Comparative analysis of the toxic responses of organic extracts from diesel/biodiesel engine emissions in human lung BEAS-2B cells

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Background

Alternative engine fuels made from renewable sources are currently of great interest and importance due to their growing production and use. Despite their undisputable benefits such as sustainability or energy security and balance, recent findings on the toxicity of their combustion-related emissions are contradictive and give rise to several concerns related to environmental and health risks.

Experimental

In the present study, we compared toxicity of organic compounds extracted from emissions of four different diesel/biodiesel fuels and their blend, respectively (DEPs): conventional diesel (B0), diesel with 30% of biodiesel (B30), pure biodiesel (B100), and alternative fuel of second generation (NEXBTL100). Human bronchial epithelial cells (BEAS-2B) were incubated 4 and 24 hours with subtoxic dose of 50μg/ml of each DEP extract. To detect transcriptional changes and generate gene expression profiles, we used whole-genome microarrays (Illumina). Detailed chemical analysis of DEP extracts was performed to assess the chemical composition possibly associated with the toxicity.

Results

Our results suggest distinct qualitative and quantitative molecular response upon 4h treatment comparing to 24h treatment. After 4h incubation, we observed modulation of many biological processes and pathways mostly related to oxidative stress response, DNA damage response or apoptosis while 24h incubation resulted in deregulation of genes involved in metabolic activation of polycyclic aromatic hydrocarbons, cell cycle, lipid and steroid hormone metabolisms and many others. We also found differences among individual DEP extracts. NEXBTL100, a low carbon biofuel, exhibited after 4h and 24 incubation modest changes and distinct molecular response comparing to others (conventional fossil diesel fuel, 30% blend with bio-component and 100% biodiesel fuel).

Conclusions

We used microarray analysis as a robust and high-throuput method to describe a complex molecular response on transcriptional level and to reveal a „fingerprint“ of genome-wide expression changes characteristic for each diesel/biodiesel engine emissions extract.

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