ABSTRACT

Serotyping is the most fundamental approach in epidemiological surveillance and outbreak investigations for Salmonella. Many multiplex PCR assays have been reported for serotyping Salmonella based on O and H antigens. The aim of this study was to apply and improve the approach in differentiation and serotyping Salmonella enterica strains by combination of sequential multiplex PCRs targeting the O, H and Vi antigens of Salmonella, and this achieved by working on 126 strains. All the strains were purified on BSA and produced black colonies of Salmonella. The strains were confirmed by PCR amplification gene that targets the *hilA*. 122 of 126 strains produced the expected band size of 789bp. A multiplex PCR (MPCR) for serogrouping targets O and Vi antigens was applied on the 122 strains: 28.7% (C2, n=35), 27.1% (B, n=33), 22.9% (D, n=29), 17.2% (E, n=21), 1.64% (C1, n=2), and 1.64% (A, n=2). Eight of the Salmonella strains from group D have the Vi antigen. A multiplex PCR for serotyping targets H1 antigens was applied on the tested strains, and were Ha, Hb, and Hd antigens detected in 19 of 122 strains. S. Paratyphi A and S. Typhi correctly are identified by MPCR for H1 antigens. The percentage of the strains were produced flagella antigens (H1; a, b, and d) was 18.1% while the percentage of non-expressed strains was 81.9%. Therefore, due to the limited information provided by H1 MPCR assay, additional primers for flagella antigens (both H1 and H2) were used. The optimization was carried out on the new primers by adjusting the concentration of buffer, time and denaturation and annealing temperature. The optimized PCR for H serotyping detected the expected amplicons of H1 and H2 antigens and further confirmation was done by DNA sequencing. The overall of multiplex PCRs of O and H

results correctly serotyped 94 of 122 strains (77%). The most frequent serovars encountered were *S*. Weltevrerden, *S*. Enteritidis, *S*. Typhimurium, *S*. Hadar and *S*. Typhi. Application of DNA based serogrouping and serotyping found to be robust, quick methods for differentiation of common *Salmonella enterica*.

ACKNOWLEDGEMENT

This research took me almost a year, by that time; I have met with a great people whose contribute in many ways to come out with this project. It is a pleasure to convey my gratitude to them all in my humble acknowledgment.

In the first place I would like to note my gratitude to Prof. Dr. Thong Kwain Lin for her supervision, advice, encouragement and guidance from the very early stage of this research as well as giving me ideas and experiences throughout the discussions of work.I am indebted to her more than she knows.

My gratitude to UM for granting me the VOT F fund which has relieved my financial worries about the research expenses incurred.

It is a pleasure to pay tribute to the all my lab mates and course mates, I am benefited with their help in particular skill in handling and running precisely delicate equipments. Many thanks go to them for science discussion and the pleasure working together in such environment.

Collective and individual acknowledgements to my colleagues at UM, particularly Dr Hasan Izadeen, Hassan Mahmoud, Mohamed Ebnouf and Khalid Abdurrahman for their advices and their bright thoughts came during science discussion we had in our beautiful house. Thanks go to my friends Omar Asmail and Dalia Osama for their especial assistance in science field.

Where would I be without my family? My parents deserve special mention for their inseparable support and prayers. My Father, Mohammed ElHassan Nori, in the first place is the person who put the fundament my learning character, showing me the joy of Intellectual pursuit ever since I was a child. My Mother, Thorya Said Ahmed, is the one who sincerely

raised me with her caring and gently love. Loay and Lamya thanks for love, respect and being supportive.

