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Determinants of Benzene Metabolism and Disposition

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The metabolism of benzene and the resulting dosimetry of benzene and its metabolites almost certainly are primary factors in determining the health risks to humans from benzene exposures. The mechanisms and pathways that determine the concentrations of benzene and its metabolites in various tissues have been the subject of considerable debate. This article describes insights into benzene dosimetry and metabolism obtained at CIIT over the past three years and subsequent implications for benzene-induced myelotoxicity and hematotoxicity. The metabolic pathways and kinetics of benzene metabolism have been explored *in vitro*, providing sufficient data to develop a mathematical model of the reactions that occur. Differences in *in vitro* benzene metabolism among mice, rats, and individual humans have been investigated. Mice metabolize benzene faster than rats, while the range of rates exhibited by human tissue samples spans that of mice and rats. Some qualitative differences have also been observed between *in vitro* and *in vivo* benzene metabolism. These differences can be explained, however, by incorporating the regional distribution of liver enzymes into a physiologically based pharmacokinetic (PBPK) model. By developing mathematical models capable of describing large data sets and observing the range of metabolic activities in samples of human liver, we expect to provide dramatically better tools for the assessment of human health risks from exposures to benzene.

Benzene was used extensively in the past for production of paints, resins, rubber, inks, and dyes. It is currently 1% of gasoline and a feedstock for the manufacture of synthetic organic chemicals (Ayres and Taylor, 1989). Benzene is a constituent of gasoline fumes, automobile exhaust, and both mainstream and sidestream tobacco smoke (Wallace, 1990). It is listed as an air toxic in the Clean Air Act Amendment of 1990. Exposure to high levels of benzene for extended periods of time is associated with aplastic anemia and acute myelogenous leukemia (AML) in humans (Infante *et al.*, 1977). Workplace exposures to benzene are now limited through safety regulations (Runion and Scott, 1985), but occupational and environmental exposures to benzene still occur (Hricko, 1994; Tompa *et al.*, 1994).

The effects of chronic exposure to low levels of benzene are not known. Uncertainties in exposure assessment in epidemiological studies have made it difficult to obtain a reliable low-dose extrapolation (Health Effects Institute, 1993). Also, a confirmed animal model does not exist for benzene-induced AML, the effect of most concern in

humans. These factors lead to considerable uncertainty about the risk to humans of low-level benzene exposure.

Benzene is myelotoxic and hematotoxic in mice and rats (MacEachern *et al.*, 1992; Snyder *et al.*, 1978). Because myelotoxicity and hematotoxicity have been observed prior to the onset of AML in humans, the incidence and degree of these acute effects in humans are presumed to correspond to risk of human AML. Further, because an animal model for benzene-induced AML has not been identified, the incidence of benzene-induced myelotoxicity and hematotoxicity in mice and rats is taken to be a surrogate for AML when considering the relationship between benzene exposure levels, tissue metabolite concentrations, and disease response. Based on the observation by Sammett *et al.* (1979) that partial hepatectomy in rats is protective against the hematotoxicity of benzene, the conversion of benzene in the liver to one or more toxic metabolites is believed to play a significant role in the induction of hematotoxicity. If this is true, then the risk to humans depends on the concentration, or dose, of these toxic

metabolites at the site of toxicity, the bone marrow. Working under this hypothesis, research at CIIT has focused on understanding the liver metabolism of benzene and on determining how this metabolism influences the dosimetry of benzene and its metabolites *in vivo*. In particular, our goal is to develop a quantitative tool—a mathematical simulation model—that relates metabolic rates in the liver to the concentrations of benzene metabolites reaching the bone marrow. This tool is to be developed using data from rats and mice, for which extensive data sets exist or can be obtained. In addition to the collection and analysis of rodent data, we have been measuring the rate of benzene metabolism by liver samples from human donors. The rodent data will be used to develop and validate the simulation model. Then, by changing the model parameters to reflect human physiology and metabolic capacities, we will be able to predict the exposure-dose relationship for benzene metabolites in human bone marrow.

The primary pathways for benzene

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Benzene Metabolism (from page 1)

metabolism in the liver are depicted in Figure 1. Oxidative reactions lead to the formation of benzene oxide (a reactive intermediate), phenol, hydroquinone, and small amounts of catechol and trihydroxy benzene. These oxidized metabolites may be further transformed by conjugation to compounds that are readily excreted in the urine. Benzene oxide can also be converted to an opened-ring metabolite, muconaldehyde, a precursor of muconic acid, which is excreted in the urine.

The conjugated metabolites of benzene are generally thought not to be responsible for its toxic effects, and a significant amount of research has focused on identifying which of the intermediate metabolites is the bad actor. Administration of either phenol or hydroquinone alone to rodents fails to reproduce the hematotoxic and myelotoxic effects of benzene exposure (Cox, 1991; Kari et al., 1992). These observations led investigators to the hypothesis that neither of these metabolites is responsible for benzene toxicity and to the conjecture that muconaldehyde, the only semistable toxic metabolite that is not produced from phenol, might be responsible. However, as with phenol and hydroquinone, muconaldehyde alone does not reproduce the toxic effects of benzene (Guy et al., 1991). Instead, benzene toxicity apparently results from the combined effects of several metabolites: muconaldehyde and hydroquinone act additively (Guy et al., 1991), and phenol and hydroquinone act synergistically (Barale et al., 1990; Eastmond et al., 1987). The risk from benzene exposure may depend on the dosimetry of all three metabolites, with catechol and trihydroxy benzene playing lesser roles.

