*. Among all the samples, the methanol extract of *E. autumnalis* exhibited greatest cytotoxicity on the cell line tested with IC<sub>50</sub> of 7.8 µg/mL). However, the water fraction of *E. autumnalis* and that of other plants showed markedly less cytotoxicity on the cell line, compared with the polar solvent fractions (Table 7.2).

The Ethyl acetate fraction of *E. autumnalis* had the least MIC (0.27 mg/mL) followed by *C. uncinulata* (0.39 mg/mL) against the test bacteria and thus demonstrated good antibacterial activities. Various biological activities of *Eucomis* were reported (Du Toit *et al.*, 2005; Gaidamashvili and van Staden, 2006). *E. autumnalis* is known for its anti-inflammatory and antispasmodic activities and these have been attributed to components such as homoisoflavones and flavonoids (Notten and Kirstenbosch, 2002). *E. autumnalis* also contains some steroidal triterpenoids which are known to be beneficial in

wound therapy (Notten and Kirstenbosch, 2002). However, the bulb was reported to be toxic (Notten and Kirstenbosch, 2002), in agreement with our findings.

Eucosterol glycoside, a lanosterol oligosaccharides isolated from *E. bicolor* have demonstrated antitumor activity by causing 44% inhibition of TPA-stimulated <sup>32</sup>P incorporation into phospholipids of HeLa. This activity has been suggested to probably relate to the use of bulb decoctions of *E. autumnalis* to relieve abdominal distensions and abdominal pain by the Tswana and Pedi tribes of South Africa (Watt and Breyer-Brandwijk, 1962). According to Koorbanally *et al.* (2006), sheep drenched with fresh bulbs of *E. autumnalis* in an animal feeding trial presented with listlessness, anorexia, foaming at the mouth, tympanites, an inactive rumen and a strong pulse leading eventually to death within twenty-four hours. Despite these submissions *Eucomis* is one of the most traded genera of plants in South Africa (Dold and Cocks, 2002), hence the need for caution in their usage.

The *Hypoxis latifolia* fraction also exhibited a considerable toxicity level (24.4 ug/mL). The antimycobacterial activity of hypoxoside has been attributed in part to the high cytotoxicity of this compound derived from *Hypoxis* species and this activity is presumed to be comparable to the cytotoxic effects demonstrated by Hypoxoside against melanoma cancer cells *in vitro* (Albrech *et al.*, 1995). *Lantana camara* which is known to have several uses in ethnomedicine possessed moderate cytotoxic effects. The folk medicine uses includes

the treatment of cancers, chicken pox, measles, asthma, ulcers, swellings, eczema and tumors (Day *et al.*, 2003). Some of the biological antagonistic or potential biocides usage includes the capability of its aqueous leachate at 1–3% to kill water hyacinth, a troublesome weed in many tropical countries even though its application as a weedicide depends on the size of the water bodies being treated and the cost of extraction of the leachate (Day *et al.*, 2003). Some taxa of the widely variable *L. camara* complex are toxic to small ruminants and this effect has been associated with the types and relative amounts of some triterpene ester metabolites (Ghisalberti, 2000). Verbascoside, a bioactive compound from *L. camara*, was reported to possess antimicrobial, immunosuppressive and antitumor activities (Day *et al.* 2003). Other compounds isolated from *L. camara*: lantanoside, linaroside and camarinic acid have been investigated as potential nematocides (Begum *et al.* 2003).

Cytotoxicity assay is a rapid inexpensive determination of significant quantities of biologically harmful contents of product measured as functions of fundamental biochemical pathways leading to cell death (Mosmann, 1983). Toxicity testing of ethnomedical preparations is essential because herbal products may contain undesirable or misidentified ingredients, sometimes toxic such as a toxic plant taken as a desired nontoxic plant or presence of heavy metals, radioactive particles, and microbes including pathogens, mycotoxins, endotoxins and pesticides (WHO, 2007). In addition, safety assessment of herbal products is necessary for the safety of the recipients since herbs are generally heterogeneous, may produce multiple effects, and may affect multiple organs systems, including the nervous, cardiovascular, gastrointestinal, hepatic, renal, and hematologic systems (Barrueto and Hirshon, 2009). Furthermore,

cytotoxicity assay is a means of forestalling financial loss due to failure of a drug making it through the developmental processes. Some reasons for the failures are due to unacceptable toxicity levels (Ricerca, 1998). Testing hence prevent unacceptable compound going through unnecessary costly developmental stages.

