Occupational exposure to pesticides is associated with differential DNA methylation
Biobank-based Integrative Omics

Published in:
OCCUPATIONAL AND ENVIRONMENTAL MEDICINE

DOI:
10.1136/oemed-2017-104787

IMPORTANT NOTE: You are advised to consult the publisher's version (publisher's PDF) if you wish to cite from it. Please check the document version below.

Document Version
Publisher's PDF, also known as Version of record

Publication date:
2018

Link to publication in University of Groningen/UMCG research database

Citation for published version (APA):

Copyright
Other than for strictly personal use, it is not permitted to download or to forward/distribute the text or part of it without the consent of the author(s) and/or copyright holder(s), unless the work is under an open content license (like Creative Commons).

Take-down policy
If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

Downloaded from the University of Groningen/UMCG research database (Pure): http://www.rug.nl/research/portal. For technical reasons the number of authors shown on this cover page is limited to 10 maximum.

Download date: 17-02-2020
ORIGINAL ARTICLE

Occupational exposure to pesticides is associated with differential DNA methylation

Diana A van der Plaat,1,2 Kim de Jong,2 Maaike de Vries,1,2 Cleo C van Diemen,3 Ivana Nedeljković,4 Najaf Amin,4 Hans Kromhout,5 Biobank-based Integrative Omics Study Consortium, Roel Vermeulen,5 Dirkje S Postma,2,6 Cornelia M van Duijn,3 H Marike Boezen,1,2 Judith M Vonk1,2

ABSTRACT

Objectives Occupational pesticide exposure is associated with a wide range of diseases, including lung diseases, but it is largely unknown how pesticides influence airway disease pathogenesis. A potential mechanism might be through epigenetic mechanisms, like DNA methylation. Therefore, we assessed associations between occupational exposure to pesticides and genome-wide DNA methylation sites.

Methods 1561 subjects of LifeLines were included with either no (n=1392), low (n=108) or high (n=61) exposure to any type of pesticides (estimated based on current or last held job). Blood DNA methylation levels were measured using Illumina 450K arrays. Associations between pesticide exposure and 420938 methylation sites (CpGs) were assessed using robust linear regression adjusted for appropriate confounders. In addition, we performed genome-wide stratified and interaction analyses by gender, smoking and airway obstruction status, and assessed associations between gene expression and methylation for genome-wide significant CpGs (n=2802).

Results In total for all analyses, high pesticide exposure was genome-wide significantly (false discovery rate P<0.05) associated with differential DNA methylation of 31 CpGs annotated to 29 genes. Twenty of these CpGs were found in subjects with airway obstruction. Several of the identified genes, for example, RYR1, ALLC, PTPRN2, LRRC3B, PAX2 and VTNRA2-1, are genes previously linked to either pesticide exposure or lung-related diseases. Seven out of 31 CpGs were associated with gene expression levels.

Conclusions We show for the first time that occupational exposure to pesticides is genome-wide associated with differential DNA methylation. Further research should reveal whether this differential methylation plays a role in the airway disease pathogenesis induced by pesticides.

INTRODUCTION

Pesticides, including insecticides, herbicides and fungicides, are widely used in the agricultural sector to protect crops against harmful or unwanted insects, weeds and fungi. Exposure to pesticides can, however, also be toxic to humans and it has been estimated that approximately 250000 people worldwide die of pesticide poisoning each year.1

In the occupational setting, it has been estimated that about 25 million workers experience unintentional pesticide poisoning each year, due to inhalation or skin absorption.2 Long-term exposure to pesticides, like in occupational settings, has been associated with an increased risk for birth defects, several types of cancer and chronic diseases such as Parkinson’s disease, diabetes, chronic obstructive pulmonary disease (COPD), atherosclerosis and autoimmune diseases.3–5 Moreover, our own previous studies have shown that occupational exposure to pesticides is associated with lower lung function levels and airway obstruction cross-sectionally and with accelerated lung function decline longitudinally.6–7

