96th Annual Meeting
April 16-20, 2005
Anaheim/Orange County, CA

Abstract Number: 36

Presentation Title: **Differential expression of the human kallikrein 10 gene (KLK10), a candidate cancer bomarker**

Presentation Start/End Time: Sunday, Apr 17, 2005, 8:00 AM -12:00 PM

Board Number: Board #15

Author Block: *Nicole Ma White*, *George M. Yousef*, *Iacovos P. Michael*, *John D. Robb*, *Eletherios P. Diamandis*. Discipline of Pathology, Memorial University, St. John's, NF, Canada, Discipline of Pathology and Laboratory Medicine, Mount Sinai Hospital, Toronto, ON, Canada

The human kallikrein gene 10 (*KLK10*) is a member of the kallikrein gene family on chromosome 19q13.4. This gene was identified by its down-regulation in breast cancer, and preliminary evidence supports that it may act as a tumor suppressor. We preformed an *in-silico* analysis of the gene expression profile in normal and cancerous tissues through different databases including the Expressed Sequence Tag (EST) and Serial Analysis of Gene Expression (SAGE), among others, from the Cancer Genome Anatomy Project.

Our SAGE analysis verifies that *KLK10* is down-regulated in breast cancer. *KLK10*-specific tags were detected in 50% of normal breast, with an average expression of 85 tpm (tags per million), as compared to no expression in 24 cancer libraries. This down-regulation is also noted in prostate cancer (average expression of 145 vs. 30 tpm, in normal and cancer libraries, respectively). The expression level of *KLK10,* on the other hand, is up-regulated in ovarian cancer. High expression density (179 tpm) was found in cancer libraries compared to 20 tpm in normal ovarian libraries. Up-regulation is also observed in gastric and colon cancers, (196 and 131 tpm, respectively) compared to no expression in normal tissues. The same pattern was observed in pancreatic cancer. Gene-specific tags were detectable in 67% of pancreatic cancer libraries with an average density of 52 tpm.

The EST results were consistent with SAGE data, with down-regulation in breast cancer (25 clones from 5 normal libraries vs. a single clone from one cancer library). Significant up-regulation was observed in ovarian cancer and cancers of the gastrointestinal tract (colon, gastric, pancreatic and esophageal). In the pancreas, two clones were identified from normal libraries, while 18 clones were isolated from cancer tissues. While four clones were identified from the normal prostate, only one clone was found in prostate cancer.

We experimentally verified the *in-silico* findings for ovarian and prostate cancer by RT-PCR analysis. While the gene was not detectable in normal ovarian tissues, a band was noted in seven of ten cancers. A moderate down-regulation was seen in prostate cancer. In four patients, bands of weaker intensity were obtained from the cancerous portion, when compared to the normal counterpart of the same patient. This study provides the basis for directing experimental efforts to investigate the possible role of *KLK10* as a diagnostic and prognostic cancer biomarker in several malignancies.

96th Annual Meeting
April 16-20, 2005
Anaheim/Orange County, CA

Citation format: Proc Amer Assoc Cancer Res 2005;46:36.