

BENZENE

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4. MECHANISTIC AND OTHER RELEVANT DATA

4.1 Toxicokinetic data

Benzene is extensively metabolized, and the fate of benzene in the body is informed by measurements of various metabolites and of benzene itself. The section on metabolism, metabolic activation, and electrophilicity (Section 4.1.1) therefore precedes the discussion of absorption, distribution, and elimination (Section 4.1.2).

4.1.1 *Metabolism, metabolic activation, and electrophilicity*

The metabolism of benzene is complex ([Ross, 1996](#); [Snyder & Hedli, 1996](#)), as summarized in [Fig. 4.1](#). Qualitatively, the same metabolites are excreted by humans after occupational or environmental exposures and in animals exposed to benzene ([Inoue et al., 1988, 1989](#); [Sabourin et al., 1988, 1992](#); [Henderson et al., 1989](#); [Boogaard & van Sittert, 1996](#)). Accordingly, the discussion below integrates findings from humans and from experimental systems in providing a synthetic overview of the metabolism and activation of benzene.

Metabolism of benzene is required for benzene toxicity. Studies in experimental systems using both pharmacological tools and genetically modified animals indicate that benzene requires metabolism to generate reactive electrophilic intermediates and subsequent toxicity ([Snyder & Hedli, 1996](#); [Ross, 2000](#)). The first step

of benzene metabolism is primarily mediated by cytochrome P4502E1 to form benzene oxide ([Johansson & Ingelman-Sundberg, 1988](#); [Koop et al., 1989](#); [Snyder & Hedli, 1996](#)), although other forms of cytochrome P450 may also play a role ([Gut et al., 1996a](#); [Powley & Carlson, 2001](#); [Sheets et al., 2004](#)). In CYP2E1-knockout mice, urinary benzene metabolites were reduced by approximately 90% with a concomitant complete lack of benzene-induced genotoxicity and cytotoxicity in bone marrow, blood, and lymphoid tissues ([Valentine et al., 1996](#)). Inhibition of CYP2E1-mediated metabolism reduced benzene-induced genotoxicity in mice ([Tuo et al., 1996](#)). Co-administration of toluene, a competitive inhibitor of benzene metabolism, reduced both benzene metabolism and benzene toxicity ([Andrews et al., 1977](#)). In agreement with rodent data that indicated a critical role for metabolism in toxicity, occupationally exposed individuals were more susceptible to benzene toxicity if they had a phenotype corresponding to rapid CYP2E1 metabolism ([Rothman et al., 1997](#)).

The sites of benzene metabolism have also been investigated. Benzene is metabolized in both liver and lung by CYP450 ([Chaney & Carlson, 1995](#); [Powley & Carlson, 2000](#)). Partial hepatectomy reduced both benzene metabolism and benzene toxicity in rats ([Sammatt et al., 1979](#)), indicating that the liver may play a primary role in benzene metabolism. Some metabolites distribute to bone marrow from

hepatic or other sites of generation, and metabolism to electrophiles can also occur in situ in bone marrow (Ross et al., 1996a). In particular, secondary metabolism of phenolic metabolites of benzene via myeloperoxidase (MPO) occurs in bone marrow to generate semiquinone radicals and quinones, providing one potential metabolic mechanism of benzene toxicity (Ross et al., 1996a; Smith, 1999). Metabolism of benzene in situ in rat bone marrow may also occur, and CYP450 has been detected at low levels in bone marrow (Gollmer et al., 1984; Schnier et al., 1989).

The main urinary metabolites of benzene in humans are phenol, hydroquinone, and catechol (the sum of free plus conjugated), *trans,trans*-muconic acid (*t,t*-MA), and *S*-phenylmercapturic acid (SPMA) (Inoue et al., 1988, 1989; Boogaard & van Sittert, 1996). *t,t*-MA and SPMA have been commonly used as biomarkers of benzene exposure in occupational and environmental studies in humans (Inoue et al., 1989; Boogaard & van Sittert, 1996). However, several metabolites have only been observed in experimental animals and/or in vitro. Benzene oxide formed by initial metabolic oxidation exists in equilibrium with its tautomer, oxepin. It can rearrange to generate phenol or undergo ring opening mediated by microsomal epoxide hydrolase to form benzene dihydrodiol; benzene dihydrodiol can spontaneously aromatize, releasing a water molecule to give phenol, and can be further oxidized to catechol and/or to a diol epoxide. Phenol can be further oxidized to catechol, hydroquinone, and benzene-1,2,4-triol. Oxidation of these phenols by MPO in bone marrow and bone marrow progenitor cells (Schattenberg et al., 1994) leads to the formation of semiquinone radicals and electrophilic benzoquinones (Gut et al., 1996b; Smith, 1996). Conjugation with glutathione (GSH) also plays an important role in the metabolism of benzene. Reaction of benzene oxide with GSH leads to SPMA.

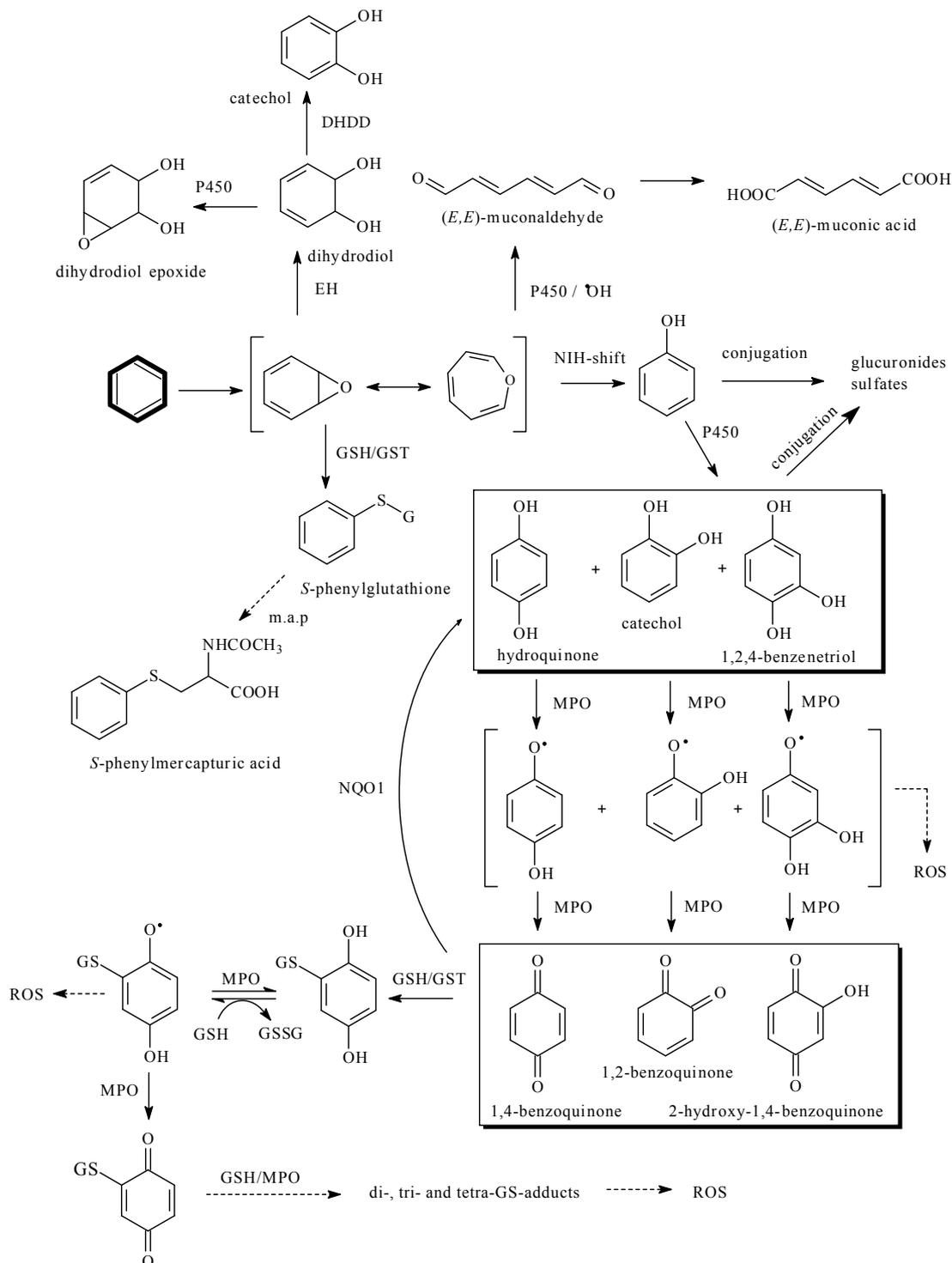
In parallel, benzene oxide or oxepin and/or benzene dihydrodiol can undergo ring opening

reactions to form *trans,trans*-muconaldehyde, which is further oxidized to *t,t*-MA. In studies using both animal and human cells in vitro, quinones generated from polyphenolic metabolites of benzene could be detoxified by NAD(P)H quinone oxidoreductase 1 (NQO1), maintaining them in their hydroquinone forms (Moran et al., 1999). Extensive glucuronidation and sulfation of phenols have been reported in animals and humans (Parke & Williams, 1953a, b; Seaton et al., 1995). GSH is also conjugated with electrophilic quinones (1,2-, 1,4-benzoquinone) leading to the corresponding *S*-(dihydroxyphenyl)glutathione (only one isomer, *S*-(2,5-dihydroxyphenyl) glutathione, is depicted in Fig. 4.1). The multiplicity of electrophilic metabolites formed during benzene metabolism, discussed in the sections that follow, are capable of reaction with GSH, which may occur chemically or be catalysed by glutathione-*S*-transferases (GSTs) (Snyder & Hedli, 1996). Benzene metabolism generates a variety of different reactive electrophiles. Several products of benzene metabolism are electrophilic and can interfere with cellular function.

(a) Epoxides

Benzene oxide is an electrophilic metabolite, identified in vitro when benzene is oxidized by human and mouse microsomes (Lovern et al., 1997) that can spontaneously rearrange to phenol by NIH shift (Jerina & Daly, 1974). It can also form adducts with GSH, cysteine residues in proteins, and DNA (Bechtold et al., 1992a; McDonald et al., 1994; Henderson et al., 2005a; Míčová & Linhart, 2012). The reaction of benzene oxide with soluble thiols such as GSH and *N*-acetylcysteine, followed by dehydration, leads to the formation of *S*-phenylglutathione and SPMA, respectively, although this reaction is relatively inefficient relative to ring opening in the generation of phenol (Henderson et al., 2005a; Míčová & Linhart, 2012). Benzene oxide is a substrate for GSTs (Zarth et al., 2015) and has sufficient stability in blood (a half-life of

Fig. 4.1 Simplified metabolic scheme of benzene



Compiled by the Working Group from [Glatt et al. \(1989\)](#), [Ross \(2000\)](#), [Snyder \(2004\)](#), [Waidyanatha et al. \(2005\)](#), and [Monks et al. \(2010\)](#).
 DHDD, dihydrodiol-dehydrogenase; EH, epoxide hydrolase; GSH, glutathione; GSSG, glutathione disulfide; GST, glutathione-S-transferase; m.a.p., mercapturic acid pathway; MPO, myeloperoxidase; NQO1, NAD(P)H:quinone oxidoreductase 1; P450, cytochrome P450; ROS, reactive oxygen species.

~8 minutes) to reach extrahepatic target sites, as indicated by the production of benzene oxide-protein adducts as biomarkers in animals ([McDonald et al., 1994](#)). Benzene oxide-protein adducts have been found in the blood and bone marrow of mice and rats exposed to benzene ([McDonald et al., 1994](#); [Rappaport et al., 1996](#)), and benzene oxide-haemoglobin and albumin adducts have been detected in the blood of workers exposed to benzene ([Yeowell-O'Connell et al., 1998, 2001](#); [Rappaport et al., 2002](#); [Lin et al., 2007](#)). Benzene oxide can form 7-phenylguanine and other DNA adducts, although its reactivity has been reported to be low relative to its reactions with thiols ([Míčová & Linhart, 2012](#)). Recent work failed to detect 7-phenylguanine in DNA from liver, lung, or bone marrow in mice exposed to benzene ([Zarth et al., 2014](#)). Benzene dihydrodiol epoxide is another putative electrophilic metabolite. Its half-life at nearly physiological conditions (pH, 7.6) was greater than 5 hours ([Waidyanatha & Rappaport, 2005](#)), suggesting it can be distributed to target tissues distal from the initial site of generation.

(b) *Muconaldehyde and other ring-opened products*

Ring opening of benzene resulting in *t,t*-MA as a metabolic end-product ([Parke & Williams, 1952](#)), commonly used as a biomarker of benzene exposure ([Carbonari et al., 2016](#); Section 1.3.1, occurs in vivo. In vitro or animal studies have identified potential metabolic intermediates in the production of *t,t*-MA. [Latriano et al. \(1986\)](#) identified muconaldehyde (*t,t*-MA dialdehyde) in mouse liver microsomes after incubation with benzene. Potential mechanisms of formation include ring opening of benzene oxide or oxepin by cytochrome P450 (CYP) or reactions mediated by oxygen radicals ([Zhang et al., 1995](#); [Golding et al., 2010](#)). Muconaldehyde is a bifunctional aldehyde and a reactive electrophilic compound ([Latriano et al., 1986](#); [Witz et al., 1996](#)) that reacts with thiols and nucleic acids ([Latriano et](#)

[al., 1989](#); [Bleasdale et al., 1993](#); [Henderson et al., 2005b](#); [Monks et al., 2010](#); [Harris et al., 2011](#)). In studies in vitro, each aldehyde functionality in muconaldehyde can be reduced or oxidized to generate alcohol and/or aldehyde (6-hydroxyhexa-2,4-dienoic acid) or acid and/or aldehyde (6-oxohexa-2,4-dienoic acid, muconic acid semi-aldehyde) derivatives that retain some of the electrophilicity of the parent dialdehyde but have greater diffusibility ([Goon et al., 1992](#); [Witz et al., 1996](#)).

(c) *Quinones and semiquinones derived from phenolic metabolites of benzene*

The phenolic metabolites, major metabolites of benzene, have been shown to reach the bone marrow of mice and rats in free or conjugated forms ([Rickert et al., 1979](#); [Sabourin et al., 1988](#)). In isolated mouse and human bone marrow cells, bi- or triphenolic metabolites could be oxidized to quinones via MPO-mediated reactions to form benzoquinones ([Smith et al., 1989](#); [Ross, 1996](#)). Phenol can be metabolized by purified human MPO and horseradish peroxidase to generate 4–4'-diphenoquinone ([Eastmond et al., 1986](#)). Quinones are electrophilic compounds that can interact with thiols, proteins, and nucleic acids ([Sadler et al., 1988](#); [McDonald et al., 1994](#); [Bodell et al., 1996](#); [Monks et al., 2010](#)). Both 1,2- and 1,4-benzoquinone protein adducts have been found in the blood and bone marrow of mice and rats exposed to benzene ([McDonald et al., 1994](#)), and 1,4-benzoquinone protein adducts have been detected in workers exposed to benzene ([Rappaport et al., 2002](#); [Lin et al., 2007](#)). The importance of quinones in humans exposed to benzene was suggested by the observation that individuals carrying a homozygous null polymorphism for the quinone-metabolizing enzyme NQO1, and therefore lacking the ability to detoxify electrophilic quinones, were more susceptible to benzene toxicity ([Rothman et al., 1997](#)). MPO-catalysed oxidation of bi- or triphenolic metabolites of benzene occurs via

semiquinone radical intermediates, which may disproportionate to generate starting compounds together with their respective benzoquinones, or may react with oxygen to generate reactive oxygen species (ROS) (Sawada et al., 1975; Kalyanaraman et al., 1985, 1988; Sadler et al., 1988; Smith et al., 1989; Smith, 1996; Bolton et al., 2000). Hydroquinone induces chromosomal damage in human lymphocytes in vitro (Eastmond et al., 1994; Stillman et al., 1997). Oxidative damage to DNA in human leukaemia HL-60 cells was induced by hydroquinone, phenol, and benzene triol (Kolachana et al., 1993). Benzene triol was the only phenolic metabolite which resulted in oxidative DNA damage in mice when administered alone; however, combinations of phenol and hydroquinone, phenol and catechol, and hydroquinone and catechol were also effective (Kolachana et al., 1993). In vitro treatment of mouse bone marrow with hydroquinone produced the same DNA adducts as found after treatment of mice with benzene (Bodell et al., 1996).

GSH conjugation of quinones is considered a detoxification reaction, and multiple studies of null polymorphisms in GST-T1 and GST-M1 genes resulting in increased benzene toxicity in exposed human populations suggest that GSTs play an important role in the detoxification of reactive benzene metabolites (Wan et al., 2002). However, GST adducts of 1,4-benzoquinone are haematotoxic and have been demonstrated in the bone marrow of mice after administration of benzene (Bratton et al., 1997). GST conjugation of 1,4-benzoquinone primarily generates 2-(S-glutathionyl)hydroquinone, which can undergo sequential oxidation and GST conjugation to produce 2,3,5,6-tetra(S-glutathionyl)hydroquinone as the final diphenolic metabolite. This process occurs via the production of both semiquinone and electrophilic quinone derivatives, which can generate oxidative stress and adducts, respectively (Lau et al., 1988, 2010).

Combined exposure to phenol and hydroquinone reproduced the myelotoxicity of benzene in mice (Eastmond et al., 1987; Legathe et al., 1994) and rats (Lau et al., 1988, 2010). Experiments in vitro showed that phenol increased the oxidation of hydroquinone, catalysed by horseradish peroxidase, as well as the binding of radiolabelled hydroquinone to rat liver protein (Eastmond et al., 1987).

In summary, benzene metabolism can generate a multiplicity of metabolites, many of which are electrophilic.

4.1.2 Absorption, distribution, and elimination

(a) Humans

Benzene is well absorbed in humans by inhalation, or by the oral or dermal routes. Inhalation is the major route of human exposure, and is the only route for which extensive human data are available. In experiments on human subjects, values of respiratory uptake (lung retention) of 47–52% were found at exposure levels ranging from 1.6 to 62.0 ppm (Nomiyama & Nomiyama, 1974; Pekari et al., 1992). For absorption of benzene at 32–69 ppm from smoking cigarettes, a higher uptake of 64% was reported (Yu & Weisel, 1996).

Skin absorption of benzene has also been studied experimentally on human subjects. The absorption rate of liquid benzene by the skin (under conditions of complete saturation) was calculated to be approximately 0.4 mg/cm² per hour. The absorption rate was determined by the amount of urinary phenol excreted, which was not corrected for urinary phenol not derived from benzene (Hanke et al., 1961). In a series of showering experiments using water contaminated with benzene (367 µg/m³) it was estimated that the total benzene dose resulting from a 20-minute shower was approximately 281 µg, about 40% of which was a result of inhalation

and the remaining 60% via skin absorption ([Lindstrom et al., 1994](#)).

Although experimental studies on oral absorption of benzene in humans are not available, case studies of accidental or intentional poisoning indicate that benzene is also absorbed by the oral route ([Thienes & Haley, 1972](#)).

After absorption, benzene is rapidly distributed throughout the human body ([Winek et al., 1967](#); [Winek & Collom, 1971](#); [Pekari et al., 1992](#)). Concentrations of benzene at 3.8 mg/L in blood, 13.8 mg/kg in the brain, and 2.6 mg/kg in the liver were reported in a young male worker who died suddenly from a short exposure to very high air concentrations of the chemical ([Tauber, 1970](#)).

Unmetabolized benzene is primarily excreted in exhaled air, but small amounts were found also in urine ([Nomiyama & Nomiyama, 1974](#)). In contrast, the main portion of the absorbed dose is excreted in the form of water-soluble metabolites in the urine. Human exposure to benzene in air at concentrations of 0.1–10.0 ppm results in urinary metabolite profiles of 70–85% phenol (free + conjugated), 5–10% each of hydroquinone (free + conjugated), catechol (free + conjugated), and *t,t*-MA, and less than 1% of SPMA ([Kim et al., 2006a](#)).

