Endoplasmic Reticulum Stress and the Unfolded Protein Response in the Pathogenesis of Asthma

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A thesis submitted in fulfilment of the requirement for the degree of Doctor of Philosophy (Medicine)

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March 2019

Statement of Originality

I hereby certify that the work embodied in the thesis is my own work, conducted under

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Acknowledgement of Authorship

I hereby certify that the work embodied in this thesis contains published papers of

which I am a joint author. I have included as part of the thesis a written declaration

endorsed in writing by my supervisor, attesting to my contribution to the joint

publications.

By signing below I confirm that Prabuddha Sanjeewa Pathinayake contributed by

critical literature review, manuscript writing, and manuscript revision to the

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Synopsis

Endoplasmic reticulum (ER) serves as a protein folding organelle and translocates correctly folded proteins into secretory pathways. Defectively folded protein aggregates are fatal and therefore the ER degrades them via ER-associated degradation (ERAD). Failure to remove terminally misfolded proteins results in an unfolded protein response (UPR) which increases the protein folding capacity while reducing the nascent protein folding load and protein translation. Unlike acute ER stress, chronic ER stress activates apoptosis, growth arrest, and cell death.

In the first study, we extensively explored the evidence of ER stress in various asthma groups using a range of different airway clinical samples and techniques. We demonstrated that chronic ER stress is a feature of severe asthma but not in mild asthma. We also observed that UPR is upregulated in those with active eosinophilic and neutrophilic inflammation. In sputum samples of those patients, expression of protein folding chaperones and ERAD function was reduced while apoptosis, and cell death markers were significantly increased.

ER stress also triggered various inflammatory signaling pathways and modulated pathogen-induced innate immune responses. In the second study, using a cell culture model we demonstrated the impact of chronic-high dose ER stress on RV1B induced inflammatory and antiviral responses in primary bronchial epithelial cells (pBEC). ER stress increased RV1B induced antiviral gene expressions; IFN-β, IFN-λ, IP-10, Viperin, and ISG56. However, the secretory profile of inflammatory and anti-viral cytokines was considerably low with UPR activation. ER stress also upregulated TSLP gene expression via CHOP dependent signaling pathway in bronchial epithelial cells but not IL-33 and IL-25. However, secretory TSLP could not be detected in the culture

supernatant. Therefore, maladaptive ER stress greatly attenuated the protein synthesis process in airway epithelial cells regardless of gene expression.

Chronic type II inflammation in asthmatic airways may induce ER-UPR and contributes to epithelial remodeling however the mechanisms are unknown. Therefore, in the third study, we investigated if exposure of airway epithelial cells to IL-13 induces ER-UPR and evaluated the efficacy of known FDA approved ER-UPR inhibitors, 4-PBA, and TUDCA on IL-13 induced mucus hypersecretion and pro-fibrotic factors in a pBEC airliquid interface cell culture model (ALI). IL-13 increased ER-UPR (XBP1s, BiP and EDEM1) in ALIs while 4-PBA markedly reduced IL-13 induced ER-UPR. IL-13 significantly induced MUC5AC gene expression in both pBEC ALIs. Treatment with TUDCA reduced MUC5AC gene expression approximately by 50% while 4-PBA reduced it by 99%. Muc5ac ELISA and IHC staining showed a significant decrease in secreted mucin with 4-PBA. None of the treatments reduced IL-13 induced STAT6 activation. However, 4-PBA significantly reduced IL-13 induced mucin transcription factors. Epithelial fibrotic factor periostin was reduced by TUDCA but not 4-PBA while SerpinB2 only reduced by 4-PBA. Therefore we demonstrate that Th2 cytokines upregulate ER-UPR in the airway epithelium and inhibiting ER-UPR reduces IL-13 induced mucus hypersecretion and epithelial remodeling.

Collectively these studies have identified potential novel pathways and molecules that are implicated in asthma. Importantly, these studies have expanded our understanding of disease pathogenesis and demonstrate that therapeutically targeting these pathways and molecules may be novel therapeutic avenues for severe asthma.

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List of commonly used Abbreviations

4-PBA 4-Phenylbutric Acid

ALI Air-Liquid Interface Cell Culture Model

BIP Binding Immunoglobulin Protein

BLF Bronchial Lavage Fluid

cDNA Complementary DNA

CHOP C/EBP Homologous Protein

COPD Chronic Obstructive Pulmonary Disease

EDEM1 ER Degradation Enhancing Alpha-Mannosidase Like Protein 1

eIF2α Eukaryotic Initiation Factor 2α

ER Endoplasmic Reticulum

ERAD ER-Associated Degradation

FACs Fluorescence-activated cell sorting

FDA Food and Drug Administration

FEV1 Forced Expiratory Volume

FVC Forced Vital Capacity

GINA Global Initiative for Asthma

HSP Heat Shock Protein

ICS Inhaled Corticosteroids

IFN Interferons

IL Interleukin

ILC2 Innate Lymphoid-2 Cells

IRE-1 Inositol Requiring Protein 1

ISGs Interferon Stimulated Gene

LABA Long-acting beta-agonists

mRNA Messenger RNA

NF-κb Nuclear Factor kappa-light-chain-enhancer of activated B cells

OVA Ovalbumin

PAMPs Pathogen Associated Molecular Patterns

pBEC Primary Bronchial Epithelial Cells

PERK Protein Kinase RNA-Like Endoplasmic Reticulum Kinase

PRRs Pattern Recognition Receptors

qPCR Quantitative Real-Time Polymerase Chain Reaction

ROS Reactive Oxygen Species

RSV Respiratory Syncytial Virus

RV Rhinovirus

TLR Toll Like Receptors

TNF Tumour Necrosis Factor

TSLP Thymic Stromal Lymphopoietin

TUDCA Tauroursodeoxycholic Acid

UPR Unfolded Protein Response

XBP1 Splicing of X-Box Binding Protein 1