

A Novel Mitochondrial DNA (mtDNA) Mutation Significantly Attenuates Transcription Termination In A Patient With A Mitochondrial Myopathy

Ravinarayan Raghupathi BSc, MSc

A thesis submitted for the degree of Doctor of Philosophy

Centre for Neuroscience, Dept. of Human Physiology, Flinders University School of Medicine Adelaide, South Australia. The scientist has a lot of experience with ignorance and doubt and uncertainty, and this experience is of very great importance, I think.

It is scientific only to say what is more likely and what less likely, and not to be proving all the time the possible and impossible.

Our imagination is stretched to the utmost, not, as in fiction, to imagine things which are not really there, but just to comprehend those things which are there.

Richard Feynman

What is science in the last analysis but the study and the love of Nature, displayed not in the form of abstract worship but in the practical form of seeking to understand Nature?

... the principal requisite for success in scientific research is not the maturity of knowledge associated with age and experience, but the freshness of outlook which is the natural attribute of youth.

Sir C.V.Raman

"...what a long strange trip it's been"

The Grateful Dead

Dedication

I dedicate this thesis to the memory of my mother, Lalitha Raghupathi (1941-2001) and my maternal grandmother, G. Ambujammal (1918-2010).

Declarationx
Acknowledgmentsxi
Abbreviationsxiv
List of figures
List of tables
Abstract
Preface
Chapter I Introduction and Literature Review1
1.1 Introduction
1.1.1 General Introduction
1.1.2 Structure of Mitochondria
1.1.3 The Electron Transport Chain
1.1.3.1 Complex I
1.1.3.2 Complex III
1.1.3.3 Complex IV
1.1.3.4 Complex II
1.1.3.5 Complex V and oxidative phosphorylation 11

1.2 Biogenesis of Mitochondria	14
1.2.1 Introduction	14
1.2.2 Structure and Organisation of Human mtDNA	15
1.2.3 Replication of mtDNA	20
1.2.3.1 Initiation of mtDNA replication	20
1.2.3.2 The strand-asymmetric (displacement) model of mtDNA	
replication	21
1.2.3.3 The strand-coupled model of mtDNA replication	22
1.2.3.4 Factors associated with mtDNA synthesis	23
1.2.4 Transcription of mtDNA	24
1.2.4.1 Initiation of mtDNA transcription	25
1.2.4.2 Mitochondrial transcription machinery	26
1.2.4.3 Elongation and termination of mtRNA transcripts	28
1.2.4.4 Post-transcriptional modifications	32
1.2.5 Translation of mitochondrial transcripts	34
1.2.6 Protein import into mitochondria	35
1.2.7 Origin and evolution of mitochondria and mtDNA	39
1.3 Mitochondrial Dysfunction	43
1.3.1 Introduction	43
1.3.2 mtDNA mutations and disease	45
1.3.2.1 Missense mutations	45
1.3.2.2 Deletions and insertions in mtDNA	46
1.3.2.3 Biogenesis mutations	48
1.3.2.4 Copy number mutations	52
1.3.3 Mitochondrial dysfunction in neurodegenerative disorders	53

1.3.4 Study of mitochondrial dysfunction	
1.3.4.1 Laboratory diagnosis	
1.3.4.2 Molecular studies of mtDNA mutations	
1.3.4.3 Cellular studies	
1.3.4.4 Animal models of mitochondrial disease	
1.4 Background to this study	59
1.5 Aims of this study	

Chapter II Materials and Methods

2.1 Materials	
2.1.1 Skeletal muscle biopsies	65
2.1.2 Cell lines	65
2.1.2.1 Lymphoblasts	65
2.1.2.2 143B206 Rho-zero cells	66
2.1.2.3 Cybrid cell lines	66
2.1.2.4 Mitochondrial extract preparation	67
2.2 Methods	68
2.2.1 Isolation of DNA from blood and cells	68
2.2.2 Diagnostic PCR and pedigree analysis by RFLP	69
2.2.3 Measurement of mitochondrial mass	71
2.2.4 RNA folding	71
2.2.5 Analysis of mtDNA transcripts	71
2.2.5.1 Real time PCR	72
2.2.5.2 Northern blotting	73