The profile of urinary metabolites may change depending on the level of exposure. When comparing workers occupationally exposed to benzene at more than 25 ppm with those exposed to benzene at less than 25 ppm, [Rothman et al. \(1998\)](#) observed that the ratios of phenol and catechol to total metabolites were significantly higher and the ratios of hydroquinone and *t,t*-MA to total metabolites were significantly lower in workers exposed to higher concentrations. Workers with less than 50 ng/g creatinine phenol in urine, corresponding to a concentration of benzene in air of approximately 10 ppm, were excluded from this analysis because phenol is not specific to exposure to benzene at lower concentrations. The differences in the ratio of each metabolite to total metabolites between

the groups of higher and lower exposure were 0.65 versus 0.61 for phenol, 0.11 versus 0.09 for catechol, 0.13 versus 0.16 for hydroquinone, and 0.11 versus 0.15 for muconic acid. A controlled study of 4 cases exposed to isotopically labelled benzene at 40 ppb resulted in a urinary muconic acid concentration of 3.2–45.0% ([Weisel et al., 2003](#)).

Multiple studies have analysed and reanalysed data first reported in [Kim et al. \(2006a\)](#) to determine if, at lower levels of benzene exposure, a nonlinear relationship exists between exposure to benzene and urinary excretion of unmetabolized benzene, phenol, hydroquinone, catechol, muconic acid, and phenylmercapturic acid. The original data were from 389 workers in Tianjin, China, 250 of whom were from factories using benzene and 139 from factories not using benzene ([Kim et al., 2006a, b, 2007](#)). In their original analysis, [Kim et al. \(2006a, b\)](#) reported nonlinear relationships between benzene exposure and urinary metabolite concentrations, adjusted for background levels based on controls who had been exposed to benzene at less than 3 ppb. Specifically, the ratio of excreted metabolites to benzene exposure increased markedly at exposures to benzene at less than 1 ppm. The presence or absence of nonlinearity for exposures at less than 1 ppm in these data has been the subject of multiple commentaries and reanalyses ([Price et al., 2012](#); [Rappaport et al., 2013a, b](#); [Cox et al., 2017](#); [McNally et al., 2017](#)).

[The Working Group noted that, overall, there are some data suggesting increased metabolism at low exposures, but the data are not definitive.]

(b) *Experimental systems*

Animal data confirm that benzene is efficiently absorbed by inhalation and by oral and dermal routes. Studies in rats and mice showed that gastrointestinal absorption was greater than 97% in both species when the animals were given benzene by gavage (in corn oil) at doses of 0.5–150 mg/kg body weight (bw) per

day ([Sabourin et al., 1987](#)). Low-temperature whole-body autoradiography of ^{14}C -benzene showed that benzene is rapidly distributed in the blood and in well-perfused organs such as the heart muscle, liver, and kidney. A very high level of radioactivity was also observed in the bone marrow, body fat, spinal cord, and white matter of the brain. The radioactivity was rapidly cleared from the central nervous system ([Bergman & Appelgren, 1983](#)). The bioavailability of benzene through the oral route was influenced by adsorption on soil. When radio-labelled benzene in soil (clay soil or sandy soil from New Jersey) was administered to rats by gavage, the area under the curve of plasma radioactivity versus time increased compared with that for benzene suspension in water, a difference that was significant with clay soil. The half-life in plasma was not affected by the type of soil used ([Turkall et al., 1988](#)). After exposing mice repeatedly to benzene, DNA adducts were detected by ^{32}P -postlabelling in peripheral blood, bone marrow, and liver. The adducts were still detectable in leukocytes 21 days after the last exposure ([Li et al., 1996](#)).

4.2 Mechanisms of carcinogenesis

This section summarizes the evidence for the key characteristics of carcinogens ([Smith et al., 2016](#)), discussing whether: benzene induces oxidative stress; is genotoxic; alters DNA repair or causes genomic instability; is immunosuppressive; alters cell proliferation, cell death, or nutrient supply; modulates receptor-mediated effects; induces chronic inflammation; and induces epigenetic effects.

In the consideration of mechanistic studies in exposed humans, the Working Group focused on studies in which the following issues were reasonably addressed in their design and/or analysis: definition and comparability of control groups, statistical power, and confounding by relevant covariates or co-exposures. An additional issue

was whether bias due to disease (i.e. a diagnosis of benzene poisoning) was avoided.

4.2.1 Oxidative stress

Several potential mechanisms may contribute to benzene-induced oxidative stress. Benzene can produce a multiplicity of electrophilic and pro-oxidant metabolites capable of depleting cellular-reduced GSH (see Section 4.1), a critical defence system against oxygen radicals. Hydroquinones can generally autoxidize in pH-dependent reactions to produce hydrogen peroxide ([Song & Buettner, 2010](#)). Polyphenolic metabolites of benzene can generate semiquinone radicals during peroxidase-mediated oxidation ([Yamazaki et al., 1960](#); [Yamazaki & Piette, 1963](#); [Kalyanaraman et al., 1991](#)). The primary fate of 1,2- and 1,4-benzosemiquinone radicals is disproportionation to quinone and hydroquinone, although reaction with oxygen can occur in the presence of superoxide dismutase ([Sawada et al., 1975](#); [Sadler et al., 1988](#); [Subrahmanyam et al., 1991](#)). The semiquinone derived from 1,2,4-benzenetriol has been shown to react with oxygen ([Kalyanaraman et al., 1988](#)), and phenoxy radicals generated during peroxidase-mediated oxidation of phenol can react with GST leading to the generation of thiyl radicals and subsequent production of oxidized GST ([Subrahmanyam & O'Brien, 1985](#); [Sadler et al., 1988](#)). Multiglutathione adducts of 1,4-benzoquinone generated by successive cycles of hydroquinone oxidation and glutathione addition retain the capability to generate active oxygen species and oxidative stress ([Lau et al., 1988, 2010](#)). Metals such as copper (II) and iron (III) may facilitate the production of reactive and oxidizing species, capable of damaging DNA and inducing lipid peroxidation, from hydroquinone and catechol ([Kasai & Nishimura, 1984](#); [Rao & Pandya, 1989](#); [Li et al., 1995](#)).

(a) *Humans*

Oxidative damage to DNA as indicated by 8-hydroxy-2'-deoxyguanosine (8-OHdG) levels has been commonly used as an indicator of oxidative stress. Examples of studies indicating oxidative damage to DNA in occupationally exposed workers or in environmentally exposed urban populations, where DNA damage was correlated with benzene exposure levels and/or metabolic biomarkers of benzene exposure, are listed in [Table 4.1](#). Four studies are further discussed in Section 4.2.3.

Decreases in GST levels, decreased superoxide dismutase, increased lipid peroxidation, and increased ROS in the blood were detected in 428 gasoline filling station workers compared with 78 unexposed controls ([Uzma et al., 2010](#)). The mean benzene exposure over the 12-hour study period in gasoline station attendants was 0.35 ppm (0.12–0.53 ppm). Individual exposure via air sampling was not monitored in controls, but the concentration of benzene in both pre- and post-shift urine and blood in gasoline station attendants was significantly higher than in controls. Both blood and urine benzene concentrations were increased in post-shift samples compared with pre-shift values. Significant correlations were observed between concentrations of benzene in the blood and changes in GST, superoxide dismutase, lipid peroxidation, and ROS ([Uzma et al., 2010](#)).

Exposure to benzene in 43 gasoline station attendants significantly increased DNA damage compared with 28 non-exposed individuals, as indicated by comet assay and micronuclei (MN) induction, increased oxidative protein damage, and decreased antioxidant capacity, including decreased GST levels ([Moro et al., 2013](#); see also [Table 4.2](#)). Gasoline station attendants were exposed to median benzene values of 76.2 µg/m³ compared with 42.0 µg/m³ in controls, and median levels of *t,t*-MA were increased 4.4-fold in gasoline station attendants

compared with the control group ([Moro et al., 2013](#)). Personal benzene exposure and urinary muconic acid levels were directly correlated with increases in oxidative protein damage and decreases in antioxidant capacity ([Moro et al., 2013](#)).

Two cross-sectional studies evaluated the relationship between benzene exposure and mitochondrial DNA (mtDNA) copy number. Compared with controls without occupational exposure to benzene, one study reported higher mtDNA levels in leukocyte DNA from highly exposed (arithmetic mean, 14 ppm) workers in China ([Shen et al., 2008](#)). A second study reported that benzene was associated with increased mtDNA among workers exposed to relatively low levels of benzene in Italy (geometric mean, 21.5 ppb among a group exposed to the highest concentrations) ([Carugno et al., 2012](#)).

(b) *Human cells in vitro*

Benzene metabolites hydroquinone, benzenetriol, and benzoquinone produced ROS in HL-60 cells and enhanced myeloid cell growth ([Wiemels & Smith, 1999](#)). A global proteomic analysis in cells after the addition of benzene revealed an enrichment of proteins involved in oxidative stress response ([Murugesan et al., 2013](#)). Oxidative DNA damage, indicated by the presence of 8-OHdG, has been detected in several studies of human cells in vitro after treatment with benzene metabolites; these are summarized in Section 4.2.2. Both GST and NQO1, which maintain reactive quinones in their reduced form and can also function as a superoxide reductase ([Siegel et al., 2004](#)), are important determinants of hydroquinone-induced toxicity in bone marrow cells ([Ross et al., 1996a, b](#); [Trush et al., 1996](#)). The addition of benzene to human myeloid cells led to the production of ROS, an effect suggested to be due to benzene alone ([Nishikawa et al., 2011](#)).

Table 4.1 Oxidative damage to DNA in humans exposed to benzene

| Oxidized DNA base measured, response, significance | Description of exposed and controls | Benzene exposure levels | Monitoring method | Measure of internal dose | Tissue or cells | Other exposures or biomarkers measured | Comments | Reference |
|---|--|---|--|--------------------------|-------------------|--|--|---------------------------------------|
| <i>(a) Occupational studies</i> | | | | | | | | |
| 8-OHdG Positive Significant correlation $P < 0.01$ between benzene exposure and 8-OHdG ($r, 0.34$) | 65 filling station attendants | Average annual concentration used as a measure of exposure: 0.06–5.85 mg/m ³ (AM \pm SD, 0.45 \pm 0.96 mg/m ³) | Estimated on the basis of seven repeated personal air samples taken at worksite over 1 yr and questionnaire on personal habits | Not used | Urine | Methyl-benzenes | Increased 8-OHdG with increasing benzene exposure; not related to toluene or xylenes | Lagorio et al. (1994) |
| 8-OHdG Positive $P < 0.05$ in medium- and high-dose groups vs controls; not significant in low-dose group | Three exposed groups and controls: low exposure (35 shoe factory workers); medium exposure (24 paint workers in car factory); high exposure (28 shoe factory workers) Controls: 30 university staff | Mean \pm SD: low ($n = 35$), 2.5 \pm 2.4 mg/m ³ ; medium ($n = 24$), 103.3 \pm 50.3 mg/m ³ ; high ($n = 28$), 424.4 \pm 181.7 mg/m ³ | Personal air sampler | Urinary <i>t,t</i> -MA | Blood lymphocytes | Toluene | 8-OHdG significantly correlated with both external and internal measures of benzene; dose–response; higher in women than men exposed to same benzene level; negative correlation of 8-OHdG with toluene levels | Liu et al. (1996) |
| 8-OHdG Positive $P < 0.015$ for coefficient different from 0; adjusted for smoking | Total of 33 men occupationally exposed to gasoline (16 auto mechanics, 14 refinery workers, and 3 gasoline pump repairmen) and 33 male non-occupationally exposed controls | Mean 8-h TWA in workers, 0.13 ppm (range, 0.003–0.6 ppm) Mean exposure of controls 0.002 ppm (range, 0.001–0.003 ppm) | Personal air sampling | Not used | Urine | NR | Late evening/next morning 8-OHdG significant ($P < 0.002$ and $P < 0.02$) relative to pre-shift; no control samples analysed late evening/next morning | Nilsson et al. (1996) |

Table 4.1 (continued)

| Oxidized DNA base measured, response, significance | Description of exposed and controls | Benzene exposure levels | Monitoring method | Measure of internal dose | Tissue or cells | Other exposures or biomarkers measured | Comments | Reference |
|---|--|---|--------------------------------|------------------------------|-----------------|--|---|--|
| Urinary markers of nucleic acid oxidation Positive $P < 0.0001$ | 239 traffic policemen, taxi drivers, and gasoline pump attendants in Parma, Italy | | Urine | Urinary <i>t,t</i> -MA, SPMA | Urine | Cotinine | Significant correlation between urinary metabolites of benzene (<i>t,t</i> -MA and SPMA) and DNA and RNA oxidation products | Manini et al. (2010) |
| 8-OHdG Positive $P < 0.001$ | 31 gasoline service station attendants, 31 petrochemical laboratory workers, and 40 temple workers exposed to incense; controls from an office site with no incense burning in Bangkok, Thailand | Individual benzene exposure (mean \pm SE): gasoline service station attendants, $360.9 \pm 44.7 \mu\text{g}/\text{m}^3$; petrochemical laboratory workers, $78.3 \pm 18.7 \mu\text{g}/\text{m}^3$; controls, $4.5 \pm 0.5 \mu\text{g}/\text{m}^3$ | Area and personal air sampling | Not used | Leukocytes | 1,3-butadiene, PAHs | For occupational exposures, gasoline service station attendants had significantly higher 8-OHdG ($P < 0.001$) than controls; 8-OHdG responding to increasing concentrations of benzene exposure; low to non-detectable 1,3-butadiene and PAHs in gasoline service station attendants and petrochemical laboratory workers | Ruchirawat et al. (2010) |
| 8-OHdG Positive $P < 0.05$ | 43 gas station attendants, 34 taxi drivers, and 22 controls with no occupational exposure, Rio Grande do Sul, Brazil | NR | NR | Urinary <i>t,t</i> -MA | Urine | Carboxy-haemoglobin | Increased 8-OHdG ($P < 0.05$) in gas station attendants and taxi drivers relative to controls; <i>t,t</i> -MA not measured in taxi drivers | Göethel et al. (2014) |

Table 4.1 (continued)

| Oxidized DNA base measured, response, significance | Description of exposed and controls | Benzene exposure levels | Monitoring method | Measure of internal dose | Tissue or cells | Other exposures or biomarkers measured | Comments | Reference |
|--|--|--|-----------------------|---------------------------------------|-----------------------|--|--|---|
| 8-OHdG Negative | 18 fuel tanker drivers, 13 filling station attendants, and 20 non-occupationally exposed controls in Bari, Italy | Benzene exposure, mean \pm SD: drivers, $279.9 \pm 248.6 \mu\text{g}/\text{m}^3$; attendants, $19.9 \pm 15.5 \mu\text{g}/\text{m}^3$; controls, $4.7 \pm 3.0 \mu\text{g}/\text{m}^3$ | Personal air sampling | Urinary <i>t,t</i> -MA, SPMA, benzene | Lymphocytes | NR | No increase in 8-OHdG in benzene-exposed groups relative to controls | Lovreglio et al. (2016) |
| <i>(b) Exposed urban populations</i> | | | | | | | | |
| 8-OHdG Positive (see comments) | 40 individuals living and working in Copenhagen | Median (range) benzene exposure, 2.5 (1.9–3.6) $\mu\text{g}/\text{m}^3$ | Personal air sampling | Urinary <i>t,t</i> -MA, SPMA | Lymphocytes and urine | Toluene, MTBE | Significant correlation between 8-OHdG in lymphocytes (but not urine) and SPMA excretion ($P < 0.04$); no correlation of 8-OHdG with external benzene, toluene or MTBE levels; external benzene was a 5-d cumulative measure while internal markers were measured for only 1 of those days | Sørensen et al. (2003) |
| 8-OHdG Positive (see comments) | Taxi-moto drivers, city residents, and village residents in Cotonou, Benin | Personal benzene exposure, mean \pm SD: taxi-moto drivers, $76.0 \pm 26.8 \mu\text{g}/\text{m}^3$; village residents, $3.4 \pm 3.0 \mu\text{g}/\text{m}^3$ | Personal air sampling | Urinary SPMA, benzene | Lymphocytes | Toluene, xylenes | Significantly higher 8-OHdG in taxi-moto drivers than village residents ($P < 0.05$) | Ayi-Fanou et al. (2006) |

Table 4.1 (continued)

| Oxidized DNA base measured, response, significance | Description of exposed and controls | Benzene exposure levels | Monitoring method | Measure of internal dose | Tissue or cells | Other exposures or biomarkers measured | Comments | Reference |
|---|---|--|--------------------------------|---------------------------------------|----------------------|--|--|---|
| 8-OHdG Positive (see comments) | 109 urban and 62 rural schoolboys in Bangkok, Thailand | Average benzene exposure: 5.50 ± 0.40 ppb in urban vs 2.54 ± 0.23 ppb in rural group | Area and personal air sampling | Urinary <i>t,t</i> -MA, SPMA, benzene | Leukocytes and urine | NR | Level of 8-OHdG in leukocytes was threefold higher in urban vs rural schoolchildren ($P < 0.001$) and was significantly associated with benzene exposure level ($P < 0.05$); urinary 8-OHdG significantly higher in urban vs rural schoolchildren ($P < 0.05$) but no correlation with benzene exposure levels | Buthbumrung et al. (2008) |
| 8-OHdG PAHs were the major contributor to 8-OHdG levels (see comments) | 165 city centre and 111 rural schoolchildren in Bangkok, Thailand | Mean ± SE benzene exposure: city, 19.38 ± 1.11 µg/m ³ vs rural, 8.40 ± 0.61 µg/m ³ | Area and personal air sampling | Not used | Leukocytes | 1,3-butadiene, PAHs | Levels of 8-OHdG were higher in city vs rural schoolchildren ($P < 0.001$); 8-OHdG levels correlated significantly with benzene ($P < 0.001$) and PAH ($P < 0.001$) levels; multivariate analysis identified PAH concentrations as the only factor significantly affecting 8-OHdG levels ($r, 0.895$; $P < 0.05$) | Ruchirawat et al. (2010) |

Table 4.1 (continued)

| Oxidized DNA base measured, response, significance | Description of exposed and controls | Benzene exposure levels | Monitoring method | Measure of internal dose | Tissue or cells | Other exposures or biomarkers measured | Comments | Reference |
|---|---|-------------------------|--|--|-----------------|--|---|--|
| 8-OHdG, 8-oxoGuo Positive (see comments) | 396 children from central Italy districts with different levels of urbanization and air pollution | | Urinary <i>t,t</i> -MA, SPMA, benzene | Urinary <i>t,t</i> -MA, SPMA, benzene | Urine | Cotinine | Multiple linear regression ($P < 0.0001$) indicated that benzene exposure (assessed by urinary SPMA and TTMA) was significantly associated with 8-OHdG and 8-oxoGuo | Andreoli et al. (2012) |
| 8-OHdG, 8-oxoGuo, 8-oxoGua Positive (see comments) | 155 children living close (< 15 km) to an oil refinery, 58 children living 70 km from the refinery and not close to an industrial hub | | Urinary <i>t,t</i> -MA, SPMA, benzene | Urinary <i>t,t</i> -MA, SPMA, benzene | Urine | Cotinine, MTBE | 8-OHdG and 8-oxoGuo significantly correlated with markers of benzene exposure ($P < 0.01$) | Andreoli et al. (2015) |

8-OHdG, 8-hydroxy-2'-deoxyguanosine; 8-oxoGua, 8-oxo-guanine; 8-oxoGuo, 8-oxo-7,8-dihydroguanosine; AM, arithmetic mean; d, day(s); h, hour(s); MTBE, methyl tertiary-butyl ether; NR, not reported; PAHs, polycyclic aromatic hydrocarbons; ppm, parts per million; ppb, parts per billion; SD, standard deviation; SE, standard error; SPMA, S-phenylmercapturic acid; *t,t*-MA, *trans,trans*-muconic acid; TWA, time-weighted average; vs, versus; yr, year(s)