To develop a simulation model for

predicting *in vivo* dosimetry and metabolism in humans based on *in vitro* data, we first need to understand *in vitro* metabolism and *in vivo* metabolism and dosimetry separately in a laboratory species such as the mouse. Only then can we merge the two levels of understanding, *in vivo* and *in vitro*, and resolve any apparent differences between the two. In this article, we first describe the ongoing research on liver metabolism, along with some tentative physiological predictions based on *in vitro* results. Secondly, the development of what is currently an independent mathematical model of *in vivo* dosimetry and metabolism is discussed. Finally, some implications of the current results and a synopsis of future directions are presented.

Differences in the In Vitro Metabolism of Benzene among Species and Individual Humans

The metabolism of benzene is fairly complicated in that it involves a number of reactions (Figure 1). To predict the dosimetry of the various metabolites, we need to know the rate of each reaction as a function of the metabolite concentrations. While these rates can be determined *in vivo* for laboratory animals, our objective is to predict human metabolism, where *in vivo* experiments are precluded and the availability of tissue samples is limited. Differences exist among species as well as among individual humans in the rates of metabolism. Since these differences affect individual risk, we seek to understand and quantify the range of rates for benzene metabolism in humans based on those measurements that can be obtained with human liver samples.

While the rates of metabolism of a

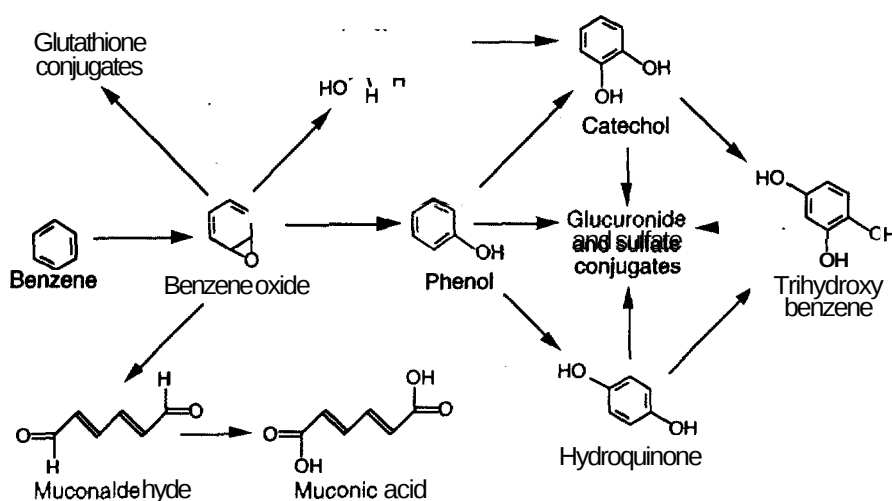


Fig. 1

Primary pathways for benzene metabolism in the liver. The oxidized metabolites phenol, hydroquinone, catechol, and trihydroxy benzene, along with the ring-open metabolite muconaldehyde, are all toxic to the bone marrow (myelotoxic) and affect the circulating blood (hemstotoxic). The conjugated metabolites and muconic acid are readily excreted in the urine.

xenobotic typically differ among species, the biochemical mechanisms of benzene biotransformation are expected to be nearly the same in all species. Therefore, our goal is to develop a mechanistically based mathematical model of metabolism in which all species and individual differences are explained by differences in parameter values such as enzyme activities. Since *in vivo* dosimetry data in mice are also being obtained and already exist for rats, these species can be used to test the extrapolation of *in vitro* rates to *in vivo* rates. Extrapolation among species or individuals can be tested by using a large *in vitro* data set for rat liver metabolism in comparison with the mouse data. In particular, we can determine if a model developed from mouse data, taken together with measurements of rat and mouse enzyme activities, can be used to predict rat metabolism. Finally, a smaller data set obtained with human tissues can be used to determine model parameter values and their ranges for humans.

Oxidative Metabolism *In Vitro*

By using different fractions from liver cells and supplying only the substrates and cofactors necessary for specific metabolic reactions, we can observe subsets of the reactions depicted in Figure 1 and reduce the complexity of developing a model for all these reactions to more manageable pieces. One specific goal is to develop quantitative descriptions or reaction rate equations for the oxidative reactions. By performing incubations with the microsomal fraction of liver and supplying NADH and NADPH as cofactors, we can observe the set of oxidative reactions in isolation. As an example, the disappearance of benzene due to oxidation by liver samples from two humans, F-344 rats, and B6C3F₁ mice is depicted in Figure 2. In these experiments, subcellular fractions of liver samples containing oxidation enzymes were incubated *in vitro* with benzene, and the amount of benzene oxidation was observed. As can be seen, mouse microsomes metabolize benzene faster than rat microsomes, which correlates with the fact that mice are more sensitive than rats to the hematotoxic effects of benzene. More importantly, the data from the two human samples illustrate the wide range in metabolic activity for benzene oxidation among humans, which spans the activity from mice and rats. Given that the same enzyme, cytochrome P450 (CYP) 2E1, is primarily responsible for benzene oxidation in mice and rats (Nakajima *et al.*, 1993) and has a similar role in humans (Seaton *et al.*, 1994), understanding the difference in metabolic rates between mice and rats should help to explain the range of rates observed for humans. In this case, the rate of a reaction may differ between two individuals, while the enzymatic mechanism is the same.

