ePOSTER • DISCOVERY SCIENCE

[PPS2]

MULTI-MODALITY STUDY BETWEEN RETINAL AND CARDIAC MR IMAGES USING DEEP LEARNING

Paul Holmes[1], Alex Frangi[2], Andres Diaz-Pinto[2], Nishant Ravikumar[2]

[1]Faculty of Medicine, University of Leeds, Worsley Building, Woodhouse, Leeds LS2 9JT

[2]Department of Computational Medicine, University of Leeds, Woodhouse, Leeds LS2 9JT

Retinal images are routine ophthalmologic practice that could be used for monitoring primary and systemic conditions such as cardiovascular disease (CVD). The connections subsist via deep learning algorithms mapping the retinal blood vessel arterial tortuosity and density. Combining this information with individual demographics can be the formula to predict and understand CVD. Important indices are left ventricular mass (LVM) and left ventricular end-diastolic volume (LVEDV). Analysing retinal images has the potential for predicting cardiovascular pathology as a cost-effective and a non-invasive alternative at your opticians, utilising cardiac magnetic resonance imaging (CMR) and retinal images for diagnosing and analysing cardiomyopathy using the United Kingdom Biobank database (UKBB).

The UKBB provided 11,000 useable images for a deep learning algorithm to map retinal tortuosity of microvasculature, specifically the fractal dimension (FD). Whilst simultaneously considering cardiovascular function, LVEDV and LVM. FD is a statistical index of complexity and in this case, represented the extent of neovascularisation of the blood vessels (BV).

20% of groups contained a $\pm 0.1 \leq 0.3$, and 16.6% of groups contained a moderate correlation, $> \pm 0.3$ between FD and LVM/LVEDV. This supported current literature that LVM and LVEDV are related to the tortuosity of retinal FD.

The microvasculature within the retina is related to LVM and LVEDV, which supports the idea of systemic disease affecting vessels throughout the body. This provides premise to continue forward in providing a cost-effective automated system for screening retinal images for CVD.

ePOSTER • DISCOVERY SCIENCE

[PPS3]

PROGESTINS EFFECT ON AN ENDOMETRIOTIC CELL LINE

Hope Rowden[1,2], Renata Pavlič[2], Maja Pušić[2], Maša Sinreih[2], Nick Hopcroft[1], Tea Lanišnik Rinžer[2]

[1]Warwick Medical School, University of Warwick, Coventry, CV4 7HL, United Kingdom

[2]Institute of Biochemistry, Faculty of Medicine, University of Ljubljana, Vrazov trg 2, Ljubljana, Slovenia

Endometriosis is a chronic inflammatory disease which affects up to 1 in 10 women of reproductive age. It occurs when endometrial cells grow outside the uterus and is categorised based on the location of ectopic lesions, namely: ovarian, peritoneal, and deep infiltrating endometriosis. The exact cause of endometriosis is yet to be determined. Nevertheless, for the last 50 years progestins (synthetic analogues of progesterone) have been used to treat endometriosis. Progestins are known to be anti-inflammatory by inhibiting the function of certain immune cells and affecting the balance of pro- and anti-inflammatory cytokines. However, the pharmacological action of progestins in endometriosis is not completely understood. Previous unpublished data from our laboratory has identified IL-1, IL-10 and OPG signalling pathways involved in progestins mechanism of action. The aim of this study was to further assess the role of progestins on the pro-inflammatory IL-1 signalling pathway. We examined the effect of progesterone and three progestins (Medroxyprogesterone acetate (MPA), Dydrogesterone (D) and Dienogest (DNG)) in a model cell line of peritoneal endometriosis (12-Z). We utilised Real Time-qPCR to assess the expression of 6 genes involved in the IL-1 signalling pathway. We found that gene encoding IL1 receptor (*IL1R*) was upregulated by MPA and DNG whereas repressors of IL-1 signalling pathway, *IL1R2* and *IL1RN*, were upregulated by all progestins. Genes *IL1A/B* showed changes depending on the progestin, and expression of IL1R1 co-receptor *IL1RAP* was not affected by any condition. Although progestins showed different effects on expression of the investigated genes, upregulation of *IL1R2* and *IL1RN* suggest that all progestins decrease pro-inflammatory IL-1 signalling in endometriotic cell line 12-Z.

ePOSTER • DISCOVERY SCIENCE

[PPS4]

CANCER GENOMIC DATABASES ANALYSIS OF IKKα (INHIBITORY-κB KINASES α) AS POTENTIAL TARGET FOR LIVER HEPATOCELLULAR CARCINOMA

Wan Yi Ngan[1], Chee Onn Leong[2], Ling Wei Hii[1], Wei Meng Lim[1]

[1]School of Pharmacy, International Medical University, Bukit Jalil, 57000 Kuala Lumpur, Malaysia

[2]Institute For Research, Development & Innovation, International Medical University, Bukit Jalil, 57000 Kuala Lumpur, Malaysia

Liver hepatocellular carcinoma (LIHC) is a deadly disease threatening human health globally over the past decade. Emerging evidence highlights Nuclear Factor-κB (NF-κB) signaling pathway's role in immune responses, inflammation and tumorigenesis, which is critical for the chemically-induced LIHC progression and compensatory liver regeneration. Genomic databases analysis is useful to predict the potential of using inhibitory-κB kinases α (IKKα) encoded by conserved helix-loop-helix ubiquitous kinase *(CHUK)* as a novel cancer treatment target due to its function in NF-κB.