Various methods are employed and these include using cell line assays and in vivo tests (use of animals). In addition, the brine shrimp (BS) mortality assay is widely accepted as a convenient probe for potential pharmacological activity in plants (Meyer *et al.*, 1982), however some known toxic plants have exhibited non-toxic effect in brine shrimp (McGaw and Eloff, 2005) generating a misgiving on the capability of BS detection of plant toxicity, hence the preference of cell-line cytotoxicity assay. Another approach to evaluate the safety of healthcare products is Bioequivalence studies in terms of toxicity effect. Two drugs are considered bioequivalent when there is no significant difference between them in terms of their absorption rates (Tu and Koh, 2010). Considering the body weight of each of two mice versus time for oral administration of two herbal products (Tyrel<sup>TM</sup> and Rumbion<sup>TM</sup>), Tu and Koh (2010) were able to conclude that there was no significant difference between the toxicity effect of Tyrel<sup>TM</sup> and Rumbion<sup>TM</sup> at 5000 mg kg<sup>-1</sup> body weight. For the determination of mycotoxins in herbs, HPLC-based technique using a monoclonal antibody immunoaffinity column is recommended (Farmacopea Argentina, 2003).

## 7.5. Conclusion

In conclusion, the results obtained indicated that the methanol extract of *E. autumnalis* exhibited much greater cytotoxicity than the methanol extract and solvent fractions of all other plants investigated even though it had strong antibacterial activities. *E. autumnalis* showed selective anticancer activity against the human hepatoma cell line, whereas the two *Aloe* spp. were non toxic on the cell line. In addition, the study showed that *Aloe arborescens*, *A. striata* and *C. uncinulata* may be candidate plants for eventual drug design. Medicinal plants are natural products and may have therapeutic potentials; however, being natural does not make them automatically safe.

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## CHAPTER 8

### GENERAL CONCLUSIONS AND RECOMMENDATIONS

#### 8.1. General conclusions

Based on the results of this study, it is concluded that

- ❖ The increasing rates of multi-drug resistant strains and emerging resistance of *E. coli* and *Salmonella* spp. to penem drugs and other antibiotics, regrettably may lead to fewer options of effective antimicrobials in the management of infections caused by the pathogens.
- ❖ Molecular analysis showed that beta-lactamase enzymes ( $bla_{CMY-2}$ ,  $bla_{SHV-1}$ ,  $bla_{TEM-20}$  and  $bla_{TEM-1}$  genes) and class 1 integron (*Int1*) genes occurred significantly among the *Salmonella* spp.
- ❖ Virulence of *Salmonella* spp. may be attributed to the virulence genes identified among the *Salmonella* strains; namely *flic*-flagellin H1, *invA*-invasion, *sefA*- fimbrial antigen while *aggR*- transcriptional activator for EAEC aggregative adherence, fimbria I expression, *eaeA*-*E. coli* attaching and effacing and LT- heat-labile enterotoxin found among the *E. coli* isolates were the main indices of virulence.
- ❖ Some of the diarrhoeogenic *E. coli* isolated from apparently asymptomatic subjects expressed some virulence genes at frequency as high as seen in cases, which was an indication that asymptomatic individuals could serve as reservoirs of pathogenic strains of enteric

bacteria and may play a role in the spread and acquisition of virulence genes.

