

COMMENTARY

DT-DIAPHORASE AND CANCER CHEMOTHERAPY

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Historical background

The first report documenting the discovery of DT-diaphorase, nowadays more properly referred to as NAD(P)H:(quinone acceptor) oxidoreductase (EC 1.6.99.2)[†], was published in 1958 by Ernster and Navazio [1]. They described the activity of a diaphorase or electron transfer enzyme in the soluble fraction of rat liver homogenates, which catalysed the oxidation of NADH and NADPH (then referred to as DPNH and TPNH) with equal facility. Subsequently, Ernster and colleagues went on to partially purify and characterize this apparently unique enzyme [2–4]. In addition to its lack of specificity for either nicotinamide dinucleotide, a striking feature of DT-diaphorase was its extreme sensitivity to dicoumarol [2]. This property initiated the use of dicoumarol as a potent diagnostic inhibitor of DT-diaphorase activity and stimulated research to determine whether the enzyme played a role in the metabolism of vitamin K or its epoxide [5–7]. A further unique property among NAD(P)H quinone reductases is the ability of DT-diaphorase to catalyse obligatory two-electron reduction [8], and it is this feature which is crucial to its role in cytoprotection against toxic chemicals.

Numerous original research papers and reviews have been published on DT-diaphorase. These have focused on various basic aspects of the enzyme, including its structure, reaction mechanism, biosynthesis and regulation, and also on its classical role as a protective, cellular defense mechanism against the cytotoxic and mutagenic effects of a variety of structurally diverse, potentially lethal compounds, including quinones, quinone epoxides, quinoneimines, azo dyes and C-nitroso derivatives of arylamines. The purpose of this commentary is to highlight more recent biochemical and molecular

advances which have increased our comprehension of the mechanism of action and regulation of DT-diaphorase and, in particular, its increasingly prominent role in current cancer chemotherapy.

Subcellular distribution and molecular biology

DT-diaphorase is a predominantly (> 90%) cytosolic enzyme [1–4]. Activity has also been detected in a number of subcellular organelles, including the endoplasmic reticulum [9], mitochondria [10] and Golgi apparatus [11]. The enzyme is widely distributed among organs, with particularly high levels being expressed in the liver, kidney and gastrointestinal tract [12–14].

The enzyme exists as a dimer of a molecular weight around 55,000 and contains two subunits of equal size and two molecules of FAD [8, 15]. At least two isofunctional forms of DT-diaphorase exist in mouse liver [16] and a minimum of three antigenically distinct variants can be detected in rat liver [17, 18]. In humans, genetic evidence indicates that the different forms of DT-diaphorase appear to be encoded by four gene loci (*DIA 1* to *DIA 4*) [19]. The product of one of these loci (diaphorase 4) has been characterized recently as a dioxin-inducible form of DT-diaphorase (termed NQO₁) [20]. It appears to account for the bulk of the DT-diaphorase activity measured in most tissues but does not occur in erythrocytes, which apparently have no measurable DT-diaphorase activity [21]. The gene for diaphorase 4 is located on chromosome 16 and is the orthologue of the rat NQO₁ gene [22]. Both the human and rat genes encode for a protein of 274 residues [22, 23]. Cloning, sequencing and expression of the human NQO₁ protein has shown that it is highly similar (84% homologous) to the rat NQO₁ protein [22] and that antisera against the rat enzyme cross-react with human NQO₁ [20].

More recently, a second constitutive human DT-diaphorase isozyme has been characterized (NQO₂) which is not induced by dioxin, and the gene encoding this product has been assigned to chromosome 6 [24]. The human NQO₂ cDNA codes for a protein of 231 amino acids, some 43 amino acids shorter than the NQO₁ protein [22, 24]. A comparison of the nucleotide sequences has demonstrated that the NQO₂ and NQO₁ cDNAs display 54% overall homology [24]. Interestingly, the NQO₂ gene locus is extremely polymorphic [24], and this finding may have important ramifications concerning inter-individual variation in both phar-

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[†] NAD(P)H:(quinone acceptor) oxidoreductase (EC 1.6.99.2) is the nomenclature recommended by the Enzyme Commission. DT-diaphorase is a trivial name for this oxidoreductase which has also been referred to previously as vitamin K reductase, phyloquinone reductase, menadiol reductase, nicotinamide menadiol oxidoreductase (NMOR), quinone reductase and quinone acceptor oxidoreductase. As suggested by Ernster (see Ref. 4), the more common term "DT-diaphorase" will be retained for the purpose of this commentary.

macodynamic and toxicological responses to certain xenobiotics.

