investigated. We analysed methyltransferase gene expression in workers exposed to high levels of metal-rich particles, and its relationship with the DNA methylation of nine inflammatory and tumour suppressor genes.

Methods We recruited 63 healthy male foundry workers. Individual exposure to arsenic and other metals was estimated based on metal components in PM10 collected in each work area (by coupled-plasma mass spectrometer) and on time spent in different areas by each worker. Methyltransferase gene expression was measured by real-time PCR in blood leucocytes DNA. Gene-specific DNA methylation was measured through bisulphite PCR-pyrosequencing. Multivariable linear regression models adjusted for age, BMI, smoking and drug consumption, were applied to assess the association between exposure and methyltransferase expression and, in turn, between methyltransferase expression and gene-specific methylation. Geometric mean ratios (GMR) were used to express results of log-transformed variables.

Results Enhanced methyltransferase (DNMT3B) gene expression was associated with increased exposure to arsenic (GMR=1.52, 95% CI: 1.06 to 2.20) and to other contaminants (Cu, Mo, Sn, Sb). DNMT3B expression was in turn associated with hypermethylation of the RASSF1A tumour suppressor gene (β=0.54, 95% CI: +0.15 to +0.94) and with hypomethylation of the Er-1 and IL-6 genes.

Discussion Our preliminary data suggest the possible role of methyltransferase gene overexpression in the pathway linking metal exposure to oncogene regulation. In particular, we found an increased DNMT3B expression in arsenic-exposed workers, that resulted also in hypermethylation (down-regulation) of RASSF1A. Interestingly, RASSF1A is a tumour suppressor gene involved in the development of cancers related to As exposure (bladder, lung).

Introduction Arsenic poisoning is a worldwide endemic disease that affects thousands of people. Growing evidence from animal, cell, and human studies indicates that arsenic has deleterious effects on immune systems, but its specific mechanism needs to be further explored.

Methods This is a population-based study that observed the association between exposure and methyltransferase expression and gene-specific methylation. Geometric mean ratios (GMR) were used to express results of log-transformed variables.

Conclusion Our preliminary data suggest the possible role of methyltransferase gene overexpression in the pathway linking metal exposure to oncogene regulation. In particular, we found an increased DNMT3B expression in arsenic-exposed workers, that resulted also in hypermethylation (down-regulation) of RASSF1A. Interestingly, RASSF1A is a tumour suppressor gene involved in the development of cancers related to As exposure (bladder, lung).