Despite the associations with a wide range of diseases and health outcomes, it is still largely unknown how pesticides affect disease development. Several mechanisms have been proposed that may underlie the detrimental effects of pesticide
Exposure assessment

exposures, such as induction of oxidative stress, disruption of the endocrine system, mitochondrial dysfunction and epigenetic modifications. A well-known epigenetic modification is DNA methylation, which is the binding of a methyl group to a cytosine base adjacent to a guanine base (a CpG) site. DNA methylation can alter gene expression without changing the DNA sequence and is increasingly recognised as an important link between environmental exposures and disease. Altered DNA methylation levels have been found to play a role in multiple complex diseases, such as cancer, respiratory and neurodegenerative diseases. An in vitro study by Zhang et al provided evidence that gene promoter DNA methylation levels are indeed altered upon exposure to pesticides. Furthermore, studies in Greenlandic Inuit as well as in Koreans have shown that exposure to persistent organic pollutants is associated with global hypomethylation, based on the Alu and LINE-1 assay. These studies thus showed that pesticide exposure affects global DNA methylation levels, and therefore it might be possible that differential methylation at specific genomic locations may contribute to the deleterious effects of pesticides.

The current study is the first large-scale epigenome-wide association study assessing associations between occupational exposure to pesticides and DNA methylation levels. Since pesticide exposure can affect organs in the entire body, we used blood methylation to assess the effects of occupational exposure to any type of pesticide on DNA methylation levels. In addition, since there might be interindividual differences in the effects of pesticides on methylation, we decided to stratify our analysis based on susceptibility groups. We stratified by gender because previous research observed gender differences in pesticide-related health effects. In our previous studies, we have shown that the association between pesticide exposure and lung function is dependent on smoking habits, and therefore we assessed if the association between pesticide exposure and DNA methylation differs between never-smokers and current-smokers. Furthermore, since the main route of pesticide exposure is via inhalation and occupational exposure to pesticides is associated with airway obstruction, we assessed if DNA methylation on pesticide exposure differs between subjects with and without airway obstruction. Finally, we assessed whether the identified differentially methylated sites are associated with gene expression levels in blood.

METHODS

Population and measurements

In total, 1656 subjects were selected of the Dutch population-based cohort study LifeLines at baseline (2006–2011). All subjects provided written informed consent and the study was approved by the Medical Ethics Committee of the University Medical Centre Groningen, Groningen, the Netherlands. Subjects were specifically selected from the larger cohort taking smoking history (never-smoker or current-smoker), airway obstruction (defined as forced expiratory volume in 1 s to forced vital capacity ratio (FEV/FVC) <70%) and occupational related exposures into account. To optimise the exposure contrast, self-reported never-smokers with 0 pack-years of smoking and current-smokers with >5 pack-years were selected. Occupational exposure to pesticides was estimated based on current or last held job using the ALOHA+ Job Exposure Matrix (JEM), which classifies subjects based on the ISCO-88 job codes into no (0), low (1) and high (2) exposure categories, as published previously. To assess whether methylation levels at the identified CpGs are associated with gene expression levels in blood, we used data of the BIOS (Bibobank-based Integrative Omics Studies) project, from the Biobanking and Biomolecular Resources Research Infrastructure for The Netherlands (BBMRI-NL). In total, 2802 subjects were selected from four population-based cohorts, LifeLines (n=727), Rotterdam Study III-2 (n=589), Netherlands Twin Registry (n=900) and Leiden Longevity Study (n=586).

Genome-wide methylation assay

The Illumina Infinium Human Methylation 450K arrays (Illumina, San Diego, California, USA) were used to determine genome-wide DNA methylation levels at approximately 485,000 CpG sites of blood taken at the baseline visit. We randomised 1656 LifeLines subjects based on sex, exposure and airway obstruction across the arrays. Using 500 ng DNA for each sample, we first performed a bisulphite conversion using the EZ-96 DNA methylation kit (Zymo Research, Irvine, California, USA), which was validated using commercially available bisulphite conversion control samples (Zymo Research). After this step, the samples were processed according to the Illumina 450K protocol. After quality control, the final data set contained data for 1561 subjects and 420,938 CpG probes (see online supplementary methods for quality control).

