

## REVIEW

# Biomonitoring of tobacco smoke carcinogenicity by dosimetry of DNA adducts and genotyping and phenotyping of biotransformational enzymes: a review on polycyclic aromatic hydrocarbons

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In this review article, we summarize the data on tobacco smoke carcinogenicity in relation to DNA adduct dosimetry and genotyping and phenotyping of biotransformational enzymes. A major class of carcinogens, polycyclic aromatic hydrocarbons, present in substantial quantities in tobacco smoke, is discussed. The historical background and an overview of the metabolic pathways are given. The epidemiological and biological data in particular on dosimetry of the representative DNA adducts and genotyping and phenotyping of the respective activating and detoxifying enzymes are presented. The salient findings are highlighted, the uncertainties are underlined and, finally, recommendations for future research are made.

**Keywords:** biotransformation, cancer, DNA adducts, polycyclic aromatic hydrocarbons (PAHs), tobacco smoke.

## Historical background

Historically, tobacco was offered to Columbus on his landing on San Salvador in the Bahamas on October 12, 1492 by the House of Arawaks. Subsequently, the seafaring European merchants brought seeds of tobacco plants to Spain and Portugal and promoted the American Indians' custom of smoking. In 1585, Jean Nicot, the French ambassador to Portugal, introduced tobacco at the Royal Court of Paris, and the tobacco plant was named *Nicotiana* in his honour. Tobacco was used first in England in 1565, followed by Italy, Germany, Scandinavia and Russia through to the year 1600 (Hoffmann and Hoffmann 1997).

Initially, tobacco was chewed or smoked in pipes, but soon cigarettes and cigars became popular. At first, cigarettes were hand-made by stuffing tobacco into a hollow reed or cane or by rolling crushed tobacco leaves in a cornhusk or in leaves of other vegetables as a wrapper. The first machine-made cigarettes were manufactured in Cuba in 1853, in London in 1856 and in North America in 1860 (Tso 1990).

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Tobacco consumption was modest in the US, UK, continental Europe and Japan until World War I. In 1920, the annual consumption of cigarettes per capita (over the age of 15 years) in Western countries ranged from 400 to 800. It then increased drastically up to 4400 until the mid-1960s (Lee 1975). Following the report of the Royal College of Physicians of London in 1962, and that of the Surgeon General of the US Public Health Service in 1964 on the health hazards of smoking, cigarette consumption declined significantly in the developed world (US Department of Health Education and Welfare 1964). In the UK, the annual consumption of cigarettes per adult male dropped from 4030 in 1960 to 1982 in 1993 (50.8% reduction) (European Bureau of Tobacco and Smoking Prevention 1994). Likewise, in the US the yearly cigarette consumption per adult male decreased from 4345 in 1963 to 2493 in 1994 (42.6% reduction). In 1965, 51.9% and 33.9% of all adult American men and women, respectively, were cigarette smokers. In 1993, the respective numbers were 27.7% and 22.5% (Giovino *et al.* 1994, WHO 1997a). Conversely, in developing countries there has been a substantial increase in annual per capita cigarette consumption since 1970 (rising from 800 to 1400 cigarettes) (World Bank 1999). Worldwide, there has also been a shift in the age group of current smokers towards younger ages (WHO 1997b). Recent surveys show an appreciable increase in smoking prevalence in youth, for example from 27.5% in 1991 to 36.4% in 1997 in the US (MMWR 1998).

### Tobacco smoking and cancer

Several decades of epidemiological research have identified tobacco smoking as the main cause of preventable mortality in developed countries (WHO 1997c, Ref. Landis *et al.* 1999). In the US, approximately one fifth of all deaths and one third of all cancers are attributable to smoking (World Cancer Research Fund/Academic Institute for Cancer Research 1997). Data from the mid-1980s confirm that among smokers aged 35–69 years, the death rate is three times higher than that in non-smokers, and that there is at least a two-fold excess mortality from all causes in old age (WHO 1997c). It is estimated that at least 50% of regular smokers who begin smoking during adolescence will eventually be killed by tobacco (WHO 1997c). Global cancer statistics show a prevailing link between tobacco smoking and a variety of human cancers, including cancers of the aerodigestive tract, lower respiratory tract, digestive and gastrointestinal system, renal and urinary tract, and colorectal system (Ferlay *et al.* 1998, Pisani *et al.* 1999, Parkin *et al.* 2001). There are one billion smokers throughout the world, one third of whom live in China, where a major smoke-associated cancer epidemic is predicted (Wald and Hackshaw 1996, Peto *et al.* 1999, Peto and Lopez 2001, Proctor 2001, Simonato *et al.* 2001): the world's most populous nation, which manufacturers and smokes 1.7 trillion cigarettes per year, will witness 100 million tobacco-related deaths in the first half of this century if current smoking trends are not changed (Peto *et al.* 1999, Proctor 2001). Taken together, although the argument for further tobacco control and improved smoking cessation strategies is powerful, the facts and figures imply that the utopian goal of a smoke-free society is still a long way off (Proctor 2001, Raw 2001). Instead, an understanding of smoke-induced carcinogenesis can lead to new strategies for decreasing risk, for identifying highly susceptible individuals and for developing innovative techniques for early detection.

