

**DEVELOPMENT OF DECISION SUPPORT
SYSTEM FOR IDENTIFICATION OF
MEDICALLY IMPORTANT
ENTEROBACTERIACEAE**

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TABLE OF CONTENT

ACKNOWLEDGEMENT	ii
TABLE OF CONTENT	iii
LIST OF TABLE	viii
LIST OF FIGURE.....	ix
LIST OF ABBREVIATION	x
LIST OF SYMBOL	xii
ABSTRAK	xiii
ABSTRACT.....	xv
CHAPTER 1	1
INTRODUCTION	1
1.1 Background of the study	1
1.2 Problem statements	2
1.3 Research questions.....	2
1.4 Objectives of the study.....	3
1.4.1 General objective.....	3
1.4.2 Specific objectives.....	3
1.5 Definition of terms	4
1.5.1 Decision support system.....	4
1.5.2 Enterobacteriaceae.....	4
1.5.3 Diagnostic test	5
1.5.4 Open Source Software.....	5
1.6 Significance of the study.....	5
1.7 Research scope.....	6
1.8 Conclusion	6
CHAPTER 2	7
LITERATURE REVIEW.....	7
2.1 Introduction.....	7
2.2 Diagnostic Procedure for Identification of Enterobacteriaceae	8
2.2.1 Principles of identification	8
2.3 Enterobacteriaceae	10
2.4 Conventional Identification Method	11
2.5 Manual Identification Systems	12
2.5.1 API 20E	14
2.5.2 API RapiD 20E.....	14

2.5.3	Crystal E/NF	15
2.5.4	Enterotube II	15
2.5.5	EPS	15
2.5.6	GN2 Microplate	16
2.5.7	ID Tri-Panel	16
2.5.8	ID 32E	17
2.5.9	Microbact	17
2.5.10	Micro-ID	17
2.5.11	RapID onE	18
2.5.12	RapID SS/u	18
2.5.13	r/b Enteric Differential	19
2.5.14	UID/UID-3	19
2.6	Automated Identification Systems	20
2.6.1	BD Phoenix 100	22
2.6.2	bioMe´rieux Vitek	22
2.6.3	Dade Behring MicroScan	22
2.7	Decision support system	23
2.8	Technological consideration	23
2.8.1	Standalone system	24
2.8.2	Client/Server	25
2.8.3	Web based	26
2.8.3 (a)	Web Server	27
2.9	Markup Language	28
2.9.1	HyperText Markup Language (HTML)	28
2.9.2	Extensible Markup Language (XML)	29
2.10	Scripting Language	29
2.10.1	Active Server Pages (ASP)	29
2.10.2	Hypertext Preprocessor (PHP)	30
2.10.3	JavaScript	30
2.10.4	VB Script	31
2.11	Database	31
2.11.1	File Maker Pro	32
2.11.2	MySQL	32
2.11.3	Microsoft Access	32
2.12	Conclusion	33

CHAPTER 3	34
RESEARCH METHODOLOGY	34
3.1 Open source software development methodology	34
3.2 Initiation phase	37
3.2.1 Problem discovery	37
3.2.1 (a) Misinterpretation of the organisms	37
3.2.1 (b) High Cost	37
3.2.1 (c) Time consuming	40
3.2.2 Solution identification	40
3.3 Execution phase	40
3.3.1 Code development and testing	41
3.3.2 Code change review	41
3.3.3 Code commit and documentation	41
3.4 Releasing phase (Microbiological part)	41
3.4.1 Calculation of sample size	43
3.4.2 Calculation of percentage comparison between identification of Enterobacteriaceae using Decision Support System with the commercial systems used in Microbiology Laboratory in Hospital Universiti Sains Malaysia	44
3.4.3 Evaluation of the currently develop system compared to manual conventional method used in Microbiology Laboratory in Hospital Universiti Sains Malaysia for identification of Enterobacteriaceae ...	45
3.5 Functional requirements	47
3.5.1 Administrative functions	47
3.5.2 User functions	47
3.6 Non-functional Requirements	47
3.6.1 Accuracy	48
3.6.2 Flexibility	48
3.6.3 User-friendliness	48
3.6.4 Efficiency	49
3.6.5 Reliability	49
3.6.6 Usability	49
3.6.7 Performance	49
3.7 Selection of Development Tools	50
3.8 Hardware Requirements	52
CHAPTER 4	54
RESULT	54

4.1	Database Design.....	54
4.1.1	Table structure for user.....	54
4.1.2	Table structure for biochemical test	56
4.1.3	Table structure for identification result	58
4.1.4	Table structure for specimen details.....	60
4.2	Entity-Relationship Diagram (ERD).....	62
4.3	Flow chart of system.....	64
4.4	Context Diagram.....	66
4.5	System overview	67
4.6	System use case diagram	67
4.7	User group.....	69
4.7.1	Administrator.....	69
4.7.2	User.....	69
4.8	Dialogue diagram.....	70
4.8.1	Dialogue diagram (Administrator)	70
4.8.2	Dialogue diagram (Microbiologist).....	72
4.9	Interface design.....	74
4.9.1	Login page	75
4.9.2	New entry.....	77
4.9.3	Input biochemical test.....	79
4.9.4	View all biochemical tests	81
4.9.5	Identify Enterobacteriaceae	83
4.9.6	Identification result	85
4.10	Comparison of DECIDER with commercial systems utilised in Microbiology Laboratory of HUSM.....	86
4.10.1	Comparison of DECIDER with automated VITEK 2 system	86
4.10.2	Comparison of DECIDER with API 20E system.....	90
4.11	Comparison of DECIDER with manual conventional system.....	92
CHAPTER 5		97
DISCUSSION		97
5.1	System development of DECIDER	97
5.2	Comparison of DECIDER with manual conventional identification system, VITEK 2 automated system and API 20E system for identification of Enterobacteriaceae	98
5.3	Advantages of DECIDER	102
CHAPTER 6		103

