

Assessment of anti-urease and consequential inhibitory potential of South African honey extracts on the multiplication of drug-resistant, vacA and cagA positive Helicobacter pylori strains under acidic conditions

by

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A thesis submitted in fulfilment of the requirements for the degree of

DOCTOR OF PHILOSOPHY (PhD) IN MICROBIOLOGY

in the Department of Biochemistry and Microbiology

FACULTY OF SCIENCE AND AGRICULTURE

UNIVERSITY OF FORT HARE

2017

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Declaration

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Dedication

Family, relatives and friends

Acknowledgements

My profound gratitude goes to Professor A.M. Clarke of the Department of Biochemistry and Microbiology, University of Fort Hare for her mentorship and diligent supervision throughout the study period. Special thanks also go to Professor G. Bradley for his timeous support of the research as well as Professor L.V. Mabinya for his continued courage and mentorship during the study period. members of the Microbial Pathogenicity and Molecular Epidemiology Research Group (MPRERG) especially Dr H.A. Njom, for their brilliant ideas, support and insight into my research, National Research and Funding (NRF) and Govan Mbeki Research and Development Centre (GMRDC) of the University of Fort Hare for funding this study. Also the German team of experts, Professor Rain Haas and Dr U. Harrison, thank you so much for all the contributions you made to my work. I would also like to extend my appreciation to my family and friends for their encouragement and support. My utmost gratitude goes to the Almighty God in the Name of Jesus Christ for being the comforter and provider of all.

List of abbreviations

Ag⁺ Silver ion

AlpA Adherence-associated lipoprotein

Am Amoxicillin

BabA Blood group antigen binding adhesin

CagA PAI Cytotoxin associated gene pathogenicity island

CJBU Commercial Jack bean urease

Cl Clarithromycin

CO₂ Carbon dioxide

Cu2+ Copper

DNA Deoxyribonucleic acid

DupA Duodenal ulcer promoting gene

GC-MS Gas chromatograph – mass spectrometry

GDH Glutamate dehydrogenase

H₂O₂ Hydrogen peroxide

Hg⁺ Mercury ion

Hop *Helicobacter* outer membrane

HPU1 Urease extracted from *H. pylori* susceptible to drugs

HPU2 Urease extracted from *H. pylori* resistant to clarithromycin

HPU3 Urease extracted from multidrug resistant *H. pylori*

HSP Heat shock protein

IceA Induced by contact to epithelium

IL Interleukin

KDa Kilo Dalton

LC-MS Liquid chromatography – mass spectrometry

MALT Mucosa associated lymphoid tissue

MBC Minimum bactericidal concentration

Met Metronidazole

MHA Muller Hinton Agar

MIC Minimum inhibitory concentration

Na₂SO₄ Anhydrous disodium sulphate powder.

NADH Nicotinamide Adenine dinucleotide

NF-KB Nuclear factor kappa-light-chain-enhancer of activated B cells

NH₃ Ammonia

Ni²⁺ Nickel

OD Optimum density

OipA Outer membrane inflammatory protein

OMP Outer membrane protein

PCR Polymerase chain reaction

PPI Proton pump inhibitor

PUD Peptic ulcer disease

RFLP Restriction fragment length polymorphism

SabA Sialic acid binding adhesin

Tet Tetracycline

VacA Vacuolating cytotoxin A

WHO World Health Organisation

General abstract

Helicobacter pylori, a neutralophile chronically infects the gastric stomach of more than half of the world's population. Infection with the organism is associated with acute or chronic duodenal/gastric ulcer disease, gastritis, gastric adenocarcinoma, mucosa-associated tissue lymphoma (MALT) and primary B-cell gastric lymphoma and has been grouped as a class one carcinogen by the World Health Organisation (WHO). Prevalence of this organism is very high in developing countries especially in Africa, including South Africa. H. pylori treatment using the common first and second line regimens, triple therapy with two antibiotics and a proton pump inhibitor (PPI) is showing inefficiency due to increasing drug resistance. However, newly developed treatment regimens seem to be more expensive and are accompanied by more side effects. Honey contains phytochemicals which are a wealthy source of biologically active compounds some of which have been put into good use in the pharmaceutical industry. Pathogenesis of *H. pylori* infection in the human stomach relies on several virulence factors which include the urease enzyme, cagA and vacA. The urease enzyme actively hydrolyses urea to produce ammonia an important by-product involved in pH regulation favouring the survival of the organism in the acidic human stomach. This study therefore focuses on screening for anti-urease solvent extracts of South African honey, and evaluate whether inhibition of urease offsets the growth of *H. pylori* under acidic conditions.

Locally produced natural honeys; Bush honey, Raw honey, Gold Crest honey, Q Bee honey, Little Bee honey, Fleures honey-radurised, Siyakholwa pure honey and Manuka honey; an import from New Zealand were purchased and the method by Syazana *et al.* (2010) was used for the extraction of compounds in honey. A standard strain ATCC 43526 (American Type Culture Collection, Manassas, VA, USA) and 48 pure cultures obtained from clinical isolates cultured from gastric corpus biopsy specimen of patients with gastric morbidities who were

visiting the endoscopy unit in Livingstone Hospital, Port Elizabeth between June 2008 to December 2008 were initially used as source of urease enzyme as per extraction method done by Amin *et al.* (2013), but with modifications. Prior to urease extraction, *H. pylori* strains were identified by biochemical tests (urease, catalase, oxidase, Gram stain), confirmed by PCR targeting the *glm*M gene (140 bp) and drug resistance profiling was done on all the 48 strains according to Seanego *et al.* (2012). The screening for anti-urease active compounds was done according to Kaltwasser *et al.* (1966), a method relying on the reduction of NADH in a coupled urease dehydrogenase (GDH) system. Acetohydroxamic acid was used as a standard inhibitor.

Prevalence of *cytotoxin-associated* gene A (*cag*A) gene and *vacuolating cytotoxin* gene A (*vac*A) gene was determined among all 48 clinical samples. The standard strains of *H. pylori*, X47 (*cag*A positive), J99 (*vac*A s1m1) and Tx30a (*s2m2*) were used as positive controls. *H. pylori*'s growth was then monitored under acidic pH in a cocktail spiked with anti-urease compounds (test samples) and in a cocktail without anti-urease compounds (negative control). Acetohydroxamic acid was used as a standard urease inhibitor. *H. pylori* multiplication was monitored in Brain Heart Infusion Broth (BHIB) adjusted to pH of 2, 3, 4, 5, 6 and 7. The strain MP01 was used as a standard urease negative strain while X47 and J99 were used as positive standards for *cag*A and *vac*A *s1m1* respectively. The compounds that had anti-urease activity and were successful towards suppressing the multiplication of *H. pylori* under acidic environment, all other factors optimised, were subjected to gas chromatograph mass spectrometry (GC-MS) and liquid chromatograph spectrometry (LC-MS) to determine volatile compounds and drugs in honey extracts respectively.

The findings of this study revealed that at a concentration of 50 mg/mL, urease inhibition by petroleum ether extracts of Gold Crest and Fleures honey, hexane extracts of Little Bee and Manuka honey, and chloroform extracts of Bush honey and Q Bee honey had a range above or equal to 50% and there was no significance difference in urease inhibition percentage (I%) of urease from different sources including that extracted from drug resistant *H. pylori* (p >0.05). Virulence factors are important for the pathogenesis of *H. pylori*. All the 48 clinical isolates were glmM (140 bp) positive and cagA was detected in 97.9% of the test isolates. The vacA gene was detected in all isolates but with different subtypes. The vacA allelic combination s1m1 was detected in 75% of the test isolates and s1m2 allelic combination was detected in 16.7% of the test isolates while the combination s2m2 was detected in 8.3% of the test isolates. None of the test isolates possessed the allelic combination s2m1. When *H. pylori* multiplication was monitored under acidic conditions in the presence of anti-urease active compounds, it was revealed that anti-urease active compounds in honey are capable of inhibiting the normal multiplication of *H. pylori* strains that are cagA positive, vacA positive and drug resistant.

The GC-MS analysis showed that Fleures honey (urease I% = 67.8 - 68.5%) and Gold Crest honey (urease I% = 50.9% - 53.3%), all petroleum ether extracts had 27 and 26 volatile compounds. The hexane extract of Manuka honey (urease I% = 50.0 - 53.2) had 43 compounds detected. The chloroform extract of Q Bee (urease I% = 64.2 - 66.2%) had 13 volatile compounds detected. All the volatile compounds considered as representative samples of GC-MS analysis had a spectral matching $\geq 90\%$ with the NIST11 library. However, the majority of compounds that were detected by LC-MS in representative honey extracts include vardenafil, urapidil, hydrocortisone, e.t.c which are drugs commonly used in the treatment of different ailments or infections that affect human beings. In addition, two

drugs, sulfaquinoxaline and hydroxyquinoline which are used in veterinary medicine and antiseptic, disinfectant and pesticide applications in agricultural activities were detected in Little Bee honey. We therefore conclude that inhibition of urease has a bactericidal effect on drug resistant, cagA positive and vacA positive H. pylori strains growing under acidic environment.

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CHAPTER ONE

1.1 GENERAL INTRODUCTION

Helicobacter pylori is a Gram-negative, microaerophilic, spiral rod-shaped bacillus that is 1–2 μm long, and 1 μm wide displaying 2–6 flagella for mobility (Lertsethtakarn *et al.*, 2011; Gu *et al.*, 2017). Since it was discovered in 1983 (Marshal and Warren, 1984), it has been associated with the development of several diseases of the human digestive system (Tanih and Ndip, 2012; Seck *et al.*, 2013; Chey *et al.*, 2017). This bacterium chronically infects the gastric mucosa of more than half of the world's population and is recognized as the main cause of gastritis (Marshal and Warren, 1984; Wu *et al.*, 2012).

Infection with *H. pylori* potentially induces chronic gastritis, peptic ulceration, adenocarcinoma of the distal stomach, mucosa associated lymphoid tissue lymphoma (MALT) and primary gastric non-Hodgkin's lymphoma (Permin and Anderson, 2005; Ahmed *et al.*, 2007b). *H. pylori* is one of the causative agents of gastric cancer and it's infection of the human host is ranked as a group 1 carcinogen (Chey *et al.*, 2007). The infection with this organism can commence early in life (Dube *et al.*, 2009; Khedmat *et al.*, 2013) and persist for life if not treated. *H. pylori* infection in paediatrics is associated with pernicious anaemia, growth faltering and susceptibility to water and food borne infections (Thomas *et al.*, 2004).

H. pylori infects approximately above 50% of the world's population (Tanih et al., 2010; Goh et al., 2011; Awuku et al., 2017). Of concern is the fact that drug resistance against commonly used drugs of H. pylori treatment is on the rise (Seck et al., 2009; Tanih et al.,

2010; Fathi *et al.*, 2013), thereby increasing the risk of serious health consequences due to prolonged infection. Some studies that have shown that urease negative mutant strains of *H. pylori* fail to effectively inhabit the acidic stomach of host and cause gastritis (Tsuda *et al.*, 1994; Amin *et al.*, 2010). In addition urease inhibition has been reported in many studies (Krajewska, 1991; Pervez *et al.*, 2008; Kumar *et al.*, 2009; Du *et al.*, 2012). Due to drug resistance, other therapeutic sources have been used in the management of the infection. These include natural products such as honey known to possess a multifaceted medicinal value due to abundance of phytochemicals in its complex that are dependent on geographical location and nectar source (Ndip *et al.*, 2007; Mandal *et al.*, 2011; Silver *et al.*, 2013). Different honey types were chosen as a template of anti-urease compounds. The experimental approach of the study was based on screening for anti-urease active compounds in honey and determining the effectiveness of identified compounds towards suppression of *H. pylori* growth under acidic conditions. This study therefore attempts to explore new ways of treating *H. pylori* infections by targeting the inhibition of the urease enzyme which is a key virulence factor required by this organism to infect the acidic environment of the human stomach.

1.2 RATIONALE

It is a concern that the prevalence and incidences of *H. pylori* infections worldwide has reached alarming rates. Several studies have highlighted high occurrences of *H. pylori* infections in the developing world (Samie *et al.*, 2007; Dube *et al.*, 2009; Tanih *et al.*, 2010). In South Africa, Samie *et al.* (2007) recorded 84% prevalence in a study conducted in Pretoria from asymptomatic individuals while Dube *et al.* (2009), recorded a prevalence of 86.8% in an asymptomatic population in the Eastern Cape Province. Prevalence studies have been done in other countries including Nigeria with 64% (Jemilohun *et al.*, 2011), Cameroon with 78.7% (Ebule *et al.*, 2017) and Egypt with 79.7% (Hanafi *et al.*, 2017), all cases with

notably high occurrences of *H. pylori* infections. In addition, drug resistance is gradually gaining momentum against currently used treatment regimens, unavoidably making this bug a severe health concern worldwide.

H. pylori infection of the human gastric mucosa is an important risk factor for the development of gastric ulcer, duodenal ulcer, and development of upper gastrointestinal tumor, adenocarcinoma and mucosa associated lymphoid tissue-MALT (Cogo *et al.*, 2011; Miernyk *et al.*, 2011; Zaki *et al.*, 2016a). It has been suggested that up to 95% of duodenal and 70% of gastric ulcers are attributable to *H. pylori* infection and most cases occur in middle aged subjects (Rothenbacher, 2007).

The organism is equipped with several virulence factors which include the vacuolating cytotoxin gene A (vacA), cytotoxin associated gene A (cagA) and the urease enzyme which all contribute positively to the colonization and pathogenicity of the organism in the human stomach. The vacA gene encodes for the production of a vacuolating cytotoxin which influences cytoskeleton changes, vacuolation and apoptosis of host cells (Pacheco $et \ al.$, 2008). A model for vacuolation suggests that anion-selective channels facilitate the transport of chloride ions into host cells resulting in intra-lumenal chloride concentration which eventually leads to diffusion of weak bases into endocytic compartments of cells causing osmotic swelling and vacuolation (Cover and Blanke, 2005). The vacuolating activity of the vacA gene in H. pylori is associated with presence of four regions, the signal (s)-, intermediate (i)-, middle (m)-, and deletion (d)- regions found as either type 1 or 2 (Bakhti $et \ al.$, 2015; Hashinaga $et \ al.$, 2016; Trang $et \ al.$, 2016). The allelic combination of s region and the m region determines cytotoxin production and severity of virulence of the bacterium

(Atherton *et al.*, 1995; Palframan *et al.*, 2012; Harrison *et al.*, 2017). The *vac*A allelic combination *s*1*m*1 is associated with high levels of vacuolating cytotoxin severity as compared to moderate level of vacuolating cytotoxin severity displayed by *s*1*m*2 allelic combination (Cogo *et al.*, 2011; Harrison *et al.*, 2017). The *s*2*m*2 allelic combination shows little or no production of vacuolating cytotoxin (Miernyk *et al.*, 2011). The *cag*A gene, which codes for a 125–145 kDa *cag*A protein is a marker for the presence of the cytotoxin associated gene pathogenicity island (*cag* PAI). Presence of *cag*A PAI seems to be influential in inflammatory response and having a link with a higher risk of developing peptic ulcer disease (PUD) or gastric cancer in comparison to persons infected by *H. pylori* strains without the *cag* PAI (Parsonnet *et al.*, 1997; Zaki *et al.*, 2016a).

The ability of *H. pylori* to produce urease enzyme is another important virulence factor that modulates survival of the organism in the hostile acidic environment of the human stomach (Amin *et al.*, 2010; 2013). Urease is a multimeric, nickel-containing enzyme which consists of six *ureA* and six *ureB* subunits (Dunn *et al.*, 1990; Hu and Mobley, 1990). This enzyme converts urea, into ammonia and bicarbonate. The ammonia is responsible for protecting *H. pylori* against the acidic environment of the human stomach through pH elevation within the microenvironment of the organism (Rektorschek *et al.*, 2000; Weeks *et al.*, 2000). The bicarbonate protects the organism against the bactericidal activity of peroxynitrite, a nitric oxide metabolite (Kuwahara *et al.*, 2000). A study positively linked production of urease by *H. pylori* and colonisation of the acidic environment when it was demonstrated that a ureasenegative mutant does not cause gastritis due to difficulties in colonization (Amin *et al.*, 2010).

As a class 1 carcinogen (Aguemon et al., 2005), high incidences of drug resistance of H. pylori has been noted worldwide. Clarithromycin and/or metronidazole drug resistance, the main components of triple therapy remedies is on the rise worldwide (Kadayifci et al., 2006; Seck et al., 2009; Fathi et al., 2013; Tanih et al., 2013; Fasciana et al., 2015). A systematic review of H. pylori resistance to clarithromycin worldwide revealed a 17.2% resistance (Francesco et al., 2010). Strains of H. pylori obtained from a population of Sicily in Italy had a representation of 25% resistance to clarithromycin (Fasciana et al., 2015). A study done in Senegal revealed 90% resistance to metronidazole (Seck et al., 2009). In Egypt, another study revealed 100% resistance to metronidazole using an E-test (Fathi et al., 2013). Also in a South African population, 20% resistance to clarithromycin and 95.5% resistance to metronidazole was recorded (Tanih et al., 2010). The triple therapy consisting of proton pump inhibitor (PPI), clarithromycin and amoxicillin or metronidazole is recommended where clarithromycin resistance is < 15%. Also, in areas with less than 40% metronidazole resistance, PPI with clarithromycin and metronidazole is preferable (Chey et al., 2017). The failure of the first line treatment regimens calls for second line or even concomitants or rescue therapies. The advanced therapies which offer better results might utilise the bismuth salt. However, this product is not available in all countries, in addition, such rescue therapies require good infrastructure for the program to be successful. Moreover, some of the drugs suggested could have more side-effects thereby posing new challenges which might eventually lead to failure of the suggested regimens.

Phytochemical research is gaining recognition, many studies have been conducted to evaluate the significance of phytochemicals in the treatment of diseases caused by some notorious pathogens including *H. pylori* (Sibanda and Okoh, 2008; Manyi-Loh *et al.*, 2010; Njume *et al.*, 2011; Seanego *et al.*, 2012). Honey is a natural product that has been shown to supress

the growth of micro-organisms including *H. pylori* (Ndip *et al.*, 2007; Manyi-Loh *et al.*, 2010; Mandal *et al.*, 2011).

In spite of the demonstrated need of urease activity during colonisation of the harsh acidic environment of the human stomach, not much work has focussed on urease inhibition as a way of treating *H. pylori* infection. Acknowledging that honey has the potential to suppress *H. pylori* growth *in-vitro* (Ndip *et al.*, 2007; Manyi-Loh *et al.*, 2010; Mandal *et al.*, 2011), it becomes necessary to screen for anti-urease active compounds in honey and assess their potential of inhibiting the growth and multiplication of *H. pylori* cells under acidic environments, a mimicry of the human stomach *in-vitro*. The success of this study could help in identifying new lead molecules, which could be used in the development of new and affordable drugs against the pathogen to circumvent the problem of increasing drug resistance.

1.3 HYPOTHESIS

The following null hypotheses were formulated:

- 1.3.1 There are no active compounds in honey that can suppress the activity of urease and *H. pylori* that is *cag*A positive, *vac*A positive and drug resistant at a neutral pH.
- 1.3.2 There are no active compounds in honey that inhibit multiplication of *cagA* positive, *vacA* positive and drug resistant *H. pylori* grown under acidic environments.

1.4 OBJECTIVES

1.4.1 Overall objective

The overall objective of this study was to identify honey extracts with anti-urease properties *in-vitro* and test their inhibitory potential on *cag*A positive, *vac*A positive and drug resistant *H. pylori* cultured under acidic environments, a mimicry of the human stomach.

1.4.2 Specific objectives

The specific objectives of this study are:

- i. Identify *H. pylori* isolates by biochemical tests (Gram stain, catalase test, oxidase test and urease test) and comfirm by PCR targeting the *glm*M gene (140 bp).
- ii. Determine drug resistance pattern of clinical isolates of *H. pylori*.
- iii. To extract and purify urease enzyme from *H. pylori* isolates.
- iv. To use organic solvents to extract honey compounds.
- v. To screen for honey solvent extracts with the most anti-urease activity.
- vi. To detect *cag*A gene and *vac*A gene among clinical isolates of *H. pylori*.
- vii. To determine the critical pH from which urease activity is a necessity for *H*.

 pylori growth in an acidic environment.
- viii. To determine if not whether kinetic inhibition of urease by anti-urease active compounds in honey can suppress the growth of drug resistant, *cag*A positive and *vac*A positive *H. pylori* strains under acidic environments.
- ix. Characterise chemical composition of honey extracts capable of inhibiting urease and hence *H. pylori* growth under acidic environments.

CHAPTER TWO

LITERATURE REVIEW

2.1 DISCOVERY OF HELICOBACTER PYLORI

Two Australian researchers, Barry J. Marshall and Robin Warren were awarded a Nobel Prize in Physiology in 2005 after they made a striking discovery of a Gram negative spiral shaped bacilli as the causal agent of gastritis and ulcers (Marshall and Warren, 1983). Evidence was provided when Marshall initially underwent gastric biopsy to prove that he was not infected with the Gram negative bacterium. He then infected himself with the bacterium resulting in a histologically proven mild gastritis over two weeks (Marshall et al., 1985). In September 1983, classification of this bug generated a lot of interest at the Second International Workshop on Campylobacter Infections held in Brussels, Belgium (Pearson et al., 1983). The resemblance of the newly discovered organism to Campylobacter included requirement of a rich growth media under microaerophilic conditions, curved morphology and failure to ferment glucose led to its naming as Campylobacter pyloridis in 1985 and later to Campylobacter pylori in 1987 (Marshall and Goodwin, 1987). However, differences observed between Campylobacter species and Campylobacter pylori were reasonable for renaming this organism as *Helicobacter pylori* which became the first member of the genus Helicobacter (Goodwin et al., 1989). Since the discovery of this pathogen, a lot of studies have been done as an attempt to fully understand its biology.

2.2 INFECTION OF THE HUMAN STOMACH AND DISEASE MANIFESTATION

H. pylori infect the stomach of about half of the world's population. The risk of getting the bacterium is more pronounced in developing nations due to precarious hygiene conditions,

overcrowding, contaminated environmental and water sources (Ndip *et al.*, 2003; Dube *et al.*, 2009). Modes of transmission of this organism are not clear, but there are acceptable suggestions raised through research which include oral-oral, faecal-oral and person-to-person transmission (Stone, 1999; Ndip *et al.*, 2003; Perry *et al.*, 2006). Infections with the bacterium can be life long without effective treatment either in an asymptomatic or symptomatic mode. Many studies have linked *H. pylori* infection as the cause of many gastroduodenal complaints such as dyspepsia, gastritis, peptic ulcers and stomach cancer (Ahmed *et al.*, 2007b; Rothenbacher, 2007; Tanih *et al.*, 2010; Kuo *et al.*, 2014).

2.2.1 Gastritis

Gastritis is the inflammation of the stomach and at advanced stages is accompanied by the erosion of the lining of the stomach, and it can either be acute or chronic (Kusters *et al.*, 2006). Animal studies revealed a positive correlation of *H. pylori* infection and development of stomach gastritis (Wirth *et al.*, 1998; Zhao *et al.*, 2015). Serum levels of IL-17 were suggested to serve as a potential biomarker for the diagnosis and prediction of gastritis caused by *H. pylori* (Zhao *et al.*, 2015). It is described as a sudden and short-lived inflammation of the gastrointestinal tract that could provoke vomiting and in serious situations can lead to bleeding and hematemesis. Acute gastritis is associated with local irritants such as bacterial endotoxins, caffeine, alcohol, and aspirin. Acute gastritis usually lasts for a few days with complete regeneration and healing occurring promptly (Porth, 2002). On the other hand, chronic gastritis on the other hand is as a result of persistent stomach colonisation by the agent provoking gastritis. There are four major types of chronic gastritis: autoimmune gastritis, multifocal atrophic gastritis, chemical gastritis and *Helicobacter pylori* gastritis (Porth, 2002; Furuta and Delchier, 2009). Prolonged colonisation of the human stomach by

H. pylori has been linked to chronic gastritis. If *H. pylori* infection is not treated successfully, chronic gastritis may last for years or even a life time.

2.2.2 Peptic ulcer disease (PUD)

PUD is a term used to refer to both stomach ulcers and/or duodenal ulcers (Kuster *et al.*, 2006; Lanas and Chan, 2017). Stomach or gastric ulcers are open sores that develop along the lining of the stomach, while duodenal ulcers develop along the intestine just beyond the pyloric sphincter. Indigestion, heartburn, burning or gnawing sensation, loss of appetite and weight loss represent the common symptoms of ulcers (Ahmed *et al.*, 2007a; Rothenbacher, 2007). Internal bleeding can happen due to ulcers especially if the spot of ulcer development coincides with a blood vessel location. The complications of peptic ulcers include hemorrhage which is caused by bleeding (Figure 2.1).

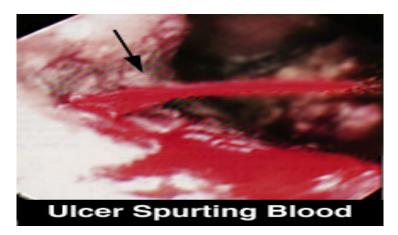


Figure 2.1: Picture showing ulcer spurting blood

Source: www.crystalgraphics.com/powerpictures/images.photos.asp?ss

2.2.3 Gastric cancer/malignant tumor

Cancer is a disease that involves abnormal and uncontrolled cell growth with the potential to invade or spread to other parts of the body. Epidemiological studies have shown that *H. pylori* is a class 1 carcinogen that causes gastric adenocarcinoma, the most common cancers worldwide

(Chey *et al.*, 2017). Gastric cancer is the second leading cause of deaths associated with cancer illnesses. A study by Lima *et al.* (2011) revealed that *vac*A *s1m1* and *cag*-PAI genes, *cag*A, *cag*E and *vir*B11 are important *H. pylori* markers for the development of gastric cancer. Tumours are adenocarcinomas developing from mucus-secreting cells in the base of the gastric crypts. About 50% and 60% of gastric cancers occur in the pyloric region or adjacent to the antrum (Furuta and Delchier, 2009) (Figure 2.2).



Figure 2.2: Picture showing gastric cancer development

Source: (www.crystalgraphics.com/powerpictures/images.photos.asp?ss)

2.2.4 Benign tumor

Benign tumors are non-cancerous cells represented as a mass of cells (tumor) lacking the ability to invade neighboring tissues. These tumors are normally surrounded by an outer fibrous sheath of connective tissue or remain within the epithelium region. The mass effect of benign tumors is a challenge even if these cells do not metastasize. Schwannomas are an example of slow growing benign tumors that originate from Schwann cells of the neutral sheath. In a recent study, a 64 year old woman having Schwannomas had chronic inflammation linked to a microorganism resembling *H. pylori* morphological (Lavy *et al.*, 2016).

2.3 H. pylori PREVALENCE AND INCIDENCE

The prevalence and incidence of H. pylori differ by geographical area and race but the prevalence of *H. pylori* is notably higher in poor developing nations as compared to wealthy developed nations (Ndip et al., 2007; Tanih et al., 2010; Watanabe et al., 2015). Incidence of H. pylori infection has been used to classify the world into two groups i.e. group one having children who become infected at childhood with chronic infection continuing into adulthood while group two comprises of developed nations whereby the minority of children are infected at childhood followed by an increase in prevalence with age (Queiroz et al., 2013). There is an *H. pylori* incidence record of 3-10% yearly in developing nations in comparison to 0.5% in developed nations (Rosenberg, 2010). Studies done in countries such as Egypt, India, Nigeria, Cameroon and South Africa show a considerably high prevalence of H. pylori infection exceeding 50%, a notable trend associated with developing nations (Dube et al., 2009; Eshraghian, 2014). There are studies that have highlighted an increased infection at childhood reaching 50% and above at the age of 5 (Bassily et al., 1999; Ndip et al., 2004; Dube at al., 2009; Awuku et al., 2017). Infections have been thought to arise through consumption of contaminated food including vegetables, contaminated water sources, contacts with animals that are H. pylori reservoirs as well as consumption of animal derived products such as sheep and cow milk (Khalifa et al., 2010). The suggested routes of transmission include direct infections through oral-oral, gastro-oral and faecal-oral routes.

2.4 THE HUMAN STOMACH AS A PREDOMINANT SITE FOR COLONISING H. pylori STRAINS

Helicobacter pylori colonises the human stomach and causes a chronic infection. The human stomach lies between the oesophagus and the duodenum of the digestive tract. The lower oesophageal sphincter and the pyloric sphincter help to control movement of the contents of

the stomach in and out of the stomach. The stomach has a mixture of gastric juices responsible for digestion. Also the stomach has a mucus lining along the walls of its inner layer which for protection against self-digestion, a common cause of stomach ulcers. Also this superficial glycoprotein-rich mucosal lining is a defensive mechanism for survival of *H. pylori* in the human stomach. The organism is known to swim through the protective gastric mucus in the stomach and attach to the epithelial cells of the stomach resulting in different disease outcomes over the duration of the infection (Peek, 2005; Celli *et al.*, 2009). Pepsin and hydrochloric acid are active ingredients secreted into the stomach by cells lining the stomach. The acid is required for the activation of the enzymes responsible for protein digestion and the human stomach pH can tolerate low pH level up to pH 1.5 (Dressman *et al.*, 1990; Russel *et al.*, 1993).

The low pH of the human stomach may unavoidably eliminate a wide range of microbial pathogens, but it is a different story with *H. pylori*. This organism actively produces urease enzymes which are either surface localised or cytoplasmic (Krishnamurthy *et al.*, 1998). *H. pylori* with cytoplasmic urease (Krishnamurthy *et al.*, 1998) and urease negative *H. pylori* (Amin *et al.*, 2010) have failed to survive an acidic environment, thereby reinforcing the belief that urease enzyme is required for *H. pylori* to colonise the human stomach. The urease enzyme is highly conserved in *Helicobacter* species and two major subunits of this enzyme have been identified which are *ureA* and *ureB* (Hu *et al.*, 1992).

The abundance of the urease produced by *H. pylori* allows rapid hydrolysis of urea producing ammonia and bicarbonate which help neutralise the gastric pH for optimum survival of the organism. Nitrogen metabolism is a requirement for normal health and it is an essential

element in all amino acids derived through dietary protein intake. Under normal conditions, renal nitrogen (urea and ammonia) excretion is equal to nitrogen intake (Weiner *et al.*, 2014). The ammonia generated by urease activity in the human stomach might be used in the metabolism of the bacterium for the synthesis of amino acids. Normally, proteins in food are hydrolysed into 9 essential and 11 nonessential amino acids (Weiner *et al.*, 2014).

2.5 VIRULENCE FACTORS OF H. pylori

Research has gradually focused on pathogenicity makers in an attempt to link virulence markers and disease manifestations. Virulence factors are molecules produced by pathogens to enable colonization of a niche in the host by evading the host's immune response and successfully causing a disease (Backert *et al.*, 2011; Cogo *et al.*, 2011; Kalali *et al.*, 2014). Several virulence factors of *H. pylori* have been documented and these include, the cytotoxin-associated gene A (*cag*A gene), vacuolating cytotoxin gene A (*vac*A) gene, induced by contact with epithelium A gene (*ice*A gene), duodenal ulcer promoting A gene (*dup*A) gene, urease enzyme, adhesins and the flagella (Backert *et al.*, 2011; Cogo *et al.*, 2011; Pereira *et al.*, 2014 Huang *et al.*, 2016).

2.5.1 The induced by contact with epithelium gene A (iceA)

There are at least two alleles of *iceA*; *iceA1* and *iceA2* (Arevalo-Galvis *et al.*, 2012; Rizzato *et al.*, 2012; Huang *et al.*, 2016). Infection with the *iceA1*-positive *H. pylori* seems to correlate with increased risk for peptic ulcer disease (Huang *et al.*, 2016), enhanced mucosal interleukin (IL)-8 and acute antral inflammation (Arevalo-Galvis *et al.*, 2012). However, infection with *H. pylori* strains having *iceA2* gene status had no significant correlation with disease manifestation (Huang *et al.*, 2016). The expression of *iceA1* is instigated by contact

between *H. pylori* and human epithelial cells (Arevalo-Galvis *et al.*, 2012). However, heat shock protein 90 (HSP90) is a crucial regulator in *H. pylori* induced IL-8 production (Yeo *et al.*, 2004). HSP90 has been revealed to be critical for intracellular signaling that participates in inflammatory response as well as carcinogenesis (Yeo *et al.*, 2004).

2.5.2 Duodenal ulcer promoting gene A (dupA)

This virulence factor is a *virb*B4 homologue (Lu *et al.*, 2005) associated with duodenal ulcer development and reduced risk of gastric carcinoma in some populations (Hussein *et al.*, 2010). The *dup*A is located in the plasticity region of *H. pylori* genome. The most common form of *dup*A (*dup*A1) encompasses parts of the jhp0917 and jhp0918 ORF which form a single continuous open reading frame by the insertion of a base C or T after position 1385 in the jhp0913 3' region (Queiroz *et al.*, 2011; Pereira *et al.*, 2014). The second common form *dup*A2 contains 2 ORFs (Hussein *et al.*, 2010).

2.5.3 Vacuolating cytotoxin gene A (vacA)

The *vac*A gene encodes for the production of *vac*A protein, a complex of 500 to 600 kDa, consisting of 87 kDa subunits (Haas, 2002). The *vac*A induces the formation of intracellular vacuoles in epithelial cell lines (Atherton *et al.*, 1995; Faundez *et al.*, 2002). The *vac*A gene is present in almost all *H. pylori* strains and not all are highly toxigenic and pathogenic (Trang *et al.*, 2016). The *vac*A gene possess four regions closely associated with the vacuolating activity of *H. pylori*, that is the signal (s)-, intermediate (i)-, middle (m)-, and deletion (d)-regions which are classified as either type 1 or 2 (Hashinaga *et al.*, 2016). The *s* region exists as *s*1 or *s*2 and in addition, has subtypes *s*1a, *s*1b and *s*1c (Faundez *et al.*, 2002). The *m* region occurs as *m*1 or *m*2. Although all strains of *H. pylori* have a *vac*A gene, there is

variation in the amount of vacuolating activity due to heterogeneity within the *vac*A gene at the 5' end *s* region and the *m* region. The allelic combination *s*1*m*1 and *s*1*m*2 strains produce high and moderate levels of toxin respectively while the *s*2*m*2 allelic combination has little or no toxin and final *s*2*m*1 combination is rare and non-vacuolating (Cogo *et al.*, 2011; Pereira *et al.*, 2014). All s1m1i1 and s1m2i1 strains are vacuolating and more virulent in comparison to s1m2i2 and s2m2i2 strains (Trang *et al.*, 2016). In addition, d1/c1 strains are associated with the production of vacuolating cytotoxin genes (s1m1i1) contrary to d2c2 association with non-vacuolating types s2m2i2 (Trang *et al.*, 2016). Studies have found correlation in the presence of the *vac*A *s*1*m*1 genotype and the presence of *cag* PAI in PUD and gastric cancer, while the *vac*A *s*2*m*2 genotype is linked with the absence of the *cag* PAI (Atherton *et al.*, 1995; Miernyk *et al.*, 2011).

2.5.4 The cytotoxin-associated gene A (cagA)

The *cag*A gene encodes a protein that is associated with increased intensity of the gastric inflammation and, subsequently severe clinical outcomes (Miernyk *et al.*, 2011). Virulence strains of *H. pylori* possess a 40 kb *cag* PAI containing 31 potential coding regions involved in different type IV secretion system (T4SS) encoding (Jones *et al.*, 2010; Jiménez-Soto and Haas, 2016; Zaki *et al.*, 2016a). During *H. pylori* infection, adhesins create close bacterial contact with host target cells followed by delivery of effector proteins into host target cells by the T4SS, a needle-like pilus device (Jones *et al.*, 2010). There are studies that have confirmed that once injected into the host cell, *cag*A can directly activate NF-κB and induce the release of IL-8 which plays a big role in the development of gatric cancer (Kang *et al.*, 2013; Lee *et al.*, 2013; Papadakos *et al.*, 2013). *Cag*A is classified as an oncogene due to its association with gastric cancer development (Pereira *et al.*, 2014).

2.5.5 Adhesins

H. pylori is highly adapted to survival in the gastric environment of the human stomach and it has been shown to encode a varied set of adhesins. More than 30 genes encoding outer membrane proteins (OMPs) have been grouped into Hop (Helicobacter outer membrane porins) and Hor (Hop related) subgroups. The adhesins that belong to the Hop family are linked with more virulent strains and they include the babA, sabA, alpA/B, HopZ and oipA (Backert et al., 2011). More focus has been on BabA and SabA adhesins, however not all H. pylori strains express functional BabA or SabA adhesins (Lopez-Bolanos et al., 2009) probably explaining the fact that in the human stomach H. pylori is found being highly motile in the mucus or attached to the epithelial cells (Oleastro and Ménard, 2013). Adherence to the gastric epithelium allows the bacterium to have persistent colonization without danger of being automatically flushed out by stomach peristalsis. Evasion of the host defense system and efficient delivery of proteins such as vacA and cagA, into gastric cells are some of the benefits of adherence (Oleastro and Ménard, 2013).

2.5.6 Flagella

H. pylori is equipped with two to six flagella that are in a lophotrich position. Possessing flagella seems to play an important role in colonisation of the host by H. pylori. A flagellated strain has been shown to be successful in colonising the stomach of experimental animals while the strain devoid of flagellates colonises the stomach of experimental animals less frequent (Eaton et al., 1992). The flagella are important for gastric colonisation through locomotion and counteraction of peristalsis. The flagella enables the organism to achieve different types of movements which include swimming, spreading and swarming motility, attained in liquid media, soft media and semi-solid media respectively (Gu, 2017). Each flagellum has four components, the basal body, the filament, sheath and the hook

(Lertsethtakarn *et al.*, 2011). The basal body consist of the c-ring, ms-ring and the type III secretion system. The c-ring (*fli*M, *fli*N, *fli*Y, *fli*G) transfers proteins as well as co-ordinating protein secretion and regulating motor rotation (Lowenthal *et al.*, 2009; Tsang *et al.*, 2013). The ms-ring (*fli*F) of the basal body is involved in the synthesis of *fl*A, *fla*B and *flg*E (Allan *et al.*, 2000). The type III secretion system (*flh*A, *fli*O, *flh*B, *fli*P, *fli*Q, *fli*R) is responsible for the transportation of flagellar proteins towards the end of the flagellar structure (Smith *et al.*, 2009; Ibuki *et al.*, 2013). The flagellar filament has proteins *fla*A, *fla*B and *fli*D with *fla*A and *fla*B playing an important role in bacterial motility (Josenhans *et al.*, 1995). The *fli*D is a filament capping protein of the flagellar assembly (Kim *et al.*, 1999). The proteins *hpa*A and *faa*A of the flagellar sheath protect the flagellar subunits from depolymerisation at low pH (Carlsohn *et al.*, 2006; Radin *et al.*, 2013).

The hook of the flagellar found in H. pylori consist of the flagellum export chaperone (fliS) and the flagellar hook proteins (flgE and flgK). The fliS chaperone help to prevent premature polymerization of the flagellin and it also participates in flagellum assembly (Lam et al., 2010). The flgE is responsible for connecting the basal body and the flagellar filament which is also linked to the powerful driving force in a viscous environment (O'Toole et al., 1994; Ryan et al., 2005). The protein flgK of the flagellar hook is responsible for controlling the length of the flagellar hook during flagellum assembly (Douillard et al., 2009).

2.6 UREASE ENZYME

Urease enzyme plays a crucial role in *H. pylori* pathogenesis. *H. pylori*, a neutralophile is able to colonise the acidic gastric mucosa of the human stomach by producing a large amount of urease enzymes (Celli *et al.*, 2009; Amin *et al.*, 2010). The urease enzyme is responsible

for the hydrolysis of urea to ammonia and bicarbonate. The by-products of urea hydrolysis result in elevated pH surrounding *H. pylori* cells from a pH 2 to almost neutral (Allen and Flemstrom, 2005). The pH regulation by urease enzyme has been shown to be crucial during locomotion. The mucus lining of the stomach has been shown to undergo reversible pH dependent sol-gel transition from viscous polymer solution to a soft gel as pH is lowered below 4 and vice versa when pH is raised (Celli *et al.*, 2009). The gastric mucin, the glycoprotein content of the mucus is responsible for the pH dependent change of viscosity. The property of the glycoprotein was observed to be important among urease producing strains of *H. pylori* since elevated pH causes alteration of rheological properties of the mucus environment to a much softer form thereby allowing easier propelling during movement (Celli *et al.*, 2009).

The crystal structure of *H. pylori* urease shows that it has two subunits (*ureA* and *ureB*) and its catalytic substance contains a dinuclear nickel active site (Lam *et al.*, 2010). However, enzymes from other bacteria including *Klebsiella aerogenes* have *ureABC* structures (Pearson *et al.*, 1997; Benini *et al.*, 1999). Colonisation of the gastric mucosa of the human stomach requires among virulence factors, production of an active metalloenzyme urease that requires nickel as a cofactor.

It has been demonstrated that urease negative strains or strains of *H. pylori* with *ure*B disruption fail to cause gastritis in mice due to colonisation difficulties (Tsuda *et al.*, 1994; Amin *et al.*, 2010). Urease enzyme neutralises the gastric acid through production of ammonia (NH₃) and carbon dioxide (CO₂). The NH₃ produced may cause the formation of

NH₃-derived compounds such as monochloramine with cytotoxic effects on host cells (Suzuki *et al.*, 1992).

2.6.1 Production and activation of urease in H. pylori

The operon of *H. pylori* urease has seven open reading frames (ORFs) *ureABIEFGH* found in a single 6.13 kb cluster of chromosomes (Cussac *et al.*, 1992; Fong *et al.*, 2013). The *ureA* and the *ureB* are responsible for encoding the urease structural proteins while the remaining five are accessary genes responsible for the synthesis of the catalytically active enzymes (Hu and Mobley, 1993). The *ureI* encodes cytoplasmic membrane protein responsible for the formation of a urea-specific pore. The urea-specific pore channels urea to the urease enzyme located in the cytoplasm of the bacteria (Rectorschek *et al.*, 2000). Work on transposon mutagenesis revealed that ure*A*, *ureB*, *ureF*, *ureG* and *ureH* of *H. pylori* are required for the production of functional urease (Cussac *et al.*, 1992; Fong *et al.*, 2013).

The comparison of urease accessory proteins from different sources including bacteria revealed that ureases contain six amino acids constituting a ligand for the Ni²⁺ metallocenter (Farrugia *et al.*, 2013; Fong *et al.*, 2013). Metalloenzymes are synthesised as precursors devoid of metalloenzyme active site. Metalloenzymes need an elaborate metallocenter assembly system to have a functional active site (Farrugia *et al.*, 2013). The Ni²⁺ metallocenter that activates the enzyme is generated through incorporation of nickel ions to the apoprotein (Fong *et al.*, 2013). The nickel is inserted into the urease active site in a GTP-dependent process with the influence of accessory proteins *ureD/ureH*, *ureE*, *ureF*, and *ureG*. The metallocenters are important as they serve crucial biological functions which include transferring electrons, stabilizing biomolecules, binding substrates, and catalysing desirable

reactions and in addition, strict control is needed during metallocenter synthesis to influence specificity of the active site (Farrugia *et al.*, 2013; Fong *et al.*, 2013; Sujoy and Aparna, 2013).

Maturation of urease requires proper insertion of two nickel ions to the active site in addition to accessory proteins (Carter *et al.*, 2009). The *ure*E and *ure*G proteins are soluble and have been researched widely in comparison to *ure*D and *ure*F proteins which are insoluble proteins (Lam *et al.*, 2010). *Ure*E seems to be responsible as a structural scaffold for recruitment of GTP to *ure*G i.e. *ure*E serves as a medium to grasp Ni²⁺ from *hyp*A and hence donate it to *ure*G (Yang *et al.*, 2015). The accessory protein *ure*D has been renamed *ure*H in *Helicobacter* species (Cussac *et al.*, 1992) and has been proposed to be a scaffold towards recruitment of other accessory proteins as well as a facilitator of activation.

UreF is a protein forming a dimer with a novel all-helical topology probably showing a possible binding surface for interaction with other urease components or for urease-related protein-protein interactions (Lam et al., 2010a). The ureG is soluble and has been highly characterised as reported by different studies (Cussac et al., 1992; Lam et al., 2010a). It forms sequential complexes with the urease apoprotein. The nucleotide-binding motif (P-loop) in the ureG sequence and the resultant seizure of urease activity corresponding to mutation of this site and in-vitro GTP-dependent ureDFG-urease apoprotein complex activation suggest that ureG protein is a GTPase for urease activation (Lam et al., 2010a; Farrugia et al., 2013).

2.6.2 Urease and inflammation of the human stomach

Urease has been shown to induce primary mucosal macrophages to produce interleukin (IL)-1 beta, IL-6 and tumour necrosis factor (TNF)-alpha (Harris *et al.*, 1998). Once in the gastric mucosa, *H. pylori* bind to CD74 on gastric epithelial cells. The urease subunit B-CD74 interaction was shown to induce NF-κB activation and interleukin-8 (IL-8) production (Beswick *et al.*, 2006). High expression of IL-8 in gastric mucosa has been linked with risk of gastric cancer (Yamada *et al.*, 2013). In addition, heat shock protein (HSP) 90 has been revealed to be critical for intracellular signalling that participates in inflammatory response as well as carcinogenesis (Yeo *et al.*, 2004). *H. pylori* also produces [Ni, Fe]-hydrogenase enzymes which oxidise molecular hydrogen to produce enough energy to compensate for the high energy used during early adaptation to survive in acidic environment of the human stomach (Yang *et al.*, 2015).

2.6.3 Urease inhibitors

Urease inhibition has been extensively studied considering potential benefits which include treatment of urease dependent microbial infections and control of pH variations in soil (Upadhyay, 2012; Amin *et al.*, 2013). Several classes of urease inhibitors have been discovered worldwide (Upadhyay, 2012; Amin *et al.*, 2013; Sujoy and Aparna, 2013; Tan *et al.*, 2013; Grant, 2014; Modolo *et al.*, 2015). These include inhibitors substrate analogues, substituted urea/thiourea, hydroxyurea, hydroxamic acids, phosphoroamides, and thioles. Varying methods of urease inhibition have been recorded, heavy metal ions seem to react with the active site sulfhydryl group in an analogous way to the formation of metal sulphide (Krajewska, 1991). The phosphoroamide compounds and hydroxamic acids inhibit urease by creating a tetrahedral intermediate with a structure similar to the tetrahedral intermediate postulated to occur during urea hydrolysis (Dixon *et al.*, 1980). The boric and boronic acids

seem to form a complex with nickel ions (Breitenbach and Hausinger, 1988). Competitive inhibition of urease has been noted with thiol compounds.

2.6.3.1 Heavy metals as urease inhibitors

Urease activity has been shown to succumb due to presence of trace elements of heavy metals. The heavy metal ions including Ag^+ , Hg^{2+} and Cu^{2+} , have been shown to inhibit urease activity with silver showing the highest inhibition effect. Time-dependent inhibition studies revealed a biphasic kinetics with all heavy metals ions (Prakash and Vishwakarma, 2001; Kumar *et al.*, 2009). The urease enzyme has been shown to quickly bind to Hg^{2+} and then attain a state of slow reversible course to inactivation (Du *et al.*, 2012). Prakash and Vishwakarma (2001), in a study showed that urease from the seeds of water melon was inhibited by heavy metal ions including copper, lead, nickel and cobalt and the effectiveness of non-competitive urease inhibition by these heavy metal ions was $Cu^{2+} > Pb^{2+} > Ni^{2+} > Co^{2+}$.