Mohammed Elbagir

LIST OF CONTENTS

Title		page	
TITLE			i
ABSTRACT			ii
ACKNOWLED	GMENT		iv
LIST IF CONT	ENTS		vi
LIST OF FIGU	RES		Х
LISTS OF TAB	LES		xi
LISTS OF APP	ENDICES		xiii
LISTS OF ABB	REVIATIONS		xiv
CHAPTER 1	INTRODUCTION		1
	1.1 Introduction		1
	1.2 Scope of study		3
	1.3 Objective of study		4
CHAPTER 2	LITERATURE REVIEW		5
	2.1Characterization of Salmonella Species		5
	2.2 Routes of transmission		6
	2.3 Detection of Salmonella		6
	2.4 Salmonellosis		7
	2.5 Serotyping of Salmonella		8
	2.6 LPS Structure of Salmonella		9
	2.7 Flagella antigens (H)		11

vi

	2.8 Capsular antigen (Vi)	12
	2.9 Molecular approaches for serotyping of Salmonella	13
	2.10 Multiplex Polymerase chain reaction	14
CHAPTER 3	MATERIALS AND METHODS	15
	3.1 Material	15
	3.1.1 Bacterial Strains	15
	3.1.2 Preparation of media and solutions	16
	3.1.2.1 Luria-Bertani (LB) Agar (Oxoid England)	16
	3.1.2.2 Luria-Bertani Broth (Oxoid England)	16
	3.1.2.3 Bismuth Sulphite agar (BSA) (Oxoid England)	17
	3.1.2.3 50% Glycerol	17
	3.1.3 Reagents for polymerase chain reaction	17
	3.1.3.1 Primers	17
	3.1.4 Solutions and reagents used for agarose gel electrophoresis	21
	3.1.4.1 1.5% agarose gel	21
	3.1.4.2 10x TBE buffer	21
	3.1.4.3 TBE buffer (0.5x)	21
	3.1.4.4 Ethidium bromide (10 mg/ml)	22
	3.2 Methods	22
	3.2.1 Purity and Storage of Strains	22
	3.2.2 Polymerase Chain Reactions	23
	3.2.2.1 DNA Template Preparation	23
	3.2.2.3 Multiplex PCR for serogrouping (O antigens) and	23

detection of Vi antigen

	3.2.2.5 Optimization of Multiplex PCR using additional	26
	flagella antigens primers	
	3.2.3 Analysis of PCR products	26
	3.2.4 Gel documentation	26
3.2.5 Validation of the Multiplex PCRs:		27
	3.2.6 Sequence Analysis	27
CHAPTER 4	RESULTS	28
	4.1 Purity and Storage of strains	28
	4.2 Multiplex PCR for serogrouping (O antigens) and detection	
	of Vi antigen	
	4.3 Multiplex PCR for serotyping (H1 antigens a, b,and d)	
	4.4 Optimization of Multiplex PCR by using additional flagella	31
	antigens primers	
	4.5 Confirmation of primers amplicons by DNA sequencing	37
	4.6 Application of optimized Multiplex PCR for serotyping of	39
	Salmonella strains using additional primers for H1 and H2 antigens	
	4.8 Validation of the Multiplex PCRs	41
	4.9 Outcome of multiplex PCRs in differentiation of Salmonella	43
	enterica based on O and H antigens	

3.2.2.4 Multiplex PCR for serotyping of (H antigens)

viii

24

CHAPTER 5	DISCUSSION	45
CHAPTER 6	CONCLUSION	52
REFERENCES		53
APPENDIX		65
RESEARCH OUT PUT		95

LIST OF FIGURES

Fig	Title	Page
4.1	A representative photo of multiplex PCR for confirmation Salmonella	28
4.2	Second replicate gel photo of multiplex PCR for confirmation <i>Salmonella</i> .	29
4.3	Multiplex PCR for O serogrouping	30
4.4	Multiplex PCR for Salmonella flagella antigens (H1).	31
4.5	Multiplex PCR for flagella antigens (H1, H2) using recommended PCR conditions described by Cardona-Castro et al., (2009).	33
4.6	Multiplex PCR for flagella antigens using PCR conditions described by Lim and Thong (2009).	35
4.7	Multiplex PCR for flagella antigens (H1) using optimized PCR conditions	36
4.8	Multiplex PCR for flagella antigens (H2) using optimized PCR	37
4.9	Multiplex PCR for flagella antigens using optimized PCR conditions	40