Information regarding the substrate preferences of the different forms of DT-diaphorase is limited, but it is generally accepted that this class of enzymes displays marked overlapping substrate specificity [4, 15, 25]. Studies by Edwards and colleagues suggested that different forms of the enzyme may exhibit distinct affinities for the prototype substrates DCPIP and menadione [19], and similar conclusions were drawn by Segura-Aguilar and Lind using DCPIP, menadione, vitamin K₁ and benzo(a)pyrene-3,6-quinone [18]. Site-directed mutagenesis studies with rat NQO₁ have revealed regions which may be involved in NAD(P)H binding [26], and similar technology may prove useful in the elucidation of other domains which govern the binding of substrates for human DT-diaphorase.

Regulation of DT-diaphorase expression

The expression of many drug-metabolizing enzymes, including both phase I and phase II components, may be induced by a number of structurally dissimilar chemicals, including drugs, steroids, industrial chemicals and dietary constituents [27]. Depending on the resultant enzyme profile, enzyme induction may prove to be beneficial or deleterious to an organism [28]. In addition to being constitutively expressed in a variety of tissues, including stomach, kidney, lung, liver, colon and breast [4, 13, 14], DT-diaphorase may also be induced by polycyclic aromatic hydrocarbons [29], coumarins, fumarates, maleates, acrylates, cinnamates, dietary phenolic antioxidants and related compounds [30, 31]. Prochaska and Talalay [32] have conveniently categorized enzyme inducing agents into *bifunctional* and *monofunctional* inducers. Bifunctional inducers include compounds like polycyclic, planar aromatic hydrocarbons, azo dyes and 2,3,7,8-tetrachlorodibenzo-*p*-dioxin (TCDD*), which co-induce the activity of both phase I (most notably members of the cytochrome P450 1A family) and phase II enzymes [such as UDP-glucuronyl transferases, glutathione-*S*-transferases (GSTs) and DT-diaphorase]. Such compounds have been shown to mediate the induction of P450 1A enzymes through the Ah (aryl hydrocarbon) receptor [33, 34], and subsequent metabolism of these chemicals by this enzyme(s) may produce highly reactive, electrophilic metabolites [34]. By contrast, monofunctional inducers selectively increase the activities of phase II enzymes only [32]. Many monofunctional inducers have been shown to possess electrophilic centres or acquire them through metabolic activation [35, 36] and are classical Michael reaction acceptors [35].

These two classes of inducers are not mutually exclusive, as the metabolites of bifunctional inducers, such as β -naphthoflavone, may be regarded as monofunctional inducers *per se*. A series of structure-activity studies by Talalay, Prochaska and co-workers

[30–32, 35, 36] have identified some of the molecular features required by inducers of DT-diaphorase. Interestingly, these workers also noted that the potency of monofunctional inducers of DT-diaphorase parallels their facility to act as substrates for the GSTs [37].

Pickett and colleagues have simultaneously reached conclusions similar to those of Prochaska and Talalay through the use of a complementary, molecular approach [38–40]. This group has identified two “responsive elements” or regulatory regions which are involved in the control of gene expression in the rat by planar aromatic compounds [38] and phenolic antioxidants [39, 40]. One of these, termed the “xenobiotic responsive element” (XRE), is a sequence within the 5′-flanking region of the rat GST Ya subunit gene which is also found in multiple copies in the 5′-flanking region of the gene encoding cytochrome P450 1A1 (*CYP1A1*) [39]. The second region (termed the “antioxidant responsive element”, ARE) is again present in the 5′-flanking region of the rat GST Ya subunit gene and is responsive to the metabolites of polycyclic aromatic hydrocarbons and phenolic antioxidants [39, 40]. The ARE is present in the 5′-flanking region of the DT-diaphorase (NQO₁) gene and appears to be involved in the constitutive expression of the GST Ya gene [40]. The core sequences of the two responsive elements XRE and ARE are distinct [40]. This is in accord with their disparate functions: ARE responds to reactive oxygen species (including hydrogen peroxide) produced by the redox cycling of metabolites, while the XRE is responsive only to planar aromatic compounds, although triggering of either regulatory region will result in elevations in both GST Ya and DT-diaphorase. The XRE functions as a transcriptional enhancer when Ah receptor ligands bind to the receptor in responsive cells. The ARE appears to be a regulatory element which activates genes encoding enzymes involved in the cellular defense mechanisms against oxidative stress and may function in a manner similar to that described for the regulators of superoxide- and hydrogen peroxide-inducible genes (*SoxR* and *OxyR*, respectively) recently characterized in bacteria [41].

