COMPARATIVE STUDY ON PROTEIN EXPRESSION OF DRUG–METABOLIZING CYP1 FAMILY GENES FROM LAKE MANZALA

By

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B.Sc. Agric. Sc. (Aquaculture), Suez Canal University, 2003
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A thesis submitted in partial fulfillment

of

the requirements for the degree of

DOCTOR OF PHILOSOPHY
in
Agricultural Sciences
(Genetics)

Department of Genetics
Faculty of Agriculture
Ain Sham University

2013

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ACKNOWLEDGEMENT

Firstly, I wish to express my great and sincere gratitude to **ALLAH** who gave me the prosperity and ability to achieve this work.

All thanks and utmost respect to my principle supervisor **Prof. Dr. Mohamed Abdel-salam Rashed** and **Prof. Dr. Aiman Hanafy Atta** professors in Genetics Department, Faculty of Agriculture, Ain Shams University, for facilitating this work, their continuous encouragement and their continuous support by the thesis requirements.

A sincere respect is offered to my **Prof. Dr. Safaa I. El-Deeb**, professor of genetics, Genetic Laboratory, National Institute of Oceanography and Fisheries (NIOF), for her continuous encouragement to finish this work.

I would like to express my great thanks to **Dr. Mohamed A. H. El-Kady**, laboratory of genetics, (NIOF), I thank him too much for assisting in methodology, also I pray God to give him good future.

My gratitudes are extended to **Dr. Mahmoud Sallam** and **Dr. Nouh Eyd Ahmed** Department of Genetics, Faculty of Agriculture, Ain Shams University, for their help in gel electrophoresis analysis.

I would like to thank **Dr. Afaf El-Menisy** Department of Plant pathology, Faculty of Agriculture, Ain Shams University, for her help in spectrophotometer measurements.

Great thanks and sincere gratitude to my family for their encouragement and continuous support.

ABSTRACT

Ahmed Mohamed Abdo Hal: Comparative Study on Protein Expression of Drug–Metabolizing CYP1 Family Genes From Lake Manzala. Unpublished Ph.D. Thesis, Department of Genetics, Faculty of Agriculture, Ain Shams University, 2013.

The cytochrome P450 superfamily (CYP) is a large and diverse group of enzymes that catalyze the oxidation of organic substances such as polycyclic hydrocarbons (PAHs), polychlorinated biphenyls (PCBs) and aryl amines. Expression of cytochrome P4501A (CYP1A) has been measured as a biomarker for possible exposure to these pollutants. Using a quantitative reverse transcription-polymerase chain reaction (Q-RT-PCR), we estimated levels of CYP1A expression in *Oreochromis aureus* from five different locations of Lake Manzala: 1) El-Gamil, 2) El-Inaniya, 3) El-Sirw, 4) El-Bashtir and 5) El-Temsah during December 2011. The area of Al-Qanater was included as a reference site from Nile River. Higher levels of CYP1A gene expression and PAHs concentrations were observed in *O. aureus* collected from different locations of Lake Manzala than the reference site. The CYP1A gene was highly expressed in the liver of all fish populations followed by gills, testes, ovaries and muscles, respectively. Muscles expressed the least CYP1A gene among the tissues studied at Lake Manzala while the expression of CYP1A in muscles at the reference site was almost negative. At the location level, El-Gamil fish population exhibited the greatest CYP1A gene expression among the studied locations while CYP1A gene expression of El-Sirw fish population was higher in gills and muscles than El-Gamil fish population. Al-Qanater and El-Temsah fish exhibited the lower expression levels in all the organs studied. Higher levels of 11 compounds of PAHs were found in El-Gamil region, followed by El-Sirw, El-Bashtir, El-Inaniya, El-Temsah and Al-Qanater regions, respectively. The correlation coefficient between PAHs and CYP1A expression of fish organs was positive and highly significant ($p<0.05$) while the correlation coefficient between PAHs and CYP1A expression of testes and ovaries was highly significant ($p<0.01$). The highest positive correlation was detected between gills and liver ($p<0.01$) however the correlation between testes and ovaries was significant ($p<0.05$). The obtained partial sequence of cDNA of *O. aureus* was 569 base pair. The phylogenetic tree based on cDNAs sequences of CYP1 of teleosts and mammalian species showed a closer relationship between CYP1A and CYP1D subfamily members than any CYP1B or CYP1C that resulted in the clustering of both subfamilies in one clade to be more correlated to each other than any CYP1B or CYP1C subfamily members. The tree clearly shows *O. aureus* CYP1A and *O. niloticus* CYP1A genes to be clustered together in the same branch showing more correlation to each other (86.8%). In conclusion, the results of the present study demonstrated that Q-RT-PCR protocol is a valuable tool and has a higher sensitivity in environmental assessment. This level of sensitivity offered by Q-RT-PCR has been used successfully of CYP1A gene expression as biomarker in Lake Manzala fish.