Table 4.2 DNA strand breaks, adducts and mutations in humans exposed to benzene

| End-point Test system | Tissue, cell type | Description of exposed and controls | Results ^a | Agent Concentration (LEC or HIC) | Comments | Reference |
|---|--|---|-------------------------|--|---|--|
| DNA damage/strand breaks DNA elution rate through filters | Blood, peripheral lymphocytes | 20 female shoemakers, 12 of which had an additional dermal exposure, 20 matched controls | + $P < 0.001$ | Benzene and toluene $4.16 \pm 4.15 \mu\text{g}/\text{m}^3$ | No evidence for contribution of skin absorption to the effect | Popp et al. (1992) |
| DNA damage/strand breaks | Blood, the pellet from centrifuged blood | 33 men occupationally exposed to gasoline, 3 unexposed controls (smokers and non-smokers) | $\pm P = 0.2$ | Benzene, VOC from gasoline HIC, 0.6 ppm | No increase overall, but in some benzene exposure subgroups | Nilsson et al. (1996) |
| Mutation/other NN GPA variant cell frequency | Blood, erythrocytes | 44 benzene-exposed workers (23 men and 21 women), 44 matched controls | + $P < 0.05$ (trend) | Benzene 100 ppm-yr | | Rothman et al. (1996) |
| DNA damage/strand breaks Comet assay, tail moment, heavily damaged cell number | Blood, peripheral lymphocytes | 12 gasoline station attendants, unspecified matched controls | + $P = 0.028$ | Benzene, gasoline vapours 0.3 ppm (8h TWA) | | Andreoli et al. (1997) |
| DNA damage/strand breaks Comet assay, percentage of damaged cells | Blood, peripheral lymphocytes | 83 exposed workers (29 low exposure, 29 high exposure, 25 benzene poisonings), 29 controls | + | Benzene HIC $< 300 \text{ mg}/\text{m}^3$ | | Wu et al. (1998) |
| Mutation/oncogene K-ras mutation | Tumour tissue, exocrine cancer of the pancreas, null | 107 patients with exocrine cancer of the pancreas, 83 K-ras mutated and 24 K-ras wildtype; among these, 16 cases were previously exposed to benzene | + $P < 0.05$ | Benzene, possibly other solvents, exposure estimated retrospectively (high, low, none) | Significant for men after the only women exposed to benzene were excluded (OR, 7.07; $P < 0.05$) | Alguacil et al. (2002) |
| DNA damage/strand breaks Alkaline comet assay, comet tail | Blood, peripheral lymphocytes | 133 traffic control policemen exposed to traffic emissions, 59 office policemen | - | Benzene, VOC from traffic HIC $9.5 \mu\text{g}/\text{m}^3$, 7-h TWA | | Carere et al. (2002) |
| DNA damage/strand breaks | Blood, peripheral lymphocytes | 158 petrochemical workers, 50 matched controls | + $P \text{ NR}$ | Benzene $1.75 \pm 3.6 \text{ ppm}$ (inhalation) | NQO1 deficiency correlated with twofold higher SSBs | Garte et al. (2005) |

Table 4.2 (continued)

| End-point Test system | Tissue, cell type | Description of exposed and controls | Results ^a | Agent Concentration (LEC or HIC) | Comments | Reference |
|--|-------------------------------|---|----------------------|--|--|--|
| DNA damage/strand breaks Comet tail moment | Blood, peripheral lymphocytes | 22 clothes vendors, 21 grilled meat vendors, 29 gasoline station attendants, 23 factory workers, 27 controls Schoolchildren: 41 from Bangkok and 30 provincial | + $P < 0.05$ | Benzene, VOCs 5.5 ± 0.4 ppb | DNA repair capacity was also altered in exposed subjects | Navasumrit et al. (2005) |
| DNA damage/adducts Comet assay, olive tail moment | Blood, peripheral lymphocytes | 41 workers from six plants: printing, shoemaking, production of nitrobenzene, benzene, methylene dianiline and carbomer | + $P = 0.001$ | Benzene, different solvents ND | | Sul et al. (2005) |
| DNA damage/adducts ³² P-postlabelling, bulky adducts | Blood, peripheral lymphocytes | 34 taxi-moto drivers from Cotonou, 6 controls from a nearby village | + $P < 0.05$ | Complex mixture containing benzene 76.0 ± 26.8 $\mu\text{g}/\text{m}^3$ | 8-oxo-dG and m ⁵ dC levels were also elevated in the exposed group | Ayi Fanou et al. (2006) |
| DNA damage/adducts Comet assay, olive tail moment | Blood, peripheral lymphocytes | 115 schoolchildren from heavy traffic area in Bangkok, 69 controls from a rural area | + $P < 0.001$ | Benzene, PAHs 17.55 ± 1.29 $\mu\text{g}/\text{m}^3$ | | Ruchirawat et al. (2007) |
| DNA damage/strand breaks SSB by alkaline elution method | Blood, peripheral lymphocytes | 158 petrochemical workers, 50 matched controls | + P NR | Benzene 1.75 ± 3.6 ppm, long-term | NQO1 deficiency correlated with a twofold higher and GSTT1 gene deletion in a 35–40% higher SSBs | Garte et al. (2008) |
| DNA damage/strand breaks Comet assay, tail intensity | Blood, peripheral lymphocytes | 20 petrol station attendants (11 smokers), 20 matched controls (11 smokers) | + $P < 0.05$ | Benzene and other petrol VOCs 0.65 ± 0.47 mg/m^3 | | Keretetse et al. (2008) |
| DNA damage/strand breaks Comet tail length, tail moment | Blood, peripheral lymphocytes | 33 petrochemical industry operators, 28 service station attendants, 21 gasoline pump maintenance workers, 51 non-exposed controls | + $P < 0.008$ | Benzene, VOCs 40 $\mu\text{g}/\text{m}^3$ | | Fracasso et al. (2010) |
| DNA damage/adducts Total DNA adducts | Blood, peripheral lymphocytes | 57 healthy inhabitants of Cotonou (high exposure), 20 suburbans (low exposure), 17 villagers (control) | + $P < 0.001$ | Benzene, PAHs 76 ± 26.8 $\mu\text{g}/\text{m}^3$ | Adducts mainly from exposure to PAHs rather than benzene | Ayi-Fanou et al. (2011) |

Table 4.2 (continued)

| End-point Test system | Tissue, cell type | Description of exposed and controls | Results ^a | Agent Concentration (LEC or HIC) | Comments | Reference |
|---|-------------------------------------|--|----------------------|---|---|---|
| DNA damage/strand breaks Comet assay, mean tail DNA (%) and tail moment | Blood, peripheral lymphocytes | 324 USA Air Force personnel maintenance workers (high), service workers (moderate), others (low exposure) | ± | Jet fuel JP-8 ND | Positive correlation between both pre-shift benzene concentrations in breath and the mean tail DNA (%) and tail moment ($P < 0.05$) | Krieg et al. (2012) |
| DNA damage/strand breaks Comet assay, DNA damage index | Blood peripheral lymphocytes | 43 gasoline station attendants with 9.1 ± 1.1 yr of exposure, 28 controls matched by age, all non-smoking | + $P < 0.001$ | Benzene, VOC 76.20 (54.34–1285.48) $\mu\text{g}/\text{m}^3$ | | Moro et al. (2013) |
| DNA damage/other Comet assay, tail intensity | Blood, peripheral lymphocytes | 18 fuel tanker drivers, 13 filling station attendants, 20 controls with no occupational exposure to benzene | – | Benzene, VOCs, fuel HIC, $280 \pm 249 \mu\text{g}/\text{m}^3$ | Smokers and non-smokers in all groups | Lovreglio et al. (2014) |

^a +, positive; –, negative; +/-, equivocal (variable response in several experiments within an adequate study)

8-oxo-dG, 8-oxo-2'-deoxyguanosine; HIC, highest ineffective concentration; LEC, lowest effective concentration; m⁵ dC, methylated deoxycytosine; ND, not determined; NQO1, NAD(P)H:quinone oxidoreductase 1; NR, not reported; OR, odds ratio; PAH, polycyclic aromatic hydrocarbons; ppb, parts per billion; ppm, parts per million; SSB, single-strand break; TWA, time-weighted average; VOC, volatile organic compounds; yr, year(s)

(c) *Experimental systems*

In rodents, benzene increased oxygen radical generation and lipid peroxidation ([Verma & Rana, 2004](#)). The exposure of mice to benzene via inhalation increased lipid peroxidation and DNA damage in bone marrow ([Yu et al., 2014](#)). The activation of bone marrow phagocytes after the administration of benzene to mice led to increased oxidative stress, nitric oxide generation, and protein-bound 3-nitrotyrosine in bone marrow ([Laskin et al., 1989](#); [Chen et al., 2005](#); [Melikian et al., 2008](#)). Oxidative stress has also been implicated in several effects induced by benzene metabolites in animal cells, including homologous recombination ([Winn, 2003](#)), DNA damage and recombination ([Tung et al., 2012](#)), and altered c-Myb transcriptional activity ([Wan & Winn, 2007](#)). Attenuation of oxidative stress in mice by transgenic overexpression of thioredoxin reductase decreased clastogenic effects and completely suppressed lymphoma of the thymus gland induced by benzene inhalation ([Li et al., 2006](#)).

4.2.2 *Genetic and related effects*

(a) *Oxidative damage to DNA*

(i) *Humans*

Representative studies examining oxidative damage to DNA in either occupationally exposed workers or in environmentally exposed urban populations, as measured by the production of oxidized DNA bases, are described in [Table 4.1](#). Oxidative damage to DNA was detected primarily using the oxidation of guanine residues, and correlated with benzene exposure levels and/or metabolic biomarkers of benzene exposure.

In several occupational studies in [Table 4.1](#) that were the focus of the Working Group's review, discussed in more detail below, significant effects of benzene exposure on oxidative damage to DNA, as indicated by increased 8-OHdG levels

or other oxidized DNA bases, were observed. Dose-response relationships between exposure to benzene and 8-OHdG levels were suggested by [Lagorio et al. \(1994\)](#), [Liu et al. \(1996\)](#), and [Ruchirawat et al. \(2010\)](#).

[Lagorio et al. \(1994\)](#) examined urinary 8-OHdG in a random sample of 65 filling station attendants, and both benzene and methylbenzene exposure levels were calculated from seven personal air samples taken over 1 year. No control group was used in this study. A significant correlation was found between urinary 8-OHdG levels and exposure to benzene ($r = 0.34$; $P < 0.01$).

[Liu et al. \(1996\)](#) demonstrated a dose-response increase in oxidative damage to DNA associated with both external and internal measures of benzene exposure. Lymphocyte 8-OHdG was assessed in blood samples of 87 benzene-exposed workers from shoemaking and car-painting factories and 30 controls from a university staff. Workers from different factories were exposed to different concentrations of benzene; median levels in environments considered to have low, medium, and high concentrations of benzene in air were measured as 2.5, 103.3, and 424.4 mg/m³, respectively.

[Manini et al. \(2010\)](#) measured urinary nucleic acid oxidation in 239 traffic policemen, taxi drivers, and gasoline pump attendants in Parma, Italy. A separate control group was not used. Urinary *t,t*-MA and SPMA were used as internal markers of benzene exposure. Multiple linear regression analyses showed that benzene exposure was associated with oxidative damage to DNA, particularly RNA as indicated by the production of 8-oxo,7,8-dihydroguanosine (8-oxoGuo). The modulating effects of NQO1 and GST polymorphisms on DNA damage and SPMA excretion, respectively, were reported.

[Ruchirawat et al. \(2010\)](#) performed a study of oxidative damage to DNA in multiple populations in Thailand, either primarily exposed to benzene (31 petrochemical laboratory workers and 31 gasoline service station attendants) or

other pollutants (165 city centre and 111 rural schoolchildren, and 40 temple workers exposed to incense). Individuals from an office building with no incense burning were used as a control population. The group exposed to the highest concentrations of benzene (gas station attendants; mean benzene exposure, 360.9 $\mu\text{g}/\text{m}^3$) had higher leukocyte 8-OHdG than control subjects, and both petrochemical laboratory workers (benzene exposure levels, 78.3 $\mu\text{g}/\text{m}^3$) and gas station attendants had significantly higher single-strand break levels and DNA repair capacity.

(ii) *Human cells in vitro*

Several studies have demonstrated that phenolic metabolites of benzene can induce oxidative damage to DNA, as indicated by 8-OHdG formation in cellular systems in vitro. [Zhang et al. \(1993\)](#) demonstrated that 1,2,4-benzenetriol induced 8-OHdG and MN formation in the human leukaemia HL-60 cell line. This and other benzene metabolites (phenol, hydroquinone, catechol) were shown to induce 8-OHdG formation in HL-60 cells ([Kolachana et al., 1993](#)). Catechol was shown to induce 8-OHdG in HL-60 cells ([Oikawa et al., 2001](#)). Hydroquinone induced DNA strand breaks, DNA–protein cross-links, and 8-OHdG formation in human hepatoma HepG2 cells ([Luo et al., 2008](#)), and single-strand breaks, chromosomal aberrations (CAs), and 8-OHdG formation in A549 human lung cancer cells ([Peng et al., 2013](#)).

(iii) *Experimental systems*

Increased 8-OHdG formation was also observed in mouse bone marrow 1 hour after administration of benzene or 1,2,4-benzenetriol ([Kolachana et al., 1993](#)). Although phenol, catechol, and hydroquinone were without effect when administered separately, binary combinations of phenol, catechol, and hydroquinone induced 8-OHdG formation in mouse bone marrow when administered together ([Kolachana et al., 1993](#)).

(b) *DNA binding, DNA strand breaks, and gene mutations*

In several occupational studies of DNA binding, strand breaks, and mutations that were the focus of the Working Group's review, discussed in more detail below, the observed effects could be reasonably attributed to benzene ([Popp et al., 1992](#); [Rothman et al., 1995, 1996](#); [Wu et al., 1998](#); [Table 4.2](#)). The study of [Rothman et al. \(1995, 1996\)](#) showed an apparent dose–response relationship. In this study, glycophorin A gene (*GPA*) loss and subsequent duplication of its NN allele in MN-heterozygous was demonstrated in subjects with long-term occupational exposure to benzene; cumulative exposures ranged from 8 to 3488 ppm-years. The NN *GPA* variant cell frequency was 13.9 ± 1.7 per million cells in workers exposed to benzene versus 7.4 ± 1.1 per million cells in control individuals. In contrast, no significant difference existed between the two groups for the null allele frequency. In this study, benzene produced gene-duplicating mutations, but did not produce gene-inactivating mutations at the *GPA* locus in bone marrow cells of humans.

There are no reports on benzene-specific DNA adducts in exposed humans or in human cells treated with benzene in vitro. However, DNA adducts were detected in human promyelocytic HL-60 cells treated with a mixture of benzene metabolites, hydroquinone and 1,4-benzoquinone, by ^{32}P -postlabelling ([Levay et al., 1991](#)). The adduct formed after treatment of the HL-60 cells with either benzoquinone or hydroquinone was later identified as *N*²-(4-hydroxyphenyl)-2'-deoxyguanosine-3'-phosphate ([Pongracz & Bodell, 1996](#)). Furthermore, two depurinating adducts, namely 7-(3,4-dihydroxyphenyl)-2'-deoxyguanosine and 3-(3,4-dihydroxyphenyl)adenine, were identified in cultured human blood mononuclear cells ([Chakravarti et al., 2006](#)).

In human lymphocytes treated in vitro, benzene and its metabolites hydroquinone, catechol, 1,2,4-benzenetriol, and 1,4-benzoquinone

(but not *t,t*-MA) significantly increased DNA damage (single-strand breaks) in the comet assay ([Anderson et al., 1995](#)). In HeLa cells treated with hydroquinone, the alkaline comet assay also showed significant DNA damage compared with untreated cells ([Galván et al., 2008](#)). In vitro studies on human cells are also listed in [Table 4.3](#).

(c) *Chromosomal damage and cytogenetic effects*

(i) *Humans*

Chromosomal damage

Chromosomal end-points, including sister-chromatid exchanges (SCEs), MN, and CAs, have typically been examined in peripheral blood lymphocytes (PBLs), although some of the benzene studies examined buccal cells, sperm, or other blood cells, such as granulocytes. Two of these end-points, CAs and MN, have been found to be associated with increased cancer risk in humans in large, prospective studies ([Liou et al., 1999](#); [Hagmar et al., 2004](#); [Boffetta et al., 2007](#); [Bonassi et al., 2007](#)). The third end-point, SCEs, is an indicator of effects on DNA; however, the relevance of SCEs to cancer risk is uncertain ([Norppa et al., 2006](#)), and the data for benzene in exposed humans are inconclusive (see [Table 4.4](#)).

Studies that examined structural CAs in humans occupationally exposed to benzene are summarized in [Table 4.4](#). Of this range of occupations, most show increases in CAs associated with jobs involving exposure to benzene, including some large studies (> 100 exposed workers) with significant positive exposure–response relationships (e.g. [Kim et al., 2004a](#); [Rekhadevi et al., 2011](#)).

Similarly, although fewer in number, the majority of studies of MN in humans exposed to benzene show increases in MN frequencies associated with jobs involving benzene exposure (see [Table 4.4](#)). In addition, several large studies have reported significant positive exposure–response

relationships (e.g. [Kim et al., 2008](#); [Rekhadevi et al., 2011](#) in buccal cells; [Zhang et al., 2014](#)).

Aneuploidy was reported in other studies of humans occupationally exposed to benzene that examined specific chromosomes, generally in lymphocytes or sperm (e.g. [Kim et al., 2004b](#); [Xing et al., 2010](#) and in studies of human cells in vitro; see [Table 4.4](#), [Table 4.5](#) and [Table 4.6](#)). [Ji et al. \(2012\)](#) compared aneuploidy results between lymphocytes and sperm in their study population and across other studies, reporting the induction of aneuploidy in different chromosomes in different cell types.

Over 20 studies of human cells in vitro are available, primarily using PBLs although some have used other lymphohaematopoietic cells or cell lines (see [Table 4.5](#)). In vitro studies using benzene without metabolic activation have been inconsistent for chromosomal end-points; however, the few that used S-9 to activate benzene metabolism were uniformly positive. In vitro studies directly assessing the benzene metabolites phenol, hydroquinone, benzoquinone, catechol, and benzenetriol have been consistently positive for the various chromosomal end-points examined, including SCEs (e.g. [Morimoto & Wolff, 1980](#); [Yager et al., 1990](#)). In the study of [Erexson et al. \(1985\)](#), catechol exhibited greater potency in inducing SCEs than benzoquinone, hydroquinone, and benzenetriol, which were in turn more potent than phenol, which was in turn more potent than benzene.

Specific cytogenetic effects

Some studies have examined specific cytogenetic changes in humans exposed to benzene to investigate the mechanisms of benzene carcinogenesis (see [Table 4.6](#)). The cytogenetic changes include alteration of the number of specific chromosomes, loss of particular regions of certain chromosomes, and acquisition of specific translocations.