TABLE 1
K_m VALUES OF SEVERAL REACTIONS FOR MICE, RATS, AND HUMANS

Species	Reaction			
	BD epoxidation (μM) ^a	BMO hydrolysis (mM) ^a	BMO glutathione (mM) ^a	Acrylonitrile epoxidation (μM) ^b
Mouse	2.00 ± 0.17	1.59 ± 0.03	35.3 ± 6.2	13 ± 1
Rat	3.75 ± 0.20	0.26 ± 0.10	13.8 ± 0.3	11 f 1
Human	5.14 ± 2.59	0.24 ± 0.10 to 1.65 f 0.12	10.4 ± 1.0	12 f 1 to 18 f 1

^aFrom Csanády *et al.* (1992); ^bFrom Kedderis *et al.* (1993).

An initial mathematical simulation model of benzene oxidation by mouse and rat liver microsomes was described by Schlosser *et al.* (1993). This model incorporates a mechanism whereby benzene, phenol, hydroquinone, and catechol all interact through competition for a common reaction site on the oxidizing enzyme, CYP. At least two CYP isozymes are responsible for benzene oxidation, with CYP 2E1 being predominant (Koop *et al.*, 1989; Nakajima *et al.*, 1993). The model of Schlosser *et al.* (1993) considers only a single enzyme, with effective parameters for the total metabolism of benzene to phenol, hydroquinone, catechol, and trihydroxy benzene. The same model structure describes metabolism by both mouse and rat microsomes, but the parameter values for the two species are quite different.

The activity or maximal rate (V_{max}) of reactions catalyzed by an enzyme such as CYP 2E1 may vary significantly among animal species, but other kinetic parameters such as saturation or affinity constants (e.g., K_m) may be very similar. For example, Csanády *et al.* (1992) examined the kinetics of 1,3-butadiene (BD) epoxidation, butadiene monoepoxide (BMO) hydrolysis, and BMO conjugation with glutathione *in vitro* with liver samples from mice, rats, and humans; apparent K_m values for these reactions are listed in Table 1. Values for acrylonitrile epoxidation obtained by Kedderis *et al.* (1993) are also listed in Table 1. While differences in K_m values among species and in some cases differences among individual humans are observed, those differences are often quite small and may not be statistically significant. Further, the differences in K_m values among species for a given reaction are, in all cases, quite small compared with the differences in K_m values between reactions. In the case of BMO hydrolysis and conjugation with glutathione, species differences of over an order of magnitude in the respective V_{max} values were observed (values not shown). Therefore we might expect

saturation parameters such as K_m generally to have similar values in different species.

The role of CYP 2E1 in benzene metabolism was further explored by Seaton *et al.* (1994), who compared biotransformation by liver samples from 10 human as well as from mice and rats. Plots of the disappearance of benzene and the formation of phenol and hydroquinone are shown in Figure 3. Benzene metabolism correlated strongly with CYP 2E1 activity across species and individuals, suggesting that a mathematical model could be developed in which this activity is the only difference among individuals or species. Such a model was developed and described by Seaton *et al.* (1994) based on the model of Schlosser *et al.* (1993). This model also assumed that a single enzyme was responsible for oxidation, with benzene, phenol, and hydroquinone competing for the enzymatic reaction site. From Figure 3, we see that the model does a fairly good job predicting data to which it has not been

The idea of a universal metabolism model in which CYP 2E1 activity alone explains individual or species differences in rates of benzene metabolism, is quite appealing. The data in Figure 3 not only suggest this possibility but also that a first-generation model capable of describing oxidative metabolism by human liver might be developed almost completely from mouse and rat data. Yet Schlosser *et al.* (1993) obtained dissimilar values of saturation and competition parameters for rats and mice. How do we explain these conflicting results of Schlosser *et al.* (1993), where saturation parameter values appear to be quite different between mice and rats, and of Seaton *et al.* (1994), where the kinetics of benzene oxidation appear very similar in mice, rats, and humans? The model of Seaton *et al.* (1994) describes the results of benzene incubations starting at a single concentration (4 μM) a

(Continued on page

tion of CYP 2E1 activity. When additional se and rat data are considered, including its from benzene and phenol incubations vo concentrations for each substrate, a le-enzyme model is no longer capable of rieving the entire data set, even for a single ies. In fact, more careful examination of re 3 reveals that there are different indi- als with nearly identical CYP 2E1 activi- but significantly different extents of me- llism.