Thus, DT-diaphorase can be induced in response to stimuli from polycyclic aromatic hydrocarbons, chemically reactive metabolites and reactive oxygen species, all of which have been implicated in carcinogenesis [34, 42, 43]. However, the system is also apparently regulated at other levels as steroids may potentiate (up to 80-fold) the coordinate induction of P450 1A1, GST and DT-diaphorase by polycyclic aromatic hydrocarbons *in vitro* [44]. High concentrations of dexamethasone may also induce directly an immunoreactive form of DT-diaphorase which has a low affinity for menadione, although the exact mechanism by which this occurs has yet to be defined [44].

DT-diaphorase and cancer

In view of the potential for DT-diaphorase to detoxify a wide range of chemically reactive metabolites and thereby protect the cell from the toxic and mutagenic effects of these species, together with its induction by a variety of pro-carcinogens, it

* Abbreviations: TCDD, tetrachlorodibenzo-*p*-dioxin; GSTs, glutathione-*S*-transferases; XRE, xenobiotic response element; ARE, antioxidant responsive element; AZQ, diaziquone; and MMC, mitomycin C.

is evident that a perturbation in the expression of this enzyme would be likely to occur during carcinogenesis. Indeed, both DT-diaphorase enzyme activity and the corresponding mRNA have been shown to be elevated markedly in rat hepatic preneoplastic nodules induced during multi-stage chemical carcinogenesis in the Solt-Farber model (6- to 7-fold higher than in surrounding normal tissue), along with mRNA for the GST Ya and Yb genes [45, 46]. The elevated mRNA has been shown to be the consequence of hypomethylation of the gene rather than the result of gene amplification [29, 38] and appears to be a reversible process since the levels of DT-diaphorase decrease in redifferentiated nodules [45]. In addition to DT-diaphorase and GST, other phase II enzymes are elevated during hepatocarcinogenesis, including UDP-glucuronyl transferase, while the activities of phase I enzymes are concomitantly decreased. These observations suggest that DT-diaphorase may provide an early cellular defense against tumorigenesis.

In addition to the hyperexpression of DT-diaphorase in chemical carcinogen-induced hepatic preneoplastic nodules compared to surrounding normal tissue [29, 38, 45, 46], elevations in DT-diaphorase have also been observed in rat brain during carcinogenesis [47], leading to suggestions that increased levels of DT-diaphorase may be a common marker for neoplasia, at least in certain model systems [48, 49]. Moreover, there is now a considerable body of literature regarding the relative expression of DT-diaphorase in neoplastic versus normal tissue, including data not only from chemical carcinogenesis models [29, 38, 45, 46, 48, 50] but also from various cell lines [51–53], spontaneous tumours in rodents [54] and various human cancers [14, 55, 56]. These studies have collectively shown that DT-diaphorase is elevated not only in preneoplastic tissue but also in established tumours, although the majority of the information was obtained in rodent hepatoma models. However, the findings have been fortified recently in an important study by Cresteil and Jaiswal [57] which demonstrated a 20- to 50-fold increase in the levels of NQO₁ mRNA in human liver tumours and surrounding tissue as compared to the levels in samples from normal individuals.

Although these studies have consistently demonstrated an increase in DT-diaphorase in tumour with respect to normal tissues of the same organ, several papers have also been published to the contrary. For example, diethylstilbestrol-induced carcinogenesis in Syrian hamster kidney has been associated with marked decreases in the activities of both cytosolic and microsomal DT-diaphorases [58], although *in vitro* studies in a fibroblastic cell line from the same strain of species suggest that transformation of these cells with *N*-methyl-*N'*-nitro-*N*-nitrosoguanidine results in a marked elevation of DT-diaphorase activity [49]. Similarly, although Schlager and Powis [14] clearly demonstrated that DT-diaphorase activity is increased in human tumours of the lung, liver, colon and breast, a more recent study has suggested that the enzyme may be elevated in some human colorectal tumours but decreased or unchanged

in others [59]. The reasons for the apparent discrepancies between studies such as these are not fully understood. It may be that there are no hard and fast rules governing the expression of DT-diaphorase in tumour versus normal tissue. This may be accounted for by the marked genetic instability and biochemical heterogeneity of the cancer cell.