## Principal chemical constituents of tobacco smoke

Tobacco combustion results in the formation of mainstream (MS) smoke and sidestream (SS) smoke (Ingebrethsen 1986). MS smoke is generated during puff drawing in the burning cone and hot zone of a tobacco product and travels through the tobacco column out toward the mouthpiece. SS smoke is formed between puffing and is emitted from the smouldering coal of the tobacco product into the ambient air (Hoffmann and Wynder 1986). Both MS smoke and SS smoke are composed of (i) a vapour phase containing volatile agents such as benzene, vinyl chloride, acrolein, etc. and (ii) a particulate phase (tar) containing semi-volatile and non-volatile agents such as alkaloids like nicotine and its derivatives, aromatic amines, polycyclic aromatic hydrocarbons (PAHs), etc. (table 1) (US Environmental Protection Agency 1992, Jaakkola and Jaakkola 1997).

Since SS smoke is generated at a lower burning temperature, its chemical composition in both the vapour and particulate phases differs from that of MS smoke (National Research Council 1986a). The ratios of selected tobacco smoke constituents in MS smoke to those in SS smoke from non-filtered cigarettes are listed in table 1.

## Environmental tobacco smoke

Environmental tobacco smoke (ETS) originates from the smouldering end of the tobacco product in between puffs and from the smoker's exhaled smoke. Other contributors to ETS include minor amounts of smoke that escape during the puff drawing from the burning cone of the tobacco product and some vapour phase agents that diffuse through the wrapping materials, such as the cigarette paper, into the environment (National Research Council 1986b). This mixture is released into the environment and is subsequently diluted by the surrounding air. It may then aggregate with pollutants already present in the environment and change character. Physicochemically, the composition of this complex mixture may differ considerably from that of MS smoke (National Research Council 1986a). Nonetheless, most toxic or carcinogenic components of MS smoke are also present in ETS, but in different concentrations (Hoffmann *et al.* 1984, National Research Council 1986a).

## Tobacco smoke carcinogens

Of the 44 chemical agents classified as 'group I carcinogens' by the International Agency for Research on Cancer (IARC) (IARC 1994), nine – benzene, cadmium, arsenic, nickel, chromium, 2-naphthylamine, vinyl chloride, 4-amino-biphenyl (4-ABP) and beryllium – are present in tobacco smoke (Smith *et al.* 1997). Based on their mode of action, these compounds are divided into two distinct types: DNA-reactive and epigenetic (Hecht 1996). Carcinogens of the DNA-reactive type possess specific structures that yield electrophilic reactants either directly or after bioactivation. Thus they can form covalently bound DNA adducts, which in turn may give rise to mutagenic events leading to, for example, DNA strand breaks, chromosomal aberrations, oncogene activation and tumour suppressor gene inactivation (Hemminki 1993, Nesnow *et al.* 1995, Ross *et al.* 1995, Denissenko *et al.* 1996, Yoon *et al.* 2001). In addition, these compounds can have other cellular and tissue epigenetic effects, such as cell proliferation and

	Emissions in MS	SS/MS ratio
<i>Vapour phase</i>		
Carbon monoxide	10–23 mg	2.5–4.7
Carbon dioxide	20–60 mg	8–11
Carbon sulphide	18–42 µg	0.03–0.13
Benzene	12–48 µg	10
Toluene	160 µg	6–8
Formaldehyde	70–100 µg	0.1– ~50
Acrolein	60–100 µg	8–15
Acetone	100–250 µg	2–5
Pyridine	16–40 µg	7–20
3-Vinylpyridine	15–30 µg	20–40
Hydrogen cyanide	400–500 µg	0.1–0.25
Hydrazine	32 ng	3.0
Ammonia	50–150 µg	40–170
Methylamine	17.5–28.7 µg	4.2–6.4
Dimethylamine	7.8–10 µg	3.7–5.1
Nitrogen oxides	100–600 µg	4–10
N-Nitrosodimethylamine	10–40 µg	20–100
N-Nitrosopyrrolidine	6–30 ng	6–30
Formic acid	210–478 µg	1.4–1.6
Acetic acid	330–810 µg	1.9–3.9
<i>Particulate phase</i>		
Particulate matter	15–40 mg	1.3–1.9
Nicotine	1.7–3.3 mg	1.8–3.3
Anatabine	2.4–20.1 µg	0.1–0.5
Phenol	60–140 µg	1.6–3.0
Catechol	100–360 µg	0.6–0.9
Hydroquinone	110–300 µg	0.7–0.9
Aniline	360 ng	30
o-Toluidine	160 ng	19
2-Naphthylamine	1.7 ng	30
4-Aminobiphenyl	4.6 ng	31
Benzo[a]anthracene	20–70 ng	2.2–4.0
Benzo[a]pyrene	20–40 ng	2.5–3.5
Cholesterol	14.2 µg	0.9
γ-Butyrolactone	10–22 µg	3.6–5.0
Quinoline	0.5–2 µg	8–11
Herman	1.7–3.1 µg	0.7–1.9
N'-Nitrosonor nicotine	200–3000 ng	0.5–3.0
4-(Methylnitrosamino)-1-(3-pyridyl)-1-butanone	100–1000 ng	1–4
N-Nitrosodiethanolamine	20–70 ng	1.2
Cadmium	100 ng	3.6–7.2
Nickel	20–80 ng	0.2–30
Zinc	60 ng	0.2–6.7
Polonium-210	0.03–0.5 pCi <sup>a</sup>	1.06–3.7
Benzoic acid	14–28 µg	0.67–0.95
Lactic acid	63–174 µg	0.5–0.7
Glycolic acid	37–126 µg	0.6–0.95
Succinic acid	112–163 µg	0.43–0.62

<sup>a</sup> Picocurie (1 curie = 3.7 × 10<sup>10</sup> becquerel).

growth promotion (Nesnow *et al.* 1995, Hecht 1996). Carcinogens of the epige-  
netic type, in contrast, do not generate reactive electrophiles and therefore are not  
likely to react with DNA (Williams *et al.* 1996). Instead, they display cellular  
effects such as neoplasm growth promotion, cytotoxicity, inhibition of tissue  
growth regulation, peroxisome proliferation, endocrine modification, immunosup-

pression and/or sustained tissue ischaemia that can be the basis for increases in neoplasia (Williams *et al.* 1996). Examples of carcinogens of the DNA-reactive and epigenetic types are 4-ABP and nickel, respectively.