2.6.3.2 Hydroximate and its derivatives as urease inhibitors

Although hydroxamic acids have previously been recorded as potent, specific and non-competitive inhibitors of urease, these inhibitors were later reported to be reversible and slow binding (Mishra *et al.*, 2002). A study by Kobash *et al.* (1975) revealed methionine-hydroxamic acid as the best inhibitor of ureases among nineteen alpha-aminoacyl hydroxamic acids which included phenylalanine, serine, alanine, glycine, histidine, threonine, leucine, and arginine-hydroxamic acids in order of decreasing inhibitory ability. Of interest is that the pH optimum required for inhibition shifted to lower pH in the presence of a carboxyl group, and to higher pH in the presence of an amino group. Hydroxamic acid seems to inhibit

urease activity with strict specificity with the exception of aspartic-β-hydroxamic acid, which inhibited asparaginase competitively among studied inhibitors (Kobash *et al.*, 1975).

2.6.3.3 Thioles as urease inhibitors

Thiol compounds having a positively charged beta-amino group are potent inhibitors while thiol compounds having an anionic carboxyl group show less inhibitory power towards urease activity (Todd *et al.*, 1989). Also their inhibitory interaction is non-specific. Disulfiram, a thiol reagent used in humans approved by FDA for the treatment of chronic alcoholism has been recently shown to inhibit urease activity (Díaz-Sánchez *et al.*, 2016).

2.6.3.4 Boric acid as urease inhibitors

Competitive inhibition of Jack bean urease by boric and boronic acids has been reported (Upadhyay, 2012). However phosphate buffering seems to influence inhibition by boric acid in a pH dependent manner with pH of 5 linked to maximal inhibition while the pH of 10 seem to be linked with minimal inhibition of urease (Reddy and Kayastha, 2006). Studies have revealed a lot more compounds showing inhibitory power against urease activity (Reddy and Kayastha., 2006; Amin *et al.*, 2013; Tan *et al.*, 2013; Díaz-Sánchez *et al.*, 2016). Hydroxyurea, sulfur compounds, alpha-hydroxyketones, alpha diketones, triketone oximes, phosphates, biscoumarin and some organic solvents are known to be urease inhibitors (Upadhyay, 2012). Phytochemicals as well have been recommended for their urease inhibition properties (Amin *et al.*, 2010; 2013).

2.7 UREASE ASSAYS

Several reliable techniques have been successfully used to confirm and study the chemistry of ureases. Some of them are the Berthlot test/ indophenol assay, pH indicator assay, potentiometric assays coupled urease-glutamate dehydrogenase (GDH) assay and coupled urease-horseradish peroxidase assay.

2.7.1 Berthlot test/indophenol assay

This test is used to determine ammonia production or presence in a sample. The Berthelot's reagent is an alkaline solution of phenol and hypochlorite. Reaction of Berthelot and ammonia results in a colorimetric blue product which determines the presence of ammonia. Another application of this method is to determine the activity of urease in the presence of urea which eventually leads to the production of ammonia and carbon dioxide. The urease activity assay kit has been used for this test. The kit provides a direct procedure for measuring urease activity in biological and environmental samples. Produced ammonia through hydrolysis of urea by urease, is determined by the Berthelot method which result in a colorimetric product that is measured at 670 nm giving a reading that is proportionate to the urease activity present in the sample.

2.7.2 The pH indicator assays

Urease is active in the pH range of 3.5 to pH 8. In acidic environments, the urease enzymes help to elevate the pH through the hydrolysis of urea to form ammonia and carbon dioxide. The rate of pH change can be monitored spectrophotometrically in the presence of a pH indicator such as phenol red (Hamilton-Miller and Gargan, 1979). This is a convenient and suitable test for routine urease tests but it is not ideal for detailed kinetic analysis.

2.7.3 Coupled urease-glutamate dehydrogenase (GDH) assay/Coupled urease-

horseradish peroxidase assay

This method is based on the fact that ammonia produced by urease can stimulate the oxidation of NADH in a coupled enzyme assay and such a reaction can be monitored by measuring reduction of NADH at 340 nm (Kaltwasser *et al.*, 1966). The coupled urease-horseradish peroxidase assay utilises the findings that ammonia can stimulate peroxidase activity on o-dianisidine resulting in an increase in absorbance at 460 nm (Stutts and Fridovich, 1964).

2.8 DIAGNOSIS OF H. pylori INFECTION

Diagnosis of an infection is crucial for proper management of the disease. There are a several methods that have been used to examine gastric colonization of *H. pylori*. Successes of tests currently used rely on representative samples which must be obtained from infected individuals. Biopsies, blood serum, exhaled air and stool samples have been widely used as *H. pylori* infection test samples (Dube *et al.*, 2009; Tanih *et al.*, 2010; Harrison *et al.*, 2017). Biopsy related methods, and serum based methods are the most common invasive methods that have been widely used to detect and confirm an active *H. pylori* infection (Tanih *et al.*, 2010; Kadi *et al.*, 2014; Saidu *et al.*, 2015; Zaki *et al.*, 2016a; Hanafi *et al.*, 2017; Harrison *et al.*, 2017). Non-invasive tests which include urease breath test and stool antigen test have been successfully used to detect *H. pylori* infection (Dube *et al.*, 2009; Harrison *et al.*, 2017).

2.8.1 Direct diagnosis tests

Endoscopy is a procedure that has been used to view the inside of the stomach in patients with gastroduodenal complaints. The magnifying narrow-band imaging endoscopy

technology allows clear visualization of the gastric epithelial lining of the stomach (Tahara *et al.*, 2009). This visualisation allows gastroenterologist to assess signs of gastritis, ulceration and cancerous cells development in the human stomach (Uemure *et al.*, 2001; Tahara *et al.*, 2009); hence the representative biopsy samples are collected near or at the area surrounding a suspected disease outcome as observed under endoscopy. Considering any *H. pylori* infection, the gastric mucosa is divided into three states, normal mucosa without a history of *H. pylori* infection (non-gastritis), current *H. pylori* infection (active gastritis), and past history of *H. pylori* infection (inactive gastritis). This requires specialisation and experience for accuracy and persistence with success of endoscopy examination (Watanabe *et al.*, 2013).

Culturing of *H. pylori* allows a lot of studies to be conducted in an effort to understand the microbiology, prevalence, virulence and drug resistance patterns of strains circulating in a population. However, to obtain live cultures from clinical specimen can be a challenge because of the fastidious nature of *H. pylori*. Obtaining viable gastric biopsy is one of the methods for diagnosing a current infection. Therefore, samples obtained by endoscopy require specialised transport media so as to maintain viability of *H. pylori* cells. Vials containing approximately 1 mL of cysteine transport medium with 20% glycerol have been successfully used as transport media (Tanih *et al.*, 2010). Inoculation of culturing plates soon after a biopsy sample has been collected and sealing cultured plates in Biobags for transportation has been reported to increase chances of recovering the organism. Portagerm pylori agar is another commercial transport media with high recovery rate of *H. pylori* from biopsy samples (Grove *et al.*, 2001). A semi-solid *Helicobacter pylori* transport media GESA (publication no. WO/2014/019696, patent pending no. PCT/EP2013/002292; Liofilchems.r.l., Rosetodegli Abruzzi, Teramo, Italy) has also been developed (Cellini *et al.*, 2014).

2.8.2 Histopathology and immunohistochemistry (IHC)

Histopathology is a process of examining biopsy or surgical specimen. Biopsy specimens need to be fixed using 10% formaldehyde soon after collection (Mégraud and Lehours, 2007; Jemilohun *et al.*, 2010). The fixation of 10% formaldehyde maintains the morphology of the bacteria and also allows different staining techniques to be used, but prolonged storage of the fixed samples lose their features making analysis difficult. *H. pylori* silver stain, modified Giemsa, modified Genta, acridine orange, cresyl violet, Gimenez, Half Gram, Ziehl-Neelsen, and Warthin-Starry are some of the stains that have been used for the histological detection of *H. pylori* in gastric biopsies with better visualization of the organism (Mégraud *et al.*, 2007). IHC is a process of selectively imaging antibodies in cells of a tissue section through antibody binding principle to antigens.

2.8.3 Culturing of H. pylori

Culturing is the gold standard method of positively identifying an infecting organism and allows direct observation of *H. pylori* growth from biopsy samples. This organism is fastidious and requires a limited and optimised condition for growth. Several studies have highlighted the suitable microaerophilic growth environment consisting of 2% – 6% O₂, 10% CO₂, 80% – 85% N₂ (Kusters *et al.*, 2006) made possible by commercial microaerophilic sachets inserted in gas jars together with culture plates, or specialised incubators capable of adjusting atmosphere to set conditions. *H. pylori* is also considered a neutralophile even though it is found inhabiting the acidic environment of the human stomach. Urease producing *H. pylori* have been found to tolerate pH range of 3.5 to 8 (Rektorschek *et al.*, 1998; Scott *et al.*, 1998; Brown, 2000). The pH of 7 has been shown to provide optimal growth of the organism while the organism's growth is totally inhibited at pH below 3.5 (Scott *et al.*, 1998).

The urease activity is over a narrower pH range of pH 6.0 - 8.0 (Scott *et al.*, 1998; Brown, 2000).

Culturing of *H. pylori* also requires a complex source of nutrients almost similar to the nutrients in the human stomach. The generally used solid media for culture of *H. pylori* is Columbia or Brucella agar and Brucella broth supplemented with horse or sheep blood or, faetal calf serum at 5–7% v/v concentration, the *Helicobacter pylori* selective supplements are also included a in the growth media. The OxoidTM *Helicobacter pylori* selective supplements (Dent) contain vancomycin, trimethoprim, cefsoludin, and amphotericin B. Another type of supplement being used is Skirrow's supplements consisting of vancomycin, trimethoprim, polymyxin B, and amphotericin B (Ndip *et al.*, 2003). Brain heart infusion growth media, Brucella growth media and the Muller Hinton growth media are the liquid formulations that are used for the growth of *H. pylori*. The optimum temperature for *H. pylori* growth is ranges from 35°C to 37°C (Grove *et al.*, 2001; Tanih *et al.*, 2010).

2.8.4 Indirect diagnosis

Indirect tests fall into two categories, the active tests which are capable of detecting an active infection and the passive tests which only reveal the presence of a marker of an organism whether it is a previous exposure or a current infection. The urea breath test and the stool antigen tests are indirect tests that have been used successfully to detect active infections (Dube *et al.*, 2009; Harrison *et al.*, 2017). Antibody-based tests (serology) also offer reliable results when determining *H. pylori* infections. However, the challenge is that serological tests do not separate between active and non-active infection. Indirect tests are less likely affected

by drugs in use hence they can easily be used as an efficient diagnostic method (Burocua *et al.*, 2013).

2.8.5 Molecular techniques

Molecular techniques have been used widely as gold standard techniques in the study of old and newly discovered micro-organisms. The complete genome of most micro-organisms including *H. pylori* and some multicellular organisms has been extensively studied through the use of molecular techniques. The analysis of nucleic acids has been done through polymerase chain reaction (PCR), gel electrophoresis and blotting techniques (Northern, Southern). The analysis of gene expression has been done using real-time PCR and microarrays (DNA chips). Also recombinant DNA technology, Sanger sequencing and next generation sequencing are some of the common techniques that have made research in molecular biology a success.

Molecular techniques have been used for the detection housekeeping genes of *H. pylori* from water, gastric biopsies, stools, luminal aspirates, vomitus, saliva, dental plaque and other oral cavities that can provide a prolonged habitat for the organism as it gains it's way to infect the host (Burocua *et al.*, 1999; Ndip *et al.*, 2003; Tanih *et al.*, 2010; Abu-Sbeih *et al.*, 2014; Miftahussurur *et al.*, 2016; Harrison *et al.*, 2017). Many studies have been published using PCR or PCR/RFLP techniques to study *H. pylori*- related issues from modes of transmission, drug resistance, pathogenesis and many more.

Several genes specific for *H. pylori* have been targeted which include 16S rRNA gene, 23S rRNA and *ure*C/*glm*M (Atherton *et al.*, 1995; Burucoa *et al.*, 1999; Al-Thwai and Ali, 2013; Nevoa *et al.*, 2017). The *ure*C gene is not related to urease production, but encodes for a phosphoglucosamine mutase hence it was renamed *glm*M. It is considered a "housekeeping" gene, which participates directly in cell wall synthesis (Espinoza *et al.*, 2011). Other PCR based techniques that have been utilised for *H. pylori* studies include reverse transcriptase PCR (RT-PCR), conventional PCR, real time- PCR, multiplex PCR and nested PCR (Wong *et al.*, 2001; Bolek *et al.*, 2007; Abu-Almaali *et al.*, 2012).

PCR has allowed more research studies to be done on virulence factors of *H. pylori* by targeting virulence genes which include cagA, vacA, iceA, dupA, ureA, ureB genes and adhesins (Essawi et al., 2013). In addition, PCR has been used to determine resistance to some of the commonly used drugs in the treatment of H. pylori infection. Molecular studies have revealed that clarithromycin resistance by H. pylori is due to point mutations in the peptidyl-transferase region encoded in domain V of 23S rRNA for example mutations as a result of the transitions in A2143C and A2142C positions of rRNA and other mutations such as A2143G, A2142G, A2142C and A2144G (Tanih et al., 2013; Xiong et al., 2013).

2.9 TREATMENT OF H. pylori INFECTION

2.9.1 First Line therapies

European and American guidelines recommend primary therapies for *H. pylori* infection to include a PPI, clarithromycin, and amoxicillin or metronidazole (clarithromycin-based triple therapy) twice a day for 7 or 7–14 days or a PPI or (Ranitidine) H₂RA, bismuth subsalicylate,

metronidazole, and tetracycline (bismuth quadruple therapy) twice a day for at least 10 days or 14 days if bismuth is unavailable, this is with regard to populations with less than 20% clarithromycin resistance (Chey et al., 2007; Malfertheiner et al., 2007). However, in areas with less than 40% metronidazole resistance, PPI with clarithromycin and metronidazole is preferable. Furthermore, a 10-day sequential therapy seems to offer better outcomes. This therapy consists of a dual administration of PPI and amoxicillin followed by triple therapy consisting of PPI, clarithromycin and tinidazole (Zullo et al., 2000; Seo et al., 2014). In a paediatric study conducted by Arenz et al. (2006), the esomeprazole-based one-week triple therapy that was directed by susceptibility testing of H. pylori was shown to be effective in eradicating the organism. However, the limitation of this method is that it is effective when there are no double-resistant strains to drugs (clarithromycin or metronidazole). Its efficacy is moreover affected by resistance patterns of amoxicillin and clarithromycin. Recently, a new sequential concomitant hybrid therapy reported a high rate (99%) of treatment success (Hsu et al., 2011). The quadruple therapy consisting of PPI, bismuth and two antibiotics (amoxicillin + clarithromycin, or metronidazole + tetracycline) offer superior eradication rates.

The increasing resistance to clarithromycin has led to investigations of fluoroquinolones such as levofloxacin as a surrogate drug for this clarithromycin. A triple therapy with PPI, amoxicillin and levofloxacin has been suggested earlier as an alternative first-line therapy (Katelaris, 2009). Resistance to fluoroquinolones is generally very low (< 10%) worldwide (Boyanova and Mitov, 2010). Recent studies have revealed a low primary and secondary resistance ranging from 6.8% to 25% for floroquinoline (ciprofloxacin, levofloxacin, moxifloxacin and gemifloxacin), which is showing uncertaint on the longevity of the used of regimens that rely on floroquinoline (Teh *et al.*, 2014; Zaki *et al.*, 2016b).

The meta-analysis of Peedikayil *et al.* (2014) revealed equality in terms of safety and efficacy of both levofloxacin-based first line therapy and the 7 days standard first-line therapy, but of concern is that levofloxacin-based first line therapy do not yield consistant results (Hung *et al.*, 2009; Lim *et al.*, 2017). However, the recommendations of Chey *et al.* (2017) are not different from those suggested by European and American guidelines in 2007, but of note is an emphasis on drug selection combination i.e. before a patient is administered with treatment, information on previous infections and drug use needs to be obtained (Chuak *et al.*, 2016).

2.9.2 Second Line therapies

The second line treatment regimens remain the alternative treatment in the event of a rise in clarithromycin and/or metronidazole resistant *H. pylori* strains. In areas with exceedingly high occurrences of clarithromycin and metronidazole resistance, bismuth-based quadruple therapy is used as the first-line treatment (Chey *et al.*, 2007; Malfertheiner *et al.*, 2007). Otherwise bismuth-based quadruple therapy is the preferred second line regimen that has yielded good eradication results (Melgraud *et al.*, 2004; Kadayifci *et al.*, 2006; Malfertheiner *et al.*, 2007). The second-line regimen currently recommended is a quadruple therapy comprising of PPI, a bismuth salt, tetracycline and metronidazole for 10–14 days (Malfertheiner *et al.*, 2007; Davis, 2014). A challenge of this second line treatment regimen is that bismuth salts are not found in all countries, hence an alternative regimen consisting of PPI, doxycycline, metronidazole and amoxicillin is recommended.

Levofloxacin, a fluoroquinolone has a broad spectrum of activity against Gram positive and Gram negative bacteria (Seck *et al.*, 2009; Bago *et al.*, 2010). Several studies have been conducted to evaluate new fluoroquinolone based regimens as standard second-line therapies

and in comparison to clarithromycin and metronidazole, the new fluoroquinolones seem to be an alternative to the standard second line regimen (Gloker *et al.*, 2007; Teh *et al.*, 2014; Zaki *et al.*, 2016b). Rates of resistance of *H. pylori* to fluoroquinolones is low in different geographical locations, unlike for metronidazole and clarithromycin (Gatta *et al.*, 2005; Boyanova and Mitov, 2010; Karczewska *et al.*, 2011; Teh *et al.*, 2014).

2.9.3 Third-line therapies/ Rescue therapy

European guidelines recommend microbial antibiotic sensitivity testing as a procedure of determining the therapy to be used. Quinolones are ready candidates for third-line therapies and have been observed to possess a wide spectrum activity against both Gram negative and Gram positive bacteria (Boyanova and Mitov, 2010). High doses of PPI plus amoxicillin and levofloxacin or rifabutin regimens have shown higher success rates (Chey *et al.*, 2017).

2.10 CHALLENGES IN H. PYLORI TREATMENT

Even though various therapeutic regimens have been suggested against *H. pylori*, a multipurpose regimen against *H. pylori* is still a dream. Over the years, the effectiveness of standard PPI triple therapies has shown a gradually deterioration mainly as a result of increasing drug resistance to key PPI combination with antibiotics (clarithromycin and metronidazole) (Kadayifci *et al.*, 2006). Triple therapy consisting of a PPI (Rabeprazole, Dexlansoprazole, Esomeprazole, Lansoprazole, Omeprazole, Pantoprazole), clarithromycin, and amoxicillin or metronidazole was the initially planned regimen for *Helicobacter pylori* eradication. A five year study conducted in Turkey found a decreasing trend in eradication success with triple therapy consisting of a PPI, clarithromycin, and amoxicillin, the PPI-based triple regimens recorded an 84% eradication success in 1997 and decreased to 55.3% in 2004 (Kadayifci *et al.*, 2006).

Several proficiently conducted studies globally, have highlighted *H. pylori* resistance against clarithromycin and amoxicillin or metronidazole which appears to vary among different countries. Using melting curve analysis, a study in Turkey revealed a 30% resistance to clarithromycin, also 79.2% of patients who had previously used clarithromycin were resistant to the drug (Kaya et al., 2007). In a separate study, Aydin et al. (2006), revealed a 58.8% (p > 0.05) resistant to clarithromycin when 500mg was administered twice daily for two weeks. A study conducted in South Africa using the GenoType Helico DR recorded 15.38% H. pylori resistance to clarithromycin (Tanih et al., 2012). Multiple drug resistance is a major problem worldwide. A systematic review of H. pylori resistance to clarithromycin worldwide revealed a 17.2% resistance (Francesco et al., 2010). Strains of H. pylori obtained from a population of Sicily in Italy had a representation of 25% resistance to clarithromycin (Fasciana et al., 2015), while a South African population revealed infection with H. pylori strains having a 15.38% resistance to clarithromycin (Tanih et al., 2013). A study done in Senegal revealed 90% resistance to metronidazole (Seck et al., 2009). In Egypt, another study revealed 100% resistance to metronidazole using an E-test (Fathi et al., 2013). A study done in Iran, revealed a double resistance to clarithromycin and metronidazole and triple resistance to clarithromycin (17.01%), metronidazole (78.86%) and amoxicillin (27.64%), this study also revealed a high rate of resistance (78.86%) to metronidazole (Ghotaslou et al., 2013). Resistant patterns of H. pylori against amoxicillin and clarithromycin, however raises doubts regarding the effectiveness of the sequential therapy that consist of a dual therapy of PPI and amoxicillin followed by triple therapy consisting of PPI, clarithromycin and tinidazole. However, cases of amoxicillin resistance are uncommon, with statistics as low as 1.9% resistance recorded among Brazilians (Picoli et al., 2014). This therefore calls for more studies on amoxicillin resistant patterns. Clarithromycin remains one of the most powerful antibiotics against *H. pylori* with minimal inhibitory concentrations (MICs) being acceptably low when compared with other molecules available. However, H. pylori resistance to clarithromycin is dampening success rates of H.

pylori eradication regimens incorporating clarithromycin. Clarithromycin resistant by *H. pylori* is instigated by point mutations of the 23S RNA gene, the main component of the 50S ribosomal subunit, mostly at positions 2142 and 2143 (2142A~G, 2142A~C, 2142A~T; 2143A~G, 2143A~C) in the peptidyl-transferase region of the variable domain (Versalovic *et al.*, 1996; De Francesco *et al.*, 2011; Tanih *et al.*, 2013; Teh *et al.*, 2014). These point mutations prevent the drug from binding with *H. pylori*. *H. pylori* contain two 23S rRNA genes and mutations usually occur in both copies. Homogenic isolates seem to be more resistant to clarithromycin. The mutation in one copy of the 23S rRNA may be easily transferred to the other 23S rRNA gene by efficient homologous DNA recombination under selective pressure. The increasing resistance to clarithromycin has led to the empiric use of levofloxacin as a surrogate drug for this antimicrobial. However, research has found that the outcome of clarythromicin based therapy in comparison to levofloxin use on eradication rates of *H. pylori* infection and ulcer recurrence are similar (Gopal *et al.*, 2013).

Metronidazole, a core-drug in H. pylori treatment, is one of the cornerstones of many triple-therapy formulations for the eradication of H. pylori. In H. pylori the rdxA and frxA genes encode reductases that are essential for the activation of metronidazole implying that their inactivation results in metronidazole resistance (Gerrits et al., 2004). Different mutations involving the rdxA gene which encodes for an oxygen insensitive NADPH nitro-reductase have been identified in metronidazole resistant strains. Presence of truncated rdxA, nucleotides insertion/deletion and frame-shift mutation at the C-terminal and missing stop codon at the end of rdxA have been observed (Gerrits et al., 2004; Teh et al., 2014). These mutations are recognized as the main explanation behind metronidazole resistance in H. pylori. There are also cases of metronidazole resistant strains involving mutation of gene frxA

even though such mutations do not result in a high MIC level of metronidazole resistance (Yang et al., 2004b).

Currently, there is no definite standard third-line therapy for treating *H. pylori*. The European guidelines recommend culture method in determining a third-line treatment according to microbial sensitivity to antibiotics (Gisbert, 2012). Efficacy of this method, relies on the availability of well-established laboratories, this however present a challenges to many communities especial in underdeveloped and developing nations.

The multi-use of quinolones due to their broad-spectrum activity against Gram-positive and Gram-negative bacteria could be the explanation for the rising resistance against these drugs by *H. pylori*. In *H. pylori*, single point mutations in the *gyr*A gene, the quinolone resistance-determining region, cause resistance to this class of antibiotics (Tankovic *et al.*, 2003). A study conducted in Germany showed that resistance to quinolones and triple resistance to metronidazole, clarithromycin, and ciprofloxacin in *H. pylori* have reached extremely high levels calling for susceptibility testing before administering quinolones especially with patients with records of failed eradication therapy before (Glocker *et al.*, 2007). Nevertheless, there is scarcity of information that reveals an effective vaccine that is quite preventive against *H. pylori* infection in various ethnic populations.

All regimens that have been suggested for first line treatment of *H. pylori* (Chey *et al.*, 2017) contain PPIs. The PPIs help to reduce the amount of hydrochloric acid released into the stomach and this unavoidably leads to increased stomach pH (Sugimoto *et al.*, 2014). Insufficient acid inhibition has been linked with treatment failure during *H. pylori* eradication (Sugimoto *et al.*, 2014). Also ingestion of PPIs has been linked to false-negative results of *H.*

pylori by diagnostics tests such as biopsy culture and rapid urease test (Saniee *et al.*, 2015). In addition, PPIs have been linked to induction of severe hypomagnesemia, community-acquired pneumonia, iron and vitamin B₁₂ deficiency, interstitial nephritis, hip fracture, microscopic colitis and *Clostridium difficile*-associated diarrhoea (Keszthelyi and Masclee, 2012). Acid tolerance of macrolides used to treat *H. pylori* infections is another factor that is important towards success of a treatment regimen. However, with the exception of levoflaxacin triple therapy and fluoroquinolone sequential therapy, all first line suggested regimens seem to contain clarithromycin.

The increasing resistance to clarithromycin has led to investigations of fluoroquinolones such as levofloxacin as a surrogate drug for this clarithromycin. A triple therapy with PPI, amoxicillin and levofloxacin has been suggested earlier as an alternative first-line therapy (Katelaris, 2009). Resistance to fluoroquinolones is generally very low (< 10%) worldwide (Boyanova and Mitov, 2010; Ahmed *et al.*, 2012). A recent study, revealed a low primary and secondary resistance of 6.8% and 25% for floroqunoline (ciprofloxacin, levofloxacin, moxifloxacin and gemifloxacin) in comparison to clarithromycin of which *H. pylori* had 6.8% primary and 87.5% secondary resistance to the drug (Teh *et al.*, 2014).

In areas with less than 40% metronidazole resistance, PPI with clarithromycin and metronidazole is preferable. Also, a 10-day sequential therapy seems to offer better outcomes. The therapy consists of a dual therapy of PPI and amoxicillin followed by triple therapy consisting of PPI, clarithromycin and tinidazole (Zullo *et al.*, 2000). In a pediatric study conducted by Arenz *et al.* (2006), the esomeprazole-based 1-week triple therapy that was directed by susceptibility testing of *H. pylori* was shown to be effective in eradicating the organism. However the limitations of this method are that it is effective when there are no

double-resistant strains to clarithromycin or metronidazole. However, its efficacy is moreover affected by resistance patterns of amoxicillin and clarithromycin. Recently, a new sequential concomitant hybrid therapy reported a high rate (99.1%) of treatment success (Hsu *et al.*, 2011). The quadruple therapy mainly consisting of PPI, bismuth and two antibiotics (amoxicillin + clarithromycin, or metronidazole + tetracycline) offer superior eradication rates.

Amoxicillin and tetracycline resistance are still relatively low, rarely exceeding 1% resistance (Megraud, 2004). Amoxicillin resistance in *H. pylori* is believed to be linked with amino acid substitutions in the penicillin binding proteins causing a structural alteration of the protein (Deloney and Schiller, 2000). Amoxicillin-resistant *H. pylori* strains seem to harbour mutations on the *pbp*-1a gene with amino acid substitution Ser-414→Arg being involved resulting in the blockage of penicillin transport (Van-Zwet *et al.*, 1999). Tetracycline, a major component of quadruple therapy inhibits bacterial growth by disrupting codon-anticodon interactions during protein synthesis by binding to the 30S subunit hence disturbing the attachment of aminoacyl tRNA to the acceptor site, in addition, mutations of the 16SrRNA-encoding genes seem to affect the binding site of tetracycline (Wu *et al.*, 2005). However, horizontal gene exchange involving foreign DNA acquisition by plasmids is common in *H. pylori* (Dharmalingam *et al.*, 2003).

2.10.2 NATURE OF ANTIBACTERIAL SUBSTANCES IN HONEY

Honey is slightly acidic, with a pH between 3.2 and 4.5. The low pH is inhibitory to many pathogenic bacteria (Molan, 1995). When honey is diluted, glucose oxidase secreted by bees is activated and converts glucose to gluconic acid and hydrogen peroxide and at this point,

antibacterial activity of honey changes from osmotic to pH and peroxide motion (Molan, 1995; Mandal and Mandal, 2011). However, the nonperoxide and other constituents of honey have been shown to play an important role in the antibacterial property of honey (Zainol *et al.*, 2013).

2.10.2.1 Hydrogen peroxide in honey (H_2O_2)

Hydrogen peroxide (H_2O_2) is a by-product of glucose oxidation catalysed by the enzyme glucose oxidase synthesized by the bees. Dilution of honey has been observed to activate the enzyme glucose oxidase that oxidizes glucose to H_2O_2 and gluconic acid, resulting in the antimicrobial activity of honey (Bang *et al.*, 2003; Brudzynski, 2006; Mandal *et al.*, 2011). The amount of hydrogen peroxide available as a honey constituency depends on the amount of glucose oxidase produced by the bees and the amount of catalase (flower origin) which actively degrade hydrogen peroxide (Brudzynski, 2007; Mandal *et al.*, 2011). The discovery that H_2O_2 is a core compound in honey led to assumptions that it plays a big role in the antimicrobial activity of honey, however, further research has shown that in most honeys, the antibacterial activity is strongly related to H_2O_2 (Brudzynski, 2006; Irish *et al.*, 2011). In contrast, Manuka honey showed antibacterial activities after the removal of H_2O_2 (Molan and Russell, 1998).

2.10.2.2 Non-peroxide constituency of honey

The non-peroxide constituency of honey includes sugars together with small amounts of organic acids, phenolic acids, flavonoids, proteins, minerals, vitamins, enzymes and other phytochemicals (Bogdanov, 1997; Kwakman and Zaat., 2012). Honey devoid of hydrogen peroxide show significant antibacterial activity (Mandal and Mandal, 2011). There are two

proteins that contribute to biological activities of honey, the glucose oxidase which originate from bees and catalase which is of floral origin (Zainol *et al.*, 2013).

2.10.2.3 Phenolic compounds

Polyphenols are a common and important class of secondary metabolites in honey. Majority of polyphenols arise from the amino acids phenylalanine or tyrosine which when deaminated to cinnamic acids and p-coumaric acids respectively, enter the phenylpropanoid pathway (Kokotkiewicz and Luczkiewicz, (2009). These molecules bear antimutagenic, antibacterial (bacteriostatic, bactericidal), antiviral, antifungul, insecticidal, keratolytic, estrogenic and antioxidant properties (Jaganathan and Mandal. 2009). There are studies that have revealed that the composition of the phenolic compounds in honey depends on the floral source where the bees collect nectar, seasonal and environmental factors, geographic origin and storage conditions (Aljadi et al., 2002; Lachman et al., 2010; Ramanauskiene et al., 2012). Phenolic compounds in honey have been classified into three groups namely flavonoids, cinnamic acids and benzoic acids. Commonly detected phenolic compounds in honey include caffeic, chlorogenic, coumaric, ellagic, ferulic, gallic, homogentisic, phenyllactic, protocatecuic, syringic and vanillic acids, while detected flavonoids include apigenin, chrysin, galangin, hesperetin, kaempferol, luteolin, myricetin, pinobanksin, pinocembrin, quercetin and tricetin (Aljadi et al., 2002; Kassim et al., 2010; Biesaga and Pyrzyn'ska K, 2013; Campone et al., 2014; Moniruzzaman et al., 2014).

Studies have revealed that plant derived phenolic compounds can inhibit enzymes (Lin *et al.*, 2005; Pereanez *et al.*, 2010; Ranilla *et al.*, 2010; Al Shukor *et al.*, 2013). The study on angiotensin-converting enzyme showed that tannic acid had the highest activity and the

number of hydroxyl groups it has on the benzene ring plays a big role in the activity of phenolic compounds (Al Shukor *et al.*, 2013). Also Ranilla *et al.* (2010) observed that even though Chanca Piedra leaves had less phenolic compounds as compared to matico leaves, extracts from Chancapiedra exhibited higher antioxidant activity probably due to free radical scavenging properties of phenolic compounds. Gallic acid, ferulic acid, caffeic acid, propylgallate and epigallocatechingallate were shown to inhibit the enzymatic activity of a phospholipase A₂ (Pereanez *et al.*, 2010). Combined extracts from different sources have also proven to offer more inhibitory potential when compared to plant extracts from a single source (Lin *et al.*, 2005).

Organisms have a way of balancing the production and removal of free radicals, known as oxidative balance. When oxygen is metabolized, by-products called free radicals are formed by cells. Free radicals move through the cell causing some disruption resulting in cellular damage. At times there are offsets of this balance resulting in increased levels of reactive oxygen species. This condition is called oxidative stress and indicates an imbalance between the production of free radicals and the antioxidant defence system resulting in damage of all components of the cell, including proteins, lipids and DNA (Wells *et al.*, 2009). Oxidative stress plays a significant role in the onset of numerous pathological conditions, thus, foods containing significant levels of antioxidants which can inhibit or delay oxidation of a substrate represent a healthy and logical diet choice. Antioxidants that occur naturally in the body or are consumed through the diet may block damage to cells. Honey intake increases blood vitamin C, beta-carotene and glutathione reductase, and improves antioxidant activity in human plasma (Ali-Waili, 2004; Khalil *et al.*, 2010). Antioxidants protect key cell components from damage by neutralizing the free radicals

There is growing evidence that honey exhibit antioxidant activity (Aljadi *et al.*, 2002; Piljac-Žegarac *et al.*, 2009). Honey antioxidant activity appears to be a result of the combined effect of a range of compounds. Phenolic compounds (flavonoids and phenolic acids), as well as non-phenolic compounds (ascorbic acid, carotenoid-like substances, organic and amino acids, and proteins including certain enzymes such as glucose oxidase and catalase) can contribute to honey antioxidant activity. Different honey types seem not to possess the same therapeutic advantages. Antioxidant potential of honey is directly related to its plant source. Considerable differences in both composition and content of phenolic compounds have been found in different uni-floral honeys. Honeys derived from several floral sources (heterofloral) seem to possess better antioxidant potency assays in comparison to monofloral source (Piljac-Žegarac *et al.*, 2009).

2.11 HONEYS AS ALTERNATIVE TO TREAT H. pylori INFECTIONS

Phytochemicals are naturally occurring compounds in plants with high biological significance. The underlying fact determining the value of these products is their chemical profile which puts a selection pressure on the use of such product in the treatment of various ailments including life threatening diseases caused by both Gram positive and Gram negative bacteria (Sibanda *et al.*, 2008; Njume *et al.*, 2011; Nkomo *et al.*, 2011). Dating back to ancient times, such biological significance attracted the use of certain plants and natural products in the traditional medicine system e.g. *Aspalathus linearis* is used in the production of herbal tea, called rooibos known to relieve hypertension and easing of severe stomach cramps (Street and Prinsloo, 2013) and *Emblica officinalis* is highly valued for its fruits which enhance digestion, reduce fever and blood purification when eaten (Franklin *et al.*, 2012). However, several studies have shown that there are many natural products with anti-*H*.

pylori compounds (Njume et al., 2009; Amin et al., 2010; Manyi-Loh et al., 2010; 2012; 2013; Nkomo et al., 2011; Franklin et al., 2012; Goswami et al., 2012; Awwad et al., 2013). Honey, a complex natural sweet substance produced by bees through a process of regurgitation, is one of the natural products that has been shown to possess a broad-spectrum of antibacterial activity against pathogenic micro-organisms (Jedder et al., 1985; Ndip et al., 2007; Manyi-Loh et al., 2010; Mandal et al., 2011) and has been used widely as a traditional remedy for the treatment of various ailments including wounds and alleviation from dyspepsia (Tonks et al., 2007; Kwakman and Zaat, 2011). The linkage of *H. Pylori* as a causative agent to gastric related illnesses sparked the possibility that honey possess antibacterial properties. In the past decades, honey has been subjected to various laboratory and clinical investigations (Ndip et al., 2007; Manyi-Loh et al., 2010; 2013; Mandal et al., 2011; Silva et al., 2013). The antimicrobial properties of honey have been attributed to both the hydrogen peroxide as well as non-peroxide components (Silva et al., 2013).

The complex natural sweet substance is also well known for its positive actions within a wound environment including those that are nonresponsive to conventional therapies (Bang *et al.*, 2003; Eddy and Gideonsen, 2005; Van den Berg *et al.*, 2008; Mandal *et al.*, 2011). Honey is known to maintain a moist wound environment that promotes healing, and its high viscosity helps to provide a protective barrier to prevent infection. It is commonly used by many people with belief that it has antibacterial properties. Honey is relatively cheap and is easily available.

2.11.1 Origin of antibacterial substances in honey

It takes a collection of several natural products for bees to construct their hive and produce honey. This collection includes bees-wax, flower volatiles, pollen, nectar, propolis and honey itself. Honey has been reported as a complex mixture of sugars which possess antibacterial activity due to the osmotic effect, together with small amounts of organic acids, phenolic acids, flavonoids, proteins, minerals, vitamins, enzymes and other phytochemicals (Al *et al.*, 2009; Kassim *et al.*, 2010; Silva *et al.*, 2013). Honey containing pollen mainly collected from a single species is classified as mono-floral, while multi-floral honey contains pollen from lots of different species (Ampuero *et al.*, 2004). The antimicrobial properties of honey have been credited to both the hydrogen peroxide as well as non-peroxide components (Snow and Manley-Harris, 2004). The non-peroxide factors correlating with antibacterial properties and antioxidant activity of honey include phenolic acids, flavonoids and lysozyme (Arreazroman and Gomezcaravaca, 2006; Silva *et al.*, 2013). In addition, low pH and high osmolarity are contributory factors in honey's antimicrobial activity. However, H₂O₂, methylglyoxal, and bee defensing-1combined presence influence the broad-spectrum activity of honey against bacteria (Kwakman *et al.*, 2010).

Honey has a wide range of phytochemicals including phenolic compounds which are known to be natural antioxidants (Ramanauskiene *et al.*, 2012). Polyphenols and phenolic acids found in the honey vary according to the source of nectar, geographical and climatic conditions (Ramanauskiene *et al.*, 2012; Silver *et al.*, 2013; Agggad and Guemour, 2014). Hence they can be used as indicators in the studies of floral and geographical origin of honey and propolis (Alzahrani *et al.*, 2012; Ramanauskiene *et al.*, 2012). Some of them were reported as a specific marker for the botanical origin of the honey. Phenolic compounds

occurring in honey have been classified into three groups, the flavonoids, cinnamic acids and benzoic acids (Valls *et al.*, 2009).

Melissopalynological analyses that consist of the qualitative and quantitative microscopic examination of honey pollen grains have been used as a traditional method of determining the geographical origin of honey (Alissandrakis *et al.*, 2003; Ruoff *et al.*, 2006). In their work (Ruoff *et al.*, 2006) validated another technique called the Front-Face Fluorescence Spectroscopy, which was directly applied on honey samples to authenticate 11 uni-floral and poly-floral honey types that have been already categorized using traditional methods of pollen analysis. Due to ever improving technology, a fast and reliable method has been developed based on fingerprinting and barcoding of proteins in honey by use of matrix assisted laser desorption ionization time-of-flight mass spectrometry (MALDI TOF MS) and MALDI Biotyper 1.1 software, respectively (Wang *et al.*, 2009). Regardless of improvement in research techniques, origin of pollen found in honey does not always correlate with the source of the nectar contributed. This poses difficulty in determining the physical, chemical, and pollen analytical characteristics of poly-floral honeys as compared to uni-floral honeys.

Research has also revealed that the geographical location plays an important role in determining the bactericidal properties of different honey types (Alzahrani *et al.*, 2012). It was demonstrated in Cameroon that four honey varieties from different geographical locations displayed antibacterial activity against *H. pylori* (Ndip *et al.*, 2007). The strongest inhibitory activity (82.22%) was demonstrated by Mountain honey at 75%v/v, followed by Capillano® and ManukaTM honeys (75.56%), and Eco-honey (73.36%) using equal concentrations. The MIC and MBC concentrations of Mountain honey were in the range 0.117 – 0.938μg/mL and 0.366 – 2.965μg/mL respectively (Ndip *et al.*, 2007). In addition,

Manuka (New Zealand) and Medihoney (Australia) honeys made from *Leptospermum* species are accepted as one of the most therapeutically useful honeys. The Manuka honey has unusual gel-like consistency (thixotropy) enhanced by its protein content and the "unique manuka factor" (Mollan, 1995; Mollan and Russel, 1998). In a study done in South Africa, a report revealed an inhibitory effect of honey on uncharacterised clinical *H. pylori* strains, it was observed that inhibitory effect of clarithromycin (zone of inhibition: $18.0 \pm 7.4 \text{ mm}$) was not significantly different (p >0.05) from honeys at a concentration of 75% v/v (Manyi-Loh *et al.*, 2010).

2.12 METHODS OF CHARACTERIZING HONEY COMPOUNDS

Harvested honey often requires an effective separation technique to enable the identification of its diverse complex constituents. Solid-phase extraction (SPME) or liquid/liquid extraction followed by the use of Capillary electrophoresis—mass spectrometry (CE-MS), High-performance liquid chromatography (HPLC), Gas Chromatography Mass Spectrometry (GC-MS) and Liquid chromatography mass spectrometry (LC-MS) have been successfully used for the analysis of compounds in honey (Arr´aez-Rom´an et al., 2006; Campone et al., 2014). These methods offer a simple and cost effective analytical technique of characterizing compounds (Campone et al., 2014).

SPME technique has been considered to be a rapid and solvent free method for the extraction of both volatile and nonvolatile organic compounds in honey. It was invented by Pawliszyn in 1989 (Vas and Ve'key, 2004). The SPME improves quality of sample obtained within a short time as well as reduction of costs involved with extraction methods that require solvents. SPME in combination with GC-MS has been exploited well and showed high

sensitivity when a total of 86 compounds in the headspace of 4 types of honey revealed marked different compositions (Wolski *et al.*, 2006). Another study demonstrated further the sensitivity of this technique when traces of *p*-dichlorobenzene and/or naphthalene (chemicals used to control wax moth; *Galleria mellonella*) residues in honey were found to exceed the maximum residue concentration (Harizanis *et al.*, 2008).

Solid-phase extraction (SP-ME) or liquid/liquid extraction followed by the use of Capillary electrophoresis—mass spectrometry (CE-MS) has also yielded good outcomes in the scientific experimental world. The combination of CE and MS provide high separation efficiency and molecular mass information in a single analysis. CE coupled with electrospray ionization time-of-flight-mass spectrometry (CE-ESI-TOF-MS) has been used also (Kamakshi *et al.*, 2013), and it requires small amount of sample, CE offers high resolution and the TOF undeniably is sensitive, highly selective and offers accurate mass and true isotopic patterns of compounds.

High-performance liquid chromatography (HP-LC), a form of improved column chromatography is one of the most powerful tools used for the analysis of compounds in chemistry. However, Liquid Chromatography Mass Spectrometry (LC-MS) which combines liquid chromatography and mass spectroscopy and GC-MS are highly sensitive, accurate and a specific quantitative analysis instruments in comparison to HP-LC (Syazana *et al.*, 2013; Moniruzzaman *et al.*, 2014).

CHAPTER THREE

In-vitro study on kinetic inhibition of urease enzymes: a focus on urease isolated from drug resistant H. pylori

3.1 ABSTRACT

The aim of the study was to evaluate inhibitory potential of South African honey extracts on urease activity. Urease enzyme is produced by pathogenic *H. pylori* so as to evade the acidic defensive mechanism of the human stomach. Commercial Jack bean urease (CJBU), Urease extracted from *H. pylori* susceptible to four drugs - clarithromycin, amoxicillin, metronidazole and tetracycline (HPU1), urease extracted from *H. pylori* resistant to clarithromycin (HPU2) and urease extracted from multidrug resistant *H. pylori* (HPU3) were all exposed in a cocktail assay based on the reduction of NADH in a coupled urease-glutamate dehydrogenase (GDH) system. NADH consumption in the presence of honey extracts (test compounds) and acetohydroxamic acids (standard inhibitor) was monitored using a SynergyMx microplate reader at 340nm. At a concentration of 50mg/ml, urease inhibition by petroleum ether extract of Gold Crest and of Fleures Honey, hexane extract of Little Bee and Manuka Honey and chloroform extract of Bush Honey and of Q had a range above or equal to 50%. The One way ANOVA Test showed no significant difference in urease enzyme inhibitory activity from different sources including urease from drug resistant *H. pylori* strains (p > 0.05).

3.2 INTRODUCTION

Nature provides an unlimited source of natural products that are of biological significance (Awaad *et al.*, 2013). Honey is a complex product with different constituents dependent on factors such as bee species, foraging behaviour of bees, geographic area, season and mode of storage (Alzahrani *et al.*, 2012; Modolo *et al.*, 2015). Honey is one of the natural products that have been shown to possess a broad-spectrum of antibacterial activity against pathogenic micro-organisms including *H. pylori* (Jeddar *et al.*, 1985; Mandal *et al.*, 2011; Alzahrani *et al.*, 2012; Nayik and Nanda, 2015). Research has also shown that the geographical location from which honey is harvested plays an important role in determining the bactericidal properties exhibited by different honey types (Alzahrani *et al.*, 2012). Apitherapy is an ancient traditional practice that has been used to treat microbial infections as well as application of honey for wound healing (Mandal and Mandal, 2011).

The occurrences of *H. pylori* related infections and incidences are on the rise worldwide especially in developing nations. Infection with *H. pylori* can be life long without an effective treatment (Kadayifci *et al.*, 2006; Nayik and Nanda, 2015). It is now widely accepted that *H. pylori* infections are associated with acute or chronic duodenal/gastric ulcer disease, gastritis, gastric adenocarcinoma, mucosa-associated tissue lymphoma (MALT), primary B-cell gastric lymphoma and acid gastric reflux (Ahmed *et al.*, 2007b; Seanego and Ndip, 2012; Tanih *et al.*, 2013; Abebaw *et al.*, 2014).

In the human stomach, urease is produced in enormous quantities by *H. pylori*. The multimeric nickel-containing urease enzyme is a vital virulence factor produced by pathogenic *H. pylori* so as to evade the defence system of the human stomach (Kuwahara *et*

al., 2000; Amin et al., 2010; 2013). Urease converts urea into ammonia and bicarbonate. Ammonia causes an increase in pH within the microenvironment surrounding profusely growing H. pylori cells in the human stomach thereby protecting the bug from the acid environment of the human stomach. The bicarbonate protects H. pylori against bactericidal action of peroxynitrite, a metabolite of nitric oxide (Kuwahara et al., 2000). Urease has been confirmed as a colonization factor of H. pylori. In the late 90s, an assessment of importance of cytoplasmic and surface localized urease on H. pylori survival in acidic environment revealed that H. pylori greatly requires surface localized urease to flourish in an acidic environment (Krishnamurthy et al., 1998). Another study revealed that urease-negative mutant strain of H. pylori does not cause gastritis due to challenges with colonization (Amin et al., 2010). The urease from different sources (plants, bacteria, invertebrates and fungi) have similar structures such as basic trimeric array possessing 1, 2 or 3 subunits that can join to form a hexameric or dodecameric structure (Seck et al., 2013). There are studies that have reported that phytochemicals have the potential to inhibit urease activity (Ndip et al., 2007; Amin et al., 2010).

Antimicrobial agents are important as control effectors of most infectious diseases. *H. pylori* infection is normally treated using a regimen comprising of a PPI, clarithromycin, and amoxicillin or metronidazole (clarithromycin-based triple therapy) given twice a day for 7–14 days or a PPI or (Ranitidine) H₂RA, bismuth subsalicylate, metronidazole, and tetracycline (bismuth quadruple therapy) given twice a day for at least 10 days or 14 days if bismuth is unavailable, in populations with less than 20% clarithromycin resistance (Chey *et al.*, 2007; Mandal *et al.*, 2011). A second-line regimen called a quadruple therapy comprising of PPI, a bismuth salt, tetracycline and metronidazole for 10–14 days has also been recommended (Gisbert., 2009; Manyi-Loh *et al.*, 2010; Mandal *et al.*, 2011). The effect of the introduction

of PPIs into the human stomach is an increase of the stomach pH causing digestive disturbances (Sugimoto *et al.*, 2014). Also there are studies that have linked the PPIs with the induction of severe hypomagnesemia, community-acquired pneumonia, iron and vitamin B₁₂ deficiency, interstitial nephritis, hip fracture, microscopic colitis and *Clostridium difficile*-associated diarrhoea (Keszthelyi *et al.*, 2012). In addition, drug resistance is threating successful treatment of *H. pylori* infections (Upadhyay, 2012; Wu *et al.*, 2012; Fathi *et al.*, 2013; Syazana *et al.*, 2013; Gosciniak *et al.*, 2014). Proposed rescue therapies seem to be related with unwelcomed side-effects which are associated with defaulting and further development of drug resistance. The European guidelines recommend culture method in determining a third-line treatment according to microbial sensitivity to antibiotics (Gisbert, 2009), however the availability of well-established laboratories determine the success of this approach. This therefore entails a need to explore new approaches that are less harmful while attaining satisfactory control strategies of *H. pylori* infections.

