UNIVERSITI TEKNOLOGI MARA

A PHYLOGENETIC INFERENCE OF NEURODEGENERATIVE DISEASES FROM PROTEIN SEQUENCES

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ABSTRACT

Neurodegenerative diseases such as Alzheimer's, Parkinson's and Huntington's disease have many similarities at cellular level. Parkinson's disease is a neurodegenerative disorder which is characterized by the loss of dopaminergic neurons in the brain. The symptoms are resting tremor and changes in facial expression. Huntington's disease is an autosomal dominant disorder that causes the breakdown of nerve cells in the brain. The symptoms are cognitive changes and problems with the ability to swallow. Alzheimer's disease is a brain disease, which is due to the accumulation of amyloid β protein in the brain. The symptoms are confusion with time and lose in memory functions. These diseases carry parallel mechanism such as protein aggregation that caused by protein misfolding. Due to the similarities found from the characteristics observed from three diseases, it is important to know if these diseases are related to each other at molecular level. Phylogenetic method used to identify the similarities of these neurodegenerative diseases proteins. From the result, most of the proteins of these three neurodegenerative diseases have low percentage identity and mixed into the different cluster. Thus, they are not related to each other, although some of them might have same functions. This study could help in the discovery of a new drug for the pharmacotherapeutics of these neurodegenerative diseases.

CHAPTER 1

INTRODUCTION

1.1 Background

Phylogenetics is the study of changes in the traits of populations or organisms over many generations. It is also known as evolution of the populations in which the traits have been changed from a common ancestor to the descendant. The change of genes due to mutation such as insertions, deletions or substitutions is one of the factors that causes the evolution (Nei & Kumar, 2000). The descendent species or population may inherit a new character which is produced by the changes in genes due to the mutation. Thus, by creating phylogenetic tree, the descendent new species with any unique character can be identified and characterized easily. Phylogenetic tree consists of branching diagram and treelike diagram in which it has been used to make an inference of inherited relationship among the populations. From the phylogenetic tree, the organisms or species can be classified according to similarities and differences in their unique characteristics. Generally, there are several steps in phylogenetic methods. It starts with making a protein sequence alignment, construct a phylogenetic tree and verify and validate the phylogenetic tree.