Statistical analysis

To assess the relationship between occupational exposure to pesticides and DNA methylation levels, we used robust linear regression models in R (MASS package), which are less sensitive to outliers and heteroscedastic errors compared with linear least-squares models. Beta values were used to represent DNA methylation levels, which is the ratio between the intensities of methylated versus unmethylated probes, ranging from 0 to 1. We included two dummy variables in the model for occupational pesticide exposure, that is, low and high, no exposure being the reference. To estimate possible batch effects, a principal component (PC) analysis was performed using the control probes included on the 450K chip. We included seven PCs in the final model that each explained >1% of the variance. Together, these seven PCs captured 95.5% of the total variance. Interestingly, the position on the chip was an important determinant of the measured variance (online supplementary methods). In addition, the model was adjusted for differential blood counts for lymphocytes, monocytes and eosinophilic, neutrophilic and basophilic granulocytes obtained using standard laboratory techniques. The final model was adjusted for sex, age, current-smoking, pack-years, batch effects (PCs) and differential blood counts. When applicable, the model was adjusted for the single nucleotide polymorphism (SNP) under the probe since it can influence the accuracy of the assay.

We analysed the association between pesticide exposure and DNA methylation in the complete cohort and stratified by gender (men/women), smoking (never/current) or by airway obstruction. In addition, we assessed interactions between pesticide exposure and gender, current-smoking or airway obstruction on genome-wide methylation levels. For all analyses, CpG sites with false discovery rate (FDR) adjusted P value <0.05 for the high pesticide exposure variable were considered genome-wide significant.

Finally, in each of the four population-based cohorts of the BIOS dataset, we assessed the association between methylation and gene expression for the identified CpGs. The linear
regression was adjusted for sex, smoking, age and batch effects (cohort-specific PCs). All genes with expression data available within 1 Mb around the CpG were assessed, and the results of the cohorts were meta-analysed based on the effect estimates (random-effect model). CpGs with a meta-analysis P value below the Bonferroni-corrected threshold (P≤0.05/number of probe sets in the 1 Mb window) were considered significant.

Additional analyses
In the online supplementary methods, additional analyses related to the association of pesticide exposure with differential blood cell counts, PCs or age acceleration based on the epigenetic age are shown. In addition, results of Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways and Gene Ontology (GO) term enrichment analyses are also included in the online supplementary methods.

RESULTS
Population characteristics
Complete data on all covariates were available for 1561 subjects of the LifeLines cohort. Of the included subjects, 883 were men and 678 were women; 903 were never-smokers and 658 were current-smokers; 595 subjects had airway obstruction and 966 subjects did not (table 1). For an overview of all analyses, see online supplemental figure 1.

Complete cohort
In the complete cohort, CpGs were not significantly associated with high exposure to pesticides on a genome-wide significant level (FDR<0.05).

Stratification by gender
In men, no CpGs were significantly associated with high exposure to pesticides on a genome-wide level (FDR<0.05).

In women, high exposure to pesticides was significantly associated with higher levels of DNA methylation at four CpGs (table 2). These CpGs are annotated to LY6/PLAUR Domain Containing 6 (LYPD6), ATP Synthase, H+Transporting, Mitochondrial Fo Complex Subunit C3 (ATP5G3), Sodium/Potassium Transporting ATPase Interacting 3 (NKAIN3) and TBC1 Domain Family Member 9 (TBC1D9). A fifth CpG (cg23116540) showed a lower DNA methylation level upon pesticide exposure and annotated to Thrombospondin1 (THBS1). For two CpGs (ATP5G3 and THBS1), the effect estimate for the low exposure variable was in the same direction as the high exposure variable, but not significant. The CpG annotated to ATP5G3 was associated with higher exposure levels of this gene (table 3).

Interaction between pesticide exposure and gender
The CpG annotated to NKAIN3 was significantly more methylated on pesticide exposure in women compared with men (table 4).