2.2.6 Analysis of mitochondrial proteins	. 75
2.2.6.1 Immunoblot analysis of COX subunits	. 75
2.2.6.2 Blue-Native PAGE analysis of mitochondrial proteins	. 76
2.2.7 Analysis of respiratory chain activity	. 77
2.2.7.1 Complex I (NADH ubiquinone oxidoreductase)	. 77
2.2.7.2 Complex II + III (Succinate-Cytochrome C oxidoreductase)	. 78
2.2.7.3 Complex IV (Cytochrome <i>c</i> oxidase)	. 78
2.2.7.4 Citrate synthase	. 79
2.2.7.5 Complex V (ATP synthase)	. 79
2.2.8 Analysis of apoptosis and oxidative stress	. 80
2.2.8.1 Apoptotic DNA ladder assay	. 80
2.2.8.2 Measurement of 8-OHdG levels	. 81

Chapter III Preliminary Analysis of the 3229.A Mutation	
---	--

3.1 Introduction	
3.2 Results	
3.2.1 Analysis of the pedigree, load and tissue distribution of	the 3229.A
mutation	
3.2.1.1 Proband	
3.2.1.2 Proband's family members	
3.2.1.2 Proband's family members	
3.2.2 Estimation of mitochondrial mass and number	
3.2.3 Prediction of tRNA ^{Leu(UUR)} secondary structure	
3.3 Discussion	

Chapter IV Molecular Analysis of the Effect(s) of the 3229.A Mutation on	
mtDNA Transcription and Translation	. 99

4.1 Introduction	100
4.1.1 Analysis of mtDNA transcription	100
4.1.2 Analysis of mt-mRNA translation	105
4.2 Results	106
4.2.1 Analysis of mtDNA expression by real-time RT-PCR (qPCR)	106
4.2.2 Analysis of mRNA levels by Northern blotting	112
4.2.3 Immunoblot analysis of COX subunit levels	115
4.2.4 BN-PAGE analysis of mitochondrial holocomplexes	115
4.3 Discussion	118

Chapter V Analysis of the Pathological Effect(s) of the 3229.A Mutation... 121

5.1 Introduction	122
5.1.1 Measurement of respiratory chain activity	122
5.1.2 Measurement of oxidative stress	124
5.1.3 Analysis of apoptotic effects of the 3229.A mutation	127
5.2 Results	128
5.2.1 Respiratory chain activity in the proband	128
5.2.2 Measurement of oxidative stress in proband cells	134
5.2.3 Analysis of apoptogenic effects of the 3229.A mutation	134
5.3 Discussion	139

Chapter VI General Discussion	142
-------------------------------	-----

6.1 Summary of findings	
6.2 Pathophysiology of the 3229.A mutation	144
6.2.1 RNA-mediated disease	
6.2.2 Protein gain of function	
6.3 Limitations of this study	147
6.4 Future scope	
6.5 Publications arising out of work contained in this thesis	

Bibliography	 151

Declaration

I certify that this thesis does not incorporate without acknowledgment any material previously submitted for a degree or diploma in any university; and that to the best of my knowledge or belief it does not contain any material previously published or written by another person except where due reference is made in the text.

Ravinarayan Raghupathi

Acknowledgments

I am deeply grateful to my Principal Supervisor, Prof. Dominic Thyagarajan, for his guidance and support during the course of my PhD study. He is an invaluable source of knowledge in the field of mitochondrial genetics and disease and I have enjoyed many hours of fruitful scientific discussion with him. Our relationship was cordial and I thank him for his patience in keeping me focused.

I am also indebted to my co-supervisors, Dr. Tim Chataway and Prof. Simon Brookes, for their wonderful support and guidance. I have spent many hours discussing everything from science to cricket with Tim and his mentoring of my project and ideas helped me immensely in gaining a better perspective of my research. I owe Simon a deep debt of gratitude for ensuring that my PhD study was relatively smooth sailing and especially for helping me win the Endeavour IPRS award that financed my degree.