This research aimed to investigate IKKα *(CHUK)* gene alteration, expression patterns and clinical attributes across 32 The Cancer Genome Atlas (TCGA) cancer studies including liver cancer, which was extracted from cBio Cancer Genomics Portal (cBioPortal). Survival analysis was analysed to determine the differences between groups by comparing their log rank p-value using Kaplan-Meier curves. The mRNA expression profile of LIHC was obtained from Genome Data Analysis Center (GDAC) Firehose.

Based on the analysis of 32 cancer types, 161 out of 10,950 patients (1.5%) had altered the *CHUK* gene. The survival outcome between altered *CHUK* gene group and unaltered group is not correlated ($P > 0.05$). Using GDAC Firehose, 26 LIHC patients have a down-regulated *CHUK* gene in their tumor samples in comparison to their normal samples (Fold difference = 0.91, $P = 0.003$). A high and low *CHUK* gene expression in 20.77% and 40.71% of LIHC patients, respectively, in the survival analysis was found to be not correlated ($P > 0.05$). However, the clinicopathological characteristics and the differentially expressed genes (DEGs) correlated with *CHUK* gene expression.

IKKα is found to be differently expressed in LIHC, but it does not substantiate the survival outcome of *CHUK* expression in patients. The results reporting IKKα correlation with LIHC are limited. Further study on clinicopathological characteristics and the DEGs are required to determine the significance of *CHUK* in tumour.

ePOSTER • DISCOVERY SCIENCE

[PPS5]

CANCER GENOMIC DATABASE ANALYSIS OF IKK ALPHA AS POTENTIAL TARGET FOR THYROID CARCINOMA

Pei Zhi Hor[1], Chee Onn Leong[2], Wei Meng Lim[1], Ling Wei Hii[1]

[1]School of Pharmacy, International Medical University, Bukit Jalil, 57000 Kuala Lumpur, Malaysia

[2]Insititute for Research, Development & Innovation, International Medical University, Bukit Jalil, 57000 Kuala Lumpur, Malaysia

The incidence of thyroid carcinoma increases by 6.2% every year. Studies reported that it is more common in women than men. It is shown that dysregulation of IKK activities will promote tumour survival proliferation, migration, metastasis and angiogenesis, which are the common characteristics of many types of human cancers. IKK and IKK-related kinases are targeted for the development of treatment for cancer due to their oncogenic effects in human cancer. In this study, the information from a genomic database is analysed to assess the potential of using IKK alpha as treatment target.

Data and clinical profile of cancers were obtained from the cBioPortal database. Different survival outcomes including progression-free survival (PFS), overall survival (OS), disease-free survival (DFS) and disease-specific survival (DSS) of cancers can be identified by analysis of Kaplan Meier survival curve available in the database. Genome Data Analysis Centre Firehose (GDAC Firehose) provides analysis across a large range of data input without any modifications.

Analysis from TCGA data obtained from cBioPortal showed that thyroid carcinoma does not show significant *CHUK* gene alteration. Analysis of mRNA expression showed that *KLK1, KLK2, KLK4, MAPK4, SLC5A8, KRAS, HRAS, BRAF* and *NRAS* were the top ten hub genes whereby they exhibit clinically significant results in tumorigenesis. By referring to the mRNA level of *CHUK* gene, the survival analysis showed that patients with high *CHUK* expression have a higher survival rate and higher probability of being event free when compared to patients with low *CHUK* expression and *CHUK* wild type. The correlation of *CHUK* with thyroid carcinoma is limited, hence the suitability of using IKK alpha as a target requires more robust evidence.

ePOSTER • DISCOVERY SCIENCE

[PPS6]

REGULATION OF NF-KB SIGNALLING PATHWAY IN B-AMYLOID INDUCED BV2 MICROGLIAL CELLS BY ORIENTIN

Wen Cong Gan[1], Pei Ying Ng[2], Anna Pick Kiong Ling[1], Rhun Yian Koh[1], Kenny Gah Leong Voon[3], Ying Pei Wong[1]

[1]Applied Biomedical Sciences and Biotechnology Division, School of Health Sciences, International Medical University, 126 Jalan Jalil Perkasa 19, Bukit Jalil, 57000 Kuala Lumpur, Malaysia

[2]School of Postgraduate Studies, International Medical University, 126 Jalan Jalil Perkasa 19, Bukit Jalil, 57000 Kuala Lumpur, Malaysia

[3]Department of Pathology, School of Medicine, International Medical University, 126 Jalan Jalil Perkasa 19, Bukit Jalil, 57000 Kuala Lumpur, Malaysia

One of the hallmarks of Alzheimer's disease (AD) is the aggregation of β-amyloid peptides (Aβ) between neurons that cause cellular damage and structural degradation, leading to cognitive and memory decline observed in AD patients. Microglial cells, which act as the macrophage of the neural immune response, can be activated by the accumulation of Aβ which triggers a neuroinflammatory response through the NF-κB signalling pathway. In this study, the role of orientin, a water-soluble flavonoid with known anti-inflammatory and neuroprotective properties, in regulating the NF-κB signalling pathway in Aβ-stimulated BV2 microglial cells was investigated through cell death analysis, determination of mitochondrial membrane potential (MMP), and NF-κB signalling pathway protein expression. The results showed that maximum non-toxic dose (MNTD) orientin (15 μM) was able to rescue MMP levels of Aβ-stimulated BV2 microglial cells, as well as increasing protein expression of IKKα, IKKβ and IκBα. Taken together, these findings suggest that MNTD orientin downregulates the NF-κB signalling pathway and improves microglial cell viability which may potentially be beneficial for AD treatment.