To date, tobacco smoke carcinogenicity has been extensively studied using dosimetry of DNA adducts. Conceptually, DNA adducts are defined as biologically effective dose markers of exposure to carcinogens; they not only reflect prior exposure to carcinogens but also imply a tangible risk for cancer (Poirier *et al.* 2000, Vineis and Perera 2000, Hemminki *et al.* 2001). The latter aspect should be interpreted quite cautiously since DNA adduct formation is only one step in the multi-stage process of carcinogenesis, and many other influential factors such as cellular proliferation are also involved in this process (Poirier *et al.* 2000, Vineis and Perera 2000, Hemminki *et al.* 2001). Therefore, it is premature to rely solely on dosimetry of DNA adducts for cancer risk estimation. At present, although recent studies have indicated the predictive value of DNA adducts for cancer (Tang *et al.* 1995, 2001, Wei *et al.* 2000), it is more realistic to use DNA adduct dosimetry as a means to evaluate carcinogenesis and its mechanisms rather than to assess cancer risk *per se* (Goldring and Lucier 1990, Hemminki 1993, Hou *et al.* 1999, Besarati Nia *et al.* 2000a).

### DNA adduct-inducing agents in tobacco smoke

Several classes of chemicals present in tobacco smoke can induce DNA adducts, including tobacco-specific *N*-nitrosamines, aromatic amines and PAHs. Of these, PAHs are the subject of the present review.

### PAHs

PAHs are formed as a product of tobacco combustion, and are found in considerable quantities in its particulate phase (IARC 1986). PAHs are also emitted into the environment as a result of incomplete pyrolysis of organic materials such as fossil fuels. Established environmental sources of PAHs are power plants, domestic heating systems, petrol and diesel engines, refuse burning and various industrial activities (Guerin 1978).

Thus far, more than 500 individual PAHs have been identified (Grimmer 1983). However, only a limited number of them exhibit carcinogenicity in test systems. Tobacco smoke contains 11 potent carcinogenic PAHs, out of which benzo[*a*]pyrene (B[*a*]P) is widely known as the representative compound (IARC 1986). Chemically, PAHs are relatively inert as they are formed at very high temperatures. Being lipid soluble, they tend to accumulate in organisms that come into contact with them. They may subsequently undergo oxidative metabolism, yielding water-soluble derivatives or highly reactive electrophiles. The latter, if not eliminated before DNA replication, can interact with cellular structures and molecules and give rise to carcinogenesis. Paradoxically, it is now known that if PAHs were not metabolized, they would not be carcinogenic (Hall and Grover 1990).

### Biotransformation of PAHs

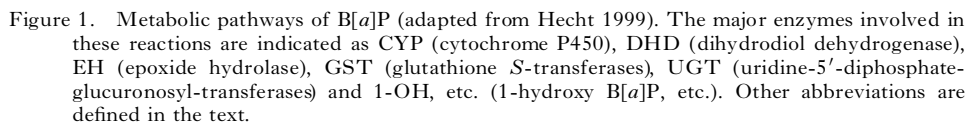
On entering the body, PAHs are enzymatically transformed to a series of either excretable end products (detoxification) or highly reactive metabolites that interact

with subcellular targets (activation) (Hall and Grover 1990). The initial step is epoxidation, which is the addition of one atom of oxygen across a double bond. This reaction is usually catalysed by cytochrome P450 (CYP450) enzymes, encoded by the *CYP* family of genes (Nebert and Gonzalez 1987). Other enzymes such as lipoxygenase, cyclooxygenases, myeloperoxidases and monoamine oxidases are also involved, but to a lesser extent (Burchell *et al.* 1997, Duffel 1997). The epoxides can undergo (i) hydration to yield diols, catalysed by epoxide hydrolases (EHs); (ii) isomerization to phenol; or (iii) conjugation with glutathione (GSH), catalysed by glutathione *S*-transferases (GSTs) (Hall and Grover 1990). The diol derivatives can conjugate to glucuronic and sulphuric acids, catalysed by uridine-5'-diphosphate-glucuronosyl-transferases (UGTs) and sulphatases, respectively (Burchell *et al.* 1997, Duffel 1997), or be further oxidated/hydroxylated to yield diol epoxides (Guenther and Oech 1981). The diol epoxides may then undergo conjugation with GSH (Armsrong 1997) or further metabolism to triols and tetraols or interaction with macromolecules to form, for example, DNA adducts (Hecht 1999). Likewise, the phenol derivatives can conjugate to glucuronic and sulphuric acids or be further metabolized to adduct-forming intermediates (Fu *et al.* 1978). The metabolic pathway of the model PAH compound, B[a]P, is simplistically outlined in figure 1.

