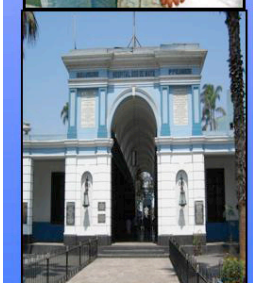

14:30 Session 2: TB Diagnosis
Chair: Bob Gilman

14:30 Proteomic fingerprinting for infectious diseases – *Dan Agranoff*

14:45 Proteomics in TB – *Gurj Sandhu*

15:00 Genetic and molecular correlates of pyrazinamide resistance – *Paty Sheen*

15:15 Unravelling the enigmatic mycobacterial pyrazinamidase – *Mirko Zimic*

15:30 Rapid and sensitive Tuberculosis diagnosis and susceptibility testing without decontamination or centrifugation - *Louis Grandjean*

15:45 Stool testing to diagnose pulmonary TB in adults and children - *Laura Martin*

Proteomic signatures in Tuberculosis

Gurjinder Sandhu, Carlton Evans, Jon Friedland, Robert Gilman, Dan Agranoff

Hypothesis: Defining the proteomic signature of TB using SELDI-TOF allows the accurate discrimination of different TB disease states: active, latent and absent.
Methods: Serum and Plasma were collected from 30 TB patients, 25 unhealthy and 18 healthy controls. Samples were processed on CM10 weak cation exchange chips using a PBSII mass spectrometer. Quality control samples were applied to each chip and data analysed using a neural network classifier. A statistical analysis was performed of 564 patients who had received both a tuberculin skin test (TST) and an interferon-γ (IFN-γ) assay.
Results: A positive biomarker for TB at 11.5 kDa and a negative marker at 13.7 kDa were identified. A neural network classified cases and controls with a sensitivity of 85.7% and a specificity of 90.0%. The percentage agreement between two currently available tests for latent tuberculosis was found to be 71.63%.
Conclusion: Previously published potential biomarkers for TB were validated. Machine learning to differentiate proteomic signatures in latent disease will be limited by the lack of a gold standard test with which to train a classifier.

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