- ❖ Ethnobotanical survey showed that traditional medicine was a popular and widely used system in the rural setting of ORTDM and was the only system available in many parts of the study areas.
- ❖ Among the commonly used plants in traditional medicine, *A. arborescens*, *A. striata*, *C. uncinulata*, *E. autumnalis* and *P. guajava* exhibited antimicrobial properties and antibacterial activity was higher in the ethyl acetate fractions of the methanol extracts than other solvents employed.
- ❖ Further fractionation and purification of bioactive components of the ethyl acetate fraction of *C. uncinulata* yielded an isolated compound, glycosylated oleanolic acid, a sugar with fatty acyl moiety, which had considerable antibacterial activities.
- ❖ Cytotoxicity testing of the medicinal plants indicated that the methanol extracts of *E. autumnalis* were more cytotoxic than the methanol extracts and solvent fractions of other plants investigated, even though it had strong antibacterial activities. The use of *E. autumnalis* may therefore be fraught with risk of disagreeable side effects. The *Aloe* spp. studied were non toxic to cell lines, indicating strong potentials for drug development.

## 8.2. General recommendations

The under-listed recommendations are made against the backdrop of the findings of the study.

- ❖ Periodic studies on antimicrobial susceptibility or resistance patterns of *E. coli* and *Salmonella* spp. should be undertaken to provide updated information for empiric management of patients.
- ❖ Public awareness campaigns or educational programs for traditional health care practitioners on the cytotoxic effects of some plants should be fore-grounded.
- ❖ Extensive studies on the structural elucidation of the active compounds of the medicinal plants, including their effects on physiological, immunological and haematological parameters are necessary to further gauge their safety and potentials as candidate templates for drug design and discovery.
- ❖ The administration of antibiotics, without results, on susceptibility testing may be fraught with risk due to increasing resistance profiles of *E. coli* and *Salmonella* spp. Therefore, antimicrobial therapy should be predicated on laboratory results of antibiograms.
- ❖ Phylogenetic studies of *E. coli* and *Salmonella* spp. from different environmental and clinical sources, including correlation with virulence markers/ genes are recommended for a better understanding of their molecular epidemiology and pathogenicity.

## APPENDICES



### APPENDIX 1A

Faculty of Health Sciences

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Private Bag X1, Mthatha 5117  
Tel/Fax: 047 502 2301

#### VOLUNTEER INFORMATION SHEET

**TITLE OF PROJECT: "MOLECULAR CHARACTERIZATION, ANTIBIOGRAMS AND ANTIBACTERIAL ACTIVITIES OF SELECTED MEDICINAL PLANTS AGAINST SOME ENTERIC PATHOGENS"**

Hello! My name is Mary Bisi-Johnson and I would like to ask you for a little of your time to explain something to you, and ask you to please assist us in a research work that we are doing. As we discuss the information below please feel free to ask any questions.

In South Africa, a substantial number of deaths due to diarrhoeal diseases have been reported. Some studies have implicated some of these enteric pathogens we are studying in cases of diarrhoea in people across ages. By doing this study, we will be able to know the germs that is making people sick of diarrhoea. We are at present doing a study that will be looking at the use of certain antibiotics/medicines and local herb in the community and how it affects the germs that infect people. We want to see if there is an increase in germs that will not be treated by antibiotics/medicines that we normally use and see if the local herb will be able to help. This will help in the control and prevention of these diseases.

We would like to make sure that all the information we have about you is correct and then ask a few more questions about use of antibiotics. We will keep this information confidential, no one else will know that it is about you and all summaries or publications will only refer to group data.

You can make the decision entirely on you own and none of us can force you to take part. If you decide to answer some of these questions, you may also change your mind at any time.

You do not have to agree, and if you decide not to be involved it will not change the way you are treated in the hospital, and your doctor will not do anything differently.

Thank you for your time. Once you have asked any questions you may have, there is a form you need to sign if you agree to take part.

