**SOX6, SOX13 and SOX9 Expression Pattern in Meningioma in East Coast Malaysia**

Nurul Balqis Md Dzali1, Wan Rohani Wan Taib1\*, Mohd Khairi Zahri1, Mohd Nizam Zahary1, Nor Hidayah Abu Bakar2, Ahmad Zubaidi Abd Latif2, Abd Manaf Ali3, Hasnan Jaafar4, Farizan Ahmad5

1Faculty of Health Sciences, Universiti Sultan Zainal Abidin, Kuala Terengganu, Malaysia.

2Faculty of Medicine, Universiti Sultan Zainal Abidin, Medical Campus, 20400 Kuala Terengganu, Terengganu, Malaysia.

3Faculty of Bioresources and Food Industry, Universiti Sultan Zainal Abidin, Besut Campus, 22200, Besut, Terengganu, Malaysia.

4Department of Pathology, School of Medical Sciences, Health Campus, Universiti Sains Malaysia,16150 Kubang Kerian, Kelantan, Malaysia

5Department of Neuroscience,School of Medical Sciences, Health Campus, Universiti Sains Malaysia,16150 Kubang Kerian, Kelantan, Malaysia

\*Author for Correspondence: wanrohani@unisza.edu.my

Abstract

SOX (Sry-related high-mobility-group-box) family plays significant functions in human development from embryonic development, organogenesis and the most recent findings, tissue regeneration. As cell key modulators, deregulation of these genes has been associated with several human diseases including cancer. SoxD and SoxE, two of the nine SOX subgroups and their molecular mechanism in carcinogenesis are widely studied. Eventhough there are a considerable number of studies done on SOX gene in glioma, such studies in meningioma, which is the most frequent brain tumor type in East Coast Malaysia are still lacking. Thus, this study aimed to determine the expression levels of SOX6 (SoxD), SOX13 (SoxD) and SOX9 (SoxE) in both WHO grade I and WHO grade II meningioma in Malaysian population. An FFPE sample of WHO grade I, WHO grade II meningioma and a normal brain FFPE tissue were sectioned by using microtome. RNA extraction were completed and the best quality and concentration of RNA were proceeded for cDNA conversion before underwent gene expression analysis, real-time PCR (qPCR). The results displayed that SOX6, SOX13 and SOX9 gene were downregulated in all low-grade meningioma compared to normal tissue. In addition, there were upregulations observed in both SOX6 and SOX9 expressions but downregulated in high-grade meningioma forSOX13. SOX6, SOX13 and SOX9 expression levels in selected brain tumours in Malaysian population provide new insights of SoxD and SoxE expression in this population. The well-known versatility functions of SOX genes and the canonical interaction of SOX genes with their co-factors may elucidate the inconsistency of SOX gene expression level across diseases and genetic backgrounds. Thus, functional studies are recommended to be carried out to observe the selected genes’ functions and mechanisms whether they should reflect their diverse roles in specific Malaysian population.

Keywords: SOX6, SOX13, SOX9, brain tumours, qPCR, meningioma