An Expression Signature to Predict Overall and Cancer-Specific Survival of Prostate Cancer

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**Background:**
Background: This study is a follow-up of findings that we previously worked on in a small Swedish group. The purpose of this study was to test if overall and cancer-specific survival of prostate cancer patients could be improved by using a panel of 189 prostate cancer patients, who were originally studied by us in an effort to use gene expression analysis of prostate cancer patients.

**Methods:**
Intermediate-Diagnosis Gene Expression Profiling

**Results:**

* **High-risk:**
  - Median overall survival: 3.23 years
  - Median cancer-specific survival: 3.47 years

* **Intermediate-risk:**
  - Median overall survival: 4.00 years
  - Median cancer-specific survival: 5.17 years

* **Low-risk:**
  - Median overall survival: 5.40 years
  - Median cancer-specific survival: 9.85 years

**Conclusion:**

- The obvious overall and cancer-specific survival difference between the three subtypes was still maintained within the patients primarily treated by hormone therapy.
- The overall survival rate at 8 years of three subtypes was 0%, 16%, and 55.6%, respectively. This obvious survival difference was independent of age, PSA level, tumor grade, and clinical stage.

**Identification of 641 ESCGPs by Simple Biostatistics**

- Using gene-median centered delta Ct values.
- Expression of these ESCGPs can be measured by microarray, RT-PCR or qPCR.

**Hypothesis of Embryonic Stem Cell Gene Predictors**

1. Embryonic stem cells are the origin of all tissue stem cells. Tissue differentiated cells and cancer stem cells.
2. Of the embryonic stem cell gene predictors, expression of these ESCGPs are also important in maintaining cancer stem cell status and overall survival (metastasis).
3. Genes with strong expression variations among different ESCs are related to overall survival.

**Identification of 641 ESCGPs**

Selected ESCGPs and control genes were analyzed by multiplex quantitative PCR using prostate tissues and other cancers. A. Original by Lapointe et al., PNAS. 2004. B. By ESCGs

**Verification of Selected ESCGPs in a Swedish Prostate Cancer Cohort with 5 Years Follow Up**

- Verification sets 1 and 2
- Verification set 1: 641 ESCGPs
- Verification set 2: 568 ESCGPs

**Verification of Selected ESCGPs in a Swedish Prostate Cancer Cohort**

- Verification set 1: 641 ESCGPs
- Verification set 2: 568 ESCGPs

**Clinical Features of 189 Prostate Cancer Patients with PSA Analyzed by qPCR**

**Cox Proportional Hazards by Univariate Analysis in the Complete Set**

**Verification of Selected ESCGPs in a Swedish Prostate Cancer Cohort**

- AUC: 0.8146962
- AUC: 0.7260167

**Expected Effect of Clinical Application**

- Accuracy of prediction of overall and cancer-specific survival can be improved to over 80% by the ESCGPs together with clinical parameters.

**References:**

1. The FNA samples were taken by a routine procedure at Karolinska University Hospital. At least one fresh cytology smear from each patient was Giemsa stained for cytological diagnosis. The remaining duplicate smears on glass slides were kept for histological examination.
2. The patients primarily treated by hormone therapy. The overall survival rate at 8 years of three subtypes was 0%, 16%, and 55.6%, respectively. This obvious survival difference was independent of age, PSA level, tumor grade, and clinical stage.

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