Investigators details:

Mrs. Mary Adejumoke Bisi-Johnson  
Prof. CL. Obi

Contact No: 0766813494  
Contact No: 047 502 2260/4

Date:

Department of Medical Microbiology,  
Nelson Mandela Drive,  
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### VOLUNTEER INFORMATION SHEET

**TITLE OF PROJECT: "MOLECULAR CHARACTERIZATION, ANTIBIOGRAMS AND ANTIBACTERIAL ACTIVITIES OF SELECTED MEDICINAL PLANTS AGAINST SOME ENTERIC PATHOGENS"**

Molo!, Igama lam ndingu Mary Bisi-Johnson, ndicela okokuba undiphe imizuzu embalwa kwixesha lakho onalo, ndinqwenela ukukucacisela nto ithile, ndikwakucela ukuba usincede kweli phulo siliqulunqayo. Xa sicacisa lo mba ongezantsi, uvumelekile ukuba ungabuza imibuzo.

Emzantsi Afrika, Isibalo esiphezulu sabantu abasweleke ngenxa yesifo Sotyatyazo sithe sabikwa. Ezinye izifundo zithe zaveza ukuba ezintsholongwane esizifundayo zolutyatyazo zikho kubo bonke abantu, ukususela komncinci ukuyakutsho komdala. Ngokwenza ezizifundo, sizakuyazi intsholongwane ebangela ukuba abantu bagule sesisifo sotyatyazo.

Okwangoku senza izifundo ezizakuthi zijonge ukuba leliphi ichiza/iyeza okanye nokuba sesiphi isityalo sasekuhlaleni nokuba liyichaphazela kanjani lentsholongwane esulela abantu. Sifuna ukubona ukuba iintsholongwane ezingenakunyangeka ngalamayeza ziyenyuka kusini na?, okanye Isityalo sasekuhlaleni singanceda na!!. Oku kunganceda Ekulawuleni nasekunqandeni ezi zifo.

Singacela ukuqinisekisa ukuba zonke inkcukacha esinazo ngawe ziyinyaniso, siphinde sibuze eminye imibuzo ngokusetyenziswa kwamayeza/kwamachiza. Sizakuzigcina ezinkcukacha ziyimfihlelo, Akukho namnye umntu ozakuyazi ukuba ezinkcukacha zingawe, kwaye wonke umpapasho uzakwenziwa ngesininzi.

Isigqibo sesakho wedwa sokuba uyafuna ukuthabatha inxaxheba kwezi ngxoxo. Ukuba ufuna ukuphendula inxalenye yalemibuzo, naleyo ikuwe, isigqibo sesakho.

Akunyanzelekanga ukuba uvume, kwaye ukuba awufuni ukubandakanyeka lonto ayizukutshintsha impatho oyifumana apha esibhedlele, noGqirha wakho akazukwenza tshintsho ngokwempatheko yokho.



Siyabulela ngexesha osiphe lona, Xa ubuzile imibuzo onganayo, kukho isivumelwano okufuneka usityikitye, ukuba uyavuma ukuthabatha inxaxheba.

Iingcukacha zabaphandi:

Mrs. Mary Adejumoke Bisi-Johnson  
Prof. CL. Obi

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UMHLA: .....

Faculty of Health Sciences

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INFORMED CONSENT

TITLE OF PROJECT: *"MOLECULAR CHARACTERIZATION, ANTIBIOGRAMS AND ANTIBACTERIAL ACTIVITIES OF SELECTED MEDICINAL PLANTS AGAINST SOME ENTERIC PATHOGENS"*

Investigators:

*Department of Medical Microbiology, WSU, Mthatha*

Mrs. Mary Adejumoke Bisi-Johnson      Contact No: 0766813494

*Directorate of Academic Affairs & Research, WSU, Mthatha*

Prof. CL. Obi      Contact No: 047 502 2260/4

Hello! My name is Mary Bisi-Johnson and I would like to ask you some information. I will need to explain what it is we would like to do. You can help us a little if you listen and tell us what you think.

We want to ask you or your mother/father/guardian some questions about you. We will ask questions about recent history of diarrhoea and about what medicines you took. We want to try and see if the germs we are studying (*Salmonella* and *E. coli*) are found in your stool and know the antimicrobial profile and the virulence factors. This is to enable us know whether the germs are causing more sickness in South Africa and if they are becoming more difficult to treat.

Would it be alright for us to ask the above questions? When we work with this information we would not require your name.

