Stephanie Greville-Heygate

Stephanie Greville-Heygate is a Specialist Registrar in Clinical Genetics for the Wessex Clinical Genetics Service and has a specific interest in Cancer Genetics and developing the interface which exists between oncology and genetics. Her research project will contribute towards a Medical Doctorate under the supervision of Professor Diana Eccles and the Department of Cancer Sciences at the University of Southampton.

Stephanie completed her undergraduate studies at the University Of Leeds School Of Medicine where she graduated with honours and was awarded the William Hey Medal. More recently she has undertaken a Master's Degree in Genomic Medicine at the University of Southampton. Over the last 10 years she has worked in London, Brighton, New Zealand and Southampton in several positions encompassing Oncology and Genetics. Her current research interests have developed through this professional and academic experience.

Stephanie lives close to the New Forest with her husband and four children.

Outline of Research (Full Time, Secondment)

Using Cancer Phenotypes to Improve Cancer Susceptibility Gene Classification

Breast cancer is the most frequently diagnosed cancer amongst women in the UK.

(1) Next Generation sequencing including panel tests are increasingly being utilised in mainstream cancer diagnostic practice to determine germline cancer susceptibility.

(2) Whilst this technology holds great potential for clinical benefit, it also significantly increases the rate of Variants of Uncertain Significance (VUS) with commensurate increase in molecular scientist workload and risk of harm through incorrect interpretation.

During this one-year research secondment, Stephanie aims to determine whether we can utilise somatic mutational profiles and histopathological subtype to better define the pathogenicity of VUS in both BRCA and other breast cancer genes.

Genetic sequence data will be derived from breast cancer patients recruited to the 100,000 Genomes Project and Prospective Outcomes in Sporadic Versus Hereditary Breast Cancer (POSH) cohort. It will be used to determine the relationship which exists between germline variation in high, intermediate and moderate risk genotypes (BRCA1, BRCA2, PALB2, ATM, CHEK2 and TP53) and reported histopathological tumour phenotype and somatic mutational profile (3-5). This should enhance routine NHS diagnostic practice by increasing the utility of genomic testing at the point of cancer

diagnosis. This will be achieved through improved VUS classification and increased opportunities for risk stratified prevention.