Possible species- and tissue-dependent regulation of expression of the enzyme may also be involved: for example, the study by Schlager and Powis [14] noted a marked decrease in the levels of human kidney tumour DT-diaphorase compared with the high levels observed in normal kidney. The diverse, multi-stage nature of neoplastic diseases in terms of their genetic, biochemical and cellular origin may also contribute to the variations in DT-diaphorase levels noted in different studies. In addition, it may well be that different classes of chemical carcinogens either decrease or increase DT-diaphorase depending on the tissue involved and the timing of the biopsy analysis. Furthermore, chemically induced cancers may affect DT-diaphorase expression in a different manner to neoplastic diseases initiated by other stimuli, such as viruses, radiation and spontaneous genetic changes in oncogenes and tumour suppressor genes.

The precise molecular basis for the alterations in DT-diaphorase expression seen in developing and established tumours remains poorly defined. Polymorphic loci on chromosome 6 (where NQO₂ is located) frequently show loss of heterozygosity during ovarian [60] and colorectal [61] cancer development. Loss of heterozygosity is associated with the unmasking of recessive mutations at tumour suppressor loci. The activity of NQO₂ may be important in carcinogen and anticancer drug metabolism, and it is therefore an intriguing possibility that somatic deletion at NQO₂ may play a role in tumour development and drug resistance. This hypothesis should be examined in more detail and the presence of several restriction fragment length polymorphisms at the NQO₂ locus [24] indicates that such a study should be technically feasible. Similarly, genetic alterations on chromosome 16, such as the loss of heterozygosity observed in breast cancer [62], may affect the expression of NQO₁ during tumour development.

Although not previously reported, the possibility also exists for amplification or translocation of DT-diaphorase in tandem with oncogenes and tumour susceptibility genes [63]. The effects of altered expression of positive and negative cancer genes on DT-diaphorase expression do not appear to have received much attention. It is interesting that the human NQO₁ promoter region contains putative binding sites for the AP-1 protein complex and the DNA-binding protein product of the *jun* oncogene [57]. The levels of these regulatory proteins can be altered during transformation, and future studies should be directed at defining their role in the regulation of the NQO₁ gene.

DT-diaphorase and the action of anticancer drugs

Although DT-diaphorase was originally considered to function as a protective enzyme which detoxifies a range of chemically reactive metabolites, recent

evidence has shown that this flavoenzyme, like many other drug-metabolizing systems, may paradoxically activate certain xenobiotics [64, 65]. In view of the general consensus that DT-diaphorase is over-expressed in tumour cells, particularly those of the liver, breast and colon [14, 31, 55–57] and the realization that DT-diaphorase may either activate or detoxify xenobiotics, depending on their chemistry [64, 65], it has become increasingly important to establish the role of DT-diaphorase in the sensitivity of tumours to anticancer drugs. Indeed, there has recently been a surge of interest in mechanistic toxicology studies designed to assess the role of DT-diaphorase in the bioactivation and/or detoxication of a number of established and experimental anticancer agents. These include the bioreductive alkylating aziridiny benzoquinones such as diaziquone (AZQ), mitomycin C (MMC), and the indoloquinone EO9, together with the dinitrophenyl aziridine CB 1954 and the benzotriazine-di-*N*-oxide SR 4233. The structures of these compounds are shown alongside menadione in Fig. 1.

In addition to understanding the molecular mechanisms responsible for the sensitivity and resistance of tumour cells to these agents, two particular aspects of the role of DT-diaphorase in the metabolism of such compounds are of particular relevance to cancer chemotherapy. The first is the possibility that measurement of DT-diaphorase in tumour biopsies, known as “enzyme profiling”, would provide a possible basis for selecting those patients most likely to benefit from a particular drug treatment. The second is the opportunity to design improved anticancer agents which would either be activated by DT-diaphorase in tumours or detoxified by the enzyme in normal tissues, a process we have termed “enzyme-directed bioreductive drug development” [66].