Among the variety of cytogenetic changes, significant exposure-related trends for -5 , -7 ,

Table 4.3 DNA damage in human cells in vitro

| End-point Test system | Tissue, cell line | Results ^a | | Agent | Concentration (LEC or HIC) | Comments | Reference |
|--|--|------------------------------------|---------------------------------|--|--|--|---|
| | | Without metabolic activation | With metabolic activation | | | | |
| DNA adducts ³² P-postlabelling | Myeloid leukaemia (HL-60) | + | NT | Benzene metabolites (HQ, 1,4-BQ) | HQ, 50 µM per 8 h; 1,4- BQ, 25 µM per 2 h | | Levay et al. (1991) |
| DNA strand breaks Comet assay | Lymphocytes | + | - | Benzene | 12 mM/h | | Anderson et al. (1995) |
| DNA strand breaks Comet assay | Lymphocytes | + | + | 1,2,4-BT | 100 µM per 30 min, <i>P</i> < 0.05 | | Anderson et al. (1995) |
| DNA strand breaks Comet assay | Lymphocytes | + | - | HQ | 200 µM/h | | Anderson et al. (1995) |
| DNA strand breaks Comet assay | Lymphocytes | NT | + | CAT | 1 mM per 2 h | | Anderson et al. (1995) |
| DNA strand breaks Comet assay | Lymphocytes | - | - | 1,4-BQ | 200 µM/h | | Anderson et al. (1995) |
| DNA strand breaks Comet assay | Lymphocytes | NT | + | 1,4-BQ | 0.5 mM per 4 h | | Anderson et al. (1995) |
| DNA strand breaks Comet assay | Lymphocytes | - | - | <i>t,t</i> -MA | 800 µM/h | | Anderson et al. (1995) |
| DNA strand breaks Comet assay, tail moment | Non-proliferating peripheral lymphocytes | + | | Benzene metabolites (HQ, BQ, BT) | LEC: HQ, 0.5 µg/mL; BQ, 0.3 µg/mL; BT, 5.0 µg/mL | | Andreoli et al. (1997) |
| DNA adducts Tandem mass spectrometry | Blood mononuclear cells | + | NT | Benzene metabolite (1,2-BQ) | 75 µM | | Chakravarti et al. (2006) |
| DNA strand breaks Comet assay, tail moment | HeLa cells | + | | HQ | 150 µM per 12 h | WRN depletion increased DNA damage (SSBs by comet assay) | Galván et al. (2008) |

^a +, positive; -, negative

BQ, benzoquinone; BT, benzenetriol; h, hour(s); HIC, highest ineffective concentration; HL, human leukaemia; HQ, hydroquinone; LEC, lowest effective concentration; NT, not tested; SSB, single-strand break; *t,t*-MA, *trans,trans*-muconic acid

Table 4.4 Chromosomal damage in humans exposed to benzene

| Description of exposed and controls | Exposure duration (years) | Exposure in air (ppm) ^a | Cytogenetic effects ^b | | | Comments | Reference |
|---|---------------------------|---|-----------------------------------|-----|----|---|---|
| | | | CA | SCE | MN | | |
| 20 (of 38) workers using benzene as solvent, 5 industrial controls from other areas of plant | 1–20 | NR (mean, ~25–150 in high-exposure area; Tough et al., 1970) | + | NT | NT | Blood samples 2–3 yr after benzene substituted with toluene | Tough & Brown (1965) |
| Factory workers (solvent) and onsite controls G1: 20 exposed, 5 controls (from Tough & Brown, 1965) G2: 12 exposed, 6 controls G3: 20 exposed, 5 controls Controls listed above from other areas of plant; 8 general-population controls | G2: 6–25 G3: 2–26 | G1: ~25–150 in high-exposure area G2: similar to G1 G3: ~12 | G1: see above G2: +/- G3: - | NT | NT | G2: blood samples almost 4 yr after benzene; G3: exposure up to time of study G2: + vs general population; - vs onsite controls; onsite controls also had some exposure, although earlier in time | Tough et al. (1970) |
| 52 workers exposed to benzene, 44 pre-employment control group | 0.1–26 | 2.1 (TWA) | + | NT | NT | + for chromosome breaks (deletions) and other CAs (rings, dicentrics, translocations, exchanges); - for chromatid breaks | Picciano (1979) |
| 22 benzene production workers, 22 controls from metallurgical factory | 11.4 (mean) | 0.2–12.4 (8-h TWA) | + | - | NT | + for chromosome-type CAs; (+) for total CAs; - for chromatid-type | Sarto et al. (1984) |
| 16 non-smoking female benzene-exposed worker, 7 controls | NR | 3–50 | NT | - | NT | | Watanabe & Endo (1984) |
| 66 ethylbenzene production workers, 20 general-population controls of same social position, etc. as exposed | 3–18 | 0.47–11.7 (8-h TWA) | (+) | + | NT | | Jablonická et al. (1987) |
| 66 refinery workers, 33 controls SCE: 28 refinery workers, 23 controls | NR | < 1–10 (TWA) | NT | (+) | NT | | Yardley-Jones et al. (1988) |
| 33 workers exposed to benzene, 15 general-population controls | 10–23 | < 31.3 | + | NT | NT | + for CAs | Sasiadek et al. (1989) |
| 36 non-smoking female shoemakers, 11 factory worker controls | 5.5 (mean) | 3–210 (GM, 54) (one 8-h shift) | NT | - | NT | | Seiji et al. (1990) |
| 66 refinery workers, 33 controls CAs: 48 refinery workers, 29 controls | > 5 | 1–10 (TWA) | + | NT | NT | | Yardley-Jones et al. (1990) |

Table 4.4 (continued)

| Description of exposed and controls | Exposure duration (years) | Exposure in air (ppm) ^a | Cytogenetic effects ^b | | | Comments | Reference |
|--|--|---|----------------------------------|-----|----|--|---|
| | | | CA | SCE | MN | | |
| 20 female shoemakers, 20 general-population controls | 3–NR (mean, 18) | 0.25–5.0 (mean, 1.3) (one 8-h shift) | NT | + | NT | | Popp et al. (1992) |
| 56 workers in plants with other exposures, 20 controls | 10–20 (not clearly reported) (average, 6 h/d as solvent) | < 10 | + | NT | NT | | Sasiadek (1992) |
| 42 benzene distillers at oil refinery, 42 controls | 2–NR | 0.3–15 (mean, 2.3) | + | + | NT | | Major et al. (1994) |
| 49 oil refinery workers, 91 historical controls, 122 industrial controls | 0–2 (<i>n</i> = 10) 2–10 (<i>n</i> = 22) > 10 (<i>n</i> = 17) | 0.9–21.5 in 1990 (start of study) 0.3–5.8 by 1992 | + | + | NT | + in both chromatid- and chromosome-type CAs and achromatic lesions (gaps); followed from 1990 to 1992, during which exposures decreased along with CAs (excluding gaps) and gaps only, but not SCEs | Tompa et al. (1994) |
| 38 high-exposure and 45 low-exposure female shoemakers, 35 worker controls | High exposure, 2–31 (mean, 13.4) Low exposure, 1–33 (mean, 17.7) | High exposure, 2–15 (mean, 8) Low exposure, 2–13 (mean, 5) | + | + | NT | | Karacić et al. (1995) |
| 35 low-benzene (high-toluene) shoeworkers, 24 medium-benzene car painters, 28 high-benzene (low-toluene) shoeworkers, 30 university staff controls | NR | Low, 0.77 (mean) Medium, 32 (mean) High, 133 (mean) (8-h TWA) | NT | NT | + | | Liu et al. (1996) |
| 58 shoemakers, 20 general-population controls | 5–50 | NR | + | NT | NT | | Tunca & Egeli (1996) |
| 437 factory workers, 150 controls | | 0.02–9.2 (mean, 1.4) | NT | NT | + | | Zhang (1996) |
| 49 exposed female shoemakers, 27 controls employed in confectionary industry | 1–33 (mean, 17) | 1.9–14.8 (median, 5.9) (at time of study) | (+) | (+) | NT | | Bogadi-Sare et al. (1997) |

Table 4.4 (continued)

| Description of exposed and controls | Exposure duration (years) | Exposure in air (ppm) ^a | Cytogenetic effects ^b | | | Comments | Reference |
|---|---|--|----------------------------------|-----|----|---|---|
| | | | CA | SCE | MN | | |
| Lymphocytes: 38 petrochemical workers, benzene plant or coke oven workers, 13 controls (included office workers) Buccal: 18 petrochemical workers, benzene plant or coke oven workers, 15 controls (included office workers) | NR | Benzene, 0.8–1.1 Coke, 0.04–0.30 (8-h TWA) | NT | NT | – | Chromosome 9; buccal cells and lymphocytes | Surrallés et al. (1997) |
| 23 painters, 22 factory controls | NR | 0.17–3.06 (TWA, 0.71) | NT | – | NT | | Xu et al. (1998) |
| 12 benzene factory workers, 5 coke oven workers, 8 rural village population controls | Benzene, 0.7–19 (GM, 4.1) Coke, 0.5–30.6 (GM, 4.8) | Benzene, 0.03–9.0 (GM, 0.41) Coke, 0.16–0.53 (GM, 0.31) | + | NT | NT | Chromosomes 1 and 9; blood smear granulocytes and lymphocytes, and stimulated (cultured) lymphocytes; + for breakages in both chromosomes in benzene factory workers in cultured lymphocytes; (+) for chromosome 1 (9 not reported) in benzene factory worker smear cells | Marcon et al. (1999) |
| 44 Chinese workers exposed to benzene, 44 controls 12 Estonian benzene production, 5 coke oven workers, and 8 controls | Estonian benzene production, 6.6 (mean) Estonian coke workers, 11.4 (mean) | Chinese, 31 (median) Estonian benzene production, 4.1 (mean) Estonian coke workers, 1.1 (mean) | – | NT | NT | | Eastmond et al. (2001) |
| 178 petroleum refinery workers, 36 office worker controls | 10.6 (mean) | 0.004–4.52 | + | NT | NT | | Kim et al. (2004a) |
| 82 coke oven workers, 76 controls | 0.75–19.67 (mean, 8) | 0.014–0.743 (GM, 0.557) (8-h TWA) | + | NT | NT | Chromosomes 8, 21 were evaluated; + for t(8,21) translocations | Kim et al. (2004b) |
| 39 ethylbenzene production workers, 55 controls | NR | 0.13–4.7 | + | NT | NT | CAs in high-CA subset decreased 10 mo after improved work conditions | Sram et al. (2004) |
| 10 oil refinery workers, 87 industrial controls, 26 matched controls | 12–28 (mean, 22.8) | 13.7 (mean) in 1994, reduced to 0.56 (mean) in 1995 | + | + | NT | Followed annually from 1990 to 2003; decreased over time as exposures decreased | Tomba et al. (2005) |
| 44 factory workers, 44 factory controls | 0.7–16 (mean, 6.3) (Smith et al., 1998) | 31 (median) 8-h TWA, based on geometric mean of five 8-h measures | + | NT | NT | Chromosomes 2, 4, 6, 11, 12, 14, 18; same study as Smith et al. (1998) and other Zhang et al. studies with different chromosomes evaluated | Zhang et al. (2007) |

Table 4.4 (continued)

| Description of exposed and controls | Exposure duration (years) | Exposure in air (ppm) ^a | Cytogenetic effects ^b | | | Comments | Reference |
|--|---------------------------|------------------------------------|----------------------------------|-----|----|---|---|
| | | | CA | SCE | MN | | |
| 108 petroleum refinery workers, 33 controls | 10.5 (mean) | 0.004–4.52 (shift TWA, 0.51) | + | NT | + | | Kim et al. (2008) |
| 30 petroleum refinery workers, 10 office worker controls | | 0.51 (mean) | NT | NT | + | | Kim et al. (2010) |
| 200 filling station workers, 200 general-population controls | 10.7 (mean) | 0.34–0.47 | + | NT | + | | Rekhadevi et al. (2011) |
| 30 workers in China who used benzene-containing glues, 11 factory controls | > 1–NR | < LOD–23.6 (GM, 2.8) | + | NT | NT | Chromosome 1 in sperm; + for “structural aberrations”, including duplications, deletions, and breaks; (+) for “numerical aberrations” (disomy, nullisomy) | Marchetti et al. (2012) |
| 459 unspecified benzene-exposed workers, 88 controls | | | NT | NT | + | | Zhang et al. (2012b) |
| 385 shoemakers, 197 controls (102 indoor local controls, 95 teachers from Shanghai as external controls) | > 1 | 0.8–17.8 (median, 2.0) | NT | NT | + | | Zhang et al. (2014) |
| 317 shoemakers, 102 office worker controls | > 1 | 0.80–12.09 (median, 1.60) | NT | NT | + | | Zhang et al. (2016) |

^a Benzene exposure level conversion: 1 ppm = 3.19 mg/m³ = 3190 µg/m³

^b +, positive; (+), positive result in a study of limited quality; –, negative

CA, chromosomal aberrations; d, day(s); G1, group 1; G2, group 2; GM, geometric mean; h, hour(s); LOD, limit of detection; MN, micronuclei; mo, month(s); NR, not reported; NT, not tested; ppm, parts per million; SCE, sister-chromatid exchanges; TWA, time-weighted average; vs, versus; yr, year(s)

Table 4.5 Chromosomal end-points in human cells in vitro

| Cells | End-point | Benzene and metabolite(s) | Results ^a | Reference |
|---------------------------------------|---|---|--|---|
| Leukocytes | Combined effects of benzene and radiation on CAs | Benzene | + for CAs | Morimoto (1976) |
| Lymphocytes | QM staining | Benzene | – for SCE, structural CAs | Gerner-Smidt & Friedrich (1978) |
| Lymphocytes | SCEs | Benzene Phenol, CAT, HQ | – for SCE + for SCE | Morimoto & Wolff (1980) |
| Lymphocytes | SCEs | Benzene CAT, HQ | + for SCE with S-9 + for SCE | Morimoto (1983) |
| Lymphocytes | SCEs | Benzene, CAT, HQ, phenol | + for SCE with S-9 | Morimoto et al. (1983) |
| T-lymphocytes | Stained using a modified fluorescence-plus-Giemsa technique for SCE | Benzene, phenol, CAT, BT, HQ, BQ <i>t,t</i> -MA, 4,4'-biphenol, 4,4'-dipheno-quinone, 2,2'-biphenol | + for SCE (+)/– | Erexson et al. (1985) |
| Lymphocytes | Modified MN assay with anti-kinetochore antibody | HQ, phenol, CAT BQ | + for MN and K+ + for MN | Yager et al. (1990) |
| Lymphocytes and HL-60 cells | MN with anti-kinetochore antibody | BT | + for MN and K+ | Zhang et al. (1993) |
| Lymphocytes | FISH (chromosomes 1, 7, and 9) | HQ | + for hyperploidy | Eastmond et al. (1994) |
| Human lymphoblast cell line (GM09948) | FISH with specific probes for chromosomes 5, 7, and 8 | HQ | + for loss of one hybridization signal for chromosomes 5, 7, and 8 | Stillman et al. (1997) |
| Lymphocytes | FISH with centromeric probes for chromosomes 1, 5, 7 and specific probes for 5q31 and 7q36-qter | HQ, BT | + for HQ and BT for monosomy 5 and 7 and –5q and –7q | Zhang et al. (1998b) |
| Human lymphoblast cell line (GM09948) | FISH with specific probes for chromosomes 5, 7, and 8 | CAT HQ | – for CAT for loss of one hybridization signal for chromosomes 5, 7, and 8 + CAT/HQ synergy; – for CAT/HQ hyperploidy [(+) for 8] | Stillman et al. (1999) |
| Lymphocytes | MN | Benzene | – for MN | Zarani et al. (1999) |
| CD34+ and CD34– cells from cord blood | FISH with probes for chromosomes 7 and 8 | HQ | + for monosomy and trisomy 7 and 8 in CD34+; + for monosomy 7 only in CD34–; – for tetrasomy 7 and 8 in both cell types | Smith et al. (2000) |

Table 4.5 (continued)

| Cells | End-point | Benzene and metabolite(s) | Results ^a | Reference |
|---|---|---------------------------|---|---|
| Human CD34+CD19– bone marrow cells | FISH with 5q31, 5p15.2, and centromeric probes specific for human chromosomes 7 and 8 | HQ | + for monosomy 7; + for –5q31; – for monosomy 5; no loss or gain of 8 | Stillman et al. (2000) |
| Lymphocytes | FISH (chromosomes 5, 7, 8, and 21) | BT, HQ, <i>t,t</i> -MA | + for aneuploidy | Chung & Kim (2002) |
| Lymphocytes | CBMN, FISH (chromosomes 7 and 8) | BT | + for MN, aneuploidy | Chung et al. (2002) |
| Metabolites incubated with human topoisomerase II α and then DNA | Measuring DNA cleavage | BT | – | Lindsey et al. (2005) |
| | | HQ | (+) | |
| | | BQ | + for targeting topoisomerase II α | |
| Whole blood | FISH with probes for chromosomes 1, 5, 6, 7, 8, 9, 11, 12, and 21; six chromosomes (1, 5, 7, 8, 9, and 21) analysed for BT and high-dose HQ | HQ | (+) for HQ for monosomy for all chromosomes except 21; ++ for 5, 7, 9, and 11; highest IRRs for 5, 6, and 12 | Zhang et al. (2005) |
| | | BT | + for trisomy for 7, 8, 9, and 21; highest IRRs for 7, 8, 12, and 21; + for BT for monosomy for 5, 7, 8, and 9 but not 1 and 21; highest IRRs for 5 and 7; (+) for BT for trisomy for all chromosomes; no selection for trisomy 8 | |
| Lymphocytes (interphase and metaphase) | FISH with probes for chromosome 1 | Benzene | (+) for MN in interphase cells, aneuploidy in metaphase | Holeckova et al. (2008) |
| HL-60 cells | Gamma-H2AX | HQ, BQ | + | Ishihama et al. (2008) |
| TK-6 cells (lymphoblastoid cell line) | Stained with DAPI, chromosomes 11 and 21 | HQ | + for structural CAs; + for translocations of chromosome 21; – for translocations of chromosome 11 | Ji et al. (2009) |
| Peripheral blood mononuclear cells | CBMN | BQ | + for MN with PMA act of MPO; – for MN without PMA | Westphal et al. (2009) |
| Lymphocytes | umuC test, CBMN assay | Benzene | – for umuC; (+)/– for MN | Bonney et al. (2012) |
| Lymphocytes | MN | Benzene with S-9, HQ | + for MN | Peng et al. (2012) |

^a +, positive; (+), positive result but in a study of limited quality; –, negative

BQ, benzoquinone; BT, benzenetriol; CA, chromosomal aberration; CAT, catechol; CBMN, cytokinesis-blocked micronucleus; DAPI, 4',6'-diamidino-2-phenylindole; FISH, fluorescence in situ hybridization; H2AX, histone H2AX; HL, human leukaemia; HQ, hydroquinone; IRR, incidence rate ratio; K+, kinetochore positive; MN, micronuclei; MPO, myeloperoxidase; PMA, phenylmercapturic acid; QM, QM protein (transcription cofactor inhibiting the activity of AP-1 transcription factors and is also a ribosomal protein participating in protein synthesis); SCE, sister-chromatid exchanges; *t,t*-MA, *trans,trans*-muconic acid

Table 4.6 Cytogenetic changes in humans exposed to benzene

| Description of exposed and controls | Exposure duration (years) | Exposure in air (ppm) ^a | Cytogenetic changes ^b | Comments | Reference |
|--|-----------------------------|--|--|--|---|
| Woman (age, 38 yr) with benzene-induced leukaemia (case study) | | | + for extra chromosomes, mostly in C group (group C trisomy) | All chromosomes | Forni & Moreo (1967) |
| Woman (age, 37 yr) with benzene-induced acute erythroleukaemia (case study) | | | + for cytogenetic changes | All chromosomes | Forni & Moreo (1969) |
| 5 women with benzene haemopathy, diagnosed 5 yr previously, 1 control | NR | NR | + | % aneuploid lymphocytes (40%) decreased from time of diagnosis (70%) | Pollini et al. (1969) |
| 4 women with benzene myelopathy diagnosed 10 yr previously, 1 control | NR | NR | Same subjects as Pollini et al. (1969) | All had lower % aneuploid cells than control | Pollini et al. (1976) |
| 4 women with benzene myelopathy diagnosed 12 yr previously, 1 control | NR | NR | Same subjects as Pollini et al. (1969) | All had lower % aneuploid cells than at previous follow-ups, but closer to control | Pollini & Biscaldi (1977) |
| 33 workers exposed to benzene, 15 general-population controls; all smokers | 10–23 | < 31.3 | + for structural CAs In exposed workers, chromosomes 2, 4, and 9 almost twice as susceptible to breaks; 1 and 2 almost twice as susceptible to gaps; chromosome 18 underrepresented for CAs In unexposed controls, more random distribution of the breakpoints | All chromosomes | Sasiadek et al. (1989) |
| 56 workers in plants, 20 controls | 10–20 (not clearly defined) | < 10 | + for structural CAs (mainly breaks and gaps) and non-random distribution of breakpoints, which accumulated mainly on chromosomes 2, 4, and 7 | All chromosomes | Sasiadek (1992) |
| 58 shoemakers, 20 general-population controls | 5–50 | NR | (+) for polyploidy | All chromosomes | Tunca & Egeli (1996) |
| 18 petrochemical workers (benzene plant or coke oven workers), 15 controls (including some office workers) | NR | Benzene plant, 1.1 (mean) Coke oven, 0.04 (mean) (8-h TWA) | – for chromosome 9 numerical abnormalities | Chromosome 9; buccal cells | Surrallés et al. (1997) |

