The Microbiome in Urine Can Indicate Higher Risk for Aggressive Prostate Cancer

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INTRODUCTION

- Prostate cancer is one of the most common cancers in the world (1 in 8 men diagnosed)
- More than 12,000 men die from prostate cancer every year (CRUK 2021)
- Infection has been established as a risk factor in many cancers (1)
- Prostate cancer has the potential to be influenced by many different bacteria in the prostate microbiome
- Bacteria has been detected in the urine of prostate cancer patients that are associated with aggressive disease (2)

OBJECTIVES

- To detect bacteria in urine using 16S sequencing data
- To compare bacterial profiles across samples from participants with different grades of prostate cancer

METHODS

- The analysis will be done on R (version 4.2.1)
- 16S Illumina sequencing on urine samples (n=46) of prostate cancer patients generates paired-end, short reads
- DADA2 (ver. 1.26.0) performed on the reads with default parameters.
- DADA2 filters and trims the reads, calculates sequencing errors, remove chimeras and assign taxonomy according to Genome Taxonomy Database (ver 86).
- Phyloseq (ver 1.42.0) was then used to combine the DADA2 output with a metadata file for all the samples to produce heatmaps and abundance plots at family taxonomic level (not shown)
- Principal Co-ordinate Analysis (PCoA) with Manhattan Distances followed by *k*-means clustering was done with *k*=3

RESULTS

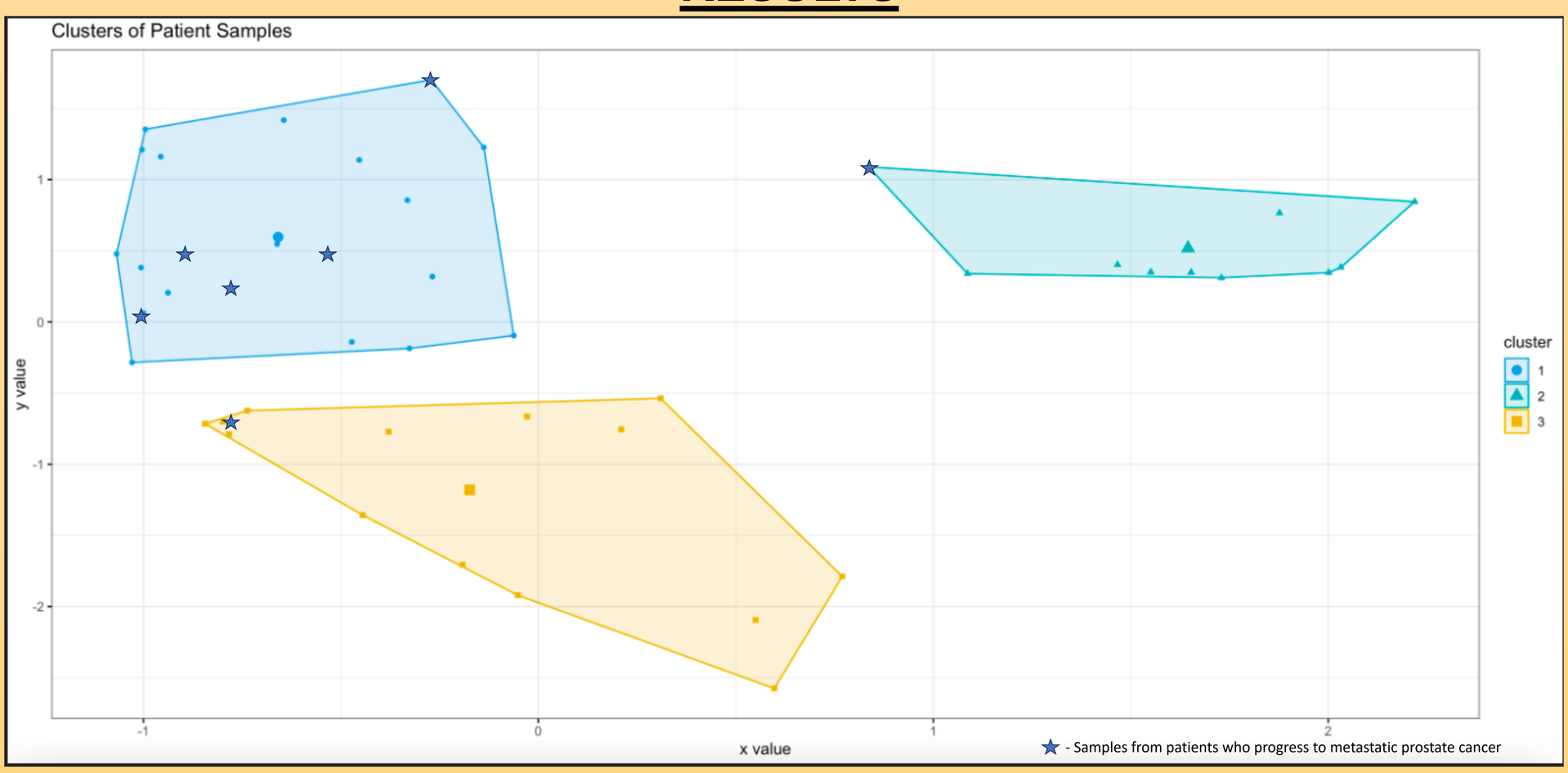

Figure 1: *k*-Means clustering with *k=3* performed on a PCoA plot (based on Manhattan distances) of patient samples. The clustering takes place based on bacterial families present

- Detected bacterial composition segregates samples into three clusters (Figure 1).
- 5 out of 7 samples from patients who progressed to have metastasis (indicated by blue stars) are in cluster 1

CONCLUSIONS

- Patients who progress to metastatic prostate cancer tend to cluster together based on shared bacterial families
- The urine microbiome can potentially indicate patients who are at higher risk for metastatic disease

REFERENCES

1. de Martel C, Georges D, Bray F, Ferlay J, Clifford GM. Global burden of cancer attributable to infections in 2018: a worldwide incidence analysis. The Lancet Global Health. 2020 Feb 1;8(2):e180-90.
2. Hurst, Rachel, et al. "Microbiomes of urine and the prostate are linked to human prostate cancer risk groups. " European Urology Oncology 5.4 (2022): 412-419.