CONCLUSION	103
6.1 Future studies	104
REFERENCES.....	105
APPENDICES	111
LIST OF PUBLICATIONS AND PRESENTATIONS.....	144

LIST OF TABLE

Table 2.1	Features of manual identification products (Adopted from O'Hara C.M., 2005).....	13
Table 3.1	Comparison of traditional and open source methodology (Adopted from Sharma <i>et al.</i> , 2002).....	35
Table 3.2	Cost of identification per isolate (Adapted from O'hara <i>et al.</i> , 1993).....	39
Table 3.3	Selection of Development Tools	51
Table 3.4	Hardware Requirement.....	53
Table 4.1	Table structure for user.....	55
Table 4.2	Table structure for biochemical test (ioe_alltest)	57
Table 4.3	Table structure for identification result (ioe_result).....	59
Table 4.4	Table structure for Specimen details (specimen)	61
Table 4.5	Comparison of DECIDER with automated VITEK 2 system for identification of Enterobacteriaceae	87
Table 4.6	Comparison of DECIDER with API 20E for identification of Enterobacteriaceae.....	91
Table 4.7	Comparison of DECIDER with manual conventional system for identification of Enterobacteriaceae	93
Table 5.1	Agreement of DECIDER with manual identification system, VITEK 2 automated system and API 20E system for identification of Enterobacteriaceae	99

LIST OF FIGURE

Figure 2.1	Flow chart for Identification of Enterobacteriaceae (Adopted from National Standard Method, 2007)	9
Figure 2.2	Algorithm for isolation and identification of Enterobacteriaceae (Adapted from Edwards and Ewing, 1972).....	12
Figure 2.3	The main hardware components of a typical standalone computer system (David, 2006).....	25
Figure 3.1	Process-data diagram of Open source software development (Adopted from Popovic <i>et al.</i> , 2013).....	36
Figure 3.2	Flow chart of methodology for microbiological part	42
Figure 3.3	Result forms used in Microbiology and Parasitology Laboratory in Hospital USM.....	46
Figure 4.1	Entity-Relationship Diagram (ERD)	63
Figure 4.2	Flow chart of the Decision Support System for Identification of Enterobacteriaceae.....	65
Figure 4.3	Context Diagram of Decision Support System for Identification of Enterobacteriaceae.....	66
Figure 4.4	Use case diagram for DECIDER	68
Figure 4.5	Dialogue diagram (Administrator)	71
Figure 4.6	Dialogue diagram (Microbiologist).....	73
Figure 4.7	Main page of Decision Support System for Identification of Enterobacteriaceae	75
Figure 4.8	New Entry.....	77
Figure 4.9	Input biochemical test.....	79
Figure 4.10	List of all biochemical test	81
Figure 4.11	Identification Page.....	83
Figure 4.12	Specimen information	85

LIST OF ABBREVIATION

Acid	: Acid
ALK	: Alkali
API	: Analytical Profile Index
ASP	: Active Server Pages
AST	: Antimicrobial Susceptibility Testing
CDC	: Centres for Disease Control and Preventions
CPU	: Central Processing Unit
DBMS	: Database management systems
DECIDER	: Decision Support System for Identification of Enterobacteriaceae
DSS	: Decision Support System
EPS	: Enteric Pathogen Screen
GUI	: Graphical User Interface
h ₂ s	: Hydrogen sulfide
HDD	: Hard drive disk
HTML	: HyperText Markup Language
HTTP	: Hypertext Transfer Protocol
HUSM	: Hospital Universiti Sains Malaysia
IIS	: Internet Information Server
JSP	: JavaServer Pages
LIS	: Laboratory Information System
MR test	: Methyl-Red test
NSM	: National Standard Method

PC	: Personal computer
PHP	: Hypertext Preprocessor
RAM	: Random-access memory
RDBMS	: Relational Database Management System
RN	: Registration Number
SQL	: Structured Query Language
TSI	: Triple Sugar Iron
UID/UID-3	: Urine Identification screen card
US	: United States
VBScript	: Visual Basic Script
W3C	: World Wide Web Consortium
XML	: Extensible Markup Language

LIST OF SYMBOL

°C	: Degree Celsius
%	: Percentage
€	: Euro currency symbol
\$: U.S. dollar
+	: Positive
-	: Negative

