

**INTERNATIONAL CONFERENCE ON INTELLIGENT
INFORMATICS & BIOMEDICAL SCIENCES 2018**

BANGKOK, THAILAND

20-25 OKTOBER 2018

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**PUSAT PENGAJIAN SAINS PERUBATAN
UNIVERSITI SAINS MALAYSIA**

09-18-16-T3FP (13:30 - 13:50)

Effect of Shoes on Lower Extremity Pain and Low Back Pain during Prolonged Standing Using Sloping Medium

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Abstract—Media with 16° slope is an effective solution to reduce low back pain risk caused by prolonged standing. In this study, we examined the effect of shoes on lower back pain caused by prolonged standing for 2 hours on sloping medium. However, prolonged standing has another major risk: lower extremity pain. Many studies have shown that this risk can be affected by shoes or characteristic. Hence, lower extremity pain risk is the main concern in this research. Two types of shoes observed in this study are Safety Shoes and Slip-On Shoes, as these are the most widely used in the manufacturing industry. Using the Surface Electromyography (S-EMG) method, the difference in Medial Gastrocnemius muscle response was measured against both types of shoes. The study showed that both types of shoes have different muscle activation values and the Safety Shoes showed greater activation. This result proves that, type of shoes may affect the amount of lower extremity pain caused while standing for 2 hours on sloping medium and Safety Shoes poses a greater lower extremity risk. Both Visual Analog Scale (VAS) and Foot Pain Questionnaire methods supported the finding. While the results of VAS method found standing for 2 hours on sloping medium has lower lower extremity pain than low back pain risk. Foot Pain Questionnaire method indicated that the activity of standing for 2 hours over sloping medium causes a high pain on thumb toe and the back of foot. Based on this study, it can be concluded that it is necessary to design a special shoes for prolonged standing occupation on a sloping medium that can reduce the lower extremity risk, besides low back pain risk.

09-18-007-T3A (13:50 - 14:10)

Expression profile of HIP1R in B-cell subsets and in silico prediction of its functions in diffuse large B-cell lymphoma ✓

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Abstract—Huntingtin-interacting protein 1 (HIP1R) is an endocytic protein involved in endocytosis of surface receptors by mediating actin polymerization. We have previously shown that HIP1R was expressed in lymphoid B cells and diffuse large B-cell lymphoma (DLBCL) associated with better survival. Herein, we examined the expression profile of HIP1R in different B-cell populations and its potential functions in DLBCL. By utilizing a validated anti-HIP1R monoclonal antibody (clone 1A10), we examined whether the following immune cells in human reactive tonsils expressed HIP1R through double immunostaining: T cells (CD3⁺), macrophages (CD68⁺), mantle zone (MZ) B cells (PAX5⁺), germinal centre (GC) B cells (BCL6⁺) and plasma cells (IRF4/MUM1⁺). HIP1R was strongly expressed in PAX5⁺ MZ B cells, moderately expressed in BCL6⁺ GC B cells, but absent in CD3⁺ T cells, CD68⁺ macrophages and IRF4/MUM1⁺ plasma cells. In particular, we observed that HIP1R was absent in IRF4/MUM1⁺ plasma cells residing within the GC or non-GC interfollicular regions, suggesting that IRF4/MUM1 might downregulate HIP1R expression in activated B cells. We have previously shown that HIP1R expression is strongly suppressed by the transcription factor FOXP1 in activated B-cell-like diffuse large B-cell lymphoma (ABC-DLBCL) cells, however FOXP1 is absent in normal plasma cells, suggesting the presence of other regulators. Our previous immunostaining results in a series of DLBCL patient cases (n=155) showed a significant inverse correlation between HIP1R and IRF4/MUM1 expression (Pearson $r = -0.495$; $p < 0.001$). Indeed, knockdown of IRF4/MUM1 expression in the ABC-DLBCL cell line OCI-LY3 by two independent IRF4 siRNA constructs increased HIP1R expression at both transcript and protein levels. In terms of functional relevance, the bioinformatics approach Gene Set Enrichment Analysis (GSEA) was adopted to examine gene sets positively-associated with HIP1R transcript expression profile in three independent gene expression profiling (GEP) datasets of DLBCL patient cases derived from Gene Expression Omnibus database *i.e.* GSE10846 (n=233), GSE23501 (n=63), and GSE19246 (n=59). Our GSEA results showed that the gene set 'Rho GTPase Activator Activity' (GO ID:0005100) was significantly positively-associated with HIP1R expression profile across all three GEP datasets GSE10846 ($p = 0.0016$), GSE23501 ($p < 0.0001$) and GSE19246 ($p = 0.0167$). These results suggest that HIP1R is involved in the activation of Rho GTPase signaling pathway, which has been documented to inhibit migration of DLBCL cells, and HIP1R expression is suppressed by transcription factors involved in B-cell activation including FOXP1 and IRF4/MUM1.

09-18-04-T3FP (14:10 - 14:30)

Biomedical Images Stitching Using ORB Feature Based Approach

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Abstract— This paper proposes a system for biomedical images stitching using feature based approach. The proposed system aims to stitch the high resolution images with low processing time. The proposed system is designed with five stages,