As urease enzyme plays a crucial role in the establishment of an effective infection by H. pylori, urease inhibitors may be targeted in search of new leads towards treatment of infections caused by organisms that are urease-dependent. There are studies that have shown that phytochemicals have anti-urease active compounds (Amin $et\ al.$, 2010; Amin $et\ al.$, 2011; Amin $et\ al.$, 2013). Heavy metals, hydroximate and its derivatives, fluoride, thiols, phosphoramides compounds, hydroxyurea, \propto -hydroxyketones and \propto -diketones, triketone oximes, phosphates, boric acid, sulfur compounds, biscoumarin have been shown to be potential inhibitors of urease (Tanih $et\ al.$, 2010; Upadhyay, 2011). However, the commercially available urease inhibitors such as hydroxamic acid derivatives are toxic, hence inapplicable for clinical use (Megraud, 2012). Continued search for low toxic urease inhibitors is ideal towards targeting urease inhibition to control diseases linked to infection by

urease dependent micro-organisms. Since, honey has been reported as a pool of phytochemicals with a broad-spectrum antibacterial activity depending on various factors such as geographical location and bee foraging behaviour, they has been no report of microorganisms gaining resistance to honey. This study therefore focuses on screening for anti-urease solvent extracts from several South African honey types in search of anti-urease active compounds that could act as a template for cheaper and easily available compounds to control *H. pylori* and other urease dependent micro-organisms.

3.3 MATERIALS AND METHODS

3.3.1 Confirming H. pylori isolates and standard strain

A standard strain, ATCC 43526 (American Type Culture Collection, Manassas, VA, USA) and clinical isolates from gastric corpus biopsy specimen of patients with gastro-duodenal disease attending the endoscopy unit at Livingstone hospital, Port Elizabeth, Eastern Cape Province from a previous study done in the MPMERG Laboratory (University of Fort Hare) by Tanih *et al.* (2010) were used for this study. *H. pylori* strains were resuscitated on Columbia Blood Agar supplemented with Skirrow's antibiotics and fetal bovine serum 5% (v/v). The plates were incubated microaerophilically (85% N₂, 10% CO₂ and 5% O₂) using OxoidTM AnaeroGenTM gas-generating envelopes (Thermo Fisher Scientific) at 37°C for 5 days. Preliminary identification of all *H. pylori* strains was done by colony morphology, Gram stain, catalase test, oxidase test, urease test followed by confirmation by PCR targeting the *glm*M gene of *H. pylori*.

3.3.2 Polymerase Chain Reaction (PCR)

DNA was isolated from presumptive pure colonies by boiling method. Briefly, colonies were suspended in 200 µL of sterile distilled water. Cells were lysed by boiling in a digital Accu dri-block (Labnet International, Woodbridge, United Kingdom) at 100°C for 15 minutes. Cell debris was removed by centrifugation at 13,000 rpm for 5 minutes and 5 µL of supernatant was used as a template in each polymerase chain reaction (PCR) assay. The glmM gene was targeted using the primer pair; Forward 5'- GAT AAG CTT TTA GGG GTG TTA GG GG-3', Reverse 5'-GCA TTC ACA AAC TTA TCC CCA ATC-3' as earlier reported (Abu-ALmaali et al., 2012). Amplification conditions included an initial denaturation of target DNA at 95°C for 5 min, 40 cycles at 95°C for 1 min, 58°C for 1 min, and 72°C for 1 min. Final elongation was done at 72°C for 5 min. A 25 µL PCR reaction was set up comprising of 12.5 µL of 2X master mix (New England Biolabs, Ipswich, United Kingdom), 6.5 µL nuclease free water (New England Biolabs), 0.5 µL of each primer (Inqaba Biotec, Pretoria, South Africa), and 5 µL of template DNA. Amplification of the 140bp glmM gene was carried out using a Bio-Rad thermal cycler (C1000 TouchTM Thermal Cycler). Products were resolved in a 1.5% (wt/vol) agarose gel containing 5 µL of ethidium bromide (Sigma-Aldrich, St Louis, MO). Electrophoresis was carried out in a 0.5X TAE buffer (40 mM Tris-HCL, 20 mM Na-acetate, 1 mM EDTA, pH 8) at 100 volts for 40 min and the gels were visualised under a UV transilluminator (Alliance 4.7 XD-79, Uvitec, Cambridge, United Kingdom).

3.3.3 Drug resistance profiling

This was done according to Seanego *et al.* (2012). In brief, 0.5 McFarland bacterial suspensions was evenly spread using sterile swabs on Muller Hinton agar (MHA) supplemented with 5% foetal bovine serum and Skirrow's antibiotics. Commercial discs impregnated with standard drugs (clarithromycin, amoxicillin, metronidazole and

tetracycline) were placed on agar followed by a 5 day incubation period at 37°C under microaerophilic conditions. Categorizing of resistance was done as recommended by McNulty *et al.*, (2002).

- Zone of inhibition < 16mm was read as resistant,
- $16\text{mm} \le \text{Zone of inhibition} \le 21\text{mm}$ was read as intermediate
- Zones of inhibition \geq to 21mm were read as susceptible.

3.3.4 Intracellular crude urease extraction

This was done as previously described by Amin *et al.* (2013) but with modifications. Briefly, 72 hours old broth cultures (50 mL, 0.5 McFarland standard) were centrifuged at $5,000 \times g$ at 4° C for 20 minutes and the bacterial mass that settled at the bottom of the tube was washed twice using phosphate-buffered saline (pH 7.4). *H. pylori* cells were suspended in buffer supplemented with complete Mini EDTA-free protease inhibitors (Roche Diagnostics S.A). An Omni Sonic Ruptor, ultrasonic homogenizer was used to disrupt cells using a setting of 40 watts for 60 seconds in ice-bath. Centrifugation at 15,000 X g, 4° C for 30 minutes was done to remove cell debris. The resultant supernatant with crude urease was precipitated in saturated ammonium sulfate solution and then tightly sealed into semipermeable snake skin dialysis tubing and then dialyzed for 24 hours. Urease activity assay kit (SIGMA) was used to determine solutions with active urease which were further eluted through HiPrep 16/60 Sephacryl S-200 High Resolution column (GE Healthcare). The resultant urease solution was stored at -80° C in aliquots until use.

3.3.5 Urease detection

This was done using Urease Activity Assay Kit (Sigma-Aldrich) according to the manufacturer's instructions. Using a 96 well microtiter plate the urease enzyme was spiked into standard cocktail to catalyse the hydrolysis of urea resulting in the production of ammonia. The ammonia was determined by the Berthelot method whereby the ammonia produced reacts with the Berthelot reagents (phenol and hypochlorite) to form a blue colorimetric product that was measured at 670 nm using SynergyMx Microplate reader.

3.3.6 Extraction of honey compounds

Seven locally produced natural honeys in South Africa, Bush honey, Raw honey, Gold Crest honey, Q Bee honey, Little Bee honey, Fleures honey-radurised, Siyakholwa pure honey and one imported honey (Manuka honey) from New Zealand were used in this study. All honey products were subjected to a test for the presence of microbial growth by sub-culturing on Colombia blood agar supplemented with Skirrow's antibiotics and 5% horse serum and incubated for 5 days at 37°C under aerobic and anaerobic conditions.

Extraction of volatile compounds was done according to the method described by Syazana *et al.* (2013) but with modifications. Three different organic solvents with increasing polarity were used; petroleum ether, hexane and chloroform. Initially, honey was initially weighed (0.5 g) and diluted with 0.5 mL sterile distilled water (w/v). Petroleum spirit (2 mL) was added to the capped glass tube containing the diluted honey. Then, the mixture was vortexed at 1500 rpm for 3 min before being centrifuged at 2500 rpm for another 5 min to separate the organic layer from the aqueous layer. The top layer containing the organic solvent was transferred to new capped glass tubes while the bottom layer was kept for subsequent

extraction processing using different organic solvents. Approximately 1.5 g of anhydrous disodium sulfate powder (Na₂SO₄₎ was added to the top layer to ensure that residual water is removed from the solvent. The sample was further vortexed for 3 minutes and for GC-MS analysis, the clear top layer containing the organic extract was filtered (using WhatmanTM 0.45 µm syringe filter) into a 1 mL autos-ampler vial before GC-MS injection. In preparation for urease/H. pylori inhibition studies, the extracts in capped tubes loosely capped were then placed in a heating block set at 28°C for 7 days to allow drying. The different concentrations of extract solutions were then prepared from dry honey solvent extracts. For the next extraction, 2 mL of hexane was added to the bottom layer from the prior extraction. The above steps were repeated. A similar process was carried out with chloroform followed by ethyl acetate and finally methanol.

3.3.7 Dilution of dried honey extracts to working concentrations (mg/ml)

Totally dried honey extracts were weighed and a 400mg/ml honey/water solution was prepared and kept for 24 hours before it vortexed at 1500 rpm for 3 minutes and filtered through a 0.45 WhatmanTM syringe filter from which serial dilutions were done to produce subsequent concentrations i.e. 200 mg/ml, 100mg/ml, 50mg/ml, 25mg/ml and 12.5mg/ml.

3.3.8 Screening for anti-urease active compounds

This was done according to Kaltwasser *et al.* (1966). The method is based on the reduction of NADH in a coupled urease-glutamate dehydrogenase (GDH). Commercial Jack bean urease was used as standard urease; acetohydroxamic acid was used as standard inhibitor, while honey extracts were used as test compounds. Reduction of NADH was monitored using a SynergyMx microplate reader at 340 nm. Inhibition percentage was calculated using the following formula:

% Inhibition =
$$\frac{A0-A1}{A0} X \frac{100}{1}$$

Where:

- A_0 is NADH decrease in absorbance rate due to urease activity (no inhibitor).
- A₁ is NADH decrease in absorbance rate due to urease (with honey extracts / acetohydroxamic acid)

The assay cocktail was prepared by mixing 240 μ L of Tris-HCL buffer [50mM, pH8], 10 μ L of NADH [8.5mM] and 10 μ L of $\dot{\alpha}$ -ketoglutaric acid [25mM pH 5] and this was injected into a 96 well micrititer plate. This was followed by equilibration at 37°C for 10 minutes. Ten microliters (10 μ L) of urease [Jack bean urease-10U/mL] and 10 μ L of GLDH [250U/mL] in phosphate buffer were then added after which test compounds were added [all 50mg/ml]/acetohydroxamic acid [all 14.3mg/ml or adjusted to 100% inhibition percentage]. Absorbance was read at 340 nm using the SynergyMx microplate reader until reading stability was obtained. This was followed by the addition of 10 μ L of 0.3 M urea and kinetic monitoring was done by reading absorbance after 30 seconds for 30 minutes. Three replications were done for each experiment, mean (\bar{x}) was calculated and data was then presented in a linear model graph showing rate of NADH reduction as a result of urease activity.

3.3.9 Statistical analysis

The Independent-Sample Kruskal-Wallis Test with the aid of the IBM SPSS statistics version 24 Package was used for statistical analysis with P < 0.05 considered statistically significant.

3.4 RESULTS

3.4.1 Confirmation of *H. pylori*

Forty eight clinical samples of *H. pylori* were successfully recovered from a pool of 250 samples that were stored at -80°C. Preliminary identification of the isolates was done by colony morphology, biochemical tests (Gram stain, oxidase test, urease test and catalase tests) and the isolates were confirmed by PCR targeting the *glm*M gene of *H. pylori* (Figure. 3.1).

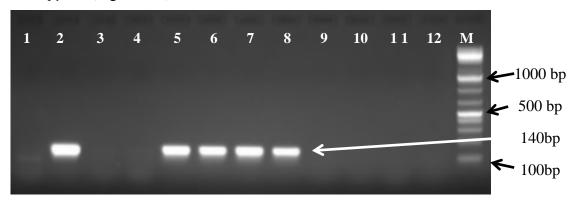


Figure 3. 1: Representative gel picture of PCR product of the *glm*M (140bp) gene of positive isolates. Lanes 1: negative control; Lane 2: positive control; Lanes 2-3, 9-12: negative isolates; Lanes 5-8: positive isolates; Lane M: 100bp ladder

3.4.2 Drug profiling of *H. pylori* strains

Of the 48 samples used in this study, 5/48 (10.4%) were susceptible to clarithromycin, amoxicillin, metronidazole and tetracycline and 3/48 (6.3%) were resistant to all the four drugs (Table 3.1). Resistance was 16.7%, 10.4%, 89.6% and 14.6% for clarithromycin, amoxicillin, metronidazole and tetracycline respectively (Figure 3.2).

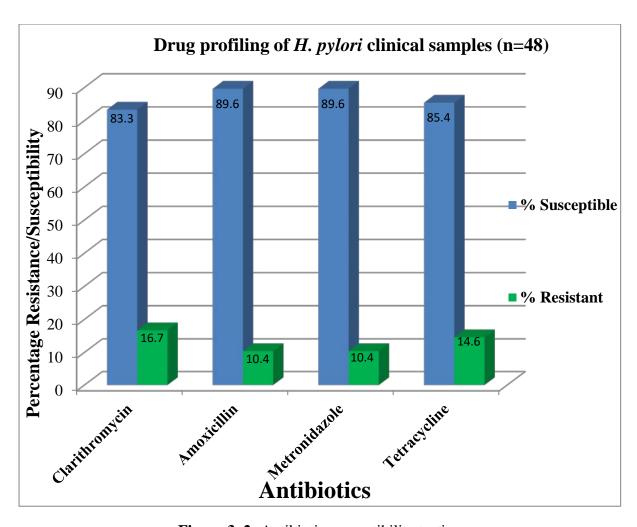


Figure 3. 2: Antibiotic susceptibility testing

Table 3. 1: Resistance of clinical *H. pylori* samples (n=48)

	<i>PYLORI</i> RAIN		DRUG R	ESISTANCE	Strain susceptible to 4	Strain resistant to 4 drugs		
		C	Am	Met	Tet	drugs		
1	10 A	NR	NR	R	R			
2	467A	R	NR	R	NR			
3	56 A	NR	R	R	NR			
4	430 A	NR	NR	R	NR			
5	96 A	NR	NR	R	R			
6	155 A	R	NR	R	NR			
7	169 A	NR	NR	NR	NR	✓		
8	11 A	NR	NR	R	R			
9	402 A	NR	NR	R	NR			
10	469 A	R	NR	R	NR			
11	265 A	NR	R	R	NR			
12	63 A	NR	NR	R	NR			
13	87 A	NR	NR	R	NR			
14	436 A	NR	NR	R	NR			
15	369 A	R	R	R	R		✓	
16	464 A	NR	NR	R	NR			
17	25 A	NR	NR	NR	NR	✓		
18	47 A	NR	NR	R	NR			
19	93 C	NR	NR	R	NR			
20	219 C	NR	NR	NR	NR	✓		
21	406 C	NR	NR	R	NR			
22	411 C	NR	NR	R	NR			
23	467 C	NR	NR	R	NR			
24	13 C	R	NR	R	NR			
25	32 C	NR	NR	R	NR			
26	105 C	NR	NR	R	NR			
27	212 C	NR	R	R	NR			
28	92 C	R	R	R	R		✓	
29	300 C	NR	NR	R	NR			
30	264 C	NR	NR	R	NR			
31	41 C	NR	NR	R	NR			
32	405 C	NR	NR	R	R			
33	10 C	NR	NR	R	NR			
34	464 C	NR	NR	R	NR			
35	213 C	R	R	R	R		✓	
36	350 C	NR	NR	NR	NR	✓		
37	98 C	NR	NR	R	NR			
38	111 C	NR	NR	R	NR			
39	404 C	NR	NR	R	NR			
40	53 C	NR	NR	R	NR			
41	77 C	NR	NR	R	NR			
42	317 C	NR	NR	NR	NR	✓		
43	299 C	NR	NR	R	NR			
44	162 C	NR	NR	R	NR			
45	430 C	R	NR	R	NR			
46	14 C	NR	NR	R	NR			
47	188 C	NR	NR	R	NR			
48	401 C	NR	NR	R	NR			
Tota	al	R=8	R=6	R=43	R=8	5	3	

3.4.3 Kinetic inhibition of ureases by different honey extracts

The results of anti-urease activity of honey extracts isolated using petroleum ether, hexane and chloroform against optimised urease activity cocktail revealed that honey possess compounds of significance importance and the presence of these compounds in honey seem to be influenced by honey type hence floral origin. With the exception of petroleum extract of Siyakholwa pure honey and chloroform extract of Little Bee honey, all the honey extracts under study revealed a level of urease activity inhibition ranging from 0.8 % to a potent level of 67.9 %. At a concentration of 50 mg/ml, petroleum ether extract of Gold Crest had inhibition percentage (I%) between 50.9% - 53.3% and that of Fleures Honey was between 67.8% - 68.5%, hexane extract of Little Bee recorded an inhibition percentage (I%) between 51.4% - 52.7% and that of Manuka Honey was between 50.0% - 53.2%, lastly chloroform extract of Bush Honey recorded an inhibition percentage (I%) between 63.8% - 66.1% and inhibition percentage of Q Bee was between 64.2% - 66.2%, all showing an inhibition percentage range $\geq 50\%$. (Table 3.2-3.4).

CJBU, HPU1, HPU2 and HPU3 were factors introduced so as to determine whether the source of urease plays a crucial role in urease inhibition by honey extracts. The findings showed that source of urease did not play a crucial role in influencing urease inhibition by anti-urease active compounds (P > 0.05). CJBU, HPU1, HPU2 and HPU3, all presented a similar inhibition trend when exposed to similar inhibitory conditions e.g. considering Table (3.2), CJBU, HPU1, HPU2 and HPU3 recorded an inhibition percentage of 20.8%, 22.1%, 21.8% and 22.3% respectively when exposed to the urease kinetic cocktail spiced with petroleum ether extract of Bush Honey.

Table 3. 2: Mean (\overline{x}) inhibition percentage (I%) of urease by petroleum ether extracts (50mg/mL) of different honey types

	Bush	Bush	Raw	Gold	Q Bee	Little	Fleures	Siyakholwa	Manauka	Standard	P value
	Honey	Honey	Crest	honey	Bee	Pure	Pure honey	Honey	inhibitor		
			Honey		Honey	Honey					
CJBU	20.8 %	20.8 %	50.9 %	1.9 %	15.1 %	67.9 %	0.0 %	22.6 %	98.2 %	0.033	
HPU1	22.1 %	18.1 %	53.3 %	0.8 %	16.2 %	68.5 %	0.0 %	23.3 %	100%	0.017	
HPU2	21.8 %	23.4 %	51.7 %	1.5 %	15.8 %	68.3 %	0.0 %	22.8 %	99.8 %	0.041	
HPU3	22.3 %	20.9 %	51.7 %	1.5 %	15.5 %	67.8 %	0.0 %	22.7 %	97 %	0.029	
P value	0.562	0.467	0.165	0.739	0.216	0.625		0.391	0.106		

Key: CJBU - Commercial Jack bean urease

HPU1 - Urease extracted from *H. pylori* susceptible to four drugs (clarithromycin, amoxicillin, metronidazole and tetracycline)

HPU2 - Urease extracted from *H. pylori* resistant to clarithromycin

HPU3 - Urease extracted from multidrug resistant *H. pylori*

Table 3. 3: Mean (\overline{x}) inhibition percentage (%) of urease by Hexane extracts (50mg/mL) of different honey types

	Bush	Raw Honey	Gold Crest	Q Bee	Little Bee	Fleures	Siyakholwa	Manauka	Standard	P value
	Honey		Honey	honey	Honey	Pure	Pure honey	Honey	inhibitor	
						Honey				
CJBU	34.5 %	20.8 %	25.9 %	39.7 %	51.7 %	25.9 %	10.3 %	50.0 %	100 %	0.022
HPU1	37.2 %	18.1 %	22.6 %	36.9 %	51.4 %	27.2 %	11.2 %	53.2 %	98.6 %	0.019
HPU2	37.6 %	23.4 %	25.1 %	40.1 %	52.7 %	25.8 %	10.5 %	51.0 %	96 %	0.031
HPU3	36.4 %	20.9 %	24.5 %	39.4 %	51.6 %	26.0 %	10.7 %	50.6 %	99.3 %	0.041
P value	0.239	0.518	0.753	0.491	0.217	0.164	0.092	0.152	0.155	

Key: CJBU - Commercial Jack bean urease

HPU1 - Urease extracted from *H. pylori* susceptible to four drugs (clarithromycin, amoxicillin, metronidazole and tetracycline)

HPU2 - Urease extracted from *H. pylori* resistant to clarithromycin

HPU3 - Urease extracted from multidrug resistant *H. pylori*

Table 3. 4: Mean (\overline{x}) inhibition percentage (%) of urease by Chloroform extracts (50mg/ml) of different honey types

	Bush	Raw	Gold	Q Bee	e Little Bee	Fleures	Siyakholwa	Manauka	Standard	P value
	Honey	Honey	Crest	honey	Honey	Pure	Pure honey	Honey	inhibitor	
			Honey			Honey				
CJBU	64.2 %	9.4 %	37.7 %	64.2 %	0.0 %	13.2%	5.6 %	15.1 %	98 %	0.029
HPU1	63.8 %	11.4 %	38.2 %	65.7 %	0.0 %	14.0 %	5.3 %	16.0 %	99 %	0.013
HPU2	66.1 %	8.5 %	35.8 %	64.9 %	0.0 %	13.8 %	6.1 %	16.3 %	98 %	0.044
HPU3	64.5 %	9.1 %	36.3 %	66.2 %	0.0 %	13.5 %	5.8 %	16.5 %	100 %	0.037
P value	0.208	0.271	0.386	0.537		0.211	0.097	0.385	0.140	

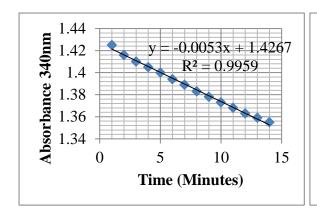
Key: CJBU - Commercial Jack bean urease

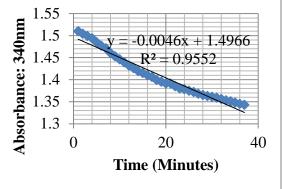
HPU1 - Urease extracted from *H. pylori* susceptible to four drugs (clarithromycin, amoxicillin, metronidazole and tetracycline)

HPU2 - Urease extracted from *H. pylori* resistant to clarithromycin

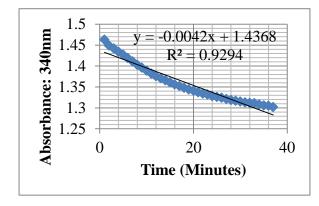
HPU3 - Urease extracted from multidrug resistant *H. pylori*

The change in absorbance at 340nm with respect to time was linear for the assay control of this experiment with rate of change being -0.0053 (Figure 3.3 (a)). After 14 minutes of the kinetic study of urease reaction, NADH reduction absorbance was between 1.34 and 1.36. However it took between 35 minutes and 40 minutes for the urease enzyme to reduce NADH to a value closer to the one recorded in the assay control when the reaction cocktail was spiked with honey extracts (Figure 3.3 (a) – (f)). The effects of spiking honey extracts into the assay cocktail seem to follow a similar trend, at 10 minutes of kinetic monitoring, the gradient of the line of best fit and NADH reduction pattern seem to be having same gradient. After 10 minutes of reaction monitoring, the actual NADH reaction continues at a faster rate and then slows down. At around 30 minutes after the commencement of the reaction, the actual NADH reduction and the line of best fit become equal with the line of best fit after which the actual rate of change slows down to almost zero as it gets nearer to 40 minutes.

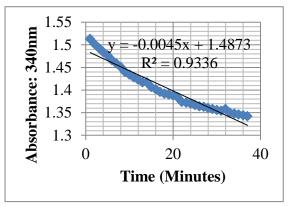




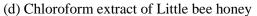
(a) Control: No inhibitor

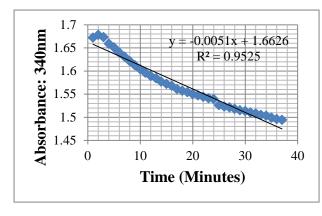


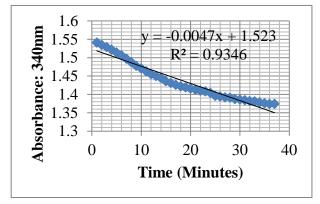
(b) Petroleum extract of Gold Crest



(c) Petroleum ether extract of Fleures honey.







(e) Hexane extract of Manuka honey

(f) Chloroform extract of Bush honey extract.

Figure 3. 3: Reduction of NADH with time due to urease activity in the presence of honey solvent extracts

3.5 DISCUSSION

H. pylori is recognised as a class 1 carcinogen infecting close to half of the world's population (Goh et al., 2011; Awuku et al., 2017). Several therapies have been formulated worldwide in an effort to carb it's spread and chronic infection. As H. pylori lacking urease fail to inhabit the acidic human stomach (Amin et al., 2010), it is ideal to focus on urease inhibitors as a control strategy for *H. pylori* infections. Overall, the current study is revealing that honey possess phytochemicals with anti-urease properties. Eight honey types (Bush honey, Raw honey-unheated, Gold Crest honey-pure, Q Bee honey, Little Bee honey, Fleures-radurised honey, Siyakholwa honey and Manuka honey) were used as source of extracts for the urease kinetics inhibition study. While Manuka honey from New Zealand has been well documented for its highly rated bioactive compounds, South African produced honey has challenged that aspect, with five solvent extracts of South African honey origin attaining an inhibition percentage (I%) greater or equal to 50% which is not significantly different to that obtained by Manuka honey, i.e. inhibition percentage (I%) of 50% (p > 0.05). The antibacterial activity of honey has been reported as both physical and chemical aspects of its nature i.e. acidity, osmolality, beeswax, nectar, pollen, propolis, volatiles, hydrogen peroxide and proteins (Weston et al., 2000; Mandal and Mandal, 2011).

The effect of origin of urease was also studied as a factor that could determine inhibition resistance of urease to honey active compounds. Commercial Jack bean urease (CJBU), *H. pylori* susceptible to four drugs urease (clarithromycin, amoxicillin, metronidazole and tetracycline-HPU1), *H. pylori* resistant to clarithromycin urease (HPU2) and multidrug resistant *H. pylori* urease (HPU3) were extracted from respective strains. On all the experiments performed, there was a similar trend on the inhibition of the different ureases. Inhibition percentage of the control (CJBU) was not significant different from those of other

ureases (p > 0.05). The findings suggest that the honey active compounds from the solvent extracts had a similar inhibitory effect on urease irrespective of the source of origin, supporting a statement by Sirko and Brodzik (2000) that ureases from different sources (plants, bacteria, invertebrates and fungi) have similar structures an indication that they might be inhibited by similar compounds.

Nowadays, drug resistance is becoming a big problem to commonly used treatment regimens, therefore the fact that irrespective of source of urease, including urease extracted from drug resistant *H. pylori*, the trend on urease inhibition seemed to be similar. This finding marks an important aspect of the study in the sense that it brings a new inference about targeting urease inhibition as a way to treat infections caused by urease-depended micro-organisms such as *H. pylori*. These data suggest additional research is needed to target the urease enzyme in an effort to offset colonisation of the human stomach by urease-depended *H. pylori*. Such a discovery could probably help surpass drug resistance treatment challenges being observed with current treatment regimes.

3.6 CONCLUSIONS

The findings if this study revealed that:

- 1. Geographical location from which honey is obtained seems to influence the inhibitory potential of honey against urease activity.
- 2. The petroleum ether extract of Fleures honey and Gold Crest honey, and the chloroform extract Q Bee honey, all South African honey types are potential candidates of being new source of urease inhibitors.

3. Irrespective of source of urease, urease extracted from drug susceptible *H. pylori* strains and drug resistant *H. pylori* strains seem to be inhibited by same compounds.

CHAPTER FOUR

Detection of cytotoxin-associated gene a (cagA) and vacuolating cytotoxin a (vacA) gene among 48 clinical isolates of H. pylori

4.1 ABSTRACT

Helicobacter pylori (H. pylori) infection is associated with various upper gastrointestinal tract (GIT) disorders. Various virulent factors are associated with the successful colonisation of the GIT by this pathogen. The aim of this study was to screen for cagA and vacA genes among 48 clinical samples of H. pylori previously isolated from gastric biopsy specimen of patients with upper gastrointestinal problems. Polymerase chain reaction (PCR) was carried out with specific primers to confirm isolates by targeting the glmM gene, and detect the presence of cagA gene and vacA gene t in H. pylori strains. All the isolates were confirmed as H. pylori and cagA was detected in 97.9% of the test isolates. The vacA allelic combination s1m1 was detected in 75% of the test isolates and s1m2 allelic combination was in 16.7% of the test isolates while s2m2 was in 8.3% of the test isolates. The vacA s2m1 allelic combination was not detected in any of the test isolates. In conclusion, the test isolates of H. pylori under study possess genes associated with upper gastrointestinal problems.

4.2 INTRODUCTION

Helicobacter pylori (H. pylori) is a medically important bacterium that expresses resistance to antibiotics in addition to a variety of virulence factors (Tanih et al., 2010; Cogo et al., 2011; Harrison et al., 2017), this eventually leads to therapy failure and serious disease manifestations due to infection. As a class-1 carcinogen, this organism infects the gastric mucosa of more than half of the world's adult population (Ndip et al., 2004; Ahmed et al., 2006). There is strong evidence that infection with the organism is the main cause of the peptic ulcers, gastritis and the development of adenocarcinomas of the stomach and primary gastric mucosa-associated lymphoid tissue lymphoma (Warren and Marshal, 1983; Oleastro et al., 2006; Braganca, 2007; Chey et al., 2017), thus being known as the main instrumental factor resulting in gastric cancer (Al-Marhoon et al., 2004). Animal studies have demonstrated that cagA plays an important role in disease progression in a Mongolian gerbil model where gastric cancer develops within 12 weeks (Peek Jr. et al., 2000; Franco et al., 2008).

H. pylori genome was fully sequenced in 1997 (Tomb et al., 1997; Alm et al., 1999), resulting in the follow up of more studies on the biology, pathology, and immunology of H. pylori infection. The clinical outcome of long-term infection is subjective and is depended on the infecting bacterial strains' virulence factors (Wang et al., 2003; Jones et al., 2010; Miernyk et al., 2011) and host genotype. H. pylori secrete many proteinaceous factors that help the bug during initial colonization and successive persistence which can be life-long without effective treatment (Aguemon et al., 2005; Dube et al., 2009). However, there are two putative bacterial markers for virulence associated with the pathogenesis of H. pylori infection, the cag A gene and the vac A gene (Achtman et al., 1999; Palframan et al., 2012;

Zaki et al., 2016a). These two virulence factors are polymorphic and affect different host cellular pathways.

The cagA gene, encodes a 125 to 145 kDa protein (cagA), a marker for the presence of the cytotoxin-associated gene pathogenicity island (cagPAI) that is associated with an increase in intensity of gastric inflammation. CagA, an oncoprotein is an abundant protein produced by H. pylori (Jimenez-Soto and Haas, 2016; Zaki et al., 2016a). The presence of the cagA gene is an indicator for the presence of all the genes found in the cagPAI including cagT, cagM and cagE. The cagPAI family gene is responsible for the bacterial type IV secretion system, which injects cagA into the cytosol of gastric epithelial cells of host (Jones et al., 2010; Jimenez-Soto and Haas, 2016). The bacterial type IV secretion system, translocate DNA and protein substrates to other target cells by a mechanism that depends on direct cell-cell contact. The subfamily of the effector translocators, are used by Gram negative bacteria (H. pylori) to deliver virulence proteins to host cells for modulation of different physiological processes during infection (Christie et al., 2013). In an unphosphorylated state, once in host cell, cagA can directly influence cellular tight junction, cellular polarity, cell proliferation and differentiation, cell scattering, induction of inflammatory response as well as cell elongation (Jones et al., 2010). In addition, in the host cell cagA localizes to the plasma membrane where it can be phosphorylated by either Abl kinase or Src family kinases.

The *vac*A gene encodes the production of the vacuolating cytotoxin. The cytotoxin has been shown to cause vacuolation of epithelial cells *in vitro* and promote epithelial cell damage and mucosal ulceration in mice (Telford *et al.*, 1994; Leunk *et al.*, 1999; Miernyk *et al.*, 2011). The *vac*A is one of the proteins secreted from the bacteria through the type V auto-transport

secretion system. The V-secretion system is important for the Gram-negative bacteria either for the secretion of virulent factors for pathogens or by secreting factors contributing to the survival of non-invasive environmental micro-organisms (van Ulsen *et al.*, 2013). *VacA* is an 88kDa toxin comprising of p33 and p55 subunits. The *vacA* toxin is believed to bind to host cells and internalised causing severe vacuolation characterized by the accumulation of large vesicles that possess hallmarks of both late endosomes and early lysosomes. The anion-selective channels seem to facilitate the transport of chloride ions resulting in increased intra-lumenal chloride concentrations (Cover and Blanke, 2005). Apart from vacuolating effects of *vacA*, it has been hypothesized that *vacA* can form membrane-embedded pores at the innermitochondrial membrane resulting in the degeneracy of the mitochondrial electrochemical membrane potential (Palframan *et al.*, 2012).

The *vac*A gene is found in almost all *H. pylori* strains, however not all infections of *H. pylori* result in cell vacuolation *in-vitro*, earmarking sequence heterogeneity of this gene (Cogo *et al.*, 2011; Palframan *et al.*, 2012). This gene has two variable regions, the *s* region and the *m* region. The *s* region encodes the signal peptide which exists as two alleles, the *s*1 or the *s*2. The *s*1 type can be re-subtyped into *s*1a, *s*1b, and *s*1c (Miernyk *et al.*, 2011). The *m* region is located in the middle region of the gene and consists of the *m*1 or *m*2 alleles. The *m*1 type can be further subtyped into *m*1a and *m*1b (Miernyk *et al.*, 2011). Bacterial strains possessing allelic combination *s*1*m*1 produce high levels of vacuolating cytotoxins while those with allelic combination *s*1*m*2 produce moderate levels. Interestingly, the *s*2 type encodes a *vac*A protein with an N-terminal hydrophilic amino acid extension which does not influence cell vacuolation (Letley *et al.*, 2003; Miernyk *et al.*, 2011), hence allelic combination *s*2*m*2 has little or no vacuolating cytotoxin effect on host cells (Miernyk *et al.*, 2011; Arevalo-Galvis *et al.*, 2012). *Cag*A, an oncoprotein, closely associated with presence of *s*1 (Atherton *et al.*,

1995). Recently, virulent strains of *H. pylori* that express *cag*A, have been shown to be significantly associated with coronary artery disease (Pietroiusti *et al.*, 2002; Kowalski *et al.*, 2006).

4.3 MATERIALS AND METHODS

4.3.1 Standard strains

Standard strains of *H. pylori* including X47 (*cag*A positive), J99 (*vac*A *s*1*m*1 positive) and Tx30a (*s*2*m*2) were supplied by Professor Rainer Haas (Ludwig-Maximilians-Universität München) in Munich, Germany.

4.3.2 DNA isolation

DNA was isolated from the clinical isolates as well as the standard strains by the boiling method as previously described in section 3.3.2.

4.3.2 Polymerase Chain Reaction (PCR)

PCR reaction was performed directly on DNA obtained from presumptive pure colonies by boiling method as explained in Chapter 3. The extracted DNA was used as a template in each polymerase chain reaction (PCR) to target the *glm*M, *cag*A, *vac*A *s1*, *vac*A *s2*, *vac*A *m1* and *vac*A *m2* using a set of primers supplied by Inqaba Biotec Industries (Pty) Ltd. A 25μL PCR reaction was set up comprising of 12.5 μL of 2X matermix (New England Biolabs, Ipswich, United Kingdom), 6.6 mL nuclease free water (New England Biolabs), 0.5 μL of each primer (Inqaba Biotec, Pretoria, South Africa), and 5 μL of template DNA. Amplification was carried out using a Bio-Rad thermal cycler (C1000 TouchTM Cycler). The following cycling

parameters were used: initial denaturation at 95°C for 5 min, followed by 40 cycles of 95°C for 1 min, 54°C for 1 min and 72°C according to amplicon length (1 min per 1000 bp). This was followed by final elongation for 5 min. The PCR products were resolved in a 1.5% (wt/vol) agarose gel containing 5 μL of ethidium bromide (Sigma-Aldrich, St Louis, MO). Electrophoresis was done in a 0.5X TAE buffer (40 mM Tris-HCL, 20 Mm Na-acetate, 1 mM EDTA, pH 8) for 40 min at 100 volts. Visualisation was done under a UV transilluminator (Alliance 4.7 XD-79, Uvitec, Cambridge, United Kingdom) in parallel with molecular size makers, GeneRulerTM 100bp DNA Ladder (Fementas).

Figure 4. 1: List of target genes, primers and amplicon size

Target	Forward primer	Reverse primer	Amplicon	Reference
gene			size	
glmM	GATAAGCTTTTAGGGGTGTTAGGGG	GCATTCACAAACTTATCCCCAATC	140 bp	Abu-ALmaali <i>et al.,</i> 2012
CagA	ACCGCTCGAGAACCCTAGTCGGTAATGGG	CAGGTACCGCGGCCGCTTAAGATTTTT	981 bp	Smith <i>et al.,</i> 2004
VacA s1	CTGCTTGAATGCGCCAAAC	ATGGAAATACAACAACACAC	259 bp	Atherton <i>et al.,</i> 1995
VacA s2	CTGCTTGAATGCGCCAAAC	ATGGAAATACAACAACAC	286 bp	
VacA m1	GGTCAAAATGCGGTCATGG	CCATTGGTACCTGTAGAAAC	290 bp	
VacA m2	CATAACTAGCGCCTTGCAC	GGAGCCCCAGGAAACATT	352 bp	

4.3 RESULTS

4.3.1 Prevalence of cagA and vacA

Of the 48 clinical samples used in this study, 47 samples (97.9%) were cagA positive. The vacA gene was also detected, 36 of the 48 isolates (75%) possessed s1m1 allelic combination, 8 of the 48 clinical samples (16.7%) possessed s1m2 allelic combination, no clinical sample possessed s2m1 allelic combination and 4 of the 48 clinical samples (8.3%) had s2m2 allelic combination (Table 4.3).

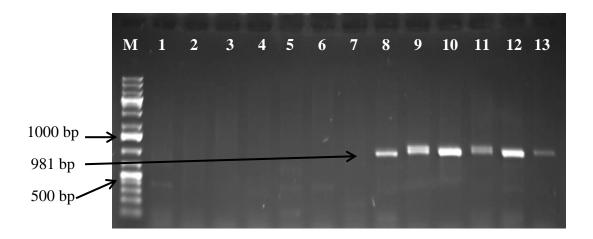


Figure 4. 2: Agarose gel electrophoresis photograph showing specific detection of 981 bp cagA gene. M-100 bp molecular weight marker, Lane 1: negative control; Lanes 2-7: negative isolates; Lanes 8-12 positive isolates; Lane 13: positive control.

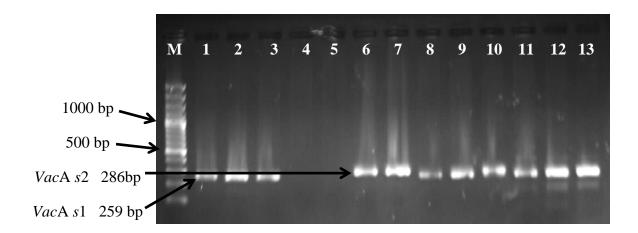


Figure 4. 3: Agarose gel electrophoresis photograph showing specific detection of 259bp $vacA\ s1$ and 286 bp $vacA\ s2$ genes. M- 100bp molecular weight marker, Lanes 1-3; 8-12: s1 positive isolates; Lane 6-7; $vacA\ s2$ positive isolates; Lane 4: negative control $vacA\ s1$

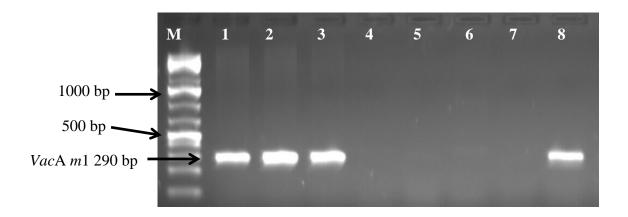


Figure 4. 4: Agarose gel electrophoresis photograph showing specific detection of 290 bp vacA m1 gene. M- 100 bp molecular weight marker, Lane 1-3: positive isolates; Lane 4-7: negative isolates; Lane 8: positive control

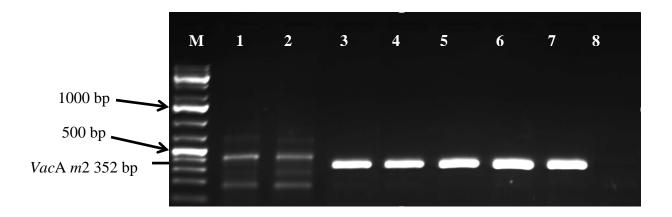


Figure 4. 5: Agarose gel electrophoresis photograph showing specific detection of 352 bp $vacA \ m2$ gene. M- 100 bp molecular weight marker, Lane 1-2: unspecified amplicons, Lanes 3-6: positive isolates; Lane 7: Positive control; Lane 8: negative control

Table 4. 1: Presence of *cag*A and allelic variants of *vac*A of *H. pylori* strains obtained from patients with upper gastrointestinal problems

				Vac	A			VacA alleli	c combinatio	ons
Strain		CagA	s1	s2	m1	m2	s1m1	s1m2	s2m1	s2m2
1	10 A	+	+	-	+	-	✓			
2	467A	+	+	-	+	-	✓			
3	56 A	+	+	-	+	-	✓			
4	430 A	+	+	-	+	-	✓			
5	96 A	+	+	-	-	+		✓		
6	155 A	+	+	-	+	-	✓			
7	169 A	+	-	+	-	+				✓
8	11 A	+	+	-	-	+		✓		
9	402 A	+	+	-	+	-	✓			
10	469 A	+	+	-	+	-	✓			
11	265 A	+	+	-	+	-	✓			
12	63 A	+	+	-	+	-	✓			
13	87 A	+	+	-	+	-	✓			
14	436 A	+	+	-	+	-	✓			
15	369 A	+	+	-	-	+		✓		
16	464 A	+	+	-	+	-	✓			
17	25 A	+	+	-	+	-	✓			
18	47 A	+	+	-	+	-	✓			
19	93 C	+	+	-	+	-	✓			
20	219 C	+	+	-	+	-	✓			
21	406 C	+	+	-	+	-	✓			
22	411 C	-	+	_	-	+		✓		
23	467 C	+	+	_	+	-	✓			
24	13 C	+	-	+	_	+				√
25	32 C	+	+	_	+	-	✓			
26	105 C	+	+	_	+	-	✓			
27	212 C	+	+	-	+	-	√			
28	92 C	+	+	-	+	-	√			
29	300 C	+	+	-	+	-	✓			
30	264 C	+	-	+	<u> </u>	+				√
31	41 C	+	+	-	-	+		√		
32	405 C	+	+	-	+	-	✓			
33	10 C	+	+	-	+	-	<u>√</u>			
34	464 C	+	+	_	+	-	√			
35	213 C	+	+	_	<u> </u>	+		√		
36	350 C	+	+	-	+	<u> </u>	√			
37	98 C	+	+		+	-	·			
38	111 C	+	+		+		<u>,</u>			
39	404 C	+	+	-		+	•	√		
40	53 C	+	+			-	√	•		
41	77 C	+	+		+ +		<u> </u>			
42	317 C						<u>√</u>			
43	299 C	+ +	+	-	+ +	<u> </u>	→			
44	162 C	+	+	+	+	+	•			√
	430 C		-		-			✓		•
45 46	14 C	+	+		-	+	√	•		
47		+	+	-	+	-	√			
	188 C	+	+	-	+	-	<u>√</u>			
48	401 C	+	+	-	+	-	Ψ			
	X47	+								
	J99 Tv20e		+		+					
T. 4. LD . ***	Tx30a	4=	4.4	+	21	+	26	0		4
Total Positi	ve	47	44	4	36	12	36	8	0	9.20/
% Total		97.9%	91.7%	8.3%	75%	25%	75%	16.7%	0%	8.3%

4.4 DISCUSSION

H. pylori infection is common in South Africa (Letley et al., 1999; Samie et al., 2007; Dube et al., 2009; Tanih et al., 2010). Drug resistant strains, cagA positive strains and vacA positive strains among those equipped with the most virulence genes have been reported among H. pylori strains circulating in South Africa (Letley et al., 1999; Tanih et al., 2013). This poses a serious health concern if attention is not given to drug resistant pattern and virulence genes of H. pylori that are circulating in South Africa.

There are studies that have associated the risk of *cagA* as an oncogen and *vacA* as a vacuolating cytotoxin (Cogo *et al.*, 2011; Miernyk *et al.*, 2011; Harrison *et al.*, 2017). This study shows that *cagA* genes (97.9%) and *vacA s1m1* allelic combinations (75%) were frequent among strains of *H. pylori* affecting the study population. This is not surprising since the study population was entirely patients who were undergoing endoscopic examination for upper gastrointestinal problems. *VacA* allelic combination *s2m1* was not detected in the *H. pylori* strains circulating in the study population however even if *s2m2* was detected, it is less common with 8.3% prevalence. The pattern of existence of these virulence genes seem to be influenced by the study population. Since, this study was done after years of sample collection, it was difficult to obtain all the patient information such as disease manifestations, hence limitations of the study to link virulence genes detected with disease manifestations. However, this study was a success in regard to the study focus of the research. We managed to obtain the drug profile of the resuscitated strains of *H. pylori* as well as the virulence genes possessed by *H. pylori* strains, the necessary findings of the next phase of the study.

4.4 CONCLUSION

CagA and vacA (s1m1) genes are highly frequent among H. pylori strains infecting patients with gastrointestinal problems. However, further studies are needed to link virulent genes of H. pylori including subtypes, to the disease manifestations in study population due to specific H. pylori strain infection. In addition, the correlation between infecting bacterial genotypes in terms of cagA and vacA in relation to patients' gastrointestinal problems contributes to earlier findings in the understanding of disease manifestations associated with H. pylori infections.

CHAPTER FIVE

Assessment of urease inhibition effect on survival of drug-resistant, vacuolating cytotoxin gene-A and cytotoxin-associated gene-A positive H. pylori strains under acidic conditions.

5.1 ABSTRACT

H. pylori produce large quantities of urease to neutralize the acidic environment of the human stomach during colonization. H. pylori lacking urease has been shown to fail to cause gastritis in animals. Highly pathogenic organisms possess cagA, an oncoprotein and vacA genes. Drug resistance is now common against H. pylori regimens currently used, and this is becoming a health concern especially in communities associated with the prevalence of highly pathogenic strains of H. pylori. Information gathered in ealier chapters of this work was used to categorise clinical isolates as drug-resistant, cagA positive and vacA positive. Agar well diffusion was used to determine zone of inhibition of honey extracts with anti-urease activity against H. pylori growth at pH of 7 and clarithromycin (0.5mg/L) was used as a standard drug. Urease inhibition studies were done by culturing H. pylori strains in Brain Heart Infusion Broth (BHIB) adjusted to pH of 2, 3, 4, 5, 6 and 7. Strain MP01 was used as a standard urease negative strain while X47 and J99 were used as positive standards for cagA and vacA s1m1 respectively. The data generated from this study reveal that anti-urease active compounds in honey have the potential to offset the normal growth of H. pylori strains that are cagA positive, vacA positive and drug resistant under acidic conditions.