If a single-enzyme model is incapable of rieving a larger data set (one that includes its from incubations with phenol as a sub- se), how can the correlation evident in Fig- 3 be explained and utilized? The rate of zene oxidation to phenol is determined sly by CYP 2E1 activity, which limits the lability of phenol during benzene incuba- s, and this limited availability may control rate at which benzene-derived phenol is equentially converted to hydroquinone. On other hand, when phenol is the substrate, vailability is not limited by CYP 2E1 activi- and a second CYP may be involved. There- the rate of conversion to hydroquinone e much more dependent on the activity CYP other than 2E1. Koop et al. (1989) ved that several CYP isozymes can con- phenol to hydroquinone. The hypothesis a CYP other than 2E1 contributes to phe- oxidation is currently being tested through development of a two-enzyme model, re the activity of one enzyme is taken to hat of CYP 2E1. Candidates for the sec- enzyme include CYP 1A1, CYP 1A2, CYP 6, and CYP 2C11 (Nakajima et al., 1993). e parameter values have been set by ching the model to a data set that includes benzene and phenol incubations at mul- 3 concentrations, the dependence of el-predicted benzene metabolism on CYP activity will be tested and compared to

the data in Figure 3. If a two-enzyme model is able to describe the existing multiple-substrate data sets, then inhibition experiments can be performed to directly test and compare the dependence of benzene and phenol metabo- lism on CYP 2E1 activity.

Conjugation In Vitro

As in the case of oxidation, the conjuga- tion reactions can also be studied separately. Phenolsulfation and hydroquinone glucuroni- dation are the primary routes for conjugation of benzene metabolites in rodents. Once con- jugated, the metabolites are readily excreted in the urine, so conjugation reactions are con- sidered to be detoxication pathways. The cir- culating levels of the oxidized metabolites are determined by the balance between oxidative rates and conjugation rates. Therefore deter- mining the rates of conjugation reactions rela- tive to the oxidative reactions and determin- ing how those rates vary among individual hu- mans are equally important as determining the rates of the oxidative reactions. The rates of conjugation reactions can be measured using the cytosolic and microsomal subcellular fractions, respectively, obtained after centrifu- gation of liver homogenates. We examined differences in the in vitro rates of conjugation among species or individuals using pooled samples of rat and mouse liver and individual samples of human liver. We observed a three- fold variation among human samples in the rate of phenyl sulfate formation (range, 0.3 to 0.9 nmole/mg/min; Table 2). For laboratory animals, phenol sulfation was much faster in rat cytosol (1.2 nmole/mg/min) than in mouse cytosol (0.5 nmole/mg/min). Hydroquinone glucuronidation varied by almost threefold among human samples (range, 0.1 to 0.3 nmole/mg/min; Table 2) and was more rapid in mouse liver microsomes (0.22 nmole/mg/ min) compared with rat liver microsomes (0.08 nmole/mg/min). No correlation was observed

among the rates of oxidation, sulfation, and glucuronidation for rats, mice, or individual humans. Therefore we can assume that these rates vary independently in risk assessment calculations, where the range of metabolism rates among humans is important.

In addition to interindividual variability among human samples in the activities of phenol sulfation, hydroquinone glucuroni- dation, and CYP 2E1 oxidation (Seaton et al., 1994), species differences observed among humans, mice, and rats are interesting and deserve comment. The mouse is more sensi- tive than the rat to the toxic effects of ben-

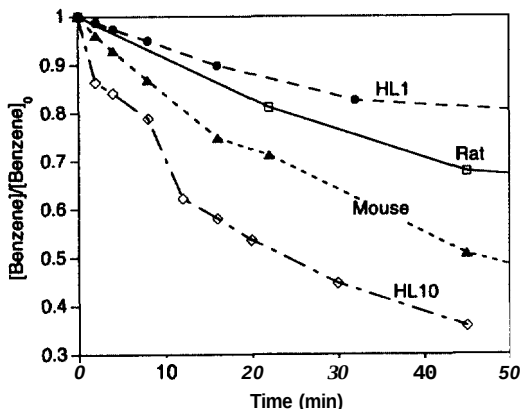


Fig. 2

Comparison of benzene metabolism with liver microsomes from B6C3F1 mice, F344 rats, and humans (HL1 and HL10). $[Benzene]/[Benzene]_0$ is the proportion of benzene remaining as a function of time relative to the initial benzene concentration. Incubations were performed with $\sim 4 \mu M$ benzene and 1 mg/ml microsomal protein, as described in Schlosser et al. (1993). Mouse and rat data were originally reported by Schlosser et al. (1993); human data were reported in Seaton et al. (1994).

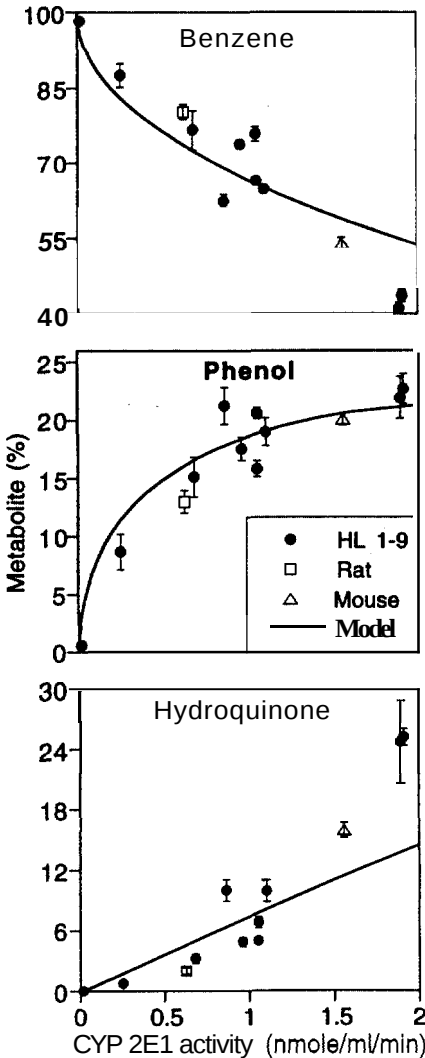


Fig. 3 Metabolism of $\sim 4 \mu M$ benzene to phenol and hydroquinone from 16-min incubations with 1 mg/ml liver microsomal protein from a number of individual humans (HL1-9), rats, and mice, shown as a function of cytochrome P450 (CYP) 2E1 activity. The amount of metabolite is displayed as a percentage of the total substrate and metabolite concentration (other metabolites not shown). Data (symbols) and model (solid line) are from Seaton et al. (1994). (Adapted by permission of Oxford University Press.)