Key words: Q-RT-PCR, CYP1A gene expression, polycyclic aromatic hydrocarbons (PAHs), *O. aureus,* Lake Manzala, water pollution.

CONTENTS

LIST OF TABLES V

LIST OF FIGURES VII

I. INTRODUCTION 1

II. REVIEW OF LITERATURE 6

1- Lake Manzala 6

2- Cytochrome P450 (CYP) 10

3- CYP1 family 12

4- Cytochrome P450 forms in fish 22

5- CYP1A subfamily 23

6- Mechanism of P450 gene induction 35

7- Molecular structure of P450s 36

8- Housekeeping genes (reference genes) 37

III- MATERIALS AND METHODS 39

Materials 39

1. Sample collection: 39

    1.1. Organs sampling 40

Methods 40

1. Total RNA isolation (AGPC method): 40

    1.1. Principle: 41

    1.2. Reagents used 41

    1.3. Protocol 41

2. Determination of total RNA concentration 43

3. Checking the integrity of total RNA 43

4. Protocol for formaldehyde gel electrophoresis 44

4.1 Reagents used 44

4.2 Gel preparation 44

5. Preparation of RNA samples for run 45

6. Primers designing 45

6.1. Primers designing for CYP1A 45

6.2. Primers designing for β-actin (internal control) 47

7. Quantitative Reverse Transcription Polymerase Chain Reaction (Q RT-PCR) 48

7.1. Principle of Competitive RT-PCR 48

7.1.1. Competitive RT-PCR Using an Internal Reference Template 48

7.2. Preparation of the RT-PCR assay 49

7.3. Reverse transcription and thermal cycling 49

8. Quantitave RT-PCR product electrophoresis stock 50

8.1. Stock solutions 50

8.1.1. Agarose gel buffer (5X Tris-borate (TBE)), pH 8.0: 50

8.1.2. Ethidium bromide dye 50

8.1.3. Polyacrylamide gel preparation 50

8.1.4. Separation on the 10% polyacrylamide 50

9. Polycyclic aromatic hydrocarbons (PAHs) analysis in 51

9.1. Extraction of water samples 51

9. 2. Column chromatography 52

9. 3. Sulphur removal 52

9. 4. Blank preparation 52

10. Sequence analysis: 53

10.1. Target Sequencing 53

10.2. Sequence alignment and phylogenetics 53

11. Statistical analysis: 54

IV. RESULTS AND DISCUSSION 55

1. Polycyclic aromatic hydrocarbons (PAHs) analysis in water samples 55

2. Extracting total RNA from tissues 60

2.1. Concentration and quality of total RNA concentration 60

2.2. Checking the integrity of total RNA. 61

3. CYP 1A and β-actin genes expression of fish populations at the different locations 62

3.1. El-Gamil population 63

3.2. El-Sirw population 65

3.3. El-Bashtir population 67

3.4. El-Temsah population 69

3.5. El-Inaniya population 71

3.6. Al-Qanater Al-Khyria (Q) population 73

4. Comparison among the expression profile for organs of fish populations based on Gelanalyzer program 75

5. Comparison among organs for fish populations using concentration measurements 77

6. Comparison among populations based on fish organs 81

6.1. CYP1A gene expression in liver among studied populations: 82

6.2. CYP1A gene expression in gills among studied populations 83

6.3. CYP1A gene expression in muscles among studied populations 83

   - 6.4. CYP1A gene expression in testes among studied populations 84
   - 6.5. CYP1A gene expression in ovaries among studied populations 85
- 7. Comparison among the different populations using the expression profile of organs based on Gelanalyzer program 86
- 8. Comparison among the different populations using the expression profile of organs based on concentration measurements. 89