5.2 INTRODUCTION

Helicobacter pylori (H. pylori) is a spiral shaped, microaerophilic and Gram-negative microorganism that colonizes the highly acidic human stomach (Allen., 2000; Lu et al., 2005; Tanih et al., 2010), an environment unsuitable for the survival of most micro-organisms. Since the discovery of H. pylori in the human stomach (Marshall and Warren, 1984), many studies have linked this organism as a causative agent of benign and malignant gastrointestinal diseases (Seck et al., 2009; Singh et al., 2009; Tanih et al., 2010; Harrison et al., 2017).

Pathogenicity of *H. pylori* is associated with the display of *cag*A gene and *vac*A genes (Faundez *et al.*, 2002; Jones *et al.*, 2010; Zabaleta, 2012; Zaki *et al.*, 2016a). The *cag*A gene is a marker for the presence of the *cag*PAI (Covacci *et al.*, 1993; Backert *et al.*, 2010). The *cag*PAI family gene is responsible for the type IV secretion system, which transports *cag*A positive strains into the cytosol of gastric epithelial cells (Viala *et al.*, 2004; Jones *et al.*, 2010). In an un-phosphorylated state, once *cag*A is inside host cells, it influences the induction of inflammatory response (Brandt *et al.*, 2005), cell proliferation and differentiation (Murata-Kamiya *et al.*, 2007; Lee *et al.*, 2010), cell scattering, cellular tight junction (Oliveira *et al.*, 2009), and cellular polarity (Zeaiter *et al.*, 2008). In addition, *cag*A has been shown to be localized in the plasma membrane where it is phosphorylated by Src or Abl kinases (Selbach *et al.*, 2002; Tammer *et al.*, 2007). *Cag*A, an oncoprotein is closely associated with the presence of *s*1 allele of the *vac*A gene (Artherton *et al.*, 1995). Presence of this gene therefore promotes intensified gastric inflammation with serious clinical outcomes which can result in severe damage to the gastric mucosa.

VacA, is a toxin that induces vacuoles in gastric epithelial cells, as well as other systemic changes such as induction of apoptosis in gastric epithelial cells (Cover et al., 2003) and inhibition of proliferation and IL-2 secretion by T cells (Gebert et al., 2003). The vacA gene is present in all H. pylori strains (Pereira et al., 2014), The four regions of vacA, the signal (s)-, intermediate (i)-, middle (m)-, and deletion (d)- regions found as either type 1 or 2 (Palframan et al., 2012; Bakhti et al., 2015; Hashinaga et al., 2016; Trang et al., 2016). Studies have shown that the mosaic combination of the alleles from both regions contribute to variations in the vacuolating activity of different H. pylori strains with strains possessing s1/m1 combination being the most cytotoxic followed by the s1/m2 strains and the s2/m2 (Atherton et al., 1995, Van Doorn et al., 1998; Cogo et al., 2011; Miernyk et al., 2011; Palframan et al., 2012). In addition, all strains possessing s1m1i1 and s1m2i1 combinations are vacuolating and more virulent as compared to the strains possessing the combinations s1m2i2 and s2m2i2 (Trang et al., 2016). Also, the strains with d1/c1 combination are linked with the production of vacuolating cytotoxin genes (s1m1i1) while the combination d2c2 is linked to failure to non-vacuolating types s2m2i2 (Trang et al., 2016).

However, current drug resistant patterns on *H. pylori* infection are worrying. The ideal antimicrobial therapy should have an eradication success of at least 90% in conjunction with tolerable levels of side effects. Several studies have highlighted high levels of drug resistant to commonly used drugs in the treatment of *H. pylori* (Seck *et al.*, 2009; Singh *et al.*, 2009; Tanih *et al.*, 2010; Fathi *et al.*, 2013). The study by Singh *et al.*, (2009), involving test samples from patients with signs and symptoms of duodenal or gastric ulcer/gastritis/gastric adenocarcinoma/non ulcer dyspepsia based on endoscopic findings; found that all test isolates were resistant to metronidazole, while 65% were resistant to amoxicillin and 4.7% were resistant to clarithromycin. Another study involving patients visiting endoscopy unit by Tanih

et al., (2010), found that 20% of the test isolates were resistant to clarithromycin and 95.5% of the test isolates were resistant to metronidazole. In Senegal 90% resistance to metronidazole were reported (Seck et al., 2009), this was not significantly different to 100% resistance to metronidazole recorded in Egypt (Fathi et al., 2013).

H. pylori infect and occupy the acidic human stomach. It has been demonstrated that H. pylori releases urease in enormous quantities as a tool to strive in the acidic environment of the human stomach (Amin et al., 2010; Amin et al., 2013; Modolo et al., 2015). Urease is a nickel-containing metalloenzyme of high molecular weight; the enzyme catalyses the hydrolysis of urea resulting in the formation of ammonia and carbon dioxide. However, there has been a demonstration that urease-negative H. pylori mutant strains fail to colonize the host resulting in the development of gastritis (Amin et al., 2010). Research has shown that in prolonged unfavourable conditions, H. pylori are capable of attaining different morphologies in a non-culturable coccoid state (Atherton., 1997; Fujimura et al., 2004).

High prevalence of *H. pylori* infection in developing nations (Samie *et al.*, 2007; Dube *et al.*, 2009; Tanih *et al.*, 2010) in conjunction with increasing drug resistance (Singh et al., 2009; Gościniak *et al.*, 2014) and virulence genes *cagA* and *vacA* put the whole world at risk in regard to diseases that occur as a result of *H. pylori* infection. Hence a search for alternative forms of *H. pylori* treatment to current treatment regimens will be of importance. In this study, we therefore focused on inhibition of urease using pre-selected honey extracts that have been demonstrated in an earlier chapter to possess anti-urease activity. Also an acidic growth environment was introduced so as to mimic the acidic human stomach when

determining the consequential inhibition of the growth of *H. pylori* when the urease enzyme is inhibited during culturing of *H. pylori*.

5.3 MATERIALS AND METHODS

5.3.1 *H. pylori* strains

Table 5. 1: List of *H. pylori* strains

Strain	Description	Source	Storage
Clinical	Resistant to clarithromycin, amoxicillin,	MPMERG UFH	Stored at -80 C
isolate 369A	metronidazole and tetracycline		
Clinical	Susceptible to clarithromycin, amoxicillin,	MPMERG UFH	Stored at -80 C
isolate 219C	metronidazole and tetracycline		
X47	CagA +ve	LMU Munich	Stored at -80 °C
199	VacA s1m1	LMU Munich	Stored at -80 C
MP01	Urease –ve	LMU Munich	Stored at -80 °C

5.3.2 Antimicrobial susceptibility testing of honey extracts at neutral pH

This was done according to Seanego *et al.* (2012), with modifications. In brief, chloroform extract of Bush honey (Inhibition percentage range = 63.8-66.1%) and the chloroform extract of Q bee (Inhibition percentage range = 64.2-66.2%) were selected for the study based on urease inhibition percentage $\geq 50\%$ observed in the previous study (Chapter 3). A colony

from 5 day cultures of strains 369A (Resistant to the four drugs tested), 219C (susceptible to the four drugs tested), X47, J99 and MP01 were taken to represent each bacterial sample.

The bacterial isolates were grown on Muller Hinton Agar (MHA) supplemented with Skirrow's antibiotics and 5% v/v fetal bovine serum with expected pH of 7.3 ± 0.1 at 25° C. Plates were swabbed with sterile swab sticks impregnated with a 0.5 McFarland standard bacterial inoculum. Five wells were bored into the agar medium using sterile 6 mm corkborer. The first three wells were filled with honey extracts at 50% v/v in respect to the diluent Phosphate buffered saline (PBS) at pH 6. The other two wells were filled with a positive control, clarithromycin (CLR) at 0.5mg/L and a negative control, PBS at pH 6. The plates were kept for 20 minutes prior to incubation to allow diffusion of the solution into the medium. The plates were incubated at 37° C for 5 days and the zones of inhibition were measured for all test organisms. The experiment was replicated three times and zones of inhibition reported as mean \pm SD.

5.3.3 Assessment of *H. pylori* growth under acidic conditions

H. pylori strains were initially grown on Columbia Blood Agar supplemented with Skirrow's antibiotics and fetal bovine serum 5% (v/v) at 37°C under micro-aerophilic conditions (85% N₂, 10% CO₂ and 5% O₂ - Helico-Campy Pack gas-generating envelopes). Urease, catalase, oxidase and PCR targeting the *glm*M gene of *H. pylori* were done to confirm presence of the organism.

Fifty milliliters (50mL) of Brain Heart Infusion Broth (BHIB) was prepared in five 100mL bottles; pH was adjusted to 2, 3, 4, 5 and 6, while normal prepared BHIB represented media

with neutral pH. The BHIB was autoclaved, allowed to cool and Skirrow's supplements and 5% fetal bovine serum added to the broth under sterile conditions and stored at 4°C until use.



Figure 5.1: Broth adjusted to pH 2; 3; 4; 5 and 6

5.3.3.1 Critical pH for urease activation

H. pylori strains, J99 (s1m1 positive), MP01 (Urease negative mutant strain) and one clinical isolate (369A) where cultured in BHIB supplemented with Skirrows antibiotics and 5% fetal bovine serum with pH ranging from 2-7. Incubation was done at 37°C under micro-aerophilic conditions (85% N₂, 10% CO₂ and 5% O₂ - Helico-Campy Pack gas-generating envelopes). The test medium cocktail consisted of 260μL of BHIB, 10μL of 0.3M urea, 5μL of 0.5 McFarland standard bacterial suspensions in BHIB with respective pH. All the experiments were replicated three times. The blank used was the absobance read at 600nm before incubation which was subtracted from the final absorbance read after an incubation of 3-5 days under micro-aerophilic conditions giving the actual difference in absorbance due to pH change.

5.3.3.2 Inhibition of *H. pylori* under acidic environment

One hundred and forty microliters (140µL) of broth was dispensed into all the wells of the microtiter plate. One hundred and forty microliters of 2X extract solution was pipetted into column 1. Using a multi-pipeter set at 120µL, contents of column 1 were mixed. One hundred and forty microliters of solution from column 1 was withdrawn and pipetted into column 2, mixed and 140µL of solution withdrawn and pipetted into column 3. The procedure was repeated up to column 10 and 140µL of solution from column 10 was discarded. Five microliters of 0.5 McFarland standard bacterial suspensions was pipetted into each well. In addition, 30µL of 0.3M of urea was pipetted into all wells of two different micro-titre plates. After mixing, the micro-titre plates were incubated for 5 days under microaerophilic conditions at 37°C. Optimum density (OD) was read at 600nm. All the experiments were replicated three times. The blank used was the absobance read before incubation which was subtracted from the final absorbance read after an incubation of 5 days under micro-aerophilic conditions giving the actual difference in absorbance due to pH acidity exposure.

Table 5. 2: Micro-titre plate experimental lay-out

	pH2	BL	рН3	BL	pH4	BL	pH5	BL	рН6	BL	pH7	pH8	Strains
	1	2	3	4	5	6	7	8	9	10	11	12	
A													X47
В													
C													J99
D													
E													MP01
F													
G													369A
H													Negative control

5.3.3.3 Ammonium test

The Urease Activity Assay Kit (Sigma Aldrich) was used to determine urease activity. In this assay, the urease enzyme catalyses the hydrolysis of urea resulting in the production of ammonia. The ammonia produced was determined by the Berthelot method resulting in colorimetric product measure at 670 nm, proportionate to the urease activity present I the sample. The estimation of ammonia production/concentration was done using the table below adapted from Urease Activity Assay Kit (Sigma Aldrich) according to the manufacturer's instructions. All the experiments were replicated three times. Actual ammonium produced was determined by subtracting OD₆₇₀ value before incubation (Blank) from OD₆₇₀ value after incubation.

Table 5. 3: The standards used for estimating ammonia concentration at OD670

	Standard OD ₆₇₀	Ammonia concentration (μΜ)
Α	1.252	500 μΜ
В	1.109	400 μΜ
С	0.912	300 μΜ
D	0.734	200 μΜ
E	0.536	150 μΜ
F	0.388	100 μΜ
G	0.233	50 μΜ
Н	0.056	0 μΜ

5.3.3.4 Re-culturing of *H. pylori* exposed to acidic and toxic environment

Samples previously cultured for 5 days in growth media with anti-urease compounds were sub-cultured for 5 days to determine biostatic/bactericidal potential of anti-urease active honey extracts. In brief, maintaining steril environment, sterile loops were used to spread bacterial inoculum on Columbia Blood Agar supplemented with Skirrow's antibiotics and fetal bovine serum 5% (v/v) and incubation was done at 37°C under micro-aerophilic conditions (85% N₂, 10% CO₂ and 5% O₂–OxoidTM AnaeroGenTM gas-generating envelopes, Thermo Fisher Scientific) in gas jars. After 5 days of culturing, observation on *H. pylori* growth was done. Three replications were done for this experiment.

5.4 RESULTS

5.4.1 Antimicrobial susceptibility testing of honey extracts

Table 5. 4 : Zone of inhibition \pm SD (mm) of honey extracts and clarithromycin (0.05 μ g/mL) at pH 7.3 \pm 0.1

Honey	Strain	Zone of inhibiti	on (mm) at diffe	rent concentration	ns (mg/mL) at pH 7.3 ± 0.1
extracts		50	100	200	Clarithromycin (0.5mg/L)
	X 47	08 ± 0.2	09 ± 0.5	11 ± 0.3	22 ± 0.7
ey	J99	09 ± 0.7	10 ± 0.2	10 ± 0.5	23 ± 1.3
Bush honey	MP01	07 ± 0.3	08 ± 0.3	11 ± 0.7	21 ± 1.1
Bus	369A	08 ± 1.2	11 ± 0.6	11 ± 0.8	10 ± 2.6
	219C	09 ± 0.5	09 ± 2.1	10 ± 0.9	22 ± 0.9
	X 47	09 ± 0.4	08 ± 2.6	11 ± 0.5	22 ± 0.7
	199	10 ± 1.9	10 ± 0.4	11 ± 2.2	23 ± 1.3
Q Bee	MP01	08 ± 0.7	09 ± 0.9	11 ± 1.6	21 ± 1.1
	369A	08 ± 1.8	08 ± 2.7	10 ± 2.4	10 ± 2.6
	219C	08 ± 0.6	09 ± 1.8	11 ± 0.9	22 ± 0.9

The results of susceptibility testing of honey extracts with anti-urease activity (Table 5.4) on growth of H. pylori strains indicate that the anti-urease activity of the selected extracts do not effectively inhibit growth of H. pylori at neutral pH, the highest inhibition zone recorded was 11 ± 2.2 at 200 mg/L for strain J99. At pH of 7.3, the growth of strain MP01 (mutant devoid of urease) was normal and not different from other strains that are capable of producing urease. The strain 369A is the only one which showed resistance to clarithromycin while strains X47, J99, MP01 and 219C were susceptible to clarithromycin.

5.4.2 Inhibition of *H. pylori* growth under acidic environments

Table 5. 5 : Inhibition of *H. pylori* growth by anti-urease honey extracts at 200mg/mL concentration

			47			J	99		MP01				CLR R	ES (369	(A)		B.I.T	
	((CagA, U	rease +ve	:)	(VacA	s1m1, ur	ease +ve)											
	N.E.T	P.T	W.E.T	P.T	N.E.T	P.T	W.E.T	P.T	N.E.T	P.T	W.E.T	P.T	N.E.T	P.T	W.E.T	P.T	N.E.T	W.E.T
pH 7	0.543	0.267	0.841	0.143	0.577	0.101	0.847	0.149	0.495	0.183	0.811	0.113	0.562	0.286	0.857	0.159	0.276	0.698
pH 6	0.429	0.258	0.748	0.098	0.432	0.061	0.754	0.104	0.238	0.067	0.690	0.040	0.441	0.27	0.739	0.089	0.171	0.650
pH 5	0.283	0.09	0.744	NON	0.281	0.088	0.769	NON	0.200	NON	0.596	NON	0.280	0.087	0.726	NON	0.193	0.778
pH 4	0.217	0.023	0.711	NON	0.210	0.016	0.710	NON	0.203	NON	0.674	NON	0.224	NON	0.714	NON	0.194	0.716
pH 3	0.178	NON	0.700	NON	0.183	NON	0.704	NON	0.256	NON	0.691	NON	0.183	NON	0.703	NON	0.247	0.692
pH 2	0.224	NON	0.643	NON	0.234	NON	0.651	NON	0.218	NON	0.658	NON	0.227	NON	0.642	NON	0.225	0.647

KEY: N.E.T: No extract turbidity; W.E.T: With extract turbidity; P.T: Projected turbidity; B.I.T: Before incubation turbidity

Table 5. 6: Inhibition of *H. pylori* growth by anti-urease honey extracts at 100mg/mL concentration

		X47 (CagA, Urease +ve)				-	J99 1, urease -	+ve)		M	P01			CLR RE	ES (369A)		B.I.T	
	N.E.T	P.T	W.E.T	P.T	N.E.T	P.T	W.E.T	P.T	N.E.T	P.T	W.E.T	P.T	N.E.T	P.T	W.E.T	P.T	N.E.T	W.E.
pH 7	0.481	0.177	0.543	0.103	0.392	0.088	0.489	0.049	0.554	0.25	0.666	0.226	0.395	0.091	0.479	0.039	0.304	0.440
рН 6	0.317	0.099	0.439	0.004	0.216	0.011	0.439	0.004	0.250	0.032	0.432	NON	0.220	0.004	0.441	0.006	0.218	0.435
pH 5	0.248	0.110	0.449	NON	0.146	0.008	0.451	0.001	0.172	NON	0.441	NON	0.241	0.003	0.450	0.000	0.238	0.450
pH 4	0.230	NON	0.407	NON	0.222	0.002	0.409	NON	0.221	NON	0.419	NON	0.221	0.001	0.413	NON	0.220	0.414
рН 3	0.244	NON	0.394	NON	0.247	NON	0.407	NON	0.219	NON	0.398	NON	0.243	NON	0.399	NON	0.237	0.403
pH 2	0.254	NON	0.406	NON	0.259	NON	0.420	NON	0.207	NON	0.406	NON	0.254	NON	0.411	NON	0.247	0.413

KEY: N.E: No extract turbidity; W.E: With extract turbidity; P.T: Projected turbidity; B.I.T: Before incubation turbidity

Table 5. 7: Inhibition of *H. pylori* growth by anti-urease honey extracts at 50 mg/mL concentration

		X47 (CagA, Urease +ve)				_	99 , urease +	ve)	MP01 CL RS (369A)						В	I.T.		
	N.E.T	P.T	W.E.T	P.T	N.E.T	P.T	W.E.T	P.T	N.E.T	P.T	W.E.T	P.T	N.E.T	P.T	W.E.T	P.T	N.E.T	W.E.T
pH 7	0.413	0.134	0.400	0.108	0.421	0.129	0.371	0.079	0.631	0.352	0.598	0.306	0.508	0.216	0.416	0.124	0.279	0.292
pH 6	0.341	0.118	0.226	0.005	0.239	0.018	0.254	0.033	0.268	0.045	0.225	0.004	0.228	0.007	0.278	0.057	0.223	0.221
pH 5	0.290	0.054	0.132	NON	0.006	0.016	0.235	NON	0.223	NON	0.164	NON	0.161	0.022	0.147	0.008	0.236	0.139
pH 4	0.200	00	0.195	NON	0.217	0.017	0.192	NON	0.211	NON	0.195	NON	0.208	0.008	0.195	NON	0.201	0.200
рН 3	0.193	NON	0.222	NON	0.213	NON	0.209	NON	0.217	NON	0.199	NON	0.223	NON	0.217	NON	0.214	0.214
pH 2	0.209	NON	0.196	NON	0.290	NON	0.216	NON	0.302	NON	0.219	NON	0.297	NON	0.205	NON	0.286	0.212

KEY: N.E: No extract turbidity; W.E: With extract turbidity; P.T: Projected turbidity; B.I.T: Before incubation turbidity

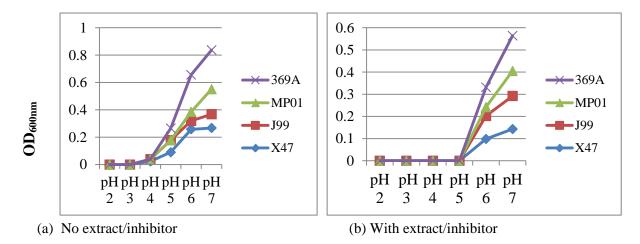


Figure 5. 2 (a-b): Inhibition of *H. pylori* growth by anti-urease honey extracts at 200mg/L concentration at different pH levels

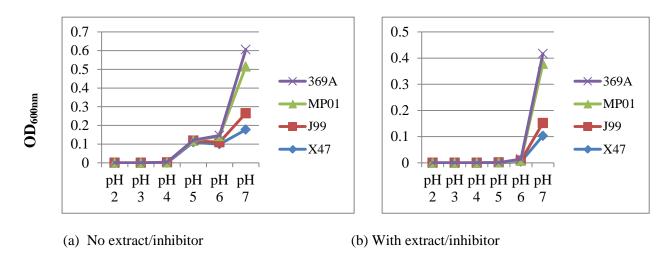


Figure 5. 3 (a-b): Inhibition of *H. pylori* growth by anti-urease honey extracts at 100mg/L concentration at different pH levels

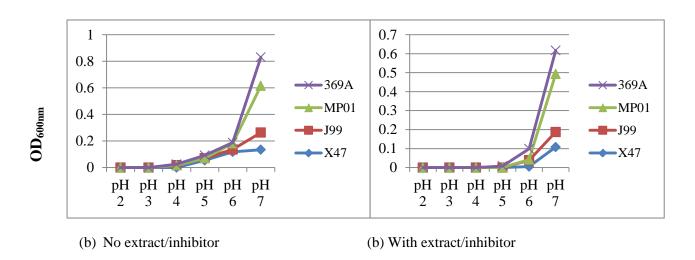


Figure 5. 4 (a-b): Inhibition of *H. pylori* growth by anti-urease honey extracts at 50 mg/L concentration at different pH levels

The urease negative mutant (MP01) recorded a good growth at pH of 7, but there was a sharp decline of viability of this strain when it was cultured at pH 6, eventually losing viability at pH 5 and downwards (Table 5.5–5.7).

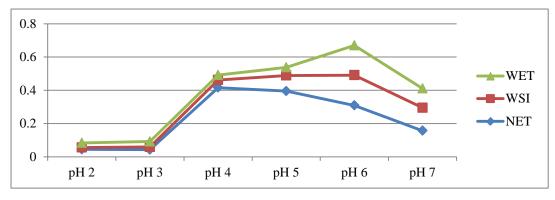
The exposure of X47, J99 and 369A to acidic growth media revealed sustainability of viability up to pH 4 (Figure 5.2-5.4). The total loss of viability or no-growth was recorded at pH 3 and 2 implying that viability might have been lost between pH 4 and pH 3. Introduction of anti-urease honey extracts into the growth media seemed to offset growth of *H. pylori* under acidic conditions. At a concentration of 200mg/mL viability of *H. pylori* strains X47, J99 and 369A was lost between pH 6 and pH 5 (Table 5.5). At a concentration of 100mg/L, viability of strains X47 and J99 was lost between pH 6 and pH 5 while the viability of strain 369A was lost between pH 5 and pH 4 (Table 5.6). Also growth of the organism was observed in growth media spiked with anti-urease honey extracts at a concentration of 50mg/L (Table 5.7). The findings reveal that strains X47 and J99 lost viability between pH 6 and pH 5, the trend notably similar to growth pattern observed when growth was monitored in growth media spiked with 100mg/L (Table 5.6). However, strain 369A lost viability between pH 5 and pH4 which is the similar trend that was noticed when growth was monitored in media spiked with 100mg/L.

5.4.3 Determining urease activity by ammonia test

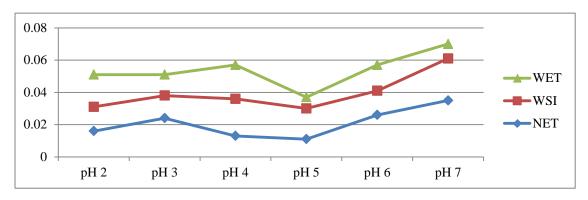
Table 5.8: Ammonia concentration (μM) after 5 days of *H. pylori* growth in media spiked with chloroform extract of Bush honey at 50mg/L concentration and acetohydroxamic acid as a standard inhibitor (14.3 mg/mL)

		X47			199		MP01			369A	
		(CagA, Ureas	e +ve)	(VacA s1r	n1, urease +ve)		(Urease neg	ative)	Cla	rithromycin	resistant
	N.E.T	W.S.I	W.E.T	N.E.T	W.E.T	N.E.T	W.S.I	W.E.T	N.E.T	W.S.I	W.E.T
pH 7	0.157	0.138	0.116	0.172	0.127	0.035	0.026	0.009	0.183	0.129	0.121
рН 6	0.309	0.182	0.179	0.299	0.154	0.026	0.015	0.016	0.311	0.188	0.183
pH 5	0.395	0.094	0.049	0.374	0.033	0.011	0.019	0.007	0.386	0.072	0.039
pH 4	0.416	0.046	0.030	0.421	0.035	0.013	0.023	0.021	0.437	0.059	0.028
pH 3	0.043	0.016	0.033	0.040	0.026	0.024	0.014	0.013	0.037	0.024	0.031
pH 2	0.045	0.011	0.028	0.037	0.030	0.016	0.015	0.020	0.032	0.017	0.023

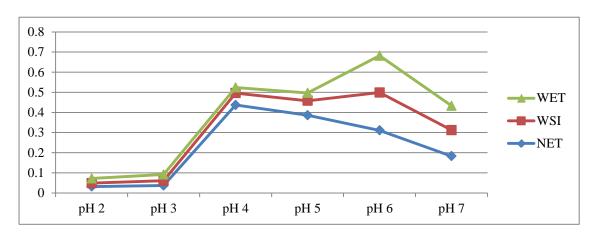
KEY: N.E.T.: No extract turbidity; W.S.I: With standard inhibitor turbidity; W.E.T: With extract turbidity



(a) Strain X47



(b) Strain MP01 (Urease negative)



(c) Strain 369A

Figure 5. 5 (a-c): Ammonia concentration (μ M) after 5 days of *H. pylori* growth in media spiked with chloroform extract of Bush honey at 50 mg/L concentration and acetohydroxamic acid as a standard inhibitor (14.3 mg/mL)

The Urease Activity Assay Kit (Sigma Aldrich) was used to determine ammonia production in samples of H. pylori cultured for 5 days under microaerophilic conditions with/without anti-urease active compounds (Figure 5.5). Ammonia was not detected in media suspension spiked with strain MP01 (urease negative). However, media spiked with strains X47, J99 and 369A (clinical isolate-clarithromycin resistant) had traces of ammonia being detected using the Urease Activity Assay Kit. Ammonia detection seemed to be dependent to pH level, all culturing media with H. pylori strains X47, J99 and 369A had traces of ammonia ranging between 0 µM and 50 µM at pH of 7. At pH of 6, culturing media without urease inhibitors but spiked with strains X47, J99 and 369A had ammonia at a concentration between 50 µM and 100 µM. At a pH of 6 as well, culturing media spiked with urease inhibitors and strains X47, J99 and 369A had an ammonia concentration between 0 μM and 50 μM. At pH level of 5, media without urease inhibition factors recorded an ammonia concentration ranging from 50 μM to 150 μM for strains X47, J99 and 369A. The same strains were also cultured at pH of 5 with media supplemented with urease inhibitors, the resultant ammonia concentration ranged from 0 µM to 50 µM. The media with urease negative mutant strain (MP01) recorded an insignificant level of ammonia concentration regardless of presence/non-presence of urease inhibitors in the culturing medium. The pH level of 4 resulted in the highest ammonia concentration detected using Urease Activity Assay Kit-spectrophotometer assay. At this pH, the concentration of ammonia ranged from 100 µM to 150 µM for media spiked with H. pylori strains X47, J99 and 369A but without urease inhibiting factors. Introduction of urease inhibitors to media at pH level of 4, led to sharp decrease in the production of ammonia in samples linked to the presence of strains X47, J99 and 369A, equating to ammonia concentration (between 0 µM and 50 µM) detected at the same pH of 4 when MP01 strain was cultured in the presence/absence of urease inhibitors. The pH level of 3 and 2 resulted in none/little production of ammonia with regard to strains X47, J99, 369A and MP01.

5.4.4 Re-culturing of *H. pylori* after acid exposure

At pH 7, strains X47, J99, MP01 and a clinical isolate (369A- clarithromycin resistant) showed good growth regardless of addition of urease inhibitors in the culturing medium during the 3—5 days culturing period. The good growth of strain MP01 (urease negative) at pH of 7 implies that *H. pylori*'s growth is not urease dependent at that pH, which explains the ineffectiveness of urease inhibitors to offset *H. pylori* growth of urease producing strains at pH of 7.

Table 5. 8: Re-growth of *H. pylori* after 3–5 day's acid exposure in growth media spiked with honey extracts at 200mg/L concentration

	(C	X47 CagA, Urease	+ve)	(VacA s1	<i>m</i> 1, urease ve)		MP01		369 A CLR RES			
	N.E.T	W.S.I	W.E.T	N.E.T	W.E.T	N.E.T	W.S.I	W.E.T	N.E.T	W.S.I	W.E.T	
pH 7	√	√	√	√	√	~	√	√	✓	√	√	
pH 6	√	√	√	~	√	X	X	X	✓	√	√	
pH 5	√	X	X	~	X	X	X	X	✓	X	X	
pH 4	√	X	X	✓	X	X	X	X	X	X	X	
рН 3	X	X	X	X	X	X	X	X	X	X	X	
pH 2	X	X	X	X	X	X	X	X	X	X	X	

Key: Growth ✓ No growth ⊠ N.E.T: No extract turbidity W.E.T: With extract turbidity

W.S.I.: With standard inhibitor

Table 5. 9: Re-growth of *H. pylori* after 3-5 days acid exposure in growth media spiked with honey extracts at 100mg/mL concentration

	(6	X47 CagA, Urease	e +ve)	(VacA s	J99 1 <i>m</i> 1, urease ⊦ve)		MP01			369A CLR RE	S
	N.E.T	W.S.I	W.E.T	N.E.T	W.E.T	N.E.T	W.S.I	W.E.T	N.E.T	W.S.I	W.E.T
pH 7	√	√	✓	✓	✓	√	√	✓	1	√	✓
рН 6	√	√	√	√	√	X	X	X	√	√	√
pH 5	√	X	X	√	X	X	X	X	√	√	√
pH 4	√	X	X	√	X	X	X	X	√	X	X
рН 3	X	X	X	X	X	X	X	X	X	X	X
pH 2	X	X	X	X	X	X	X	X	X	X	X

Key: Growth ✓ No growth ☑ N.E.T: No extract turbidity W.E.T: With extract turbidity

Table 5. 10: Re-growth of *H. pylori* after 3—5 day's acid exposure in growth media spiked with honey extracts at 50mg/L concentration.

	(C	X47 CagA, Urease	+ve)	J99 MP01 (VacA s1m1, urease +ve)					369 A CLR RES				
	N.E.T	W.S.I	W.E.T	N.E.T	we) W.E.T	N.E.T	W.S.I	W.E.T	N.E.T	W.S.I	W.E.T		
pH 7	✓	✓	√	√	✓	✓	✓	~	✓	√	✓		
рН 6	√	✓	√	✓	√	X	X	X	√	√	√		
pH 5	√	X	X	√	✓	X	X	X	~	√	✓		
pH 4	X	X	X	√	X	X	X	X	√	X	X		
рН 3	X	X	X	X	X	X	X	X	X	X	X		
pH 2	X	X	X	X	X	X	X	X	X	X	X		

Key: Growth ✓ No growth ⊠ N.E.T: No extract turbidity W.E.T: With extract turbidity

The urease negative strain MP01 succumbed and lost viability when exposed to pH of 2, 3, 4, 5 and 6. Strains X47, J99 and 369A (clinical isolate) maintained viability in media without urease inhibiting compounds when exposed to pH 6, 5 and 4, at pH 3 and pH 2, none of the strains were successfully re-cultured after 5 days of exposure to the stated pH values. Strains X47, J99 and 369A could not be re-cultured from 5 day old cultures spiked with urease inhibiting compounds at pH levels 2, 3, 4, 5 and 6. X47 lost viability between pH 5 and 6 regardless of the concentration of urease inhibiting compounds. J99 and 369A lost viability between pH 5 and 6 at a concentration of 200mg/mL (Table 5.8) of urease inhibiting compounds while viability was lost between pH 4 and 5 at a concentration of 100mg/ml of urease inhibiting compounds (Table 5.9). At 50mg/ml, viability of strain J99 was lost between pH 5 and 6 while the viability of strain 369A was lost between pH 4 and 5 (Table 5.10).

5.5 DISCUSSION

H. pylori release urease in the human stomach. The urease enzyme is released in abundance by *H. pylori* and plays an important role in pH regulation by splitting urea into ammonia and carbon dioxide. Ammonia eventually leads to elevation of the pH in the human stomach. In this controlled experiment, we targeted inhibition of urease so as to observe the growth of *H. pylori* under acidic environments.

The organism is also equipped with several virulence factors, which include the cagA, an oncoprotein and the vacA genes. The allelic combination of these two genes influences risk of disease outcome due to H. pylori infection. The organism is recognised as a class 1 carcinogen by WHO, and many eradication protocols have been suggested due to drug

resistance development to currently approved therapies. In the present experiment, honey extracts with anti-urease activity were selected as test compounds. The anti-urease extracts were used to eliminate activity of urease enzyme among *H. pylori* strains grown under acidic environments, a mimicry of the human stomach so as to determine the value of targeting urease inhibition as a treatment strategy of *H. pylori* infections.

Our findings support previous studies that urease dependent micro-organisms could be controlled by application of urease inhibition techniques (Zaborska *et al.*, 2001; Zhang *et al.*, 2006; Amin *et al.*, 2012; Amin *et al.*, 2013). The strain MP01 is a mutant devoid of urease enzyme. There was an important observation when this mutant strain was cultured in media with different pH values. Strain MP01 succumbed to a dramatic drop in the growth between pH 7 and 6 when grown in media without urease inhibitors, probably because the change of pH from 7 to 6 signalled more production of urease enzyme so as to stabilise pH at a neutral level. Since this is a mutant strain that is unable to produce urease, the acidic environment led to poor growth implying that the critical pH for urease activation lies between pH 7 and pH 6. Also this observation implies that the optimum pH for growth of *H. pylori* is pH 7. The current findings support earlier reports that surface localisation of urease help to maintain a neutral pH around the organism (Phadnis *et al.*, 1996).

There are other studies that have shown that at pH 7, honey has a greater inhibitory effect on Gram negative bacteria (Ali-Naama, 2009; Manyi-Loh *et al.*, 2010; Alzahran *et al.*, 2012). In this study, at the pH of 7 (a presumptive pH for commercial media for the growth of *H. pylori*) the honey extracts with urease inhibition compounds did not show much inhibitory effect on the growth of *H. pylori* probably because of the screening of honey extracts to only

those with high concentration of urease inhibitors. The findings of this study suggest that at a neutral pH, urease inhibition does not suppress the growth of *H. pylori*.

Contrary, important observations were made when strains of *H. pylori* (X47, J99 and 369A) growth was monitored in the absence/presence of urease inhibitors in acidic growth media (pH adjusted from pH 7 to pH 2). In comparison to the mutant strain, these strains (X47, J99 and 369A) showed a reasonable decline in growth rate when cultured in media without urease inhibitors when subjected to decreasing pH up to pH of 4 after which no growth was observed. However, spiking of anti-urease active extracts of honey (200mg/L) led to a sharp decline in growth of H. pylori with growth undetectable between pH 5 and pH 6 for strains X47, J99 and 369A. The 100mg/L and 50mg/L anti-urease extracts of honey resulted in no growth of strain X47 and J99 between a pH of 5 and 6 while strain 369A showed no growth between pH 4 and 5. In comparison to cultures grown without anti-urease active compounds, where growth was lost between the pH of 3 and 4 or pH4 and 5, urease inhibiting compounds in honey seem to be playing an active role which causes H. pylori to lose its multiplication capabilities. Surface localised urease enzyme is known to maintain an optimum pH for the growth of the organism in an acidic environment (Phadnis et al., 1996; Amin et al., 2010). The observed results therefore suggest that urease inhibitors in honey weaken the protective effect of the urease enzyme causing the organism to succumb to the acidic pH. The current observations demonstrate that the urease enzyme is an important virulent factor required by H. pylori to colonise the acidic environment such as the human stomach.

This study revealed that the concentration of urease inhibiting compounds in culturing media did not affect re-growth of H. pylori after exposure to culturing media with pH of 7 (Tables

5.9–5.10). However, it was observed that all the strains showed no growth between pH 3 and pH 4 and re-culturing of these strains was not successful after 5 days of incubation at 37°C under miroaerophilic conditions. This could suggest that urease activity was totally stalled between pH 3 and pH 4, probably marking bactericidal pH range of honey extracts, or could be that because of prolonged unfavourable growth conditions, *H. pylori* cells changed to its coccoid state which is viable but non-culturable.

The standard strain X47 is *cag*A positive and the *cag*A gene encodes a protein that is linked with increased intensity of gastric inflammation. J99 is *vac*A *s*1*m*1 positive while strain 369A is a clinical isolate that is multidrug resistant. The findings of this study therefore may imply that the selected anti-urease honey extracts have the potential to eradicate the growth of *cag*A positive, *vac*A positive and drug resistant strains exposed to acidic environment.

5.6 CONCLUSION

H. pylori devoid of urease (MP01) were shown to have difficulties in surviving the acidic environment while urease producing H. pylori tolerated acid exposure with success. This leads to a conclusion that the urease enzyme is an important virulence factor for the organism's survival under acidic conditions. The data generated in this study also demonstrate that anti-urease compounds in honey extracts are bioactive against urease depended H. pylori under acidic conditions and have the potential to offset the growth of H. pylori strains that are cagA positive, vacA positive and drug resistant under acidic conditions. In addition, anti-urease active compounds have been shown to be antibacterial against urease producing H. pylori under acidic conditions.

CHAPTER SIX

Characterisation of bioactive compounds in honey extracts by GC-MS and LC-MS

6.1 ABSTRACT

Gas chromatography-mass spectrometry (GC-MS) and liquid chromatography-mass spectrometry (LC-MS) are sensitive techniques frequently used in the detection of volatile and non-volatile compounds respectively. Extracts for analysis were chosen on the bases of known urease inhibition potential of the extracts as determined in chapter 3. Volatile compounds in honey were detected using the GC-MS technique while commonly used drugs/pesticides/insecticides applied during agricultural activities were screened using LC-MS run on a positive mode. Fleures honey (I% = 67.8-68.5%), Gold Crest honey (I% = 50.9%-53.3%), Raw honey (I%=8.1-23.4%) and Siyakholwa honey (I% = 0), all petroleum ether extracts recorded 27, 26, 22, and 29 compounds respectively that were positively identified by spectral matching ≥ 90% with the NIST11 library during GC-MS analysis. Manuka honey (I% = 50.0 - 53.2%) and Siyakholwa honey (I% = 10.3% - 11.2%), all hexane extracts recorded 43 and 23 compounds respectively that were positively identified by spectral matching $\geq 90\%$ with the NIST11 library during GC-MS analysis. Regarding chloroform extracts, Raw honey (I% = 8.5 - 11.4%), Q Bee (I% = 64.2 - 66.2%) and Siyakholwa honey (I% = 5.3% - 6.1%), revealed 19, 13 and 12 compounds respectively with spectral matching ≥ 90% with the NIST11 library during GC-MS analysis. There were six compounds that were identified by LC-MS to be constituents of both Q Bee honey and Little Bee honey hexane extracts. The majority of compounds detected in Little Bee honey are drugs commonly used in the treatment of a variety of ailments affecting human beings. Two drugs, sulfaquinoxaline and hydroxyquinoline used in veterinary medicine and, antiseptic, disinfectant and pesticide applications in agricultural produce were also detected in Little Bee honey. To conclude, geographical location influences honey's value as a rich source of urease inhibiting compounds.

6.2 INTRODUCTION

Honey is a natural sweet product commonly used for food or food additive and traditional medicinal applications (Selcuk and Nevin, 2002). This natural sweet product has been used in ethno-medicine dating back to ancient times. Treatment of wounds, burns, skin ulcer and gastro-duodenal disorders are some of the complications that have been alleviated by use of honey (Selcuk and Nevin, 2002; Orhan *et al.*, 2003).

The geographical location and floral origin affect the physiochemical composition, antioxidant activities and phenolic components of honey (Eleazu *et al.*, 2013). Several studies have documented different classes of chemical compounds in honey including acids, aldehydes, alcohol, ketones, terpenes, hydrocarbons, furans (Sirko and Brodzik., 2000; Barra *et al.*, 2010; Manyi-Loh *et al.*, 2010; Modolo *et al.*, 2015). While it is acceptable that geographical location from which bees forage play an important role in determining the medicinal value of honey, veterinary medicines and insecticides used in agriculture always get incorporated into the honey passively by foraging bees (Hoopingarner and Nelson, 1998; Kuhn and Wittrig, 2007).

Different techniques are being used for determining chemical components in honey. Capillary electrophoresis—mass spectrometry (CE-MS), High-performance liquid chromatography (HPLC), Gas Chromatography Mass Spectrometry (GC-MS) and Liquid chromatography mass spectrometry (LC-MS) are the most commonly used techniques (Arr´aez-Rom´an *et al.*, 2006; Campone *et al.*, 2014).

GC-MS has been widely used in the analysis of chemical components of honey with much success. Liquid Chromatography Mass Spectrometry (LC-MS) which combines liquid chromatography and mass spectroscopy is a highly sensitive, accurate and specific quantitative analysis method. The GC-MS is suitable for the analysis of volatile chemicals, mostly non-polar or chemicals amenable to changes to enhance volatility (Wolski *et al.*, 2006; Syazana *et al.*, 2013). The LC-MS is highly recommended for more polar chemicals (Campone *et al.*, 2014). The purpose of this study was therefore to assess the composition of volatile and non-volatile compounds in South African honey that have anti-urease potential as well as determining whether there are any likelihood of insecticide or chemical traces in honey that have been incorporated by bees after foraging on plants or pollen sprayed using pesticides.

6.3 MATERIALS AND METHODS

6.3.1 Honey preparation for GC-MS and LC-MS

Extraction of honey compounds for GC-MS and LC-MS analysis was done according to the method described by Syazana *et al.* (2013) as already explained in chapter 3. However the anhydrous disodium sulfate powder (Na₂SO₄₎ was not added to honey extracts prepared for LC-MS analysis.

6.3.2 GC-MS analysis

Analysis of compounds was done at the Mass Spectrometry Laboratory, School of Chemistry; University of KwaZulu Natal-Pietermaritzburg, South Africa. GC-MS analysis was performed using a Shimadzu GC-MS-QP2020 mass spectrometer. The column was an SH-RtxTM-VMS (30m X 0.25mmID, 1.40 µm) column, and helium, a carrier gas was kept at a constant linear velocity of 34cm/sec at 40°C. One microliter volumes were injected using a splited mode at an injector temperature of 200°C. The oven temperature was ramped from 40 to 220°C (4 minute hold) at a rate of 16°C/min, then at 32°C/min (hold 5 minutes). The oven temperature was held at 150oC for 6 minutes following each analysis. The total run time for each sample was almost 90 minutes. The GC-MS interface temperature was set to 150oC. Mass spectrometry mode was used during analytical scanning from 35-300 atomic mass unit (amu). The ion source temperature was set to 200°C. The blank was first injected, and was followed by the sample injection. The chromatograms obtained from the total ion count (TIC) were integrated without any correction for co-eluting peaks and the results were expressed as total abundance. All the peaks were identified based on mass spectral matching (≥ 90%) from both the NIST and Wiley libraries. Only compounds with 90% or greater spectral matching accuracy are reported. Qualitative analysis report obtained from the total ion count (TIC) was summarised without any alteration for co-elution peaks. All the peaks were identified based on mass spectral matching greater or equal to 90% ($\geq 90\%$) with the NIST11 library. Only compounds with 90% or greater spectral matching accuracy were reported.

6.3.3 Liquid Chromatography-Mass Spectrometry (LC-MS)

Hexane extracts of Raw Honey, Goldcrest Honey, Q Bee Honey, Fleures Honey and Little Bee Honey were subjected to Liquid Chromatography Mass Spectroscopy (LC-MS) so as to identify possible compounds responsible for urease inhibition. LC-MS analysis was done using Triple TOFTM 5600 System Technology and DuosprayTM Ion Source on a positive electrospray ionisation mode according to Andrews et al., 2017 but with modifications. The following conditions for MS were used: ion spray voltage, 4.5KV-4.5KV; ion source temperature, 600°C; curtain gas (GS 1) at 30 psi; nebulizer gas at 50 psi; heater gas (GS 2) at 50 psi; declustering potential at 80 V. The following mass ranges were used, m/z 100-600 for TOF MS scan, 50-600 for TOF MS/MS experiments. In the TOF MS/MS experiments, the most intensive 8 ions were selected for MS/MS fragmentation. The dynamic background subtraction was done to match the information dependent acquisition (IDA) criteria. The collision energy (CE) was set at 30eV-40eV and the collision energy was at 10eV for MS/MS experiments. The data was analysed using PeakView Software TM and the Metabolite Pilot Software on Drug Discovery was used to determine compounds in honey extracts and the potential compounds were selected based on being positive in mass error, isotope and library hit scores.

6.4 RESULTS

6.4.1 Volatile compounds in honey detected by GC-MS

6.4.1.1 Petroleum ether extracts and urease inhibition

There were 27, 22 and 26 compounds that were detected in Fleures honey, Raw Honey and Gold Crest honey respectively by GC-MS by spectral matching greater than 90% with the NIST11 library (Figure 6.1). The compounds in Fleures honey petroleum ether extract compared very well with compounds detected in Gold crest honey with a spectral matching greater or equal to 90%. Tetradecane, heneicosane, nonadecane and octadecanoic acid were potential compounds found in Gold crest honey with spectral matching \geq 90% and inhibition percentage (%) of 50.9% but not in Fleures honey that had an inhibition percentage of 67.9%.

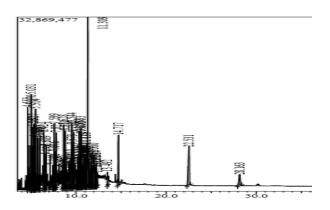
6.4.1.2 Hexane extracts and urease inhibition

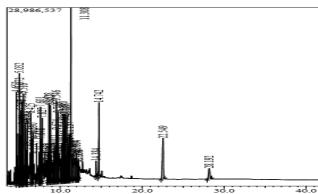
All the peaks were identified based on mass spectral matching \geq 90% from both the NIST11. Two hexane extracts were analysed with GC-MS (Figure 6.1). The hexane extract of Manuka honey had forty three of the eighty four (51.2%) compounds with 90 % or greater spectral matching with NIST11 library (Table 6.2). Siyakholwa honey recorded a lower number of compounds with a 90% or greater spectral matching compared to Manuka honey, twenty three out of eighty two (28%) of the compounds revealed a 90% or greater spectral matching (Table 6.2). Comparing volatile compounds with spectral matching from 90% and above in both extracts, it was observed that twenty two (88%) out of twenty five compounds identified in Siyakholwa honey hexane extract were also found in the Manuka honey hexane extract. Hexadecane, phenol and tetradecanamide were the three compounds that were not positively identified in Manuka honey by spectral matching (\geq 90%) even though they were identified

by spectral matching (\geq 90%) in Siyakholwa honey hexane extract. Manuka honey exhibited an inhibition percentage ranging from 50% to 53.2% on urease activity under observation. Siyakholwa honey hexane extract performed poorly on urease inhibition with an inhibition percentage ranging from 10.3% to 11.2% on the ureases selected for this study.

