Mitochondrial DNA Copy Number and Exposure to Polycyclic Aromatic Hydrocarbons

Sofia Pavanello1, Laura Dioni2, Mirjam Hoxha3, Ugo Fedeli2, Danuta Mielzynska-Svach4, Svach4, and Andrea A. Baccarelli5

Abstract

Background: Increased mitochondrial DNA copy number (mtDNAcn) is a biologic response to mtDNA damage and dysfunction, predictive of lung cancer risk. Polycyclic aromatic hydrocarbons (PAHs) are established lung carcinogens and may cause mitochondrial toxicity. Whether PAH exposure and PAH-related nuclear DNA (nDNA) genotoxic effects are linked with increased mtDNAcn has never been evaluated.

Methods: We investigated the effect of chronic exposure to PAHs on mtDNAcn in peripheral blood lymphocytes (PBLs) of 46 Polish male noncurrent smoking coke-oven workers and 44 matched controls, who were part of a group of 94 study individuals examined in our previous work. Subjects’ PAH exposure and genetic alterations were characterized through measures of internal dose (urinary 1-pyrenol), target dose (anti-benzo[a]pyrene diol epoxide (anti-BPDE)–DNA adduct), genetic instability (micronuclei and telomere length), and DNA methylation (p53 promoter) in PBLs. mtDNAcn (MT/S) was measured using a validated real-time PCR method.

Results: Workers with PAH exposure above the median value (>3 µmol 1-pyrenol/mol creatinine) showed higher mtDNAcn [geometric means (GM) of 1.06 (unadjusted) and 1.07 (age-adjusted)] compared with controls [GM 0.89 (unadjusted); 0.89 (age-adjusted); (P = 0.029 and 0.016)], as well as higher levels of genetic and chromosomal [i.e., anti-BPDE–DNA adds (P < 0.001), micronuclei (P < 0.001), and telomere length (P = 0.053)] and epigenetic [i.e., p53 gene-specific promoter methylation (P < 0.001)] alterations in the nDNA. In the whole study population, unadjusted and age-adjusted mtDNAcn was positively correlated with 1-pyrenol (P = 0.043 and 0.032) and anti-BPDE–DNA adds (P = 0.046 and 0.049).

Conclusions: PAH exposure and PAH-related nDNA genotoxicity are associated with increased mtDNAcn.

Impact: The present study is suggestive of potential roles of mtDNAcn in PAH-induced carcinogenesis.

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Exposure to PAHs was assessed by measuring 1-pyrenol in a urine sample (50 mL) collected from each of the workers at the end of their work shift (after at least 3 consecutive working days) and in the late afternoon from controls. At the same time when urine was collected, blood samples were taken and placed in EDTA (20 mL) and heparin tubes (10 mL) for adduct and micronuclei analysis, as described previously (29). Samples were brought at the Institute of Occupational Medicine and Environmental Health in Sosnowiec where: (i) PBL cultures for micronuclei detection were prepared and micronuclei analyses were conducted; (ii) PBLs for adduct analyses were isolated in Ficoll solution (Seromed) within 4 hours after blood collection and kept frozen at −80°C until shipment to the Occupational Health section of the University of Padova, Italy, where DNA was extracted. Data on other possible nonoccupational PAH exposure (diet and environment) and consumption of fruits and vegetables were collected by means of a structured-questionnaire, as described previously (6, 29). Individuals with high dietary intake of PAHs were defined as those who reported consumption of PAH-rich meals (charcoaled meat and pizza) more than once a week; individuals with indoor exposure to PAHs were those who used wood or coal heating at home; and individuals with environmental exposure to PAHs were those with high-exposure index based on the location of their residence in areas with intense local traffic and/or presence of industries. The study was reviewed by the Ethics Committee of the Institute of Occupational Medicine and Environmental Health in Sosnowiec. All participants gave their written informed consent before enrolling.

Analysis of exposure to PAHs

Internal dose: 1-pyrenol. Exposure to PAHs was determined as previously described (29) by measuring 1-pyrenol in urine samples by high-performance liquid chromatography/fluorescence. Creatinine levels were used to estimate urinary dilution using a colometric test, based on the Jaffe reaction between creatinine and sodium picrate. Urinary 1-pyrenol was expressed as micromoles per mole of creatinine.

Analysis of nDNA alterations

Target dose: anti-BPDE–DNA adduct. Anti-BPDE–DNA adduct formation was detected after DNA isolation from exposed individuals.