I must acknowledge Dr. Wei Ping Gai for having invited me to be a Visiting Academic in 2005, which led to my eventually studying at Flinders University the following year. He, along with his Research Assistants Fariba Chegini and Xiao-fan Shen, welcomed me to Australia and to the Flinders University scientific fraternity and I am grateful to all of them for doing so.

My thanks go to my laboratory colleagues Dr. Mark Slee, Malgorzata Krupa, Patrick Fernandes and James Finkemeyer for their collegiality and assistance. I wish to place on record my gratitude to the Government of Australia and Flinders University for the Endeavour International Postgraduate Research Scholarship, without which this study would have been impossible. I thank the Departments of Human Physiology and Neurology for giving me the opportunity to undertake my PhD study.

One of the many wonderful things about studying at Flinders University is the camaraderie shared by the faculty, staff and students, especially in the Dept. of Human Physiology. During my PhD study, I have been fortunate to interact with and/or receive assistance from several people, who are too numerous to list here. I thank them all individually for their friendliness and support and I am grateful to all the laboratories that allowed me use of their facilities.

I would be remiss if I did not acknowledge the proband, whose cells and tissues formed the basis of this study. I had the pleasure of interacting with him on several occasions and I wish him well.

I would never have come this far were it nor for the support of my parents, (Varadachar and Lalitha Raghupathi), my maternal grandmother and my family and friends. I am deeply grateful to all of them for their love and support, especially when the going got tough.

There are no words to really describe my gratitude to my wonderful wife, Dr. Anuradha Mundkur, without whom my life would not have been the same. Her love and support have carried me through the good times and the bad and she has been an incredible source of strength and inspiration.

Abbreviations

8-OHdG	8-hydroxy-2-deoxyguanosine
AD	Alzheimer's Disease
ADP	Adenosine diphosphate
ADPD	Alzheimer's Disease and Parkinson's Disease
adPEO	Autosomal Dominant Progressive External
	Ophthalmoplegia
ALS	Amyotrophic Lateral Sclerosis
ALT	Alanine transaminase
AP	Alkaline phosphatase
AST	Aspartate aminotransferase
ATP	Adenosine triphosphate
BN-PAGE	Blue-Native Polyacrylamide Gel Electrophoresis
bp	Base-pair
BSA	Bovine serum albumin
CaCl ₂	Calcium chloride
CaCl ₂ cDNA	Calcium chloride Complementary DNA
_	
cDNA	Complementary DNA
cDNA CK	Complementary DNA Creatine kinase
cDNA CK CNS	Complementary DNA Creatine kinase Central Nervous System
cDNA CK CNS CoA	Complementary DNA Creatine kinase Central Nervous System Coenzyme A
cDNA CK CNS CoA CoQ	Complementary DNA Creatine kinase Central Nervous System Coenzyme A Coenzyme Q

CS	Citrate synthase
CSB	Conserved Sequence Blocks
DIG	Digoxigenin
DMEM	Dulbecco's modified Eagle's medium
DNA	Deoxyribonucleic acid
DTNB	5,5'-dithiobis(2-nitrobenzoic acid)
EBV	Epstein-Barr virus
EDTA	Ethylene diamine tetra-acetic acid
EEG	Electroencephalography
ELISA	Enzyme-linked immunosorbent assay
EtBr	Ethidium bromide
ETC	Electron Transport Chain
FMN	Flavin mononucleotide
GGT	gamma-glutamyl transferase
HCl	Hydrochloric acid
HD	Huntington's Disease
HMG	High mobility group
Hsp	Heat shock protein
HSP	Heavy strand promoter
IMS	Inter-membrane space
KCl	Potassium chloride
KCN	Potassium cyanide
KSS	Kearns-Sayre syndrome
LHON	Leber's Hereditary Optic Neuropathy
LIMM	Lethal Infantile Mitochondrial Myopathy