6.4.1.3 Chloroform extract and urease inhibition

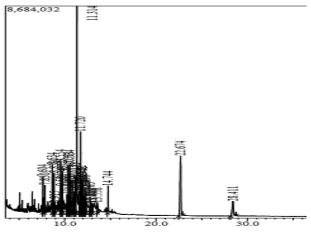
Chloroform was also used as an extraction solvent for honey compounds. Three honey extracts were analysed using GC-MS (Figure 6.1). Few compounds reached a 90% library hit in comparison to petroleum extracts and hexane extracts. Raw honey had nineteen out of sixty seven (28.4%) compounds with spectral matching of 90% and above in the NIST11 library (Table 6.3). Q Bee honey recorded thirteen of the thirty five (37.1%) compounds reaching a spectral matching of 90% and above in the NIST11 library (Table 6.3). Siyakholwa honey extract had twelve out of thirty eight (31.6%) of the compounds reaching 90% and above spectral matching with the NIST11 library (Table 6.3). Of the three, Siyakholwa honey extracts gave the lowest urease inhibition percentage (%) ranging from 5.3% to 6.1% which did not differ much from a range of 8.5% to 11.4% attained by Raw honey extracts under similar experimental environments.

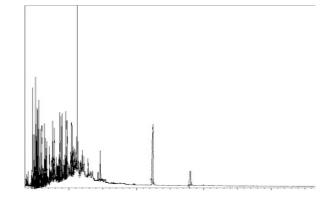




(a) Petroleum ether chromatogram of Fleures honey

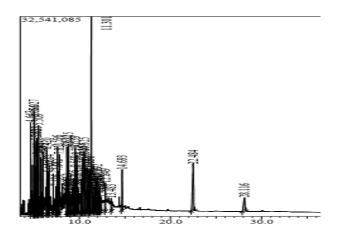
(b) Petroleum ether chromatogram of Gold Crest honey

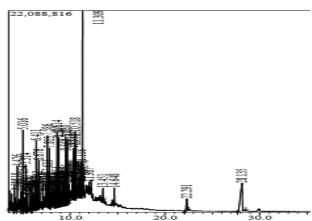




(c) Hexane chromatogram of Little Bee honey

(d) Hexane chromatogram of Manuka honey





(e) Chloroform chromatogram of Bush honey

(f) Chloroform chromatogram of Q Bee honey

Figure 6. 1 (a-f): GC-MS chromatograms of honey extracts

 Table 6. 1: GC-MS analysis of petroleum extracts in reference to inhibition percentage

	Compound	Fleures ho I%=67.8-		Gold Crest 1% = 50.9		Raw Hon I% = 8.1- 23.4%	•	Siyakholw I% = 0.0%	
		Relative %	√/X	Relative %	√/X	Relative %	√/X	Relative %	√/X
1	Benzene	0.87	✓	0.84	✓	0.54	✓	1.00	√
2	Undecane	0.91	✓	0.92	✓	0.54	✓	1.05	√
3	Octane	0.91	✓	0.92	✓		X	1.05	✓
4	Decane	0.91	✓	0.92	✓	0.54	✓	1.05	✓
5	Dodecane	0.91	✓	0.75	✓	0.47	✓	1.05	✓
6	Tetradecane	0.91	✓	0.75	✓	0.47	✓	1.05	✓
7	Ethanol	0.63	✓	0.65	✓	1.89	✓		X
8	Tridecane	0.79	✓	0.75	✓	0.54	✓	0.90	√
9	Pentadecane	0.91	✓	0.83	✓	0.54	✓	0.90	✓
10	Nonane	1.00	✓	1.02	✓	0.48	✓	1.18	✓
11	Hexadecane	0.75	✓	1.02	✓	0.48	✓	1.04	✓
12	Heptadecane	0.59	✓	1.02	✓	0.73	✓	0.76	✓
13	Eicosane	0.80	✓	0.83	✓	0.73	✓	0.93	✓
14	Heneicosane	1.52	✓	1.62	✓	0.73	✓	1.70	✓
15	Tetracosane	0.58	✓		X	0.90	✓	0.84	✓
16	Tetradecane		X		X	0.47	✓	1.05	✓
17	Tetratetracontane	1.91	✓	0.57	✓	0.90	✓	2.13	✓
18	Hexatriacontane	1.02	✓	1.43	✓		X	0.85	✓
19	Hexadecanamide	1.11	✓	0.65	✓		X	1.10	✓
20	Dodecanamide	1.11	✓	0.65	✓		X	1.10	✓
21	Octadecanamide	1.11	✓	0.65	✓		X	1.10	✓
22	Decanamide	1.11	✓	0.65	✓		X	1.10	✓
23	Tetradecanamide	1.11	✓	0.65	✓		X	1.10	✓
24	Tetratriacontane	1.25	✓	1.28	✓		X	1.21	✓
25	2-methyloctacosane	1.25	✓	0.57	✓		X	0.75	✓
26	9-Octadecenamide	5.88	✓	4.76	✓	2.22	✓	5.93	✓
27	Cholesta-3,5-diene	1.86	✓	2.53	✓		X	1.42	✓
28	Cholesterol	1.86	✓	2.53	✓		X	1.42	✓
29	Heneicosane		X		X	0.73	✓	1.70	✓
30	9,12-Octadecadienoic acid		X		X	1.89	✓		X
31	Cis-13,16-Docasadienoic acid		X		X	1.89	✓		X
32	Oxacycloheptadec		X		X	1.89	✓		X
33	Phthalic acid		X		X		✓		X
34	Diisooctyl phthalate		X		X		X	1.26	$\overline{}$
	al compounds identified of all peaks	$\frac{27}{70}$		<u>26</u> 84		<u>22</u> 86		<u>29</u> 72	
%to	otal compounds identified of all peaks	38.5%	/ o	31%	D	25.6% 40.3%			

Key: \checkmark - detected, X - not detected

Table 6. 2: GC-MS analysis of hexane extracts in reference to inhibition percentage

	Compound	Manuka Hon I% = 50-53.2		Siyakholwa I%=10.3-11.	2%
		Relative %	√/X	Relative %	√/X
1	n-Butyl ether	0.44	✓		X
2	Isobutyl ether	0.44	✓		X
3	Oxalic acid	0.44	✓		X
4	Malonic acid	0.44	✓		X
5	Nonane	0.51	✓	0.82	√
6	Heptane	0.51	✓		X
7	Decane	0.51	✓		X
8	Dodecane	0.51	✓	0.82	√
9	D-Limonele	0.46	✓		X
10	Cyclobutane	0.46	✓		X
11	Cyclohexene	0.46	✓		X
12	Octane	1.72	✓		X
13	Undecane	1.72	✓		X
14	Nonane	1.72	✓		X
15	Benzene	0.45	√		X
16	Ethanol	0.79	✓		X
17	Naphthalene	0.51	√		$\frac{X}{X}$
18	Azulene	0.51	√		$\frac{X}{X}$
19	2,4-Dimethyldodecane	0.82	√		$\frac{X}{X}$
20	Tridecane	0.82	√		X
21	Eicosane	0.61	√		$\frac{X}{X}$
22	Hexadecane	0.53		0.79	
23	Tetradecane	0.53	·	0.79	
24	Heptadecane	0.53	·	2.20	·
25	3-Ethyl-3-methylheptane	0.52	·	2.20	
26	Pentadecane	1.00	,		$\frac{X}{X}$
27	Sulfurous acid	0.51	<u>,</u>		
			<u>,</u>	2.20	X
28	Heneicosane	0.45	<u> </u>	2.20	
29	Nonadecane	0.76	<u> </u>	0.79	
30	Tetratetracontane	0.76		0.00	X
31	2-Methyloctacosane	0.51		0.90	
32	Tetracosane	2.74		1.05	X
33	Hexatriacontane	0.68	√	1.85	
34	2-Methylhexacosane	1.48	√	2.82	√
35	Hexadecanamide	1.38	√	1.84	√
36	Octadecanamide	1.38	<u>√</u>	1.84	<u> </u>
37	Tetradecanamide	1.38	√	1.84	- ✓
38	Dodecanamide	1.38	✓	1.84	√
39	Decanamide	1.38	✓	1.84	✓
40	Tetratriacontane	1.38	✓	1.85	✓
41	Tetracosane	1.38	✓	1.12	✓
42	9-Octadecenamide	10.32	✓	10.63	✓
43	Cholesta-3,5-diene	1.00	✓	1.25	✓
44	Eicosane		X	0.79	✓
45	Phenol		X	0.90	✓
46	Tetratetracontane		X	3.27	√
47	Pentadecane		X	1.06	✓
Total o	compounds identified out of all peaks	43 84		23 82	
0/ tota	al compounds identified out of all peaks	51.2%		28%	

Key: ✓ - detected, *X* - not detected

Table 6. 3: GC-MS analysis of hexane extracts in reference to inhibition percentage

Compound		Raw honey		Q Bee honey I%= 64.2-66.2%		Siyakholwa 5.3-6.1%	
		Relative %	√/X			Relative %	√/X
1	Ethanol	0.81	✓		X		X
2	Dodecane	1.29	✓		X	1.46	✓
3	Nonane	1.29	✓		X		X
4	Hexadecane	1.29	✓	2.09	✓	1.46	✓
5	Tetradecane	1.29	✓		X	1.46	✓
6	Decane	0.91	✓		X		X
7	Pentadecane	0.91	✓		X	1.46	✓
8	Heptadecane	0.83	✓	2.09	✓	1.46	✓
9	Heneicosane	0.83	✓	2.21	✓	2.12	✓
10	Eicosane	2.43	✓	2.09	✓	2.12	✓
11	Phenol	0.97	✓		X		X
12	Tetratetracontane	2.75	✓	2.21	✓	2.66	✓
13	2-methyloctacosane	2.75	✓	2.21	✓	2.66	✓
14	Tetracosane	0.72	✓	1.99	✓	1.78	✓
15	Tetratriacontane	1.70	✓	1.88	✓		X
16	Hexatriacontane	1.50	✓	2.06	✓	1.96	✓
17	2-methylhexacosane	0.75	✓	2.06	✓		X
18	Cholesta-3,5-diene	2.24	✓	2.66	✓		X
19	Cholesteryl benzoate	2.24	✓	2.66	✓		X
20	Cholesterol		X	2.66	✓		X
21	Benzoic acid		X		X	1.20	✓
Total compounds identified		<u>19</u>		<u>13</u>		<u>12</u>	
_	of all peaks	67		35		82	
% total compounds identified out of all peaks		28.4%		37.1%		14.6%	

Key: \checkmark - detected, X - not detected

6.4.2 Volatile compounds in honey and urease inhibition

The solvent extracts that resulted in urease kinetic inhibition of 50% and more were selected for this analysis. Two extracts of petroleum ether (Gold Crest honey and Fleures Honey), one hexane extract of Manuka honey and one chloroform extract of Q bee honey were selected to link compounds in honey with inhibitory power on kinetic activity of the urease enzyme. The area percentage was the only variable considered for this analysis.

Thirty seven compounds were detected by GC-MS in the petroleum ether extract of Gold Crest honey with eicosane having the highest area percentage of 26.11% followed by cholester-5-en-3-ol (3.beta) with 13.72% (Table 6.4). The petroleum ether of Gold Crest honey had an inhibition percentage of urease activity ranging from 50.9% to 53.3%. The urease percentage inhibition of Fleures honey ranged from 67.8% to 68.5%.

The petroleum ether extract of Fleures honey had 35 compounds detected by GC-MS. The cholesteryl valerate had the highest area percentage of 20.94% of the compounds followed by eicosane with 16.79%. Cholesterol- pentafluoropropionate had 9.35% area representation while 9-octadecanamide recorded 6.56% area representation (Table 6.5). The hexane extract of Manuka honey had an inhibition percentage of urease activity ranging from 50% to 53.2%. GC-MS analysis revealed that 38.42% of the area % of compounds was represented by eicosane followed by 10.32% of 9-octadecenamide and 8.62% of 1,4-epoxynaphthalene-1(2H)-methanol (Table 6.6). The chloroform extracts were represented by Q Bee honey which had urease inhibition percentage ranging from 64.2% to 66.2%. Also eicosane had the largest share of area percentage (23.19%) followed by 9- octadecanamide (16.65%) and silane, diethylheptyloxyoctadecyloxy with 12.29% (Table 6.7).

 Table 6. 4: Petroleum ether extracts of Gold Crest honey showing area %

No	Volatile compounds	RT (min)	Area %
1	Mesitylene	4.655	0.85
2	Nonane, 5-(2-methylpropyl	5.035	1.36
3	Spiro [3.5]nona-5,7-dien-1-one, 5,9,9-trimethy	5.075	1.16
4	Benzene, 1-ethyl-3,5-dimethyl	5.272	0.89
5	Undecane	5.332	1.07
6	Benzene, 1,2,3,5-tetramethyl-	5.494	3.00
7	Ethanol, 1-(2-butoxyethoxyl)	5.896	0.77
8	Dodecane, 4,6-dimethyl, 4-methyl	5.969	3.34
9	Azulene	6.004	0.93
10	Tetradecane, 5-methyl	6.346	1.44
11	Tridecane, 6-methyl	7.185	0.53
12	Heptadecane	7.376	3.43
13	Hexadecane,1-iodo	7.445	4,51
14	Eicosane	7.605	26.11
15	Pentadecane	7.651	0.91
16	Phenol, 2,4-bis(1,1-dimethylethyl)	7.712	0.87
17	Octacosyl triflouroacetate	8.764	0.72
18	Heneicosane	9.233	3.84
19	Silane, trichlorooctadecyl	9.579	1.01
20	Benzenepropanoic acid, 3,5-bis (1,1-dimethyle	9.645	0.84
21	Hexatriacontyl trifluoroacetate	9.675	0.70
22	11-Bromoundecanoic acid	9.747	0.90
23	9-Octadecanamide. (Z)	9.817	5.66
24	Cis-13,16-Docasadienoic acid	10.449	1.56
25	Hexadecanamide	10.612	0.81
26	Cholest-5-en-3-ol (3.beta)-,	10.712	13.72
27	Octadecanoic acid, 2-hydroxyethyl ester	10.805	2.85
28	Tetratetracontane	10.860	2.69
29	Bis(dodecanamido) methane	11.388	0.62
30	Cholesta-3,5-diene	11.544	3.19
31	Hexatriacontane	11.857	0.98
32	Bis(tridecyl) phthalate	12.006	1.59
33	2-methylhexacosane	12.183	0.64
34	Silane, diethylheptyloxyoctadecyloxy	22.594	3.47
35	1.4-Epoxynaphthalene-1(2H)-methanol, 4,5,7	28.243	1.16
36	Propanoic acid, 3.3'-thiobis-, didodecyl ester	30.274	0.23
37	Longifolenaldehyde	87.317	0.71
Tota	al	100%	

 $\textbf{Table 6. 5:} \ \text{Petroleum ether extracts of Fleures honey showing area } \%$

No	Volatile compounds	RT (min)	Area %
1	Mesitylene	4.651	0.86
2	Pentadecane	5.031	1.22
3	Spiro[3.5]nona-5,7-dien-1-one, 5,9,9-trimethy	5.070	1.06
4	Benzene	5.267	3.54
5	Undecane	5.327	0.91
6	Dodecane, 4,6-dimethyl	5.965	2.67
7	Naphthalene	6.000	0.86
8	Tetradecane	6.559	1.34
9	Eicosane	7.440	16.79
10	Pentadecane	7.646	0.68
11	Phenol, 2.4-bis(1,1-dimethylethyl)	7.708	0.70
12	Heneicosane	8.487	0.58
13	Docosyl pentafluoropropionate	8.760	0.60
14	Nonane, 5-methyl-5-propyl	8.905	0.91
15	Heptadecane	9.054	0.64
16	Silane, trichlorooctadecyl	9.573	0.99
17	Hexadecane, 1-iodo	10.078	2.06
18	Octadecane, 1-chloro	10.152	0.72
19	E,E,Z,1,3,12-Nonadecatriene-5,14-diol	10.443	0.66
20	Bis(dodecanamido)methane	10.533	2.45
21	Hexadecanamide	10.600	1.11
22	Cholesta-3,5-diene	10.727	3.32
23	Octadecanoic acid, 2 hydroxyethyl ester	10.819	3.74
24	Tetratetracontane	10.997	2.84
25	Cholest-5-en-3-ol (3.beta)	11.163	1.7
26	9-Octadecanamide	11.309	6.56
27	Bis(tridecyl) phthalate	12.000	1.97
28	Hexatriacontane	12.261	0.78
29	5.5-Diethylheptadecane	12.391	0.68
30	13-Docosenamide, (Z)	13.492	0.74
31	Silane, diethylheptyloxyoctadecyloxy	22.531	3.43
32	1.4-Epoxynaphthalene-1(2H)- methanol, 4,5,7	28.163	1.26
33	Cholesteryl valerate	85.148	20.94
34	3Beta-methoxy-5-cholesten-19-oic acid	85.345	1.34
35	Cholesterol, pentafluoropropionate	86.493	9.35
Tota	al	100%	

 $\textbf{Table 6. 6:} \ \textbf{Hexane extracts of Manuka honey showing area \%}$

No	Volatile compounds	RT (min)	Area %
1	n-Butyl ether	3.829	0.44
2	4-Butoxy-2-butanone	4.118	0.72
3	Oxalic acid, cyclohexyl propyl ester	4.428	1.44
4	Nonane, 2,6-dimethyl, 5-butyl	4.786	4.91
5	D-Limonene	4.880	0.46
6	Octane, 5-ethyl-2-methyl	5.015	3.6
7	Decane, 3,7-dimethyl, 2,3,7-trimethyl	5.350	1.3
8	Benzene, 1,2,4,5-teteamethyl	5.498	1.05
9	Ethanol, 1-(2-butoxyethoxy)	5.880	0.79
10	Tetradecane	5.952	0.78
11	Naphthalene	5.994	0.51
12	Undecane, 2,5-dimethyl	6.030	1.1
13	Dodecane, 4,6-dimethyl	6.275	3.72
14	Tetradecane	7.107	0.68
15	Hexadecane	7.168	1.43
16	Eicosane	7.428	38.42
17	Pentadecane, 2,6,10,14-tetramethyl	7.632	1.71
18	Phenol, 2,4-bis (1,1-dimethylethyl)	7.693	1.04
19	1-Dodecanol, 2-hexyl	7.729	0.48
20	Sulfurus acid, pentadecyl 2-propyl ester	8.157	0.51
21	1-Heptanol, 2,4-diethyl	8.745	0.97
22	Heptadecane	9.040	0.74
23	Phthalic acid, butyl tetradecyl ester	9.340	0.47
24	n-Tetradecyltrichlorosilane	9.559	1.58
25	Benzenepropanoic acid, 3,5-bis(1,1-dimethyl	9.625	0.79
26	Tetracontyl	9.655	2.31
27	Ethanone, 1-phenyl	10.290	0.56
28	Hexadecanamide	10.583	1.38
29	Octadecanoic acid, 2 hydroxylethyl ester	10.808	1.17
30	9-Octadecenamide, (Z)	11.293	10.32
31	Bis(dodecanamido)methane	11.375	0.82
32	Tetratetracontane	11.984	0.43
33	5,5-Diethylpentadecane	12.198	0.57
34	Cholesta-3,5-diene	14.644	1.00
35	Silane, diethylheptyloxyoctadecyloxy	22.296	2.51
36	1,4-Epoxynaphthalene-1(2H)-methanol	28.051	8.62
Tota	al	100%	

Table 6. 7: Chloroform extracts of Q Bee honey showing area %

No	Volatile compounds	RT (min)	Area %	
1	Eicosane	23.19		
2	Nonane, 5-methyl-5-propyl	18.915	1.03	
3	Silane, trichlorooctadecyl	9.584	1.21	
4	Pentadecanoic acid	9.749	1.73	
5	9-Octadecanamide, (Z)	10.620	16.65	
6	Octadecanoic acid, 2-hydroxyethyl ester	10.813	3.91	
7	Hexatriacontane	11.019	5.41	
8	1,3,5-Trisilacyclohexane	11.720	6.52	
9	1H-Indene, 1-hexadecyl-2,3-dihydro	11.822	3.21	
10	Squalane	11.873	4.54	
11	Hexadecanoic acid, 2-hydroxy-	11.948	2.73	
12	5,5-Diethylpentadecane	12.210	5.06	
13	1,3,5-Trisilacyclohexane	12.763	2.41	
14	Oxalic acid, 3,5-difluorophenyl tetradecyl ester	12.891	1.05	
15	2-Methylhexacosane	13.558	2.19	
16	Cholesta-3,5-diene	14.744	2.66	
17	Silane, diethylheptyloxyoctadecyloxy	22.674	12.29	
18	1,4-Epoxynaphthalene-1(2H)-methanol,4,5,7	28.411	4.20	
Tota	al	100%		

6.4.3 LC-MS analysis

Six hexane extracts of different honeys were analysed using LC-MS (Appendix C). The honey extracts showed differences in compound composition. The hexane extract of Little Bee honey which scored an inhibition percentage (I%) \geq 50% during urease inhibition assays in the previous chapter has 16 compounds positively identified according to mass error, isotope and library of Metabolite Pilot Software on Drug Discovery Software installed in the Triple TOFTM 5600 System Technology and DuosprayTM Ion Source system. The hexane extract of Little Bee honey (I% = 51.6% - 52.7%) and hexane extract of Q Bee honey (I% = 36.9% - 40.1%) both had 6 similar compounds in their matrix namely vardenafil, caproylresorcinol, hydrocortisone, altretamine, urapidil and oxeladin (Table 6.8). The 10 compounds that were found in hexane extract of Little Bee honey but not in other hexane

extracts of other honeys are clotiapine, sulfaquinoxaline, Lisinopril, raubasine, hydroxyquinoline, pilocarpine, levocabastine, aceclidine, diazoxide and benzylpenicillin (Table 6.8). There were 13, 5, 18, 14 and 16 compounds that were positively identified in hexane etracts of Raw honey, Gold Crest honey, Q Bee honey, Fleures honey and Siyakholwa honey respectively.

Table 6. 8: Compounds detected by positive mode of LC-MS in hexane extract of South African honey according to mass error, isotope and library scores

Raw Honey)	Goldcrest)	Q Bee	(Fleures)	Siyakholwa)	DHE (Little Bee)
ALL POSITIVE	ALL POSITIVE	ALL POSITIVE	ALL POSITIVE	ALL POSITIVE	ALL POSITIVE
(Mass error, isotope and	(Mass error, isotope and	(Mass error, isotope	(Mass error,	(Mass error, isotope	(Mass error, isotope
Library)	Library)	and Library)	isotope and Library)	and Library)	and Library)
			Library)		
Vardenafil	Trapidil	Vardenafil	Vincamine	Vardenafil	Vardenafil
Vincamine	Urapidil	Caproylresorcin ol	Yohimbine	Alprenolol	Clotiapine
Yohimbine	Pergolide	Alprenolol	Caproylresorc inol	Nandrolone	Sulfaquinoxalin e
Tamoxifen	Oxprenolol	Moxisylyte	Grepafloxaci n	Urapidil	Lisinopril
Urapidil	Benzoctamine	Amisulpride	Ropinirole	Diltiazem	Raubasine
Dihydralazine		Quinine	Oxymetazolin e	Adenine 7-	Caproylresorcin ol
Theophylline		Acetylsalicylam id	Pilocarpine	aminodesmethyl	Urapidil
Sulfalene		Chinine	•	flu	8-
Sulfamethoxypyrida			Urapidil Benzylpenicil	Vincamine	Hydroxyquinoli ne
Aceprometazine		Viquidil	lin	Yohimbine	Pilocarpine
•		Hydrocortisone	Moxisylyte	Tamoxifen	Hydrocortisone
Hydrocortisone		Altretamine	Floctafenine	Salsalate	21-ac
8-Hydroxyquinoline		Urapidil	Levobunolol		Altretamine
Azapropazone		Cyclovalone		Hydrocortisone	Levocabastine
			Etiroxate	Oxprenolol	A 11 11
		Oxeladin	Quinidine	Caproylresorcin ol	Aceclidine
		Theophylline		**	Diazoxide
		Theobromine		Flupentixol	Benzylpenicillin
		7-			Oxeladin
		Aminodesmethy Iflu			
		Buprofezin			
Total = 13	Total = 5	Total = 18	Total = 14	Total = 16	Total = 16

6.5 DISCUSSION

Acids, aldehydes, alcohol, ketones, terpenes, hydrocarbons, furans are chemical compounds that have been observed as components of honey in previous studies (Awaad et al., 2010; Alzahrani et al., 2012; Seanego et al., 2012). This current study, as well confirmed the presence of the named chemical compounds in honey extracts of South African honey. A compilation based on a spectral matching (≥ 90%) from NIST11 library was made on four petroleum extracts, two hexane extracts and three chloroform extracts. With reference to petroleum extract GC-MS analysis, Fleures honey, Gold Crest honey, Raw honey and Siyakholwa honey recorded 38.5%, 31%, 25.6% and 40.3% respectively, compounds that had 90% or greater spectral matching with the NIST11 library. Fleures honey and Gold Crest honey had an inhibition percentage above 50 % while Raw honey and Siyakholwa honey recorded an inhibition percentage (I%) that is less than 10%. However, the major difference in chemical composition was with Raw honey versus Fleures honey and Gold Crest but not Siyakholwa honey. hexatriacontane. hexadecanamide. dodecanamide. Octane. octadecanamide, decanamide, tetradecanamide, tetratriacontane, 2-methyloctacosane, cholesta-3,5-diene and cholesterol are compounds that were detected in Fleures honey, Gold Crest and Siyakholwa honey but not in Raw honey. If these compounds mattered the most towards urease inhibition, this could imply that an inhibition percentage of zero (0%) obtained by Siyakholwa extract of petroleum ether could be attributed to experimental error.

GC-MS analysis of Manuka honey and Siyakholwa honey extracts of hexane revealed a 51.2% and 28% respectively of NIST11.1 library matching greater or equal to 90%. Furthermore, Manuka honey had a urease inhibition percentage (I%) of 50–53.2% compared to 10.3–11.2% scored by Siyakholwa honey. Octane, hexatriacontane, dodecanamide, octadecanamide, decanamide, tetradecanamide, tetratriacontane, 2-methyloctacosane,

cholesta-3, 5-diene and with the exception of hexadecanamide and cholesterol are the compounds with spectral matching of 90% or greater with the NIST11 library in the hexane extract of Manuka honey which scored an inhibition percentage (I%) that is greater than 50%. However, the Siyakholwa honey extract of hexane possessed most of these compounds. Chloroform extracts were also analysed by GC-MS technique, 28.4 % of compounds in Raw honey chloroform extract had a 90% or greater spectral matching with the NIST11 library while 14.6% of the Siyakholwa honey chloroform extracts revealed a 90% or greater spectral matching with the NIST11 library. The chemical compounds that were recorded had a 90% or greater spectral matching with the NIST11 library which leaves out unknown compounds which might also have contributed to high urease inhibition percentage.

The honey extracts that exhibited 50% or more inhibition percentage (%) of urease kinetic activity had an enormous area percentage represented by eicosane, cholest-5-en-3-ol, 9-octadecanamide (Z), cholesteryl valerate, silane, diethylheptyloxyoctadecyloxy, hexatriacontane and 1,4-epoxynaphthalene- 1(2H)-methanol. Therefore, these named compounds seem to be potential candidates responsible for urease inhibition. However, this does not rule out the other compounds as potential candidates for urease inhibition. Nevertheless, the findings of this study suggest that honey possesses a pool of valuable compounds for the medical fraternity that aims to utilise urease inhibitors to control/treat infections caused by urease depended organism.

LC-MS is a sensitive instrument in detecting molecules (Kamakshi *et al.*, 2013). Several compounds were detected in South African honey based on mass error, isotope and library scores. The number of compounds detected by LC-MS per honey extract was dependent on the type of honey supporting the idea that compounds in honey depend on honey source or

geographical area from which the honey is harvested. However, the LC-MS analysis of drugs present in these honeys showed that agricultural activities such as pesticides application did not influence the medicinal value of the different types of honeys under study. This might be so because the majority of the compounds detected are not recommended as agricultural chemicals. Compounds that were detected include vardenafil, an oral drug used to treat impotence. This drug inhibits phosphodiesterase type 5 (PDE₅) resulting in an increased arterial blood leading to enlargement of corpus cavernosum (Ormrod et al., 2012). Also vincamine was detected and is a peripheral vasodilator leading to increase blood flow to the brain, mainly used to boost brainpower, memory and focus, this drug is a monoterpenoid indole alkaloid found in the leaves of Apocynaceae family (Na et al., 2016). Tamoxifen was also detected in Raw honey. This drug is used in the treatment of oestrogen receptor-positive breast cancer (Cuzick et al., 2015). Urapidil is an α-1-adrenoreceptor antagonist drug, important in lowering blood pressure (Grimm and Flack, 2011). In addition, dihydralazine can induce peripheral vasodilation resulting in lowered peripheral vascular resistance which leads to a drop in blood pressure (Yang et al., 2004). Hydrocortisone is a steroid hormone produced by the adrenal gland at a rate of 1mg/kg body mass per day under non-stressful conditions (Goding, 2009) and atretamine is a drug approved for minimising the symptoms of ovarian cancer (Kwon et al., 2009). Final, oxeladin also a common compound that was found in both Q Bee and Little Bee hexane extracts is a cough suppressant use to treat different cough etiologies (Zayed and Issa, 2013).

However, the detected drug such as sulfaquinoxaline, might have been incorporated into honey matrix through contaminated environment and water commonly visited by foraging bees. Sulfaquinoxaline is a sulphonamide antibiotic used in veterinary medicine, meat and poultry industries to treat coccidiosis a common protozoan disease (Adewole, 2012).

Administration of sulfaquinoxaline can be through drinking water or feed. Hydroxyquinoline has antiseptic, disinfectant and pesticide properties (Mandewale *et al.*, 2015). Due to such properties, hydroxyquinoline has been shown to be active in preserving longevity of cut Gerbera flowers (Banaee *et al.*, 2013).

Nevertheless, the identified compounds may act as bases for further studies in search of answers that will elucidate the anti-urease activity of honey extracts. While it remains difficult to pin point which compounds carry inhibitory activity towards urease, the identified compounds can be isolated and inhibition tests run on pure compounds so as to ascertain the effectiveness of individual compounds and combined effect of these compounds towards urease inhibition.

6.6 CONCLUSION

- South African honey serves as a rich source of natural compounds whose importance
 calls for further studies, in addition the compounds in South African honeys compared
 very well with Manuka honey which is well known for its high level of medicinal
 value.
- 2. The anti-urease activity of honey seems to be influenced by geographical area being foraged by bees and agriculturally used chemicals did not influence the urease inhibitory potential of honey extracts.

CHAPTER 7

7.1 GENERAL DISCUSSION

Research on the treatment success of *H. pylori* infections has been on-going for years, however the challenges surpass discovery of correct antibiotic combinations including the high cost of combination therapy to counteract drug resistance, therapy failures and adverse side effects. Also rescue drugs, such as tetracycline, quinolones, rifambutin or bismuth salts, are either contraindicated or not approved for children. However, there is a growing trend in research towards the use of new therapeutic approaches such as traditional medicines because of proven effectiveness. Several studies have shown that there are natural products with anti-*H. pylori* compounds (Manyi-Loh *et al.*, 2010; Manyi-Loh *et al.*, 2013; Nkomo *et al.*, 2011; Franklin *et al.*, 2012; Goswami *et al.*, 2012) and honey being one of the readily available natural products that has been shown to possess bactericidal activity on different species of pathogenic micro-organisms (Ndip *et al.*, 2007; Manyi-Loh *et al.*, 2010). Of interest, the prolonged use of honey seems not to result in eradication resistant patterns as its action is not mediated via a single mechanism (Mohammad and Mohammad, 2007).

While Warren and Marshal., (1983) were the first to discover *H. pylori* in the human stomach, and the first as well to show that infection of the human stomach by *H. pylori* causes gastritis, there are many studies that have looked into the pathogenesis of *H. pylori*. Several virulence factors have been outlined which include the cytoxin-associated gene A (cagA), vacuolating cytotoxin gene A (vacA) and the urease enzyme. The presence of the cagA gene has been shown to be associated with increased intensity of gastric inflammation leading to serious clinical outcomes (Miernyk et al., 2011; Papadakos et al., 2013). Also cagA is associated with development of gastric cancer, hence it is referred to as an oncogene (Pereira et al., 2014). The vacA gene is present in all strains and has two variable regions, the s and m

regions. There is variation of vacuolating rate due to heterogeneity within the vacA gene. The strains possessing allelic combinations s1/m1 and s1/m2 produce high and moderate toxin levels while s2/m2 has little or no toxin (Cogo $et\ al.$, 2011; Pereira $et\ al.$, 2014).

The urease enzyme is produced by *H. pylori* in enormous quantities and is known to catalyse conversion of urea to ammonia and carbon dioxide, resulting in neutralisation of the pH in the human stomach. There are studies that have reported that H. pylori devoid of urease have difficulties in colonising the acidic environment (Tsuda et al., 1994; Amin et al., 2010). The strain MP01 is a mutant devoid of urease enzyme. Its failure to withstand a small deviation of pH 7 to pH 6 which led to significant loss of viability of the strain supports earlier findings by Amin et al. (2010) where they reported that urease-negative mutant strain of H. pylori does not enhance gastritis due to challenges with colonisation. The urease enzyme was extracted from different strains, including a commercial Jack bean urease, of interest is that honey active compounds affected these ureases in a similar fashion, this support earlier reports that ureases from different sources possess similar structures (Seck et al., 2013). The mucus lining of the human stomach undergoes reversible pH dependent solution-gel transition from viscous polymer solution to a soft gel at low pH (Celli et al., 2009). This implies that if urease inhibitors are to be a target towards H. pylori infection management, incidences of H. pylori infections might drop dramatically because infecting cells will fail to move through the mucus layer and attach to the epithelial lay of the human stomach where H. pylori cells normally attach with the help of adhesins. Attachment by adhesins is important in helping the organism to dodge being automatically flushed out by the continual peristaltic movement of the digestive tract.

Different honey types seem to have different therapeutic advantages; otherwise antioxidant potential of honey seems to be directly related to floral source. Therefore, to obtain much more positive results pertaining antimicrobial activity of honey, floral source of both monofloral and hetero-floral honey needs consideration when searching and screening for the most active components of honey. Of interest, the prolonged use of honey seems not to result in eradication resistant patterns as its action is not mediated via a single mechanism (Mohammad and Mohammad, 2007). Therefore, this factor makes honey an important source of anti-*H. pylori* compounds if its mechanism of antibacterial action is understood.

The overall objective of the study was to identify honey extracts with anti-urease properties *in-vitro* and test their inhibitory potential on *cag*A positive, *vac*A positive and drug resistant *H. pylori* cultured under acidic environments, a mimicry of the human stomach. This study revealed that geographical location plays an important role in determining the medicinal value of honey. In South Africa, there are honey types that have urease inhibiting compounds i.e. petroleum ether extracts of Fleures honey and Gold Crest honey; the hexane extract of Little Bee honey; and the chloroform extract of Bush honey and Q Bee honey. Of importance is that the named South African honey extracts, compared very well with Manuka honey, a New Zealand product that has been well documented for its antibacterial activity.

The honey extracts with urease inhibiting activities were also used to determine the effect of inhibiting urease activity of *H. pylori* grown in acidic media. Strains of *H. pylori* possessing cagA, vacA and multidrug resistance properties were grown under controlled environments for 5 days. The observations made revealed that urease inhibitors can offset growth of *H. pylori* under acidic environments. The strains possessing cagA, vacA and drug resistance properties were affected in a similar manner which implies that targeting urease enzyme with

urease inhibitors as a way of treating *H. pylori* infection might be a success. Of importance is that the *in-vitro* analysis on urease inhibition is showing that current drug resistance patterns noticed with clarithromycin, amoxicillin, metronidazole and tetracycline is totally eliminated when using an approach that targets urease inhibition by solvent honey extracts to offset growth of *H. pylori* in acidic environments.

7.2 CONCLUSION

In line with the current study, the following can be drawn:

- 1. Treatment success with commonly used regimens for the treatment of *H. pylori* infections is under threat due to drug resistance.
- 2. *H. pylori* rely on the urease enzyme to survive the acidic gastric niche of the human host.
- 3. South African honeys are a source of valuable medicinal compounds with chemical constituents influenced by geographical location from which bees forage.
- 4. Inhibition of urease unavoidably impact negatively on the growth of *H. pylori* under acidic conditions.
- GC-MS and LC-MS are useful techniques of identifying compounds in fractions of solvent extracts.

7.3 RECOMMENDATIONS

- 1. Further studies involving more advanced separation techniques are required to purify the anti-urease active compounds in honey so as to identify the exact compounds responsible for urease inhibition.
- 2. Melissopalynogy studies need to be done to determine the original source of compounds.
- 3. More studies are needed to elucidate the mechanism of action by which honey extracts inhibit urease activities.
- 3. Toxicology experiments to evaluate suitability of the honey extracts on safety measures prior to clinical trials.
- 4. Also animal studies to determine the therapeutic potential of the identified compounds would be of importance prior to subsequent clinical evaluation.

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APPENDICES

APPENDIX A: BUFFERS

A 1: 36% HCl to 1M HCl

 Add 83.5 mL of 36% HCl acid to 600mL of deionised water in a 1L measuring cylinder and top up with deionised water to 1L.

A 2: 1M NaOH

- Dissolve 40 grams of NaOH in 1L deionised water.

A 3: Phosphate buffered saline (PBS) pH 7.4

NaCl	8g
KCl	0.2g
NaHPO ₄	1.44g
Kh_2PO_4	0.272g
Deionised water	800ml

- Adjust pH to 7.4 using HCl/NaOH before filling up to 1L with deionised water

A 4: 0.1 M potassium dihydrogen phosphate

- Dissolve 13.61g KH₂PO4 in 1000mL deionised water

A 5: 0.1M Disodium hydrogen phosphate

- Dissolve 17.8g Na₂HPO₄ in 1000mL of deionised water.

A 6: 10x TAE electrophoresis buffer

- Dissolve 48.4g of Tris base [tris(hydroxymethyl)aminomethane], 14.4mL of glacial acetic acid (17.4 M) and 3.7 EDTA, disodium salt in 1L deionised water.

A 7: Preparation of Tris-HCl buffer (50mM, pH 8) from 100X concentrate

-Ratio is 10 mL Tris-HCl buffer concentrate: 990 mL deionised water

A 8: Preparation of NADH (8.5 mM)

- Ratio: add 6.32757g of NADH to 1 L NaOH (0.01M) buffer

A 9: Preparation of α-ketoglutaric acid: 25mM

- Ratio: 3.65275g α-ketoglutaric acid : 1L of deionised water.

A 10: Preparation of 10U/mL of urease

- Weigh 1g of urease and add 10mL of Tris-HCl buffer

A11: Preparation of glutamate dehydrogenase (GLDH), 250u/mL

- Weigh 5.682 mg and add 10mL phosphate buffer

A12: Preparation of 0.3 M urea

- Weigh 18.018g urea and add 1 L of deionised water.

APPENDIX B: GC-MS QUALITATIVE ANALYSIS REPORT OBTAINED

FROM THE TOTAL ION COUNT (TIC)

B 1: Petroleum extract of Gold Crest honey

		Peak Report TIC						
Peak#	R.Time	Area	Area%	_	Height%	A/H Name		
1 2	4.655 5.035	16400976 26320774	0.85 1.36	16464410 21813930	2.35 3.11	1.00 Mesitylene 1.21 Nonane, 5-(2-methylpropyl)-		
3	5.075	22380949	1.16	18579715	2.65	1.20 Spiro[3.5]nona-5,7-dien-1-one, 5,9,9-trimethy		
4	5.272	17271472	0.89	13789079	1.97	1.25 Benzene, 1-ethyl-3,5-dimethyl-		
5	5.332	20637957	1.07	15112427	2.15	1.37 Undecane		
6	5.494	14967390	0.77	11404529	1.63	1.31 Benzene, 1,2,3,5-tetramethyl-		
7 8	5.520 5.733	20002441 23312308	1.03 1.20	17583325 12108313	2.51 1.73	1.14 Benzene, 1,2,3,5-tetramethyl- 1.93 Benzene, 1,2,4,5-tetramethyl-		
9	5.896	14835622	0.77	7498483	1.07	1.98 Ethanol, 1-(2-butoxyethoxy)-		
10	5.969	17879243	0.92	12024439	1.71	1.49 Dodecane		
11	6.004	17910191	0.93	12239880	1.74	1.46 Azulene		
12	6.346	12716936	0.66	6307082	0.90	2.02 Tetradecane, 5-methyl-		
13 14	6.429 6.564	25009414 18730104	1.29 0.97	14932093 9639668	2.13 1.37	1.67 Dodecane, 4,6-dimethyl- 1.94 Tetradecane		
15	6.693	21806144	1.13	11230527	1.60	1.94 Dodecane, 4-methyl-		
16	7.125	15134614	0.78	9480514	1.35	1.60 Tetradecane		
17	7.185	10285063	0.53	3935769	0.56	2.61 Tridecane, 6-methyl-		
18 19	7.376 7.445	11576837 20035414	0.60 1.03	3526697 6177599	0.50 0.88	3.28 Heptadecane 3.24 Hexadecane		
20	7.605	40102776	2.07	16424426	2.34	2.44 Eicosane		
21	7.651	17682964	0.91	10275029	1.46	1.72 Pentadecane		
22	7.712	16775828	0.87	7063938	1.01	2.37 Phenol, 2,4-bis(1,1-dimethylethyl)-		
23	7.830	34986943	1.81	14106506	2.01	2.48 Eicosane		
24 25	7.986 8.145	10497878 12340014	0.54 0.64	3519689 7064259	0.50 1.01	2.98 Eicosane 1.75 Hexadecane		
26	8.368	12576900	0.65	3887386	0.55	3.24 Heptadecane		
27	8.417	13476016	0.70	4859729	0.69	2.77 Eicosane		
28	8.491	14589113	0.75	5765066	0.82	2.53 Heptadecane		
29	8.548	10645318	0.55	4402774	0.63	2.42 Heptadecane		
30 31	8.633 8.671	46865375	2.42	15695787	2.24 1.03	2.99 Eicosane 2.43 Eicosane		
32	8.764	17574795 13959555	0.91 0.72	7242594 6004570	0.86	2.32 Octacosyl trifluoroacetate		
33	8.825	34303980	1.77	15948665	2.27	2.15 Eicosane		
34	8.926	25173776	1.30	5513184	0.79	4.57 Hexadecane, 1-iodo-		
35	9.059	16946545	0.88	4508315	0.64	3.76 Heptadecane		
36 37	9.233 9.302	17095657	0.88	6582938 4526358	0.94 0.65	2.60 Heneicosane 2.58 Eicosane		
38	9.414	11694965 18014361	0.60	7454132	1.06	2.42 Heneicosane		
39	9.464	14000156	0.72	6931150	0.99	2.02 Eicosane		
40	9.549	25320748	1.31	15911486	2.27	1.59 Eicosane		
41	9.579	19485276	1.01	11446221	1.63	1.70 Silane, trichlorooctadecyl-		
42 43	9.645 9.675	16211319 13488813	0.84 0.70	8807961 7166836	1.26 1.02	1.84 Benzenepropanoic acid, 3,5-bis(1,1-dimethylet		
44	9.720	23526929	1.22	14273879	2.03	1.88 Hexatriacontyl trifluoroacetate 1.65 Eicosane		
45	9.747	17385580	0.90	10687319	1.52	1.63 11-Bromoundecanoic acid		
46	9.787	12434041	0.64	6586489	0.94	1.89 Heneicosane		
47	9.817	12777863	0.66	6869209	0.98	1.86 Octadecanamide		
48 49	9.900 10.020	22721878 11306167	1.17 0.58	6141276 4207446	0.88 0.60	3.70 Eicosane 2.69 Eicosane		
50	10.020	23184722	1.20	4936521	0.70	4.70 Eicosane		
51	10.161	18219509	0.94	4875585	0.69	3.74 Hexadecane, 1-iodo-		
52	10.241	36907940	1.91	8350229	1.19	4.42 Eicosane		
53	10.374	42127753	2.18	12992811	1.85	3.24 Eicosane		
54 55	10.449 10.529	30202664 37915236	1.56 1.96	11574558 13500978	1.65 1.92	2.61 cis-13,16-Docasadienoic acid 2.81 Eicosane		
56	10.612	15697733	0.81	11411002	1.63	1.38 Hexadecanamide		
57	10.635	16158648	0.83	7680535	1.09	2.10 Heneicosane		
58	10.712	16777387	0.87	5024821	0.72	3.34 Cholest-5-en-3-ol (3.beta.)-, 3,5-dinitrobenzoa		
59 60	10.775	10482492	0.54 1.69	5810194	0.83 2.07	1.80 Eicosane		
61	10.805 10.860	32769513 13495992	0.70	14526973 6281952	0.90	2.26 Octadecanoic acid, 2-hydroxyethyl ester 2.15 Tetratetracontane		
62	11.003	28088346	1.45	7172022	1.02	3.92 Tetratetracontane		
63	11.043	10422857	0.54	5260146	0.75	1.98 Tetratetracontane		
64	11.095	16693815	0.86	5584149	0.80	2.99 Eicosane		
65 66	11.141 11.315	31666273 96736032	1.64 5.00	9175927 30140432	1.31 4.30	3.45 Eicosane 3.21 9-Octadecenamide, (Z)-		
67	11.388	12020644	0.62	5294031	0.75	2.27 Bis(dodecanamido)methane		
68	11.544	10425134	0.54	3345373	0.48	3.12 Cholesta-3,5-diene		
69	11.605	22515928	1.16	5524752	0.79	4.08 Octadecanoic acid, 2-hydroxyethyl ester		
70	11.808	10797201	0.56	3423877	0.49	3.15 Heneicosane		
71 72	11.857 12.006	18897517 30685361	0.98 1.59	3983436 4710909	0.57 0.67	4.74 Hexatriacontane 6.51 Bis(tridecyl) phthalate		
73	12.183	12340975	0.64	3318037	0.47	3.72 2-methylhexacosane		
74	12.268	11703250	0.60	3081905	0.44	3.80 Hexadecane, 1-iodo-		
75	12.385	11146850	0.58	2357107	0.34	4.73 Cholest-5-en-3-ol (3.beta.)-, nonanoate		
76	14.390	6404605	0.33	2736747	0.39	2.34 Cholesta-3,5-diene		
77 78	14.750 22.594	44951463 67100710	2.32	13420856 7840155	1.91	3.35 Cholesta-3,5-diene 8.55 Silane, diethylhentylogynotydecylogy-		
78 79	28.243	67109710 22453261	3.47 1.16	7849155 2184559	1.12 0.31	8.55 Silane, diethylheptyloxyoctadecyloxy- 10.28 1,4-Epoxynaphthalene-1(2H)-methanol, 4,5,7-		
80	30.274	4381239	0.23	446999	0.06	9.80 Propanoic acid, 3,3'-thiobis-, didodecyl ester		
81	86.515	237527641	12.27	1315773	0.19	180.52 Cholest-5-en-3-ol (3.beta.)-, 9-octadecenoate,		
82	87.317	13832939	0.71	552705	0.08	25.03 Longifolenaldehyde		
		1935916008	100.00	701568152	100.00			

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B 2: Petroleum extract of Fleures honey