Table 4.6 (continued)

| Description of exposed and controls | Exposure duration (years) | Exposure in air (ppm) ^a | Cytogenetic changes ^b | Comments | Reference |
|--|--|--|---|--|--|
| 43 Chinese factory workers, 44 other factory controls | 0.7–16 (mean, 6.3) | 1–328 (median, 31) (8-h TWA, based on geometric mean of five 8-h measures) | + dr for hypo- and hyperdiploidy of chromosome 8; hyperdiploidy of chromosome 21; t(8,21), t(8;?), t(21,?), and chromosome 8 breaks but not deletions | Chromosomes 8 and 21; same study population as some Zhang et al. studies (2007 and others), different chromosomes evaluated | Smith et al. (1998) |
| 43 Chinese factory workers, 44 factory controls | 0.7–16.0 (mean, 6.3) | 1–328 (median, 31) (8-h TWA, based on geometric mean of five 8-h measures) | + dr for monosomy 5 and 7 but not 1; trisomy 1, 5, and 7; tetrasomy 1, 5, and 7; –5q; –7q; total structural CAs in 5 and 7 (+) for chromosome 1 breaks at the centromere | Chromosomes 1, 5, and 7; same study population as for some Zhang et al. studies (2007 and others), different chromosomes evaluated | Zhang et al. (1998a) |
| 12 benzene factory workers, and 5 cokery workers; 17/8 rural village population controls | 0.7–19 (GM, 4.1) | 0.0–9.0 (GM, 0.41) | (+) for hyperploidy in both chromosomes 1 and 9 in cultured lymphocytes; (+) for chromosome 1 hyperploidy and breakages (9 not reported) in smear cells; + for breakages in chromosomes 1 and 9 in cultured lymphocytes | Chromosomes 1 and 9; blood smear granulocytes and lymphocytes, and stimulated (cultured) lymphocytes | Marcon et al. (1999) |
| 5 cokery workers, 8 rural village population controls | 0.5–30.6 (GM, 4.8) | 0.16–0.53 (GM, 0.31) | (+) for hyperploidy in both chromosomes 1 and 9 in cultured lymphocytes | | |
| 43 Chinese factory workers, 44 factory controls | 0.7–16 (mean, 6.3) | 1–328 (median, 31) (8-h TWA, based on geometric mean of five 8-h measures) | + dr for monosomy (one hybridization signal) 7 and 8 in metaphase but not interphase + dr for trisomy (3 hybridization signals) 7 and 8 in metaphase and interphase, but more pronounced in metaphase | Chromosomes 7 and 8; same study population as for other Zhang et al. studies (e.g. 2007), different chromosomes evaluated; compared sensitivity of metaphase and interphase FISH, metaphase more sensitive | Zhang et al. (1999) |
| 44 Chinese workers, 44 controls | NR | 1.6–328.5 (median, 31) | (+) dr for hyperploidy in Ch chromosome 1 | Chromosomes 1 and 9 | Eastmond et al. (2001) |
| 12 Estonian benzene production workers, 5 coke oven workers, 8 controls | Benzene workers, 6.6 (mean) Coke workers, 11.4 (mean) | Benzene workers, 4.1 (mean) Coke workers, 1.1 (mean) | | | |

Table 4.6 (continued)

| Description of exposed and controls | Exposure duration (years) | Exposure in air (ppm) ^a | Cytogenetic changes ^b | Comments | Reference |
|--|---|---|--|---|--------------------------------------|
| 82 coke oven workers, 76 controls | 0.75–19.67 (mean, 8) | 0.014–0.743 (GM, 0.557) (8-h TWA) | + for both monosomy and trisomy of both 8 and 21; + for t(8,21) translocations | Chromosomes 8 and 21 | Kim et al. (2004b) |
| 43 factory workers, 44 factory controls | 0.7–16 (mean, 6.3) (from Smith et al., 1998) | 1–328 (median, 31) (8-h TWA, based on geometric mean of five 8-h measures) | + dr for monosomy and trisomy of all 7 chromosomes; + for exposed vs non-exposed for tetrasomy of all 7 chromosomes; some selectivity at lower exposures: only monosomy 6 and trisomy 4, 6, and 11 were + in the < 31 ppm group; + for –6q and t(14;18); – for t(4,11) and t(6,11) | Chromosomes 2, 4, 6, 11, 12, 14, and 18; same study population as for Smith et al. (1998) and other Zhang et al. studies, different chromosomes evaluated | Zhang et al. (2007) |
| 57 Chinese factory workers exposed to benzene (20 low-dose and 37 high-dose), 31 unexposed factory workers (not clearly reported) Subset: 37 benzene-exposed workers, 20 unexposed factory workers (not clearly reported) | NR | Low, 1.8 (mean) High, 21.9 (mean) Subset, 22.6 (mean) | t(14,18) signif ↓ no t(8,21) observed 2 t(15,17), but 1 in unexposed, 1 in exposed | t(15;17) and t(8,21) t(14,18) in subset | McHale et al. (2008) |
| 649 MDS cases, 80 with benzene exposure (13.2%), 29 highly exposed > 21 ppm | High, > 0.5 (mean, 12) | > 21 | – * | –5/5q–, –7/7q–, +8, del(20q) and 11q23/ <i>MLL</i> * – for benzene-exposed vs non-exposed MDS cases | Irons et al. (2010) |
| 30 petroleum refinery workers, 10 office worker controls | | 0.51 (mean) | + for chromosomes 7, 9 for aneuploidy | Chromosomes 7 and 9 | Kim et al. (2010) |
| 33 Chinese male factory workers using benzene-containing glues, 33 factory worker controls | > 1 | < 0.2–23.6 (median, 2.9) (8-h TWA) | + for disomy X and disomy Y; – for disomy 21 | Chromosomes 21, X, and Y in sperm; same population as Ji et al. (2012) (PBL results) | Xing et al. (2010) |
| 47 shoemakers (22 exposed to benzene at < 10 ppm, 25 at ≥ 10 ppm), 27 clothing factory controls | NR | Low, 4.95 (mean) High, 28.33 (mean) (Based on multiple samples over 3 mo) | + selectivity; + dr for monosomy 5, 6, 7, 10, 16, and 19; + dr for trisomy 5, 6, 7, 8, 10, 14, 16, 21, and 22 | All chromosomes; OctoChromosome FISH: chromosome-wide aneuploidy study (CWAS) | Zhang et al. (2011) |

Table 4.6 (continued)

| Description of exposed and controls | Exposure duration (years) | Exposure in air (ppm) ^a | Cytogenetic changes ^b | Comments | Reference |
|---|---------------------------|---|---|--|---|
| 33 Chinese male factory workers, 33 control factory workers | > 1 | < 0.2–23.6 (median, 2.9) (8-h TWA) | (+) for trisomy 21; – for gain X and gain Y | Chromosomes 21, X, and Y; same population as Xing et al. (2010) (sperm results) | Ji et al. (2012) |
| 30 workers in China who used benzene-containing glues, 11 factory worker controls | > 1–NR | < LOD–23.6 (GM, 2.8) | (+) for disomy 1 | Chromosome 1 in sperm | Marchetti et al. (2012) |
| Man (age, 43 yr) with MDS and AML (case study) | 16 (HQ) | | + CAs in chromosomes 5 and 7 | | Regev et al. (2012) |
| 28 shoemakers (18 exposed to benzene at < 10 ppm, 10 at ≥ 10 ppm), 14 clothing factory controls | NR | Low, 2.64 (mean) High, 24.19 (mean) (Based on multiple samples over 3 mo) | + dr for monosomy 7 and 8; no trisomy effects | Chromosomes 7 and 8; in interphase CFU-GM cells | Zhang et al. (2012a) |
| 722 AML cases, 78 with benzene exposure (10.8%), 38 > 0.31 ppm | | | – * | –5/5q–, –7/7q–, +8, del(20q) and 11q23/ <i>MLL</i> ; t(8,21), t(15,17) * – for benzene-exposed vs non-exposed AML cases | Irons et al. (2013) |

^a Benzene exposure level conversion: 1 ppm = 3.19 mg/m³ = 3190 ug/m³

^b +, positive; (+), positive but in a study of limited quality; –, negative

AML, acute myeloid leukaemia; CA, chromosomal aberration; CFU-GM, colony-forming-unit granulocyte-macrophage; CWAS, chromosome-wide aneuploidy study; dr, dose-response relationship; FISH, fluorescence in situ hybridization; GM, geometric mean; h, hour(s); HQ, hydroquinone; LOD, limit of detection; MDS, myelodysplastic syndrome; *MLL*, mixed lineage leukaemia gene; mo, month(s); NR, not reported; PBL, peripheral blood lymphocyte; ppm, parts per million; TWA, time-weighted average; vs, versus

–5q, and –7q, as well as for +8 in PBLs, have been observed ([Zhang et al., 1998a, 1999, 2011](#)). [Zhang et al. \(2012a\)](#) also observed a significant exposure-related trend for –7, but not +7 or +8, in circulating interphase colony-forming-unit (CFU) granulocyte-macrophage (GM) cells, myeloid progenitor cells that are probable targets for the induction of myeloid leukaemia. In independent studies with PBLs, the benzene-associated aneuploidy of chromosome 7 ([Kim et al., 2010](#)) and +8 ([Kim et al., 2004b](#)) were confirmed. [Zhang et al. \(2007\)](#) also observed a significant exposure-related trend for trisomy 12.

In studies on several translocations implicated in some cancers of the lymphoid and haematopoietic tissues, [Smith et al. \(1998\)](#) observed a significant exposure-related trend using fluorescence in situ hybridization testing for t(8,21). This association was independently confirmed by [Kim et al. \(2004b\)](#), but not replicated using polymerase chain reaction analysis ([McHale et al., 2008; IARC, 2012](#)). Similarly, using fluorescence in situ hybridization [Zhang et al. \(2007\)](#) observed a significant exposure-related increase in t(14,18) in the group exposed to the highest concentration of benzene, but this was not replicated in the polymerase chain reaction analyses of [McHale et al. \(2008\)](#). In addition, [Zhang et al. \(2007\)](#) did not observe significant trends for some common translocations involving the *MLL* (mixed lineage leukaemia) gene on chromosome 11q23; however, a significant exposure-related trend was observed for –6q. [McHale et al. \(2008\)](#) did not observe an exposure-related effect on t(15,17).

In vitro studies similarly report certain cytogenetic changes with exposure to benzene or its metabolites. For example, [Chung & Kim \(2002\)](#) reported significant concentration-related trends for –5 and –7, as well as inductions of +8 without significant trends, in human lymphocytes treated with the benzene metabolites hydroquinone, benzenetriol, or *t,t*-MA, although no t(8,21) translocations were observed.

Similarly, [Zhang et al. \(1998b\)](#) reported significant increases in –5 and –7, as well as in –5q and –7q, in human lymphocytes treated with hydroquinone or benzenetriol. [Smith et al. \(2000\)](#) reported that hydroquinone also induced significant positive dose–response relationships in +8 in CD34+ cells and in –7 in both CD34+ and CD34– cells from human cord blood, CD34+ cells being haematopoietic progenitor cells. [Stillman et al. \(1997, 1999\)](#) observed increased –5 and –7 in a human lymphoblastoid cell line from exposure to hydroquinone, but not to catechol. [Stillman et al. \(1999\)](#) further found that catechol acted synergistically with hydroquinone to induce significant positive dose–response relationships in –5 and –7, as well as –5q, which was not observed for hydroquinone alone. A concentration-related trend for +8 was also observed, although it was reportedly not statistically significant. In addition, [Stillman et al. \(2000\)](#) treated human CD34+CD19– bone marrow cells with hydroquinone and reported significant concentration-related trends for –7 and –5q but not –5 or +8; further, a greater susceptibility to hydroquinone-induced –5q and –7 was seen in the bone marrow cells than in the lymphoblastoid cell line. [Zhang et al. \(2005\)](#) exposed lymphocytes in whole blood to hydroquinone or benzenetriol, and reported that chromosomes 5 and 7 were selectively more susceptible to loss induced by those benzene metabolites than several other chromosomes that were examined; further, chromosome 8 was one of a few chromosomes that were more susceptible to gain. Also of note, similar to the findings of [Zhang et al. \(2007\)](#) in workers exposed to benzene, no increases in translocations involving 11q23 were observed in a lymphoblastoid cell line (TK6) treated with hydroquinone ([Ji et al., 2009](#)).

In addition to the investigation of chromosomal end-points in healthy people exposed to benzene, some studies have examined cytogenetic changes in cases of acute myeloid leukaemia (AML) or myelodysplastic syndromes

(MDS) in people who have likely been exposed to benzene. [Zhang et al. \(2002\)](#) reviewed 18 cases of AML attributed to benzene exposure from case reports with cytogenetic analyses. Only 1 of the 18 cases had a normal karyotype ([Zhang et al., 2002](#)), in contrast to some cytogenetic studies which reported over 40% of de novo cases of AML with a normal karyotype ([Schoch et al., 2004](#); [Sanderson et al., 2006](#)). [Zhang et al. \(2002\)](#) also reviewed over 30 abnormal karyotypes from leukaemia patients with likely prior benzene exposure from several large-scale leukaemia studies, and noted that several cases exhibited the same translocation (e.g. t(8,21) for AML and t(9,22) for chronic myeloid leukaemia). Overall, [Zhang et al. \(2002\)](#) found that there were insufficient data from which to discern a specific pattern of clonal chromosomal changes in patients with leukaemia associated with benzene, indicating that benzene produces a variety of cytogenetic changes that may induce or contribute to leukaemogenesis.

[Irons et al. \(2013\)](#) investigated 722 AML cases identified in Shanghai, China and determined that 78 cases had likely benzene exposure. [Irons et al. \(2013\)](#) compared the cytogenetic findings in the 78 cases exposed to benzene first with those from the 644 unexposed cases and then with those from several studies of therapy-related AML. In a subsequent study of 710 of these AML cases, 75 of which were determined to have likely been exposed to benzene, [Kerzic & Irons \(2017\)](#) assessed chromosome breakpoints across 441 identifiable regions. Likewise, [Irons et al. \(2010\)](#) studied 649 MDS cases in Shanghai, China, and determined that 80 cases had likely been exposed to benzene, 29 of which had likely been exposed to high concentrations (> 21 ppm) of benzene. [Irons et al. \(2010\)](#) first compared the cytogenetic findings in the cases exposed to benzene with those from all of the MDS cases. A case–case analysis was then conducted, in which each of the 29 highly exposed cases was matched by age and sex to two cases with no suspected

benzene exposure, and levels of various abnormalities characteristic of t-MDS in the highly exposed cases were compared with levels in the unexposed cases. [The Working Group noted that the implications of the reported comparisons between cases exposed to benzene and unexposed cases are uncertain, given that only a portion of the MDS cases in those exposed to benzene were actually attributable to benzene, which can have a diluting effect.]

(ii) *Experimental systems*

Benzene induced CAs, MN, and SCEs in bone marrow cells of mice, CAs in bone marrow cells of rats, rabbits, and Chinese hamsters, and sperm-head anomalies in mice treated in vivo. Most of the induced aberrations were breaks or deletions. Chromosome-type aberrations also occurred however, particularly after prolonged exposure when toxicity, manifested by a drop in the peripheral blood leukocyte count, appeared. Benzene did not induce SCE in rodent cells in vitro, but it did induce aneuploidy and CAs in cultured Syrian hamster embryo cells. Benzene induced mutation and DNA damage in some studies in rodent cells in vitro. In *Drosophila*, benzene was reported to be weakly positive in assays for somatic mutation and for crossing-over in spermatogonia; in single studies, it did not induce sex-linked recessive lethal mutations or translocations. It induced aneuploidy, mutation, and gene conversion in fungi. Benzene was not mutagenic to bacteria ([IARC, 1982, 1987, 2012](#)). In agreement with a possible role of combinations of multiple metabolites of benzene in genotoxicity, [Barale et al. \(1990\)](#) demonstrated that combinations of phenol and hydroquinone were highly genotoxic to mouse bone marrow as indicated by the formation of MN.

In utero exposure to benzene increased the frequency of MN and SCEs in haematopoietic tissue of fetal and postnatal mice ([Ning et al., 1991](#); [Xing et al., 1992](#)). [French et al. \(2015\)](#) observed a dose-dependent increase in benzene-induced

chromosomal damage and estimated a benchmark concentration limit of 0.205 ppm benzene using Diversity Outbred mice. This estimate is an order of magnitude below the value estimated using B6C3F1 mice.

After exposure of mice to benzene, DNA adducts were detected by ^{32}P -postlabelling in both the bone marrow and leukocytes (Bodell et al., 1996; Lévy et al., 1996). Mild but statistically significant mutagenic responses were found in transgenic mice carrying the *lacI* reporter gene exposed to benzene (Mullin et al., 1995; Provost et al., 1996). The clastogenic potential of benzene is partly due to its metabolites. Specifically, benzene oxide, benzoquinones, muconaldehydes, and benzene dihydrodiol epoxides are electrophiles that readily react with peptides, proteins, and DNA (Bechtold et al., 1992b; McDonald et al., 1993; Bodell et al., 1996; Gaskell et al., 2005; Henderson et al., 2005a; Waidyanatha & Rappaport, 2005), and can thereby interfere with cellular function (Smith, 1996).

The importance of CYP2E1 (see Section 4.1) in inducing benzene toxicity was shown in studies of *Cyp2e1*^{-/-} mice, in which no benzene-induced cytotoxicity or genotoxicity were observed (Valentine et al., 1996). Similar studies showed the importance of NQO1, which detoxifies benzoquinones, proposed toxic metabolites of benzene. Compared with *NQO1*^{+/+} mice, *NQO1*^{-/-} mice exhibited more severe benzene-induced haematotoxicity and were more sensitive to benzene-induced MN formation in peripheral blood cells. These results indicate that NQO1 deficiency results in substantially greater benzene-induced toxicity. However, the specific patterns of toxicity differed between the male and female mice (Bauer et al., 2003). In fact, male mice were more sensitive than females to the induction of MN by benzene administered either orally or intraperitoneally (Meyne & Legator, 1980; Siou et al., 1981). This may be due, at least in part, to a function of greater oxidative metabolism in male mice (Kenyon et al., 1996). Castration of males

reduces their sensitivity to that of females (Siou et al., 1981).

4.2.3 Altered DNA repair or genomic instability

Several DNA reactive metabolites are formed during benzene metabolism, and the type and the frequency of lesions, the respective DNA repair systems involved in their removal, and the repair capacity of the target organ are influenced by the different metabolites (Winn, 2003; Pandey et al., 2009; Au et al., 2010; Hartwig, 2010). Table 4.7 reports examples of in vivo and in vitro studies indicating altered DNA repair or epigenetic alterations related to benzene exposure or its metabolites.

Benzene exposure at occupational and environmental concentrations influences DNA repair systems in human studies in vivo, as reviewed by Ravegnini et al. (2015). In subjects who worked at a spray-painting plant, the exposure to benzene had significantly altered mRNA expression of some critical cell regulatory and DNA repair genes such as *Xpc*, *Xpa*, and *Apel* (Wang et al., 2012). Exposure to a time-weighted average concentration of benzene in a workplace of up to 1.8 mg/m³ may cause chromosomal damage in workers; in particular, the *XRCC1* rs25487 and rs1799782 polymorphisms may be associated with an increase in MN frequency (Huang et al., 2016). Frequencies of MN and CAs in 108 petroleum refinery workers exposed to 0.51 ppm of benzene (full-shift time-weighted average) were higher than in 33 office workers, and the frequencies were influenced by the polymorphism of the *XRCC1* gene (Kim et al., 2008).

In human cell systems and in exposed mice, chemically reactive benzene metabolites, particularly 1,4-benzoquinone and hydroquinone, directly inhibited isolated topoisomerase II (Frantz et al., 1996; Hutt & Kalf, 1996; Eastmond et al., 2001, 2005; Ji et al., 2009). Possible mechanisms of this inhibition include covalent binding

Table 4.7 Studies of benzene or metabolites indicating altered DNA repair, genomic instability, or epigenetic alterations

| Description of exposed and controls Study type Tissue | Benzene exposure (range or median) or its metabolites | Comments | Reference |
|--|--|---|---|
| <i>DNA repair or genomic instability</i> | | | |
| In vitro Isolated topoisomerase II α | BQ, 10 μ M; HQ 10 mM | Metabolites catalytically inhibited topoisomerase II | Baker et al. (2001) |
| In vitro Isolated topoisomerase II α ; human CEM leukaemia | BQ, 0–100 μ M BQ, 10 μ M | BQ strongly inhibited topoisomerase II BQ underwent covalent binding with topoisomerase II α | Lindsey et al. (2004) |
| 108 exposed petroleum refinery workers, 33 controls Occupational exposure | 0.004–4.52 ppm | Both the CA and MN frequencies were significantly higher in exposed compared with unexposed workers and influenced by polymorphism of XCCR1 gene | Kim et al. (2008) |
| Spray painters: A, 46 direct exposed; B, 26 indirect exposed; C, 29 controls Occupational exposure | A, 0.21 \pm 0.19 mg/m ³ ; B, 0.06 \pm 0.12 mg/m ³ ; C, ND | The mRNA expression levels of <i>Rad51</i> , <i>Bcl-2</i> , <i>Bax</i> , <i>Apel</i> , <i>Xpa</i> , and <i>Xpc</i> in groups A and B were downregulated significantly compared with group C | Wang et al. (2012) |
| Haematopoietic stem and progenitor cells, human CD34+ cells In vitro | 0.5–1 mg/mL | DNA breakage | Thys et al. (2015) |
| CD-1 mouse fetal liver cells In vitro | BQ, 5, 15, and 25 μ M | Benzoquinone exposure significantly decreased the transcript levels of 8-oxo-guanine glycosylase | Philbrook & Winn (2016) |
| <i>Epigenetic alterations</i> | | | |
| <i>DNA methylation</i> | | | |
| 78 gas station attendants, 77 urban traffic officers, and 57 controls Occupational exposure | 0.040–0.132, 0.09–0.031, and < 0.006–0.014 mg/m ³ | Airborne benzene was associated with hypomethylation of <i>Line-1</i> and <i>AluI</i> | Bollati et al. (2007) |
| In vitro Human lymphoblastoid TK6 cells | Benzene: 1, 10, and 100 μ M; HQ, 0.005, 0.05, and 0.5 μ M | Benzene and its metabolite HQ exposure induced global DNA hypomethylation in TK6 cells | Tabish et al. (2012) |
| In vitro Human hepatic L02 cells | Benzene, HQ, and BQ: 5, 10, 25, and 50 μ M | HQ and 1,4-BQ, but not benzene, induced global DNA hypomethylation | Hu et al. (2014) |
| <i>Histone modifications</i> | | | |
| In vitro Human myeloid leukaemia HL-60 cells | HQ Single treatment: 1, 5, 15, and 25 μ M Repeated treatment: 1, 5, and 15 μ M four times every 48 h Long-term treatment with 1 μ M: five times a week for 5 wk | Epigenetic modifications (instauration in <i>LINE-1</i> sequences) after in vitro treatment with HQ were transitory and reversible | Mancini et al. (2017) |

BQ, benzoquinone; CA, chromosomal aberration; CEM, human acute lymphoblastic leukaemia cells; h, hour(s); HQ, hydroquinone; *LINE-1*, long interspersed nuclear element-1; MN, micronuclei; ND, not detectable; ppm, parts per million; wk, week(s)

or catalytic action ([Baker et al., 2001](#); [Lindsey et al., 2004, 2005](#); [Chen et al., 2016a](#)).