Stereoisomerically, most PAH derivatives exist as pairs of enantiomers (*anti* or *syn*), two compounds related to one another as non-superimposable mirror images. Physically, each member of a given pair differs from its antipode in the direction by which it rotates the plane of polarized light (+ or -), and also in the absolute configuration of the groups around a chiral centre (*R* or *S*) (Thakker 1985). Biologically, two members of a pair of enantiomers may exhibit large differences, both in terms of their activity and in the details of their metabolism (Trager and Jones 1987). For example, the 7,8-diol 9,10-oxide-B[a]P (BPDE), generally regarded as the ultimate carcinogenic form of B[a]P, is produced as two diastereomers, each comprising two enantiomers. Of these four, the (+)-*anti*-7*R*,8*S*-dihydroxy-9*S*,10*R*-epoxy-7,8,9,10-tetrahydro-B[a]P [(+)-*anti*-BPDE] has been found to possess greater biological activity than the other three in most test systems (Dipple *et al.* 1984). (+)-*Anti*-BPDE can bind covalently to the 2-amino group of guanine at its C-10 position, thereby forming a major DNA adduct, (+)-*anti*-BPDE-dG (Weinstein *et al.* 1976).

### **Epidemiological and biological data on PAHs**

In 1775, Percival Pott noted a high incidence of skin cancer in chimney sweeps, probably induced by B[a]P, which occurs at a concentration of 0.2% in soot. Around a century later, von Volkman demonstrated the link between skin cancer and exposure to PAH in German coal tar workers (Alloway and Ayres 1994). In 1947, Kennaway showed the high risk of lung cancer in workers in the coal tar and gas industries (Alloway and Ayres 1994). This work was extended in 1972 by Sir Richard Doll (Alloway & Ayres 1994), who made a longitudinal study of mortality in workers in the same industries. Subsequent studies in individuals exposed occupationally, medically or environmentally to PAHs implicated these compounds in the aetiology of several human cancers, including cancers of the lung, oral cavity, larynx, skin, stomach, rectum, cervix and breast (IARC 1994). The history of the evaluation of PAHs has been extensively reviewed by Sir Ernest Kennaway (Kennaway 1955).



Thus far, the involvement of PAHs in smoking-associated cancers in humans has been investigated in the target organs (tumour-arising organs) or in the surrogate matrices such as peripheral blood cells (Phillips 1996, Poirier and Weston 1996). The latter have been used mainly in studies where the population under investigation consists of healthy individuals. Conceivably, most target organs for smoking-related cancers are not readily obtainable and require surgical or somewhat invasive procedures, precluding, for practical or ethical reasons, widespread population sampling or repeated sampling of the same individual (Phillips 1996).

*Lung.* In the lung, dosimetry of PAH-DNA adducts has consistently shown a higher level of adducts in smokers compared with non-smokers (Phillips *et al.* 1988, Van Schooten *et al.* 1990, Geneste *et al.* 1991, Lewtas *et al.* 1993, Lodovici *et al.* 1998, Hussain *et al.* 2001). In  $^{32}\text{P}$ -postlabelling analyses, smokers show a typical diagonal radioactive zone (DRZ) generated by the resolution of labelled



DNA digests on two-dimensional thin-layer chromatograms. This is widely regarded as an indication of the formation of a complex mixture of adducts in the respiratory tract as a result of exposure to tobacco smoke (Phillips 1996). More recently, ammonium hydroxide-based thin layer chromatography solvents have been introduced, which resolve adduct DRZ into discrete spots and allow determination of adducts derived from various classes of compounds, including PAHs (Spencer-Beach *et al.* 1996). The PAH-derived nature of DNA adducts in the lungs of smokers is shown by the specific detection of BPDE-dG adducts using fluorescence spectrometry and enzyme-linked immunosorbent assay (ELISA) (Van Schooten *et al.* 1990, Weston and Bowman 1991). Also, using a robust and sensitive gas chromatography/mass spectrometry (GC/MS) method, Goldman *et al.* (Goldman *et al.* 2001) have recently shown dose-dependent formation of a spectrum of PAH-DNA adducts in the lungs of smokers. In contrast, non-urea-based  $^{32}\text{P}$ -postlabelling analysis failed to demonstrate any typical PAH-DNA adducts in the lung tissue of smokers (Gupta *et al.* 1999).

Mechanistically, distribution of ( $\pm$ )-*anti*-BPDE-dG adducts has been mapped within the *p53* tumour suppressor gene, which is mutated in 60% of human lung cancers (Hollstein *et al.* 1991), in both HeLa cells and normal human bronchial epithelial cells (Denissenko *et al.* 1996). Accordingly, it has been shown that this major adduct of PAHs is preferentially formed at lung cancer mutational hotspots (codon 154, 157, 158, 245, 248, 249 and 273) (Hollstein *et al.* 1991, Denissenko *et al.* 1996). Subsequent mapping of other active diol epoxides of smoke-related PAHs (chrysene, 5-methylchrysene, 6-methylchrysene, benzo[*c*]phenanthrene and benzo[*g*]chrysene) in normal human bronchial epithelial cells has also shown that the DNA damage induced by these compounds is mostly located at the same codons previously reported for ( $\pm$ )-*anti*-BPDE (Smith *et al.* 2000). This indicates that other PAHs also contribute to the total load of adducts in the *p53* gene and probably impact on its mutational spectrum (Smith *et al.* 2000). Furthermore, it has been shown that the *p53* mutational spectra differ significantly between smokers and non-smokers in that smokers have a higher frequency of G $\rightarrow$ T transversions (reviewed by Hainaut and Pfeifer 2001). Recently, the G $\rightarrow$ T transversion hotspots in *LacI*, *cII* and *SupF* transgenes have been shown to correlate with the preferential binding sites of BPDE at methylated CpG dinucleotides in these reporter genes (Yoon *et al.* 2001). Also, *in vitro* treatment of human bronchial epithelial cells with BPDE induced the frequency of G $\rightarrow$ T transversions at several mutational hotspots of the *p53* (Hussain *et al.* 2001). Altogether, these data reiterate a plausible link between the formation of smoke-derived PAH-DNA adducts and lung cancer.

