**BACKGROUND**

- Proliferation (PCa) remains a major cause of death. However, clinicians always have to balance between risk and benefit. This dilemma suggests that the majority of PCa falls into the low-risk category.
- Historically, >90% of low-risk PCa is treated immediately with either radical prostatectomy (RP) or radiation therapy (RT).
- Active surveillance with close clinical follow-up and repeat biopsies may be an important option for men with low-risk PCa, especially in light of emerging oncologic data supporting the use of active surveillance for certain patients.

**STUDY OBJECTIVES**

- To determine whether gene expression profiles in PCa can predict clinical outcome.
- To identify genes whose quantitative expression predicts clinical recurrence (cRFI) after RP.
- To compare the association between gene expression and clinical recurrence in primary and highest Gleason patterns (PGP and HGP).

**RESULTS**

- **Sample Preparation**: The tissue samples were microdissected and placed in separate tubes.
- **Assessment of Heterogeneity**: The association between gene expression and clinical recurrence was assessed using a supervised analysis of gene expression data.
- **Comparison of Gene Expression**: Gene expression was compared between primary and highest Gleason patterns (minimum size = 5 mm).
- **Comparison of the Association**: The association between gene expression and clinical recurrence was compared between primary and highest Gleason patterns.
- **Evaluation of the Findings**: The findings were validated using additional weight in the analysis.

**Figure 3. Evaluative Parameters, Samples, and Genes**

**Figure 4. Distribution of Patients by Clinical Recurrence Status**

**Figure 5. Most Significant Genes Associated with Clinical Recurrence in Both Primary and Highest Gleason Pattern Samples**

**Table 1. Patient Sample Status**

**Table 2. Baseline Characteristics**

**Table 3. Multivariate Analysis: Surgical Gleason Score, Baseline PSA, and Year of Surgery are Associated with Clinical Recurrence**

**Table 4. Genes Associated with Clinical Recurrence in Both Primary and Highest Gleason Pattern Samples**

**Figure 6. p-Values and q-Values for the Association of Gene Expression and Clinical Recurrence in Both Primary and Highest Gleason Pattern Samples**

**Figure 7. Genes Associated with Clinical Outcomes and Gene Expression**

**Figure 8. Genes and Biological Pathways Associated with Clinical Recurrence in Both Primary and Highest Gleason Pattern Samples**

**Figure 9. Clinicopathological Parameters Associated with Clinical Recurrence in Both Primary and Highest Gleason Pattern Samples**

**Table 5. Univariate Std. HRs for cRFI Including AUA Risk Group**

**Table 6. Multivariate Analysis: Effects of Clinicopathological Parameters on cRFI**

**Additional Methods**

- **Studies**
  - **Precision Digital Enzyme**
  - **Quantitative Gene Expression**
  - **Multivariate Analysis**

**Conclusion**

- This study provides evidence that gene expression data can be used to predict clinical outcomes in PCa.
- The findings have implications for the development of personalized treatment strategies and the potential for novel therapeutic targets.
- Further validation studies are needed to confirm these findings in larger, more diverse populations.