Prostate cancer (PCa) risk stratification is based on tumour size, PSA level and Gleason Score, but it remains imprecise. The purpose of this study was to identify gene expression profiles for predicting tumour progression after radical prostatectomy.

Methods

- Retrospective study which includes 188 PCa patients who attended at our department between 2000 and 2007.
- Formalin-fixed paraffin embedded PCa tissue samples were collected.
- Biochemical recurrence (BCR) was defined as 2 consecutive PSA values ≥ 0.2 ng/mL or any salvage treatment 6 months after radical prostatectomy.

Results

- Median follow-up of the series was 131.8 months (range 120-194).
- During the surveillance period, 55 patients developed BCR (33%) and 6 metastatic recurrence (3.6%).
- Overall, three patients died of PCa (1.8%), and 22 due to other causes (13%).

Conclusions

- Gene expression levels in PCa tissue can be useful for distinguishing patients with clinically localized disease who will develop BCR or metastatic recurrence after radical prostatectomy.
- These gene expression biomarkers could have potential clinical utility for identifying the subset of patients that would benefit from closer surveillance and adjuvant therapy.