Stratification by never-smoking and current-smoking
In never-smokers, one CpG (cg03181524) was genome-wide significantly associated with high exposure to pesticides. This CpG was annotated to Ryanodine receptor 1 (RYR1), named after the natural plant-derived insecticide ryanodine. This CpG was more methylated in both low and high exposed subjects, and the P value of the low exposure variable was borderline significant (table 2 and figure 1A). The CpG was associated with lower exposure levels of three genes, namely RYR1, Calpain 12 (CAPN12) and CTD-2540F13.2 (table 3).
Table 2  Genome-wide significant associations between DNA methylation and exposure to pesticides stratified by gender, smoking status and by the presence of airway obstruction

<table>
<thead>
<tr>
<th>Chr</th>
<th>BP</th>
<th>Str</th>
<th>Gene</th>
<th>Island</th>
<th>Position</th>
<th>Low pesticide exposure</th>
<th>High pesticide exposure</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Mean beta (%)</td>
<td>B</td>
</tr>
<tr>
<td>2</td>
<td>39</td>
<td>0.14</td>
<td>cg10770187</td>
<td>2</td>
<td>150,186,923</td>
<td>−0.15</td>
<td>0.29</td>
</tr>
<tr>
<td>8</td>
<td>66</td>
<td>0.53</td>
<td>cg19476538</td>
<td>8</td>
<td>176,451,185</td>
<td>−0.32</td>
<td>0.33</td>
</tr>
<tr>
<td>13</td>
<td>94</td>
<td>0.25</td>
<td>cg18275640</td>
<td>13</td>
<td>311,400,799</td>
<td>−0.63</td>
<td>0.16</td>
</tr>
<tr>
<td>4</td>
<td>28</td>
<td>0.30</td>
<td>cg25564547</td>
<td>4</td>
<td>141,677,874</td>
<td>−0.24</td>
<td>0.17</td>
</tr>
<tr>
<td>19</td>
<td>39</td>
<td>0.04</td>
<td>cg03181524</td>
<td>19</td>
<td>39,048,014</td>
<td>0.77</td>
<td>0.07</td>
</tr>
<tr>
<td>5</td>
<td>35</td>
<td>0.18</td>
<td>cg03181524</td>
<td>5</td>
<td>39,151,939</td>
<td>0.46</td>
<td>0.60</td>
</tr>
<tr>
<td>2</td>
<td>39</td>
<td>0.22</td>
<td>cg19476538</td>
<td>2</td>
<td>4,383,573</td>
<td>0.15</td>
<td>0.12</td>
</tr>
<tr>
<td>5</td>
<td>35</td>
<td>0.20</td>
<td>cg03181524</td>
<td>5</td>
<td>38,446,916</td>
<td>0.64</td>
<td>0.60</td>
</tr>
<tr>
<td>19</td>
<td>39</td>
<td>0.04</td>
<td>cg10770187</td>
<td>19</td>
<td>4,638,197</td>
<td>0.15</td>
<td>0.12</td>
</tr>
<tr>
<td>5</td>
<td>35</td>
<td>0.20</td>
<td>cg03181524</td>
<td>5</td>
<td>38,446,916</td>
<td>0.64</td>
<td>0.60</td>
</tr>
</tbody>
</table>

*Additionally adjusted for single nucleotide polymorphism (SNP) under the probe.

There were no significant associations between DNA methylation and pesticide exposure in the full cohort and in the stratified analysis in men or in individuals without airway obstruction.

B, beta; Bp, base pair; Ch, chromosome; CpG, DNA methylation site; Str, strand; UTR, untranslated region; TSS, transcription start site.
Gene stratification according to airway obstruction

Had lower DNA methylation levels on pesticide exposure and are annotated to the long intergenic RNA gene VTRNA2-1, which is located in an intron of the ELK1 gene, and with lower expression of the gene HLA-S, which is associated with lower levels of DNA methylation at two CpGs, annotated to the gene VTRNA2-1.

No data in BIOS-BBMRI were available for cg08855288, cg15793258 and cg27484412. In online supplemental table 5, the results of all CpGs and genes with expression data are shown.

* CpG also identified in pesticide exposure×airway obstruction analysis.

B, beta; CpG, DNA methylation site; P adjusted, Bonferroni-corrected P values based on all probesets located within the 1 Mb window.