Materials and Methods

Study design

The study participants (n = 90) were all males, noncurrent smokers, including 46 coke-oven workers in 3 polish cokeries and 44 controls matched by gender and ethnicity, who were part of a group of 94 study individuals examined in our previous work (6) with DNA, still available (enrolled from January through May 2006). All coke-oven workers performed tasks (i.e., charging, coking, and pushing operations at the coke-oven battery section) involving exposure to high levels of PAHs. We excluded individuals whose work involved exposure to benzene (i.e., workers in byproduct operations). Controls were clerks of the Institute of Occupational Medicine and Environmental Health in Sosnowiec, recruited during their periodic check-ups at the Preventive Health Services of the Institute. All individuals were non-current smokers, defined as either never-smokers or former smokers who had quit smoking at least 1 year before sample collection. Urine analysis of nicotine and its metabolites (29) confirmed that all individuals were nonexposed to tobacco smoke as they had urine nicotine concentrations less than 0.01 mg/mmol creatinine.

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analyses of a standard curve repeated five times on five different days was 10%. The highest CV value was 5.70% for those samples (n = 8) with more than 200 μg DNA, repeated twice.

Genetic instability: micronuclei. Micronuclei analysis was conducted on coded slides scored by light microscopy at ×400 magnification, as described previously (29). To exclude artifacts, the identification of micronuclei was confirmed at ×1,000 magnification in 10% of samples. The scoring of bi-, tri- and tetra-nucleate cells and micronuclei analysis was done and the cytokinesis block proliferation index was calculated as being equal in both groups (P = 0.60).

Genetic instability: telomere length measurement by quantitative PCR. Telomere length was measured in PBL DNA using the real-time quantitative PCR method developed by Cawthon (30) and described previously (6). This method measures the relative telomere length in genomic DNA by determining the ratio of telomere repeat copy number (T) to single copy gene (S) copy number (T:S ratio) in experimental samples relative to the T:S ratio of a reference pooled sample (6). The single-copy gene used in this study was human β-globin (hbg). An “eight-point” standard curve was generated from a serially diluted DNA pool (obtained from 20 DNA samples randomly selected from the samples tested in the present study), ranging from 30 to 0.234 ng in each plate, so that relative quantities of T and S (in nanograms) could be determined from it. All samples and standards were run in triplicate and the average of the 3 T:S ratio measurements was used in the statistical analyses. The PCR runs were conducted in triplicate on a 7900HT Fast Real Time PCR System (Applied Biosystems; ref. 6). After PCR amplification, the specificity and absence of primer dimers. All samples were run in triplicates on 384-plate. The average of the three Mt PCR run, a fresh standard curve, which ranged from 20 ng/μL to 0.25 ng/μL. The primers for qRT-PCR analysis of MtDNA and hbg were previously described (32). All PCRs were performed on 7900HT Fast Real-Time PCR System (Applied Biosystems). The thermal cycling conditions for mtDNA PCR were: initial 2 minutes at 50°C, and 3 minutes at 95°C to activate the hot-start iTaq DNA polymerase, followed by 35 cycles comprised of 15-second denaturation at 95°C and 60-second anneal/extend at 60°C. The thermal cycling conditions for the hbg PCR were 3 minutes at 95°C to activate the hot-start iTaq DNA polymerase, followed by 35 cycles comprised of 15-second denaturation at 95°C and 60-second anneal/extend at 58°C. Each run was completed by melting curve analysis to confirm the amplification specificity and absence of primer dimers. All samples were run in triplicates on 384-plate. The average of the three Mt measurements was divided by the average of the three S measurements to calculate the MT/S ratio for each sample. The CV for the MT/S ratio in duplicate samples analyzed on two different days was 7.8%.

Statistical analysis
Statistical comparisons between groups were carried out using the non-parametric Mann–Whitney U-test for continuous variables or the χ² test for categorical variables. Linear regression analysis was used on the entire study population to test the association of PAH exposure (urinary 1-pyrenol), anti-BPDE–DNA adduct, micronuclei, p53 DNA methylation levels, or telomere length (independent variables) with mtDNAcn (dependent variable) in unadjusted or age-adjusted models. Linear regression was also applied to compare mtDNAcn between the first and fourth quartiles of the above explanatory variables. Multiple linear regression analysis was used to assess the influence of urinary 1-pyrenol, anti-BPDE–DNA adduct, micronuclei, p53 DNA methylation levels, telomere length and age (independent variables), all fitted in the same model, on mtDNAcn (dependent variable). PAH exposure was fitted in univariate and multivariate analysis as a categorical variable (0 = controls; 1 and 2 = workers with 1-pyrenol ≤ and
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Table 1. Characteristics of Polish noncurrent smoker male coke-oven workers and nonexposed controls