					Peak Rep	ort TIC
Peak#	R.Time	Area	Area%	Height	Height%	A/H Name
1	4.651	14877252	0.86	15582063	3.28	0.95 Mesitylene
-2 -3	5.031 5.070	21234601 18471921	1.22	18010715 15978645	3.79 3.37	1.18 Pentadecane 1.16 Spirot2 Shows 5.7 diem 1 and 5.0.0 trimethy.
4	5.267	15107383	0.87	11871373	2.50	 Spiro[3.5]nona-5,7-dien-1-one, 5,9,9-trimethy. Benzene, 1-ethyl-3,5-dimethyl-
3	5.327	15856301	0.91	12434156	2.62	1.28 Undecane
6	5.489	12227900	0.70	9907490	2.09	1.23 Benzene, 1,2,3,5-tetramethyl-
7	5.514	15788308	0.91	15211003	3.20	1.04 Benzene, 1,2,3,5-tetramethyl-
8	5.728 5.965	18399722 13678323	1.06 0.79	9752151 9687890	2.05 2.04	1.89 Benzene, 1,2,4,5-tetramethyl- 1.41 Dodecane
10	6.000	14879303	0.79	10174171	2.14	1.46 Naphthalene
ñ	6.424	17291112	1.00	10724896	2.26	1.61 Dodecane, 4,6-dimethyl-
12	6.559	12977785	0.75	6522005	1.37	1.99 Tetradecane
13	6.689	15195754	0.88	8099491	1.71	1.88 Dodecane, 4-methyl-
14 15	7.120 7.440	10267174 13824140	0.59 0.80	6273682 4456858	1.32 0.94	1.64 Tetradecane 3.10 Eicosane
16	7.599	26343003	1.52	12211539	2.57	2.16 Eicosane
17	7.646	11892463	0.68	7001775	1.47	1.70 Pentadecane
18	7.708	12189287	0.70	4611363	0.97	2.64 Phenol, 2,4-bis(1,1-dimethylethyl)-
19	7.825	24677399	1.42	10502377	2.21	2.35 Eicosane
20	8.487 8.628	10153813	0.58	4020298	0.85 2.52	2.53 Heneicosane
21 22	8.760	33138368 10385121	1.91 0.60	11939384 4187480	0.88	2.78 Eicosane 2.48 Docosyl pentafluoropropionate
23	8.821	23776143	1.37	10822822	2.28	2.20 Eicosane
24	8.905	15869668	0.91	3786271	0.80	4.19 Nonane, 5-methyl-5-propyl-
25	9.054	11180279	0.64	3047688	0.64	3.67 Heptadecane
26	9.229	13898349	0.80	4508266	0.95	3.08 Eicosane
27 28	9.410 9.544	11019076 18802772	0.63 1.08	5322615 12235134	1.12 2.58	2.07 Eicosane 1.54 Eicosane
29	9.573	17199634	0.99	8118769	1.71	2.12 Silane, trichlorooctadecyl-
30	9.714	26652049	1.54	10400151	2.19	2.56 Eicosane
31	9.895	17779985	1.02	4157621	0.88	4.28 Eicosane
32	10.078	11739019	0.68	3371933	0.71	3.48 Hexadecane, 1-iodo-
33 34	10.152 10.236	12548231 26448657	0.72 1.52	3372532 5722874	0.71 1.21 _	3.72 Octadecane, 1-chloro- 4.62 Eicosane
35	10.368	29473716	1.70	10570940	2.23	2.79 Eicosane
36	10.443	11517846	0.66	5301356	1.12	2.17 E,E,Z-1,3,12-Nonadecatriene-5,14-diol
37	10.533	42593305	2.45	11098160	2.34	3.84 Bis(dodecanamido)methane
38	10.600	19342940	1.11	10007004	2.11	1.93 Hexadecanamide
39 40	10.632 10.727	11198451 12440884	0.65 0.72	5382848 3397328	1.13 0.72 _	2.08 Hexadecane, 1-iodo- 3.66 Cholesta-3,5-diene
41	10.819	34250021	1.97	7944187	1.67	4.31 Octadecanoic acid, 2-hydroxyethyl ester
42	10.997	20660393	1.19	5912932	1.25 _	3.49 Tetratetracontane
43	11.091	14553744	0.84	4981239	1.05	2.92 Tetratetracontane
44 45	11.135 11.163	14516567 13212243	0.84 0.76	7981125 5406010	1.68	1.82 Eicosane
46	11.309	102001375	5.88	31978246	1.14 6.74	2.44 Cholest-5-ene, 3-ethoxy-, (3.beta.)- 3.19 9-Octadecenamide, (Z)-
47	11.382	11720876	0.68	5266061	1.11	2.23 Octadecanamide
48	11.538	16259910	0.94	3048388	0.64	5.33 Cholest-5-en-3-ol (3.beta.)-, 3,5-dinitrobenzoa
49	11.648	30806333	1.77	4573369	0.96	6.74 Octadecanoic acid, 2-hydroxyethyl ester
50 51	11.742 11.851	12767808 12732906	0.74 0.73	3225518 4022600	0.68 0.85	3.96 Cholesta-3,5-diene 3.17 Hexadecane. 1-iodo-
52	12.000	34126762	1.97	5868492	1.24	5.82 Bis(tridecyl) phthalate
53	12.179	14091257	0.81	3697852	0.78	3.81 Tetratetracontane
54	12.224	11094576	0.64	4422430	0.93	2.51 Eicosane
55	12.261	13547825	0.78	3426431	0.72	3.95 Hexatriacontane
56	12.391	11877170	0.68	2564494	0.54	4.63 5,5-Diethylheptadecane
57 58	13.492 14.717	12800840 32335258	0.74 1.86	2572728 9430406	0.54 1.99	4.98 13-Docosenamide, (Z)- 3.43 Cholesta-3,5-diene
59	22.531	59463291	3.43	7237503	1.52	8.22 Silane, diethylheptyloxyoctadecyloxy-
60	28.163	21925658	1.26	2103157	0.44	10.43 1,4-Epoxynaphthalene-1(2H)-methanol, 4,5,7-
61	85.148	186289946	10.73	2399357	0.51	77.64 Cholesteryl valerate
62	85.345	23242043	1.34	2205971	0.46	10.54 3Beta-methoxy-5-cholesten-19-oic acid
63 64	86.493 86.870	162334008 177177773	9.35 10.21	2421764 2238954	0.51 0.47	67.03 Cholesterol, pentafluoropropionate 79.13 Cholesteryl valerate
04	00.070	1736126020	100.00	474714331	100.00	79.10 Castestery variate

B 3: Hexane extract of Manuka honey

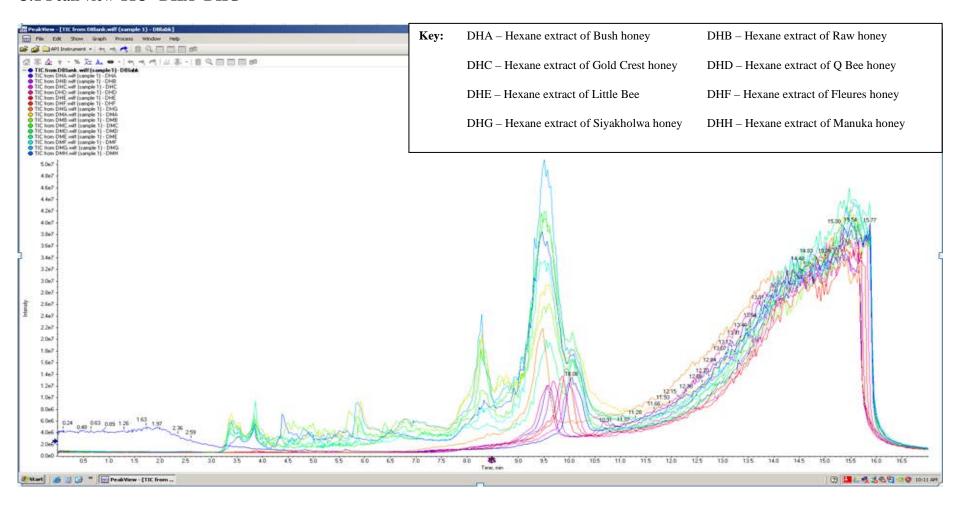
					Peak Rey	oort TIC
Peak#	R.Time	Area	Area%	Height	Height%	A/H Name
1 2	3.596 4.118	3155427 2405530	0.58 0.44	2098612 2773939	0.85 1.12	1.50 0.87
3	4.426	5030864	0.92	4802600	1.12	1.05
4	4.880	2360391	0.43	2043366	0.83	1.16
5	5.016	8542635	1.57	8786982	3.55	0.97
6	5.054	3823808	0.70	3576786	1.45 2.01	1.07
7 8	5.314 5.350	5612964 2483237	1.03 0.46	4974876 2319810	0.94	1.13 1.07
9	5.400	2283859	0.42	1168207	0.47	1.96
10	5.498	2868613	0.53	1655746	0.67	1.73
11	5.716	2804503	0.52	1518213	0.61	1.85
12 13	5.877 5.952	4515788 4089032	0.83 0.75	2465075 2124257	1.00 0.86	1.83 1.92
14	5.990	2305535	0.42	1719989	0.70	1.34
15	6.030	2564217	0.47	1287569	0.52	1.99
16	6.202	2380622	0.44	1332678	0.54	1.79
17 18	6.275 6.329	3803217 4179176	0.70 0.77	1237961 2196459	0.50 0.89	3.07 1.90
19	6.411	11691825	2.15	7252429	2.93	1.61
20	6.462	3190348	0.59	2110123	0.85	1.51
21	6.497	2818667	0.52	1847594	0.75	1.53
22 23	6.542 6.676	6104181 8478054	1.12 1.56	2622243 4999517	1.06 2.02	2.33 1.70
24	6.731	2608037	0.48	1560488	0.63	1.67
25	6.780	2409752	0.44	1594096	0.64	1.51
26	7.108	3610021	0.66	2481028	1.00	1.46
27 28	7.169 7.428	4996751 5351795	0.92 0.98	1199183 2008354	0.49 0.81	4.17 2.66
29	7.586	16261512	2.99	7501098	3.03	2.17
30	7.633	5773812	1.06	3610723	1.46	1.60
31	7.665	2660307	0.49	1650832	0.67	1.61
32	7.693	3174452	0.58	2251190	0.91	1.41
33 34	7.813 7.863	15486192 2789438	2.84 0.51	6280465 1995716	2.54 0.81	2.47 1.40
35	7.913	2393473	0.44	1551229	0.63	1.54
36	7.969	2812019	0.52	1267582	0.51	2.22
37	8.127	2489860	0.46	2266558	0.92	1.10
38 39	8.157 8.350	2550614 3110348	0.47 0.57	15426 <u>7</u> 9 1269491	.0.62 0.51	1.65 2.45
40	8.400	3950378	0.73	1548967	0.63	2.55
41	8.475	4489489	0.82	2185221	0.88	2.05
42 43	8.515	3570001	0.66 3.55	1450202	0.59	2.46
44	8.614 8.654	19354591 4177492	0.77	7957534 2826537	3.22 1.14	2.43 1.48
45	8.746	5074309	0.93	2112960	0.85	2.40
46	8.807	14580979	2.68	7275337	2.94	2.00
47 48	8.850 8.910	3169317 5964696	0.58 1.10	2246139 1840232	0.91 0.74	1.41 3.24
49	8.960	4264366	0.78	2203254	0.89	1.94
50	9.039	3284638	0.60	1523067	0.62	2.16
51	9.128	2898214	0.53	920504	0.37	3.15
52 53	9.215 9.280	3860292 2585186	0.71 0.47	2223155 1204713	0.90 0.49	1.74 2.15
55 54	9.280	2886098	0.47	1526090	0.49	1.89
55	9.396	4623734	0.85	2618735	1.06	1.77
56	9.445	5809526	1.07	2151559	0.87	2.70
57 58	9.530 9.560	12448901 8404795	2.29 1.54	7189501 5650309	2.91 2.29	1.73 1.49
59	9.626	4390648	0.81	2828237	1.14	1.55
60	9.655	4688218	0.86	2262874	0.92	2.07
61	9.700	13909298	2.55	6636693	2.68	2.10
62 63	9.792 9.882	7353470 5329005	1.35 0.98	2055431 1931713	0.83 0.78	3.58 2.76
64	10.220	10055350	1.85	2437564	0.99	4.13
65	10.354	8855113	1.63	5287722	2.14	1.67
66	10.380	3528190	0.65	2149953	0.87	1.64
67 68	10.480 10.518	6466418 13753315	1.19 2.53	2362376 7136697	0.96 2.89	2.74 1.93
69	10.585	8411165	1.54	5638015	2.28	1.49
70	10.635	3715113	0.68	1709822	0.69	2.17
71 72	10.807	11265505	2.07 0.86	1922278 2102550	0.78 0.85	5.86 2.23
73	10.984 11.075	4694378 4664736	0.86	1357438	0.85	3.44
74	11.118	5695200	1.05	3412883	1.38	1.67
75	11.150	2357903	0.43	1537444	0.62	1.53
76 77	11.309 11.370	67704564 4058078	12.43 0.75	20178939 2270515	8.16 0.92	3.36 1.79
78	11.987	2425883	0.75	1055945	0.43	2.30
79	13.451	3037801	0.56	1238750	0.50	2.45
80	14.648	3803451	0.70	1772154	0.72	2.15
81 82	22.291 28.135	9227437 43792012	1.69 8.04	1292681 3064040	0.52 1.24	7.14 14.29
02	20.133	544550129	100.00	247242473	100.00	27.23

B 4: Chloroform extract of Q Bee honey

Peak# R Time						Peak Rej	port TIC	
2 7.830 2390731 1.58 1131640 2.32 2.11 Eicosame 3 8.634 2991472 1.98 1968532 4.04 1.52 Eicosame 4 8.829 2841721 1.88 1629013 3.34 1.74 Eicosame 5 8.915 1562360 1.03 397199 0.82 3.93 Noname, 5-methyl-5-propyl- 6 9.554 2700481 1.78 2094341 4.30 1.29 Eicosame 7 9.584 1838091 1.21 1093911 2.25 1.68 Silme, trichlorooctadecyl- 8 9.725 2367689 1.56 1726608 3.54 1.37 Eicosame 9 9.749 2624520 1.73 1415993 2.91 1.85 Pentadecanoic acid 10 10.249 2799896 1.85 760033 1.56 3.68 Eisosame 11 10.381 4059280 2.68 1899454 3.90 2.14 Eicosame 12 10.534 6149473 4.06 1968951 4.04 3.12 Eicosame 13 10.620 2877749 1.90 970550 1.99 2.97 Cadadecanomide 14 10.813 2952856 1.95 1353493 2.78 2.18 Octadecanomide 15 11.019 2460055 1.62 882941 1.81 2.79 Herschitzoortane 16 11.113 1669465 1.10 669652 1.37 2.49 Eicosame 17 11.153 4335929 2.86 1450926 2.98 2.99 Eicosame 18 11.314 22336836 14.75 8465906 17.37 2.49 Eicosame 19 11.611 2960820 1.96 897028 1.84 3.30 Octadecanoic acid, 2-hydroxyethyl ester 20 11.720 9876224 6.52 3326395 6.83 2.97 1.3,5-Trisilacyclohexame 21 11.822 4864848 3.21 1327537 2.72 3.66 1H-Indene, 1-hersadecyl-2,3-dihydro- 21 11.822 4864848 3.21 1327537 2.72 3.66 1H-Indene, 1-hersadecyl-2,3-dihydro- 22 11.873 4806114 3.17 1214045 2.49 3.96 Squalame 23 11.948 4122064 2.73 1280246 2.63 3.23 Hexadecanoic acid, 2-hydroxyethyl ester 24 12.039 5736947 3.79 958131 1.97 5.99 Hexatriacontane 25 12.210 2519369 1.66 684321 1.40 3.68 5,5-Diethylpentadecane 26 12.255 2350934 1.55 945177 1.94 2.49 5,5-Diethylpentadecane 27 12.294 2801099 1.85 734412 1.51 3.81 5,5-Diethylpentadecane 28 12.763 3642084 2.41 647344 1.33 5.63 1,3,5-Trisilacyclohexame 30 13.018 2077340 1.37 382760 0.79 5.43 Squalame 31 1.558 3314008 2.19 414478 0.85 8.00 2-methylpentadecane 31 1.544 4021092 2.66 1106722 2.27 3.63 Cholesta-3,5-dieme 32 14.744 4021092 2.66 1106722 2.27 3.63 Cholesta-3,5-dieme 33 22.674 18611831 12.29 54242068 5.01 7.62 Silane, diethylpentyloxyoctadecyloxy-	Peak#	R.Time	Area	Area%	Height	Height%	A/H	Name
3 8.634 2991472 1.98 1968532 4.04 1.52 Eicosane 4 8.829 2841721 1.88 1629013 3.34 1.74 Eicosane 5 8.915 1562360 1.03 397199 0.82 3.99 Norman 2.97 6 9.554 2700481 1.78 2094341 4.30 1.29 Eicosane 7 9.584 1838091 1.21 1093911 2.25 1.68 Silane, trichlorooctadecyl- 8 9.725 2367689 1.56 1726608 3.54 1.37 Eicosane 9 9.749 2624520 1.73 1415093 2.91 1.85 Pentadecanoic acid 10 10.249 2799896 1.85 760033 1.56 3.68 Eicosane 11 10.381 4059280 2.68 1899454 3.90 2.14 Eicosane 12 10.534 6149473 4.06 1968951 4.04 3.12 <td>1</td> <td>7.604</td> <td>2810308</td> <td></td> <td>1482470</td> <td>3.04</td> <td>1.90</td> <td>Eicosane</td>	1	7.604	2810308		1482470	3.04	1.90	Eicosane
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22 11.873 4806114 3.17 1214045 2.49 3.96 Squalane 23 11.948 4129064 2.73 1280246 2.63 3.23 Hexadecanoic acid, 2-hydroxy-1-(hydroxymet) 24 12.039 5736947 3.79 958131 1.97 5.99 Hexatriacontane 25 12.210 2519369 1.66 684321 1.40 3.68 5,5-Diethylpentadecane 26 12.255 2350934 1.55 945177 1.94 2.49 5,5-Diethylpentadecane 27 12.294 2801099 1.85 734412 1.51 3.81 5,5-Diethylpentadecane 28 12.763 3642084 2.41 647344 1.33 5.63 1,3,5-Trisilacycloherane 29 12.891 1588659 1.05 407568 0.84 3.90 Oxalic acid, 3,5-diffuorophenyl tetradecyl este 30 13.018 2077340 1.37 382760 0.79 5.43 Squalane 31 13.558 33								
23 11.948 4129064 2.73 1280246 2.63 3.23 Hexadecanoic acid, 2-hydroxy-1-(hydroxymet) 24 12.039 5736947 3.79 958131 1.97 5.99 Hexatriacontane 25 12.210 2519369 1.66 684321 1.40 3.68 5,5-Diethylpentadecane 26 12.255 2350934 1.55 945177 1.94 2.49 5,5-Diethylpentadecane 27 12.294 2801099 1.85 734412 1.51 3.81 5,5-Diethylpentadecane 28 12.763 3642084 2.41 647344 1.33 5.63 1,3,5-Trisilacyclohexane 29 12.891 1588659 1.05 407568 0.84 3.90 Oxalic acid, 3,5-diffuorophenyl tetradecyl este 30 13.018 2077340 1.37 382760 0.79 5.43 Squalane 31 13.558 3314008 2.19 414478 0.85 8.00 2-methylhexacosane 32 14.744								
24 12.039 5736947 3.79 958131 1.97 5.99 Hexatriacontane 25 12.210 2519369 1.66 684321 1.40 3.68 5,5-Diethylpentadecane 26 12.255 2350934 1.55 945177 1.94 2.49 5,5-Diethylpentadecane 27 12.294 2801099 1.85 734412 1.51 3.81 5,5-Diethylpentadecane 28 12.763 3642084 2.41 647344 1.33 5.63 1,3,5-Trisilacyclohertane 29 12.891 1588659 1.05 407568 0.84 3.90 Oxalic acid, 3,5-diffuorophenyl tetradecyl este 30 13.018 2077340 1.37 382760 0.79 5.43 Squalane 31 13.558 3314008 2.19 414478 0.85 8.00 2-methylhexacosane 32 14.744 4021092 2.66 1106722 2.27 3.63 Cholesta-3,5-diene 33 22.674 18611831								
25 12.210 2519369 1.66 684321 1.40 3.68 5,5-Diethylpentadecane 26 12.255 2350934 1.55 945177 1.94 2.49 5,5-Diethylpentadecane 27 12.294 2801099 1.85 734412 1.51 3.81 5,5-Diethylpentadecane 28 12.763 3642084 2.41 647344 1.33 5.63 1,3,5-Trisilacyclohexane 29 12.891 1588659 1.05 407568 0.84 3.90 Oxalic acid, 3,5-diffuorophenyl tetradecyl este 30 13.018 2077340 1.37 382760 0.79 5.43 Squalane 31 13.558 3314008 2.19 414478 0.85 8.00 2-methylbexacosane 32 14.744 4021092 2.66 1106722 2.27 3.63 Cholesta-3,5-diene 33 22.674 18611831 12.29 2442068 5.01 7.62 Silane, dierhylberyloxyoctadecyloxy- 34 28.411								
26 12.255 2350934 1.55 945177 1.94 2.49 5,5-Diethylpentadecane 27 12.294 2801099 1.85 734412 1.51 3.81 5,5-Diethylpentadecane 28 12.763 3642084 2.41 647344 1.33 5.63 1,3,5-Trisilacyclohertane 29 12.891 1588659 1.05 407568 0.84 3.90 Oxalic acid, 3,5-diffuorophenyl tetradecyl este 30 13.018 2077340 1.37 382760 0.79 5.43 Squalane 31 13.558 3314008 2.19 414478 0.85 8.00 2-methylhexacosane 32 14.744 4021092 2.66 1106722 2.27 3.63 Cholesta-3,5-diene 33 22.674 18611831 12.29 2442068 5.01 7.62 Silane, diethylheptyloxyctadecyloxy- 34 28.411 6354534 4.20 595229 1.22 10.68 1,4-Epoxynaphthalene-1(2H)-methanol, 4,5,7-								
27 12.294 2801099 1.85 734412 1.51 3.81 5/5-Diethylpentadecane 28 12.763 3642084 2.41 647344 1.33 5.63 1,3,5-Trisilacyclohertane 29 12.891 1588659 1.05 407568 0.84 3.90 Oxalic acid, 3,5-diffuorophenyl tetradecyl este 30 13.018 2077340 1.37 382760 0.79 5.43 Squalane 31 13.558 3314008 2.19 414478 0.85 8.00 2-methylhexacosane 32 14.744 4021092 2.66 1106722 2.27 3.63 Cholesta-3,5-diene 33 22.674 18611831 12.29 2442068 5.01 7.62 Silane, diethylheptyloxyoctadecyloxy- 34 28.411 6354534 4.20 595229 1.22 10.68 1,4-Epoxynaphthalene-1(2H)-methanol, 4,5,7-								
28 12.763 3642084 2.41 647344 1.33 5.63 1,3,5-Trisilacyclohestane 29 12.891 1588659 1.05 407568 0.84 3.90 Oxalic acid, 3,5-diffuorophenyl tetradecyl ester 30 13.018 2077340 1.37 382760 0.79 5.43 Squalane 31 13.558 3314008 2.19 414478 0.85 8.00 2-methylhexacosane 32 14.744 4021092 2.66 1106722 2.27 3.63 Cholesta-3,5-diene 33 22.674 18611831 12.29 2442068 5.01 7.62 Silane, diethylheptyloxyoctadecyloxy- 34 28.411 6354534 4.20 595229 1.22 10.68 1,4-Epoxynaphthalene-1(2H)-methanol, 4,5,7-								
29 12.891 1588659 1.05 407568 0.84 3.90 Oxalic acid, 3,5-diffuorophenyl tetradecyl ester 30 13.018 2077340 1.37 382760 0.79 5.43 Squalane 31 13.558 3314008 2.19 41.4478 0.85 8.00 2-methylhexacosane 32 14.744 4021092 2.66 1106722 2.27 3.63 Cholesta-3,5-diene 33 22.674 18611831 12.29 2442068 5.01 7.62 Silane, diethylheptyloxyoctadecyloxy-34 28.411 6354534 4.20 595229 1.22 10.68 1,4-Epoxynaphthalene-1(2H)-methanol, 4,5,7-								
30 13.018 2077340 1.37 382760 0.79 5.43 Squalane 31 13.558 3314008 2.19 414478 0.85 8.00 2-methylhexacosane 32 14.744 4021092 2.66 1106722 2.27 3.63 Cholesta-3,5-diene 33 22.674 18611831 12.29 2442068 5.01 7.62 Silane, diefnylheptyloxyoctadecyloxy- 34 28.411 6354534 4.20 595229 1.22 10.68 1,4-Epotynaphthalene-1(2H)-methanol, 4,5,7-								
31 13.558 3314008 2.19 414478 0.85 8.00 2-methylhexacosane 32 14.744 4021092 2.66 1106722 2.27 3.63 Cholesta-3,5-diene 33 22.674 18611831 12.29 2442068 5.01 7.62 Silane, diethylheptyloxyoctadecyloxy- 34 28.411 6354534 4.20 595229 1.22 10.68 1,4-Epoxynaphthalene-1(2H)-methanol, 4,5,7-								
32 14.744 4021092 2.66 1106722 2.27 3.63 Cholesta-3,5-diene 33 22.674 18611831 12.29 2442068 5.01 7.62 Silane, diethylheptyloxyoctadecyloxy- 34 28.411 6354534 4.20 595229 1.22 10.68 1,4-Epoxynaphthalene-1(2H)-methanol, 4,5,7-								
33 22.674 18611831 12.29 2442068 5.01 7.62 Silane, diefnylheptyloxyoctadecyloxy- 34 28.411 6354534 4.20 595229 1.22 10.68 1,4-Epoxynaphthalene-1(2H)-methanol, 4,5,7-								
34 28.411 6354534 4.20 595229 1.22 10.68 1,4-Epoxynaphthalene-1(2H)-methanol, 4,5,7-								
	24	20.721	151423879	100.00	48725074	100.00	20.00	4, 1 aport juliproduction a (as a) tantamitor, 4,5,1

APPENDIX C: LC-MS RESULTS ANALYSIS USING METABOLITE PILOTE SOFTWARE ON DRUG DISCOVERY

C:1 Peak view TIC -DHA- DHG



C: 2 XIC manager (DHC- Hexane extract of Gold Crest wiff sample 1)

Manage														NI.		
С	1111.	None	Formula	leolope	Mess (Dx)	Adduct / Modifications	Extraction Mass (De)	Vridin (Ow)	Found At Mann (Da)	Error (ppm)	Expected RT (min)	RT (vlidth (min)	Found At RT (min)	Intensity	Library Hit	Purity Score
E ST		Sufequinoseline	C14H12N402S	0	300 0681	481	301,07537	0.01	201.07476	- 2	0	2.	13.5	14054	Sulleganossine	38.0
P		Alprenolol	C15H23N02	0	249.17288	+11.	250.50016	0.01	250 17567	-2.3	0	2	334	9624	Alprendel	61.1
R		Trapidli	C10H15N5	0	205.13275	4H	206.14002	0.01	206 13923	-0.1	0	2.	15.83	6416	Topidi	38.3
P		Histidine	C6H9N302	0	155,06948	+84	156,07679	0.01	156,07668	-0.5	0	2	15.9	3330	Heldre	16.2
2	• • •	Unpdi	C29H29H5O3	0	387,22704	+H	300.23432	0.01	3012326	-44	0	2.	10.43	2505	Unpidd	75.0
P		Pergolide	C19400002S	0	314.15167	+01	315.10195	0.01	316,38001	-0.5	0	2	12.07	1882	Perpolde	93.5
R		Fludrocortisone Acetz	CZSHSTFOR	0	422.21047	+H	423.21778	0.01	423.21894	26	0	2.	8.79	1339	Fluidrocortisone Acess	100
P		Caproylesoronol	C12H1603	0	208.10994	+81	209.11722	0.01	209 11725	0.1	0	2	5438	6660	Capoyteoconii	38.7
P.		Dignenoloi	C15H23NQ3	0	265.16779	+H	266.17507	0.01	296 17295	-0.1	0	2.	12.03	3431	Organold	67,9
P	•	Dosazosini	C32H43N505	0	577 32542	+01.	579.3337	0.01	57833429	3	0	2	3.45	3000	Dhydroegokryptow	60.8
R		Berandamine	CIGHIGH	0	349.15175	4H	250.15907	0.01	250 16035	53	0	2.	9.14	2122	Sercoctanine	\$1.0
P		Adenosine	C10H13N504	0	267.09675	+24	268.10403	0.01	268.10362	-15	0	2	7.00	1646	Adentisins	99.9
2		3.4-Methylenedoxym	C11H15NO2	0	193,11029	+H	194.11796	0.01	194 11754	-0.1	0	2.	15.17	271107		
P		2.4-Methylenedoxyar	C10H13N02	0	179.09463	+01.	350,10191	0.01	180,10167	-13	0	2	13.76	110024	Proben	26.6
R		Desamethasone	C22H29F06	0	392.1999	+H	393.20718	0.01	293.2082	26	0	2.	18.02	64796		
P		Diaveridos	C13H16N402	0	260.12733	+84	251.134E	0.01	251.13065	-913	0	2	8.54	37775	Daverdon	100
2		Flufenamic Acid	C24H30F2O6	0	452,20105	486	453.20832	0.01	410.20062	0.7	0	2.	9.13	36836	Fluorolone Acatons	11.7
P		Verlataure	C17H27N02	0	277.20418	+01.	279.25146	0.01	276.21121	-0.9	0	2	13.97	32168		
2		Berzocere	C9H11NO2	0	165,07896	+H	166.00636	0.01	166.00614	-0.7	0	2.	8.32	16706		
P		Etherzanide	C9H11N02	0	165.07896	+81	166,00625	0.01	166.08614	-0.7	0	2	8.32	16706		
2		Aceprometazine	C19H22NQOS	0	326.14529	486	327,15296	0.01	327,19434	112	0	2.	13.06	17934	Запропасня	.04
R.		Acepromissine	C19H22NQO5	0	326.14529	+01.	327.15256	0.01	327.55624	11.2	0	2	13.06	17934	Ampromative	.04
R		Bunitold	C14H20N202	0	248.15248	+H	249.15975	0.01	249 15687	-11.6	0	2.	9.14	13232	Pindolol	60.5
P		Pindolol	C14H20N2O2	0	248.15248	+81	249.19975	0.01	249 15687	-11.6	0	1	3.14	13232	Pindolol	60.5
2		Bunazonin	C34H50O7	0	570.05565	+H	571.36293	0.01	571.36342	0.9	0	2.	15.83	11529		
P		Mexistine	C11H17N0	0	179.13101	+01.	380,13029	0.01	180 13836	0.3	0	2	35.37	11334		
D.		Ni-Methylephedrine	C11H17ND	0	179.13101	+14	180.13829	0.01	100 13835	0.3	0	2.	15.37	11384		
P		Methylephodone	C11H17N0	0	179.13101	+84	100.13029	0.01	100 13036	0.3	0	1	15.37	11334		
2		Azapropazone	C16H20NH02	0	300.15863	+H	301.1658	0.01	201.16477	-0.8	0	2.	14.12	10011		
P		National Institution	C24H33NO3	0	383.24504	+01	364.25332	0.01	384.25256	- 4	0	2	13.75	10000	No March	No Marc
R		Desaverine	C24H03NQ3	0	383.24904	411	384.25332	0.01	104.25256	- 4	0	2.	13.79	10080	No Matrix	No Marc
P		Phenelzine	C8H12N2	0	136.10005	+84	137.10732	0.01	137.1071)	-15	0	1	10.27	2714		
P		Caffeire	C2H10N4C2	0	194 08038	48	116.06768	0.01	195 09132	111	0	2.	12.07	8237	Caffere	62.4

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г	1111	Name	Fornula	leotope	Mass (Ds)	Addust/ Modifications	Extraction Mass (De)	Inlide (De)	Found At Mass (Da)	Error (ppm)	Espected RT (min)	RT Width (min)	Found At RT (min)	Intensity	Library Hit	Purity Score
P		Desaverine	C24H33NO3	0	383,24604	+14	384 25332	0.01	384.25256	- 2	0	2	13.79	10000	No Match	No Manh
₽.		Phaneltine	C8H12N2	0	136.10005	+11	137 10732	10-0	337.98711	-15	0	2	10.27	1714		
Г		Coffeire	CEH10N4C2	0	194.08038	+14	195.08765	0.01	196.09132	383	0	2	12.07	8237	Celeva	51.4
₽.		Faraceteriol	CSH6NO2	0	151 06333	+11	152,07061	10-0	192,07022	-2.6	0	2	13.79	6134		
P		p-(Aminomethyl)benz	CSHSNCS	0	151.06333	+14	152,07061	0.01	152 07022	-28	0	2	13.79	2134		
₽.		Crotetamide	C12H22N202	0	226.16813	-11	227.1764	10.0	227.17516	-5.3	0	2	9.13	7755		
P		17-olpha-Methyltestin	C20H3002	0	302.22458	+14	303.23186	0.01	303 23187	0	0	2	345	1102		
₽.		Directuron	C15H19C8W03	0	238.11457	+11	339.12154	10.0	339,12021	-4.5	0	2	14.35	6609	Directures	77.4
P		Physioligmine	C19421N302	0	275.16338	+14	276.17065	0.01	276.17186	44	0	2	10.43	6762		
₽.	****	Adversione	C9H11NG3	0	181 07389	-11	182,08117	0.01	162,00109	-0.4	0	2	7.72	6156	Administra	21.7
P		Feberale	£15H14G3	0	242,09429	48	243,10167	0.01	340,10162	0.7	0	2	14.71	5254		
₽.		Eterovan	C12H17NO3	0	223.12084	48	224,12812	0.01	204,12700	-13	0	2	7.41	4700		
P		Bulesamac	C12H17N03	0	223.12084	+81	234 32112	0.01	224,12712	-13	0	2	7.41	4700		
₽.		Bucetin:	C12H17NO3	0	223.12084	48	224,12812	0.01	234 (2783	-13	0	2	7.41	4700		
P		Meterolone acetate	C22H0203	0	344 23515	48	345-24242	0.01	345 24205	-11	0	2	15.75	3531		
₽.		Footopri	C13H16N406	0	324.10698	-11	325.15426	0.01	325,11263	-4.5	0	2	3.97	2993	No Metals	No Marie
P		Acetylsoficylic Acid	C3H604	0	180 04725	48	181.04954	0.01	121.04953	0	0	2	11.61	2628		
₽.		Phonethylamin	CBHIN	0	121 08915	-81	122 09642	0.01	322 09631	-0.0	0	2	8.87	2927	No Metals	No Mary
P		Montplyte	C16H25N03	0	279.10344	48	280 19072	0.01	290,19027	-16	0	2	10.33	2555	Monteylyte	212
		5-Hydroxyquinoline	C947N0	0	145.05276	-81	146.06004	10.0	146,09964	-2.7	0	2	4.0	2412	\$Hydosysinder	16.8
P		Setane	CBH11NO2	0	117,07898	48	118.08526	0.01	- TIE 00606	-13	0	2	0.23	2216		
₽.		3.4 Methylenedoxyst	C12H17NO2	0	207,12593	-81	206 13321	0.01	208 13711	-0.4	0	2	231	2106		
P		Senzybeniolile	C16H18H2O45	0	234 09873	48	335 10401	0.01	305 10973	11.1	0	2	6.79	2117	flerzytjenistin	92.0
		Anbucetenide	C11H12N3O	0	202.09804	-81	203 10531	0.01	203 10565	17	0	2	14-13	2095		
P		Disferine	C20H31NO2	0	317.23548	+81	318.34276	0.01	318.24238	0.7	0	2	14.58	3974		
P		Nationatione	C15H1602	0	228.11500	-11	229 12231	0.01	229.12164	-23	0	2	13.27	1715		
P		Levestatin	C24H36O5	0	404.25627	48	405 36355	0.01	406.26311	-11	0	2	18.63	1625		
		Repoglinide	C27H06N204	0	452,26751	-11	450.27478	10.0	453.27633	- 34	0	2	520	3569		
P		Tetrospren	C164221404	0	234.16411	+81	335 17138	0.01	335 16714	-127	0	2	85	3181	Tehnopin	25.4
		Propionylpromapine	C20424N205	0	340.16094	-81	341,16621	0.01	341.96783	-5.3	0	2	35.00	1097		
P		Gestolere	C19H22O6	0	345.54164	+14	347.54812	0.01	347.54745	-42	0	2	10.67	1045		
		Propranolol	C16H21NO2	0	250.15723	-11	260,16451	0.01	260,16328	-47	0	2	35.64	1008		
P.		Testoslarune	C19H2SO2	0	288.20893	+84	289.21621	0.01	209.21747	44	0	2	13.16	1006		
			-		101,000	100	- many	1 000000		144		- 1	1141	-	11.16.1	H11H11

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г	Mir.	Name	Formula	leotope	Mass (Ds)	Adduct / Modifications	Extraction Mass (De)	Width (Du)	Found At Mass (Da)	Error (ppm)	Expected RT (min)	RT Width (min)	Found At RT (min)	Intensity	Library Hit	Purity Scor
P		Gestodere	C19HQ2O6	0	346,14164	+H	347 14832	0.01	347.14745	42	0	2	1007	1045		
P		Programolof	C16H21N02	0	259.15723	+H	260 16451	0.01	260.16328	-47	0	2	15.66	1000		
П		Testosterore	C19HQ8C2	0	288.20893	+H	289.21621	0.01	255.21747	4.4	0	2	1316	1006		
P		Acquirex	C9494203	0	154.03784	+H	156.04512	0.01	155,04548	11	0	2	1131	27701	No Malch	No March
P		Betarrethasone-17-bx	C29H03F06	0	496.22612	+H	497 23339	0.01	497 234 16	13	0	2	3.22	34292	No Match	No March
R		Innosibere	C14H16N4	0	240.1375	+H	241.54077	0.01	241.14314	-6.0	0	2	14.52	19890	No Match	No March
I P		Sulfalene	C11H12N4C3S	0	280.06301	+H	281 07029	0.01	261 07048	5.7	0	2	3.96	3400		
R		Sulfamethoopsyndam	C11H1ZN4O3S	0	280,06301	+H	201,07929	0.01	281 07048	0.7	0	2	336	. 8400		
P		Betweending	C10H15N3	0	177.1266	+H	178.13367	0.01	178.1305	-13.9	0	2	11.06	7097	Dethanides	23.8
1 12		Cycloberasprine.	C20H21N	0	275.1674	+4	275.17468	0.01	276.17218	-91	0	2	1043	6500	Cycloberuspore	242
P		Tempolen	C26H29NO	0	371.22431	+H	372 23233	0.01	372.23041	43	0	2	3.02	5627		
		Cydovalone	C22HQ2O5	0	366,14672	44	367,154	0.01	367.15586	3.3	0	2	8.88	5396		
P		Azstadne	C20402N2	0	290.1783	+H	291.18558	0.01	291.18846	33	0	2	12.12	5091		
P		Toceride	CTTH16N2O	0	192,10636	48	190.10054	0.01	190.13053	154	0	2	11.86	4556	1-(4-methosyphenylly	66.3
P		Ampiolin.	C16H19N3O5S	0	365.10454	+H	36631182	0.01	366 10846	92	0	2	3.96	3634		
F		Indenazoline	C12H19N3	0	201.1266	48	202,13367	0.01	202,13567	53	0	2	3.25	3240		
P		Bisoprotol.	C18H31NOA	0	325.22531	+14	326 23253	0.01	326.23239	-0.6	0	2	3.99	3043		
R		Deploraçõe	C19427NS	0	125,22665	eH.	326.23392	0.01	326.23238	-4.7	0	2	3.99	2954		
P		Rampril	C23H32N2O5	0	416.23112	+14	#17.250#	0.01	417 23829	-0.3	0	2	3.02	2709		
P		Atopine	C21H0003	0	330.2195	+H	331.22677	0.01	331,22956	-0.7	0	2	1433	2685		
P		Mesusmide	C21H0003	0	330.2195	+H	331 22677	0.01	331.22655	-0.7	0	2	1453	2685		
P		Iprazochronie	C12H16N403	0	264.12224	+14.	266.12962	0.01	265.13152	75	0	2	3.15	2617		
P		Genfbrial	C15HQ2O3	0	250.15629	+H	251.16417	0.01	251.1638	-1.5	0	2	14.72	2349		
P		Levamepromatine	CTSHQUNQOS	0	328,16094	48	328 16821	0.01	329 16362	-4	0	2	14.23	2201		
P		Didanosine	C20H34O5	0	354.24062	+H	355,2475	0.01	368.24579	-8.9	0	2	1334	2200		
P		Anteronium	C20H04O6	0	354.24062	+H	255,2471	0.01	256.24579	-8.9	0	2	13.34	2200		
P		Attetanine	CSH18N5	0	210.15929	+H	211.16657	0.01	211.16836	8.5	0	2	34.0	2103		
R		Labetolol	C19404NQ03	0	320,17869	44	328 18897	0.01	329 19779	55	0	2	347	2057		
P		Promethazine	C17HQ0NQS	0	2(4.13472	+H	285.142	0.01	255.14436	8.3	0	2	14.76	1776		
P		Promitione	CITHQUIQS	0	284.13472	48	285.142	0.01	285 54436	13	0	2	1476	1776		
P		Dhydralszne	C8H10N6	0	750.09663	+H	191.10387	0.01	191 10755	10.7	0	2	13.7	1763	Doydani	473
1 17		Thyrosperdin	CZ3H32N002S	0	400.21845	+14	401 22573	0.01	401,22547	-0.7	0	2	1436	1742		
P.		Nomfensine	C16H18N2	0	238.147	+H	238.15428	0.01	235 15499	3	0	2	15.48	1732		

C: 3 XIC manager (DHD- Hexane extract of Q Bee wiff sample 1)

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-	the.	Name	Formula	liotope	Mass (Da)	Adduct / Modifications	Extraction Mass (Da)	Vrlidth (De)	Found At Mass (Ds)	Error (ppm)	Expected RT (min)	RT Width (min)	Found At RT (min)	Intensity	Library Hit	Punity Soo
P	• • •	Vardenalil	C23H32N6O45	0	418.22058	+81	489-22795	0.01	489:22569	42	0	2	13.01	53393	Vardenali	94.6
R	****	Caproylesorsinol	C12H16O3	0	208.10994	48	209 11722	0.01	209.11728	0.3	0	2	13.96	1001	Coprophenomial	49.2
P		Alprenolal	C15H23N02	0	249 17288	+11	250.58016	0.01	250 17967	-13	0	2	8.7	4637	Alprendel	41.6
Ø.		Hydrocorisone 21-ac	C23H02O6	0	404.21989	48	405.22717	0.01	406.22955	14	0	2.	15.47	3421	Hydrocortianne 21-ac	69.1
P		Moninylyte	C18HQ5NO3	0	279.18344	+84	280.19072	0.01	290 19049	-0.0	0	2	2.3	2679	Moninglyte	51.6
R		Anis/Ipride	C17H27N304S	0	369.17223	+14	370,1796	0.01	370 18232	7.6	0	2	14.45	19353	Amendaride.	39.7
P		Quinine	C20H24N2O2	0	324.18378	+84	325.19106	0.01	325.19251	4.5	0	2	35.43	8607	Quintine	81.1
Ø.		Acetylsolicylamid	C20HQ4N2O2	0	324.18378	48	325 79105	0.01	325.19251	4.5	0	2.	15.45	9607	Quindre	81.1
P		Chinine	C20H24N2O2	0	324.18378	34H	325.19106	0.01	325.79251	4.5	0	2	35.49	8607	Quintine	81.1
R		Viquidii	C20H24N2O2	0	324.18378	+H	325 79105	0.01	125,19251	45	0	2.	15.45	9607	Quindre	81.1
P		Sulfaquinoxaline	C14H12N402S	0	1590.000	+86	301.07537	0.01	301.07497	-13	0	2	.12.6	6460	Subsummative	833
Ø.		Hydrocottoone	C21H0005	0	362.20032	48	363,2166	0.01	363.21425	-62	0	2.	13.60	5339	Hydrocortisone	71.7
P		Histidne	C6H9N302	0	155.06348	+84	156.07675	0.01	156,07684	0.6	0	2	9.95	3754	Heldre :	35.2
Ø.		Abstance	CSHISNE	0	210.19929	48	211,19657	0.01	211.1679	63	0	2.	13.8	3679	Abstance:	50.0
P		Ungidil	C20H29N5G3	0	387.22704	+86	386.23432	0.01	366.23167	-63	0	2	3.55	2993	(Impid)	67
p.		Cyclovalone	C22H22O5	0	366 14672	48	367.154	0.01	367,18881	52	0	2.	12	2016	Cycloalone	75.2
P.		Oseladirs	CZDHSSNOS	0	335.24604	+84	336.25332	0.01	136.28736	4.0	0	2	10.95	2472	Delade	90.2
Ø.		Dougonin	C32H43N5O5	0	577.32642	48	578.3337	0.01	579.33405	0.6	0	2.	8.07	1942	Dhydroepikystne	55.6
P		Theophyline	C7H8N402	0	180.06473	+86	181 073	0.01	181.0712	-44	0	2	7.03	1415	Theobramine	81.1
Į.		Theobromine	C7H8N402	0	180.06473	48	181.072	0.01	181.0712	-44	0	2	7.63	1415	Theobromine.	81.1
P		3.4-Methylenedoxym	CTIKISNOZ	0	190,11028	1481	394,31796	0.01	19431708	-24	0	2	1421	424349	No Match	No Mars
D.		3.4-Methylenedioxyar	C10H13NG2	0	179.09463	48	180 10191	0.01	180 10134	-41	0	2	12.54	157501	Prophum	26.3
P		Acetylsalicylic Acid	CSHSO4	0	180.04226	+14	181 04954	0.01	181,04889	-55	0	2	30.71	100195		
Ø.		Desamethasone	C22H29F06	0	392,1999	48	260.20718	0.01	310,20066	1.8	0	2.	834	29423		
P		Yohimbine	C21H26N2O3	0	354.19434	×81	355-30162	0.01	356/20156	-0.2	0	2	75.51	30004		
Ø.		Viscarrine	C21H26N2O3	0	354.19434	48	358.20162	0.01	386,20156	-0.2	0	2.	15.51	38004		
P		Verlataure	C17H27NO2	0	277.20418	*11	278.21146	0.01	276.21132	-0.5	0	2	35.36	23942		
2		Flufenamic Acid	C24H30F2O6	0	452.20105	48	450.20032	0.01	410.20022	-0.2	0	2.	8.40	19724	Fluxoncione Acetonic	11.7
P		Physiostigninie	C15H21N302	0	275 16338	+44	276,17065	0.01	276.37347	3	0	2	312	13599		
D.		Ethengamide	C9H11NO2	0	165,07896	486	166 00636	0.01	166.00569	-24	0	2	14.22	16805	No March	No Mare
D		Berzocene	C9H11N02	0	165,07896	+14	166.00526	0.01	166 08569	-3.4	0	2	14.22	16809	No March	No Mars
D		Diavendre	CISHIBNAGE	0	260.12733	486	261 13/6	0.01	251 13078	-14.6	0	2	7.76	16245	Dawridne	100
P		Phenetzine	CBH1252	0	136 10005	+24	137.10732	0.01	137.10636	-27	0	2	360	16070		
		3 - 1 -	40.00	3		900	- 1000000	920	11171111	- 70	- 0	10	300	10.000		100