zene (Snyder and Kalf, 1994). Our results reveal a greater capacity for activation and less for detoxication in mice compared with rats, whereas human values include slow activation and detoxication (Table 2, HL 2), moderate activation and rapid detoxication (Table 2, HL 6), and rapid activation and slow detoxication (Table 2, HL 10). Observations in mice and rats are in agreement with the suggestion that susceptibility to benzene toxicity results from a balance between oxidative and conjugative reactions. Moreover, these observations agree with *in vivo* data from Sabourin *et al.* (1987) and physiological model simulations by Medinsky *et al.* (1989). Those studies demonstrated greater urinary excretion of phenyl sulfate and less excretion of hydroquinone conjugates in rats compared with mice following benzene exposure, consistent with higher CYP 2E1 activity and lower phenol sulfotransferase activity measured *in vitro* in mouse liver.

A Physiological Compartmental Model

As discussed in the introduction, benzene-induced hematotoxicity and myelotoxicity and the risk of AML in humans are probably a function of the circulating levels of oxidized metabolites that occur during benzene exposure. Given the range of activities for oxidation, sulfation, and glucuronidation indicated in Table 2, what phenol and hydroquinone blood levels would occur? We have developed a physiological compartmental model for estimating steady-state blood concentrations of phenol and hydroquinone that might have been achieved during continuous exposure of those 10 individuals to 0.01 μ M benzene in blood (Seaton *et al.*, 1995). This blood concentration is likely to result from exposure to

benzene at the current permissible exposure limit of 1 ppm under the Occupational Safety and Health Act (Wallace, 1990).

The steady-state phenol and hydroquinone concentrations for the individual humans, rats, and mice are depicted in Figure 4. According to model calculations, predicted steady-state phenol concentrations varied six-fold among humans and correlated inversely with measured microsomal activity of CYP 2E1. This inverse relationship is most likely due to the fact that CYP 2E1 is also responsible for phenol oxidation to hydroquinone in this model. In particular, while the rate of phenol formation increases with CYP 2E1 activity, the rate of removal also increases with CYP 2E1 activity, resulting in a net decrease in concentration. Steady-state hydroquinone concentrations varied fivefold among humans. With laboratory animals, model simulations predicted that steady-state concentrations of phenol and hydroquinone would be higher in mice than in rats during exposure to this very low benzene dose. These predictions are in agreement with *in vivo* observations from studies with higher benzene concentrations (Sabourin *et al.*, 1987). Predicted steady-state concentrations in mice were higher than in humans, whereas rat values fell among the range of predictions for humans. These simulations suggest that the rat may be a good model for humans with respect to tissue dosimetry of benzene metabolites.

Higher levels of oxidized metabolites in mice are due in part to the faster blood flow per unit body weight in this small species compared with humans. More benzene is brought to the liver per unit time for metabolism. The model predictions for higher concentrations of oxidized metabolites in mouse blood, if correct, also suggest that development of leuke-

mia in humans is a function of tissue response in addition to dosimetry. In particular, mice exhibit levels of the putative leukemogenic benzene metabolites that are at least as high as is predicted in humans at exposure levels associated with AML in humans, but these levels do not give rise to AML in mice. Therefore mouse bone marrow apparently responds to these agents in a manner that is qualitatively different from humans.

Variability in rates of conjugation plays a definite role in determining steady-state blood concentrations of phenol and hydroquinone. Although the *in vivo* rate constants for benzene oxidation vary 13-fold among human samples, the steady-state concentration of phenol in blood varies only 6-fold. Moreover, steady-state concentrations of hydroquinone do not correlate with rates of oxidation reactions and appear to be influenced more by competition between phenol sulfation and phenol oxidation and detoxication due to hydroquinone glucuronidation. While the effect of the hydroquinone:phenol concentration ratio in blood on susceptibility to benzene toxicity is not clear, a synergistic relationship between these metabolites has been demonstrated *in vitro* (Smith *et al.*, 1989; Irons *et al.*, 1992; Kolachana *et al.*, 1993; Chapman *et al.*, 1994).

The results described above suggest a significant interaction between Phase I (oxidation) and Phase II (conjugation) pathways in determining blood and tissue levels of benzene metabolites. The quality of these predictions must be tested experimentally in laboratory animals *in vivo* before utilizing them for human risk assessment. Once this has been done, a model like that described here, taken together with the observed ranges of enzyme activities among humans, can be used to predict risk to individual humans with given enzyme activity profiles and subsequently the range of risk to human populations.

