

LTRC Concept Sheet # 05-04-0001

**Microarray Analysis of Gene Expression Profiles Associated With
Unique Phenotypic Variations in COPD**

Abstract: Understanding patient phenotypes in COPD requires a fresh and unbiased look at the disease. Characterization of subjects with evolving clinical tools provides insights into distinct disease phenotypes. In this application we propose a funnel-shaped analytic effort designed to identify and highlight key molecular events and pathways that determine patient phenotype in COPD. We believe that elucidation of the complex molecular networks that underlie these characteristics will lead to identification of novel rational molecular targets for intervention in each of these phenotypes. Unique phenotypic aspects of COPD derived from lung mechanics and quantitative computed tomography parameters are associated with unique gene expression patterns in the lung parenchyma measured by microarray analyses. The specific phenotypes in COPD are determined by local interaction of specific cell types (lymphocytes, airway epithelial cells, fibroblasts and endothelial cells) at the alveolar or small airway level. Our research strategy, based on innovative statistical approaches, has the potential to lead to a new understanding of COPD, to the generation of new, specific, hypotheses regarding the distinct phenotypes that characterize the disease and most importantly to the identification of new targets for therapeutic intervention.