I have read and/or I understand the contents of the information sheet and understand that I have been invited to participate, that my agreeing is fully voluntary, and that I can withdraw at any time.

Consent given:	Date:
Witness: A	Date:

Department of Medical Microbiology,  
Nelson Mandela Drive,  
Private Bag X1, Mthatha 5117  
Tel/Fax: 047 502 2301

## INFORMED CONSENT

TITLE OF PROJECT: *"MOLECULAR CHARACTERIZATION, ANTIBIOGRAMS AND ANTIBACTERIAL ACTIVITIES OF SELECTED MEDICINAL PLANTS AGAINST SOME ENTERIC PATHOGENS"*

## Investigators:

*Department of Medical Microbiology, WSU, Mthatha*

Mrs. Mary Adejumoke Bisi-Johnson      Contact No: 0766813494

*Directorate of Academic Affairs & Research, WSU, Mthatha*

Prof. CL. Obi

Contact No: 047 502 2260/4

Molo!, Igama lam ndingu Mary Bisi-Johnson, ndicela ukukubuza Imibuzo nje embalwa. Kuzakunyanzeleka ndikucacisele ukuba yintoni na le ndifuna siyenze. Ungasinceda ngokuba simamelane kwaye uyitsho into oyicingayo.

Sicela ukubuza, wena No-Mama/No-Tata/Umniki Ncedo kwimpilo(Unomakhaya) wakho imibuzo ngempilo yakho nesigulo eso onaso. Sizakubuza imibuzo ngesigulo onaso nangamayeza obuwathabatha phambi kokuba uze Esibhedlele. Sifuna ukuzama, sibone ukuba intsholongwane le Siyifundayo/Siyihlodayo ayinguye na unobangela wezigulo esinazo apha emzantsi Afrika.

Ingaba sivumelekile ukukubuza lemibuzo sele ndiyikhankanyile apha ngasentla, Xa sisebenza ngezinkcukaca asizukulibiza/ukulisebenzisa igama lakho.

Ungaxhalabi xa uqonda ukuba kukho umbuzo ongacacelanga ukuwuphendula, akukho nento ezakujika ngempatho oyifumana kugqirha.

Ndiyifundile/Ndiyawuqonda umxholo oqulethwe yile-ncwadilkwaye ndiyavuma ukuba ndimenyiwe ndithabathe inxaxheba, kwaye ukuvuma kwam sisigqibo endizithabathele sona ngokokwam kwaye ndingarhoxa nangaliphi ixesha ndithanda.

IMVUME:	UMHLA:
INGQINA:	UMHLA:

SURVEY INFORMATION FROM TRADITIONAL HEALERS ON HERBAL PLANTS IN TRADITIONAL TREATMENT OF DIARRHOEA

DATE OF VISIT: \_\_\_\_\_ PLACE OF VISIT: \_\_\_\_\_  
 NAME OF TRADITIONAL HEALER: \_\_\_\_\_  
 CONTACT ADDRESS & NO: \_\_\_\_\_

*Department of Medical Microbiology, WSU, Mthatha*  
 Mrs. Mary Adejumoke Bisi-Johnson      Contact No: 0766813494

- i) Do you treat Diarrhea?    Yes     No
- ii) Do you treat some of other diseases linked to diarrhea?  Yes  No
- iii) Do you treat both males and females?    Yes     No
- iv) Which age group do you treat for diarrhoea?

Children	Young adult	Adult

- v) Do patients try self-treatment of diarrhea before consulting you?  
\_\_\_\_\_
- vi) How effective is your treatment of diarrhea? \_\_\_\_\_  
\_\_\_\_\_
- vii) Do you experience cases where patients show adverse reactions to your treatment?    Yes     No
- viii) How do you feel about patients going to hospitals or clinics for further or (alternative) treatment? \_\_\_\_\_  
\_\_\_\_\_
- ix) Which plant/plants do you use for the treatment of diarrhea?  
\_\_\_\_\_
- x) Do you use cultivated plants for the treatment of diarrhea? Yes     No

xi) Which plant parts do you use?