Benzoquinone exposure significantly decreased the transcript levels of the critical base excision repair gene, 8-oxo-guanine glycosylase, in CD-1 mouse fetal liver cells in vitro ([Philbrook & Winn, 2016](#)); it was also able to rapidly increase ROS production, followed by a statistically significant increase in both c-H2A.X foci and DNA recombination in fetal haematopoietic cells ([Tung et al., 2012](#)).

4.2.4 Immunosuppression

This section focuses on the studies that directly or indirectly inform immune response outcomes, and is divided into haematotoxicity (inclusive of all such data in Section 4), genes related to immune function, and immunoproteins.

(a) Humans

(i) Haematotoxicity

Acute exposure to benzene has been associated with diseases and symptoms in the blood-forming system such as aplastic anaemia, specific cytopenias, and pancytopenia ([Aksoy et al., 1971](#); [Yin et al., 1987](#); [IARC, 2012](#)). These diseases are associated with a functional reduction in immune competence by virtue of the reduced number of immunocompetent cells resulting from impaired haematopoiesis ([IARC, 2012](#); [McHale et al., 2012](#)). In addition, several studies have found that various levels of severity of benzene-associated haematotoxicity have been associated with a future risk of developing a haematological malignancy or related disorder ([Aksoy & Erdem, 1978](#); [Yin et al., 1987](#); [Rothman et al., 1997](#)).

Many studies investigating the association between benzene exposure and altered blood cell counts reported haematological changes in exposed humans, especially at relatively high levels of exposure (e.g. > 10 ppm) ([Rothman et al., 1996](#); [Ward et al., 1996](#); [Qu et al., 2002](#); [Lan](#)

[et al., 2004](#)); some studies have demonstrated that haematological alterations can also occur at lower levels of exposure (< 10 ppm) ([Ward et al., 1996](#); [Zhang, 1996](#); [Qu et al., 2002](#); [Lan et al., 2004](#); [Miao & Fu, 2004](#); [Uzma et al., 2008](#); [Robert Schnatter et al., 2010](#); [Chen et al., 2012](#); [Wang et al., 2012](#); [Zhang et al., 2016](#)). In particular, leukocyte counts were consistently reduced in an exposure-related manner ([Rothman et al., 1996](#); [Ward et al., 1996](#); [Qu et al., 2002](#); [Lan et al., 2004](#); [Robert Schnatter et al., 2010](#)). Reductions in leukocyte counts were observed with median benzene air concentrations of 1.2 ppm in [Lan et al. \(2004\)](#) and 3.8 ppm (4-week average) in [Qu et al. \(2002\)](#), with lowered counts in subgroups of workers exposed to less than 1 ppm. Decreased neutrophil counts were associated with benzene exposure down to a level of about 7.8–8.2 ppm ([Robert Schnatter et al., 2010](#)). However, numbers of band neutrophils, which are precursors and later mature into granulocytes, were increased as well as mean corpuscular volume ([Bogadi-Sare et al., 2003](#)).

A few studies reported no statistically significant differences in blood cell counts ([Hancock et al., 1984](#); [Kipen et al., 1989](#); [Biró et al., 2002](#)). Additionally, several studies reported no or minimal changes in haematological parameters in workers with occupational exposures of less than 5 ppm, in particular, less than 1 ppm. Several of these studies used historical haematological data collected as part of routine surveillance ([Collins et al., 1991, 1997](#); [Tsai et al., 2004](#); [Swaen et al., 2010](#)). [The Working Group noted that the timing of collection of blood samples relative to the most recent benzene exposure was not reported.]

Total lymphocyte counts were reduced in humans exposed to benzene ([Rothman et al., 1996](#)). Numbers of circulating CD19+ B-lymphocytes were consistently reduced in several studies ([Rothman et al., 1996](#); [Bogadi-Sare et al., 2000, 2003](#); [Lan et al., 2004](#)). CD4+ T-lymphocytes were consistently decreased in

multiple studies ([Luan, 1992](#); [Lan et al., 2004](#); [Kirkeleit et al., 2006](#); [Uzma et al., 2008](#); [Chen et al., 2007, 2012](#); [Wang et al., 2012](#)); however, CD8+ T-lymphocyte populations were increased ([Chen et al., 2012](#)). In a study of paint factory workers exposed to benzene, a continual increase in the percentage of CD8+ T-cells measured every 4 months for a year was observed ([Chen et al., 2012](#)). No significant change in absolute number of CD8+ cells was observed in other studies (e.g., [Chen et al., 2007](#)). The decreased CD4+ and increased CD8+ T-cells resulted in a lowering of the CD4+/CD8+ ratio ([Luan, 1992](#); [Lan et al., 2004](#); [Chen et al., 2007, 2012](#); [Wang et al., 2012](#)). Increased CD3+ lymphocytes were additionally noted ([Chen et al., 2012](#)).

Benzene exposure also reduced T-cell receptor excision circles (TREC), a marker of T-cell maturity. Decreased TRECs in peripheral blood mononuclear cells (PBMCs) of patients with benzene poisoning were found in two separate studies, suggesting impaired T-cell immune function ([Li et al., 2005, 2009a](#)). Decreased TRECs were also found in the peripheral blood mononuclear cells in 62 workers exposed to benzene at a concentration in air of 1.72–37.8 mg/m³ compared with 11 healthy controls ([Han et al., 2004](#)). However, [Lan et al. \(2005a\)](#) reported no significant difference in TREC levels in shoe factory workers exposed to benzene at a mean concentration in air of 15.8 ppm.

Relatively low levels of benzene (i.e. < 5 ppm) could result in haematological suppression after continuous exposure with no observed threshold for a response ([Ward et al., 1996](#)). Most types of blood cells, with the exception of leukocytes, from complete blood count levels were decreased in workers exposed to benzene, correlated with length of employment ([Khuder et al., 1999](#)).

Overall, decreased red blood cell counts ([Rothman et al., 1996](#); [Khuder et al., 1999](#); [Qu et al., 2002](#); [Miao & Fu, 2004](#); [Koh et al., 2015](#)), platelets ([Rothman et al., 1996](#); [Qu et al., 2002](#); [Uzma et al., 2008](#); [Ye et al., 2008](#); [Chen et al.,](#)

[2012](#); [Wang et al., 2012](#)), and haemoglobin content ([Bogadi-Sare et al., 2003](#); [Wang et al., 2012](#); [D'Andrea & Reddy, 2016](#)) were consistently reported. Benzene exposure increased haemoglobin content and platelets. Haemoglobin content and red blood cell counts in workers who had been exposed to benzene for longer periods were significantly increased compared with controls ([Uzma et al., 2008](#)). Chemical and rubber factory workers who had been exposed to benzene at 0.07–872.0 mg/m³ (median level, 7.4 mg/m³) had reduced red blood cell count and mean platelet volume, the most affected haematological peripheral blood parameters ([Robert Schnatter et al., 2010](#)).

Finally, several studies examined circulating haematopoietic stem and/or progenitor cells, which may also be affected in individuals exposed to benzene. In a cross-sectional study of 17 petroleum refinery workers exposed to very low levels of benzene (0.28–0.41 ppm), increased burst-forming-unit erythroid and CFU-GM colonies without any growth stimulation were observed compared with 20 unexposed controls; this effect was not observed after the addition of growth factors, either erythropoietin (EPO) or granulocyte colony-stimulating factor ([Quitt et al., 2004](#)). However, another study of 10 subjects with occupational exposure to more than 10 ppm benzene (mean, 24.2 ppm), 19 subjects with exposure to less than 10 ppm benzene (mean, 2.6 ppm), and 24 controls with no occupational exposure to benzene reported an inverse monotonic exposure–response relationship with haematopoietic progenitor cell colony formation in cultured peripheral blood, including: CFU granulocyte, erythroid, macrophage, and megakaryocyte (with EPO stimulation); CFU-GM (with and without EPO stimulation); and burst-forming-unit erythroid cells (with EPO stimulation) ([Lan et al., 2004](#)).

(ii) *Genes related to immune function*

Several studies have investigated human susceptibility to benzene exposure and its relationship with single-nucleotide polymorphisms in genes that encode immune-related proteins. For instance, the tumor necrosis factor alpha (TNF- α) single-nucleotide polymorphism was associated specifically with an increased risk of persistent benzene-induced dysplasia in workers (Lv et al., 2007), and a significantly higher frequency of TNF- α was observed in benzene-poisoned patients (Lv et al., 2005).

Corresponding to altered leukocyte counts in benzene-exposed shoe factory workers, changes were reported in the expression of various genes, including the vascular cell adhesion molecule VCAM1, interleukin (IL)-1A, IL-4, IL-10, IL-12A, CSF3, MPO, and CRP (Lan et al., 2005b; Shen et al., 2011). Gene expression related to T-cells was also altered. The distributions of the T-cell receptor variable (TCRV) family TCRV α , TCRV β , and TCRV γ gene repertoires in individuals exposed to benzene were significantly lower compared with the reference group (Chen et al., 2006; Li et al., 2007, 2008, 2009b). PBMC gene expression levels of CD3 δ , CD3 ϵ , and CD3 ζ were increased in workers exposed to benzene versus controls; in workers diagnosed with benzene poisoning, however, some regions were decreased in severe cases and other regions were unchanged (i.e. CD3 γ and CD3 ϵ) in mild cases (Li et al., 2012). CXCL16, a gene responsible for encoding a chemokine that activates T-cells and natural killer cells, was found to be consistently upregulated in workers exposed to benzene (Forrest et al., 2005; McHale et al., 2009).

(iii) *Immunoproteins*

Regarding B-cell effects, immunoglobulin (Ig) G production was positively correlated with air benzene levels (Bogadi-Sare et al., 2000). Increased IgG was also reportedly correlated with benzene urinary metabolite *t,t*-MA measured in petrochemical workers exposed to

benzene (Dimitrova et al., 2005). IgM and IgA were reduced in cargo tank workers exposed to benzene (Kirkeleit et al., 2006). Furthermore, one study reported that plasma concentrations of soluble CD27 and CD30, two immune markers indicative of B-cell activation, were decreased by 17% for sCD27 but non-significantly reduced for sCD30 in the group exposed to the highest concentration of benzene (≥ 10 ppm) compared with control workers, after adjusting for age and sex (Bassig et al., 2016). [The Working Group noted that several prospective cohorts, although not specifically related to benzene, found that higher levels of sCD27 were associated with increased risk of non-Hodgkin lymphoma (Purdue et al., 2011; De Roos et al., 2012; Bassig et al., 2015a; Hosnijeh et al., 2016; Späth et al., 2017).]

Similar to effects in cytokine gene expression, cytokine serum concentrations were also modified. TNF production was significantly reduced in paint factory workers exposed to benzene vapours (Haro-García et al., 2012). IL-10 serum concentrations were positively correlated with the number of working years in those exposed to benzene (Spatari et al., 2015).

(b) *Human cells in vitro*

Alterations in cytokine production were also observed in studies of human cells in vitro. Both IL-1 α and IL-1 β were decreased in human blood monocytes after exposure to hydroquinone (Carbonnelle et al., 1995). Catechol, hydroquinone, 1,2,4-benzenetriol, and *p*-benzoquinone were also found to stimulate the production of T-helper cell (Th2) cytokines IL-4 and IL-5 (Gillis et al., 2007).

Supporting the haematotoxicity observed in humans, phenol, hydroquinone, and 1,2,4-benzenetriol decreased haemoglobin synthesis in K562 cells in a concentration-dependent manner (Wu et al., 2011). CD34+ haematopoietic progenitor cells treated with hydroquinone inhibited erythroid differentiation in an

exposure-related response, and miRNA-451a and miRNA-486-5p were upregulated during erythroid differentiation ([Liang et al., 2017](#)).

(c) *Experimental systems*

(i) *Mouse*

Several murine studies demonstrated consistent immunosuppressive effects on assays for humoral and cell-mediated immune function after oral and inhalation exposure. The only animal study to evaluate the effect of benzene exposure on the ability of T-cells to respond to a tumour challenge was conducted by [Rosenthal & Snyder \(1987\)](#), who exposed C57Bl/6 male mice to three concentrations (10, 30, and 100 ppm) of benzene for 100 days before tumour challenge. Inhalational exposure to 100 ppm increased lethal tumour incidence, which suggests reduced tumour surveillance ([Rosenthal & Snyder, 1987](#)). Further examination demonstrated that the same benzene concentration reduced T-cell cytolytic activity after 20 days of exposure, and reduced proliferative responses in the spleen in the mixed lymphocyte reaction ([Rosenthal & Snyder, 1987](#)). These reductions in cytotoxic and proliferative activity all occurred without any corresponding changes in the total number of T-cell or lymphocyte subpopulations in the spleen ([Rosenthal & Snyder, 1987](#)). In addition, [Rosenthal & Snyder \(1985\)](#) also demonstrated that 9 days of continuous inhalation exposure to benzene reduced cell-mediated immunity to bacterial infection. Exposure to benzene at several concentrations (30–300 ppm) increased bacterial load after a 4-day infection by the intracellular pathogen *Listeria monocytogenes*. Accompanying this effect, total lymphocytes and T- and B-cell populations were all reduced in the spleen for up to 7 days post-infection under the same benzene exposure concentrations ([Rosenthal & Snyder, 1985](#)).

Changes in assays for humoral immune function were first observed in BALB/c male mice

after inhalation exposure to benzene at concentrations of 50 or 200 ppm for 14 days ([Aoyama, 1986](#)). Seven days after immunization with sheep red blood cells (SRBC), both benzene concentrations reduced IgM SRBC-specific plaque-forming cells (PFC) by up to 87% relative to controls, and IgG PFCs were reduced by approximately 94% ([Aoyama, 1986](#)). IgG PFCs remained suppressed 10 days after immunization, and IgM PFCs were not significantly different from controls. Reductions in total lymphocytes and B- and T-cells in the blood were also observed at the same concentration.

The oral exposure database of assays for immune function is less robust than that for inhalation; only one study has reported reduced humoral immunity. Male CD-1 mice were exposed to benzene in drinking-water at a concentration of 166 mg/L (the only tested dose) for 28 days, resulting in reduced IgM SRBC-specific PFCs as well as anti-SRBC antibody titres ([Hsieh et al., 1990](#)). Reductions were also observed in the mixed lymphocyte response and T-cell proliferation in response to concanavalin A and phytohaemagglutinin stimulation, and in the B-cell proliferative responses to pokeweed mitogen and lipopolysaccharide stimulation. In addition, benzene exposure increased serum corticosterone, which is known to suppress immune function ([Hsieh et al., 1991](#)). Different results were observed in a study of BALB/c male mice exposed to benzene by oral gavage at a concentration of 150 mg/kg bw per day (8 hours per day/5 days a week, for 2 weeks); no changes in total serum antibody titres were reported, but reduced counts of leukocytes, total lymphocytes, monocytes, and neutrophils in the blood were observed ([Wen et al., 2016](#)). In C57BL/6 mice exposed orally to benzene at 27 mg/kg bw per day for 28 days, briefly increased splenic natural killer cell activity was observed by day 21 and splenic production of IL-2 was reduced by day 28 ([Fan, 1992](#)).

The haematotoxic effects of benzene exposure are well established in experimental animals ([Cronkite et al., 1985](#); [Farris et al., 1997a](#)). Rats and mice of both sexes exhibited leukocytopenia and anaemia after subchronic inhalation exposure, but only mice demonstrated evidence of severe femoral hypoplasia ([Ward et al., 1985](#)). Nucleated bone marrow cells were significantly reduced in B6C3F₁ mice after inhalation exposure at a concentration of 100 ppm benzene for 8 weeks ([Farris et al., 1997a](#)). From analysis of the differentiation and maturation of haematopoietic precursor cells, exposure to benzene at 200 ppm for 8 weeks resulted in a sustained reduction of the primitive precursor CFU high proliferative progenitor cells, downstream progenitor CFU-GM cells, bone marrow granulocytes, and leukocytes in the blood ([Farris et al., 1997a](#)). In C57BL/6 mice exposed intraperitoneally to hydroquinone at 50 mg/kg bw per day or to benzene at 600 mg/kg bw per day for 2 days, or in DBA/2J mice exposed to benzene at 10 ppm via inhalation for 5 days, CFU-GM proliferation was not significantly affected but differentiation was significantly increased ([Dempster & Snyder, 1991](#); [Hazel et al., 1996](#)). When Swiss Webster mice of both sexes were exposed to benzene in utero at 10 ppm and re-exposed to benzene at 10 ppm at age 10 weeks, greater reductions in splenic CFU-GM were observed compared with mice that were not exposed to benzene in utero ([Keller & Snyder, 1986](#)). Intraperitoneal exposure to benzene increased the production of nitric oxide in bone marrow cells, which may contribute to the reduced proliferation ([Punjabi et al., 1994](#)). Benzene exposure was also found to suppress the progenitor cell cycle of CFU-GM in the bone marrow of C57BL/6 mice by overexpressing the cyclin-dependent kinase inhibitor p21 ([Yoon et al., 2001](#)).

(ii) Rat

Two rat studies examined the effect of benzene exposure on assays for immune function: one oral and one inhalation. In male Wistar rats exposed to a single dose of benzene in drinking-water at 0.6 mL/kg of drinking water per day for 90 days, reductions in the total number of SRBC-specific antibody-forming cells in the spleen by 40%, and in the total anti-SRBC serum titres by 64% after immunization with SRBC (immunization protocol not specified), were observed ([Karaulov et al., 2017](#)). Cell-mediated immunity, assessed by the delayed-type hypersensitivity response, was also reduced by 52% compared with controls. [Karaulov et al. \(2017\)](#) additionally examined the effect of benzene exposure after 45, 90, and 135 days by stimulating splenocytes *ex vivo* with the concanavalin A; increased cytokine production of IL-4 and IL-6 and a reduced number of CD4+ T-cells were reported for all time periods.

In male Sprague-Dawley rats exposed to benzene via inhalation at a range of concentrations (30–400 ppm) for 2 or 4 weeks, no changes in anti-SRBC serum antibodies were induced ([Robinson et al., 1997](#)). However, the highest tested concentration reduced the numbers of splenic B-cells after 2 and 4 weeks of exposure and of CD4+/CD5+ T-helper cells after 4 weeks of exposure.

4.2.5 Altered cell proliferation, cell death, and nutrient supply

(a) Humans

Representative studies were included if the biological end-point was considered relevant for this key characteristic (studies of peripheral blood cell counts, benzene poisoning, cultured haematological progenitor cells, and genetic susceptibility to these events are presented in Section 4.2.4(a)). The Working Group focused on studies in which presence of benzene in the

study population was documented, the presence of co-exposures was evaluated and addressed, the control group was comparable to the exposed study population, and the study had adequate statistical power.

