

were observed across the four different demand-control categories in the full sample. In stratified analysis, passive work environments (low control and low demands) and low-strain environments (high control and low demands) were associated with increased risk of heart disease (HR=1.94, 95% CI 0.99–3.81; HR=2.06, 95% CI 1.01–4.17), compared to active work (high demands and high control) among women. No similar relationship was observed among men.

Among a representative sample of Ontario workers, high strain work environments were not associated with increased risk of heart disease. Passive and low strain environments (both characterised by low psychological demands) were associated with increased risk of heart disease among women, but not men. Implications of these findings for assessment of the psychosocial work environment in Canada will be discussed.

## Biomarkers of Exposure

### 06D.1 INFLAMMATORY MARKERS IN THE PLASMA OF FIREFIGHTERS HEAVILY EXPOSED TO PARTICULATES

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10.1136/OEM-2019-EPI.153

**Introduction** In 2016 firefighters from Alberta, Canada deployed to a catastrophic fire in Fort McMurray. In the first few days, firefighters experienced heavy smoke exposures during greatly extended work shifts. Blood samples were collected to determine whether inflammatory markers might constitute a useful biomarker of exposure. In first responders exposed during the World Trade Center disaster, inflammatory markers in serum samples collected within 6 months post-event were associated with poor recovery from exposure-related lung disorders.

**Methods** Blood samples were collected at two fire services. At Service A, first samples were drawn two weeks from the start of the fire and second samples after 3–4 months. At Service B samples were collected over 4 weeks, starting 4 months from the first exposure. Samples were immediately centrifuged and the plasma stored at –80C before being evaluated for 42 cytokines or chemokines using a multiplex assay. A principal component analysis was carried out to reduce the number of correlated outcomes. Exposure to particulates was estimated for each firefighter using environmental PM<sub>2.5</sub>, total hours exposed, tasks carried out and the use of respiratory protection. Respiratory symptoms immediately before the fire, immediately post fire and at 4 months were collected using visual analogue (VA) scales.

**Results** Inflammatory markers were assayed for 242 plasma samples from 175 firefighters. Six components were extracted of which only one, labelled the inflammatory marker component (IMC) was related to estimated exposure ( $p < 0.001$ ): values decreased with time since last exposure ( $p < 0.001$ ). All respiratory symptoms post-fire were greater in those with higher estimated PM<sub>2.5</sub>. IMC scores were independently related to cough and wheeze at 4 months, but the biomarker did not contribute to models for these endpoints that also included PM<sub>2.5</sub>.

**Conclusions** Inflammatory markers were related to exposure but did not improve prediction of symptoms in the first months post fire.

### 06D.2 EVIDENCE OF DNA METHYLATION CHANGES BY CARBON NANOTUBES IN A TRANSLATIONAL STUDY DESIGN

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10.1136/OEM-2019-EPI.154

**Introduction** While studies have addressed genotoxic effects of CNT, only limited information are available on epigenetic effects. We designed a study to investigate DNA methylation alterations *in vitro*, *in vivo* and in occupationally exposed workers.

**Material and methods** *In vitro* studies were performed in 16-HBE and THP-1 cells. For the *in vivo* study, BALB/c mice were administered intratracheally with single-wall CNT (SWCNTs) and multi-wall (MWCNTs) at high (2.5 mg/kg) and low (0.25 mg/kg) doses. For the cross sectional study, 24 workers exposed to aggregates of MWCNT of 500 nm–100 µm with concentrations of 4.6–42.6 µg/m<sup>3</sup> and 43 unexposed referents were recruited. Global DNA methylation and demethylation patterns were analysed by LC-MS/MS. Methylation of specific genes was measured by Pyromark 24<sup>®</sup> (Qiagen). Genome-wide assessment of DNA methylation was performed with Infinium HumanMethylation450 BeadChip Array.

**Results** In general, we did not find global DNA methylation alteration for both CNTs. In 16-HBE cells, differentially methylated and expressed genes (MWCNTs>SWCNTs) from p53 signalling, DNA damage repair and cell cycle pathways were observed. In THP-1 cells, CNTs induced promoter-specific methylation of genes involved in several signaling cascade, vascular endothelial growth factor and platelet activation pathways. In lungs of BALB/c mice CNTs affected methylation of ATM gene. Finally, analysis of gene-specific DNA methylation in exposed workers revealed significant changes for DNMT1, ATM, SKI, and HDAC4 promoter CpGs.

**Conclusions** Epigenetic changes seem to occur at sub cytogenotoxic concentrations *in vitro*. Alteration in DNA methylation pattern could be a natural reaction of cells but could also silence critical genes and reprogram cellular functions.

### 06D.3 EVALUATION OF POLYCYCLIC AROMATIC HYDROCARBONS EXPOSURE ACROSS OCCUPATIONS IN KOREA USING URINARY METABOLITE 1-HYDROXYPYRENE

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10.1136/OEM-2019-EPI.155

**Objectives** Polycyclic aromatic hydrocarbons are a well-known carcinogen causing lung and skin cancers in exposed workers. Several occupations such as coke production have been reported to be associated with high PAHs exposure. However, previous reports have been