Leaves	Stem	Tree bark	Whole plant	Root	Tuber	Combination

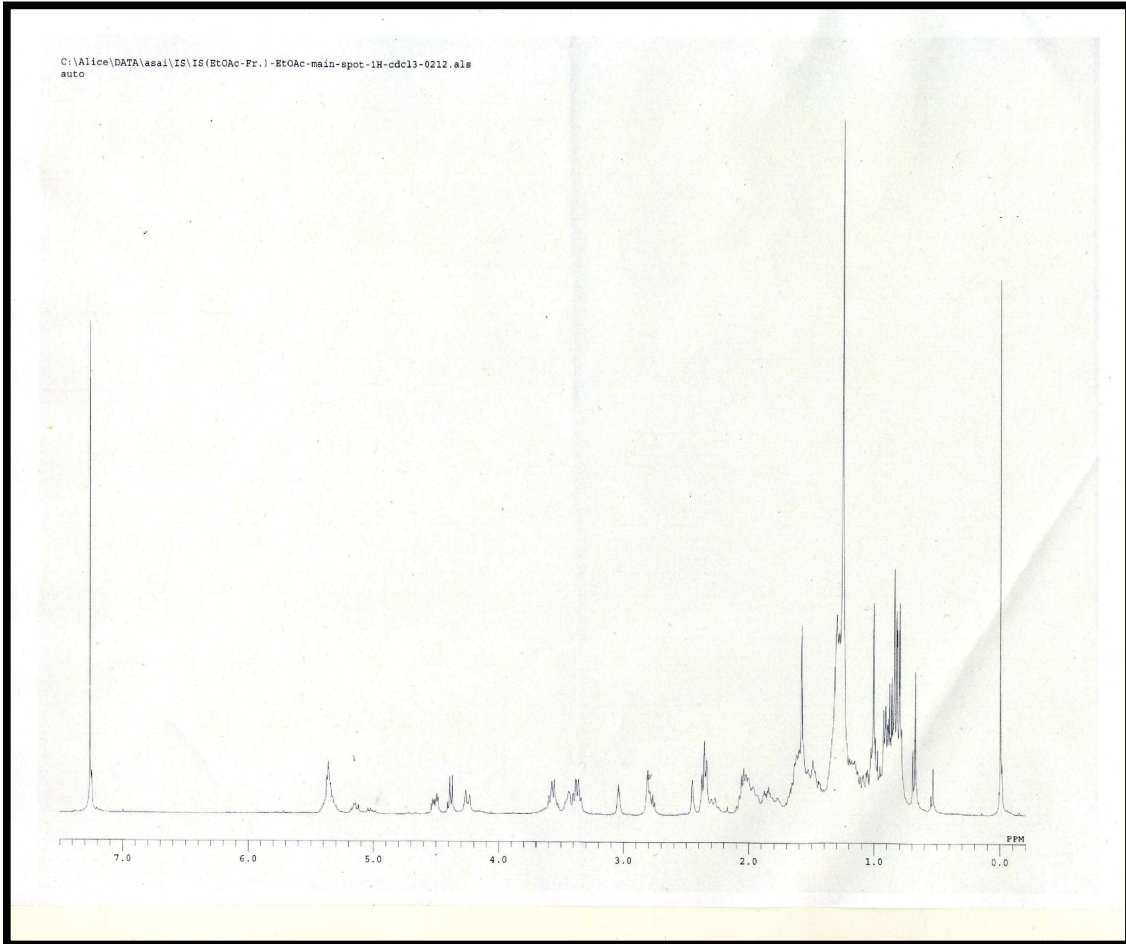
xii) How did you learn about the plant? From parent or during training\_\_\_\_\_