х

LISTS OF TABLES

Table	Title	page
3.1	Known bacterial strains used as positive and negative controls	15
3.2	Oligonucleotide primers used for O- multiplex PCR and H1- multiplex PCR	18
3.3	Additional oligonucleotide primers used for H1 and H2- multiplex PCR	20
3.4	PCR reaction mixture for multiplex PCR serogrouping of A, B, C1, C2, D,	24
	E and Vi (Lim and Thong, 2009)	
3.5	PCR cycling parameters for multiplex PCR serogrouping of A, B, C1, C2,	24
	D, E and Vi (Lim and Thong, 2009)	
3.6	PCR reaction mixture for multiplex PCR serotyping for Ha, Hb, and Hd	25
	flagella antigens (Lim and Thong 2009)	
3.7	PCR cycling parameters for multiplex PCR serotyping for Ha, Hb, and Hd	25
	flagella antigens (Lim and Thong 2009)	
4.1	Optimized PCR condition recommended by Cardona-Castro et al. (2009)	32
4.2	PCR cycling parameters for multiplex PCR serotyping of flagella antigens	32
	(H1, H2)	

- 4.3 PCR conditions for multiplex PCR serotyping H1, H2 according to Lim and 33 Thong (2009) optimized conditions
- 4.4 The optimized PCR conditions for multiplex PCR serotyping H1and H2 35
- 4.5 Optimized PCR reaction cycling parameters for multiplex PCR serotyping 36
- **4.6** Results of blast search of DNA sequences showing the percentage of **38** identity, score and E value.
- 4.7 Salmonella strains used for blind testing and verification of the sequential41Multiplex PCRs results compared to conventional serotyping
- **4.8** Overall results of *Salmonella* typing based on mPCR detection O, H and Vi **44** genes

LIST OF APPENDICIES

Appendix	Title	Page
Α	Information of tested Salmonella strains	65
В	Results of multiplex PCR for O and Vi antigens	68
С	Results of multiplex PCR for H antigens (Ha, Hb, Hd, fliC-r, fliC-i, fliC- g.m and fliC-e.h)	71
D	Results of multiplex PCR for H antigens (fliC-z ₁₀ , fliC-z ₆ , fliC- i,z13, fljB-1.5, fljB-1.2, fljB-1.6, and fljB-enx)	74
Ε	PCR Product of Primers (fliC e.h) - DNA sequencing blast result	77
F	PCR Product of Primers (flj B enx) - DNA sequencing blast result	79
G	PCR Product of Primers (fliC z6) - DNA sequencing blast result	80
Н	PCR Product of Primers (fliC r) - DNA sequencing blast result	82
I	PCR Product of Primers (fliC- i) - DNA sequencing blast result	84
J	PCR Product of Primers (fljB-1.5) - DNA sequencing blast result	86
K	PCR Product of Primers (fljB- 1.6) - DNA sequencing blast result	88
L	PCR Product of Primers (fliC- g.m) - DNA sequencing blast result	90
Μ	PCR Product of Primers (fliC- z_{10}) - DNA sequencing blast result	92
Ν	PCR Product of Primers (fljB-1.2) - DNA sequencing blast result	94

LIST OF ABBREVIATIONS

Abbreviations	Stand for
BSA	Bovine serum albumin
DNA	Deoxyribonucleic Acid.
dNTP	Deoxynucleotide triphosphates
MgCl2	Magnesium Chloride
Taq	Thermus aquaticus
Ml	Microlitre
μΜ	Micromolar
Mg	Milligram
UMMC	Universiti Malaya Medical Centre
USM	Universiti Sains Malaysia
DMSO	Dimethyl sulfoxide
LB	Luria-Bertani
PCR	Polymerase Chain Reaction.
mPCR	Multiplex polymerase chain reaction
ddH2O	Double-distilled water
TBE	Tris-borate EDTA
Вр	base pair
Ml	Milliliter
mM	Millimolar

U	Unit
G	Gram
IMR	Institute of Medical Research
WHO	World Health Organization
&	And