

The “BUG” project: nasal microbiota, bronchiolitis and air pollution

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Background:

Exposure to pollutants such as atmospheric particulate matter (PM) can induce nasal microbiota alterations, which can determine host response diversities to infectious agents, leading to aggravated pathological states, such as bronchiolitis in infants. Nasal microbiota could be a key mediator between hosts and risk factors such as pollutants.

Methods and Results:

The microbiota analysis was conducted via 16S rRNA sequencing on nasal swabs from 103 cases and 46 controls. Adjusting for both PM10 and PM2.5 exposure, *Dolosigranulum* genus abundance was decreased and *Haemophilus* increased in cases; a significant positive correlation was observed between *Haemophilus* and PM 10 exposure level at 3 weeks before sampling (p-value of interaction= 0.0489). *Haemophilus influenzae* (Hi), predicted to be the most represented species, was adopted to set up a zebrafish model to study the immunomodulatory effects of the short-term exposure to PM via Hi-derived extracellular vesicles, observing a strong pro-inflammatory potential in zebrafish embryos.

Conclusions and Significance:

We described a modifier effect of PM10 and PM2.5 on *Haemophilus*, with a greater impact as exposure levels increased, modifying its relative abundance between cases and controls. Moreover, we found that bacterial EVs may be involved in the microbiota-host immune response interaction, modulating airways inflammation and promoting viral infections.

Keywords:

Nasal microbiota, Pollutants, extracellular vesicles, bronchiolitis, Haemophilus

References:

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Thematic Area:

- Frontiers in Microbiome Research

Infrastructures:

N.A.