xiii) What dosage/quantity do you give you patient?\_\_\_\_\_

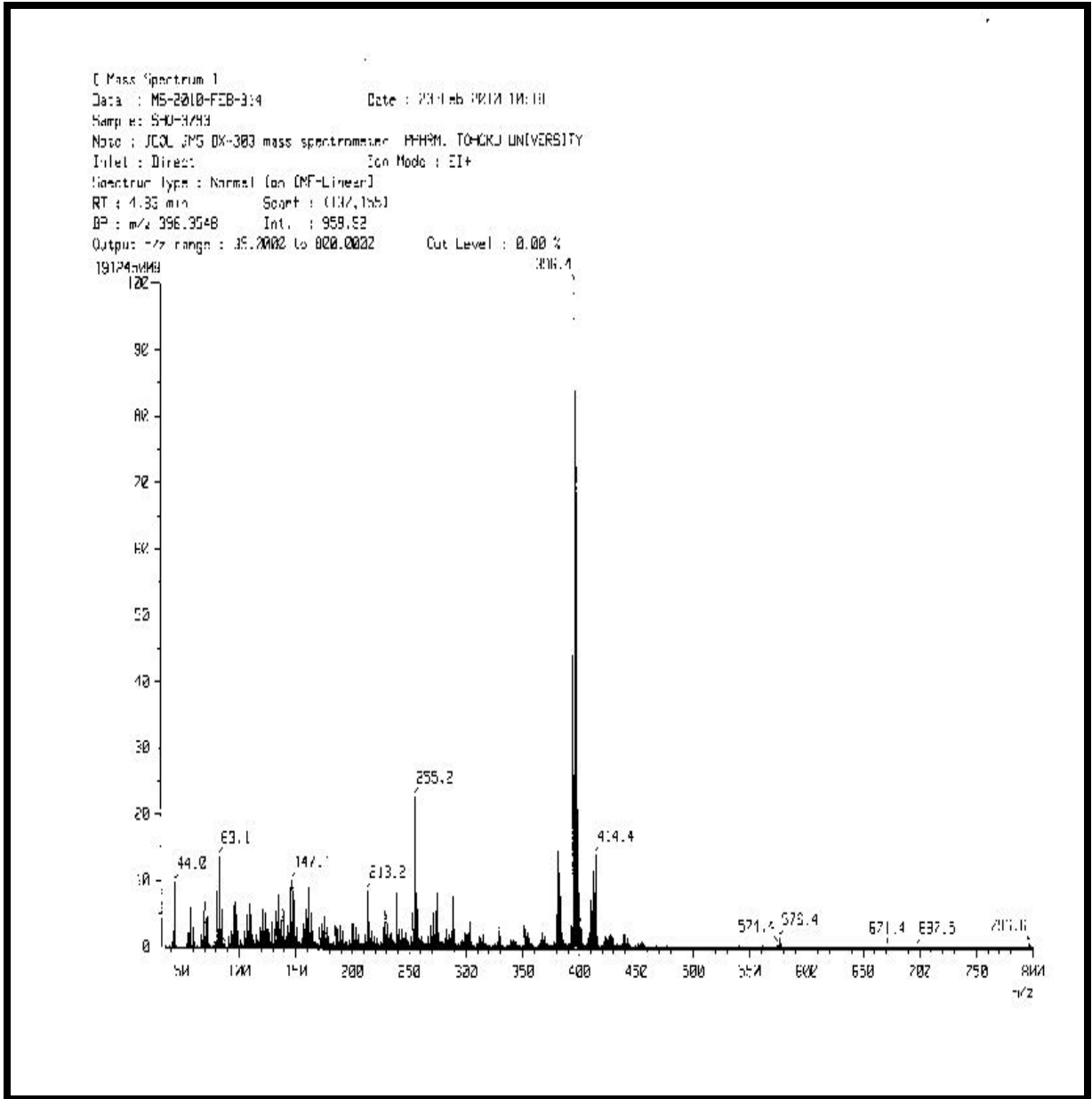
xiv) For how many days do they take the herb?\_\_\_\_\_

xv) How do you prepare your medication?

