Genomics Education Programme

NHS
Health Education England

# Richard Turner

Dr Richard Turner is a registrar in Clinical Pharmacology and Therapeutics (CPT) with an interest in pharmacogenomics and precision medicine. He graduated in medicine in 2010 from the University of Cambridge. He completed his foundation training in the East of England deanery between 2010-2012, which included a CPT academic component investigating the pharmacogenomics of fluoropyrimidine toxicity.

Richard moved to Liverpool in 2012 after being awarded an NIHR academic clinical fellowship in CPT. During his two years In Liverpool he completed core medical training and was involved in a large cardiovascular pharmacogenomics study. From 2014-2017 Richard undertook a sustained period of doctoral research as an MRC fellow on the North West England MRC CPT Fellowship scheme, investigating the pharmacogenomics of statin-induced muscle toxicity.

In his spare time Richard enjoys running, both cross-country and now around the room after his crawling baby.

## Outline of Research (Part Time, Postdoctoral)

## Evaluating the potential of pharmacogenomics using whole genome sequences to reduce drug toxicity.

Richard's project is entitled, 'Evaluating the potential of pharmacogenomics using whole genome sequences to reduce drug toxicity'. The NHS in England spent £15.5bn on medicines in 2014-2015, and drug expenditure is rising. There is, however, notable variation between patients in response to a given drug, affecting both efficacy and safety.

Pharmacogenomics is the study of the genetic determinants of drug response and their application to improve patient care. Most pharmacogenomics research has focussed on common genetic variants. However, the majority of variants within gene regions (~98%) occur in less than 1% of people. Therefore, this fellowship aims to determine the impact of rare genetic variation on adverse drug reactions (ADRs) and healthcare utilisation using the world-leading 100,000 Genomes Project (100k GP).

Firstly, during this fellowship all genetic variants in a large set of drug relevant genes will be catalogued. Secondly, the impact of genetic variation (common and rare) on ADRs and healthcare use associated with specific therapeutics (fluoropyrimidines, irinotecan, statins, oral anticoagulants and citalopram/escitalopram) will be investigated using genetic association and cost consequence analyses. Novel natural language processing techniques will identify the ADRs from 100k GP participant

records.  It is envisaged that this fellowship will increase the pharmacogenomics evidence base and inform clinical guidelines.