Table 3 Significant associations between DNA methylation and gene expression (n=2802)

<table>
<thead>
<tr>
<th>CpG</th>
<th>Annotated gene</th>
<th>Ensembl_ID</th>
<th>Gene</th>
<th>B</th>
<th>SE</th>
<th>P adjusted</th>
</tr>
</thead>
<tbody>
<tr>
<td>cg16884400</td>
<td>ATP5G3</td>
<td>ENSG00000154518</td>
<td>ATP5G3</td>
<td>0.098</td>
<td>0.005</td>
<td>2.94×10^{-2}</td>
</tr>
<tr>
<td>cg03181524</td>
<td>RYR1</td>
<td>ENSG00000196218</td>
<td>RYR1</td>
<td>−0.881</td>
<td>0.157</td>
<td>6.74×10^{-7}</td>
</tr>
<tr>
<td>cg10059942</td>
<td>HMX2</td>
<td>ENSG00000138161</td>
<td>CUD01</td>
<td>1.474</td>
<td>0.536</td>
<td>4.18×10^{-2}</td>
</tr>
<tr>
<td>cg20869844</td>
<td>RAB19</td>
<td>ENSG00000146955</td>
<td>RAB19</td>
<td>−3.479</td>
<td>1.134</td>
<td>2.37×10^{-2}</td>
</tr>
<tr>
<td>cg11465769</td>
<td>MYT1</td>
<td>ENSG00000130508</td>
<td>PXXN</td>
<td>4.973</td>
<td>1.445</td>
<td>2.32×10^{-3}</td>
</tr>
<tr>
<td>cg19084031*</td>
<td>RP11-1008C21.2</td>
<td>ENSG00000259225</td>
<td>RP11-1008C21.1</td>
<td>−1.711</td>
<td>0.177</td>
<td>2.34×10^{-2}</td>
</tr>
<tr>
<td>cg04035638</td>
<td>PSORS1C3;POU5F1</td>
<td>ENSG00000225851</td>
<td>HLA-S</td>
<td>10.888</td>
<td>1.621</td>
<td>7.57×10^{-10}</td>
</tr>
</tbody>
</table>

Interaction between pesticide exposure and current-smoking

Four CpGs had a genome-wide significant interaction with high pesticide exposure and current-smoking and three of these are annotated to VTRNA2-1. Current-smokers who are highly exposed to pesticide exposure have lower DNA methylation levels at these VTRNA2-1 loci compared with exposed never-smokers. The other CpG is located in an intron of the Elongator Acetyltransferase Complex Subunit 4 (ELP4). None of these four CpG sites were associated with gene expression levels.

Stratification according to airway obstruction

In subjects without airway obstruction, no CpGs were significantly associated with high exposure to pesticides on a genome-wide level (FDR<0.05).

In subjects with airway obstruction (FEV1/FVC<70%), 20 CpGs were significantly associated with high exposure to pesticides (table 2). Nine CpGs had higher levels of DNA methylation on pesticide exposure and are annotated to the long intergenic non-protein-coding RNA 391 (LINC000319), AK053272, H6 Family Homeobox 2 (HMX2), RAB19, Kinesin Family Member 6 (KIF6), Paired Box 2 (PAX2), LOC101928227, Serine/Threonine Kinase 38 Like (STK38L) and WD Repeat Domain 46 (WDR46). The other 11 CpGs had lower DNA methylation levels on pesticide exposure and annotated to Tumour Necrosis Factor, Alpha-Induced Protein 8-Like 1 (TNFAIP8L1), figure 1C, Allantoicase (ALLC), two CpGs, figure 1D, Protein Tyrosine Phosphatase Receptor Type N2 (PTPRN2), Leucine Rich Repeat Containing 3B (LRRC3B), BCO16361, Collagen Type IX Alpha 1 Chain (COL9A1), Growth Differentiation Factor 6 (GDF6), Myelin Transcription Factor 1 Like (MYT1L), Psoriasis Susceptibility Candidate 3 (PSORS1C3) and Endothelial PAS Domain Protein 1 (EPAS1). For 11 CpGs, the effect estimate for the low exposure variable was in the same direction as the high exposure variable, and for the three CpGs annotated to ALLC and COL9A1, the effect estimate for the low exposure variable was significant. The CpGs annotated to RAB19 and RP11-1008C21.2 were significantly associated with lower gene expression levels in blood (table 3) and the CpGs annotated to HMX2 and MYT1L were associated with higher gene expression levels. The CpG annotated to PSORS1C3 was associated with higher gene expression levels of HLA-S, DDR1 and TCF19, and with lower expression of HCG22 and HLA-B.