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г	Mr.	Name	Formula	lackspe	Mass (Da)	Adduct / Modifications	Extraction Mass (Da)	Volume (Day)	Found At Mass (Da)	Error (ppm)	Espected RT (min)	RT Width (min)	Found At RT (min)	Intensity	Library Hit	Punity Score
P		Benzoowne	CSH11NO2	0	165.07098	+86	166 08626	0.01	166.03563	-34	C	2	14.22	16205	No Match	No Month
P		Diaverione	C13H16N402	0	290.12733	48	261.1346	0.01	261 13078	-146	0	2	7.78	16245	Dieveridine	100
Г		Phenelzine	CBH12N2	0	136.10005	+86	137.10732	0.01	137.10695	-27	0	2	9.63	16070		
P		p-(Aminomethyl)benz	CBHMNO2	0	151.06333	+H	152.07061	0.01	152,00999	41	0	2	12.64	15471	Paracetaries	10.5
P		Paracetanol	CSH6NO2	0	151.06333	+86	152,07061	0.01	152 06355	41	0	2	12.84	19471	Parioclariol	10.6
P		Betoridre	C10H15N3	0	177.1266	(48)	179.13387	0.01	178 13000	-21.3	0	2	10.62	15374	Bettaridee	60.9
P		Acepromazine	C19HQ2NQOS	0	326.14529	+86	327.15256	0.01	327 19636	11.6	0	2	15:17	14544	Acepromisine	83.4
P		Aceprometazine	C19HQ2NQOS	0	326.14529	+H	327.15256	0.01	227,15436	13.6	0	2	15.17	14944	Acapromisson	23.4
P		Methaqualore	C16H14N2O	0	250.11061	+86	261.11789	0.01	251.11735	-22	0	2	35.1	14920	Methopialore	22.6
P		Setemethesone-17-bi	C29H03F06	0	496.22612	(48)	497.23339	0.01	497,2341	14	0	2	3.6	13146	No Match	No Mand
P		Methylephebine	C11H17NO	0	179 13101	+86	180 13829	0.01	180 13805	43	0	2.	14.53	12776		
P		Maxietre	C11H17NO	0	179 13101	+H	180,13829	0.01	180 13005	-1.3	0	2	14,53	12776		
P		N-Methylephedine	CTIHIT/NO	0	179.13101	+36	180 13829	0.01	180 13805	41	0	2	14.53	11775		
P		Cafeine	C8H10N402	0	194,00038	(48)	195.06765	0.01	155.09008	16.5	0	2	11.20	11218	Cafeire	42
P		Feltomale	C15H14O3	0	242.09429	+36	243.10157	0.01	243.50125	43	C	2.	13.65	11005		
P		17-sighe-Methyltesto:	C50H30C5	0	302.22458	48.	303.23136	0.01	363,23185	0	0	2	1457	7300		
P		Finduki	C144201Q02	0	245.15245	+36	243.16975	0.01	245 15685	-11.7	0	2	8.38	£43	Pindolel	60.5
P		Bunitolal	C14HQ0NQ02	0	248.15248	(48)	248 10978	0.01	245 15685	-11.7	0	2	8.30	.00	Feddel	60.5
P		Dehydrocholic add	C24H3405	0	402.24062	+36	403.2479	0.01	403/24781	-02	0	2	13.45	6185		
P		Adonvestation	C33H05FNQ05	0	558.253	1486	150 25028	0.01	589.29112	23	0	2	1.29	4050	No Match	No Match
P		Phenettylenia.	CBHIIN	0	121,08915	+36	122.09643	0.01	122.09627	-13	0	2	736	4525	No Match	No March
P		Crotetarvide	C12H22N2O2	0	226.16813	(148)	227,1754	0.01	227.17548	0.3	0	2	8.07	4422		
P		Elansvon	C12H17N03	0	223.12084	+86	224.12812	0.01	224.12784	-12	0	2	5.63	3412		
P		Superior	C12H17NO3	0	223.12084	+86	224.12812	0.01	224 52764	-12	0	2	5.63	3412		
P	• ••	Bulesamec	C12H17N03	0	223.12084	+86	224 12812	0.01	224 12784	-12	0	2	5.63	3412		
P		N.N-Diethyl-m-toluem	C12H17NO	0	191,13101	186	192.13829	0.01	192,13620	-0.1	0	2	12.82	3165		
P		Acebutolol	C18-081004	0	336,20491	+86	337,21218	0.01	337,21368	- 1	C	2.	14.5	2952		
P		Difenosuron	C19/18/Q03	0	286.13174	+8	267 13902	0.01	207 13912	0.4	0	2	15.48	2548		
P		Mephysosine	C12H13N02	0	203.09463	+86	204 10191	0.01	20410116	37	0	2	14.33	2010		
P		Pettanidee	C19+Q4N402	0	340.18993	186	341.1972	0.01	341.19852	14	0	2	14.42	2460		
P		Methantholinium	C21H26NQ3	0	340.19127	+86	341.19355	0.01	341.13852	-01	0	2.	16.61	2611		
P		Salsalate	C14H1006	0	258.05282	+8.	259,0601	0.01	259-06302	11.3	0	2	15.34	1967	Alternated	75.6
P		Delaire	CSH11NO2	0	117.07098	+86	118,00626	0.01	118.0862	-0.5	0	2	6.16	1811		

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г	Mir.	Name	Formula	luolope	Maes (Da)	Adduct / Modifications	Extraction Mass (De)	Inlidit (Da)	Found At Mass (Da)	Error (ppm)	Expected RT (min)	RT Width (min)	Found At RT (min)	Intensity	Library Hit	Purity Score
P	***	Methanthelmian	C21H2SNO3	0	340,19127	+41	343,19856	0.01	341.13652	-61	0	2	34.41	2411	10	
P		Selselate	C14H1005	0	258.05202	-88	259.0601	0.01	250 06302	113	0	2	15.64	1967	Atemand	75.6
Г		Selaine	C0H11N02	0	117,07898	+81	118.00526	0.01	116.0652	-0.5	0	2	616	1811		
P		Melesanic acid	C15H15NC2	0	241 11028	-84	242,11756	0.01	242.11715	-1.7	0	2	33.35	1676		
P		Bussions	C34H8007	0	\$70,35565	+81	171 36211	0.01	571.36513	3.8	0	2	19.62	1639		
P		Eprosetan	C23HQ4NQO45	0	424.14568	-84	425.15296	0.01	425.15433	52	0	2	13.03	1672		
P		Benzyberiolite	C19H18H2O4S	0	334.09673	+81	336 10601	0.01	226 10997	318	0	2	8.06	1433	llerzybenolie.	32.6
P	• • •	Cenarizee	C20-C81/2	0	368 22525	+84	363.23253	0.01	369 23333	22	0	2	33.45	1206		
P		Sulfalene	C11H12H4035	0	280.06301	+81	281 07029	0.01	281 07547	0.6	0	2	36.31	1210		
P		Sullamethorphysidasi:	C11H12N4035	0	280.06301	-84	261 07029	0.01	281.07047	0.6	0	2	36.31	1280		
P		Conine	CBH17N	0	127.1361	+8	126 14138	0.01	128 14293	-35	0	2	19.36	1270		
P		Deposide	C9H15N02	0	163 11028	. 164	170.11756	0.01	170 13683	43	0	2	9.77	1125		
P		Acedidre	C9H15N02	0	169.11028	+81	175 11756	0.01	170,11623	43	0	2	9.77	1125		
R		5-Hydroxygunoline	C9H7NO	0	145,05276	+81	146.06004	0.01	146,09332	-4.9	0	2	100	1096		
P		Olanzapine	CTHODAS	0	312.14087	+14	313.14015	0.01	313 14666	47	0	2	13.41	1042		
P		Repagliside	C27H06N2O4	0	452.26751	. 164	453.27478	0.01	453.27308	-38	0	2	939	1002		
P		7-Aninodesrettyttle	CISHI2FIGG	0	269.09644	+14	27610372	0.01	270.10204	42	0	2	14.52	36229	7-Amendesmethytha	45.3
P		Buprofezin	C16H23N005	0	305.15618	-84	306.16346	0.01	306 16068	-85	0	2	(4)	4567.	Banker	447.
P		Ininostitane	C14H19W	0	240.1375	+14	241.14477	0.01	241 94273	-45	0	2	13.96	32664	No Statute	No Ment
P		Adpirox	CBH6N203	0	154.03784	. 164	155,04512	0.01	155-04537	55	0	2	10,88	10079	No Henry	No Meson
P		Aminopromazine	CINCINGS	0	327,17692	+81	328.1842	0.01	126 16705	67	0	2	19.66	12275		
P		Benedyaire	C20H25NO3	0	327.18344	-84	328.19072	0.01	328.18796	-84	0	2	15.66	11904		
P		Naturnetone	C15H1902	0	228.11903	+14	225.12221	0.01	229 12044	-42	0	2	71.53	10162		
P		Seleplin	C25HG605	0	418.27192	+84	419 2792	0.01	416:27639	-63	0	2	33.94	8767		
P		Moperone	CZ2H29FNO2	0	255.19476	+14	384 30303	0.01	286 20489	-1	0	2	19.52	3553		
P		Nandrolone	C18H2602	0	274.19328	+H	275.20096	0.01	275,1980	-2.7	0	2	14:14	6299		
P		Trapidl	CTOHTSNS	0	206.13275	+81	206 14002	0.01	256 14001	0	0	2	19.53	6702	No Statute	No Menth
P		Indonazoline	CT2H15N3	0	201,1266	-84	202 13387	0.01	202.13622	67	0	2	18	6062		
P		Enturaride	C17H27NO3	0	293 19909	+81	294 20637	0.01	294.20784	- 5	0	2	19.79	5351	No Statute	No Ment
P		Nonvanide	C17H27NO3	0	293.19909	+81	254 20637	0.01	254.20794		0	2	35.29	5351	No Hunch	No Meson
P		Batosytaine	C17H27NO3	0	253.13909	+8	294 20637	0.01	294.20784	- 5	0	2	19.79	5351	No Statute	No Ment
P		Butallylonal	C25H54O6	0	430 23554	-84	43134282	0.01	431.24458	- 6	0	2	970	4942		
Ø		Tocaride	CTIHTENCO	0	192,10626	+16	193 13394	0.01	193.13084	-34		2	11.00	4423	1-14-methosypheny();	56.2

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г	the.	Name	Formula	lactope	Mass (Da)	Addust / Modifications	Extraction Mess (Da)	Voldth (Da)	Found At Mass (Ds)	Error (ppm)	Expected RT (min)	RT Width (min)	Found At RT (min)	Intensity	Ubrary Hit	Purity Score
D.		Butosyosine	C17H27N03	0	293.19909	484	294.20637	0.01	294.20784	- 5	0	2	15.79	5361	No March	No March
F		Butallylonal	C25H34O6	0	430.23554	486	40134017	0.01	431,34455	4.	0	2.	9.78	4942		
П		Toomride	C11H161Q0	0	192,12626	+84	193.13354	0.01	193 13064	-14	0	2	11.09	4422	1-(4-methosyphenyl);	56.2
P		Dhydralszine	CBH10N6	0	190 09669	48	391.10357	0.01	391.1061	11.1	0	2.	12.76	3623	Dicyclanii	63.7
Ø		Metenolone acetate	C22H32O3	0	344 23515	484	36524342	0.01	34524121	-33	0	2	14.38	3633		
P		Levonegromazine	C194Q4XQQ5	0	328.16094	48	329.16821	0.01	329,17107	1.7	0	2.	15.36	3410		
Ø		Terroviler	C26H29N0	0	371.22431	+84	372.23219	0.01	372.23648	115	0	2	9.76	3367	Tamales	76.0
F		Valacyclovir	C13H29N604	0	324.1546	+16	325.16188	0.01	325.76158	-03	0	2.	12.01	3197		
g.		Genfbrook	C15H22O3	0	250.15639	484	251 16417	0.01	251 16421	8.3	0	2	13.91	3007		
P		THC	C21H3002	0	314.22458	+16	215.23186	0.01	316 23336	4.1	0	2	13.31	2754		
Ø		Antiuostamide	C11H12H00	0	202.09804	+84	203-10531	0.01	203.10516	-0.8	0	2	15.53	2296		
P		Adrenatone	C9H11NO3	0	181 07389	+16	182.00317	0.01	102.0007	2.5	0	2.	10.36	2100		
Ø		Timolof	C13H24N403S	0	316.15691	+14	317.16419	0.01	317 96422	8.1	0	2	12.67	2063		
F		Metarrifepramone	CTTHISNO	0	177,11536	+16	179.12264	0.01	178.32314	25	0	2	14.13	2961		
P		Hymeoromone	C10H003	0	175.04734	484	177.05462	0.01	177.05401	-33	0	2	13,49	1665		
P		Selbutamol	C13HQ1NO3	0	229.15214	+36	240.16942	0.01	240,15843	-33	0	2.	12.05	1555		
Ø.		Bazitramide	C31H32HN402	0	453,26035	+14	494.26763	0.01	454.25006	25	0	2	9.22	1478		
P		Metipranolol	C17H27NO4	0	300.19401	+16	310,20129	0.01	310.29006	+14	0	2	15.51	1306		
Ø.		Nadoliil	C17H27NO4	0	309.19401	+84	310.20129	0.01	310.20006	-14	0	2	15.51	1200		
P		Badolen	C10H12CN02	0	213.05566	+36	214.06251	0.01	214.06229	- 0	0	2.	14.30	1367		
g.		Methylphenidale	C14H19N02	0	233.14158	+84	234 14336	0.01	234.14867	-12	0	2	11.09	1322		
P		Diszep	C31H44N2O10	0	604,2996	+16	605.30687	0.01	405,30058	25	0	2	155	1203		
g		Tramadul	C10425N02	0	263.16853	48	264 19581	0.01	264 19545	-13	0	2	13.24	1239		
P		Butetamate	C19H25N02	0	263 18853	+31	254.19581	0.01	254.19545	-13	0	2	13.34	1220		
D.		Labetskiil.	C19HQ4HQ03	0	328.17069	+14	329.10997	0.01	129 18733	43	0	2	8.09	1125		
P		Denogest	C20H25NO2	0	311.18853	+16	312.19561	0.01	312.19445	43	0	2	14.5	1120		
F		Rupredryldene 21-A	C20H25NO2	0	311 16853	+81	31219581	0.01	372.13445	40	0	2	146	1120		
P		Bote	C10H16N2035	0	244.08316	+36	345,09544	0.01	245.09447	4.	0	2.	11.55	1000		
P		Prazeparo	C19H17CM20	0	324 10294	48	325.11022	0.01	325 11127	32	0	2	0.04	1057		
P		Arropinmethy/bromid	C8H1904	0	188.10486	+16	189.71234	0.01	189,11300	5.7	0	2.	157	1021		
F		Reamptas	C15H19N5	0	265.16405	+81	276.17132	0.01	270 17198	2.4	0	2	13.71	1008		
P		Methyldopa	C10H13NO4	0	211,08445	+36	212,09173	0.01	212.00000	.54114.5	0	2.	13.13	20996		
D		Cycloberosprine	C20H21N	0	275.1674	+14	276.17458	0.01	276 17181	-104	0	2	332	16603	Cyclidentagrine	17.0

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г	the.	Name	Formula	lackope	Mass (Ds)	Adduct / Modifications	Extraction Mass (De)	Volidith (Da)	Found At Mass (Ds)	Error (ppm)	Expected RT (min)	RT Width (min)	Found At RT (min)	Intensity	Library Hit	Purity Scor
P		Restriptor	C15H19N5	0	255.16405	48	276 17132	0.01	270 17190	2.4	0	2	13.71	1008		
F		Methyldopa	C10H13NO4	0	211,00445	+H	212,09173	0.01	212.00031	-114	0	2.	13.13	20096		
П		Cycloberzsprine	C20H21N	0	275.1674	+#	276.17458	0.01	276 17381	-104	0	2	3.02	16603	Cyclobenzagenoe	17.8
P		Cyamericaine	C19HQ1N35	0	323.14562	+H	324.1629	0.01	324 14356	-13.4	0	2.	13.96	15754	Commission	78.7
F		Phenobarbital-05	C10H164203	0	212.11609	+#	213.12337	0.01	213.12615	133	0	2	15.06	5660		
P		Glenepiride	C24H34N4O65	0	410.22419	+H	491,20227	0.01	491,23413	36	0	2.	13.64	4321		
F		Prometryn	CTOHISMAS	0	241.13612	+#	242.14339	0.01	242 14567	10.2	0	2	13.87	4554		
P		Timbutryn	C10H19M6S	0	241.13612	+H	242.54330	0.01	242,34587	10.2	0	2.	13.97	4554		
F		Carlcan	C13H20H2035	0	284,11946	+81	285.12874	0.01	255 13004	118	0	2	3.45	4025		
P		Mesotari	CZSHQBNGO	0	428.23245	+H	429,23974	0.01	429 22879	-22	0	2.	12.66	3997		
F		Galopani	C28H01Q05	0	454.28372	+#	485.301	0.01	485:30327	4.7	0	2	13.2	3756		
P		Proceinamide	C13HQ1N3O	0	226.16845	+H	236.17574	0.01	236,17397	5-153	0	2.	1538	3317		
F		N2-Ethylpuenin	CTHINISO	0	179.00071	44	160.06799	0.01	180 (8362	342	0	2	12.86	3066		
P		Norethisterone acetal	C22H28C3	0	340,20385	+H	341,23112	0.01	341,20964	-33	0	2.	14.29	2976		
Ø		Ethyl sultate	C4H803	0	104.04734	+#	105.05462	0.01	106.05785	30.6	0	2	12.39	2726	No March	No Man
P		Famprofazione	CZ3H06N20Z	0	372,27768	+H	373,28436	0.01	373.28406	12.4	0	2.	13.96	2161		
F		Aproline	C20+Q64Q02	0	325.19943	+#	327.2067	0.01	327,2066	-0.3	0	2	13.82	2144		
P		Carbenovolone	C19/09/2065	0	358.15524	+H	250 16352	0.01	0	0	0	2.	15.71	2140	Clastein	36.1
Ø		Etherrbutol	C10HQ4HQ02	0	204.18378	+#	206.19106	0.01	205.1934	1974	0	2	15.1	2119		
P		Gleorepide	C6413NO5	0	179.07907	+H	180,00665	0.01	180.06362	-368	0	2.	12.85	2074		
F		Dobutanine	C18H23N03	0	301.16779	+#	302.17507	0.01	30237476	-3-	0	2	15.12	1050		
P		Incisuprine	C18HQ3NO3	0	301.16779	+H	302,17507	0.01	302,17476	2	0	2.	15.12	1850		
F		Dihydrocodeine	C18HQ3NO3	0	301.16779	+#	302.17507	0.01	302.17476	-3	0	2	15.12	1050		
P		Granisetron	C10H14O4	0	190.08921	+H	190,09649	0.01	159.00036	-157	0	2.	10.55	1436		
F		Coticosterone	C21H0004	0	346.21441	+#	347.22169	0.01	347.22029	- 4	0	2	345	1878		
P		Azoluron	C12H14N4O	0	230.11676	+H	231.12404	0.01	221.11992	5-17.8	0	2.	7.00	1343		
F		Meprobamate	C9H18N2O4	0	218.12666	+#	219 10330	0.01	219 13773	173	0	2	14.11	3180		
R		Ethyl glucuronide	CZHEO4S	0	125.99068	+H	127 00596	0.01	127 00166	-033	0	2.	10.84	3150		
P		Amidotranic Acid	C12H804	0	216.04226	44	217.04954	0.01	217 04647	-141	0	2	12.06	3197		
P		Azapropazone	C16-09N402	0	300.15863	+16	301 1669	0.01	301.36383	-63	0	2.	13.37	14136		
F		Alopund	CSHANAO	0	136.03051	+81	137.04573	0.01	137.04651	53	0	2	12,84	7801	Allepainel	11.2
P		Pergolide	C194QQQ5	0	214.10167	48	215.18096	0.01	315 19116	7.	0	2.	14.43	2683		
P		Ausen	C10H14N2O4	0	225.09536	+#	227 10263	0.01	227 10462	1.3	0	2	15.21	2517		

C: 4 XIC manager (DHE- Hexane extract of Little Bee wiff sample 1

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г	Mir.	Name	Formula	lectope	Mass (Da)	Adduct / Modifications	Extraction Mass (Da)	Width (Du)	Found At Mass. (Da)	Error (ppm)	Especial RT (min)	RT Width (min)	Found At RT (min)	Interesity	Library Hit	Purity Scor
P		Vardenafit.	C23H32N6O4S	0	455.22058	+H	489.22785	d-01	489.22575	43	0	2	15.45	121506	Vardenalif	522
R		Clotispine	C19H25N03	0	319.21474	-eH	330 22202	0.01	320,22194	-0.3	0	2	10.15	13605	Cyclotive	46.1
P		Sultaquinosaline	C14H12N4Q2S	0	300.0681	+H	301.07537	0.01	301.07475	41	0	2	13.11	12017	Substanceire.	30.5
R		Alprenolol	C15H23N02	0	249.17288	-eH	250.33016	0.01	250,17954	-25	0	2	9.06	10327	Alpendel	60.8
P		Hydrocorlisone	C21H0005	0	362.20932	+24	363.2166	0.01	363.21559	-21	0	2	14.29	9639	Hydrocetaine	73.3
P		Lisropel	C21H01N005	0	405.22637	ald.	406 23365	0.01	406.23386	0.5	0	2	3.95	0.006	Langel	323
P		Raybasine	C21HQ4NQ03	0	352,17069	+H	353.76557	0.01	363.18678	23	0	2	14.33	8000	Radenes	73.5
R		Caproylesorcinal	C12H16C3	0	208.10994	ald.	200.11722	0.01	209 1166	- 21	0	2	14.43	1675	Carcyheorina.	46.3
P		Doxazosin	C32H43N505	0	877.32642	+24	576 3337	0.01	578.33583	33	0	2	92	4048	Dilydroegukryptne	55.2
R		Orapidi	C20H29N503	0	387.22704	ald.	388 23432	0.01	308.2327	42	0	2	19.2	3566	Unput	10
P		Histoine	C6H9N302	0	155.06948	+H	156,07675	0.01	156.07557	- 6	0	2	15.76	2500	Holdre	30.5
R.		5-Hydroxyquinoline	CSH7NO	0	145.05275	+H.	146-06004	0.01	146,05336	46	0	2	8.40	2410	3.Hydrospanoles	42.7
P		Fluid ocortisone Acetz	C23H01F06	0	422.21047	+H	423.21774	0.01	423.21885	26	0	2	2.51	1384	Flubocontoone Acets	100
Ø		Adenosine	C10H13N504	0	267.09675	ald.	258 10403	0.01	298.10258	+1.7	0	2.	17.21	1250	Adentine	100
P		Plocerpine	C11H16N202	0	208.12118	+H	201 12545	0.01	209 13001	74	0	2	15.44	7196	Placepine	557
P		Hydrocorteone 21-eo	CZ3HG2O6	0	404.21989	+H.	406.22717	0.01	405.2257	-1.1	0	2	3244	4675	Hydrocartoone 21 oc	645
P		Attetamine	CSHISNS	0	210.15929	+H	211.19657	d-01	211.16765	5.1	0	2	14.36	6148	Altertamine	44
P		Leocabastine	CZGHZSFNQQZ	0	420.22131	eH.	421 22850	0.01	421,23091	35	0	2	738	4222	Covoceleative :	90.4
P		Acedidine	CSHISNOZ	0	369.11028	+H	170.11756	0.01	175 11721	-21	0	2	10.24	3065	Acadelese	30 4
P		Disposide	CSH15NO2	0	169.11026	+H.	170,11756	0.01	170.11721	-2.1	0	2	10.34	3865	Aceditive	30.4
P		Benzylpeniollin	C16H18HQO4S	0	334.09873	+H	335.10621	0.01	335 10532	33	0	2	85	2008	Benzylpmoute	86.1
P		Methylphenidate	C14H15NO2	0	233.14158	-H	234 1488E	0.01	234.14856	-13	0	2	11.53	2189	piperman	39
P		Oveledn	C20H33NO3	0	335.24604	+H	336.25332	0.01	336-25269	-1.9	0	2	11.02	1061	Dielate	73.4
F		3.4-Mathylenedoxyrs	CTTHISNOD	0	193.11026	-H	194 11756	0.01	194.11753	-0.1	0	2	14.57	430010	No Match	No Marc
P		3.4-Methylenedoxyer	C10H13NO2	0	179.09463	+H	180 10191	0.01	180 10166	-7.4	0	2	13.34	260797	Prophen	26.2
P		Desarrethasone	C22H29F05	0	392.1999	-M	383 26718	0.01	393,33846	33	0	2	8.74	.99553		
P		Aceprometazine	C19HQ2NQOS	0	326.14529	+H	327 18256	0.01	327 15638	10.7	0	2	15.71	53685	Approvative	72.1
F		Acepromezine	C19HQ2NQOS	0	325.14529	-H	327.16256	0.01	337 15408	10.7	0	2	15.71	53685	Aceptomictive	72.1
P		Flutenamic Acat	C24H30F2O6	0	452.20105	+H	453,20632	0.01	453.20817	-0.3	0	2	2.86	40247	Plantinolone Acetoni	11.7
P		Vincamine	C21HQ9IQ03	0	384.19434	-H	355.20562	0.01	255 20186	0.7	0	2	33.55	30832	Yohinkins	233
P	• • •	Yohinbine	C21HQ6NQ03	0	354.13434	+H	368-20162	0.01	368-20186	5.7	0	2	13.39	30032	Yohindana	23.9
F		Disveridine	CTSH16N402	0	260.12733	-84	267.1366	0.01	261 13064	-14.4	0	2	8.22	32536	Disverident	100
P		Physostymne	C15421N302	0	275.16338	+24	276.17068	0.01	276.17161	35	0	2	10.11	31696		
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п	thi.	None	Formula	Isotope	Mass (Ds)	Adduct / Modifications	Extraction Mass (De)	Width (De)	Found At Mass (Ds)	Error (ppm)	Expected RT (min)	RT Width (min)	Found At RT (min)	Internity	Library Hit	Purity Score
P		Yohimbine	C21H29N2O3	0	354.19434	+14	355-20162	0.01	265,20186	0.7	0	2	12.00	30337	Yeliobre	23.9
P		Dieveridine	CIGHIBNAGS	0	260.12733	+H	261.1346	0.01	261.53084	-14.4	0	2	8.22	32536	Disversion	100
г		Physiosignose	C15HZ1N302	0	275.16330	+14	276 17065	0.01	276.17161	3.5	0	2	10.11	31696		
P		Verlatorine	C17HQ7NO2	0	277.20418	+H	278.21346	0.01	278 21052	-1.9	0	2	13.16	27302		
P		Berzossine:	CIHITMOZ	0	165.07899	+H	166 09626	0.01	166 00532	-2	0	2	14.63	25219	This Materia.	No March
P		Etherzamide	C9H11NO2	0	165.07398	+11	166.00626	0.01	166.00002	2	0	2	14.60	25219	No Match	No Malch
R		p-(Aminomethyl)tenz	CSH9NO2	0	151.05333	+14	152,07061	0.01	182.07011	-32	0	2	13.33	22945	This Mariette.	No March
Ø		Parecelamol	C8H6NO2	0	151.06333	+H	152,07061	0.01	152 07011	-0.2	0	2	1333	22345	No Manch	No Malch
F		Phenelpine	CBH12N2	0	136.10005	-M	137 19732	0.01	137,10706	-2	0	2	9.92	20239		
P		Tanostes	C36453NO	0	371.22451	+H	372.23219	0.01	372.23681	12.4	0	2	10.05	20140	Tamoden	53.3
P.		Caffeire	CSH10N4C2	0	194,00030	+14	195.06765	0.01	196.09127	18.5	0	2	117	19904	Caffeire	68.1
P		Alonyastatin	C33H35FN2O5	0	558.253	+H	868 26038	0.01	558 26152	2.9	0	2	9.58	19358	No Match	No Malch
Ø.		Denaverne	C24H03N03	0	383,24604	+H	384.25332	0.01	36423241	24	0	2	15.63	14367	Netidonayi	216
P		Natidologi	C24H03N03	0	383,24604	+H	384.25332	0.01	384,25241	-24	0	2	15.63	14967	Nebdologi	21.6
Ø.		Bunitolol	C14H20N202	0	248.15243	+14	249.35975	0.01	249.19662	-12.6	0	2	3.02	13707	Pindololi	60.5
P		Findolol	C14H20N202	0	248.15248	+H.	249.19975	0.01	249.55662	12.6	0	2	8.92	13707	Pints (cf.	60.5
P		Grepoloxaco	C16H27NO4	0	297,19401	+H	298,20129	0.01	290.20075	14	0	2	34	12019		
P		Methylephodrine	CTIHI7NO	0	179.13101	+11	100.13029	0.01	186 13755	-1.9	0	2	1434	9672		
Ø.		Neclotice	C11H17NO	0	179.13101	+14	100.13029	0.01	100 13795	1.9	0	2	1434	1672		
P		NiMetylephodine	CTIH17NO	0	179.13101	+H	100,13029	0.01	186 13795	-1.9	0	2	1434	9672		
P		Crotetanide	C12H22N2O2	0	276.16813	+14	227,1764	0.01	727,1749	22	0	2	3.02	1072		
P		Felbanate	C15H14C3	0	242.03429	+11	243.10157	0.01	243.10152	-0.2	0	2	14.25	8010		
Ø.		Pergolide :	C19H26H25	0	314.18167	-14	315.1805	0.01	216 19229	10.6	0	2	11.71	7565	Perpolde	95.7
P		17-alpho-Methyltestor	C50H3003	0	302.22458	+H	363 23186	0.01	30523147	-13	0	2	15.39	7119		
P		Nandrokene	C18H2902	0	274.10320	+14	275.20056	0.01	275 19984	2.6	0	2	14:93	5507		
P		Phenethylamin	CBH11N	0	121.00915	+11	172.09643	0.01	172.09596	-3.1	0	2	2.45	5676	No Match	No Malch
P		Trapidit	C10H15N5	0	205.13275	+14	206.14002	0.01	206 13932	341	0	2	15.75	5045	No March	No March
P		Milelosine	C12H16425	0	220.10342	+H	221.1107	0.01	221.11428	16.2	0	2	10.42	4903	ejatre	100
P		Ibesatar	C25HQSN6O	0	428.23246	+14	429 22974	0.01	429 23888	-2	0	2	15.74	4573		
Ø		Metamphetamine	CTOHTSN	0	149.12045	+11	190.12773	0.01	150 32743	2	0	2	836	4258	No Match	No Malch
P		Bulexamac	C12H17NO3	0	223.12084	+14	224.12812	0.01	224 12799	-0.6	0	2	7.06	1001		
P		Bucelin	C12H17NO3	0	223.12084	+H	224.03102	0.01	224.12799	-0.6	0	2	7.06	4001		
P		Etarriyan	C12H17NO3	0	223.12084	-M	224.12812	0.01	224.12799	0.6	0	2	2.06	4061		

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г	the.	Name	Formula	lookspe	Mass (Ds)	Adduct / Modifications	Extraction Mass (De)	Width (De)	Found At Mass (De)	Error (ppm)	Expected RT (min)	RT Width (min)	Found At RT (min)	Intensity	Library Hit	Punty Score
F	*1**	Bulesamac	C12H17NO3	ā	223 12084	+H	224 (2812	0.01	224 12799	-0.6	0	2	756	4061		
P	****	Sucete	CT2HT7NO3	0	223.12054	+8	224 12812	0.01	224.12799	-0.6	0	2	7.00	4061		
г	****	Eleminan	C12H17NO3	0	223 12084	+H	224,32832	0.01	224 12799	-0.6	0	2	7.06	4061		
₽		Anbucelamide	C11H12NGO	0	202,09804	+8	203.10531	0.01	203 30595	33	0	2	13.31	3706		
P		Genfánszk.	C15H22O3	0	250.15689	+H	281.16417	0.01	251 16522	42	0	2	14.27	2555		
₽		17alpha-Hydroxyprop	CBHTSNO	0	151.09971	+8	152,10839	0.01	152.10053	-3	0	2	10.23	5484	Norperudosphidrow	35.6
P		Norpseudosphiltine	CIHTINO	0	151.09971	+H	152 10699	0.01	152 10653	-3	0	2	1023	3454	Siepsealosphiline	15.4
P		Nonphebrine	CBHTSNO	0	151.09971	+8	152,10899	0.01	152 10053	- 3	0	2	10.23	3484	Norperudosphidrow	35.6
P		D-Norpseudoephedia	CIHTINO	0	151 09971	+H	152 10009	0.01	152 10653	-3	0	2	1023	3454	Siepsealosphiline	15.4
P		Phenylproporolamini	CSHTSNO	0	151.09971	+8	152,10099	0.01	152 10053	- 3	0.	2	10.23	3484	Norproudoephidrone	35.6
P		Advendore	C9H11NO3	0	181 07389	+H	182.08117	0.01	152 06009	-32	0	2	730	3307	Administra	27
₽		Valacyclove	C13H20N6O4	0	324.7546	+8	325 16188	0.01	225.36182	-02	0.	2	12.64	2304		
P		Testosterone	C19HGBO2	0	288.20093	+H	285 21621	0.01	289.23963	- 2	0	2	14.84	3196		
F		Predrisone -	C21H29O5	0	358.17002	+8	258.1862	0.01	368 18539	0.3	0.	2	9.3	2104		
P		Arrenolin	C28H42CI2N4CI2	0	53625548	+H	537,27576	0.01	537 27837	4.3	0	2	1226	2676		
₽		Betalve	CSH11NO2	0	117,07098	+8	11)(.08626	0.01	118.09622	-03	0	2	16.01	2390		
P		Dawnshion	C22H29FO4	0	375 20499	+H	377.21228	0.01	37721377	- L	0	2	9.27	2112		
F		Flyocortin Sutyl	CZ2H29FO4	0	375.20499	+8	377,21226	0.01	377,21377	4	0	2	327	2102		
P		Sulfalere	C11H12N4O05	0	280.06301	+H	281 07029	0.01	281 07034	0.2	0	2	3.78	1629		
₽		Sultemethosypyridate	C11H12N4O35	0	290.06301	+8	281 07029	0.01	281,07034	0.2	0	2	3.76	3629		
P		Corine	CBH17N	0	127.1361	+H	128.14138	0.01	126 14232	-36	0	2	15.89	1493		
P		Perbutolol	C18H29NOZ	0	291,21983	+8	292.22711	0.01	292,22524	-3	0	2	11.03	3172		
P		Dopamin	C12H14N2O4	0	250.09536	+H	251.10363	0.01	251 50308	33	0	2	1236	1120		
F		Cyclopertobation	C9H10N9O	0	182 09161	+8	163,09889	0.01	183 09914	14	0.	2	14.74	1054		
P		Baproleon	C19-03N3OS	0	305.15618	+H	306 16346	0.01	306 16049	-87	0	2	8.43	13941	Burofein	44.7
F		Metamoton	C10H10N40	0	202,08545	+8	303.99274	0.01	203.09099	46	0.	2	12.01	5054	Metandron	39.5
P		Osprevolal	C16H23NO3	0	265.16779	+H	256.17907	0.01	266 17275	47	0	2	11.67	2823	Opensid	57
F		Butallylonal	C25H0406	0	430,23554	+8	421,24212	0.01	42124568	66	0.	2	3.00	108132		
P		Amisulpode	C17H27H3O4S	0	369.17223	+H	370,1798	0.01	370 18254	93	0	2	15.02	45203	Armigrale	11.1
P		Setamethasone-17-b.	C29H33F06	0	496-22612	+81	497 23331	0.01	497,23428	338	0.	2	1.96	38716	No Malch	No Heath
P		Appinox	CRHM203	0	154,03784	+H	150-04512	0.01	155,04616	67	0	2	1121	31926	No Materia	No Matei
P		Innositiene.	C14H16N4	0	240 1376	+8	241.74477	0.01	241 14291	37	0.	2	34.44	19999	No Malch	No Hand
F		Selegiin	C25H38O5	0	418.27192	+H	419.2792	0.01	419.27577	42	0	2	19.55	14797		
-		1200	-	-	******	1000	Service -		- And the last	-	- 4	_	40	-	196.981.0	-

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г	11/1	Name	Formula	Isotope	Maes (Da)	Adduct / Modifications	Extraction Mass (De)	Inlidth (Da)	Found At Mass (Da)	Error (ppm)	Expected RT (min)	RT Vildh (min)	Found At RT (min)	Intensity	Library Hit	Purity Score
P		Adpinox	CRH6N203	0	154.03784	+H	155.04112	0.01	115.04516	67	0	2	1121	31926	No Statute	No March
P		Innotibere	C14H16N4	0	240.1375	+H-	241 14477	0.01	245 54295	-7.7	0	2	14.44	10999	No Match	No Mesti
P		Seleplin	C25H38O5	0	418.27192	+14	419.2792	0.01	419-27577	42	0	2	19.56	16797		
P		Indonazoline	C12H15N3	0	201,1266	-84	202,13387	0.01	202.13517	64	0	2	8.62	14222	No Heath	No Metal
P		Directories	C201-Q41/Q	0	292.19395	+14	290 20123	0.01	293 20317	66	0	2	13.99	10747		
P		Bunazosan	C34H50C7	0	579.36565	+84	571,36251	0.01	571:36206	-15	0	2	16.71	7509		
P		Gallopanil	C28H0N2O5	0	454.29372	+14	485.501	0.01	48530165	13	0	2	19.32	7155		
P		Cyclovalone	C22HQ2O5	0	366.14672	-84	367.194	0.01	367.55588	5.7	0	2	1.5	6657		
P		Tocaride	C11H16N2O	0	192.10626	+14	193 12384	0.01	193 13112	-12.5	0	2	115	5791	1-(4-methosyphery());	45.5
P		Christe.	C20+Q4/Q02	0	-324.18378	-14-	325.19105	0.01	225,19284	55	0	2	13.55	5753		
P		Voidl	C20HQ4NQ02	0	324.18378	+14	335.19106	0.01	225.19284	55	0	2	13.95	5753		
P		Quinne	C20+Q4/Q02	0	-324.18378	.66	325.19105	0.01	325,19284	55	0	2	13.55	5753		
P		Acetylsoloylamid	C20HQ4NQ02	0	324.18378	+14	335 19106	0.01	325.19284	55	0	2	13.95	5753		
P		Dehydrocholic and	C24H34O5	0	402,24062	-14-	403.2479	0.01	403.24721	-1.2	0	2	15.16	5611		
P		Moneylyte	C1RIOSNO3	0	279.18344	+14	280 19072	0.01	280 19176	37	0	2	10.7	4255		
P		Glooperin	C23H34O5	0	390.24062	-84	2912479	0.01	391,24686	-2.7	0	2	35.77	4242		
P		Metrylthoursoil	CSHGNOOS	0	142,02008	+14	143.02736	0.01	143 02596	-93	0	2	10.98	3541	Methylthinesol	17.8
P		Sisoprolol	C18H01NO4	0	-325-22531	-14-	326 23258	0.01	226 23149	-0.4	0	2	142	3675		
P		Pherobarbital-D5	C10H161003	0	212.11609	+14	213.12337	0.01	213 12548	5.3	0	2	19.53	3375		
P		Beztranide	C31H02HN402	0	483,26035	-84	494.26763	0.01	494.2927	22	0	2	9.55	3366		
P		Nonvaride	C17H27NC1	0	293 19909	+14	294,30637	0.01	294,20548	-23	0	2	13.96	3333		
P		Butonycoine	C17H27NO3	0	293.19909	-14-	254,20637	0.01	254 20568	-23	0	2	13.96	3333		
P		Enfurerade	C17H27NO3	0	293.19909	+14	294.20637	0.01	294 20548	-23	0	2	13.96	3333		
P		Tetrosoprim	C16HQ2N4O4	0	334.36411	.84	336,17138	0.01	335 17634	568	0	2	10.36	2973	Tehmoprim.	92.5
P		Laberalsk	C19HQ4HQ03	0	328.17069	+14	329 14187	0.01	229 13678	25	0	2	325	2001		
P		Mephroceine	C12H13NO2	0	203.09463	+84	254 10131	0.01	204 10101	44	0	2	14.51	2877.		
P		Prometrys	CTOHTSMSS	0	241 13612	+14	202,54339	0.01	242.14551	67	0	2	14.45	2350		
P		Terbutryn	CTOHTOMSS	0	241,13612	-84	24234038	0.01	242,14551	17.	0	2	14.45	2850		
P		Melitracies	CZ1H2SN	0	291.1907	+14	212.20130	0.01	292 20307	-53	0	2	3.10	2712		
P		Terbusine	CZ1H25N	0	291.1967	+84	292.20558	0.01	292.20307	-0.9	0	2	1.95	2782		
P		3.4-Methylenedosyst	C12H17NG2	0	207 12593	+14	208.13321	0.01	208 11323	0.5	0	2	19.25	2719		
P		Isoproturon	C12H18N2O	0	206.14191	-84	207,34319	0.01	207.35335	9.5	0	2	136	2660		
P		Nadelel	C17H27NO4	0	309.19401	+14	310 20129	0.01	310/20085	-14	0	2	19.25	2551		

	tool tool total	888 2														
г	11/1	Name	Formula	lectope	Mass (De)	Addust / Modifications	Extraction Mass (Da)	Volato (Da)	Found At Mass (Ds)	Error (ppm)	Espected RT (min)	RT Width (min)	Found At RT (min)	intensity	Library Hit	Purity Soor
P		3.4-Methyleredoxyet	C12H17N02	0	207,12593	+H	208 13321	0.01	208 (3323	01	0	2	1525	2719		
P	***	Inoprofusor	C12H1IN2O	0	206.14191	+8	207.14319	0.01	207,15115	31	0	2	8.95	260		
Г		Nadokii	C17H27NQ4	0	309.19401	+95	310.20129	0.01	310.20005	-14	0	2	1525	2661		
P		Metipranolol	C17H27NO4	0	309.19401	+H	310.20129	0.01	310,20005	-1.6	0	2	15.25	2551		
P		Prolonamide	C9H12N2S	0	180,07212	+86	181,8794	0.01	181.66212	- 15	0	2	0.0	2367	Protomende	58.7
P		Desnedoham	C19/16N2O4	0	300.11101	+8	301.31828	0.01	301.11529	-9.9	0	2	12.41	2270		
P		Phennedipham	C16H16N2O4	0	300.11101	+16	301 11828	0.01	301.11529	- 65	0	2	12.01	2270		
P		Amphelamine	CSHTSN	0	135 104E	+H	136 11208	0.01	136,1118	- 21	0	2	8.57	2107		
P		brazodvone	C12H16N403	0	264,12224	+36	26512962	0.01	265 13182	87	0	2	8.82	2073		
P		Tolycome	C19-02N203	0	278.16304	+8	279.17002	0.01	279 17366	4.1	0	2	10.13	1900		
P		Meprobamate	CSH18N2O4	0	218.12666	+16	218 13393	0.01	215 13473	34	0	2	10.15	1786		
P		Ampiolin	C10H19N3O85	0	365.10454	+H	366.11182	0.01	366 13851	- 0	0	2	5.32	1773		
P		Olanzapine	C17H20N45	0	312,14387	+16	313.14815	0.01	313.14634	38	0	2	15.76	1773		
P		Midodrine	C12H18N2O4	0	254.12666	48	256 13383	0.01	255.13462	2.7	0	2	13.5	1164		
P		Orybuproceine	C174Q81Q03	0	308.20999	+86	309.21727	0.01	309 21378	8.1	0	2	9.2	1516		
Ø.		Carazolol	C18H22N2O2	0	298.16813	+8	299,1754	0.01	299 17709	0.3	0	2	15.71	1487		
P		Backelen	C10H12CN02	0	213.05566	+16	214.06293	0.01	214.06258	-18	0	2	14.81	1426		
P.		Metamlepramone	CTIHISNO	0	177,11536	48	179.12264	0.01	178 12259	-0.3	0	2	1447	1477		
P		Levobunold	C17H25N03	0	291.10344	+86	292.19072	0.01	292 19053	-0.6	0	2	10.38	1402		
P		Elirocate	C17H25N03	0	291,18344	+8	292.19072	0.01	292.19053	-0.6	0	2	10.38	1402		
P		Quindine	C17HQ5NQ3	0	291.10344	+86	292.19072	0.01	292 19053	-0.6	0	2	10.38	1402		
P	6.00	Floctelenine	C29H17F3N2O4	0	405.11404	+86	407 12132	0.01	407.12307	6.5	0	2	10.36	1352		
P		Acetyleologiic Acid	C5H6O4	0	180.04226	+86	121.04954	0.01	181 64904	-28	0	2	11.2	1251		
P		Fluratione	C15H13F02	0	244.08996	48	245.09723	0.01	245.09792	2.8	0	2	1.49	1250		
P		Selbutarrol	C13H21N03	0	239.15214	+86	240.15342	0.01	240.15866	32	0	2	12.64	1231		
P		Oxedosyl	C16H18N2O4	0	278.12666	(48)	779.13393	0.01	279.13665	9.7	0	2.	15.27	1215		
P		Metsulfuron-methyl."	C14H15N506S	0	381,07431	+86	382.06158	0.01	302.00241	22	0	2	3.75	1012		
P		Fosinopril	C13H16N406	0	324,10698	48	325.11425	0.01	225 11402	-0.7	0	2	10.09	1012		
P		Lobeline	CZZHQTNQZ	0	337,20418	+86	330.21145	0.01	330 21266	36	0	2	1579	1007		
P		Decemberry	C22H27NO2	0	337.20418	48	338.2114E	0.01	330.25266	34	0	2	15.79	1007		
p		Cycloberzaprine	C20H21N	0	276 1674	+86	276.17468	0.01	226 17173	-10.7	0	2	10 11	20578	Cycloberaspone	22.1
R		Tronantadrie	C19414N2035	0	314.07251	+86	315,07979	0.01	315.00316	11.9	0	2	12.41	13038		
P		Certicain	C13H20N203S	0	284.11946	+16	285 12674	0.01	265.12577	10.6	0	2	9.75	6492		
1		2772			******		Telephone .		- correction	1167		- 5	100	100		

C: 5 XIC manager (DHF- Hexane extract of Fleures wiff sample 1)

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г	the.	Name	Formula	Solope	Mass (Ds)	Adduct / Modifications	Extraction Mass (De)	Voliditi (Da)	Found At Mass (Ds)	Error (ppm)	Expected RT (min)	RT tolidih (min)	Found At RT (min)	Intensity	Ubrary Hit	Purity Score
P		Suffaquenciales	C14H12N4O2S	0	300.0681	+81	301.07537	0.01	301.07475	-21	0	2	13.32	17602	Subsummaire	91.7
F		Alprenokal	C15HQ3NQ2	0	245.17288	485	250.10016	0.01	250,17952	-2.5	0	2.	192	16257	Alprendel	55.3
Ø		Vincennie	C21HQ6NQ03	0	354.19434	484	368 20162	0.01	365 2018	0.5	0	2	15.23	12097	Yolothe	37
R		Yohimbine	C21H29HQ03	0	354.19434	+81	255 20162	0.01	366 2018	0,6	0	2.	15.23	12997	Yukinbee	37
Ę.		Caproylesoronol	C12H1603	0	208.10994	484	205 11722	0.01	205 3168	- 2	0	2	14.63	6176	Coprophenoronal	45
F		Hatidne	09/8/002	0	155.06548	485	156,07675	0.01	156 07533	-1.5	0	2.	16.50	3039	Heldee	86.7
Ø.		Methylphenidale	C16H19N02	0	233.14158	484	234 14336	0.01	234 14812	-0.2	0	2	11.75	2702	ppercen	58.7
F		Fludrocortisone Acets	C23H31F06	0	422.21047	401	423.21774	0.01	423 2185	2	0	2.	8.66	2261	- Pudrocortoure Acets	100
Ø		Grepatosacin	C16/27NO4	0	297,19401	484	298.20129	0.01	290,20068	-14	0	2	9.35	2155	Gustrosmil	76.1
P.		Adenosine	C10H13N504	0	267,09675	+01	258 10421	0.01	268 10337	-2.5	0	2.	7.61	1756	Alersine	99.4
g.		Roperiole	C10/Q4/Q0	0	260,18886	484	261.19614	0.01	261.19671	2.2	0	2	15.52	5415	Dynetusies	75.5
R.		Osymetazolese	C19494N2O	0	260 18886	401	261.19614	0.01	261,19675	2.2	0	2.	15.52	2415	Digmetassiere	79.8
Q.		Plocarpine	C11H16AQ02	0	206.12118	484	208 12645	0.01	209 12952	5.3	0	2	15.53	6236	Plocupine	55.1
Į.		Urspidil	C20+29N503	0	387.22794	+01	369.23412	0.01	366,23233	-61	0	2.	10.32	4942	Unpidi	68.4
Ø		Benzylpenicillin	C16H18N2O45	0	334.09873	484	335 10601	0.01	335 10921	36	0	2	8.67	4366	Senzylpeniolie	.54
Ø		Dokazoski	C32H43N505	0	577 32642	401	578.3337	0.01	576 33542	3	0	2.	336	4301	Dhydoirpilestini	45.5
g.		Moximylyte	C10425N03	0	279.18344	484	250 19072	0.01	200 19029	-1.6	0	2	10.2	4041	Montplyte	32.5
p.		Flootalenine	C20H17F3N2O4	0	406,11404	+01	407.12132	0.01	407.12504	9.2	0	2.	15.33	3456	Rodelesine	\$2.3
Ç.		Levobunolol	C17H25NO3	0	291.16344	484	292 19672	0.01	202 13067	-02	0	2	10.45	1454	Exceptions	53.4
Ø		Etiroxate	C17H25NO3	0	291.18344	401	292.19072	0.01	252,19067	-0.2	0	2.	10.46	1454	Excatopine	59.4
g.		Quinidine	C17H25NO3	0	291.18344	484	292 19672	0.01	202 13067	-02	0	2	10.46	1454	Excellegine	53.4
p.		3.4-Hethylenedosym	C11H15NO2	O.	193.11029	401	134.31756	0.01	194.11752	-0.2	0	2	34.33	140306	No Match	No Match
g		3.4-Methylenedissyst	C10H13N02	0	179-09453	484	365 30331	0.01	180 10184	-04	0	2	13.56	421835	Prophan	25.0
Ø.		Dexamethosone	C22H29F06	0	392,1999	401	300.20718	0.01	393,20825	4	0	2	8.88	129652		
g .		Flufenamic Acid	C24H30F2O6	0	452,20108	484	453,20632	0.01	453,20654	0.5	0	2	9	57163	Placeoline Acetoni	117
P		Disvendine	C13H16N402	0	290 12733	+24	261.1346	0.01	261.13305	-13.6	0	2.	101	51980	Durendee	100
g.		Betamethasone-17-br	C29H33F06	0	496.22612	48	497 23339	0.01	457.23454	25	0	2	9.1	43997	No March	No March
Ø.		p-(Aninomethyl)benz	CEHSNO2	0	151.06333	401	152,07061	0.01	152,07018	23	0	2.	13.57	39947	No Materi	No Materi
g.		Perscetamol	CEHSNOZ	0	151.06333	48	152 07061	0.01	152,07018	2.8	0	2	1157	38947	No March	No March
p.		Etherganide	C9H11MO2	0	165 07898	+01	166,00625	0.01	166.00597	-1.7	0	2	14.95	39930	No Materi	No. Match
g.		Beroscaine	C9H11N02	0	165.07898	484	166,00036	0.01	166,08597	-17	0	2	14.95	39938	No March	No March
Ø		Physostigmine	C15HZ1N307	0	275.16338	+01	276.17066	0.01	276,17119	4.1	0	2	10.25	27589		
g.		Verlateure	C17H27N02	0	277.26418	+44	278.21146	0.01	278.21086	-21	0	2	13.82	25433		
	1000		-	- 1	100,0000		100000			-		-	1111	- 17.11		