Diaziquone (AZQ)

AZQ is one of a number of aziridiny benzoquinone analogues synthesized at the National Cancer Institute, U.S.A., by Driscoll and co-workers [67–69]. Extensive screening of quinoid compounds for anti-tumour activity revealed that *p*-benzoquinone analogues containing aziridine moieties were among the most active against many tumour models [68]. AZQ was selected on the basis that it would penetrate the central nervous system, while retaining adequate water solubility to be administered parenterally [67, 68]. Subsequently, this bioreductive drug has entered clinical trials in the U.S.A., some of which have indicated activity in brain tumours and non-lymphocytic leukaemia [70, 71].

Aziridiny benzoquinone anticancer drugs are believed to undergo activation to potent alkylating agents upon reduction of the quinone moiety [72]. Reduction of the quinone nucleus to either the one-electron reduction product, the semiquinone, or the two-electron reduction product, the hydroquinone, is thought to facilitate protonation of the aziridine ring and subsequent ring opening leading to the formation of the ultimate potent alkylating species [73]. Quinone bioreductive drugs may be enzymatically reduced by a direct two-electron reduction catalysed by DT-diaphorase [4, 15, 25] or via one-

electron reduction by a variety of enzymes, including NADPH-cytochrome P450 reductase [72, 74]. Although either of these routes of bioactivation could, in theory, result in the formation of the ultimate toxic metabolite of AZQ, recent evidence has shown that DT-diaphorase may be a major reductase involved in the bioactivation of AZQ to genotoxic and cytotoxic metabolites in cancer cells [65, 75, 76]. Interestingly, the hydroquinone product of the reduction of AZQ by DT-diaphorase may auto-oxidize in air and the ensuing redox cycling may also contribute to the cytotoxic and genotoxic effects of this drug [76].

In vitro reduction of AZQ to a product which introduces DNA interstrand cross-links has been demonstrated using an agarose gel technique [77]. This cross-linking is facilitated at low pH [77]. In addition, it has been suggested that DT-diaphorase may bioactivate AZQ analogues to sequence-selective alkylating species and that this effect is a function of the chemistry of the substrate [78]. AZQ has been shown to undergo obligatory two-electron reduction by DT-diaphorase from MCF-7 human breast carcinoma cells [76], HT-29 human colon carcinoma cells [75] and rat liver [75]. Studies with two human colon carcinoma cells lines have shown that cells containing at least 300-fold higher levels of DT-diaphorase (HT-29 cells) may be around 2-fold more sensitive to AZQ than cells which express virtually no activity (BE cells). This occurs despite the fact that the sensitive cells exhibit higher levels of reduced glutathione and GSTs [75], both of which may be involved in cellular defense mechanisms against AZQ [65]. The differences in the levels of these additional cytoprotective mechanisms may explain why there is not an even greater difference in sensitivity between the two cell lines, given the disparity in DT-diaphorase levels. Additionally, the involvement of alternative bioreductive enzymes cannot be excluded.

Mitomycin C (MMC)

MMC is a naturally occurring antibiotic which exhibits activity against a variety of animal and human tumours [79]. It is used quite widely in human gastrointestinal and bladder cancer therapy [79]. The precise mechanisms responsible for the anti-tumour effects of MMC are unclear, although bioreductive activation to genotoxic metabolites appears to be a prerequisite for its activity [80, 81]. Chemical reduction and acid-mediated degradation of MMC have also been shown to activate the drug to a reactive form which can cross-link adjacent guanines at the N² position in the minor groove of DNA via the 1 and 10 positions of the MMC molecule [82, 83]. As for AZQ, generation of a highly reactive bifunctional alkylating metabolite may occur through one- or two-electron reduction of the quinone moiety [81, 84]. The one-electron reduced semiquinone intermediate may give rise to reactive oxygen species through interactions with molecular oxygen, which could account for some of the activity demonstrated in normoxic tumour cells [85]. MMC displays modest preferential toxicity towards hypoxic as opposed to aerobic (or normoxic) tumour cells *in vitro* and *in vivo* [86–88]. Cellular reductases which reduce MMC