**PEMBANGUNAN SISTEM SOKONGAN KEPUTUSAN UNTUK
MENGENALPASTI ENTEROBACTERIACEAE YANG PENTING DALAM
PERUBATAN**

ABSTRAK

Majoriti daripada organisma gram-negatif yang dikenalpasti di makmal klinikal mikrobiologi adalah terdiri daripada famili Enterobacteriaceae. Pada masa ini, famili ini terdiri dari lebih 20 genus dan lebih dari 100 spesis, dimana kira-kira 50 spesis boleh membawa penyakit kepada manusia. Buat masa ini, di Makmal Mikrobiologi dan Parasitologi, Hospital Universiti Sains Malaysia, Enterobacteriaceae dikenalpasti dengan secara rutin menggunakan ujian biokimia yang konvensional. Selain daripada itu, sistem komersial iaitu API 20E dan sistem automatik VITEK 2 juga digunakan terutamanya bagi mengenal pasti sampel Enterobacteriaceae yang kritikal disebabkan oleh kosnya yang tinggi. Pengenalpastian secara manual menggunakan kaedah konvensional sering cenderung menyebabkan salah tafsiran berpunca daripada kesilapan manusia semasa percampuran dan pepadanan ujian biokimia, manakala penggunaan sistem komersil pula memerlukan kos yang tinggi. Untuk mengatasi masalah ini, Sistem Sokongan Keputusan perlu dibangunkan untuk membantu ahli mikrobiologi mengenalpasti Enterobacteriaceae. Sistem Sokongan Keputusan untuk Enterobacteriaceae (DECIDER) telah dibangunkan menggunakan perisian sumber terbuka yang percuma iaitu, PHP dan MySQL dengan menggunakan metodologi pembangunan perisian sumber terbuka. Sistem yang baru dibangunkan ini telah dibandingkan dengan cara sebelum ini; iaitu sistem konvensional, sistem API 20E dan sistem automatik Vitek 2 dengan menggunakan 356 rekod sedia ada kultur darah positif

bagi tahun 2011 yang diambil dari Makmal Mikrobiologi dan Parasitologi. Peratus persamaan telah dikira. Peratus tertinggi bagi kesamaan penuh adalah dari perbandingan antara DECIDER dan Vitek 2, dengan 82 (87.23%) organisma yang dikenal pasti secara tepat. Perbandingan antara sistem konvensional dan DECIDER menghasilkan 274 (76.97%) persamaan penuh organisma yang dikenalpasti secara tepat. Keputusan menunjukkan DECIDER boleh mengenalpasti Enterobacteriaceae dengan aras penerimaan dengan tepat yang tinggi. Sistem ini adalah ringkas dan mudah digunakan oleh pengguna.

DEVELOPMENT OF DECISION SUPPORT SYSTEM FOR IDENTIFICATION OF MEDICALLY IMPORTANT ENTEROBACTERIACEAE

ABSTRACT

Members of the family Enterobacteriaceae are the majority of gram-negative organisms identified in a clinical microbiology Laboratory. The family now has over 20 genera and more than 100 species, of which about 50 are associated with human disease. Currently, in Laboratory of Microbiology and Parasitology, of Hospital Universiti Sains Malaysia, the identification of Enterobacteriaceae is utilised routinely by conventional biochemical tests. Other than that, commercial system such as API 20E and Vitek 2 automated system are also been utilised specifically for identification of critical samples, due to its expensive cost. Identification manually by conventional method prone to human error during mixing and matching biochemical tests, which further cause misidentification, while identification using commercial methods require high cost. To overcome this problem, there is a need to develop a computerised decision support system to assist microbiologists for identification of Enterobacteriaceae. Decision support system of Enterobacteriaceae (DECIDER) were developed using free open source software, PHP and MySQL by following open source software development methodology. The newly develop system has been compared to previous method; conventional manual system, API 20E system and VITEK 2 automated system by back tested using a total of 356 positive blood culture previous record in year 2011 gathered from Laboratory of Microbiology and Parasitology. Percentage agreement was calculated. The highest percentage of complete agreement

was by comparing DECIDER and Vitek 2, with 82 (87.23%) correctly identified organisms. Manual conventional system compared with DECIDER yield about 274 (76.97%) complete agreement for correctly identified organisms. Result has shown that DECIDER, identified a highly acceptable level of identification accuracy for members of the family Enterobacteriaceae. The system is simple and provides ease of use for user.

CHAPTER 1

INTRODUCTION

1.1 Background of the study

Diagnostics laboratories in Hospital Universiti Sains Malaysia (Hospital USM) have started using Laboratory Information System (LIS) since 2005. LIS was developed in-house by the hospital's Information System Unit using proprietary software for interface design and open-source software for database and server management. Currently, the implementation of LIS at Hospital USM is in the use of test request confirmation module and result entry module. Ever since its implementation, users have given many constructive feedbacks to enhance the system. While most of the laboratories are quite similar in the standard operating procedures, the Microbiology Laboratory, in particular, has additional diagnostic investigation procedures. One of the procedures is in the identification of microorganism. This procedure, which consists of a range of biochemical analysis, is being performed manually by the medical laboratory technologist and confirmed by Microbiologist. The identification procedure manually, is time consuming and prone to human errors, whereas automated identification might affect increase in cost. There is a need to develop a computerised decision support module to assist microbiologists in the process of identifying the microorganism specifically Enterobacteriaceae.

1.2 Problem statements

Identification of Enterobacteriaceae requires complex matching of various biochemical reactions. Human errors are more likely to happen during mixing and matching, causing misinterpretation of the organisms. In the year 2011 there were more than 356 isolates from blood specimen, 201 isolates from urine specimen and 120 isolates from stool specimen at Hospital USM Microbiology Laboratory. Commercial methods that are available in the market are very expensive; therefore they are not feasible to be purchased. Hospital USM Microbiology Laboratory is currently using an Analytical Profile Index (API) 20E system installed in a standalone dedicated computer system and VITEK 2 automated system.

In order to overcome the weaknesses and to reduce the cost, a decision support system should be developed to assist microbiologist in conducting the identification of Enterobacteriaceae.

1.3 Research questions

1. What are the strength and weaknesses of existing system?
2. What are the specifications of decision support system that is suitable for identification of Enterobacteriaceae conducted in diagnostic microbiology laboratory?

1.4 Objectives of the study

1.4.1 General objective

To develop decision support system for identification of Enterobacteriaceae using open source technology.

