The Role of Misfolded Proteins in Neurodegenerative Diseases

An Essay

Submitted for Partial Fulfillment of Master Degree in Neuropsychiatry

By

Marwa Mohamed moawed

M.B.,B.Ch.

Faculty of Medicine-Benha University

Under supervision of

Prof. Dr/ Magd fouad Zakaria

Professor of Neurology and Psychiatry Faculty of Medicine, Ain Shams University

Prof. Dr/ Nagia Aly Fahmy

Professor of Neurology and Psychiatry Faculty of Medicine, Ain Shams University

Dr/ Mohamed Khaled Elewa

Lecturer of Neurology and Psychiatry Faculty of Medicine, Ain Shams University

Faculty of Medicine

Ain shams university 2014



Acknowledgment

First, I would like to thank **Allah** the merciful and compassionate for making all this work possible and for granting me with the best teachers, family, friends, and colleagues that many people would wish and dream of having.

I am honored to have **Prof. Dr. Magd Found Zakaria**, Professor of Neurology, Faculty of Medicine, Ain Shams University, as a supervisor of this work. I am greatly indebted to his for his kind guidance and patience.

I am deeply thankful to **Prof. Dr. Magia**Aly **Fahmy**, Professor of Neurology, Faculty of
Medicine, Ain Shams University, for her great help
and effort to make this work possible. I was honored
to work with her.

Words can not express my deep gratitude and sincere appreciation to **Dr. Mohamed Khaled Elewa**, Lecturer of Neurology, Faculty of Medicine, Ain Shams University, who assisted me in most of the work. I am greatly grateful for his generous help, kind advice, and kind guidance.

Furthermore I would like to convey my special thanks to all my staff members, my colleagues and last but not least my wonderful family.

Contents

	Page
List of Tables	Ι
List of Figures	II
List of Abbreviations	III
Introduction	1
Aim of the Work	4
Chapter 1: Proteins: structure and folding process	5
Chapter 2: Protein misfolding: aggregation and amyloid formation	21
Chapter 3: Proteins misfolding in neurodegenerative diseases: Cause or Response?	32
Chapter 4: Diagnostic and Therapeutic approaches to protein misfolding neuro-degenerative diseases	
Discussion	7 3
Conclusions and Recommendations	80
Summary	83
References	88
Arabic Summary	_

List of Tables

Table No. Pag		e No.	
Table (1):	Summary of protein-modifying conditions and their affected proteins or peptides	.23	
Table (2):	Proteins susceptible to misfolding and their associated diseases	.35	

List of Figures

Figure No. Page No.	
Fig (1):	Models alpha-helix and beta sheets8
Fig (2):	Schematic representation of the structural component of proteins9
Fig (3):	Schematic energy landscape for protein folding
Fig (4):	Energy state of protein folding under physiological and misfolding conditions12
Fig (5):	Molecular chaperones regulate several important cellular processes
Fig (6):	Protein misfolding and aggregation24
Fig (7):	Composition of amyloid cross-β structure27
Fig (8):	Microscopic image of brain tissue form an Alzheimer disease
Fig (9):	Structure of amyloid fibrils in Parkinson's disease
Fig (10):	Induction of the heat shock response72

List of Abbreviations

α	Alpha
β	Beta
γ	Gamma
α-syn	α-synculein
17AAG	17-allylamino-17-demethoxy geldanamycin
Αβ	Beta-amyloid
AA	Amino acid
ABri	British amyloid peptide
AD	Alzheimer's disease
ADan	Danish amyloid peptide
AIF	Apoptosis inducing factor
ALS	Amyotrophic lateral sclerosis
ApoE	Apolipoprotein E
APP	Amyloid precursor protein
AR	Androgen receptor
ATP	Adenosine triphosphatases
BACE	Beta secretase
Ca ⁺²	Ionized Calcium
Cdk	Cyclin-dependent protein kinase
CFTR	Cystic fibrosis conductance regulator

CIDNP	Chemically induced nuclear polarization
CJD	Creutzfeld-Jackob disease
DMSO	Dimethyl sulfoxide
DNA	Deoxyribonucleic acid
DRPLA	Dentatorubral pallidolysian atrophy
ER	Endoplasmic reticulum
ERAD	Endoplasmic-reticulum associated degradation
ERK	Extracellular regulated kinase
FAD	Familial Alzehimer's disease
FBD	Familial British Dementia
FDD	Familial Danish Dementia
FFI	Fatal familial insomnia
FTDP-17	Frontotemporal dementia with Parkinsonism-17
GPI	Glycophosphatidylinositol
GRP	Glucose-regulated protein
GSK	Glycogen synthease kinase
GSS	Gerstmann-straussler-scheinker syndrome
HD	Huntington's disease
HDX	Hydrogen/deuterium exchange
HIBM	Hereditary inclusion body myopathy
HRP	Heat shock responsive protein
HSC 70	Heat shock cognate 70