**Larynx.** In the larynx, aromatic DNA adducts have been detected in smokers but not in non-smokers using both enrichment methods of the  $^{32}\text{P}$ -postlabelling assay, the nuclease P1 (NP1) digestion and butanol extraction techniques (Degawa *et al.* 1994). Applying the NP1 version of this assay, Szyfter *et al.* (1994) demonstrated the formation of aromatic/hydrophobic DNA adducts in both tumour and non-tumour laryngeal tissues, with adduct levels being higher in the former. Analysis of laryngeal tumours by single-strand conformation polymorphism (SSCP) and direct DNA sequencing of exons 5–8 revealed that 46% of the mutations detected in these tissues were the typical *p53* mutations observed in lung cancer (G $\rightarrow$ T transversions, and G $\rightarrow$ A and C $\rightarrow$ T transitions) (Hainaut *et al.*



1998). Additionally, 54% of the detected mutations were within the hotspot region of the *p53* gene, covering codons 238–248 (Zhang *et al.* 1994).

*Oral and nasal cavity.* Initial reports on dosimetry of DNA adducts in the oral mucosa cells were inconclusive both in smokers versus non-smokers and in different groups of tobacco users, such as betel nut chewers, Khaini tobacco chewers and inverted smokers (Dunn and Stich 1986, Chacko and Gupta 1988). Subsequently, NP1- and butanol-enhanced <sup>32</sup>P-postlabelling analyses showed a higher level of adducts in the oral mucosa cells of smokers and suggested the aromatic amines and/or nitroaromatic nature of these adducts (Jones *et al.* 1993, Stone *et al.* 1995). Also, immunohistochemistry of PAH–DNA adducts showed a higher level of adducts in the oral cells of smokers compared with non-smokers (Hsu *et al.* 1997, Romano *et al.* 1999, Besarati Nia *et al.* 2000a). Likewise, in nasal epithelial cells obtained by biopsy or nasal lavage, smokers had a higher level of adducts compared with non-smokers in NP1-enriched <sup>32</sup>P-postlabelling analyses (Peluso *et al.* 1997, Zhao *et al.* 1997).

*Cervix, placenta and sperm.* In the cervical epithelium, smokers showed higher level of adducts compared with non-smokers in both versions of the <sup>32</sup>P-postlabelling assay; the differences were more pronounced when the butanol extraction method was utilized (Simons *et al.* 1993, 1995). A recent immunohistochemical study has also shown a higher level of PAH–DNA adducts in the cervical smears of smokers compared with non-smokers (Mancini *et al.* 1999). Also, elevated levels of DNA adducts were observed in the placentas of smoking pregnant women compared with their non-smoking counterparts by both <sup>32</sup>P-postlabelling assay and ELISA (Everson *et al.* 1988, Hansen *et al.* 1992, Arnould *et al.* 1997). In addition, the level of adducts in the umbilical cord vein was significantly lower than in the placenta, and marginally lower than in the umbilical cord artery of the same donor (Hansen *et al.* 1992, Arnould *et al.* 1997, Hoffmann and Hoffmann 1997). This implies a transplacental exposure of the fetus to smoke-derived carcinogens as well as the capability of the fetus to metabolize these compounds.

<sup>32</sup>P-postlabelling analysis of human sperm cells failed to differentiate between smokers and non-smokers (Gallagher *et al.* 1993, Little and Vainio, 1994). However, pre-implemented embryos from smoking parents showed higher immunoreactivity for BPDE–DNA adducts compared with those from non-smoking parents (Zenzes *et al.* 1999a). The similar levels of immunostaining in embryos from both types of smoking couples (either one parent smoker or both parents smokers) in the same study (Zenzes *et al.* 1999a), together with the relatively higher immunoreactivity for BPDE–DNA adducts in the sperm cells of smokers compared with non-smokers in another study (Zenzes *et al.* 1999b), suggest that transmission of modified DNA is mainly through the spermatozoa.

*Breast.* In a pilot study in breast cancer cases and mastoplasty controls, only breast tissues (tumour and/or tumour-adjacent) from cases who were current smokers displayed a DRZ in NP1-enhanced <sup>32</sup>P-postlabelling analyses (Perera *et al.* 1995). Applying the same methodology, a large scale case control study showed a higher level of DNA adducts in the adjacent non-tumour tissues of the cases (Li *et al.* 1996). However, both studies were subsequently shown to be biased because of their inappropriate controls and unadjusted confounders. Recently, a well-designed hospital-based case control study has shown an association between

immunohistochemically detected PAH-DNA adducts and breast cancer risk (odds ratio = 4.43, 95% confidence interval = 1.09–18.01) after controlling for known risk factors for breast cancer and adjusting for confounding factors for PAH exposure. Smoking behaviour, however, did not correlate with the level of adducts or with the case-control status (Rundle *et al.* 2000a).

