

# Dissecting the Expression Landscape of Urogenital Cancers\*

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**Summary** The Gender Summit celebrates differences and similarities between genders and this reaches a cellular level. The research identified a difference in variation of gene expression between males and females.

## 1. Relevance

Cancers of the urogenital system are among the top ten most common cancers found in both men and women in Canada. Currently, the common methods used to diagnose some of these cancers are by: cystoscopy, biopsy, and surgery, which may be very frightening for the patient and costly for society. Most symptoms for such cancers can often be caused by other health problems, such as persistent abdominal pain and blood in urine, so diagnosis requires testing. For these reasons it is essential to develop a diagnostic tool that is simple and economic, offering an alternative to making patients endure such discomfoting procedures.

## 2. Aims & Objectives

Analyse the difference of expression of genes in normal and cancerous tissue of different cancers of the urogenital system. Comparing these cancers to research genes with a change in expression specific for one cancer, or present in every cancer of the system. Study their potential as biomarkers for these cancers that are present in urine.

## 3. Methods

Statistical targets were applied to data provided by TCGA so that the genes with the most modified expression between healthy and cancerous tissue would be retained. As the genes were observed to be expressed differently in men than in women, the data was divided into male and female cancers. The data in each cancer separated by gender conforming to the statistical conditions was compared with those having significant modification in other urogenital cancers. Those found to be uique to each cancer were assessed to determine with genes hand proteins present in urine. Analysis of paired and unpaired data, with the application of statistical tests, was accomplished for the top ten most up- and down-regulated to choose genes for validation as potential biomarkers in urine.

## 4. Results

In BLCA, with data from male patients, 2880 modified genes were retained. By comparing these genes with those having significant modification in other urogenital cancers, 1183 genes were found to be unique to BLCA. Of these, the proteins of 129 genes are present in urine. Analysis of paired and unpaired data, with the application of statistical tests, was accomplished for the top ten most up- and down-regulated to choose five genes to be validated in BLCA.

## 5. Conclusions

Overall, the modification of expression in 24 genes will be validated in tissues by qPCR and in the urine of patients by mass spectrometry. This should result in finding biomarkers unique to each urogenital cancer as well as perhaps one in every cancer for males to use in diagnosis.

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