ATS 2021 Highlights

Respiratory Structure and Function Early Career Professionals

Get to know members of the RSF Assembly

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Is your research clinical, basic science or translational?

Basic Science

Tell us about your research?

My PhD project aims to elucidate the contribution of the sex chromosomes and sex hormones to the pathology of respiratory diseases. Recently, I have investigated changes DNA methylation and gene expression in asthma patients who smoke using bioinformatics analysis. This work highlights molecular changes to tobacco smoke response pathways in asthma.

Where do you see yourself in 5 years?

I hope to continue working in respiratory research in an academic postdoc position. I want to be working overseas, expanding on my current skillset and knowledge base in a challenging new environment.

What do you find is the major benefit of RSF Assembly Membership?

As an early career researcher, being a member of RSF offers the opportunity to establish valuable connections which can grow into collaborations for future research.

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If you or someone you know would like to be featured as an ATS RSF ECP please email Katrina Tonga (katrina.tonga@sydney.edu.au)

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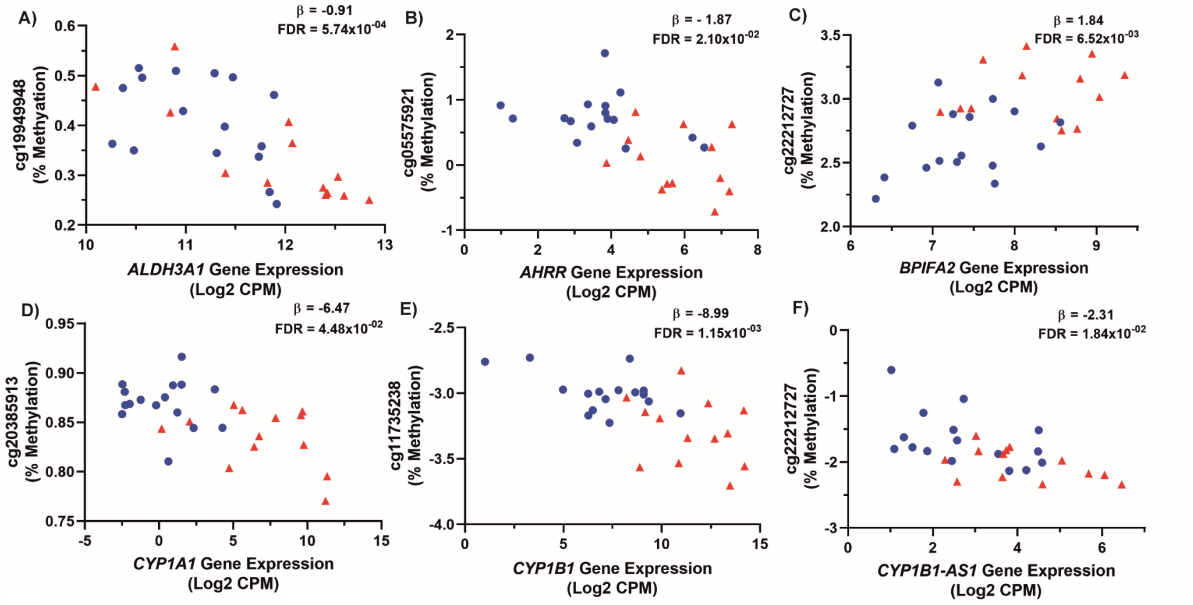

Representation of the relationship between DNA methylation status and gene expression in ex-smoker (blue) and current-smoker (red) patients. A) – F) Normalised percentage (%) methylation values are reported on the y-axis and normalised gene expression (Log2 CPM) reported on the x-axis. The β-value indicates the slope of the correlation. All results returned an FDR < 0.05; n = 29.

Abstract Title: Current Smoking Alters Gene Expression and DNA Methylation in the Nasal Epithelium of Asthmatics

Objective: To investigate the connection between differential gene expression and DNA methylation between current and ex-smoker asthma patient nasal epithelium.

Methods: Matched gene expression and epigenome-wide DNA methylation samples collected from nasal brushings of 55 patients. Differential gene expression and DNA methylation analyses were conducted comparing current- vs ex-smokers. Expression quantitative trait methylation (eQTM) analysis was completed to explore smoking relevant genes by CpG sites that differ between current and ex-smokers.

Results: 809 genes and 18,814 CpG sites were differentially associated with current-smoking in the nasal epithelium of asthma patients. The cis-eQTM analysis uncovered 171 CpG sites whose methylation status associated with smoking-related gene expression, including *AHRR, ALDH3A1, CYP1A1 and CYP1B1*.

Conclusion: Current-smoking affects the genes *ALDH3A1*, *CYP1A1*, *CYP1B1*, and *AHRR,* which are involved in physiological responses in detoxification and oxidative stress. Differentially methylated sites in current smokers demonstrate a correlation with the expression of the identified genes.

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