HSEs	Heat shock elements
HSF1	Heat shock transcription factor 1
HSP	Heat shock protein
HSR	Heat shock response
Ig	Immunoglobulin
JNK	c-jun N-terminal kinase
KDa	Kilo Dalton
LAMP	Lysosomal associated membrane protein
LDL	Low density lipoprotein
MAP	Mitogen activated protein
MAPK	Mitogen-activated protein kinase
MSA	Multiple system atrophy
NAC	Non A beta component
NFT's	Neurofibrillary tangles
NMDA	N-methyl-D-aspartate
NMR	Nuclear magnetic resonance
NO	Nitric oxide
NSAID	Non-steroidal-anti-inflammatory drugs
PABP2	Poly (A) binding protein 2
PD	Parkinson's disease
PK	Protein kinase-k
PrDs	Prion related disorders

PrP ^c	Cellular prion protein
PrP ^{sc}	Prion protein scrapie
PS	Presenilin
RNA	Ribonucleic acid
ROS	Reactive oxygen species
SBMA	Spinal & bullar muscular atrophy
SCA	Spinocerebellar ataxias
sHSPs	Small heat shock proteins
SIBM	Sporadic inclusion body myositis
SOD	Superoxide dismutases
UPR	Unfolded protein response
vCJD	Variant Creutzfeld-Jackob disease

Introduction

A growing numbers of neurodegenerative diseases are associated nowadays with the expression of misfolded proteins. As known that protein molecules are responsible for almost all biological functions in the cell. In order to fulfill their various biological roles, these chain-like molecules must fold into precise three-dimensional shapes (*Hartl*, 2010).

The order of the amino acids determines the *primary* structure of the protein by creating a unique polypeptide chain, which is relatively flexible. Protein folding is the process by which the newly synthesized protein molecule folds into its unique, three- dimensional structure as polypeptides can fold into three *secondary* elements: the alpha-helix and the beta-sheet, which determine the three-dimensional structure of the protein, and the random coil. The *tertiary* structure refers to the distribution of the alpha-helices, beta-sheets and random coils in the protein, where in these elements are folded into a compact conformation stabilized by hydrogen bonds or ionic interaction. To become functional, the protein has to be packed into its particular *native* conformation. In the cell, a variety of proteins named chaperones assist the newly synthesized

polypeptide to attain its native conformation (Bryngelson et al., 1995; Herczenik and Gebbink, 2008).

Polypeptides and proteins may undergo misfolding processes resulting in aggregates: oligomers and fibrils possessing toxic properties. Genetic mutations are the main cause for protein misfolding in rare families, but the majority of patients have sporadic forms possibly related to environmental factors that results in the unfolding of the proteins which have a tendency to aggregate. Recent studies suggest that generation of excessive nitric oxide (NO) and reactive oxygen species (ROS), in part due to overactivity of the N-methyl-D-aspartate (NMDA) - subtype of glutamate receptor, can mediate protein misfolding in the absence of genetic predisposition (Nelson et al., 2005; Nakamura and Lipton, 2009).

Protein aggregation can result in several neurodegenerative diseases such as: Alzheimer's disease (deposits of amyloid beta and tau), Parkinson's disease (deposits of alpha synculein), Myotonic Dystrophies, Inclusion-Body Myositis and Prion related Disorders (PrDs) which also known as Transmissible spongiform encephalopathies (deposits of prion protein) (Matus et al., 2011).

Recent findings provide new concepts for inhibition of protein aggregation and its proinflammatory and cytotoxic effects. The main approaches fall into the following categories: Small compounds that inhibit aggregation; such as 2,4-dinitrophenol, di- and tri substituted aromatic molecules, Immunotherapy (antibody therapy and vaccination), and Compounds that interfere with amyloid-cell or amyloid-protein interactions (Verdier and Penke, 2006; Herczenik and Gebbink, 2008).

Some recent studies proposed that molecular chaperones are neuroprotective because of their ability to modulate the earliest aberrant protein interactions as they may convert toxic conformations of misfolded proteins to nontoxic forms that can be tolerated by cells, also they prevent the formation of toxic pre-fibrillar intermediates, or accelerate their conversion to nontoxic amorphous aggregates that can be turned over more easily by the proteolytic machinery (Muchowski et al., 2002).

Aim of the Work

To Review:

- 1- Why and how proteins are misfolded.
- 2- The role of misfolded proteins in pathogenesis of neurodegenerative diseases.
- 3- Recent diagnostic procedures and therapies for neurodegenerative diseases.
- 4- Future prospect of neurodegenerative disease' therapy.

<u>For</u> better understanding, diagnosis and therapy of neurodegenerative diseases.

Chapter (1):

Proteins: Structure and Folding Process

Proteins are essential elements for life. They are building blocks of all organisms and the operators of cellular functions. Humans produce a repertoire of at least 30,000 different proteins, each with a different role. The function of a protein can only be interpreted from its structure. The nervous system is a network of cells, and the peculiar functional properties of these cells can be derived from the properties and interactions of their proteins. Proteins are involved in all stages of neural activity. Those embedded wholly or partly in membranes regulate the transport of ions and molecules as a means of signal exchange with other cells and the external medium. Some of them have enzymatic functions to catalyze the chemical processes essential for function (Makhatadze and Privalov, 1995; Baldwin, 2007).

The structure of proteins

Proteins are molecules composed of an amino acid chain, in which each amino acid is connected to the next one by a peptide bond. Proteins are very diverse and vary in size from small peptides to large multimers. The variation