

Research Award:

Identification of epigenetic DNA methylation marks for asthma and allergic sensitization using Oxford Nanopore in the Isle of Wight (IoW) F2 generation

Awarded to: Negusse Kitaba and John Holloway **Amount:** £9,284.20

Lay summary

For this project, using Oxford Nanopore Technologies (ONT) sequencing we profiled methylation for 18 samples from the Isle of Wight Birth cohort. We successfully generated genome-wide DNA methylation profiles, interrogating over 51 million positions across the genome. This is a step change in the level of detail at which we can observe epigenetic changes in genes compared to the previous technology we have used, Illumina EPIC arrays (850,000 CpGs). By profiling Isle of Wight Cohort samples where we already have data from the EPIC platform, we have been able to directly compare the two methodologies against each other.

With the opportunity provided by the AAIR funding, we have now fully developed a bioinformatic analysis pipeline for the ONT data using the software packages Dorado and Modkit. The resulting workflow provides the foundation for replication and extension of methylation profiling at genomic loci previously associated with severe asthma and maternal smoking-related epigenetic signatures. We are currently drafting a pilot manuscript for publication. In addition, the preliminary results from this work were also used to support a grant application aimed at scaling up the analysis to a larger cohort focused on identifying epigenetic biomarkers for predicting treatment responses in severe asthma.

We wish to thank the AAIR charity for their support of this project that has allowed us to establish this technology in Southampton which will not only benefit our own research into the early life origins of asthma, but also other researchers within the Faculty of Medicine.