<table>
<thead>
<tr>
<th></th>
<th>Coke-oven workers (n = 46)</th>
<th>Controls (n = 44)</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age, mean (range)</td>
<td>36 (20–59)</td>
<td>38 (21–58)</td>
<td>0.95</td>
</tr>
<tr>
<td>Diet high in PAH contenta, n</td>
<td>4</td>
<td>1</td>
<td>0.18</td>
</tr>
<tr>
<td>Fruit and vegetablesb, n</td>
<td>27</td>
<td>21</td>
<td>0.30</td>
</tr>
<tr>
<td>Environmental exposure to PAHsc, n</td>
<td>15</td>
<td>15</td>
<td>0.88</td>
</tr>
<tr>
<td>Indoor exposure to PAHsd, n</td>
<td>24</td>
<td>18</td>
<td>0.28</td>
</tr>
<tr>
<td>Ex-smokers, n</td>
<td>20</td>
<td>15</td>
<td>0.36</td>
</tr>
<tr>
<td>Years of work in the cokery, mean (range)</td>
<td>12 (1–40)</td>
<td>NA</td>
<td></td>
</tr>
<tr>
<td>PAH exposure, urinary 1-pyrenol µmoles/mol creatininea, median (range), nDNA alterations</td>
<td>3.00 (0.20–7.48)</td>
<td>0.09 (0.01–0.40)</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Anti-BPDE-DNA, adducts per 10^8 nucleotidesb, median (range)</td>
<td>4.97 (0.90–12.2)</td>
<td>0.21 (0.12–5.56)</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>MN per 1,000 binucleate cells, median (range)</td>
<td>3 (1–11)</td>
<td>1 (0–4)</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Relative TL, median T/S (range)</td>
<td>1.01 (0.31–3.00)</td>
<td>1.20 (0.43–2.12)</td>
<td>0.053</td>
</tr>
<tr>
<td>p53, median % mCg, (range)</td>
<td>12.2 (5.63–25.1)</td>
<td>18.0 (6.85–46.2)</td>
<td>&lt;0.001</td>
</tr>
</tbody>
</table>

Abbreviations: MN, micronuclei; TL, telomere length.

aNumber of individuals with charcoaled meat consumption more than or equal to once a week.
bNumber of individuals with daily consumption of fruit or vegetables.
cNumber of individuals with high environmental exposure from residence in town, intense traffic, and presence of industries near home (see Materials and Methods).
dNumber of individuals with wood- or coal-based heating at home.

Results

Participants’ characteristics, exposure, and biomarker levels

The study population of 46 coke-oven workers and 44 controls (Table 1) included all noncurrent smoking males. The two groups were similar for age range, dietary behaviors (PAH-rich meals and daily consumption of fruit and vegetables), as well as for their environmental or indoor exposure to PAHs (Table 1). Coke-oven workers had a median of 12 working years and were heavily exposed to PAHs as reflected in their urinary 1-pyrenol with a median value of 3 µmoles/mol creatinine. Workers exhibited significantly higher levels of different genotoxic alterations as reflected in higher anti-BPDE–DNA adduct (P < 0.001) and micronuclei (P < 0.001), and lower telomere length (P = 0.053) and DNA promoter methylation of p53 (P < 0.001) compared with controls. Among former workers, no correlation was found between mtDNA and years since they quit smoking.

mtDNA copy number according to PAH exposure

Coke-oven workers were divided in low and high exposure groups using the median levels of urinary 1-pyrenol (1-pyrenol ≤ and >3 µmoles/mol creatinine), taken as a measure of exposure to PAHs. Blood mtDNAcn GM was significantly higher in the high exposure group of coke-oven workers (GM 1.06) compared with controls (GM 0.89 MT/S, P = 0.029; Table 2). Age-adjusted analysis confirmed the finding of higher mtDNAcn in highly-exposed workers (1.07 MT/S) compared with controls (0.89 MT/S, P = 0.016). MtDNAcn in the low-exposure group of workers was not significantly different from controls, suggesting that mtDNAcn levels were similar in low-exposed workers and controls. Tests for trend for increased mtDNAcn across the three exposure categories [controls, low (1-pyrenol ≤3) and high exposed (1-pyrenol > 3)] workers were statistically significant in both unadjusted (PTrend = 0.043) and age-adjusted (PTrend = 0.032) analyses. As regards long-term exposure assessment, no measures were available and the only information was on duration of exposure as a coke-oven worker. There was no significant association between mtDNAcn and years worked in the coke-oven factory (linear regression r = 0.081, P = 0.52).

