

ANALYSIS OF EPIGENETIC FACTORS IN HUMAN NEURAL STEM CELLS EXPOSED TO HIGH GLUCOSE

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2:00PM – 2:45PM

ANATOMY SEMINAR ROOM
L2, MD10, DEPARTMENT
OF ANATOMY, NUS

MISS DEEPIKA KANDILYA

Graduate Student
Department of Anatomy
Yong Loo Lin School of Medicine
National University of Singapore

SYNOPSIS:

Gestational diabetes mellitus (GDM), which is characterised by hyperglycemia during pregnancy, is a major risk factor contributing to metabolic and cognitive impairments in the newborn. Studies suggest that alterations in molecular and epigenetic profile in fetal neural stem cells (NSCs) may be responsible for GDM-induced neurodevelopmental and cognitive impairments. It is hypothesised that high glucose alters the gene-specific epigenetic mechanisms that regulate brain development. In the present study, DNA methylation, histone modifications and miRNA regulatory mechanisms were found to be altered in human neural stem cells (hNSCs) when exposed to high glucose *in vitro*. High throughput DNA methylation array analysis suggests that expression levels of genes involved in neurodevelopmental and axon guidance pathway were epigenetically regulated in hNSCs exposed to high glucose. In parallel, Wharton jelly-derived mesenchymal stem cells (WjMSCs) which are multipotent cells having a very high proliferation capacity and low immunogenicity have been used to generate neural stem cells (NSCs). NSCs-derived from WJMSCs (obtained from normal and GDM mothers) express neuronal markers suggesting its potential to form neural derivatives which can be used for future theranostics.