

European Respiratory Society Annual Congress 2013

Abstract Number: 5204

Publication Number: P669

Abstract Group: 3.3. Mechanisms of Lung Injury and Repair

Keyword 1: COPD - exacerbations **Keyword 2:** Infections **Keyword 3:** Bacteria

Title: Precision cut lung slices: A novel method for examining mechanisms underlying respiratory diseases

Dr. Carla 26923 Bauer carlamtbauer@gmail.com¹, Dr. Javad 32681 Golgi javad.golgi@gmail.com², Ms. Kristen 32682 Lambert lambert.kn@gmail.com³, Dr. Donovan 32683 Cheng donavan.cheng@gmail.com², Mr. Mario 32684 Giron mario.giron@roche.com², Dr. John 32686 Allard john.allard@roche.com², Dr. Holly 32687 Hilton holly.hilton@roche.com², Dr. Hans 32688 Bitter hans.bitter@roche.com², Dr. Martin 32689 Stampfli stampfli@mcmaster.ca³ and Dr. Christopher 32696 Stevenson stevenson.cs@googlemail.com¹.¹ pRED, Pharma Research and Early Development, Inflammation DTA, Hoffmann-La Roche, Nutley, NJ, United States, 07110 ;² pRED, Pharma Research and Early Development, Translational Research Sciences, Hoffmann-La Roche, Nutley, NJ, United States, 07110 and³ McMaster Immunology Research Center, Department of Pathology and Molecular Medicine, and Firestone Institute of Respiratory Health at St. Joseph's Healthcare, Department of Medicine, McMaster University, Hamilton, ON, Canada, L8N3Z5 .

Body: Bacterial infections and smoking have been linked to exacerbations of many respiratory diseases. To this end, responses to toll-like receptor (TLR) agonists and bacterial pathogens were studied in precision cut lung slices (PCLS) from room air and smoke-exposed mice. Ex vivo cultured PCLS were either left untreated or stimulated with toll-like receptor agonists, lipopolysaccharide (LPS), or Pam3CSK. An additional set of PCLS were challenged with either live or heat-killed *Haemophilus influenzae*, or *Streptococcus pneumoniae*. RNA was isolated and microarray analysis performed. Principal component analysis showed that live *S. pneumoniae* stimulation of PCLS led to a distinct response and a greater number of differentially expressed genes (DEGs) when compared to the responses elicited by the two TLR agonists or *H. influenzae*. Unsupervised hierarchical clustering analysis was performed on 1846 DEGs identified 24 hours post-stimulation in room air exposed PCLS, and two distinct clusters were present, confirming the principal component analysis. Of the 1354 genes identified following live *S. pneumoniae* challenge of room air PCLS, several signaling cascades were identified following ingenuity pathways analysis (IPA); these included the IL-1 and IL-10 signaling cascades. In the context of cigarette smoke exposure, IPA analysis captured pathways involved in airway pathology in COPD. These data highlight the strength of this technique for evaluating pathways that may be linked to disease (or exacerbation) susceptibility. Finally, mechanisms that have been implicated in COPD pathogenesis are captured in this model, and therefore increase the validity of this method to test interventions.