1.4.2 Specific objectives

1. To develop a decision support system for identification of Enterobacteriaceae that suits the needs of Microbiology Laboratory in Hospital Universiti Sains Malaysia.
2. To compare the identification of Enterobacteriaceae using newly develop decision support system with the commercial systems used in Microbiology Laboratory of Hospital Universiti Sains Malaysia.
3. To evaluate the current system compared to manual conventional method used in Microbiology Laboratory of Hospital Universiti Sains Malaysia for identification of Enterobacteriaceae.

1.5 Definition of terms

1.5.1 Decision support system

Power (2010) defines a Decision Support System (DSS) as an interactive computer-based system or subsystem intended to help decision makers use data, documents, communications technologies, knowledge and/or models to identify and solve problems, complete decision process tasks, and make decisions. DSS is a general term for any computer application that improves a person or group's ability to make decisions (Power, 2010). In general, Decision Support Systems are a class of computerised information system that supports decision-making activities (Power and Eom, 2006).

1.5.2 Enterobacteriaceae

According to National Standard Method (NSM) (2007) for Identification of Enterobacteriaceae, members of the Enterobacteriaceae are Gram-negative, straight rods, most species grow well at 37°C, some are motile, facultatively anaerobic, oxidase-negative and catalase-positive (except *Shigella dysenteriae* Type 1). They are distributed worldwide and may be found in soil, water, plants and animals (Standards Unit, Evaluations and Standards Laboratory, 2007). In 1972 there were 26 recognised species, now the current edition of Bergey's Manual of Systematic Bacteriology lists 42 genera and over 140 validly published species in this family (Brenner *et al.*, 2005; Standards Unit, Evaluations and Standards Laboratory, 2007). Enterobacteriaceae is a type of microorganism that are responsible for a variety of

human diseases, including wound infections, urinary tract infections, gastroenteritis, meningitis, septicemia, and pneumonia (Lerner and Lerner, 2003).

1.5.3 Diagnostic test

Diagnostic test is conducted for prevention or treatment of diseases. The measures of quality in a diagnostic test are reliability, reproducibility, speed and cost-benefit ratio. (Vandepitte *et al.*, 2003)

1.5.4 Open Source Software

According to Open Source Initiative (2007), open source have several criteria which are free redistribution, include and allow distribution of source code, integrity of the author's source code, allow modifications and derived works, no discrimination against persons or groups, no discrimination against fields of endeavor, distribution of license, license must not be specific to a product, license must not restrict other software and license must be technology-neutral.

1.6 Significance of the study

Microbiology and Parasitology Laboratory in Hospital Universiti Sains Malaysia has limited resources in terms of budget and human resource. At the point of this study, it cannot afford to purchase any existing decision support system

because most of the software are very expensive. Based on the advancement of open source technology, the researcher proposed to develop a decision support system to solve the problems in microbiology laboratories. With the use of decision support system, the laboratory can expedite the test procedures for the benefit of patients. The laboratory managements do not need to purchase expensive license to use the system.

1.7 Research scope

Decision support system for identification of Enterobacteriaceae was evaluated by retested all positive blood results for year 2011. Urine, stool and others record are not taken due to time constraint.

1.8 Conclusion

Decision support system for identification of Enterobacteriaceae was develop according to the requirements from the Microbiology and Parasitology Laboratory in Hospital Universiti Sains Malaysia. The main advantage for this system is to assist microbiologist in identification of Enterobacteriaceae. This study applied Open source software to reduce cost in the implementation of the system.

CHAPTER 2

LITERATURE REVIEW

2.1 Introduction

The increase in identification of members of the family Enterobacteriaceae has been proportionate with the significant increases in hospital acquired infection due to these gram-negative bacilli (Washington II, 1976). Many automated and non-automated systems have been developed and are commercially available for the identification of gram-negative rods (Wauters *et al.*, 1995). All commercial identification systems are based on of five different technologies or a combination of pH-based reactions that require from 15 to 24 hours of incubation, enzyme-based reactions that require 2 to 4 hours, utilization of carbon sources, visual detection of bacterial growth, or detection of volatile or nonvolatile fatty acids via gas chromatography (O'Hara, 2005).

These organisms are commonly identified by the use of commercial system, either manual or automated. Commercially available systems provide more in-depth identification to the species level and also detect new and unusual strains (O'Hara, 2005). Cost limitations are the major problem face by clinical microbiology laboratories. Most published methods either involve the use of expensive consumables or are too labour-intensive for routine implementation (Peterson *et al.*, 2001).

Nowadays, there are several computerised system that can be use in the identification of Enterobacteriaceae. Each system has its own strength and weaknesses which determine the reliability of the system. Literature review has been done to compare each system available according to their features. This will lead to the determination of the most appropriate application that can be used to develop a decision support system that can assist user in laboratory to identify Enterobacteriaceae that fulfill the specification required.

2.2 Diagnostic Procedure for Identification of Enterobacteriaceae

National Standards Method (NSM) describes the identification of members of the family Enterobacteriaceae in diagnostic clinical microbiology laboratories are usually by using biochemical tests (Standards Unit, Evaluations and Standards Laboratory, 2007).

2.2.1 Principles of identification

Colonial morphology, Gram stain, oxidase and the use of several biochemical tests are the basic principles to identify isolates from clinical materials (Standards Unit, Evaluations and Standards Laboratory, 2007). If further identification or confirmation required, isolates should be sent to the Reference Laboratory, while careful consideration should be given to isolate that give an uncommon identification (Standards Unit, Evaluations and Standards Laboratory, 2007). All evidence including growth characteristics, colonies morphology and serology should be considered before accepting commercial identification system results (Standards

Unit, Evaluations and Standards Laboratory, 2007). Figure 2.1 illustrates the procedure to identify Enterobacteriaceae.