In Vivo Metabolism of Benzene and Phenol in Mice

The underlying goal of our *in vivo* metabolism studies in mice has been the development of a quantitative, mechanistically based description of the relationship between a phase benzene exposure concentration (ppm) and the amount of active metabolite being delivered to the target tissue. Oxidative metabolism by CYP 2E1 is required for manifestation of the hemato-toxic and genotoxic effects of benzene, but the dosimetry of a putative benzene metabolites in the target tissue bone marrow, is a net result of competitive toxification (oxidation) and detoxification (conjugation) reactions. Therefore we need to understand how these processes interact *in vivo* to determine tissue concentrations of benzene metabolites.

TABLE 2
INITIAL RATES FOR BENZENE OXIDATION, PHENOL SULFATION,
AND HYDROQUINONE GLUCURONIDATION IN INDIVIDUAL HUMAN LIVER
SAMPLES AND IN POOLED LIVER SAMPLES FROM MICE AND RATS^a

Liver sample	Initial rate		
	Benzene oxidation (nmole/mg/min)	Phenol sulfation (nmole/mg/min)	Hydroquinone glucuronidation (nmole/mg/min)
Human			
HL 1	0.344	0.309	nd ^b
HL 2	0.926	0.581	0.117
HL 6	1.433	0.867	0.281
HL 7	1.499	0.919	0.167
HL 10	4.442	0.485	0.106
Mouse	1.558	0.485	0.218
Rat	0.625	1.195	0.077

^aResults from Seaton *et al.* (1995). ^bNot determined due to insufficient sample.

Phenol metabolism is of interest in this text since phenol is a major oxidized metabolite of benzene, and there are distinct differences in both carcinogenic and toxic responses between benzene and phenol in mice. For example, while benzene is carcinogenic in a number of tissues in the following both oral and inhalation exposure (Huff et al., 1989), no increased incidence of tumors was found in a two-year National Cancer Institute (NCI) bioassay in which male and female B6C3F₁ mice were exposed to phenol in drinking water at levels of up to 5000 ppm (NCI, 1980). Benzene has been consistently found to induce micronuclei in mouse bone marrow cells (Huff, 1987). In contrast, both weakly positive and negative results have been reported for micronuclei induction in mouse bone marrow cells by phenol following intraperitoneal and oral administration (ATSDR, 1993). These dramatic differences in carcinogenicity and genotoxicity between benzene and its major oxidized metabolite, phenol (Figure 1), have puzzled benzene researchers and led to different hypotheses about metabolites responsible for benzene toxicity. Insight into a possible metabolic basis for the high potency of benzene as both an oral carcinogen and genotoxicant and the lack of genotoxicity and carcinogenicity of phenol can be gained by comparing the urinary metabolite profiles after comparable doses of benzene and phenol. This comparison is presented in Table 3, using

data from CIIT for urinary excretion of phenol metabolites following oral gavage of phenol in male B6C3F₁ mice (Kenyon et al., 1995) and similar data reported by Sabourin et al. (1989) following oral gavage with benzene. Differences in the excretion of hydroquinone glucuronide are quite marked, particularly at the lower dose (~1 mg/kg). Hydroquinone glucuronide excretion in urine was sixfold and twofold greater after benzene compared with phenol at doses of approximately 1 and 10 mg/kg, respectively. The *in vitro* studies described above indicate that hydroquinone is produced by sequential oxidation of benzene via phenol. How then could more hydroquinone be produced after administration of benzene than after phenol?

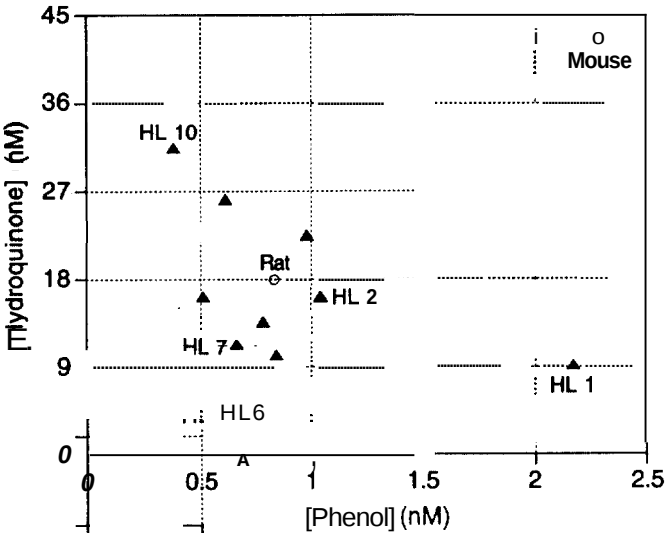
The differences in hydroquinone formation after benzene and phenol administration are of interest for three reasons. First, hydroquinone itself is an inducer of micronuclei and chromosomal aberrations in various test systems (IPCS, 1992). Thus greater production of hydroquinone after benzene administration compared with phenol administration, together with production of other putative toxic metabolites such as muconaldehyde that are unique to benzene, provide a possible metabolic basis for the carcinogenic and genotoxic effects observed with benzene but not with phenol. Secondly, these data are in contrast to *in vitro* data (liver microsomes and isolated hepatocytes) that suggest greater production of hydroquinone after phenol compared with benzene (Schlosser et al., 1993; Schrenk and Bock, 1990). The implication

here is that a mechanistic basis for this difference should be incorporated into our quantitative *in vivo* description of the relationship between benzene exposure and target tissue dosimetry. Finally, this difference points out the need for caution when interpreting *in vitro* metabolism studies.

