Characterization, Identification, and Comparative Proteomic Kinetics of Innate Host Defense Proteins in Experimental IPA and *Pseudomonas* Pneumonia

> Thomas Walsh, MD NIH/NCI

Pulmonary Aspergillosis & Pseudomonas Pneumonia



Normal



Neutropenic Pseu





37

ic Pseudomonas Aspergillus







Expression of Serum and BAL Galactomannan



Comparison of Spectral Regions of Plasma in Aspergillus and Pseudomonas Pneumonia



Hierarchical Clustering of Spectra

31 high intensity ■ peaks decreased by D3

26 low intensity peaks increased by D3



SELDI-TOF Spectra peaks > 10 x S/N - ratio, 0.3%width

Animals ordered by time in columns.

Peak clusters with p < 0.001 shown in each row, ordered by unsupervised hierarchical clustering



Plasma Protein Peak (*m/z*)

Random Forest Analysis of Top 30 Spectral Points ⁴⁰ Distinguish Between *Aspergillus* and *Pseudomonas* Pneumonia











Figure A: SELDI-TOF shows the peaks of 11.7kDa and 13.7kDa in sample #34 and #38.



The image of 1D SDS-Page gel with coomassie blue stain. Line 1 is molecular markers; Line 2 is sample #34 (pseudomonas) and Line 3 is sample #38 (aspergillus). On the right image, 23k, 28k, 40k and 44k are just band labels. They do not necessarily represent their actual molecular weight. The protein IDs with significant hit (p<0.05) are listed on the left. The numeric value in the parenthesis () is Mowse score.

Reverse antibody array



This RPA image (contrast adjusted) shows an array immuno-stained with anti-rabbit HPT antibody and indicates the layout of samples on the slide. Each unique sample has 16 spots composed of 8, 4, 2 and 1 deposition curves printed in quadruplicate.





Protein validation with reversed phase array of ApolipoproteinA1

The change of relative CRP level with time course in Aspergillus and Pseudomonas animals by reverse phase array



Protein validation with reverse phase array for transthyretin (pre-albumin)



Conclusions

- Proteomic analysis of serum and BAL proteins in experimental Aspergillus and Pseudomonas pneumonia demonstrate spectral regions that are shared in early infection and distinguish between the two etiologies at later stages of infection
- These data support the concept that a pattern of proteins are expressed with different microbial infections
- Haptoglobin, apolipoprotein A1, and C-reactive protein display distinct kinetic profiles and with probable roles in the pathogenesis of invasive pulmonary aspergillosis
- This approach may enhance our understanding of hostpathogen interactions, detection and prognosis

Acknowledgments

- Ruta Petraitiene (NCI)
- Vidmantas Petraitis (NCI)
- Honghui Wang, PhD (CCMD)
- Chris Devor, MD (NCI)
- Densie Gonzales, MD(CCMD)
- Steve Kern, MS (CCMD)
- Anthony Suffredini, MD (CCMD)