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= =	the.	Name	Formula	Instage	Mass (Da)	Adduct / Modifications	Extraction Mass (De)	Vrlidth (De)	Found At Mass (Da)	Error (ppm)	Expected RT (min)	RT Voldth (min)	Found At RT (min)	Intensity	Library Hit	Punity Score
N P		Berascane	CSHTSNOZ	0	165,07298	-+H	166.03625	0.01	166,02587	-17	g	2	1435	39131	No Match	No March
0 17		Physiolognine	C16+Q1N3O2	0	275.16338	+84	276 17065	0.01	276.17339	4.1	0	2	10.29	27329		
Г		Verlataure	C17H27N02	0	277.20418	-14	278.21546	0.01	279.21086	31	0	7	0.0	25413		
P		Phenelone	C8H12N2	0	136.10005	+84.	137.10732	0.01	137 10707	-1.0	0	2	10.00	25190		
I V		Caffeine	CBHTDN4CZ	0	194 00038	-H	195 00765	0.01	195.09305	17.4	0	7.	11.9	21741	Cafferre	68.2
P		Acetyleslicylic Acet	C9H8O4	0	180.04225	+H	181.04954	0.01	101.04942	-0.7	0	2	15.44	19530		
Ø.		Aceprometizine	C19H22N2O5	0	325.14529	-H	327.15294	0.01	227 15614	10.9	0	7	12.9	74002	Асерпечатия	14
P		Acepromazine	C19422NQOS	0	326 14529	+84	327.15256	0.01	327.15614	10.9	0	2	12.9	18002	Aceptomisme	54
P.		Pindolol	C14HQ0N202	0	248 15248	-H	245.15975	0.01	245.15671	-122	0	7.	8.97	17629	Pindolel	50.5
P		Buntrolid	C14HQ0N202	0	245.15248	+84	249 19975	0.01	245 15671	-122	0	2	8.97	17633	Pindolei	40.5
P.		Indensystem	CT2HISNO	0	201.1266	-H	202 13347	0.01	202 13445	23	0	2	9.01	12612	No Match	No Mano
P		Ciotetamide	C12H22N2O2	0	226.16813	+84	227.1754	0.01	227.17463	-34	0	2	8.97	13432		
Ø.		Mexistre	C11H17NO	0	179.13101	+H	180 13429	0.01	180 13822	-0.4	0	2	15.2	10056		
P		Methylephedrine	CTIHITNO	0	179.13101	+84	180 13829	0.01	100 13022	-0.4	0	2	15.2	10056		
Ø.		N-Methylephedine	C11H17NO	0	179,13101	-H	180 13429	0.01	180 13822	-0.4	0	2	152	10054		
P		Atoniestatin	C33H35FN2O5	0	688-263	+84	558.26028	0.01	555,26242	23	0	2	200	10014	No Match	No State
Ø.		Physotylania	CSHITIN	0	121,00915	+H	122.09643	0.01	122,89521	-1.8	0	7	166	1766	No Match	No Marc
P		Denaverne	C24K33NO3	0	383.24604	+84	364.25332	0.01	364.25262	-33	0	2	13.64	2506	No Match	No Mari
P.		Natidiologi	C24H33NO3	0	383.24934	-H	384.25332	0.01	384.25292	-13	0	7	1364	8598	No Match	No Marc
P		Felbanale	C15H14O3	0	242.09429	+84	243,10157	0.01	243,10162	0.2	0	2	34.51	7017		
Ø.		Foundpril	C13H16N406	0	324.10698	+H	325 15426	0.01	325.11297	43	0	7	5.87	6564	No Match	No Marc
P		3.4-Methylenedoxyet	C12H17NO2	0	207,12593	+84	208.13321	0.01	206 13275	42	0	2	15.53	6376		
P.		Pergolide	C19406A25	0	314.10167	-H	315.18895	0.01	315 19297	11.8	0	2	1134	5440	Perpolde	35.7
P		Advensione	C9H11NO3	0	181,07329	+84	182.08117	0.01	162 00001	-2	0	2	7.54	5254	Adventories	21
P.		Buleranac	C12H17NO3	0	223.12084	+H	224,12812	0.01	224,12797	33	0	2	7.19	4457		
P		Bootin	C12H17NO3	0	223.12084	+H	224 12912	0.01	224.12797	41	0	2	7.19	4407		
P.		Elemen	C12H17NO3	0	223.12004	-11	224.12812	0.01	224,12797	33	0	2	7.19	4457		
P		Dobutamine	C18H23N03	0	301.16779	+H	302,17507	0.01	302,17434	QA.	0	2	15.00	4105		
P.		Isosoprine	C18H23N03	0	301.16779	-8	302 17507	0.01	302,17434	24	0	2	15.69	4106		
P		Dihydrocodeine	C18H23NC3	0	301.16779	+H	302 17507	0.01	302,17434	24	0	2	1540	4105		
R		Nitrendiprie	C18H20N206	0	365.13214	-11	361.13941	0.01	361.14347	23	0	2	15.11	3505		
P		Seoprolol	C18HG1NO4	0	325-22531	+H	326-23258	0.01	326.23188	42	0	2	3.95	3676		
		Ambucetamide	C11H12N30	0	202 09004	-14	201 10531	0.01	203,10574	21	0	2	12.94	3552		

				2		100.00			40000					NO.		
п	1111	Name	Fornula	Inotope	Mass (Da)	Adduct./ Modifications	Extraction Mass (De)	Width (De)	Found At Mass (Ds)	Error (ppm)	Expected RT (min)	RT Width (min)	Found At RT (min)	Intensity	Library Hit	Purity Scor
P		Nitrendigine	C18HQ0NQ06	0	360,13214	-+H	361.13941	0.01	361 14347	23	0	2	1511	3500	1 1	
P		Sisoprolol	C18HQ1NO4	0	325-22531	+84	326-23259	0.01	326.23188	-22	0	2	3.95	3676		
П		Anbucelamide	C11H12N30	0	202 09004	-H	20110531	0.01	203.10574	2.1	0	7	13.94	3552		
P		Caprenolal	C16H23NG3	0	268.16779	+14	266.17507	0.01	266.17187	-12	0	2	11.86	3427	Openiul	647
R.		Gernibrool	C15H22O3	0	250,15689	-H	251.16417	0.01	251 16307	-4.4	0	7	14.5	2206		
P		E-Hydroxygunoline	C9H7NO:	0	145.05276	+H	146,06004	0.01	146.0537E	-1.0	0	2	8.85	3323	0-Hydronysanoline	21.4
P.		Prednisone	C21HQ6O5	0	358.17902	-H	359 1952	0.01	353 18436	-0.9	0	7	9.43	2917		
P		Iprozochrome	C12H16N400	0	254.12224	+84	368 52962	0.01	265 13062	43	0	2	8.97	2797		
P.		Acadeline	CSHISNOZ	0	169 11028	-H	178.31754	0.01	178.11721	- 4	0	7	10.45	2647	Aceddon	17.4
P		Dispusión	C9H15NO2	0	169.11028	+H	170 11756	0.01	170 11721	- 3	0	2	10.45	2647	Acecides	17.A
R.		Methanthelinium	CZ1HONNO3	0	340.19127	-H	341.19855	0.01	341,19095	12	0	7	15.4	2545		
P		Novethisterone acetat	C22H3803	0	340.20385	+H	34121112	0.01	341,2095	47	0	2	38.66	2313		
R.		Norephedrine	CSH13NO	0	151 09971	+H	112 10099	0.01	152 10661	-25	0	7	10.46	2279	Norpreudosphidose	32.9
P		17alpha-Hydroxyprog	C9H13NO	0	151.09971	+H	152,10039	0.01	152 10061	-2.5	0	2	10.46	2279	Norpreudosphidose	12.0
P.		D-Norpseudoephedre	CSH13NO	0	151.09971	-H	152 10099	0.01	152 10661	-25	0	7	10.46	2279	Norpreudosphidose	12.9
P		Phenylproporolamine	CSHTSNO	0	151.09971	+84	152,10639	0.01	152 10661	-2.5	0	2	10.46	2279	Norpreudosphidose	12.8
P.		Norpeeudoephidrens	CSH13NO	0	151 09971	-H	152,10099	0.01	152 10661	-25	0	7	10.46	2279	Norpreudosphidose	32.9
P		Raubasine	C21HQ4N203	0	352,17009	+84	363.19597	0.01	363.18667	12	0	2	14.32	2200	Badowe	72.8
P.		Norethisterone	C50H5605	0	298.19328	-H	299 20004	0.01	299,20049	-02	0	7	14.45	2153		
P		Nandrolone	C18H2602	0	274.19329	+84	275.20096	0.01	375,20115	22	0	2	15:91	2131	Numbelow	65
P.		Setaine	CSHTSNOZ	0	117.07098	-14	118.00625	0.01	118,88601	31	0	7	. 8.33	1811		
P		Valacyclovir	C13H00N604	0	324.1546	+86	325 16188	0.01	325.35113	-23	0	2	12.93	1529		
P.		Conine	CBH17N	0	127,1361	-H	176 14336	0.01	128 14305	-26	0	7	1531	1417		
P		Diopropione	C24HG0C3	0	366 2196	+84	367.23677	0.01	267 22528	41	0	2	14.53	1351		
P.		Etofenamute	C18H18F3NO4	0	363.11679	-H	378 12507	0.01	370 12736	35	0	7	12.63	1318		
P		Diffuontokove	C29H0N2O4	0	450.29881	+8	481 30008	0.01	481 30648	0.0	0	2	14.53	1206		
P.		Clotapine	C19H29N03	0	319.21474	-14	320 22202	0.01	320 22 161	-13	0	7	10.29	1172		
P		Trimethoprim	C14H18N403	0	290.13729	+H	291,34517	0.01	291.34137	-0	0	2	.8.13	1009	Directopin	95.5
P.		Directuron	C15H19CR403	0	338.11457	-14	338 12184	0.01	339 12514	- 4	0	7	14.65	10021	Directuron	75.8
P		Hydrocodisone	C21H0005	0	362.20932	+H	363.2166	0.01	263.21391	-24	0	2	14.50	2001	Hydrocordonne	75.3
D.		Terbutryn	CICHINAS	0	241.13612	-14	24234009	0.01	242.14552	11	0	7	14.72	4576	Prometryn	30.2
P		Prometryn	C10H19N65	0	241.13612	+84	20,1031	0.01	242 14552	11	0	2	14.72	4576	Prometyn:	30.2
P	0.00	Oxelomide	C27H00NHO	0	426.24196	-14	427 24924	0.01	427.24561	47	0	7	15.14	2243	Chatomde	55.5

г	1114.	Name	Formula	Jackspe	Mass (Da)	Adduct / Modifications	Extraction Mass (Cla)	Width (Da)	Found At Mass (Da)	Error (ppm)	Expected RT (min)	RT Width (min)	Found At RT (min)	Interesty	Library Hit	Punty Sco
D		Terbutye	CIOHISNES	0	241.13612	40	242 14379	0.01	242,14552	88	0	2	14.72	4876	Prometryn	30.2
D.		Prometryn	CIOHISMIS	0	241.13612	+14	242,34339	0.01	242.14552	11	0	2	14.72	4576	Prometon	30.2
Г		Oxatomide	C27H00N4O	0	425.24196	+11	427,24524	0.01	427.24551	4.7	0	2	15.34	2243	Oustorride	46.6
D.		Appimox	C9H6N203	0	154.00784	+14	185 94532	0.01	155,04611	64	0	2	11.37	A3169	No Match	No Main
D		Amoulpride	C17H27N3O4S	0	369.17223	+11	370.1796	0.01	370.16177	63	0	2	1534	40210		
D.		Ininosibera	C14H1G94	0	240 1375	+14	241.14477	0.01	241.14234	75	0	2	1471	27658	No Match.	No Main
D		Cyclobergaprine	C20H21N	0	275 1674	+11	276.17462	0.01	276,17212	-83	0	2	10.25	26261	Cyclobergapone	21.1
D.		Sutallylonel	C25H0406	0	430.23554	+14	431.24382	0.01	431,34538	53	0	2	10.1	12031		
D		Azapropazone	C16H20N402	0	300.15363	+11	301.1059	0.01	301.1641	4	0	2	34.00	12501	No March	No Marci
D.		Sulfalere	C11H12N4O3S	0	280 06301	+16	281 07029	0.01	201,07038	0.3	0	2	3.00	12208	No Match.	No Main
D		Sufamethorypyndadi	C11H12H403S	0	280.06301	+81	261,07029	got	281,07038	0.3	0	2	386	12200	No Metch	No Marc
D.		Bunazosin	C34H5007	0	570,35565	+16	571.36293	0.01	571,36266	-01	0	2	1570	11022		
P		Molindone	C10404N202	0	276.36378	40	277.19105	0.01	277.19106	3	0	2	15.7	9765	No March	No Marc
P		Cyclovalone	C22H22O5	0	366.14672	+11	367.184	0.01	367,35696	83	0	2	8.76	2112		
P		Trapidil	CTOHISMS	0	205.13275	+81	206.54002	0.01	206.13039	-33	0	2	1579	6622	Trioldi	13.7
P		Becontypine	C20HQ5NO3	0	327.19344	+16	328 19072	0.01	226.16762	-0.5	0	2	1376	4743		
D		Abretanine	CSH18N6	0	210.15929	+10	211.19657	0.01	211.10801	63	0	2	14.6	4603	No March	No Mate
P.		Rampel	C23H32N2O5	0	416 20112	+16	417.2384	0.01	417.23827	-0.3	0	2	3.55	4217		
D		Ampiolin	C19H19N3O5S	0	365,10454	+10	366.11182	0.01	366.10809	46	0	2	15.78	3000		
P.		Carazolisi	C18H22N2O2	0	290.16013	+14	.299.1754	0.01	299 17435	-3.5	0	2	15.79	3738		
D.		Irridapel	C14H11N	0	193.00915	+10	194.09643	0.01	194.09644	0.5	0	2	14.93	3276		
P		Beoltweide	C31H32HN4G2	0	453.29035	+14	494 26763	0.01	494.255A	1.6	0	2	9.65	3142		
P		Anbenorium	C29H34O5	0	354 24062	+11	395.2479	0.01	355.2453	73	0	2	13.13	3006		
P		Didanosine	C20H3405	0	354.24062	+16	765.2479	0.01	255,2453	73	0	2	13.13	3000		
P		Anosolio	C28H42CI2N4O2	0	536.26848	148	537,27576	0.01	537.27732	29	0	2	12.49	2900		
P		Mequitagne	C20H22N25	0	322,16037	+16	322 18765	0.01	323 1606E	9.3	0	2	9.00	2946		
P		Metamiron	C10H10N4O	0	202,00546	+81	203.09274	0.01	203.0919	41	0	2	12.64	2002	Metarologic	17.1
F		Laberalol	C19H24N2O3	0	325.17069	+16	325.18557	0.01	229.18671	2.7	0	2	9.37	2687		
P		Daunorubion	C22H29F04	0	376.20439	748	377.21226	0.01	377,21407	4.1	0	2	9.41	2982		
P		Fluocortin Buryl	C22H29F04	0	376.20499	+16	377.21226	0.01	377.21407	4.0	0	2	9.41	2652		
D		Berzoctamine	CIBHIN	0	249.15175	+11	250,15303	0.01	250,15367	3.4	0	2	1.90	2676		
P		Methylthiourasil	CSHONOOS	0	142,02008	- 11	143.02736	0.01	143,0201	52	0	2	11.34	2530	Helythousol .	19.0
P		Butorycoine	C17H27NO3	0	293.19909	+11	294.29637	0.01	294,2006	0.0	0	2	14.26	2136		

Manage													9	N.	1.11	
г	the.	Name	Formula	lastope	Mass (Ds)	Adduct / Modifications	Extraction Mass (De)	Width (De)	Found At Mass (De)	Error (ppm)	Expected RT (min)	RT Width (min)	Found At RT (min)	Intensity	Library Hit	Purity Score
P.		Berzoctamine	CTBHSM	0	249.15175	-H.	250,75903	0.01	250 15167	34	0	7	136	2576		
P		Metrythiourack	CSHRNZOS	0	142,02008	+H	143.02736	0.01	342 0081	5.2	0	2	11.14	2530	Rehylhousol	70.0
Г		Butorycaine	C17H27N03	0	293.19909	-11	294.20637	0.01	794.2066	0.0	0	7	14.25	2136		
P		Nonverside	C17H27N03	0	293 19909	+81	294,20077	0.01	294.2066	0.1	0	2	34.26	2136		
₽.		Enturanide.	C17H27N03	0	293 19909	-14	294.20637	0.01	794.2066	0.8	0	7	14.25	2136		
P		Amphetamine	CSHT3N	0	135 1048	+H	136 11208	0.01	136.11133	-8.5	0	2	8.07	2019		
P.		Norfoxaon	C16H18FH003	0	319 13322	-11	220 1405	0.01	320 13951	- 31	0	7	2.65	1776		
P		Clonipravine	C19HZ3CNQ	0	314.15498	+H	215.16225	0.01	315.13919	-67	0	2	15.85	1714		
R.		Dosorution	C20H28N	0	212.22218	-H	793.22345	0.01	283 22712	-7.5	0	7	14.53	1954		
P		leoproturon	C12H18N2O	0	206.14191	+H	207.34313	0.01	207.15063	73	0	2	9.13	3654		
R.		Flurarcine	C15H13F02	0	244.00996	-14	245,09723	0.01	245 (9865	5.5.	0	7	215	1455		
P		Testosterone	C19H2802	0	210.20893	+H	205/21621	0.01	209.21430	-4.2	0	2	13.67	3422		
P		Tolycame	C15H22N2O3	0	278.16304	-H	279 17032	0.01	279 16528	-37	0	7	344	1387		
P		Fluoroutsol	C24H29FD6	0	432.19432	+H	433,20209	0.01	433.20426	8	0	2	8.62	1307		
P.		Cinetidne	CTOHTENES	0	252,11572	-14	253 12299	0.01	253 1237	2.8	0	7	1.65	1072		
P		Benzoyleogonine	C16H19NO4	0	288 10141	+H	290,13958	0.01	290 13817	-880	0	2	15.05	1001		
P.		Selbutanol	C13HZINO3	0	239.15214	+H	240.15142	0.01	240 15364	0.9	0	7	12.85	1047		
P		Hekazinone	C12H20N402	0	252.15363	+H	253.1650	0.01	253.16439	4	0	2	.876	3036		
P.		Metamphetamine	C10H15N	0	149.12045	-8	150 32773	0.01	150 12677	-64	0	7	971	1006		
P		Fluorisone	C21H25FNQ02	0	356.19001	+84	267,19728	0.01	367,20044	1.0	0	2	15.81	1027		
P	***	Descriptortore 21-Ch	C30H38O4	0	462.27701	-8	463.26429	0.01	463.29039	-8.4	0	7	10.69	1020		
P		7-Aninodesmethyffur	C16H12FN3O	0	269.09644	+8	270 10372	0.01	270.50311	42	0	2	34.0	1016		
P.	***	Amidotraoic Acid	C12H904	0	216.04226	-H	217.04954	0.01	217.04741	- 51	0	7	12.77	1007		
P		Aminodaritylene	C14H12N403	0	294.09094	+84	205-09022	0.01	205 00006	-18.2	0	2	54.97	100550		
P		Betweende	C10H15N3	0	177 1266	-8	178.13387	0.01	176 13022	-70.5	0	7	10.96	10230		
P		17-alpha-Methyltestor	C20HG0C2	0	302.22458	+H	303.23196	0.01	303.23178	-03	0	2	15/07	2645		
P.		Minazone	C17H16N402	0	308.12733	-8	339 1546	0.01	309 13094	-118	0	7	13.99	7112		
P		Methapytions	C14H19N35	0	261.12997	+H	262,13725	0.01	262 13415	-11.2	0	2	131	1606		
P		Tronsitadine	C19H14N203S	0	314 07251	-8	215.07979	0.01	315 88332	112	0	7	10.29	5200		
P		Melenide	C7H10N202S	0	186,0463	+H	187,05358	0.01	187 05136	-11.0	0	2	12.36	400	No Match	No Statut
P.		Certimazole	C7H10N202S	0	186,0463	-H	107.05358	0.01	107/05136	-118	0	7	1236	4481	No Match	No Munch
P		Granisation	C10H14O4	0	196.08921	+H	190,00643	0.01	109 09353	-162	0	2	1123	3400		
P		Procamamide	C13HZ1N30	0	235 16545	-11	236.17574	0.01	236 17221	-14.9	0	7.	13.53	3341		

C: 6 XIC manager (DHG- Hexane extract of Siyakholwa honey wiff sample 1

lanager				2										0		
г	11/11	• Name	Formula	lastope	Mass (Da)	Adduct / Modifications	Extraction Mass (De)	Velidite (Che)	Found At Mass (De)	Error (ppm)	Expected RT (min)	RT Width (min)	Found At RT (min)	Intensity	Library Hit	Purity Soo
P.		Vardenski	C23H32N6O4S	0	488.22058	-H.	489-22785	0.01	489 22581	- 21	0	7	13.45	45301	Vardenski	35.7
P		Sulfequinocoline	C14H12N4D2S	0	300.0681	+84	301.07537	0.01	201.07543	8.4	0	2	12.51	13504	Subspinissing.	31
P.		Alprenolat	C154G3N0Z	0	245.17288	-H	250 38016	0.01	250 19023	0.3	0	2	1.63	15975	Algrendel	56
P		Nandrolone	C18H2902	0	274,19329	+84	275.20096	0.01	375,20049	-02	0	2	15.76	15513	Nurdrolone	29
R.		Urapidil	C20H29M5C3	0	387.22704	-H	388 23432	0.01	386 23272	4.9	0	2	3.53	1000	Unpdi	72
P		Difficzem	C22H26H2O45	0	414.16133	+84	416.16961	0.01	415.36821	-0.9	0	2	10.02	4774	Ditease	32.3
P.		Fludrocortisone Acets	CZHITEOE	0	422.21047	-H	423.21774	0.01	423.21362	42	0	2	8.11	2676	Flubrocortiones Aceds	100
R		Admire	CSHSNS	0	135.0545	+84	136 06177	0.01	136 06178	0.1	0	2	0.6	2295	Aderes	79.8
P		7-Aminodesmethylflur	CISHIZENSO	0	268.09644	-H	279.10372	0.01	770 10249	-4.5	0	2	54.A	52217	7-Annodemetyffur	43.1
P		Vincamere	C21HQ9NQ00	0	354.19434	+84	365 20162	0.01	355 20248	2.4	0	2	18.51	12000	Yshelbee	36.4
P.		Yolombine	C21H09N203	0	354.19434	-H	265 20162	0.01	366 20248	24	0	2	15.51	10000	Yototave	36.4
R		Tarrosteri	C26H29NO	0	371.23491	+84	372 23233	0.01	372.23155	4.7	0	2	8.35	14196	Tansoles	79.8
P.		Salcatate	C14H1006	0	258.05282	-H	251 0601	0.01	259 05825	-7.5	0	2	11.47	11578	Alternated	A15
F		Hydrocodisone	C21H0006	0	362 20932	+84	363.2166	0.01	363.21877	-6.	0	2	1276	6882	Hydrocordonne	55.6
P.		Methylpheridate	C14H19NOZ	0	233.14158	-H	214,14886	0.01	234.54889	0.2	0	2	11.09	4506	pipercoan	33.7
F		Oxprenotal	C16H23N03	0	268.16779	+84	266.17507	0.01	266.17336	-65	0	2	11.14	4705	Openial	542
P		Caproylesceninol	C12H1603	0	208.10994	-H	20111722	0.01	209 11666	-27	0	2	13.99	4716	Capro/resorced	36.6
R		Flapented	CZSHQSF3NQOS	0	434.16397	+84	436.17125	0.01	435.1743E	83	0	2	10.91	1556	Papertial	39.2
P.		14-Methylenedosym	C11H15NOZ	0	193 11028	-H	194.53754	0.01	194.11734	43	0	2	1434	214298		
₽		3.4-Mathylenedoxyar	C10H13NO2	0	179 09463	+84	180 10191	0.01	180.10167	-13	0	2	12.9	111602	Prophen	263
P.		Fluienamic Acid	C24H30F20K	0	452.20105	-H	453 20832	0.01	453.20192	3.5	0	2	2.45	74770	Fluorotore Acetons	11.7
P		Verlatuine	C17H27NO2	0	277.20418	+84	279.21146	0.01	279.21131	-05	0	2	15.48	67630		
D.		Setamethosone-17-bi	C29H33F06	0	496.22617	-H	497.23339	0.01	497.23558	4.4	0	2	8.57	36731	No Match	No Mano
P		National	C24H33NO3	0	383.24604	+84	364.25332	0.01	384.25301	-011	0	2	15.13	12934	Thirtedologi	313
P.		Denzierine	C24H33NO3	0	363.24904	-H	384.25332	0.01	384.25301	-0.0	0	7	15.11	18934	Nationality	51.1
P		Diaveridine	C13H16N402	0	260.12733	+84	261.1346	0.01	261 13141	-122	0	2	7.00	19729	Devention	100
P.		Phensione	C8H12N2	0	136.10006	-H	137.10732	0.01	137,30701	-23	0	7	954	13061		
F		Denetor-O	C8H1903PS2	0	258.05133	+84	259.0506	0.01	259 05825	-14	0	2	11.47	12202		
P.		Betweende	C10H15N3	0	177.1266	-H	178.12367	0.01	178 1305	-19	0	7.	10.61	11414	Detracións	40.6
P		p-(Aminomethyl)benz	CEHSNO2	0	151.06333	+84	152 07061	0.01	152,07061	-0.6	0	2	12.00	10431		
P.		Paracetamol	CSH5NO2	0	151.06333	-H	152,07061	0.01	152,07051	-06	0	7	12:57	10425		
P		Caffone	C8H10N4C2	0	194,00038	+84	196 00765	0.01	195 09138	19.2	0	2	1131	10395	Ceferre	40 A
R.		Etherganide	CSHTINGS	0	165.07298	-H	166.03625	0.01	166,00581	-27	0	7	14.27	10152	No Match	No Marc

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п	Ilir.	Name	Formula	Inologie	Mass (Da)	Adduct / Modifications	Extraction Mass (De)	Width (Dw)	Found At Mass (Da)	Error (ppm)	Espected RT (nin)	RT Inlight (min)	Found At RT (min)	Intensity	Library Hit	Punity Score
R		Paracetamol	CBH5NO2	ū	151.06333	-14	152.07061	0.01	152,07051	-06	0	2	1210	10428	1	
P		Ceffeine	C8H10N4O2	0	194,00038	+H	196 00765	0.01	116 09139	19.2	0	2	1131	10295	Cellene	65.4
F		Elterasmide	CBH11NO2	0	195.07838	-11	166.08626	0.01	166 00581	47	0	2	14.27	10152	No Match	No Mater
P		Berasceine	CBHTTMO2	0	145.07896	+H	166,00626	0.01	166 00321	-27	0	2	14.27	10152	No Match	No Mand
R		Ampropazone	C19420N402	0	300.15863	-14	201,1659	0.01	301.16466	45	0	2	14.03	10041	Azspropazone	23
2 17		Lovestatio	C2010605	0	401,25627	+H	406.26355	0.01	435,2638	06	0	2	1348	8907		
P		17-alpha-Methyltestor	C20H0002	0	302,22458	+H.	3012118	0.01	303 23201	8.5	0	2	14.63	8370		
P		Dehydrocholic soid	C20H0405	0	400.24062	+14	103 2479	0.01	403 34723	117	0	2	12.26	7825		
P		Metenolone scetate	CZ2H02O3	0	344.23515	-44	345.24242	0.01	3852007	0.7	0	2	1426	7653		
P		Acetylaslicylic Acid	CSHEDE	0	180.04226	+H	181.04354	0.01	181 04935	- 31	0	2	10.12	7559		
P		Crotetanide	C12H22N202	0	225.16813	-14.	227.1754	0.01	227.1754		0	2	830	5554		
P		Noniverside	C17H27NO3	0	293.19909	+91	294,20637	0.01	294.20763	8	0	2	10.70	5000		
P		Enbutramide	C17HQ7NO3	0	293.19909	-14.	294-20637	0.01	79420783	- 6	0	2	1578	5000		
P		Butosyceine	C17H27N03	0	293,19909	+H	294.20637	0.01	294.20783	- 5	0	2	15.79	5000		
P		N Nethylophedine	CT1H17NO	0	179.13101	-14.	185 13429	0.01	180 12809	43	0	2	14.53	5272		
P		Methylephedrine	C11H17NO	0	179,13101	+H	180 13829	0.01	180 13800	-1.1	0	2	14.53	1272		
P		Nesistne	C11H17NO	0	179.13101	-14	185 13429	0.01	180 12809	43	0	2	14.53	5272		
P		Gentlonal	C15H22C3	0	250,15689	+H	291.16417	0.01	251.1641	-0.1	0	2	9.82	5063		
P		Doozzoen	C32H43N505	0	577.32642	-11.	A78.3337	0.01	578.33464	16	0	2	8.83	4420		
P		Mosseylyte	C16425N03	0	279.18344	+H	260,19072	0.01	250 19108	13	0	2	3.00	4414	Municiples	17.3
P		Prednisone	C21HQ605	0	358.17902	-11	288 1853	0.01	358 13529	-81	0	2	8.93	3504		
D		Phenethylamin	CBritis	0	121,08915	+91	122 09643	0.01	122 09631	-0.9	0	7	7.91	3000	No March	No March
D		Butathylonal	C25H3406		430.23554	-#	431.24212	0.01	431 74347	15	0	2	9.71	3690		
Ø		Englapel	C20HQ8NQO5	0	375.19902	+H	377.2071	0.01	377 20752	11	0	2	1276	2547		
D		THC	C21H0002		314.22458	-#	315.23186	0.01	315.23198	84	0	2	1217	3384		
D		Bulexamac	C12H17NO3	0	223.12084	+H	224 12812	0.01	224 12904	-0.4	0	ž	4.8	2198		
P		Sucein	C12H17N03	0	220,12084	-#	224.12012	0.01	224 12804	-0.4	0	2	436	3150		
D		Elanivari	C12H17N03	0	223.12084	+H	224 12812	0.01	224 T2904	-0.4	0	2	4.8	2198		
P		Adversione	CHITMOT		181,07389	-#	192 08117	0.01	102.06137	11	0	2	440	3193		
D		Norethisterone sortat	C22HQ803	0	340,20385	+14	34121112	0.01	341,21073	41	0	7	1371	2150		
D		Berzy/penicifin	C19H18H2O4S		334,09873	-#	335 10601	0.01	305 11006	121	0	2	7.54	2055	Berzybenciën	94
10		Hydrocorisone 21-ac	C23H02O6	0	404.21989	+H	406.22717	0.01	405.22713	-01	0	7	1554	2682		
D		Methopostone	C19H14N2O		250,11061	-#	251,11785	0.01	251.11734	42		2	15.15	24%		
			200			1 100				- 17				-		

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г	114	Name	Formula	luolope	Maes (Da)	Adduct / Modifications	Extraction Mass (De)	Infidth (Da)	Found At Mass (De)	Error (ppm)	Expected RT (min)	RT Width (min)	Found At RT (min)	Intensity	Library Hit	Purity Score
P		Bercyberiolin	C16H18N2O4S	0	234 09873	+14	336 10601	0.01	235 11006	12.1	0	2	754	2366	Berz/pencile	34
R		Hydrocortocne 21-ac	C23H3206	0	404,21988	-84	405.22717	0.01	406 22713	-03	0	2	35.54	2602		
г		Methapatine	CIRHARO	0	250.11061	+14	251,11789	0.01	251 11734	-22	0	2	19.15	3496		
R		Dropropialne	C24H3003	0	366.2196	-84	367.22677	0.01	367,22715		0	2	14.03	2491		
P		Setaine	CSH11NO2	0	117.07898	+14	118.00526	0.01	118.00634	0.8	0	2	0.09	2255		
R		Pliocarpine	C11H16N202	0	208,12118	-84	205 12545	0.01	209.12831	-0.7	0	2	15.16	2225		
P		Genolative	CTEHQUINACI	0	312 19501	+H	313 20229	0.01	313.20092	-44	0	2	12.36	2019		
R		Gestodene	C11H22O6	0	346.14164	. 164	347,34812	0.01	347.54301	0.3	0	2	10	1900		
Ø		Conine	CBH17N	0	127.1361	+H	126 14138	0.01	128 14366	14	0	2	19.35	1821		
R		Naturetone	C15H1602	0	228.11503	+84	225 12231	0.01	229.12307	33	0	2	12.01	1519		
P		Euconspine	C201/Q402	0	256.17763	+H	297.15491	0.01	297 18415	-25	0	2	12.55	1454		
R		3-Hydroxyquinoline	C9H7NO	0	145,05276	-64	146.06004	0.01	146,09336	46	0	2	103	1309		
P		Telrosopres	C16H22N4O4	0	234.16411	+81	335.17138	0.01	236 36775	-10.8	0	2	756	1253	Tehnogein	813
P		Theotoprine	C7H8N402	0	180.05473	-64	161.072	0.01	181,07201	g g	0	2	7.57	1216		
Ø		Thesphyline	C7H8N402	0	180.06473	+H	181 072	0.01	181.07201	0	0	2	757	1216		
P		Buprolezin	C16H23N005	0	305.15618	. 44.	306.16346	0.01	306 16154	-5.2	0	2	7.88	13643	Banker	44.7
P		Deconettasone	C22H29F06	0	292.1999	+81	350:20718	0.01	383,30954	- 4	0	2	8.20	140719		
R		Mesazone	C17H16N402	0	308.12733	-84	309 1346	0.01	309 13304	- 4	0	2	12:17	79092		
Ø		Adpinox	C9H6N203	0	154.03784	+H	155.04512	0.01	115.04654	9.1	0	2	10.84	61562	No Mature	No March
R		Innotibere	C14H16N4	0	240.1375	. 44.	241.14477	0.01	245.34336	-63	0	2	33.95	19027	No Hatch	No Mest
Ø		Oxatorode	C27H00N40	0	426.24196	+14	427.24924	0.01	427.24558	-41	0	2	13.32	3635	Outstale	13.5
R		Teoseide	C11H16N2O	0	192,12626	-64	190.13354	0.01	183,13089	-13.7	0	2	31.1	9539	1-(4-methosyphosy0);	45.1
p		Cydovaline	C22H22O5	0	366 14672	+H	367.154	0.01	367 55636	7.8	0	2	8.15	8135		
P		Olanzapine	C17H20N4S	0	312.14087	.66	313,34835	0.01	313.34779	-53	0	2	15.75	7760		
P		Feltavole	C15H1403	0	242.09429	+81	243.10157	0.01	243.1014	-0.7	0	2	13.72	5425		
R		PlanipiE	CZ3H02N2O5	0	416.20112	-64	417.2364	0.01	417.23869	0.7	0	2	106	6421		
P		Celszedone	C22H3004	0	258.21441	+8	359 22159	0.01	389.22301	-1.9	0	2	13.48	1623		
P		Testosterone benzzat	C22HG0G4	0	358.21441	.66	369.22169	0.01	369:22101	-1.5	0	2	32.48	5825		
P		Sisoprolei	CTEHOTNOS	0	325.22531	+H	335-23259	0.01	336,7334	-0.6	0	2	3.43	5503		
P		Dapiprocole	C19H27N5	0	-325.22965	-64	326 23332	0.01	336,2334	43	0	2	349	5399		
Ø		Disspyramide	C21H29N3O	0	339.23106	+H	340 23834	0.01	340 23409	-66	0	2	14.66	550		
P		Altretarrine	C9H18N5	0	210 15029	. He	211.16957	0.01	211,1686	9.6	0	2	1156	3740		
Ø.		Redusine	C21H24N2O3	0	252,17069	+81	263 14187	0.01	303 1646	-33	0	2	19.21	3523		

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Е	Mir	• Name	Formula	lackspe	Mass (Da)	Adduct / Modifications	Extraction Mass (Dx)	Width (De)	Found At Mass (De)	Error (ppm)	Expected RT (nin)	RT Width (min)	Found At RT (min)	Intensity	Ubrary Hit	Purity Soo
P		Indonazoline	C12H15N3	0	201.1266	+11	202 13387	0.01	200 13557	8.1	0	2	842	3409		
P		Perbutolol	C18H29NO2	0	291,21963	(40)	292.22711	0.01	290.22732	0.7	0	2	15.5	3343		
г		Heroin	C21HQ8O4	0	344.19876	+16	345.20004	0.01	345,20643	13	0	2	11.00	3123		
P		Valacyclove	C13H20N6O4	0	324.1546	+11	325.16138	0.01	325.76233	1.4	0	2	130	2042		
R		Bensenand	C11H13NSO5	0	295.09167	-14	294,09895	0.01	296 09663	7.8	0	2	13.62	2741		
D		Carteroxolone	C16H26N2O6S	0	358.15624	+10	368.16362	0.01	359,16253	28	ů.	2	15.52	2629		
R		Heldre	C9H9N302	0	155,06948	+14	194,07675	0.01	156.07671	-0.3	0	2	14	2517		
D		Timolol	C13H24N4D3S	0	316.15691	+11	317.16419	0.01	317.16517	3.5	ů.	2	12.50	2502		
R		Florocemine	C15H21F3H202	0	318.15551	+14	219.16279	0.01	319.16415	43	0	2	15.67	2056		
D		Amen	C10H14N2O4	0	226.09536	148	227.10363	0.01	227.10469	5.3	ů.	2	15.24	2034		
R		Hymecromone	C10H803	0	175.04734	+16	177.05462	0.01	177.054	-0.5	0	2	13.52	1705		
D		Mephacaine	C12H13NO2	0	203.09463	+81	204.10191	0.01	254.30167	43	ů.	2	3423	1546		
P		Nordine	C12HQ1M50252	0	331,11367	+16	332 12095	0.01	332 11933	-4.9	0	2	12.16	1500		
P		Develuron	C15H19CRMO3	0	336.11457	+10	335.32184	0.01	339 11964	44	ů.	2	10.06	1129		
R		Anbuostanide	C11H12N00	0	202.09804	+14	203.10531	0.01	203,196	34	0	2	15.77	1430		
D		Metarstron	C10H10N4O	0	202,08546	+81	203.09274	0.01	203.09236	-13	ů.	2	12.01	1322		
P		Oxonematine	C18H22N2O2S	0	300.1402	+16	221.14748	0.01	331.14575	-52	0	2	929	1263		
P		Metrylthoursell	CSHRIQOS	0	142.02008	140	143.02736	0.01	143.02493	-37	ů.	2	10.64	1220	Mehythousol	31.7
P		Norlosson	C16H18FN003	0	319,13322	+16	320,1405	0.01	220 13967	-2.6	0	2	7.95	1101		
D		Transvarvic acid	CBH15NO2	0	157,11028	+81	156.11756	0.01	156.51005	3.1	ů.	2	921	1093		
P		Acecidine	C9H15NG2	0	169.11026	:+16	170 11756	0.01	170 11095	-1.6	0	2	8.90	1062		
D		Diagrande	C9H15NO2	0	169,11026	140	179 11756	0.01	170.33136	3.6	ů.	2	8.90	1063		
R		Fluorinoride	C29405F05	0	446.24685	+16	447,25413	0.01	447.25607	43	0	2	13.54	1059		
D		Aminodantrolene	C14H12N4G3	0	284,09094	+11	265.09622	0.01	285 09451	-11	ů.	2	13.95	56228		
P		Tromentadine	C16H14N2O3S	0	314.07251	+16	215.07979	0.01	315.0636	12.7	0	2	9.87	9100		
D		Carboan	C13H20N2O2S	0	284,11945	+0	265 12674	0.01	285.1306	13.2	ů.	2	3.47	9636		
P		Seleplin	C25H08O5	0	418.27192	+11	419 2792	0.01	419.27811	-2.6	0	2	13.95	8120		
D		Virenol	C21H01CM20	0	362.21249	+0	363.21977	0.01	363.21938	43	ů.	2	12.79	7322		
P		Pindolol	C14H20N2O2	0	248.15248	+16	249.15975	0.01	349.15719	-10.3	0	2	8.33	5404		
D		Burstrotol	C14H20N202	0	248.15248	+0	248 19975	0.01	245 35719	-10.3	ů.	2	833	5404		
P		Monocrotophos	C7H14NO5P	0	223.06096	+11	224.06824	0.01	224.96429	-172	0	2	12.60	5331		
P		Methylprednisolone	C22H3005	0	374-20932	+0	375.2166	0.01	375/21484	47	ů.	2	11.69	4520	January II	15.9
P		Granieron	C10H14O4	0	198.08921	+16	199,09949	0.01	119,09312	-12.0	0	2	10.01	4321		

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г	the.	Name	Formula	lactope	Mass (Da)	Adduct / Modifications	Extraction Mass (De)	Width (Da)	Found At Mass (Da)	Error (ppm)	Expected RT (min)	RT Width (min)	Found At RT (min)	Intensity	Library Hit	Purity Score
P	***	Monocratophen	C7H14NO6P	0	223.06096	+16	224,06824	0.01	224,06428	-172	0	2	12.65	5331		
P		Methylprednisolone	C22H30O5	0	374.20932	+H	375.2166	0.01	375,21464	4.7	0	2	11.69	4520	Jasenske II	35.0
Г		Gransetter:	C10H14O4	0	198.00921	+86	139.09643	0.01	199 09992	-128	0	2.	10.61	4321		
P		Didanosine	C20H34O5	0	354.24062	+H	365,2479	0.01	355,24669	-0.4	0	2	12.32	3866		
P		Anbenorium	C20H34O5	0	354 24062	486	355.2479	0.01	388/24668	-34	0	2	12:32	3966		
P		Corticosterone	C21H30Q4	0	346.21441	+H	347,22163	0.01	347,221	-2	0	2	13.19	3750		
P		Testosterone	C19H2802	0	258.20053	+86	20121621	0.01	289.23636	0.5	0	2	143	3680		
P	* **	Techutryn	CTOHIONES	0	241.13612	+H	242.14331	0.01	242.14668	13.6	0	2	13.99	3671		
P		Prometryn.	CIDHISMSS	0	241,10612	+96	242.14339	0.01	242 14668	13.6	0	2	1339	3671		
P	* **	Megutazine	C20HQ2NQ5	0	322.15037	+86	323.15765	0.01	223.16238	137	0	2	13-13	3381		
P		Glmepiride	C24H34N4O65	0	450,22499	+86	491.23227	0.01	491,23266	0.0	0	2	13.3	2990		
P	****	Ethyl glucuronide	C2H6Q45	0	125 99008	+H	127,00056	0.01	127 00159	-344	0	2	10.83	2402		
P		3-Hydrorynsperidone	CZ3HZ7FN4O3	0	426.20672	+94	427.234	0.01	427.2135	-12	0	2	12:38	2436		
P	* **	Phecobarbital-DS	C10H16N203	0	212.11609	+86	213.12237	0.01	213.12567	15.4	0	2	15,25	2376		
P		Apolaron	C12H14N4O	0	230.11676	+96	231 12454	0.01	231 12006	-172	0	2	7.85	2301		
P	* **	Methapyriene	C14H10N35	0	261.12997	+86	262.13725	0.01	262,13433	-115/	0	2	7.66	2294		
P		Norethisterone	C50HG605	0	298.19328	+36	299 20056	0.01	299.2006	0.2	0	2	12.79	2265		
P		Bunazosin	C34H5007	0	570.35565	+81	571.36293	0.01	571.36067	-3.6	0	2.	13.96	2207		
P		Practiciol	C14H22N2O3	0	266.16304	+34	267.17032	0.01	267 17052	0.7	0	2.	15.55	2196		
P		Aterold	C14422N203	0	266.16304	+H	267 17032	0.01	267,17052	0.7	0	2	15.56	2196		
P		Cyclopentoberbital	C6H10N6CI	0	182.09161	+36	163,09619	0.01	383 30364	15	0	2	10.85	2006		
P	* **	Carbinacole	C7H10N2O2S	0	186 0463	(+H	187.05358	0.01	187.05166	-10.2	0	2	11.03	1970		
P		Malende	C7H10N2O2S	0	186 0463	+36	187.05358	0.01	187.05166	-10.2	0	2	11.83	1970		
R		Nitrendpine	C18H20M2O6	0	360,13214	+H	361,13941	0.01	361 13943	0.1	0	2	11.60	1900		
P	• • •	Isosuprine	C18H23NQ3	0	301.16779	+16	302.17507	0.01	302.17447	- 2	C	2	15:05	1721		
P		Dobutamine	C18H23N03	0	301.16779	+H	362.17507	0.01	302.17447	-2	0	2	15.05	1721		
P	• ••	Dhydrocodeine	C18H23N03	0	301.16779	+86	302.17507	0.01	302,17447	- 2	0	2.	15.05	1721		
P	• ••	Dapsone	C27H29NO10	0	527.17915	+H	121.186Q	0.01	528.18793	2.8	0	2	19.26	1610		
P		Tenposide	C56H35O3	0	302.23515	+86	393.24242	0.01	203/24424	45	0	2	1221	1561		
R		Detajmium	C27H42N3C3	0	456.32262	+H	457,32903	0.01	457,33074	1.9	0	2	11.61	1239		
P	****	Melesamide	C15H24N2O3	0	280,17868	+16	28118997	0.01	281.18972	13.4	0	2	13.65	1019		
R	• ••	Quinidine	C17H2SNO3	0	291,18344	+H	292.19072	0.01	292,19209	47	0	2	10.13	1000		
P		Levoburold	C17HQ5N03	0	291.16344	496	292.19072	0.01	292,13209	4.7	0	2.	10.13	1003		