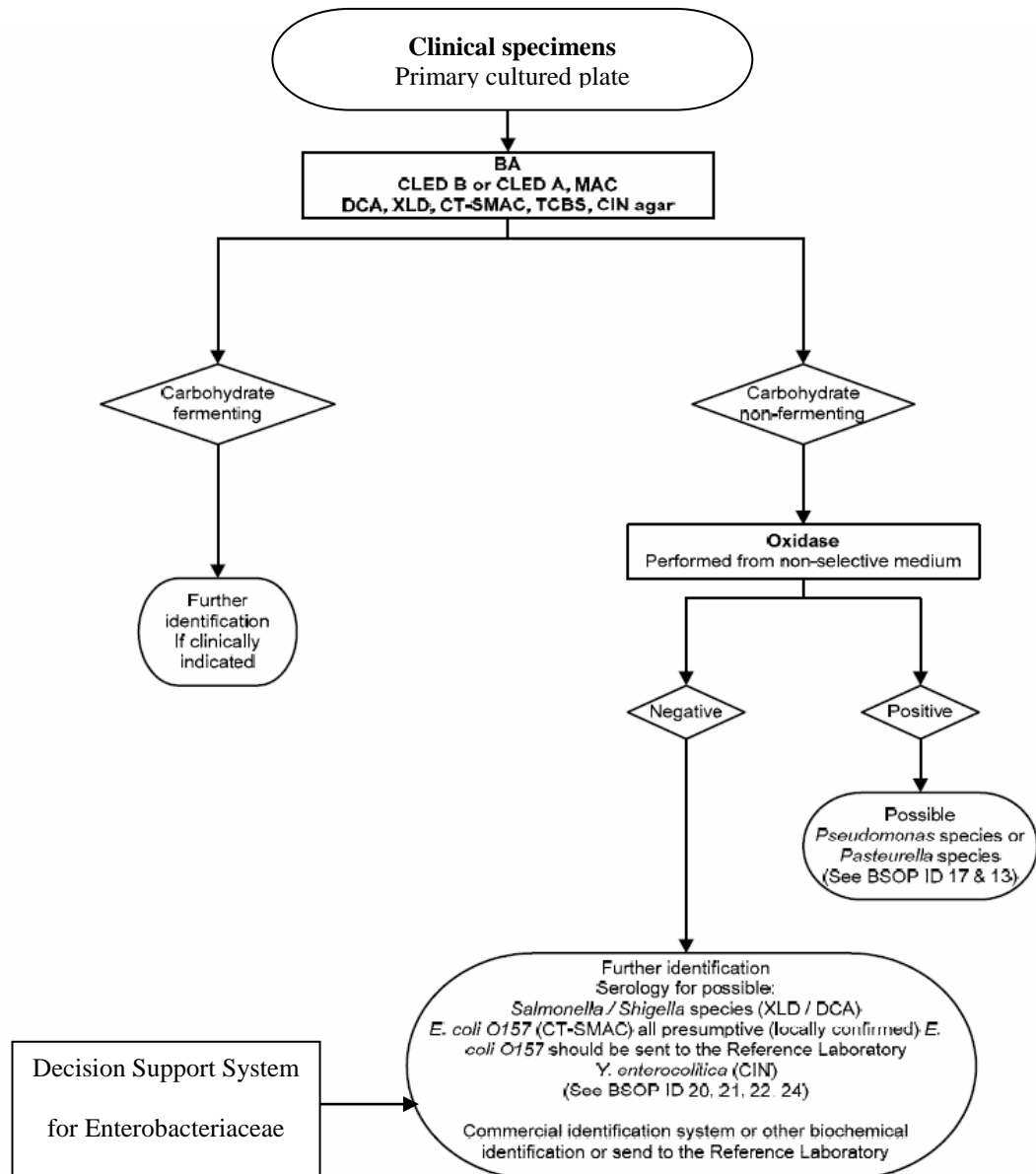


Figure 2.1 Flow chart for Identification of Enterobacteriaceae (Adopted from National Standard Method, 2007)

2.3 Enterobacteriaceae

Enterobacteriaceae is a family of Gram-negative bacilli that is most widely studied family of organisms in the world (Peter, 2006). They have a worldwide distribution, and numerically important to the medical microbiologist, as they may account for 80% of clinically significant Gram-negative bacilli (Peter, 2006). The family now has over 20 genera and more than 100 species, of which about 50 are definitely or probably associated with human disease (Farmer *et al.*, 1985). Peter (2006) has listed four reasons why clinical microbiologists need to identify microorganisms:

1. To predict the likely outcome of the infection.
2. To predict likely sensitivity to antimicrobials.
3. To identify potential cross-infection risks.
4. To obtain research information on new disease associations with microorganisms.

The common genera of the family Enterobacteriaceae includes *Citrobacter* species, *Enterobacter* species, *Escherichia* species, *Hafnia alvei*, *Klebsiella* species, *Morganella morganii*, *Proteus* species, *Providencia* species, *Salmonella* species, *Serratia* species, *Shigella* species and *Yersinia* species (Standards Unit, Evaluations and Standards Laboratory, 2007).

Various species of the Enterobacteriaceae are able to cause pneumonia, urinary tract infections, wound infections, bacteremia, meningitis and other

nosocomial infections (Samuel, 1996). These bacteria are estimated to be responsible for about 100,000 deaths each year in the United States, and account for about half of all the clinically significant bacteria isolated by hospital laboratories (Deepa *et al.*, 2010). Enterobacteriaceae can cause severe, often fatal infection in severely ill patients (Souli *et al.*, 2008).

