Name

Sean Corbett

Email

scorbett@bu.edu

Institutional Affiliation

Boston University

Campus

Charles River Campus

School

GRS

Department

Bioinformatics Program

Position Held at Institution

Graduate

Poster Submissions

Poster Title

The Lung Connectivity Map: A High Throughput Genomics Approach
for Identifying Novel Lung Therapeutics

Authors and their Affiliation

Sean Corbett, Elizabeth Moses, Teresa Wang, Josh Campbell, Catalina Perdomo, Xiaodong
Lu, Ted Natoli, Rajiv Narayan,
 Aravind Subramanian, Marc Lenburg, Avrum Spira

Please describe the extent of your work in this research

This poster represents a detailed analysis of in-vitro experimental data generated by
Elizabeth Moses. All but two subportions of the analysis were conducted by me, with the
exceptions being conducted by me.

Abstract Submission

- **Evans-Day-Abstract-2015-CMap_v3.docx**

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

No

The Lung Connectivity Map: a high throughput genomics approach to identifying novel lung therapeutics

ES Moses[1], S Corbett[1], T Wang[1], J Campbell[1,2], C Perdomo[1], X Lu[2], T Natoli[2], R Narayan[2], A Subramanian[2], ME Lenburg[1], A Spira[1]

[1]BU, Boston MA. [2]The Broad Institute, Cambridge MA.

Objectives: Gene-expression profiling offers functional insight into the molecular changes underlying the presence and progression of disease. Importantly, these profiles can be assessed for the functional connections between disease states and the effects of therapeutic compounds, as shown by the Connectivity Map (CMap) database at the Broad Institute.

Methods: Here we utilize the CMap concept, which tests compounds in a variety of tissue types, in a lung-tissue specific fashion to identify potential therapeutic candidates for respiratory diseases. To do so, we exposed six lung cell lines to 322 CMap compounds. These perturbations included a variety of small molecules and commonly used therapeutics. RNA from cell lysates was extracted and hybridized to the Luminex-1000 array, a novel high-throughput platform that leverages the direct measurement of 1000 "landmark" genes to subsequently impute expression levels for all genes.

Results: We found that each lung cell line exhibited a range of responses across the 322 unique perturbations. In addition, each compound elicited a range of concordant and discordant responses across the six lung cell lines. Furthermore, perturbation signatures clustered by cell type. These preliminary results reflect the presence of cell-type specific genomic responses to small molecule and exposure-oriented perturbations, highlighting the importance for additional profiling of genome-scale signatures in lung-resident cell lines.

Conclusions: As in the original CMap, these perturbations may allow for the characterization of the relationships between genes, drugs, and disease through common gene changes, but in a lung cell specific manner. Importantly, the elucidation of these relationships in a lung-relevant context will provide greater understanding of the molecular pathogenesis of lung diseases and will facilitate the identification of novel pulmonary therapeutics.