Correlation of mtDNA copy number with nDNA alterations

In the whole study population (n = 90; Table 3), mtDNAcn (MT/S) was positively correlated with anti-BPDE–DNA adduct levels in both unadjusted (P = 0.046) and age-adjusted analyses (P = 0.049). MtDNA was not...
associated with micronuclei, telomere length, and p53 promoter methylation (Table 3). A linear regression model applied to compare mtDNAcn between the first and fourth quartiles of the explanatory biomarkers showed higher levels of mtDNA in the highest telomere length quartile in both unadjusted and age-adjusted analyses ($P = 0.044$ and $P = 0.036$), but no associations with the other variables (micronuclei and p53 methylation; data not shown). When biomarkers were analyzed separately in exposed workers and controls, no significant associations were found. However, although not statistically significant, the positive correlation between number of adducts and mtDNAcn was also found among exposed workers, with a regression coefficient higher than in the whole study population ($b = 0.03$ vs. $b = 0.02$). The multiple linear regression analysis of urinary 1-pyrenol, anti-BPDE–DNA adduct, micronuclei, p53 DNA methylation levels, telomere length, and age, all fitted in the same model as determinants of mtDNAcn, revealed that telomere length, but not the other markers, was the only independent significant determinant of increasing mtDNAcn ($P = 0.031$).

### Discussion

In the present study, we showed that workers with exposure to PAHs above 3 μmol 1-pyrenol/mol creatinine had significantly higher mtDNAcn in PBLs compared with controls. Workers also exhibited higher levels of genetic and chromosomal alterations in anti-BPDE–DNA adducts, micronuclei, telomere length, and epigenetic changes (i.e., p53 hypomethylation) as previously reported (6, 31). Increased levels of mtDNAcn in PBLs have been associated with a future risk of lung cancer (22). Our findings extend those observations by showing that increased mtDNAcn may also occur in healthy individuals who are occupationally exposed to considerably higher levels of carcinogenic PAH(BP) than Biological Exposure Index proposed by Jongeneelen (34), i.e., 1-pyrenol of 2.28 μmoles/mol creatinine. At this value, corresponding to the post-shift excretion value at an environmental exposure equal to the airborne threshold limit value of coal tar pitch volatiles (i.e., 0.2 mg/m$^3$ of "benzene soluble matter", ACGIH (35), coke-oven workers have been shown to be at a 30% increased risk of lung cancer (34). Alterations in mtDNA have long been

<table>
<thead>
<tr>
<th>nDNA alterations</th>
<th>mtDNAcn (MT/S) [Model 1]$^a$</th>
<th>$b$ (SE)</th>
<th>$P$</th>
<th>$b$ (SE)</th>
<th>$P$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Adducts</td>
<td>0.021 (0.010)</td>
<td>0.046</td>
<td></td>
<td>0.020 (0.010)</td>
<td>0.049</td>
</tr>
<tr>
<td>MN</td>
<td>0.013 (0.014)</td>
<td>0.336</td>
<td></td>
<td>0.008 (0.014)</td>
<td>0.52</td>
</tr>
<tr>
<td>TL</td>
<td>0.073 (0.066)</td>
<td>0.273</td>
<td></td>
<td>0.090 (0.066)</td>
<td>0.18</td>
</tr>
<tr>
<td>p53</td>
<td>−0.006 (0.004)</td>
<td>0.133</td>
<td></td>
<td>−0.005 (0.006)</td>
<td>0.18</td>
</tr>
</tbody>
</table>

Abbreviations: MN, micronuclei; TL, telomere length.

$^a$Unadjusted analyses.

$^b$Analysis adjusted by age.
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Mitochondria have been shown to compensate for damage and dysfunction by replicating their mtDNA and increasing mtDNAcn (16). A rise in mtDNA content has been directly associated with DNA damage (42, 43) and reduced respiratory chain function, secondary to oxidative damage (17, 44). In our study, anti-BPDE-related mtDNAcn changes were detected at high PAH-exposure doses. Although PAHs are still considered the primary genotoxic carcinogens produced by coal combustion emissions (for a comprehensive review see ref. 3 and references therein), the presence in coke emissions of toxic metals, or alternatively of reactive oxygen species produced by PAH (12) or metal (45) metabolism, might have contributed, along with BP exposure, in determining the mtDNAcn alteration observed in our study. Also, alterations of mitochondrial lipids and proteins produced by PAHs and/or anti-BPDE may have operated as concurrent events contributing to the increased mtDNAcn. However, we cannot exclude that different socio-economic statuses might have contributed, along with PAH exposure (for which we have supplied a measure of internal dose and biologically effective dose, i.e., the specific promutagenic anti-BPDE–DNA), in the increase of mtDNAcn that we observed in PBLs of coke-oven workers.