- 9. The correlation coefficient between Gelanalyzer program and spectrophotometric measurements 91
- 10. The relationship between CYP1A gene expression of organs and PAHs concentrations 92
- 11. Sequencing of partial sequence of CYP1A mRNA of *Oreochromis aureus* 94
- 12. Alignment of partial sequence of CYP1A mRNA of *O. aureus* and *O. niloticus* 97

V- SUMMARY 102

VI- REFERENCES 106

ARABIC SUMMARY

LIST OF TABLES

1. Sequences, start, stop and GC % contents of used CYP1A primer for competitive RT-PCR. 47
2. Sequences, start, stop and GC % contents of used β-actin primer for competitive RT-PCR. 47
3. The analysis of Water samples by a Hewlett Packard 5890 series II Gas Chromatograph (concentration unit is µg/l). 59
4. The concentration of total RNA by A_{260} reading of spectrophotometer of organs. 60
5. The concentration of CYP1A gene expression of organs for El-Gamil population using Gelanalyzer program (ng/0.15µl) and spectrophotometric measurements (ng/µl). 64
6. The concentration of CYP1A gene expression of organs for El-Sirw population using Gelanalyzer program (ng/0.15µl) and spectrophotometric measurements (ng/µl). 66
7. The concentration of CYP1A gene expression of organs for El-Bashtir population using Gelanalyzer program (ng/0.15µl) and spectrophotometric measurements (ng/µl). 68
8. The concentration of CYP1A gene expression of organs for El-Temsah population using Gelanalyzer program (ng/0.15µl) and spectrophotometric measurements (ng/µl). 70
9. The concentration of CYP1A gene expression of organs for El-Inaniya population using Gelanalyzer program (ng/0.15µl) and spectrophotometric measurements (ng/µl). 72

10. The concentration of CYP1A gene expression of organs for Al-Qanater population using Gelanalyzer program (ng/0.15µl) and spectrophotometric measurements (ng/µl). 74
11. The correlation between Gelanalyzer program and spectrophotometer analysis. 91
12. The correlation between PAHs concentration and CYP1A gene expression. 93
13. Percentage identities of DNAs sequences of CYP1A, CYP1D, CYP1B and CYP1C gene subfamilies. 98

LIST OF FIGURES

1. AHR-mediated expression of CYP1A gene 36
2. Location of sampling sites in Lake Manzala. 1: El-Inaniya, 2: El-Sirw, 3: El-Temsah, 4: El-Gamil, 5: El-Bashtir and 6: Al-Qanater. 39
3. The phenotypic characteristics of the *Oreochromis aureus* that used as a model to measure the expression of CYP1A gene at Lake Manzala. 40
4. Graphical summary on Conserved Domain of CYP superfamily. 46
5. Polycyclic aromatic hydrocarbons (PAHs) analysis by GC-FID in water of El-Gamil region. 55
6. Polycyclic aromatic hydrocarbons (PAHs) analysis by GC-FID in water of El-Sirw (a) and El-Bashtir (b) regions. 56
7. Polycyclic aromatic hydrocarbons (PAHs) analysis by GC-FID in water of El- Temsah (a) and El- Inaniya (b) regions. 57
8. Polycyclic aromatic hydrocarbons (PAHs) analysis by GC-FID in water of Al-Qanater region. 58
9. Total RNA extracted from liver and gills incubated with 100% ethanol (a) and total RNA extracted from organs stored at normal saline 0.9% (b). Position of 28S and 18S ribosomal RNA is indicated by the arrows. 61
10. Representative electrophoretic patterns of Q-RT-PCR for liver (L), gills (G), muscles (Mn), testes (Y) and ovaries (X) taken from wild *O. aureus* of El-Gamil population. M: DNA standard marker. 63