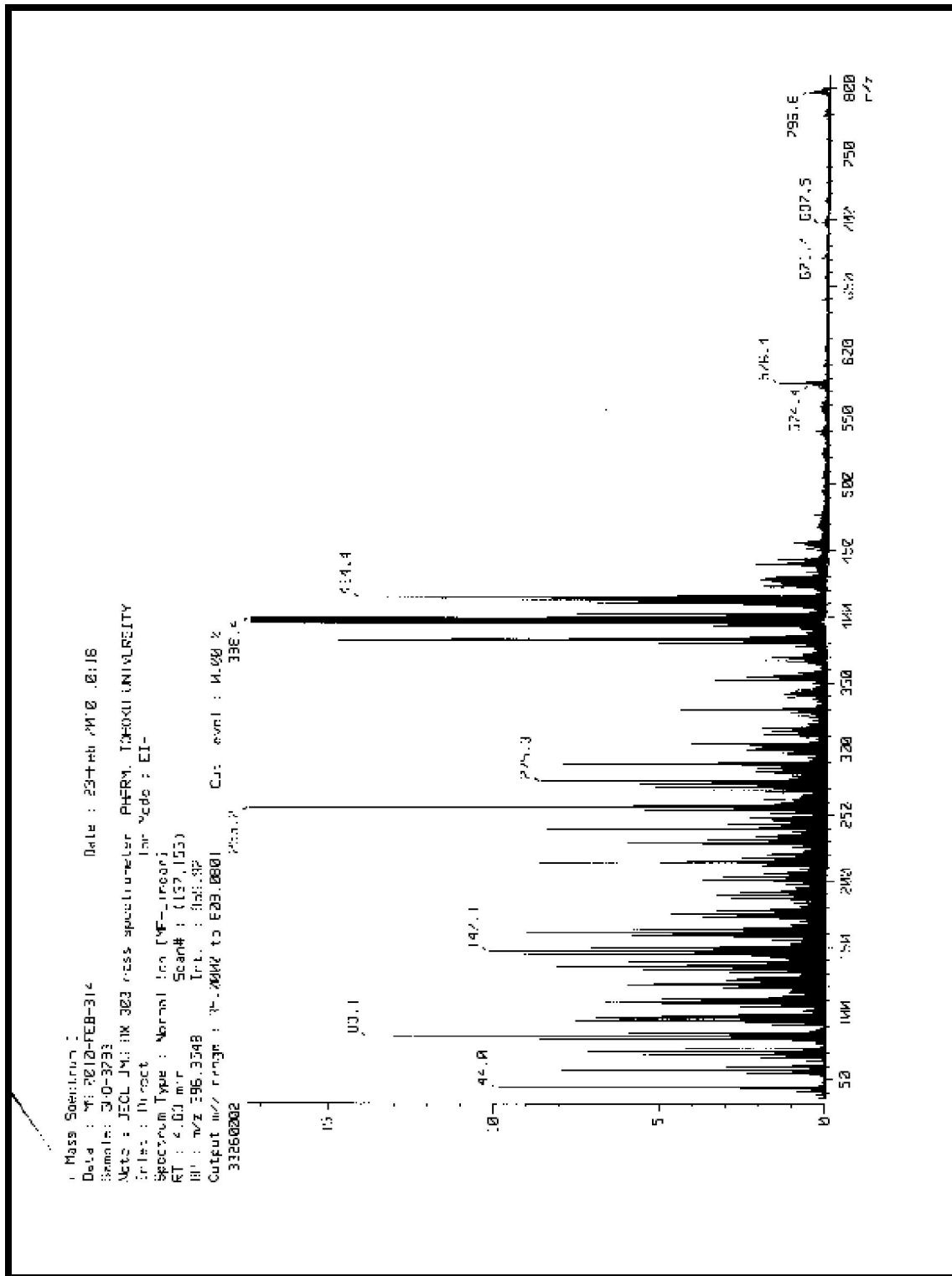
Appendix 4A. NMR spectrum for the isolated compound (SSC3-9-10).



Appendix 4B. Mass spectrum 1 for the isolated compound



Appendix 4C. Mass spectrum 2 for the isolated compound





Appendix 4D. Structure of the isolated compound