*Miscellaneous.* Scant  $^{32}\text{P}$ -postlabelling data have shown the elevated level of DNA adducts in tumour tissues from gastric cancer patients compared with respective controls (Dyke *et al.* 1992). Also, in a pilot study in human colon mucosa, (+)-anti-BPDE-dG adducts were detected using high performance liquid chromatography with fluorescence detection (HPLC-FD) (Phillips 1996). In the skin, adduct measurement was performed in relation to occupational/medical exposure to PAHs rather than tobacco smoking. For example, in psoriasis patients treated with coal tar, specific nuclear staining for ( $\pm$ )-anti-BPDE-DNA adducts detected by the indirect immunofluorescence method was observed in skin biopsies (Zhang *et al.* 1990). The same samples revealed a pattern of multiple DNA adducts in NP1  $^{32}\text{P}$ -postlabelling analyses (Zhang *et al.* 1990). Similar results were also reported by our group in coal tar-treated eczema patients (Godschalk *et al.* 1998).

*Peripheral blood, bronchoalveolar lavage and sputum.* In peripheral blood cells, dosimetry of PAH-DNA adducts initially produced controversial results when this matrix was analysed in its entirety (Reddy *et al.* 1990, Rothman *et al.* 1990, Van Schooten *et al.* 1992). Later, it became evident that, since white blood cells (WBCs) are composed of different cell types with varying life spans and metabolizing capacities (Boggs and Winkelstein 1983), both the recency of exposure and the formation/persistence of adducts may vary within this matrix (Savela and Hemminki 1991). For instance, granulocytes, which comprise approximately 60% of the total WBCs and have a short half-life of 7–24 h (Boggs and Winkelstein 1983), had a considerably lower level of PAH-DNA adducts than mononuclear cells (monocytes [15%] plus lymphocytes [75%]) (Boggs and Winkelstein 1983, Savela and Hemminki 1991). Moreover, when treated separately with B[a]P *in vitro*, only short-lived monocytes (life span 8 h), but not unstimulated lymphocytes (life span 1–5 years), formed DNA adducts. Subsequent formation of DNA adducts in both cell types incubated simultaneously with B[a]P suggested that *in vivo* formation of adducts in lymphocytes occurs after other cell types activate the procarcinogens (Holz *et al.* 1991). Accordingly, use of total WBCs for the measurement of DNA adducts has increasingly been replaced by mononuclear cell DNA adduct dosimetry. Although more recent studies lend support to the relevance of DNA adduct analysis in subpopulations of WBCs for both exposure and risk assessment (Wiencke *et al.* 1999, Wei *et al.* 2000, Li *et al.* 2001, Tang *et al.* 2001), adduct dosimetry in fractionated WBCs is still subject to bias. Understandably, circulating blood cells are exposed to diverse routes of exposure, such as inhalation, ingestion and dermal absorption, thereby reflecting an integrated rather than a specific body burden for DNA adducts. This liability is of most concern when the carcinogen of interest enters the body via a specific route. Such non-specificity of DNA adducts in WBCs may explain the controversial data on PAH-DNA adducts in the WBCs of smokers versus non-smokers and of other groups of PAH-exposed versus non-exposed individuals (Tang *et al.* 1995, Phillips 1996, Poirier and Weston 1996, Palli *et al.* 2000, 2001). In addition, the lack of

correlation between the level of adducts in the WBCs and that in the target organs is to some extent expected (Phillips 1996, Poirier and Weston 1996). Interestingly, few studies (Izzotti *et al.* 1991, De Flora *et al.* 1993, Van Schooten *et al.* 1997, Piipari *et al.* 2000) have utilized bronchoalveolar lavage (BAL) cells, which are mainly (> 90%) composed of bronchoalveolar macrophages (BAMs), having an efficient metabolic machinery and a predominant exposure to inhalatory carcinogens (Harris *et al.* 1978, Petruzzelli *et al.* 1988). Although adduct analyses in BAL cells have been much more promising than those in WBCs, the invasiveness of the method of sampling hinders routine application of BAL cells in molecular dosimetry studies. Recently, we have examined the applicability of induced sputum, a non-invasively obtainable matrix from the lower respiratory tract, for dosimetry of inhalatory carcinogens (Besarati Nia *et al.* 2000b). Applying both versions of the  $^{32}\text{P}$ -postlabelling assay, we found a higher level of DNA adducts in the induced sputum of smokers compared with non-smokers, with the differences being more explicit with the NP1 enrichment procedure (Besarati Nia *et al.* 2000b). Subsequent analysis of the samples by immunohistochemistry showed a non-significantly higher level of PAH-DNA adducts in the induced sputum of smokers compared with non-smokers ( $p = 0.07$ ) (Besarati Nia *et al.* 2000c). These observations were confirmed in a follow-up study, in which we also demonstrated the superiority of adduct analysis in induced sputum to that in WBCs (Besarati Nia *et al.* 2000d).