11. Representative electrophoretic patterns of Q-RT-PCR for liver (L), gills (G), muscles (Mn), testes (Y) and ovaries (X) taken from wild *O. aureus* of El-Sirw population. M: DNA standard marker. 65

12. Representative electrophoretic patterns of Q-RT-PCR for liver (L), gills (G), muscles (Mn), testes (Y) and ovaries (X) taken from wild *O. aureus* of El-Bashtir population. M: DNA standard marker. 67

13. Representative electrophoretic patterns of Q-RT-PCR for liver (L), gills (G), muscles (Mn), testes (Y) and ovaries (X) taken from wild *O. aureus* of El-Temsah population. M: DNA standard marker. 69

14. Representative electrophoretic patterns of Q-RT-PCR for liver (L), gills (G), muscles (Mn), testes (Y) and ovaries (X) taken from wild *O. aureus* of El-Inaniya population. M: DNA standard marker. 71

15. Representative electrophoretic patterns of Q-RT-PCR for liver (L), gills (G), muscles (Mn), testes (Y) and ovaries (X) taken from wild *O. aureus* of Al-Qanater population. M: DNA standard marker. 73

16. Log mean number of CYP1A transcripts of total RNA from El-Gamil (a) and El-Sirw (b) populations of *O. aureus.* 75

17. Log mean number of CYP1A transcripts of total RNA from El-Bashtir (a), El-Temsah (b), El-Inaniya (c) and Al-Qanater (d) populations of *O. aureus.* 76

18. Log mean number of CYP1A transcripts of total RNA from El-Gamil populations of *O. aureus.* 77

19. Log mean number of CYP1A transcripts of total RNA

from El-Sirw (a), El-Bashtir (b) and El-Temsah (c) populations of *O. aureus* using spectrophotometer. 78

20. Log mean number of CYP1A transcripts of total RNA from El-Inaniya (a) and Al-Qanater (b) populations of *O. aureus* based on spectrophotometer. 79
21. Electrophoretic patterns of Q-RT-PCR of liver of *O. aureus* from El-Bashtir (B), El-Inaniya(E), El-Gamil (G), El-Sirw(S), El-Temsah (T) and Al-Qanater Al-Khyria (Q) populations. **M**: DNA standard marker. 82
22. Electrophoretic patterns of Q-RT-PCR of gills of *O. aureus* from El-Bashtir (B), El-Inaniya(E), El-Gamil (G), El-Sirw(S), El-Temsah (T) and Al-Qanater Al-Khyria (Q) populations. M: DNA standard marker. 83
23. Electrophoretic patterns of Q-RT-PCR of muscles of *O. aureus* from El-Bashtir (B), El-Inaniya(E), El-Gamil (G), El-Sirw(S), El-Temsah (T) and Al-Qanater Al-Khyria (Q) populations. M: DNA standerd marker. 84
24. Electrophoretic patterns of Q-RT-PCR of testes of *O. aureus* from El-Bashtir (B), El-Inaniya(E), El-Gamil (G), El-Sirw(S), El-Temsah (T) and Al-Qanater Al-Khyria (Q) populations. M: DNA standerd marker. 85
25. Electrophoretic patterns of Q-RT-PCR of ovaries of *O. aureus* from El-Bashtir (B), El-Inaniya(E), El-Gamil (G), El-Sirw(S), El-Temsah (T) and Al-Qanater Al-Khyria (Q) populations. M: DNA standerd marker. 86
26. Log mean number of CYP1A transcripts of total RNA from liver (a) and gills (b) of *O. aureus.* 87
27. Log mean number of CYP1A transcripts of total RNA from muscles (a) and gonads (b, c) of *O. aureus.* 88