Interrelationships between the mtDNA and nDNA is however suggested in our study by the finding that individuals with lower mtDNAcn, even after adjusting for age, also had lower telomere length. This finding specifically suggests a link between nuclear telomere attrition, a marker of biologic aging, and mitochondrial alterations. This observation is in line with previous findings by Sahin and colleagues (46) that showed a potential unifying mechanism connecting the nucleus and mitochondria in cellular aging. In that work, progressive nuclear telomere shortening, mediated by the activation of a p53-dependent pathway, was found to determine a reduction of mitochondrial function and mtDNAcn (46).

The present study has several strengths. The enrollment of the study participants was carefully designed to minimize potential confounding and increase the capability to reveal PAH effects by selecting non–current smoking males, all living in the same residential area. The selection of non–current smokers minimized the probability that the observed associations were dependent on factors other than the occupational PAH exposure. We also evaluated several other potential sources of PAH exposure, including dietary PAHs, indoor PAH exposure, and environmental PAH exposure, which showed no differences between coke-oven workers and controls. Our study had reliable measurements of PAH(BP) internal and target doses. Also, we measured in the study participants, biomarkers of genetic instability and methylation that allowed for characterizing the intercorrelation between mtDNAcn and nDNA alterations. Finally, the results of this study appear to be biologically plausible and the direction of the effects is consistent with the available literature data on mtDNAcn mechanisms.
We also recognize limitations to our study. This is a small-sized study and its results need to be confirmed in a larger independent investigation. Its cross-sectional design does not allow for investigating the temporal relationship of PAH exposure with mtDNAcn, as well as of the biomarkers of damage, genetic instability, and DNA methylation. The absence of air monitoring, as well as of repeated biologic sampling, are limitations of the study exposure assessment strategy. However, PAH exposure was assessed using biomarkers of internal dose (urinary 1-pyrenol) and target dose (anti-BPDE–DNA adduct), which may more appropriately represent the effective exposure dose. To limit confounding, we matched coke-oven workers and controls for their individual characteristics, including age, gender, and ethnicity. In addition, we adjusted the analysis contrasting highly exposed workers, as well those based on continuous exposure or biomarker variables, for age. Because of the limited number of study subjects, it is possible that the associations observed were due to confounding or chance. The small sample size might have also caused false negative findings. For instance, we did not find any difference in mtDNAcn between low-exposed coke-oven workers and controls. Future studies with augmented sample size are warranted to better characterize the effects of PAH exposure on mtDNAcn at low doses.

In conclusion, coke-oven workers exposed to high levels of PAHs exhibited significantly higher PBL mtDNAcn, as well as genetic alterations in nDNA (i.e. anti-BPDE–DNA adduct, micronuclei, shorter telomere length, p53 hypomethylation). Individuals with shorter telomere length showed lower mtDNAcn, thus linking PAH exposure and mitochondrial dysfunction with cellular aging. These features were found in PBLs of individuals chronically exposed to PAHs. As previous investigations have shown that increased mtDNAcn is predictive of future risk of lung cancer, the results of the present study are highly suggestive that mtDNAcn may serve as a biomarker of cancer risk due to PAH exposure. Although these results imply a role of mtDNAcn in PAH carcinogenesis, whether mtDNAcn mediates the risk of lung cancer, determined by PAH exposure, should be determined in future mechanistic investigations.

Disclosure of Potential Conflicts of Interest
No potential conflicts of interest were disclosed.

Authors’ Contributions
Conception and design: S. Pavanello, A.A. Baccarelli
Development of methodology: S. Pavanello, L. Dioni, M. Hoxha, A.A. Baccarelli
Acquisition of data (provided animals, acquired and managed patients, provided facilities, etc.): S. Pavanello, L. Dioni, A.A. Baccarelli
Analysis and interpretation of data (e.g., statistical analysis, biostatistics, computational analysis): S. Pavanello, U. Fedeli
Writing, review, and/or revision of the manuscript: S. Pavanello, L. Dioni, M. Hoxha, U. Fedeli, A.A. Baccarelli
Administrative, technical, or material support (i.e., reporting or organizing data, constructing databases): S. Pavanello, D. Mielczynska-Swach
Study supervision: S. Pavanello

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