LSP	Light strand promoter
MELAS	Mitochondrial encephalomyopathy, lactic acidosis, and
	stroke-like symptoms
MERRF	Myoclonic Epilepsy and Ragged-Red Fibre Disease
MgCl ₂	Magnesium chloride
MMC	Maternally Inherited Myopathy and Cardiomyopathy
MND	Motor Neuron Disease
MRI	Magnetic Resonance Imaging
mRNA	Messenger RNA
mtDBP	Mitochondrial displacement (D)-loop binding protein
mtDNA	Mitochondrial DNA
mTERF	Mitochondrial transcription termination factor
MTG	MitoTracker Green
mt-Hsp	matrix heat shock protein
mtRNA	Mitochondrial RNA
MTS	Matrix targeting sequences
mtSSB	mitochondrial single-stranded binding protein
mtTFA/TFAM	Mitochondrial transcription factor A
NAD	Nicotinamide adenine dinucleotide
NADH	reduced Nicotinamide adenine dinucleotide
NADH-TR	NADH-tetrazolium reductase
NARP	Neurogenic ataxia retinitis pigmentosa
NCR	Non-coding regions
nt	Nucleotide
OXPHOS	Oxidative phosphorylation

PAGE	Polyacrylamide gel electrophoresis
PAM	Presequence Translocase Associated Motor
PCR	Polymerase Chain Reaction
PCR-RFLP	Polymerase chain reaction-restriction fragment length
	polymorphism
PCR-RSM	PCR-mediated restriction site modification
PD	Parkinson's Disease
PEG	Poly-ethylene glycol
PEM	Progressive encephalomyopathy
POLRMT/mtRPOL	Mitochondrial RNA Polymerase
PPR	Pentacotripeptide Repeat
РТР	Permeability Transition Pore
PVDF	Polyvinylidene fluoride
qPCR	Quantitative PCR
REST	Relative Expression Software Tool
RFLP	Restriction fragment length polymorphism
RNA	Ribonucleic acid
ROS	Reactive Oxygen Species
RRF	Ragged-Red Fibres
rRNA	Ribosomal RNAs
RT-PCR	Reverse Transcriptase-Polymerase Chain Reaction
SAM	Sorting and assembly machinery
SD	Standard deviation
SDH	Succinate dehydrogenase
SEM	Standard error of the mean

SSC	Saline sodium citrate
TAE	Tris acetate EDTA
TBE	Tris borate EDTA
TIM	Translocase of the inner membrane
ТОМ	Translocase of the outer membrane
tRNA	Transfer RNA
Wt	Wild type

List of figures

Fig. 1.1	Structure of a typical mitochondrion	6
Fig. 1.2	Schematic of the electron transport chain	.8
Fig. 1.3	The complete set of electron carriers in the ETC	9
Fig. 1.4	Flowchart of electron transport and ATP synthesis	13
Fig. 1.5	Map of human mtDNA	16
Fig. 1.6	Human mtDNA transcription	31
Fig. 1.7	Illustration of the various protein import pathways into	
	mitochondria	36
Fig. 1.8	Pathological mutations in tRNA ^{Leu(UUR)}	51
Fig. 1.9	Electropherogram of proband's muscle mtDNA showing the novel	
	adenine insertion at nt 3230	51
Fig.3.1	Schematic of primer design for the PCR-RSM analysis of the	
	3229.A mutation	34
Fig. 3.2	Analysis of mutant load and pedigree by PCR-RSM	37
Fig. 3.3	Analysis of the mutation load in cell lines	88
Fig 3.4	Measurement of mitochondrial mass by MTG staining	92
Fig. 3.5	mFOLD analysis of $tRNA^{Leu(UUR)}$ secondary structure formation	
	and energy change	93
Fig.4.1	The Pfaffl equation used in REST to calculate the relative expression	l
	(R) of a target gene1	01
Fig.4.2	The mitochondrial genes analysed by qPCR10)2
Fig. 4.3	Standard curve for each qPCR primer pair10)5
Fig. 4.4	Quality and purity of qPCR products1	06