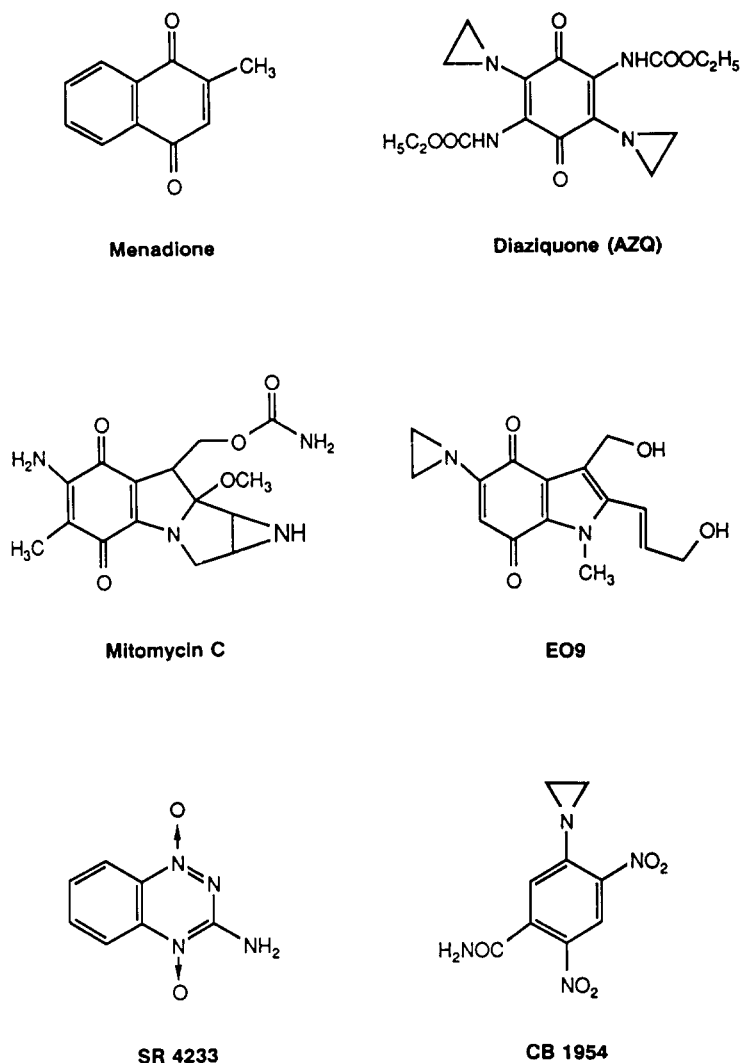


Fig. 1. Chemical structures of the prototype quinone menadione and several anticancer drugs which have been shown to be substrates for DT-diaphorase.

under anaerobic conditions include cytochrome P450 reductase [84, 89], xanthine oxidase [89] and DT-diaphorase [90]. However, the role of DT-diaphorase in the reductive bioactivation of MMC has been the subject of much controversy [91].

Early studies by Sartorelli and co-workers [84, 92, 93] relied on the use of dicoumarol as a specific inhibitor of DT-diaphorase to probe for the role of this enzyme in the cellular toxicity of the drug. Dicoumarol was shown to inhibit the cytotoxicity of MMC in EMT-6 mouse mammary tumour cells, which suggested a role for DT-diaphorase in the bioreductive activation of this drug. However, under hypoxic conditions, MMC cytotoxicity was increased by dicoumarol in these same cells [84, 92, 93]. At this time, the authors concluded reasonably that DT-diaphorase activates MMC in air but detoxifies the drug under hypoxic conditions. However, problems associated with the

use of dicoumarol as a cellular diagnostic inhibitor of DT-diaphorase have been highlighted recently [91, 94]. Indeed, when one considers that dicoumarol has been shown to exert a plethora of effects on the cell, including the uncoupling of mitochondrial respiration [4] and inhibition of UDP-glucuronyl transferases [95] and xanthine oxidase [96], results obtained in studies relying solely on this line of evidence should be interpreted with extreme caution.

Subsequent, unsuccessful attempts to demonstrate that MMC was a substrate for purified DT-diaphorase from rat liver [97], human kidney [98] and DT-diaphorase-fortified preparations from human HT-29 colon carcinoma cells and rat Walker 256 mammary tumour cells [91] disputed the role of DT-diaphorase in the metabolism of MMC [91]. However, more recently, MMC has been shown to be a substrate for DT-diaphorase purified from both rat liver [99], rat Walker tumour [100] and HT-29

