**Application number/Title:** 29273 - Genetic analysis of peripheral artery disease and migraine

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**Keywords provided by the Applicant PI to describe the research project:** cardiovascular, carotid-stenosis, genetics, migraine, peripheral-artery-disease

**Application Lay Summary:**

Genes involved in vascular development and function have been implicated in numerous human diseases. These include atherosclerotic diseases, such as peripheral artery disease (PAD), as well as non-atherosclerotic conditions, such as migraine headaches. The aim of our proposed study is to use the large sample size and concomitant statistical power of the UK Biobank to identify novel genetic markers of incident non-coronary vascular diseases including PAD, carotid stenosis, stroke, varicose veins, and migraine. Cardiovascular disease remains the leading global cause of death despite numerous advances in prevention, diagnosis, and treatment. The global prevalence of PAD is ~200 million individuals, and this disease has significant implications in terms of morbidity and mortality for patients. In addition, migraines lead to significant morbidity and productivity loss, and they have also been linked to stroke. Compared to coronary artery disease, our understanding of the pathophysiology of non-coronary vascular disease is limited. Our proposed study has the potential of achieving the UK Biobank’s purpose of improving the care of patients with these serious diseases. First, we will identify all patients with each sub-type of vascular disease of interest. These patients will be defined using pre-existing data fields within the Biobank. We will also identify a reference cohort of control patients from within the UK Biobank that are matched for age, sex, tobacco use, and other known risk factors. We will then perform genome-wide and candidate gene association analyses to identify genetic variation, predominantly in the form of single nucleotide polymorphisms significantly associated with each disease. For the proposed study, we will require access to the full cohort.