Interaction between pesticide exposure and airway obstruction

Three CpGs annotated to TNFAIP8L1, ALLC and LRRC3B were significantly lower methylated on pesticide exposure in subjects with airway obstruction compared with those without airway obstruction (table 4). In addition, two CpGs were higher methylated on pesticide exposure in subjects with airway obstruction compared with subjects without airway obstruction, and are located in the body of the RNA gene CTD-2555A7.2 (AK053272) and LOC101928227. None of these CpGs were associated with gene expression levels.

Additional information

The Manhattan, volcano and Q-Q plots of all analyses are shown in online supplemental figures 1–11 and the regional
**Table 4** Genome-wide significant interactions between pesticide exposure and gender, current-smoking or airway obstruction on DNA methylation levels.

<table>
<thead>
<tr>
<th>Gene</th>
<th>Island</th>
<th>Position</th>
<th>Chr</th>
<th>Str</th>
<th>Gene</th>
<th>CpG Chr</th>
<th>Gene Island</th>
<th>Position</th>
<th>P</th>
<th>SE</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td>NKAIN3</td>
<td>5</td>
<td>TSS1500</td>
<td>8</td>
<td>S′ UTR</td>
<td>3′ UTR</td>
<td>63.7</td>
<td>0.32</td>
<td>0.89</td>
<td>0.0098</td>
<td>0.02</td>
<td>0.71</td>
</tr>
<tr>
<td>VTRNA2-1</td>
<td>5</td>
<td>TSS1500</td>
<td>13</td>
<td>S′ UTR</td>
<td>3′ UTR</td>
<td>36.7</td>
<td>0.32</td>
<td>0.89</td>
<td>0.0098</td>
<td>0.02</td>
<td>0.71</td>
</tr>
<tr>
<td>VTRNA2-1</td>
<td>5</td>
<td>TSS1500</td>
<td>11</td>
<td>S′ UTR</td>
<td>3′ UTR</td>
<td>30.8</td>
<td>0.32</td>
<td>0.89</td>
<td>0.0098</td>
<td>0.02</td>
<td>0.71</td>
</tr>
<tr>
<td>ALLC</td>
<td>5</td>
<td>TSS1500</td>
<td>19</td>
<td>S′ UTR</td>
<td>3′ UTR</td>
<td>35.8</td>
<td>0.32</td>
<td>0.89</td>
<td>0.0098</td>
<td>0.02</td>
<td>0.71</td>
</tr>
<tr>
<td>PAX2</td>
<td>15</td>
<td>TSS1500</td>
<td>31</td>
<td>S′ UTR</td>
<td>3′ UTR</td>
<td>35.8</td>
<td>0.32</td>
<td>0.89</td>
<td>0.0098</td>
<td>0.02</td>
<td>0.71</td>
</tr>
</tbody>
</table>

**DISCUSSION**

To our knowledge, this is the first study to assess the association between occupational exposure to pesticides and genome-wide DNA methylation levels. There were no significant associations between pesticide exposure and DNA methylation in the complete population. However, we identified a total of 31 CpG sites, annotated to 29 genes, that were associated with high pesticide exposure in the stratified analyses or the interaction analyses based on gender, smoking or airway obstruction status. Of these 31 CpGs, 5 CpGs were genome-wide significant in women, of which one CpG annotated to NKAIN3 was significantly different between men and women. In addition, one CpG annotated to RYR1 was identified in never-smokers and two CpGs annotated to VTRNA2-1 and EGFLAM were identified in current-smokers. In the interaction analysis between smoking and pesticide exposure, four CpGs were genome-wide significant, of which three CpGs were annotated to VTRNA2-1 and one was also identified in the current-smokers. Lastly, 20 of these 31 CpGs were genome-wide significantly associated with high pesticide exposure in subjects with airway obstruction. The associations of these 20 sites were not significant in subjects without airway obstruction, and in addition, 5 of these 20 sites were genome-wide significant in the interaction analysis between the presence of airway obstruction and pesticide exposure. Our data therefore suggest that differential methylation at specific genomic locations as induced by pesticides may play a role in airway disease pathogenesis.