human colon cancer cells [99]. The metabolism of MMC, unlike the majority of other DT-diaphorase substrates, is markedly pH dependent, being readily apparent only at pH < 7 [99]. This marked pH dependence in DT-diaphorase-mediated metabolism has also been demonstrated for porfiromycin [101], an MMC analogue, and has been explained in terms of the ambivalent nature of the quinone methides formed upon reduction of these drugs [90, 101, 102]. The quinone methide of MMC can act as an electrophile at pH 7.8 and may alkylate the enzyme, resulting in a loss of catalytic activity. However, at pH 5.8 it can be protonated giving rise to 2,7-diaminomitosene, thereby preserving enzyme activity. The pharmacological relevance of bioreductive activation at such low pH levels remains to be established. However, recent studies with a more sensitive spectrophotometric assay, showed that MMC was reduced, albeit at a low rate and with a high K_m (around 1 mM), by rat Walker tumour DT-diaphorase at pH 7.8 [100]. Perhaps a relatively small number of DT-diaphorase-activated molecules, resulting in potent DNA cross-links, would be sufficient to account for the cytotoxicity of MMC. But it is likely that other reductases which may exhibit a higher affinity for MMC are also involved [103]. In contrast to AZQ, the hydroquinone of MMC does not readily auto-oxidize [99] and hence redox cycling is unlikely to accompany reduction of MMC by DT-diaphorase in normoxic tissues.

Studies with HT-29 and BE cells have demonstrated that the cells expressing higher levels of DT-diaphorase were some 6-fold more sensitive to the toxic effects of MMC [99]. Furthermore, HT-29 cells were also more susceptible to the development of MMC-induced DNA inter-strand cross-links, which could be reduced markedly by dicoumarol [99]. These data are in agreement with previous studies conducted in L5178Y/HBM10 lymphoblasts, which possess 24-fold higher levels of DT-diaphorase than the parent line L5178Y [104]. These cells, although deemed to be "quinone resistant" having been induced by exposure to hydrolysed benzoquinone mustard [104], were found to be highly sensitive to MMC [104] and also trenimon (a therapeutically obsolete aziridinybenzoquinone which is an excellent substrate for DT-diaphorase) [105]. These results are consistent with the hypothesis that DT-diaphorase bioactivates both these anticancer agents under aerobic conditions. Several studies employing more molecular approaches have supported this hypothesis and have demonstrated that a loss of DT-diaphorase activity in Chinese hamster ovary cells [103] and non-transformed human skin fibroblasts from a cancer-prone family [106, 107] may render these cells resistant to the cytotoxic effects of MMC and its analogues, such as the methylated derivative porfiromycin. Furthermore, it has been suggested that there may be a causal link between decreased levels of DT-diaphorase and the predisposition of such individuals to cancer, presumably because these subjects have a diminished capacity to detoxify and eliminate potential carcinogens [108].

Indoloquinone EO9

EO9 is the lead compound in a series of

indoloquinones synthesized by Oostveen and Speckamp [109]. The drug is structurally related to the quinone antitumour antibiotic MMC and is about to enter clinical trial as an anticancer agent with the EORTC in Europe on the basis of its distinct antitumour profile and lack of myelosuppression. Recent data from our laboratory have shown that EO9 is metabolized by DT-diaphorase in rat Walker 256 mammary tumour cells and human HT-29 colon carcinoma cells [110]. The rat enzyme reduced EO9 at a much faster rate than the human enzyme, and the respective apparent K_m values (around 3 and 15 μ M) suggested that EO9 may have a reduced affinity for the human enzyme [110]. Using a highly purified DT-diaphorase preparation from the rat Walker 256 tumour cell line, EO9 was found to undergo reductive bioactivation under aerobic conditions *in vitro* to a reactive species which produced single-strand breaks in pBR 322 plasmid DNA [110]. Our recent data have also shown that EO9 causes DNA cross-links in Walker tumour cells (Baily SM, Knox RJ and Workman P, unpublished observations). In contrast to MMC, the metabolism of EO9 is not pH dependent in the range 5.8 to 7.8 [110]. Moreover, the V_{max} for the Walker enzyme is 20–30 times higher than for MMC and only 3–4 times lower than that for menadione [110].