Fig. 4.5	Melting curve analysis of qPCR products107
Fig. 4.6	Results of qPCR using REST-RG109
Fig. 4.7	Separation and transfer of total RNA111
Fig. 4.8	Northern blot results
Fig. 4.9	Immunoblot results
Fig. 4.10	Blue-Native PAGE analysis of mitochondrial holocomplex
	Levels
Fig. 5.1	Preliminary analysis of 8-OHdG levels in a novel 12S rRNA
	mutation124
Fig. 5.2	Citrate synthase (CS) specific activity in proband cells and tissues,
	compared to controls
Fig. 5.3	Complex I (CI) specific activity in proband cells and tissues,
	compared to controls
Fig. 5.4	Complex II + Complex III (CII + CIII) specific activity in proband
	cells and tissues, compared to controls
Fig. 5.5	Complex IV (CIV) specific activity in proband cells and tissues,
	compared to controls
Fig. 5.6	Complex V (CV, ATP synthase) specific activity in proband cells,
	compared to controls
Fig. 5.7	Measurement of 8-OHdG levels in proband and two controls134
Fig. 5.8	Analysis of DNA laddering due to apoptosis in proband and
	controls cells
Fig. 5.9	Analysis of DNA laddering after induction of apoptosis in
	proband and controls cells

List of tables

Table 1.1	Mammalian mitochondrial genetic code	.19
Table 2.1	List of primers used to analyse various mtDNA transcripts	
	from the proband and control cDNA samples	72
Table 3.1	Summary of the tissue distribution and percentage of load	
	of the 3229.A mutation in the proband and family members	90

Abstract

This PhD study aimed to characterise the pathophysiology of a novel mitochondrial mutation in a patient with a mitochondrial myopathy. This mutation, an adenine insertion at nucleotide (nt) position 3230 of the human mitochondrial genome (RefSeq NC_012920), was shown to significantly disrupt transcription termination, leading to increases in the levels of both the genome-length mitochondrial DNA (mtDNA) polycistronic transcript and selected mRNAs encoding subunits of the respiratory chain complexes. A corresponding increase in the levels of two subunits of Cytochrome *c* oxidase (COX, Complex IV) was observed; however, there was no increase in the levels of any of the respiratory chain holocomplexes. Complex I and Complex IV activities were elevated in the proband's tissues. No evidence of DNA damage through apoptosis or necrosis was found and the proband's cells did not show elevated levels of 8-hydroxy-2-deoxyguanosine, a biomarker of oxidative stress. Attenuation of transcription termination in human mitochondria appears to be a novel mechanism of mitochondrial disease.

Preface

This thesis is divided into six chapters. Chapter I provides a comprehensive review of pertinent literature in the field of human mitochondrial disease. It covers the biogenesis of mitochondria, mitochondrial function and dysfunction and explores the approaches commonly used in the study of mitochondrial disease. It ends with the background to this project, including the clinical case study, and outlines the aims of the project.

Chapter II details the biological samples used in this study, which included lymphoblasts, cytoplasmic hybrids (cybrids) and skeletal muscle biopsy samples obtained from the proband and six controls and the experimental procedures used to obtain the results described.

In Chapter III, the initial molecular genetic analysis of the mutation is described. Using a PCR-RFLP assay, the pedigree and tissue distribution of the mutation and its load in different samples was studied. Mitochondrial mass and number were assayed using a mitochondrion-selective fluorophore, MitoTracker Green. The effect of this mutation on tRNA^{Leu(UUR)} folding was analysed using mFOLD.

Chapter IV describes the study of the effects of the mutation on mtDNA transcription and translation. The levels of the polycistronic transcript and three mtDNA mature transcripts (ND1, ND2 and COX 1) were measured by Real-time RT-PCR and Northern blotting. Respiratory chain holocomplex levels were analysed by Blue-Native PAGE and mass spectrometry. The levels of COX sub-

xxiii

units I, II and IV were measured by immunoblotting with monoclonal antibodies against each subunit.

The penultimate Chapter (V) details the study of the effects of this mutation on mitochondrial function. Standardised spectrophotometric assays were used to measure respiratory chain activity. DNA damage was analysed by gel electrophoresis to look for the typical DNA laddering associated with apoptosis. A commercial ELISA kit was used to measure 8-OHdG levels.

Chapter VI presents an in-depth discussion of the overall findings and looks at their implication in a novel mechanism of mitochondrial disease in humans. This project has paved the way for interesting future projects, some of which are introduced in this chapter.

Note: unless otherwise mentioned, all artwork presented in this thesis is original.