2.4 Conventional Identification Method

Enterobacteriaceae are usually identified using biochemical tests in routine clinical microbiology laboratories. Biochemical and enzymatic tests form the basis for most identification procedures performed in clinical microbiology laboratories. In general, biochemical characteristics refer to the formation of distinct biochemical end products from defined substrates, the production of acid from various carbohydrates, and the presence of certain bacterial enzymes as determined by chromogenic substrates or other methods (Washington *et al.*, 2006).

The conventional tests were generally described by Edwards and Ewing (1972). Figure 2.2 shows methods that may be used to isolate and identify Enterobacteriaceae from all sorts of clinical specimens.

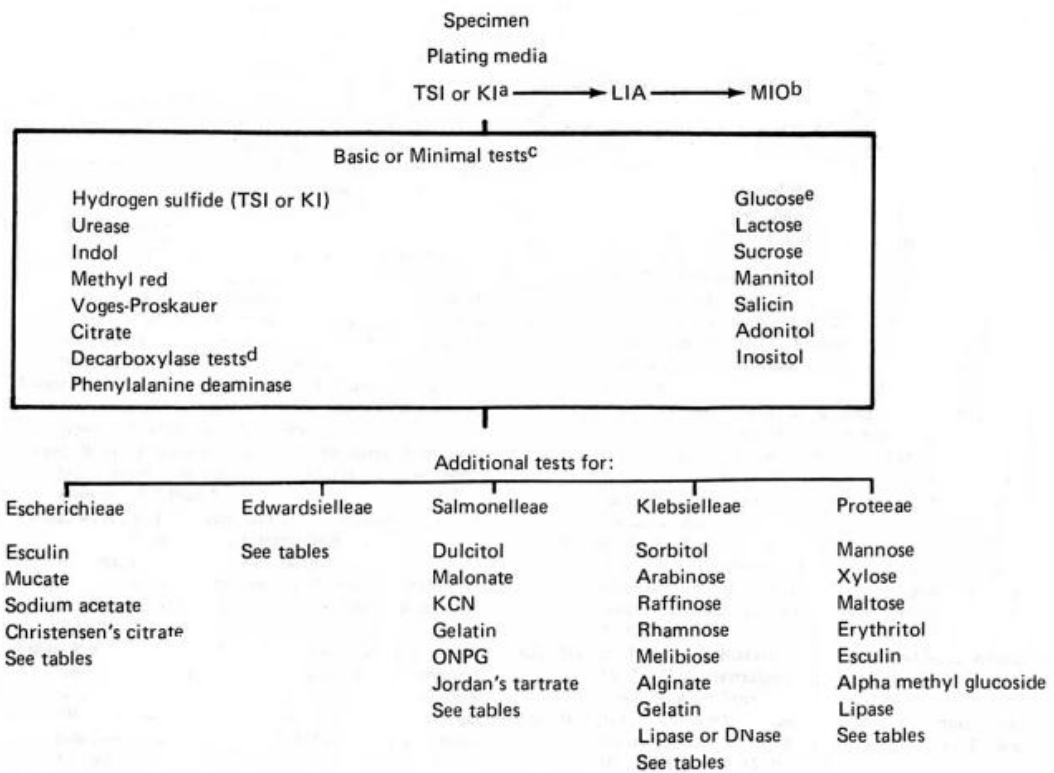


Figure 2.2 Algorithm for isolation and identification of Enterobacteriaceae (Adapted from Edwards and Ewing, 1972)

2.5 Manual Identification Systems

The studies by O'Hara C.M. (2005) compared manual identification systems to identifications obtained by using conventional biochemical tests. Table 2.1 show details relevant to each product or system.

Table 2.1 Features of manual identification products (Adopted from O'Hara C.M., 2005)

Name of product	Manufacturer	No. of tests on product	No. of products per package	Incubation time (h)	No. of additional reagents	No. of organisms for quality control	List cost per test
API 20E	bioMe´rieux	20 ^c	25	18–24	6	5	\$6.56
API RapiD 20E	bioMe´rieux	20	25	4	2	3	\$5.96
Crystal E/NF	BD ^d	30	20	18–20	2	6	\$5.91
Enterotube II	BD	12	25	18–24	2	4	\$9.89
EPS	bioMe´rieux	10	20	4–6	1	4	\$4.85
GN2 Microplate	Biolog	95	1	4–6, 16–24	0	0	\$7.40
ID Tri-Panel	BD	30		18–24	6	5	\$8.94
ID 32E	bioMe´rieux	32	25	24	1	5	€68
Microbact	Oxoid	24	40, 60, 80, or 120	18–24	4	5	\$3.97
Micro-ID	Remel	15	10	4	2	4	\$6.94
RapID onE	Remel	19	20	4	1	4	\$5.05
RapID SS/u	Remel	12	20	2	3	5	\$2.73
r/b Enteric Differential	Remel	15	Various	18–24	1	7	\$3.22
UID/UID-3	bioMe´rieux	9	20	1–13	0	5	\$4.60/\$2.01

2.5.1 API 20E

API system is a plastic strip holding 20 miniaturized compartments, each containing a dehydrated substrate for a dissimilar test (O'Hara, 2005). The biochemical tests used in the identification of enteric bacteria have long been a prime target of investigators interested in miniaturizing microbiological methods (Smith *et al.*, 1972). The API 20E strip is a gold standard among commercial systems because of its large acceptance by clinical microbiology laboratory market (O'Hara, 2005).

