TRAFFIC-RELATED AIR POLLUTION, CHILDHOOD ASTHMA AND THE INFLUENCE OF CANDIDATE GENES INVOLVED IN OXIDATIVE STRESS

Elaina MacIntyre, *School of Environmental Health, University of British Columbia, Vancouver, Canada - Institute of **Epidemiology**, Helmholtz Zentrum Muenchen, Munich, Germany*
Erik Melén, *Unit of Environmental Epidemiology, Karolinska Institute, Stockholm, Sweden*
Elaine Fuertes, *School of Environmental Health, University of British Columbia, Vancouver, Canada*
Joachim Heinrich, *Institute of Epidemiology, Helmholtz Zentrum Muenchen, Munich, Germany*
Marjan Kerkhof, *Department of Epidemiology, University Medical Center Groningen, Groningen, The Netherlands*
Göran Pershagen, *Unit of Environmental Epidemiology, Karolinska Institute, Stockholm, Sweden*
Ulrike Gehring, *Institute for Risk Assessment Sciences, Utrecht University, Utrecht, The Netherlands*
Michael Brauer, *School of Environmental Health, University of British Columbia, Vancouver, Canada*
Chris Carlsten, *Department of Medicine, University of British Columbia, Vancouver, Canada*
for the TAG Study Team

Background and Aims: We combined previously collected data from two Canadian and four European birth cohorts to examine whether exposure to traffic-related air pollution interacts with a child's genetic profile to impact their risk of developing asthma.
Methods: Logistic regression was used to evaluate the association between traffic-related NO_2 (land use regression or dispersion model) and physician-diagnosed asthma or parent reported 'ever wheeze' at school age, stratified by *glutathione S-transferase P1* (*GSTP1*) and *tumor necrosis factor* (*TNF*) genotypes. Interaction terms were included to test for interaction between genotype and NO_2 in models for asthma and wheeze. Analyses were adjusted for gender, cohort, city, maternal age, parental atopic disease, and environmental tobacco smoke exposure (and intervention status for relevant studies).
Results: The combined dataset contained information for 4,902 children (380 asthma cases; 2,182 wheeze cases) and included three single-nucleotide polymorphisms (SNPs): rs1799811 (*GSTP1*; $C>T^{114}$), rs947894 (*GSTP1*; $A>G^{105}$) and rs1800629 (*TNF*; $G>A^{308}$). Pooled estimates for asthma by rs1799811 were elevated for carriers of the minor (CT,TT) alleles [OR per 10 $\mu g/m^3$ of NO_2: 2.12(95%CI: 1.12-4.00)] but not for major (CC) allele carriers [1.12(0.80-1.56)]. Accordingly, the interaction between rs1799811 and NO_2 was statistically significant (p-value=0.012) for asthma. The estimates for asthma for the remaining two SNPs were not statistically significant and interactions for both were also non-significant (p-value=0.152 for rs947894 and 0.051 for 1800629). Pooled estimates for wheeze, stratified by allele, were not statistically significant for any of the SNPs considered. Interactions for the *GSTP1* SNPs were not statistically significant in models for wheeze (p-value=0.889 for rs1799811 and 0.819 for rs947894), but the interaction for rs1800629 was significant (p-value=0.008).
Conclusions: In the largest study of its kind to date, we find that children with the rs1799811 minor alleles are at increased risk for developing asthma when exposed to traffic-related air pollution.