A case series report in China of 23 subjects with a history of benzene poisoning, with quantitative data for 17 subjects indicating very high exposure to benzene before diagnosis (i.e. concentration in air at 50–300 ppm), described a distinct pattern of bone marrow dysplasia including marked dyserythropoiesis, eosinophilic dysplasia, and abnormal cytoplasmic granulation of neutrophilic precursors. In addition, clonal and oligoclonal proliferation in bone marrow T-lymphocytes, including clonal rearrangements in T-cell receptor gene segments, was present in 14 out of 23 cases ([Irons et al., 2005](#)).

Several cross-sectional studies of workers with occupational exposure to benzene and unexposed controls measured miRNA in peripheral leukocytes or plasma and mRNA in leukocytes, and found altered levels of these end-points for genes that play a role in apoptosis; these studies provided indirect evidence of the possible influence of benzene on apoptosis in healthy subjects ([Forrest et al., 2005](#); [Sun et al., 2009](#); [McHale et al., 2011](#); [Wang et al., 2012](#); [Li et al., 2014](#); [Chen et al., 2016b, 2017](#); [Hu et al., 2016](#); [Liu et al., 2016](#)).

In studies in vitro, benzene or its metabolites induced apoptosis in CD34+ human bone marrow progenitor cells, PBLs, PBMCs, bone marrow mesenchymal stem cells, and HL-60 human promyelocytic leukaemia cells ([Moran et al., 1996](#); [Ross et al., 1996a](#); [Wiemels & Smith, 1999](#); [Bratton et al., 2000](#); [Nishikawa et al., 2011](#); [Hu et al., 2012](#); [Lee et al., 2012](#); [Peng et al., 2012](#); [Zolghadr et al., 2012](#)). Inhibition of nuclear-factor kappa-light-chain-enhancer of activated B-cells (NF- κ B) by hydroquinone sensitizes human bone marrow progenitor cells to TNF- α -induced apoptosis ([Kerzic et al., 2003](#)). Inhibition of DNA-dependent protein kinase,

catalytic subunit, potentiated the apoptotic and growth inhibitory effects of hydroquinone in proerythroid leukaemia K562 cells ([You et al., 2013](#)). Apoptosis was prevented when NQO1 was induced by hydroquinone in KG-1a human promyeloblastic leukaemia cells. Induction of NQO1 by hydroquinone in human bone marrow cells depends on its genotype ([Moran et al., 1999](#)); in cells with a T/T genotype, NQO1 activity and protein were not detected ([Ross et al., 1996b](#); [Traver et al., 1997](#)). This finding is consistent with the observation that the NQO1 null genotype increases the risk of benzene poisoning (i.e. haematotoxicity) ([Rothman et al., 1997](#)).

The benzene metabolite orthoquinone stimulated hyperproliferation of human mononuclear cells cultured with T- and B-cell mitogens ([Chakravarti et al., 2006](#)).

(b) *Experimental systems*

Benzene is reported as a bone marrow depressant as it decreases cell counts in circulating blood, bone marrow, and haematopoietic progenitor cells of animals treated with benzene ([IARC, 1982](#)). The cycling fraction of bone marrow or progenitor cells is also suppressed during exposure to benzene, although this suppression is rapidly reversed when exposure to benzene ceases ([Moeschlin & Speck, 1967](#); [Irons et al., 1979](#); [Cronkite et al., 1982](#); [Lee & Garner, 1991](#); [Farris et al., 1997a](#)). Suppression of the number of progenitor cells as well as of their cycling fraction is induced by a p53-mediated checkpoint for damaged cells ([Kastan et al., 1991](#); [el-Deiry et al., 1994](#)), as evidenced by the lack of suppression of either parameter in the Trp53 knockout mouse ([Yoon et al., 2001](#)). On and off regulation of Trp53 therefore results not only in the direct suppression of haemopoiesis but also in a dynamic recovery proliferation after suppression of haemopoiesis during and after benzene exposure in wildtype mice. These dynamic changes may be responsible for the oscillatory proliferation of bone marrow cells to

counter any additional epigenetic haematopoietic neoplastic impacts (Yoon et al., 2001). Indeed, the studies of Snyder and co-workers (Snyder et al., 1981; Dempster & Snyder, 1990) demonstrated that exposing mice to benzene by inhalation for varying periods of time resulted in a growth advantage for granulopoietic cells and proliferation of myeloblasts and/or promyelocytes.

Benzene has been shown to induce apoptosis in murine haematopoietic cells in vitro (Martínez-Velázquez et al., 2006; Gao et al., 2011), as well as spleen cells, femoral B-lymphocytes, and thymic T-lymphocytes in vivo (Farris et al., 1997b; Wen et al., 2016). In mice exposed to benzene by inhalation at 100 ppm for 6 hours per day, 5 days per week for 2 weeks, no change in the level of apoptosis in bone marrow as measured by flow cytometric analysis using Annexin V staining (Faiola et al., 2004) was observed. However, genes involved in apoptosis (Trp53-mediated *caspase 11*, *bax*, and *ccng*) were upregulated in the bone marrow cells of mice exposed to benzene by inhalation at 300 ppm for 6 hours per day, 5 days per week for 2 weeks (Yoon et al., 2003). In mice exposed to benzene by inhalation at 300 ppm for 6 hours per day, 5 days per week, a higher ratio of apoptosis (i.e. Annexin V staining) in bone marrow cells was observed on day 60 after the start of the experiment when compared with control mice (Das et al., 2012). Trp53-mediated gene expression alterations were also observed in the bone marrow cells of mice exposed to benzene by inhalation at 100 ppm for 6 hours per day, 5 days per week for 15 weeks (Boley et al., 2002). Simultaneously, in mice exposed to benzene a reduction of immune function (phagocytic capacity and cytotoxic efficacy) of cells derived from bone marrow, a reduced generation of adherent stromal cells, and a decreased expression of the adhesion molecule (CXCR4) in bone marrow cells were observed, which might be responsible for inducing myelodysplasia (Das et al., 2012).

Inhalation of benzene at 300 ppm for 23 hours per day for 7 consecutive days induced apoptotic changes in the parenchymal components of the lung of Sprague-Dawley rats. An assay for terminal deoxynucleotidyl transferase dUTP nick end-labelling (TUNEL) and electrophoretic analysis of internucleosomal DNA fragmentation of benzene-exposed lung tissue exhibited 180–200 base pairs of laddering subunits, indicative of genomic DNA degradation (Weaver et al., 2007).

4.2.6 Receptor-mediated effects

Although no data on aryl hydrocarbon receptor (AhR) were available in exposed humans or in human cells, several experimental studies in vitro and in vivo have examined the potential role of AhR in benzene carcinogenicity. This transcription factor appears to be involved in the regulation of immature haematopoietic stem or progenitor cell populations, and AhR dysregulation may result in changes to the bone marrow microenvironment that can lead to excessive or unnecessary proliferation (Singh et al., 2009, 2014). Yoon et al. (2002) reported that AhR-knockout (AhR^{-/-}) mice do not show any haematotoxicity after exposure to benzene (Yoon et al., 2002). Follow-up studies reported that mice in which the bone was ablated by irradiation and repopulated with marrow cells from AhR-knockout mice did not display any sign of benzene-induced haematotoxicity (Hirabayashi et al., 2008; Hirabayashi & Inoue, 2010). Benzene and its metabolites hydroquinone and benzoquinone did not activate AhR in mouse hepatoma cells in vitro, suggesting that direct interaction with AhR is not involved in these haematotoxic effects (Badham & Winn, 2007).

4.2.7 Chronic inflammation

(a) Humans

TNF- α (an important mediator of inflammation), IL-6 (a pro-inflammatory cytokine), and IL-8 (a chemokine) were studied in 196 rural Indian women who used benzene-contaminated biomass to cook, and compared with 149 age-matched women who cooked with the cleaner fuel of liquefied petroleum gas ([Dutta et al., 2013](#)). This study analysed sputum samples and revealed markedly elevated levels of TNF- α (6.9-fold) as well as significantly higher IL-6 and IL-8 levels in the exposed women, suggesting airway inflammation and trafficking of inflammatory cells from circulation to the airways, compared with control women who cooked with the cleaner fuel ([Dutta et al., 2013](#)). [The Working Group noted that the women using biomass were not only exposed to benzene, but also to particulate matter of diameter less than 10 μm (PM₁₀) and other toxic chemicals such as formaldehyde, which may also induce inflammation.]

Several studies in human cells in vitro indicate that several benzene metabolites (*t,t*-MA, hydroquinone, catechol, benzoquinone, and 1,2,4-benzenetriol) may play important roles in the mechanisms of benzene toxicity and inflammation. Hydroquinone (1–10 M) inhibited TNF- α -induced activation of NF- κ B in primary human CD4+ T-lymphocytes and in primary human CD19+ B-lymphocytes ([Pyatt et al., 1998, 2000](#)). [Gillis et al. \(2007\)](#) showed that benzene metabolites (catechol, hydroquinone, 1,2,4-benzenetriol, and benzoquinone) increased production of pro-inflammatory cytokines (TNF- α and IL-6) in PBMCs. TNF- α production was increased in a dose-dependent manner. Concurrently, suppression of anti-inflammatory cytokine IL-10 expression was also observed in the activated PBMCs treated with higher concentrations of hydroquinone and catechol ([Gillis et al., 2007](#)).

(b) Experimental systems

(i) Mouse

Exposure to benzene for 14 days has been demonstrated to affect inflammation in mouse models in two studies. [Aoyama \(1986\)](#) reported that exposure to benzene by inhalation at 200 ppm for 14 days increased ear swelling in BALB/c mice immunized with the contact sensitizer picryl chloride. In mice given benzene by oral gavage at 150 mg/kg bw per day (8 hours per day/5 days a week, for 2 weeks), slight, but not significant, paw swelling was observed in the delayed-type hypersensitivity test ([Wen et al., 2016](#)).

Benzene metabolites were also shown to directly induce inflammatory responses in mice. In C57BL/6 female mice given a single subcutaneous injection (100 nmol/mouse), benzoquinone and (to a lesser extent) hydroquinone, but not benzene itself, was observed to increase popliteal lymph node cell count indices 6 days later as determined by popliteal lymph-node assay ([Ewens et al., 1999](#)). [Bando et al. \(2017\)](#) also demonstrated the direct inflammatory capacity of hydroquinone. The ears of BALB/c and C57BL/6 mice were observed to swell within 24 hours of dermal application of hydroquinone at concentrations of as low as 1% and 8%, respectively. Further examination revealed accumulation of Th2 cytokines such as IL-4, decreased Th1 cytokines, and increased accumulation of T-, B-, and natural killer cells, total serum IgE, hydroquinone-specific IgE, macrophages, neutrophils, and eosinophils ([Bando et al., 2017](#)). In female BALB/c mice, hydroquinone induced IL-4 and IgE and increased total and keyhole limpet haemocyanin-specific IgE ([Lee et al., 2002](#)).

(ii) Rat

In a single study in rats that examined the effect of 1 hour of dermal exposure to benzene of hairless male rats, occlusive and unocclusive dermal exposure increased erythema at the site

of application. Blood IL-1 and skin concentrations of TNF- α increased by 2.4-fold and 3.7-fold, respectively ([Chatterjee et al., 2005](#)).

4.2.8 Epigenetic alterations

Epigenetic alterations related to benzene exposure were observed in studies in vivo and in vitro, as reviewed by [Zhang et al. \(2010\)](#), [Chappell et al. \(2016\)](#), and [Salemi et al. \(2017\)](#).

Epigenetic alterations, including DNA methylation and non-coding RNA, were correlated with benzene exposure ([Fenga et al., 2016](#)). Occupational or environmental exposure to benzene can produce epigenomic changes. More recently, the effect of benzene exposure on miRNA expression has been reported in occupationally exposed workers ([Liu et al., 2016](#)). Downregulation of miR-133a was observed in 50 workers exposed to benzene at 3.50 ± 1.6 mg/m³ compared with 50 controls exposed to benzene at 0.06 ± 0.01 mg/m³ ([Chen et al., 2016b](#)). Overexpression of miR-221 was observed in PBLs of 97 petrol station attendants exposed to benzene at 0.073 ± 0.02 mg/m³ compared with 103 controls exposed to benzene at 0.008 ± 0.001 mg/m³ ([Hu et al., 2016](#)).

The results of in vitro studies of benzene-induced changes in DNA methylation are influenced by cell line type and substance used for the specific experiment, that is, benzene or its metabolite. A global DNA hypomethylation was observed in human lymphoblastoid TK6 cells after exposure to benzene at concentrations of 1, 10, and 100 μ M ([Tabish et al., 2012](#)), and after exposure to hydroquinone at concentrations of 2.5, 5, 10, 15, and 20 μ M in a dose-dependent manner ([Ji et al., 2010](#)). In human normal hepatic L02 cells a global DNA methylation change was observed only after exposure to hydroquinone and 1,4-benzoquinone, but not to benzene itself or other metabolites ([Hu et al., 2014](#)). A reversible poised state of chromatin, identified by the simultaneous presence of histone modifications

associated with both gene activation and repression in long interspersed nuclear element-1 (*LINE-1*) sequences, was observed after an in vitro long-term treatment of human myeloid leukaemia HL-60 cell line with a low-concentration dose (1 μ M (correspond to 110 ng/mL)) of hydroquinone ([Mancini et al., 2017](#)). In human leukaemia U937 cells exposed to 1,4-benzoquinone, [Chen et al. \(2016b\)](#) observed dose-dependent alterations in miR-133a expression.

4.2.9 Other mechanisms

Other effects of benzene primarily concern telomere length and transformation. [Bassig et al. \(2014\)](#) reported that workers who had been exposed to high concentrations of benzene (> 31 ppm) had a mean telomere length that was increased by about 10% compared with matched unexposed workers. A study of human lung cells in vitro reported that exposure to benzene (0.01 and 1 μ M) increased telomerase activity in the fibroblast-like human lung LL24 cell line, but not in the human adenocarcinoma A549 cell line at higher concentrations (10 and 1000 μ M) ([Giuliano et al., 2009](#)).

Two studies in vitro examined indicators of transformation. [Tsutsui et al. \(1997\)](#) reported increases in transformed colonies of Syrian hamster embryo cells after treatment with benzene and its metabolites phenol, catechol, or hydroquinone (1–100 μ M), and [Ibuki & Goto \(2004\)](#) described anchorage-independent growth in soft agar after treatment of NIH3T3 cells with benzoquinone and hydroquinone.

4.3 Data relevant to comparisons across agents and end-points

This section analyses the responses and/or activity of benzene, its metabolites ([Fig. 4.1](#)), and its agents, as evaluated by IARC in a diverse set of in vitro assays performed as part of the United States Environmental Protection Agency Toxicity

Forecaster (ToxCast) ([Kavlock et al., 2012](#)) and Toxicology in the 21st Century (Tox21) ([Tice et al., 2013](#)) initiatives. The inclusion of analyses from high-throughput in vitro assays in the evaluation of the carcinogenicity of agents has been identified as a priority by IARC ([Straif et al., 2014](#)). Consequently, analyses involving these assays have been part of recent *Monographs* that have evaluated the carcinogenicity of 2,4-dichlorophenoxyacetic acid (2,4-D) and 4,4'-dichlorodiphenyltrichloroethane (DDT) ([Loomis et al., 2015](#)).

Benzene has not been tested as part of ToxCast and Tox21. The benzene metabolites that have been evaluated are phenol (IARC Group 3), hydroquinone (IARC Group 3), catechol (IARC Group 2B), and 1,4-benzoquinone (IARC Group 3).

Exposure to agents could potentially lead to human cancer through a diverse set of mechanisms. Each individual agent has a specific pathway or a set of pathways leading to a particular kind of cancer. Despite this heterogeneity in the possible mechanisms, [Smith et al. \(2016\)](#) have identified 10 common characteristics of carcinogens by examining all agents classified as Group 1 carcinogens by IARC. The IARC *Monographs* Volume 113 Working Group ([Loomis et al., 2015](#); [IARC, 2017](#)) systemically evaluated the assays performed as part of ToxCast and Tox21 and assigned an estimation of activity in each assay for an agent as an indication of 1 of the 10 key characteristics of the carcinogens. In this *Monograph*, we use these same assignments of activities (i.e. mapping of assays) to the key characteristics. Assays were assigned to 6 out of the 10 key characteristics of carcinogens, namely: is electrophilic or can undergo metabolic activation (31 end-points); induces epigenetic alterations (11 end-points); induces oxidative stress (18 end-points); induces chronic inflammation (45 end-points); modulates receptor-mediated effects (92 end-points); and alters cell proliferation, cell death, or nutrient supply (68 end-points).

The 10 key characteristics are listed in full as follows.

- (1) *Is electrophilic or can be metabolically activated*: 31 assay end-points consisting of CYP biochemical activity assays and aromatase, which regulates conversion of androgens to estrogens. [The Working Group noted that these assays largely indicate inhibition of CYP activity, and do not directly measure metabolic activation or electrophilicity.]
- (2) *Is genotoxic*: 0 assay end-points.
- (3) Alters DNA repair or causes genomic instability: 0 assay end-points.
- (4) *Induces epigenetic alterations*: 11 assay end-points including 4 DNA-binding assays in HepG2 liver cell lines, biochemical assays targeting histone deacetylases, and other enzymes modifying chromatin, as well as cellular transcription factor assays involved in epigenetic regulation. [The Working Group noted these end-points have not been extensively validated with reference compounds for epigenetic alterations.]
- (5) *Induces oxidative stress*: 18 assay end-points, all cellular assays, targeting nuclear erythroid-related factor-2, antioxidant response element, and other stress-related transcription factors, as well as protein upregulation in response to ROS.
- (6) *Induces chronic inflammation*: 45 assay end-points, mostly using primary human cells, measuring protein expression levels indicative of inflammatory responses, including cytokines, cell adhesion molecules, and NF- κ B. [The Working Group noted these in vitro end-points are short-term assays and therefore not directly indicative of chronic inflammation.]
- (7) *Is immunosuppressive*: 0 assay end-points.
- (8) *Modulates receptor-mediated effects*: 92 assay end-points targeting nuclear receptors (e.g. AhR, androgen receptor (AR),

estrogen receptor (ER), farnesoid X receptor, peroxisome proliferator-activated receptor (PPAR), pregnane X receptor (PXR), and retinoic acid receptor, among others) in cellular assays for transactivation, receptor dimerization, and nuclear translocation, as well as biochemical radioligand binding assays and coregulatory recruitment assays.

(9) *Causes immortalization*: 0 assay end-points.

(10) *Alters cell proliferation, cell death, or nutrient supply*: 68 assay end-points measuring cell cycle markers, proliferation, cytotoxicity, and mitochondrial toxicity by a wide variety of assay formats in cell lines, primary human cells, and developing zebrafish larvae.

