**Aims**

Bladder cancer is the 10th most common cancer diagnosed in Australia. A biologically heterogeneous disease, phenotypic and genotypic tumour heterogeneity is observed across patients. Cases range from highly recurrent to non-muscle invasive disease, to muscle invasive disease (Figure 1), which sees a much poorer prognosis. High variability is seen in clinical outcomes of patients with bladder cancer, and there is a need to further understand the cellular interactions that mediate therapeutic response, at the level of the tumour microenvironment itself.

A more sophisticated understanding of the biology that underpins this variation in therapeutic efficacy may aid in informing treatment decisions where immune cell infiltrates may predict immunotherapeutic responses.

**Objective:** to identify biomarkers that can predict patient responses and help inform clinical decisions and improve patient outcomes.

**Methodology**

1. Spatially profile the differential expression of proteins of interest across variants of BC in the tumour-immunocytic microenvironment of our BC biobank.
2. Using flow cytometry, enumerate tumour-infiltrating lymphocyte populations and expression of immune checkpoint inhibitors (ICIs) in BC tumour specimens.
3. Establish a urine-derived lymphocyte extraction protocol and investigate the correlation between immune cell subset populations present in patient-matched urine and tumour specimens.

**Results & Reference Acknowledgements**

*Future work will aim to further investigate novel proteins of interest discovered in this study and provide a more comprehensive understanding of BC responses to immunotherapy.*

**Conclusions**

Future work will aim to further investigate novel proteins of interest discovered in this study and provide a more comprehensive understanding of BC responses to immunotherapy.

**References & Acknowledgements**


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