The Analytab system of 20 biochemical tests for identification of Enterobacteriaceae was evaluated in parallel with conventional tests on 128 Enterobacteriaceae, where 88% of Enterobacteriaceae were correctly speciated with the Analytab system; on repeat testing with heavier inocula of organisms failing to ferment glucose initially, the proportion of Enterobacteriaceae correctly speciated became 93% (Washington II *et al.*, 1972).

2.5.2 API RapiD 20E

API RapiD 20E system is designed to identify Enterobacteriaceae in 4 hours. Similar to the API 20E in its test configuration, this system has 20 microtubes that contain substrates for the demonstration of enzymatic activity or fermentation of carbohydrates (O'Hara, 2005). The seven-digit profile number that is compiled from the test reactions is entered into the APILAB software, where the database contains 26 genera and 65 species (O'Hara, 2005). Identifications are also available by using the Analytical Profile Index (O'Hara, 2005).

2.5.3 Crystal E/NF

Crystal E/NF is a plastic panel includes 30 tests for the fermentation, oxidation, degradation, or hydrolysis of various substrates (O'Hara, 2005). The current software version is 4.0 and contains 38 genera and 104 species with category of miscellaneous gram-negative bacilli includes an additional 20 taxa that may require up to 17 additional off-line tests for completion of identification via an algorithm (O'Hara, 2005).

2.5.4 Enterotube II

The Enterotube II is a self-contained, compartmented plastic tube contains 12 conventional media and an inoculating wire (O'Hara, 2005). A five-digit profile number is generated, and the Computer Coding Identification System is consulted for the identification and the database includes 22 genera, 79 species, and 6 CDC enteric groups (O'Hara, 2005).

2.5.5 EPS

Marketed by bioMe´rieux, the Enteric Pathogen Screen (EPS) is to be used in conjunction with the Vitek Legacy instrument as a screen for isolates of the common oxidasenegative enteric pathogens, which include *Edwardsiella tarda*, *Salmonella* spp., *Shigella sonnei* and other *Shigella* spp., and *Y. enterocolitica* (O'Hara, 2005). Incubations are carried out in the instrument, and reports are generated automatically at the end of the cycle (O'Hara, 2005). The most recent evaluation of this product, in

1993, reported a sensitivity of 99.5% in the screening for possible enteric pathogens (Imperatrice and Nachamkin, 1993).

2.5.6 GN2 Microplate

The GN2 MicroPlate product is based on the exchange of electrons produced during an organism's respiration, leading to a subsequent tetrazolium-based color change, with each of the 96 wells of the microtiter-style plate contains tetrazolium dye, which changes from colorless to purple as the actively growing cells oxidize the carbon source (O'Hara, 2005). The current GN database is release 6.01 and contains identification patterns for 526 species or taxa that encompass not only Enterobacteriaceae but many other gram-negative nonfermenters and fastidious organisms (O'Hara, 2005).

2.5.7 ID Tri-Panel

The ID Tri-Panel is a panel which accommodates the testing of three isolates at one time or can be used as part of a combination MIC-ID configuration, contains 30 colorimetric-based substrates (O'Hara, 2005). A profile number is generated, and the answer is obtained from either an Electro-Code computer program or the data management system with the database contains 31 genera and 118 species (O'Hara, 2005). The most recent evaluation was in 1994 by Edinger et al., who reported that 86% of 127 non-glucose-fermenting isolates were correctly identified (Edinger *et al.*, 1994).

2.5.8 ID 32E

The ID 32E is an upgraded version of the API 20E and contains 32 substrates in a plastic-strip configuration similar to the API (O'Hara, 2005). A numerical profile is generated and entered into the APILAB PLUS software for identification with the current database contains 40 genera and 103 species (O'Hara, 2005).

2.5.9 Microbact

Identification of Microbact is based on pH changes in various substrates and substrate utilization tests (O'Hara, 2005). The reactions are converted into an octal code and then entered into the Microbact computerized identification package, which provides the identification. (O'Hara, 2005).

2.5.10 Micro-ID

The Micro-ID is a self-contained plastic unit containing 15 reagent impregnated disks that detect the presence of specific enzymes and/or metabolic end products produced by the microorganism (O'Hara, 2005). A five-digit, octal number is composed from the 15 reactions, and the MICRO-ID Identification Manual is consulted for the identification (O'Hara, 2005).

2.5.11 RapID onE

RapID onE employs conventional and chromogenic substrates for the identification of Enterobacteriaceae and other clinically relevant oxidase-negative, gram-negative bacilli from human sources (O'Hara, 2005). The same plastic panel with 18 reaction cavities will give 19 test results, as one cavity is bifunctional after the addition of a single reagent (O'Hara, 2005). The current database is dated 30 April 2003 and contains 28 genera, 60 species, and several biogroups within species (O'Hara, 2005). Two studies in 1994 reported accuracy rates exceeding 91%. Kitch et al. evaluated 364 strains of Enterobacteriaceae and 15 strains of oxidase-negative, gram-negative nonfermenters and found an accuracy rate of 97.6% without additional tests (Kitch *et al.*, 1994). Lee et al. studied 125 strains of Enterobacteriaceae and *Acinetobacter calcoaceticus* (Lee *et al.*, 1994). They reported accuracy rates of 92.9% with fresh clinical isolates and 90.2% with frozen stock isolates.