*Genotyping and phenotyping of biotransformational enzymes.* A complementary area of interest is the polymorphisms of genes involved in the biotransformation of PAHs. The enzyme complex responsible for the initial activation of PAHs, arylhydrocarbon hydroxylase (AHH), consists of a battery of enzymes that includes CYP1A1 (Nelson *et al.* 1996). CYP1A1 mRNA reflects gene induction, while AHH and 7-ethoxyresirufun *O*-deethylase (EROD) are measures of enzyme activity (Cosma *et al.* 1993, Zhang *et al.* 1996). Among the four known polymorphisms identified in the *CYP1A1* gene, two closely linked mutations (mostly in Asians) have been extensively studied in relation to AHH inducibility, DNA damage and cancer risk: the *CYP1A1*\*2 allele, which results in a new restriction site (*Msp*I) in the 3'-untranslated region of the gene, and the *CYP1A1*\*3 allele, located in exon 7, which results in an amino acid exchange (Ile 462→Val) (Hayashi *et al.* 1991, Crofts *et al.* 1994). In most studies, but not all, these alleles have been associated with increases in the catalytic activity of the enzyme and with higher AHH inducibility (Cosma *et al.* 1993, Zhang *et al.* 1996). The alleles have also been associated with increased frequency of *p53* mutations in lung and oral tumour tissues (Kawajiri *et al.* 1996, Park *et al.* 1997). The extent of AHH activity in human lung microsomes has been positively correlated with the level of PAH-DNA adducts in the same lung samples (Geneste *et al.* 1991). In leukocytes, however, such a correlation has not been consistently shown (Ichiba *et al.* 1994, Rothman *et al.* 1995). Regarding *CYP1A1* polymorphism and susceptibility to DNA damage or cancer, contradictory results have been reported. This has mostly been the case when different populations with varying mutated allele frequencies were investigated or when the analyses were performed in surrogate tissues (Phillips 1996, Poirier and Weston 1996, Bartsch *et al.* 2000, Piipari *et al.* 2000). Overall, lack of agreement in these studies may have arisen from differences in the experimental approaches used to determine polymorph-

isms, to detect DNA adducts within specific organs, and to demonstrate subtle effects whilst having incomparable statistical power (IARC 1999a).

A major pathway of detoxification for PAHs is formed by the multi-gene family of cytosolic enzymes, the GSTs. These enzymes catalyse the conjugation of PAHs or their reactive metabolites to GSH, thereby making them readily excretable (Mannervik and Danielson 1988). Four different gene families of *GSTs* are known –  $\alpha$ ,  $\mu$ ,  $\pi$  and  $\theta$  (Hayes and Pulford 1995), although most of the available literature with regard to PAHs and cancer relates to *GST $\mu$*  and *GST $\pi$* . Each *GST* family comprises several genes; for example, the *GST $\mu$*  family consists of at least five known genes, *GSTM1–5* (Hayes and Pulford 1995). The various GSTs have different but often overlapping substrate specificities (Hayes and Pulford 1995). Also, diverse patterns of expression in different cells and tissues have been shown (Hayes and Pulford 1995). The most studied human GST, *GSTM1*, is lacking in approximately 50% of Caucasian populations (Seidegård *et al.* 1988). Absence of this enzyme is caused by an 8 kb deletion at the entire coding region of the *GSTM1* gene, producing the null genotype (Seidegård *et al.* 1988). A meta-analysis of 12 case control studies has concluded that the *GSTM1* null genotype is a moderate risk factor for lung cancer (odds ratio = 1.41, 95% confidence interval = 1.23–1.61,  $p < 0.0001$ ) (McWilliams *et al.* 1995). In some studies, but not all, this genotype has also been associated with an increased incidence of other types of cancer, including adenocarcinoma of stomach and caecum, multiple skin cancers, carcinoma of bladder, and oral nasopharyngeal and laryngeal cancer (Bell *et al.* 1993, Heagerty *et al.* 1994, Park *et al.* 1997, Nazar-Stewart *et al.* 1999). Additionally it has been shown that possession of the *GSTM1* null genotype may affect the susceptibility to DNA damage of various organs (Kato *et al.* 1995, Jourenkova *et al.* 1998, Bartsch *et al.* 1999). A number of studies have reported an association between the *GSTM1* null genotype and the level of PAH–DNA adducts in the non-tumorous tissues of lung cancer cases (Shields *et al.* 1993, Kato *et al.* 1995, Ryberg *et al.* 1997). Also, the *GSTM1* null genotype has been shown to be a major determinant of PAH–DNA adduct levels in both malignant and non-malignant breast tissues in cases but not in controls (Rundle *et al.* 2000b). However, the influence of this genotype on DNA adduct levels in leukocytes is not yet clear. Studies of subjects exposed occupationally, environmentally or medically to PAHs, e.g. chimney sweeps, coke oven and foundry workers, bus drivers, firefighters, soldiers and coal tar-treated patients, as well as studies of smokers have mainly shown no or an insignificant increase in the leukocyte DNA adduct levels dependent on the *GSTM1* null genotype (Butkiewicz *et al.* 1998, Bartsch *et al.* 1999, Rojas *et al.* 2000).

