**Poster Number 49**

**Abstract 0240_0346_000079**

**Inhaled diesel exhaust alters plasma proteome signature**

**Mahadevappa Hemshekhar**, University of Manitoba; **Min Ryu**, University of British Columbia; **Victor Spicer**, University of Manitoba; **Christopher Carlsten**, University of British Columbia; **Neeloffer Mookherjee**, University of Manitoba

**Background:**

Recent evidence suggests that traffic-related air pollution (TRAP) impacts pregnancy outcome and development of childhood disease such as asthma, thus has a profound impact on child health. Diesel exhaust (DE) a paradigm for TRAP is associated with respiratory and cardiovascular diseases. Changes in plasma proteins following DE exposure in humans have not been defined.

**Objective:**

The aim of this study was to delineate global proteins (proteome) changes in plasma following exposure to inhaled DE, using a controlled human exposure study.

**Methods:**

Individuals (n=6) inhaled filtered air (FA) and DE (300 mg $PM_{2.5}/m^3$) for 2h (crossover; random order), and plasma was obtained 24h after each exposure. Plasma samples were probed using Slow off-rate modified aptamer (SOMAmerÒ)-based proteomic array. Pairwise differential analysis with Welch's t-test was used to identify proteins that were significantly altered by inhaled DE compared to FA. To examine if this was a DE-driven response, abundance of selected proteins were quantified independently using western blots, in plasma samples obtained from healthy individuals following DE and FA exposure.

**Results:**

Expression of 342 plasma proteins were significantly ($p<0.05$) altered in response to DE compared to FA. The top 20 proteins enhanced in response to DE were enriched to GO biological process of immune response, primarily related to either inflammation or cardiovascular disease. Expression of proteins that were dysregulated in response to DE included chemokines CCL23 and CX3CL1, Apolipoprotein M and Apolipoprotein B, and metalloproteinase MMP-12.

**Conclusion:**

This is the first comprehensive interrogation of the plasma proteome following inhaled DE exposure in humans. This study details proteins that are altered following exposure to TRAP and adds functional plausibility to epidemiological observations of adverse health effects therein.