Some of the annotated genes of the 20 CpGs identified in subjects with airway obstruction were previously associated with lung function or lung diseases, like ALLC, PTPRN2, LRRCB3 and PAX2. Moreover, genetic variants in the ALLC gene were previously associated with changes in FEV1 following inhaled corticosteroid treatment.29 Hypermethylation of PTPRN2 was seen in squamous cell lung cancer samples, and the gene’s methylation profile is included in prediction models for a COPD, pulmonary fibrosis and lung cancer diagnosis.29 30 LRRCB3 was differentially methylated in several cancer types and suggested to be a tumour suppressor gene in non-small-cell lung cancer.31 The PAX2 gene is of interest since PAX2 is abnormally higher expressed in Foxp1/2/4-deficient developing lungs, is a biomarker for lung cancer and is lower expressed in zebra fish exposed to glyphosate-based herbicides.32–34 Unfortunately, no expression data were available for ALLC and LRRCB3, and the association of cg15577272 with PTPRN2 gene expression was non-significant. However, the association between cg03943218 and PAX2 expression levels was nominal significant (B=3.29, SE 1.20, P=0.006, online supplemental table S4). Five other CpGs were significantly associated with gene expression levels...
Exposure assessment


Interestingly, CpG cg04035638 is located within the HLA superlocus and was associated with expression levels of multiple genes within this region, including HLA-B, HLA-S and DDR1. The HLA region plays an important role in the immune response and has been associated with asthma and lung cancer. Therefore, differential DNA methylation on exposure to pesticides may alter gene expression levels and subsequently play a role in the development of airway diseases.

Another interesting finding of this study is the observation of higher DNA methylation of a CpG located in an intron of RYR1 with high exposure to pesticides. Higher DNA methylation at this CpG was associated with lower RYR1 expression levels. In addition, the observed association between pesticide exposure and higher DNA methylation levels at the RYR1 intron was only significant in never-smokers, but a similar trend was seen in the complete cohort, in men and in subjects without airway obstruction (figure 1A). The RYR1 gene codes for a skeletal muscle calcium release channel that can be targeted by anthranilic diamide insecticides. In the current study, it is not possible to assess the effects of specific pesticides, like the anthranilic diamide insecticide ryanodine. Moreover, this is a relatively new class of insecticides introduced around 2006. Since our data collection started in 2006, it is therefore unknown if the subjects were exposed to this type of insecticide. Our findings do, however, indicate that higher methylation on pesticide exposure is associated with lower RYR1 expression levels, and it could therefore be a biological plausible mechanism through which pesticides act, but experimental studies are warranted.

In women, we also identified possible interesting differently methylated CpGs on pesticide exposure in, among others, the transcription start sites (TSSs) of the genes THBS1 and LYPD6. Alterations in the expression of the transcription factor THBS1 were found on in vitro exposure of human peripheral blood lymphocytes to the pesticides cypermethrin and mancozeb. The LYPD6 protein was found to directly interact with the nicotinic acetylcholine receptor in brain extracts, which is also a target for several classes of insecticides. Although we were not able to assess the effects of these specific pesticides, these findings do point to plausible genes related to pesticide exposure.

We also identified three CpGs located in the TSS of the vault RNA VTRNA2-1 (or MIR886) that are lower methylated with high pesticide exposure in current-smokers compared with never-smokers (figure 1B). This vault RNA is located between Transforming Growth Factor Beta 1 (TGFBI) and SMAD Family Member 5 (SMAD5), and both genes have been implicated in COPD development. Gene expression data of VTRNA2-1 were
Exposure assessment

Several of the annotated genes are biologically plausible genes previously linked to either pesticide exposure or lung-related diseases. Of the 31 differentially methylated CpGs, 7 CpGs were associated with gene expression levels and thus might have a biological function. Further research should reveal whether these identified CpGs are true findings and whether they play a role in the pathogenesis of airway diseases.

Acknowledgements

The authors wish to acknowledge the services of the Lifelines Cohort Study, the contributing research centres delivering data to Lifelines and the participating general practitioners, and all the study participants.

Contributors

DAvdP participated in the study design, analysis and interpretation of the data, and drafting of the manuscript, tables and figures. HMB, DSP, CCdV and CMvd obtained funding. JMV, Kdj, HMB, DSP, CCdV, CMvd, MdV, IN and NA determined the study design, participated in the analysis and interpretation of data, and critically supervised writing of the manuscript. HK and RV designed and provided the ALOHA+-jem. All researchers part of the group author BBMRI BIOS participated in collecting the BIOS data. All authors approved the final version of the manuscript.