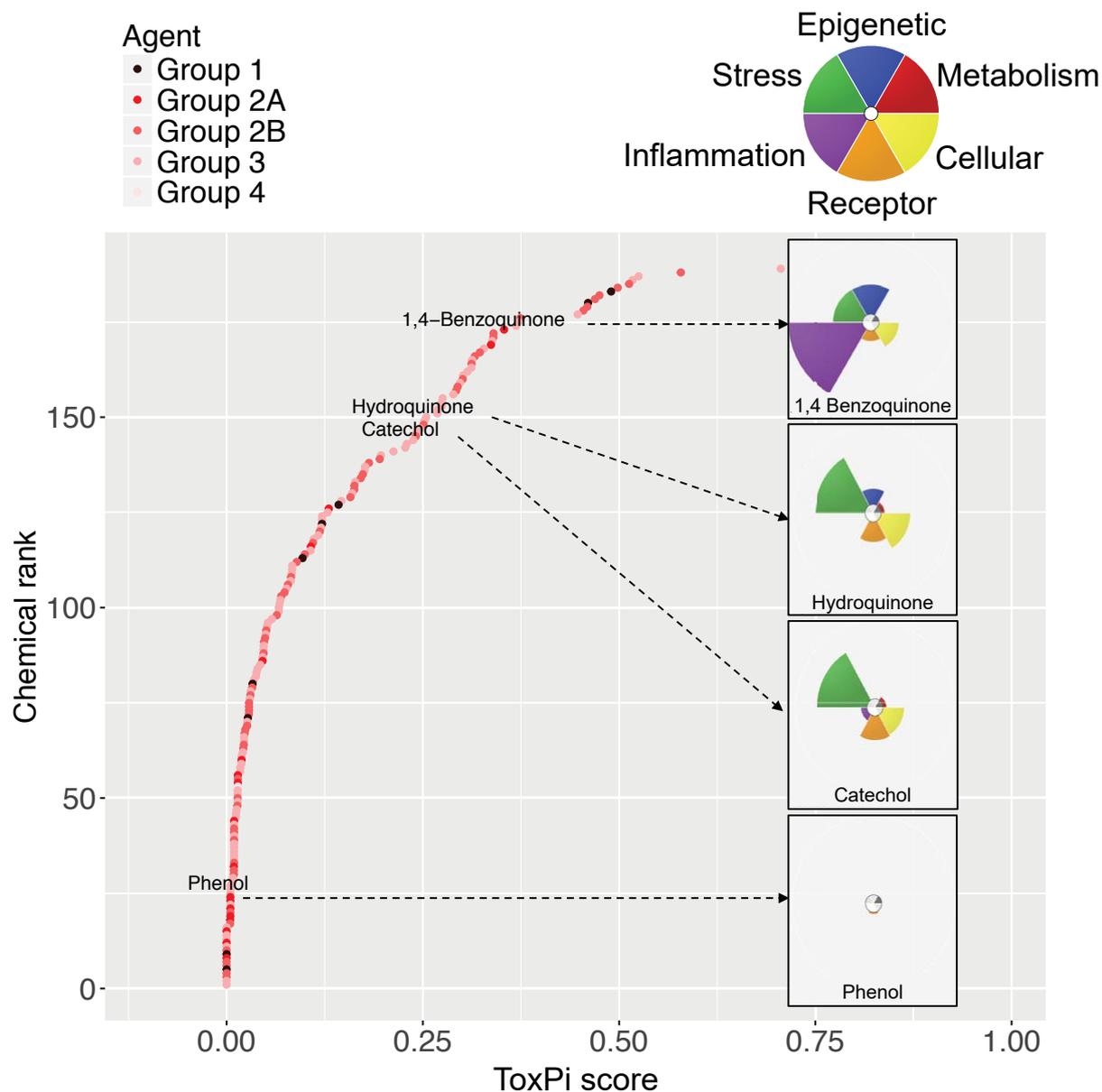
The activity of an agent on a given assay is determined by the statistical significance of the association between all tested concentrations of the agent with assay response (Sipes et al., 2013). The activity of each agent in each assay and across groups of assays was summarized using the Toxicological Prioritization Index (ToxPi) approach (Reif et al., 2010). In the Working Group's analysis, each agent–assay pair was summarized as “active” (1) or “inactive” (0). Within each key characteristic slice for a given agent, the distance from the origin represents the relative agent-elicited activity of the component assays (i.e. slices extending further from the origin were associated with “active” calls on more assays). The overall score of an agent is the aggregation of all slice-wise scores (Fig. 4.2, inset) and provides an activity ranking relative to the 189 agents screened in ToxCast/Tox21 that have been evaluated in the *IARC Monographs* (Fig. 4.3, rank chart).

A tabular and graphical summary of the results is given in the supplementary material (Annex 1), and a summary for each relevant compound follows. Note that the activity calls across these assays represent exposure to each of the four individual metabolites, and may not

necessarily be indicative of exposure to benzene or its other metabolites.

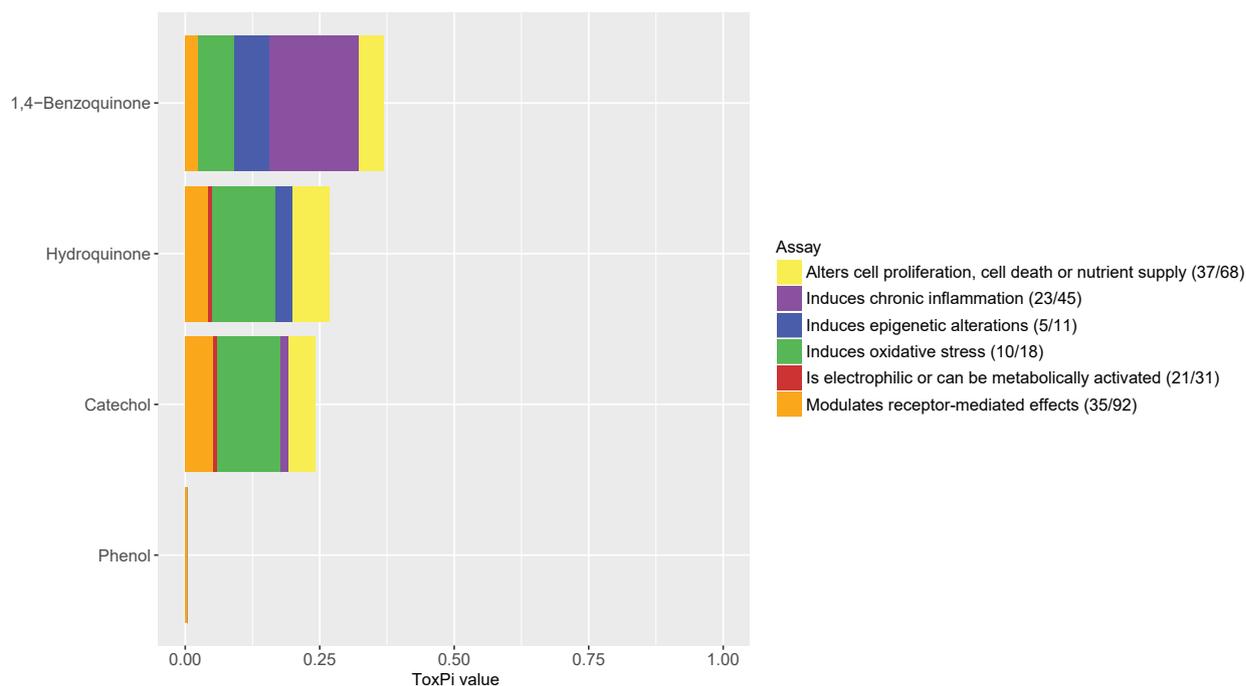
1,4-Benzoquinone (Chemical Abstracts Service, CAS, Registration No. 106-51-4) has the highest ToxPi value among the benzene metabolites evaluated, and has the 16th highest value among the 189 agents (16/189) evaluated by IARC (see Fig. 4.2). The largest contribution to this ToxPi value is from active hits to assays mapped to the “*Induces chronic inflammation*” category (Fig. 4.2). This represents the maximum number of hits to this category among the 189 evaluated IARC agents. Exposure results in upregulation of cell adhesion proteins E-selectin, P-selectin, and vascular cell adhesion molecule 1 (VCAM1), and in the upregulation of chemokines and cytokines such as CXCL9, CXCL10, CCL2, IL-1a, IL-8, TNF α , CD38, CD40, and CD69 in multiple human cell cultures and co-cell cultures. NF- κ B is also upregulated in the HepG2 cell line. The second-largest contributor to the ToxPi value derives from active hits mapped to the “*Induces epigenetic alterations*” category, with two hits out of four assays mapping to DNA binding (the seven assays associated with measuring chromatin alterations were not performed). Assays indicating upregulation of matrix metalloproteinase 1 in two cells cultures are linked to the “*Induces oxidative stress*” category, and the tissue inhibitor of metalloproteinases 2 is also upregulated in a co-culture involving one of the former lines. Assays suggesting upregulation of hypoxia-inducible factor-1 and metal regulatory transcription factor-1 in HepG2 liver cell lines are also linked to 1,4-benzoquinone exposure. Hits associated with upregulation of six genes, including *TGF β 1*, *MYC*, and vascular endothelial growth factor *VEGFR2*, which are markers of cell-cycle across multiple platforms, downregulation of cellular proliferation across multiple cell-cultures as assayed by the sulforhodamine B colorimetric assay, and upregulation of two markers of cell proliferation were mapped to the “*Alters cell proliferation, cell death, or nutrient*

Fig. 4.2 ToxPi ranking for benzene metabolites phenol, catechol, hydroquinone, and 1,4-benzoquinone and all agents evaluated by IARC with available data using ToxCast and Tox21 assay end-points mapped to six key characteristics of carcinogens



Inset are the ToxPi diagrams for these metabolites. ToxPi diagram colour coding is provided in the legend. Each agent in the rank chart is plotted in a colour according to its IARC classification

Fig. 4.3 Stacked bar plots of ToxPi values by assay category for benzene metabolites phenol, catechol, hydroquinone, and 1,4-benzoquinone using ToxCast and Tox21 assay end-points mapped to six key characteristics of carcinogens



The numbers in the parentheses next to each category represent the ratio of the maximum number of hits to assays assigned to category over 189 IARC agents to the total number of assays assigned to the category

supply” category. Upregulation of the gene expression of six receptors, including AhR, AR, glucocorticoid receptor, and retinoid X receptor, all on the Attagene platform performed on HepG2 liver cell line, were linked to the “*Modulates receptor-mediated effects*” component of the ToxPi value.

Hydroquinone (CAS 123-31-9) has the second-highest ToxPi value of the benzene metabolites and the 39th highest ToxPi value among the 189 agents (39/189) evaluated by IARC (see Fig. 4.2). The largest contributor to this value came from active hits linked to the “*Induces oxidative stress*” category. This represents the ninth-highest number of hits to this category among the 189 evaluated IARC agents. This category contains assays mapped to regulation

of matrix metalloproteinase 1 in one of the three cell cultures, regulation of oxidative stress and stress kinase after 72 hours of exposure, and four (hypoxia-inducible factor- α , metal regulatory transcription factor-1, nuclear erythroid-related factor-2, and antioxidant response element) out of six markers of oxidative stress measured in three separate assay platforms (Apredica, Attagene, and Tox21). The second-largest contributor came from hits linked to the “*Alters cell proliferation, cell death, or nutrient supply*” category, with indications of upregulation of cell cycle, downregulation of proliferation, and upregulation of mitochondrial toxicity. For assays assigned to “*Modulates receptor-mediated effects*” there are active hits for AhR, AR, glucocorticoid receptor, PPAR-response element, PXR-vitamin D

response element, ER, and PPAR γ . One out of the four assays associated with DNA binding (from the “*Induces epigenetic alterations*” category) is active for hydroquinone exposure.

Catechol (CAS 120-80-9) has the third-highest ToxPi value of the benzene metabolites and the 45th highest ToxPi value among the 189 agents (45/189) evaluated by IARC (see [Fig. 4.2](#)). The largest contributor to this value came from the exact same active hits as for hydroquinone in assays linked to the “*Induces oxidative stress*” category. For assays assigned to “*Modulates receptor-mediated effects*” there are active hits for AhR, AR, ER, and PPAR. The assays linked to “*Alters cell proliferation, cell death, or nutrient supply*” category suggested upregulation of cell cycle and downregulation of proliferation across multiple cell cultures.

Phenol (CAS 108-95-2) was only active on a biochemical assay for ER, with no activity hits on any other assays assigned to the six categories of carcinogenicity.

In conclusion, 1,4-benzoquinone is the benzene metabolite most strongly associated with assays mapped to the six key characteristics of carcinogens, and with the “*Induces chronic inflammation*” category in particular. Hydroquinone and catechol showed a moderate number of hits. Phenol showed activity on only one assay. These four benzene metabolites were tested in different phases of the ToxCast or Tox21 programmes, resulting in different percentages of missing data (i.e. “not-tested” in a given assay). Relative to the full assay set, 1,4-benzoquinone was tested in 46% of all assays and catechol, hydroquinone, and phenol were tested in 88% of all assays. [The Working Group noted that a reanalysis of data, in which only assays with data for most of the full list of IARC chemicals tested were considered, resulted in similar ToxPi scores.]

4.4 Observed exposure–response relationships in mechanistic studies

Based on the *Report of the IARC Advisory Group to Recommend on Quantitative Risk Characterization* ([IARC, 2014](#)), a more detailed review of the availability of exposure–response information for mechanistic and other data from studies in exposed humans was performed. The purpose of this review was to explore the observed exposure–response relationships by summarizing information across studies on the magnitudes of response (e.g. relative percentage change) and the corresponding levels of exposure.

First, the representative studies of human benzene exposure that were the focus of Sections 4.1 and Section 4.2 relating to the key characteristics of carcinogens were further reviewed for availability of information relating level of exposure to degree of response. Only studies relating to key characteristics of carcinogens for which there was strong evidence in exposed humans were considered (see Section 5.4). Additional considerations for selecting studies included the availability of multiple exposure categories with associated measurements of benzene concentrations in air, adequate sample size, consideration of potentially confounding co-exposures, and/or completeness of reporting. Candidate studies were evaluated for their adequacy in terms of exposure assessment.

Based on these considerations, it was determined that exposure–response information was available for the key characteristics of carcinogens of “is genotoxic” and “is immunosuppressive”, the second of which includes measures of haematotoxicity. Specifically, exposure–response information was available for the end-points for which there was strong evidence in exposed humans (see Section 5.4): (i) genotoxicity (oxidative DNA damage, indicated by 8-OHdG, and

chromosomal effects, indicated by MN and CAs); and (ii) immunosuppression and haematotoxicity (peripheral pluripotent stem cell and leukocyte counts).

Representative studies, independent of the presence or direction of a statistically significant effect, were then selected (see Section 4.2), and numbers in the exposed and reference groups, duration of exposure, and level of exposure among those exposed were examined. Further, for each end-point the measure of response, the evidence of an exposure–response gradient, the central tendency and measure of variance of end-point in the reference group, and the measure of exposure were all considered. Finally, considerations of each exposure category included: the central tendency and measure of variance of exposure; the central tendency of difference in response from the reference group as a percentage change (i.e. (mean of category – mean of the reference group)/mean of the reference group); and a test for significance of difference from the reference group (e.g. *t*-test) and *P* value.

[The Working Group noted that, because representative studies were selected, the existence of additional mechanistic studies with exposure–response information cannot be excluded. The possibility of publication bias on mechanistic end-points also cannot be excluded.]

4.4.1 Genotoxicity

Two studies with exposure–response information for oxidative DNA damage (8-OHdG) were selected ([Lagorio et al., 1994](#); [Liu et al., 1996](#)). Both had statistically significant exposure–response trends, but the population in [Lagorio et al. \(1994\)](#) were exposed to benzene at much lower concentrations (mean, 0.45 mg/m³ or 0.14 ppm) compared with those in [Liu et al. \(1996\)](#) (mean, 166.1 mg/m³ or 51 ppm). Of the two studies, only the study conducted by [Liu et al. \(1996\)](#) divided exposed populations into categories; the group exposed to low concentrations

(mean, 2.46 mg/m³ or 0.76 ppm) was not statistically different, with an effect size of 25%, and the group exposed to medium concentrations (mean, 103.3 mg/m³ or 31 ppm) was statistically significantly increased, with an effect size of 600%.

Four studies with exposure–response information for MN were selected ([Liu et al., 1996](#); [Rekhadevi et al., 2011](#); [Zhang et al., 2014, 2016](#)). [The Working Group noted that the study by [Rekhadevi et al. \(2011\)](#) was not informative for exposure–response because it had a narrow range of benzene exposures (1.1–1.5 mg/m³ or 0.34–0.46 ppm) that was further divided into three categories.] All studies except for that of [Rekhadevi et al. \(2011\)](#) tested for exposure–response trends, all of which were statistically significant. Exposures in the [Rekhadevi et al. \(2011\)](#) (mean, 1.32 mg/m³ or 0.41 ppm), [Zhang et al. \(2016\)](#) (median, 1.6 ppm), and [Zhang et al. \(2014\)](#) (median, 6.4 mg/m³ or 2 ppm) studies were lower than those of the [Liu et al. \(1996\)](#) study (mean, 166.1 mg/m³ or 51 ppm). Three of these studies divided exposed populations into categories that were compared with the reference group and, in each case, the group exposed to the lowest concentrations demonstrated a statistically significant increase in MN compared with the reference group, with effect sizes of 45–55% ([Liu et al., 1996](#); [Zhang et al., 2014, 2016](#)).

Numerous publications with exposure–response information for CAs were selected ([Bogadi-Sare et al., 1997](#); [Zhang et al., 1998b, 2007, 2011, 2012b](#); [Kim et al., 2004b](#); [Xing et al., 2010](#); [Rekhadevi et al., 2011](#); [Marchetti et al., 2012](#)), although many were of the same study population. All had statistically significant exposure–response trends with the exception of [Rekhadevi et al. \(2011\)](#) (see Working Group comment, above) and [Bogadi-Sare et al. \(1997\)](#). Exposure concentrations considered by [Rekhadevi et al. \(2011\)](#) (mean, 1.322 mg/m³ or 0.41 ppm), [Kim et al. \(2004b\)](#) (geometric mean, 0.56 ppm), [Marchetti et al. \(2012\)](#) (mean, 2.8 ppm), [Xing et al. \(2010\)](#) (median, 2.9 ppm), and [Bogadi-Sare et al. \(1997\)](#)

(median, 5.9 ppm) were lower than those in the Zhang et al. studies (median, 10–31 ppm). Among the studies of exposure to lower concentrations, two divided exposed populations into categories that were compared with the reference group: [Xing et al. \(2010\)](#) and [Marchetti et al. \(2012\)](#). The response of the group exposed to the lowest concentration (median, 1.2 ppm) in the study by [Marchetti et al. \(2012\)](#) was statistically significantly different from the reference group, with an effect size of 33%. In the case of [Xing et al. \(2010\)](#), the group exposed to the lowest concentration (median, 1.0 ppm) was not statistically different with an effect size of 50%; the group exposed to the higher concentration (median, 7.7 ppm) was statistically significantly increased, with an effect size of 70%.

[The Working Group noted that, in the majority of studies examined, an exposure–response gradient between benzene exposure and both MN and CAs was reported.]

4.4.2 *Immunosuppression and haematotoxicity*

Numerous studies with exposure–response information for leukocyte counts were selected ([Liu et al., 1996](#); [Rothman et al., 1996](#); [Ward et al., 1996](#); [Qu et al., 2002](#); [Lan et al., 2004](#); [Robert Schnatter et al., 2010](#); [Swaen et al., 2010](#); [Zhang et al., 2016](#)). All had statistically significant exposure–response trends with the exception of the study by [Swaen et al. \(2010\)](#), which was not statistically significant, and by [Liu et al. \(1996\)](#), in which no trend test was performed. Exposures in the studies by [Swaen et al. \(2010\)](#) (mean, 0.22 ppm), [Zhang et al. \(2016\)](#) (median, 1.6 ppm), [Robert Schnatter et al. \(2010\)](#) (median, 2.3 ppm), [Qu et al. \(2002\)](#) (mean, 3.8 ppm), and [Lan et al. \(2004\)](#) (mean, 5.1 ppm) were lower than in the studies by [Rothman et al. \(1996\)](#) (median, 31 ppm) and [Liu et al. \(1996\)](#) (mean, 166.1 mg/m³ or 51 ppm). [Ward et al. \(1996\)](#) only reported the maximum exposure level (34 ppm).

Six studies divided exposed populations into categories ([Liu et al., 1996](#); [Rothman et al., 1996](#); [Qu et al., 2002](#); [Lan et al., 2004](#); [Swaen et al., 2010](#); [Zhang et al., 2016](#)). The groups exposed to the lowest concentrations in these studies had effect sizes ranging from a 0.8% increase to a 14.5% decrease in leukocytes, with the effects observed in [Lan et al. \(2004\)](#) (14.5% decrease at a mean exposure of 0.57 ppm) and [Qu et al. \(2002\)](#) (4.3% decrease at a mean exposure of 3.07 ppm) being statistically significant. In the case of [Swaen et al. \(2010\)](#), none of the groups (< 0.5 ppm, 0.5–1.0 ppm, > 1.0 ppm) demonstrated statistically significant changes (effects ranging from 1% increase to 1% decrease). In [Zhang et al. \(2016\)](#), the groups exposed to the two lowest concentrations (3.55 ppm-yr and 6.51 ppm-yr) had non-significant decreases of 5.3%, whereas the third exposure group (10.72 ppm-yr) had a significant decrease of 11.2%. In [Liu et al. \(1996\)](#), the lowest exposure category (mean, 2.46 mg/m³ or 0.76 ppm) demonstrated a 0% change, but the middle exposure category (mean, 103.3 mg/m³ or 31 ppm) showed a 17% decrease (no statistical tests were performed). In [Rothman et al. \(1996\)](#), the group exposed to the lower concentration (median, 13.6 ppm) demonstrated a non-significant decrease of 5.8%, whereas the group exposed to the higher concentration (median, 91.9 ppm) had a significant decrease of 17.6%.

[The Working Group noted that, in the majority of studies examined, an exposure–response gradient between exposure to benzene and leukocyte count was reported. Some other studies discussed in Section 4.2.4(a), which evaluated populations exposed to relatively low levels of benzene, reported no effects on leukocytes; these studies are not included here, however, because they were not informative for exposure–response analyses (e.g. they only compared all levels of exposure with the reference group).]

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