We hypothesize that differences in the urinary metabolite profile of phenol compared with benzene following oral administration result from quantitative zonal differences in the distribution of metabolizing enzymes within the liver acinus, as illustrated in Figure 5. Phenol absorbed from the gut lumen has relatively greater opportunity for conjugation than for oxidation, initially in gastrointestinal mucosal cells (sulfation and glucuronidation) and subsequently in the periportal hepatocytes of zone 1 (sulfation) when absorbed into the portal circulation. The greater opportunity for phenol conjugation over oxidation is due to the relatively greater abundance of conjugating enzymes compared with oxidative enzymes in the areas where phenol would be distributed when initially absorbed (Gebhardt, 1992; Morris and Pang, 1987). The net effect of this hypothetical scenario is that less phenol reaches hepatic zone 3, where oxidative enzyme activity is greatest, resulting in less hydroquinone production.

In contrast to phenol, benzene is only a substrate for CYP2E1, and CYP2E1 activity is much greater in the pericentral hepatocytes of zone 3 (Tsutsumi et al., 1989). Thus metabolism of benzene would be minimal as benzene passes through periportal and midzonal hepatocytes prior to reaching hepatocytes in zone 3, where CYP2E1 oxidation capacities are relatively greater (Gebhardt, 1992; Morris and Pang, 1987). Consequently, administration of benzene may result in the delivery of more free phenol to zone 3 oxidative enzymes than administration of phenol itself. The metabolic implications of these hypothetical scenarios are reflected in the observed urinary metabolite profiles presented in Table 3. Phenyl sulfate excretion is approximately twofold higher and phenyl glucuronide excretion approximately four- to ninefold higher after phenol compared with benzene exposure, and oxidation products such as hydroquinone are higher after benzene exposure.

Returning to the question of benzene toxicity, Smith et al. (1989) hypothesized that benzoquinone, formed from the myeloperoxidase-mediated oxidation of hydroquinone in the bone marrow, is responsible for benzene-induced hematotoxicity. The net effects of heterogeneous distribution of enzymes in the liver and the resulting preferential oxidation of benzene and conjugation of phenol are a higher blood level of hydroquinone after benzene administration compared with phenol and more hy-



3.4 Steady-state blood concentrations of phenol and hydroquinone for 10 individual humans, B6C3F₁ mice, and F344 rats when the blood concentration of benzene is constant at 0.01 μ M. This blood concentration is approximately what would be expected for a continuous exposure to 1 ppm benzene. The steady-state phenol and hydroquinone concentrations are calculated from *in vitro* oxidation and conjugation activities, such as those listed in Table 1, using a physiological compartment model, reported by Seaton et al. (1995). (Adapted by permission of Oxford University Press.)

TABLE 3
COMPARISON OF URINARY METABOLITES EXCRETED AS PHENOL SULFATE, PHENOL GLUCURONIDE, AND HYDROQUINONE GLUCURONIDE FOLLOWING GAVAGE ADMINISTRATION OF PHENOL OR BENZENE IN MALE B6C3F₁ MICE

Chemical administered	Dose (mg/kg)	Total metabolites in urine (%) ^a		
		Phenol sulfate	Phenol glucuronide	Hydroquinone glucuronide
Benzene ^b	1	26 ± 0.3	42 ± 0.3	43 ± 0.8
Phenol ^c	1.4	56 ± 0.9	39 ± 1.1	7.2 ± 0.4
Benzene ^b	10	32 ± 0.8	5.9 ± 0.3	36 ± 0.4
Phenol ^c	9.4	57 ± 7.7	26 ± 6.4	15 ± 1.6

^aValues are means ± SE.

^bUrinary metabolite data following benzene exposure are from Sabourin et al. (1989).

^cData are from Kenyon et al. (1995).

