

**P-028****DNA METHYLATION AND EXPOSURE TO AIR POLLUTION IN CHILDREN RESIDENT IN THE VALLE DEL MELA (SICILY) AREA****Authors:**

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**Background:** DNA methylation is associated to asthma-related inflammation. Short-term exposure to air pollution was suggested to be associated with epigenetic markers variations, either global or specific to some gene promoter.

**Objectives:** To study the association between individual DNA methylation markers and exposure to air pollutants among children with respiratory disorders resident in the high risk area of Milazzo – Valle del Mela (Sicily, Italy).

**Methods:** A panel study on 35 asthmatic children 8-11 years old with personal air pollution monitors was conducted on December 2007 – April 2008 in a high risk area. Two nasal-cell DNA samples were collected on different days by nasal brushings. We correlated DNA methylation of IL-6, iNOS, Alu and LINE-1 with daily average concentrations of NO<sub>2</sub>, SO<sub>2</sub> and PM<sub>2.5</sub>.

**Results:** Alu was consistently associated with SO<sub>2</sub> concentrations at lag12 in confounder adjusted single- and multipollutant (beta=-0.01; p=0.079) models. None of those associations was present after adjustment for confounders for LINE-1 marker. IL-6 was weakly associated with SO<sub>2</sub> lag12 (multipollutant beta=-0.004; p=0.227). iNOS methylation was consistently associated with the three pollutants at lag12 (SO<sub>2</sub> beta=-0.04 p=0.067; NO<sub>2</sub> beta=-0.05 p=0.10; PM<sub>2.5</sub> beta=-0.02 p=0.01).

**Conclusions:** We found evidence of association between air pollution level measured by personal monitors and hypomethylation of the inducible nitric oxide synthase (iNOS) gene promoter.

**Keywords:** Epigenetics, Air Pollution, Childhood Respiratory Disorders, Epidemiology, particulate matter