Funding

This study is sponsored by grant number 4.1.13.007 of Lung Foundation Netherlands (Longfonds). The Lifelines Biobank initiative has been made possible by funds from FES (Fonds Economische Structuurversterking), SNN (Samenwerkingsverband Noord Nederland) and REP (Ruimtelijk Economisch Programma). The Biobank-Based Integrative Omics Studies (BIOS) Consortium is funded by BBMRI-NL, a research infrastructure financed by the Dutch government (NWO 184.021.007). The sponsors of this study played no role in the design of the study, data collection, analysis, interpretation or in the writing and submission of the manuscript.

Competing interests

DSP reports: The University of Groningen has received money for Professor Postma regarding a grant for research from Asta Zeneca, Chiesi, Genentec, GSK and Roche. Fees for consultancies were given to the University of Groningen by Astra Zeneca, Boehringer Ingelheim, Chiesi, GSK, Takeda and TEVA. All other authors declare they have no actual or potential competing financial interest.

Patient consent

Obtained.

Ethics approval

The study was approved by the Medical Ethics Committee of the University Medical Center Groningen, Groningen, the Netherlands.

Provenance and peer review

Not commissioned; externally peer reviewed.

Data sharing statement

Lifelines data are available (at costs) to all scientists. Scientists can apply for access to Lifelines data and samples by submitting a research proposal to the Lifelines biobank (www.lifelines.nl). Data on occupational exposures in Lifelines can be obtained from Professor H M Boezen. Access to the Biobank-based Integrative Omics Studies (BIOS) data is available by application to the BIOS Data Access Committee (www.bbmr.nl/acquisition-use-analyse/bios/).

Open Access

This is an Open Access article distributed in accordance with the Creative Commons Attribution Non Commercial (CC BY-NC 4.0) license, which permits others to distribute, remix, adapt, build upon this work non-commercially, and license their derivative works on different terms, provided the original work is properly cited and the use is non-commercial. See: http://creativecommons.org/licenses/by-nc/4.0/

© Article author(s) (or their employer(s) unless otherwise stated in the text of the article) 2018. All rights reserved. No commercial use is permitted unless otherwise expressly granted.

REFERENCES

Occupational exposure to pesticides is associated with differential DNA methylation

Diana A van der Plaat, Kim de Jong, Maaike de Vries, Cleo C van Diemen, Ivana Nedeljkovic, Najaf Amin, Hans Kromhout, Biobank-based Integrative Omics Study Consortium, Roel Vermeulen, Dirkje S Postma, Cornelia M van Duijn, H Marike Boezen and Judith M Vonk

*Occup Environ Med* published online February 19, 2018

Updated information and services can be found at: [http://oem.bmj.com/content/early/2018/02/19/oemed-2017-104787](http://oem.bmj.com/content/early/2018/02/19/oemed-2017-104787)

**References**

This article cites 46 articles, 6 of which you can access for free at: [http://oem.bmj.com/content/early/2018/02/19/oemed-2017-104787#ref-list-1](http://oem.bmj.com/content/early/2018/02/19/oemed-2017-104787#ref-list-1)

**Open Access**

This is an Open Access article distributed in accordance with the Creative Commons Attribution Non Commercial (CC BY-NC 4.0) license, which permits others to distribute, remix, adapt, build upon this work non-commercially, and license their derivative works on different terms, provided the original work is properly cited and the use is non-commercial. See: [http://creativecommons.org/licenses/by-nc/4.0/](http://creativecommons.org/licenses/by-nc/4.0/)

**Email alerting service**

Receive free email alerts when new articles cite this article. Sign up in the box at the top right corner of the online article.

**Topic Collections**

Articles on similar topics can be found in the following collections

- Open access (143)

**Notes**

To request permissions go to: [http://group.bmj.com/group/rights-licensing/permissions](http://group.bmj.com/group/rights-licensing/permissions)

To order reprints go to: [http://journals.bmj.com/cgi/reprintform](http://journals.bmj.com/cgi/reprintform)

To subscribe to BMJ go to: [http://group.bmj.com/subscribe/](http://group.bmj.com/subscribe/)