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Poster Submissions

Poster Title

VALIDATING A GENE EXPRESSION--BASED BIOMARKER FOR LUNG CANCER PREMALIGNANCY IN THE AIRWAY

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Please describe the extent of your work in this research

I carried out the entire project, from data cleaning and preparation to designing computational experiments and their implementation to developing the biomarker, analyzing results and carrying out validations.

Abstract Submission

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Would you like your abstract to be considered for an oral presentation (students and post docs only)?

Yes

VALIDATING A GENE EXPRESSION-BASED BIOMARKER FOR LUNG CANCER PREMALIGNANCY IN THE AIRWAY

Anna Tassinari, Gang Liu, Sherry Zhang, Hanqiao Liu, Stephen Lam, Mary Beth Pine, Samjot Dhillon, Suso Platero, Mary Reid, Marc Lenburg, Avrum Spira, Jennifer Beane

Objectives: Bronchial premalignant lesions (PMLs) are precursors of squamous cell carcinoma (SCC) and are associated with elevated risk for developing lung cancer (LC). PMLs can be detected using autofluorescence bronchoscopy with limited sensitivity and specificity, as well as availability. As an extension of "airway field of injury" hypothesis, whereby airway epithelial cell gene expression is altered by cigarette smoking and can be predictive of lung cancer status, we propose that these gene expression changes may also indicate the presence of PMLs and offer a surrogate for monitoring changes in PMLs.

Methods: Using mRNA-Seq data from cytologically normal bronchial brushings from LC free subjects with (nDysplasia = 38) and without (nControl = 20) bronchial PMLs, we developed a biomarker to detect the presence of PMLs. We examined 6,650 combinations of parameters (models) that included different feature selection and prediction methods. The selected model had highest test-set AUC among the top 10% least overfitting and most consistent models in terms of gene selection.

Results: The selected biomarker consisted of 200 genes and utilized the weighted voting prediction algorithm. The biomarker achieved an AUC of 0.868 across the training set (n = 58) and an AUC of 0.883 across the validation set (n = 17) not used during biomarker discovery. The biomarker was used to score mRNA-Seq data from serial bronchial brushings from subjects undergoing screening for LC at Roswell Park Cancer Center (n = 26 subjects, n = 54 samples). The change in biomarker score was predictive of PML regression or stable/progressive disease (AUC = 0.733).

Conclusion: The biomarker is promising in its ability to detect presence of bronchial PMLs, suggesting that the concept of airway field of injury can be applied in the premalignant setting. Specifically, the biomarker's power to predict changes in PMLs, and thus disease progression, may be efficacious in selecting or monitoring subjects in chemoprevention trials.