Project Details		
Project Code	MRCPHS25Ca Jurkowska	
Title	Targeted reprogramming of epigenetic signals for lung regeneration.	
Research Theme	Population Health Sciences	
Summary	 What most of us do naturally and take for granted – the breathing - 500 million people struggle with as they suffer from incurable lung disease. Epigenetic mechanisms control what genes are switched on or off. They get dysregulated by environmental exposures, causing disease. Despite the identification of epigenetic changes in lung diseases, their functional role remains unknown. This project will establish an exciting new technology called epigenetic editing to precisely manipulate epigenetic signals in lung cells. It will probe which epigenetic changes drive disease phenotypes and if their correction will boost cell regeneration, accelerating the discovery of novel treatments. 	
Description	 Background: Chronic lung diseases, including asthma, chronic obstructive pulmonary disease and lung fibrosis are one of the most pressing biomedical challenges of our generation. They affect over 540 million people worldwide and cost the UK economy a staggering £188 billion annually. The molecular mechanisms driving lung diseases are poorly understood and there are no effective treatments. Thus, innovative approaches to the discovery of curative therapies are urgently needed to help restore the lung regeneration programs altered in disease and transform patients' lives. To develop new treatments, we need to understand how healthy individuals develop lung diseases and identify suitable targets for drug development. Epigenetic modifications are chemical groups on our genetic information that determine which genes are active and which are shut off. They get dysregulated by environmental exposures causing disease. Excitingly, they can also be manipulated with the potential to cure disease. Thus, epigenetic signalling provides an exciting and largely unexplored level of regulation for the identification of disease-driving events, novel disease regulators, and biomarkers. DNA methylation is a key epigenetic signal used for the control of gene expression. It is introduced at cytosine residues by DNA methyltransferases and removed by DNA demethylases. Several groups identified global DNA methylation changes in patients with lung diseases, implying the pathogenic role of epigenetic approaches for lung regeneration. This is because the methodologies for targeted manipulation of epigenetic approaches for lung regeneration. This is because the methodologies for targeted manipulation of epigenetic signals. It employs a programable DNA targeting domain (e.g. INA methyltransferase or demethylase), which can be specifically targeted to a desired genomic region to change its epigenetic states, and 	

consequently gene expression. It was used to study epigenetic regulation
in human cells and animal models and offers exciting prospects for
future therapeutic interventions for lung diseases.
This innovative project will pioneer the use of this cutting-edge
technology in primary human lung cells and organoids. It will develop a
versatile platform for understanding how epigenetic signalling drives
lung disease development, thereby accelerating the discovery of
epigenetic therapeutics and biomarkers for chronic lung diseases.
Aims:
Our group works collaboratively with stakeholders from different sectors
to determine how epigenetic dysregulation drives the development of
lung diseases and harness this information to develop curative therapies.
This PhD project will develop the epigenetic editing technology for use in
primary lung cells to understand which epigenetic changes drive disease
phenotypes and if their correction will boost the regeneration capacity
of lung cells.
Objectives:
Objective 1: To develop and validate our innovative epigenetic editing
tools for locus-specific rewriting of epigenetic signals in human lung
cells.
Objective 2: To apply these tools to introduce aberrant epigenetic
changes (identified by us from patient profiling) at selected genomic
regions and examine their functional relevance in driving lung disease
phenotypes (focusing on cell regeneration).
Using human cell lines, we have already developed combinations of
epigenetic domains for sustained activation or repression of target genes
upon transient delivery. As primary human lung cells are difficult to
transfect but can be efficiently transduced, we will establish epigenetic
editing using viral vectors and novel aptamer-based technology for the
co-delivery of epigenetic editing domains. After technology
establishment, we will demonstrate its power and versality. Using high-
resolution epigenetic profiling, we identified numerous sites within the
genome severely disrupted in chronic lung diseases. This project will test
the functional relevance of these alterations. We will introduce specific
epigenetic changes at selected regions in lung cells, model what we
observed in patient samples, and examine their impact on driving gene
expression changes. Through this innovative approach, we will
determine which sites play a causal role in lung disease development
and therefore provide the most promising targets for interventions and
drug development.
Ownership and co-creation of the project by the student:
The exact project will be co-designed together with the student. The
student will be able to steer the direction of the project, drive the
selection of the best epigenetic tools and cloning strategies, as well as
shape the selection of the most interesting targets and disease contexts
for functional validation.
Innovation:
Our group pioneered the use of cell-type resolved epigenetic profiling
across disease stages for the identification of novel disease regulators.
The innovative aspect of this studentship is the application of epigenetic
editing to lung diseases, as this powerful technology has not yet been

	applied to primary lung cells. Thus, this project will deliver a step-change approach for future identification and validation of epigenetic therapeutics and biomarkers for chronic lung diseases.	
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