The *GSTP1* gene is also known to be polymorphic at different sites (Zimniak *et al.* 1994). A common polymorphism occurs in exon 5 of this gene, causing an exchange of amino acids (Ile 105→Val) with a mutant frequency of 30–35% (Butkiewicz *et al.* 2000). The two isoforms, *GSTP1-1/V-105* (GG: Val/Val, GA: Ile/Val) and *GSTP1-1/I-105* (AA: Ile/Ile), differ in activity, specificity and catalytic efficiency (Zimniak *et al.* 1994, Hu *et al.* 1997). Epidemiological studies indicate that individuals carrying the *GSTP1-1/V-105* rather than the *GSTP1-1/I-105* allele are more susceptible to tumour formation at sites such as the oral cavity, oesophagus, breast, bladder and testis (Harries *et al.* 1997, Helzlsouer *et al.* 1998, Katoh *et al.* 1999). In addition, the levels of hydrophobic DNA adducts in non-cancerous lung tissues from smoking lung cancer patients have been shown to

be associated with the *GSTP1-I/V-105* genotype (Ryberg *et al.* 1997). However, studies of *GSP1* polymorphisms in relation to PAH exposure are too few and limited to allow any definite conclusions (for more information on recent meta-analyses, see IARC 1999b).

Overall, it appears that a combination of different metabolic polymorphisms, rather than a single one, is a better determinant of DNA damage and cancer susceptibility (IARC 1999c, Bartsch *et al.* 2000, Rojas *et al.* 2000). For instance, in a study of non-small cell lung cancer (NSCLC), the prevalence of combined *GSTM1* null and *CYP1A1\*2B* genotypes was significantly higher in the adenocarcinoma group (Butkiewicz *et al.* 1999). In the same study, patients with the *GSTM1* null and *CYP1A1\*3* combined genotypes had a significantly higher level of PAH-DNA adducts in non-tumorous tissues of the lung compared with those with other genotype combinations (Butkiewicz *et al.* 1999). Also, smoking lung cancer patients as well as coke oven workers who had a combination of *CYP1A1\*2* or *\*3* and *GSTM1* null genotypes had a higher level of (+)-anti-BPDE-DNA adducts compared with those with *CYP1A1* and *GSTM1* wild-type genotypes at a similar or even lower smoking dose (Bartsch *et al.* 1999). Furthermore, smoking individuals with mutated *CYP1A1* and *GSTM1* null genotypes had a 100-fold higher level of bronchial BPDE-DNA adducts than those with other combined genotypes (Bartsch 1996). Among the moderate smokers, those who carried the combined *CYP1A1\*2* and *GSTM1* null alleles showed the highest level of adducts (Ichiba *et al.* 1994). Likewise, lung cancer patients with *GSTM1* null and *GSTP1-I/V-105* combined genotypes had the highest level of hydrophobic DNA adducts in non-tumorous tissues of the lung ( $p = 0.011$ ) (Ryberg *et al.* 1997). The distribution of combined *GSTM1* null and *GSTP1-I/V-105* genotypes was also significantly different in cases and controls (Ryberg *et al.* 1997). In a Japanese population, individuals who carried the mutated *GSTP1* and *GSTM1* null alleles had a higher risk of head and neck cancer compared with those who had other combined genotypes (odds ratio = 2.58, 95% confidence interval = 0.77–1.79) (Kihara *et al.* 1997). Also, the level of PAH-DNA adducts in the mononuclear WBCs of smokers with *GSTM1* null and *GSTP1-I/V-105* combined genotypes was non-significantly higher than that in smokers with other genotype combinations (Butkiewicz *et al.* 1998).

Taken together, the results of adduct dosimetry and genotyping/phenotyping studies partially support the contribution of PAHs to smoking-associated cancer, in particular cancer of the lower respiratory tract, in humans. The remaining uncertainties cannot be resolved unless the following issues are fully addressed: (i) the ubiquity of confounding exposure to PAHs; (ii) the complexity of exposure to a spectrum of PAHs with different carcinogenic potencies; and (iii) the statistical power criteria for genotyping/phenotyping of the relevant biotransformational and DNA repair enzymes. These, together with the need to validate the currently used surrogate matrices and/or to introduce innovative biological materials, should define the strategy for future research on PAHs, smoking and cancer.

## Summary and conclusions

Although the carcinogenicity of tobacco smoke to humans is no longer a matter of dispute, the identity of the constituents involved in this process still is. Ample studies have attempted to address this issue by dosimetry of smoke-related DNA

adducts and genotyping/phenotyping of the relevant biotransformational enzymes. The majority of these investigations have implicated smoke-derived PAHs in the aetiology of several human cancers, in particular cancer of the lower respiratory tract. The results have been more straightforward when the target tissues have been analysed. Of course, since most target organs for PAH-associated cancers are only invasively accessible, routine biomonitoring of the general population has mainly been achieved by the analysis of the surrogate matrices. To some extent though, the incomparability of exposure patterns and the differences in cell compositions (with varying activation/detoxification and DNA repair capacities) have cast a shadow on the credibility of these matrices to portray the events occurring in the target sites. Such liabilities have introduced biases in the results of many studies. Nevertheless, cautious interpretations of the results have still shed light on the epidemiological observations and helped resolve partially the dilemma of causal/casual relationship between PAH exposure and cancer. This is best exemplified by a single recent nested-case control study in which dosimetry of PAH-DNA adducts in WBC could significantly predict the risk for lung cancer (Tang *et al.* 2001).

In the future, to better understand smoking-induced carcinogenesis in humans and the roles played by chemical carcinogens, large-scale research is needed. Such investigations should be conducted in a multi-disciplinary way to elucidate the impact of specific DNA adducts on target and relevant surrogate matrices, along with genotyping/phenotyping of biotransformational and DNA repair enzymes. Fortunately, great advances in adduct dosimetry techniques, enabling specific and sensitive detection of DNA adducts, together with major breakthroughs in DNA chip technology, which offer high-throughput gene analysis, have partly paved the way to embark upon such investigations.

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