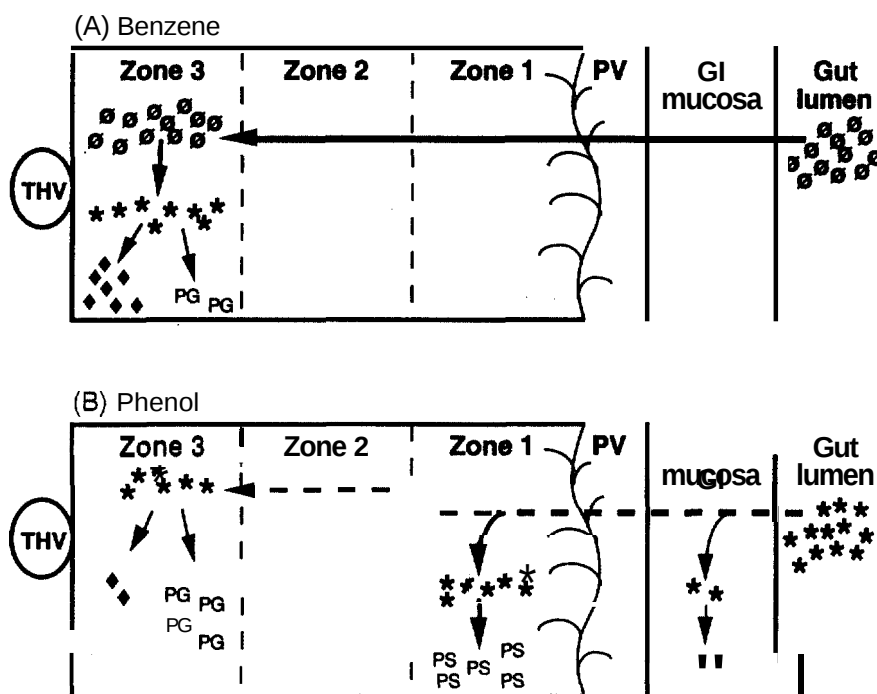


Fig. 5

Hypothesized major relative hepatic zonal differences in metabolism of benzene (A) compared with phenol (B) following gavage administration during an initial pass through the liver. Symbols and abbreviations denote benzene (●), phenol (*), hydroquinone (◆), portal vein (PV), and the terminal hepatic venule (THV). Benzene and phenol absorbed from the gastrointestinal (GI) tract are sequentially available for metabolism in the GI mucosa and periportal (zone 1) and pericentral (zone 3) regions of the liver. The overall capacity of GI mucosal metabolism is low relative to the liver. Periportal localization of the enzymes (sulfotransferase) responsible for phenol sulfation suggests that less free phenol would reach the pericentral hepatocytes where higher levels of CYP 2E1 activity are localized. The necessity for oxidation of benzene prior to conjugation suggests that more benzene will reach the pericentral hepatocytes for oxidation to phenol and hydroquinone. Phenol sulfate, PS; phenol glucuronide, PG.

droquinone in bone marrow available for oxidation to benzoquinone. Localization of enzymes in the liver provides explanations for differences both in observed toxicity and in *in vitro* metabolism of benzene and phenol. Thus both the location and the quantities of benzene-metabolizing enzymes must be incorporated into *in vivo* models to predict risks for humans exposed to benzene.

The concept that the metabolic fate of a metabolite derived from a precursor differs from that of a preformed metabolite is new. It was, in fact, proposed by Pang and Gillette in 1978 for drugs. The kinetics of a drug and its metabolite can differ due to differences in diffusional barriers between drug and hepatocyte, the rate of communication of the drugs between hepatocytes, and the distribution of drug-metabolizing enzyme systems within the liver parenchyma (Pang and Terrell, 1981). Using the drug-metabolite pair phenacetin and acetaminophen, Pang and colleagues noted differences in clearance of the chemicals from an isolated perfused liver depending on whether perfusion was conducted in a normal (portal centrilobular) or retrograde (reversed) direction. They attributed these differences to preferential localization of P450 demethylation enzymes and sulfation enzymes in different zones of the liver and suggested that existing models of well-stirred livers were oversimplifications and could only be used in limiting cases when the distribution of enzymes was viewed as operationally uniform.

Using a combination of experimental and mathematical modeling approaches, Pang and Terrell (1981) determined that substrate concentration at any point is influenced by preceding events during the metabolic processing of a substrate along the length of the liver sinusoid. Enzymes, systems such as sulfation, when present upstream along the sinusoidal flow path, modify residual substrate available for metabolic activities such as oxidation with downstream hepatocytes. In the case of benzene and phenol, we propose that the residual phenol available for oxidation in the centrilobular region is very low when phenol is administered directly because most of it is conjugated upstream of this region. In contrast, when benzene is administered, the phenol is produced in the centrilobular region and thus is more available for subsequent oxidation to hydroquinone.

Conclusions

We cannot yet claim to have completely elucidated the factors that determine benzene metabolism and dosimetry, let alone toxicity. Nevertheless, the research described here does represent considerable

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progress in understanding and quantitating the factors that determine the distribution of benzene and benzene metabolites in the body. In particular, we have seen that the quantity of a benzene metabolite produced is the result of subtle interplay among various enzymes competing for substrates at a given location, the distribution of those enzymes in the liver, and relative rates of perfusion in different species. Given the complexity of this system, it is not surprising that many, sometimes contradictory, mechanisms for benzene metabolism have been proposed. At this point in time, many experimental observations must be explained by any proposed model. One example is the fact that *in vivo* administration of benzene yields higher levels of hydroquinone than *in vivo* administration of phenol but that *in vitro* metabolism of phenol yields greater quantities of hydroquinone than *in vitro* metabolism of benzene. The mechanisms proposed here are capable of resolving these disparate observations and can be tested experimentally. In the case of hepatic enzyme localization, experiments with isolated hepatocytes (in a well-mixed suspension) can be compared with the results of normal grade and retrograde perfused liver experiments to determine if this is indeed a significant factor.

A second important point is that the individual pieces of research described here, taken together with further planned *in vitro* experiments, will allow us to quantify the relationship between rates of biotransformation determined *in vitro* and benzene metabolite dosimetry *in vivo* based on quantitative, mechanistic data. Once this has been done for laboratory animals (mice and rats), we will have a sound basis for predicting metabolism and dosimetry in humans. These predictions should then lead to significantly improved risk assessments for human exposures to benzene, since they will allow us to track the amount of critical benzene metabolites that reach the target tissue, bone marrow. Risk assessments can then be based on target tissue dosimetry rather than on ambient air concentration. Given the differences among species and among individual humans, such assessments should provide much better characterizations of risk.

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