2.5.12 RapID SS/u

RapID SS/u is a combination of conventional and chromogenic substrates for the identification of organisms isolated from urine (O'Hara, 2005). This plastic panel has 10 reaction cavities, with one being bifunctional after the addition of spot indole reagent (O'Hara, 2005). The current database is dated 29 April 2003 and contains nine gram-negative and two gram-positive genera as well as two taxa of yeasts (O'Hara, 2005). An evaluation by Halstead et al. reported that 95.9% of 170 isolates were identified correctly in 2 h (Halstead *et al.*, 1987). A subsequent evaluation by

DeGirolami et al. reported an accuracy of 86.5% for 185 isolates (DeGirolami *et al.*, 1988).

2.5.13 r/b Enteric Differential

The two-tube r/b, designated r/b1 and r/b2, are the components of the r/b system, along with an auxiliary tube, the Cit/Rham Expander (O'Hara, 2005). The current database is dated October 1990 and includes 13 genera and 37 species. An organism can be identified by using the chart in the package insert or by generating a biogram code number and using the computer code book (O'Hara, 2005).

2.5.14 UID/UID-3

The Urine Identification screen card (UID/UID-3) comprises of 10 wells in the UID card, 9 of which contain substrates and metabolic inhibitors whose reactions are specific for a given genus (O'Hara, 2005). Huber reported that 90.1% of 1,634 specimens were both correctly enumerated and identified within 9 h with the UID-3 card (Huber, 1985). Dalton et al. studied the use of the UID-3 as a screening test for bacteriuria and reported a sensitivity and a specificity of 93 and 55%, respectively, when the colony counts were $\geq 10^5$ CFU/ml (Dalton *et al.*, 1993).

2.6 Automated Identification Systems

The growth of technology has resulted in introduction of new commercial automated identification systems to laboratories environment. Technology had enabled valid results to be obtained in as quickly as 4 hour (O'Hara, 2005). Table 2.2 show features of automated instruments currently available.

Table 2.2 Features of automated identification products (Adopted from O'Hara, 2005)

Name of product	No. of tests on product	No. of products per package	Incubation time (h)	Additional tests required	Cost of instrument	Cost per test
BD Phoenix NID	45	25	2-12	Spot tests only	\$95,000	\$7.40
Vitek GNI+	28	20	2-12	70	\$137,850	\$5.35
Vitek 2 ID-GNB	41	20	3	5	\$159,000	\$7.15
MicroScan Neg ID type 2	32	20	16-20	Yes	\$153,038	\$12.79
MicroScan Rapid Neg ID type 3	36	20	2 h 20 min	Yes	\$153,038	\$14.39
Trek Sensititre GNID	32	10	5-24	4	\$72,380	\$9.41

2.6.1 BD Phoenix 100

The BD Phoenix 100 has been introduced in 2003, was designed and marketed by Becton Dickinson with the goal of rapid identification of gram-negative and gram-positive bacteria of human origin (O'Hara, 2005). The Phoenix 100 instrument is capable of processing 99 panels at one time; one panel holder is reserved for the internal thermometer (O'Hara, 2005). Once the panels are inoculated and loaded into the instrument, all operations are totally automated and results print when each panel is completed (O'Hara, 2005).

2.6.2 bioMérieux Vitek

VITEK 2 (bioMérieux, Marcy l'Étoile, France) is an integrated system that automatically performs rapid identification using algorithms based on fluorescence and colorimetry and antimicrobial susceptibility testing (AST) based on kinetic analysis of growth data (Barry *et al.*, 2003). An early evaluation by Isenberg *et al.* reported an accuracy of 97.8% for 1,020 isolates compared to conventional biochemical with turnaround times averaged 8 hour (Isenberg *et al.*, 1980).

2.6.3 Dade Behring MicroScan

American MicroScan introduced the autoSCAN-3, a semiautomated instrument that utilized microdilution trays containing frozen conventional substrates for identification of bacterial isolates (O'Hara, 2005). An early evaluation, incorporating both Enterobacteriaceae and nonfermenters, by Ellner and Myers in

1981 reported an agreement of 95.0% between visually read and automated identifications, thus ensuring that machines were capable of accurate interpretations of the reactions in each well (Ellner and Myers, 1981).

2.7 Decision support system

Decision support systems (DSS) is an organized collection of people, procedures, software, databases and devices used to help make decisions to solves problems (George and Ralph, 2013). It is an interactive, computer-based system that assists users in judgment and choice activities by providing data storage and retrieval with support for model building and model-based reasoning (Marek and Roger, 2002). Fundamentals components of DSS are database management system (DBMS), model-base management system (MBMS) and dialog generation and management system (DGMS).

2.8 Technological consideration

In order to develop a decision support system, appropriate technological consideration must be made. Technology that will be used must meet the needs the requirements of the system.

System architecture is the conceptual model that defines the structure, behavior, and further views of a system (Hannu and Bernhard, 2011). An architecture description is a formal description and representation of a system, organized in a way that supports reasoning about the structure of the system which includes system

components, the externally visible properties of those components, the relationships between them, and provides a plan from which products can be obtained, and systems developed, that will work together to implement the overall system (Carlos, 2013)

2.8.1 Standalone system

A standalone computer system is a computer (CPU and peripherals) that the operator has individual use of and which are not connected to any other computer systems, although they may be connected to the internet (David, 2006). The operating system, applications software and user data files are all stored on the computer's drive without shares features (David, 2006). Standalone system is not part of any Local Area Network.

The advantage of the system are portable, low cost and if the personal computer breaks down it will not affect any other personal computers because it is completely separate (David, 2006). A disadvantage of standalone computer is not being part of a network to share information with other computers. In this 21st century, this architecture is not suitable because it could reduce work productivity.