**Investigating Microbe Associated Prostate Cancer from Short Read Whole Genome Sequences**

Prostate cancer is the most common cancer in men in the UK with more than 52,000 new diagnoses annually. We recently discovered that a subset of anaerobic bacteria appears to be associated with aggressive prostate cancer – the ABBS genera[1]. In this study, we explored whether these findings could be validated in the Pan-Prostate Cancer Group (PPCG, *N*=2,176), using the taxonomic classification of short non-human whole genome sequencing reads.

As in our initial report we found that the detection of at least one ABBS genera in the primary tumour samples was associated with a poorer outcome in the patient (log-rank *p*=0.023, relapse free survival). We also confirmed that ABBS positive samples tend to originate from older participants (*p*=5.5x10*-11*).

Investigating *pks*, an experimentally validated genotoxic bacterial pathogenicity island, alongside evidence for *Escherichia* reveals four distinct groupings of samples: 41 samples contained evidence for the pks gene without *Escherichia*, suggesting that the gene may exist in genera other than *Escherichia* in samples from patients with prostate cancer.

In this study we have provided further evidence for the important role that anaerobic bacteria may play in the development of prostate cancer and revealed that a bacterial gene driven approach may be more reflective of impact on cellular biology than a purely taxonomic driven approach.

[1] Hurst R, Meader E, Gihawi A, Rallapalli G, Clark J, Kay GL, et al. Microbiomes of Urine and the Prostate Are Linked to Human Prostate Cancer Risk Groups. Eur Urol Oncol. 2022.