These findings suggest that tumours rich in DT-diaphorase may be particularly sensitive and therefore represent attractive targets for EO9. Indeed, our own recent unpublished data (with Dr. J. Plumb) have shown that EO9 is around 25-fold more toxic towards DT-diaphorase-rich HT-29 human colon carcinoma cells compared to enzyme-deficient BE cells. In addition, when the DT-diaphorase levels were compared in two transplantable mouse colon adenocarcinomas growing as solid tumours in their syngeneic hosts, it was found that the tumour more sensitive to EO9 expressed around 15 times the level of DT-diaphorase in the resistant tumour, whereas the activities of cytochrome P450 reductase were identical [111]. However, further studies are required to elucidate the relative roles of one-electron versus two-electron donating enzymes in the bioactivation and detoxication of this novel anticancer agent.

Dinitrophenylaziridine CB 1954

CB 1954 was synthesized by Kahn and Ross [112, 113] at the Chester Beatty Institute, U.K., as one of a series of anti-tumour nitrophenylaziridine analogues. It proved to be highly potent and selective in its effects against the Walker 256 rat tumour line [112–114] but comparatively inactive against a series of other tumours originally tested [114, 115]. The demonstration of the remarkable and selective activity of CB 1954 towards the Walker tumour [112–114] initiated extensive studies on the mechanism of action of this agent [52, 116, 117]. Although CB 1954 is, chemically, a monofunctional alkylating agent by virtue of its aziridine ring, Knox and colleagues have shown that the selectivity of action of CB 1954 is a consequence of its ability to undergo aerobic nitroreduction by DT-diaphorase to a bifunctionally reactive species [52, 117].

DT-diaphorase in Walker cells has been shown to

reduce the nitro group in the 4-position of CB 1954 to the hydroxylamine derivative [52]. The product, 5-(aziridin-1-yl)-4-hydroxylamino-2-nitrobenzamide, is a highly toxic metabolite which reacts bifunctionally in cells and induces DNA-DNA interstrand cross-links [52, 117]. Further studies demonstrated that DT-diaphorase-rich rat cell lines other than the Walker 256 line were sensitive to CB 1954 but human cells were comparatively resistant, even though they expressed significant levels of DT-diaphorase [118]. The species differences in sensitivity to CB 1954 may be explained by inequalities in the kinetics of CB 1954 reduction by the human and rat forms of DT-diaphorase; both forms are capable of reducing CB 1954 to the hydroxylamine but the rate of reduction by the human enzyme is very much lower [118].

Interestingly, all cell types so far examined appear to exhibit a similar sensitivity to the hydroxylamine of CB 1954 [118]. Moreover, this compound has been shown to induce DNA-DNA interstrand cross-links in cells but not in naked DNA, suggesting that a further activation step may be required to convert the hydroxylamine to the proximal reactive species [117]. The situation thus appears analogous to that observed with a wide range of chemical toxins, including 4-nitroquinoline 1-oxide and *N*-acetylaminofluorene, whereby the respective hydroxylamine is relatively chemically inert *per se* and requires further metabolism by phase II (conjugation) enzymes to elicit its cytotoxic or mutagenic effects [119, 120]. Indeed, a recent report by Knox and co-workers [121] has shown that the hydroxylamine of CB 1954 can be activated non-enzymatically through a chemical reaction with acetyl-coenzyme A and other thioesters. The ultimate DNA reactive species was not defined conclusively but it seems likely that it is 4-(*N*-acetoxy)-5-(aziridin-1-yl)-2-nitrobenzamide or a further derivative of this compound.

As a direct result of these detailed enzymological studies, Sunters and co-workers [122] and Connors [123] have suggested that CB 1954 may be a useful drug for antibody directed enzyme pro-drug therapy or ADEPT. These authors are looking at the potential for using CB 1954 in combination with an immunoconjugate comprising Walker rat DT-diaphorase and an anti-carcino-embryonic antigen monoclonal antibody in the ADEPT system against colon cancer [122]. In this context, the relatively poor performance of human DT-diaphorase towards CB 1954 is a significant advantage for selective chemotherapy.

Benzotriazine di-N-oxide SR 4233 (WIN 59075)

SR 4233 (WIN 59075; 3-amino-1,2,4-benzotriazine-1,4-oxide) is the lead compound in a series of highly selective hypoxic cytotoxins, the benzotriazine di-*N*-oxides, which exhibit improved efficacy and increased selectivity compared with their predecessors, the mitomycins and nitroimidazoles [124]. The compound is reduced preferentially under anaerobic conditions to both two- and four-electron reduction products [125, 126], neither of which is toxic to cells under aerobic or hypoxic conditions [125, 127]. Consequently, it has been proposed that a one-electron reduced species, by definition a free

radical intermediate, is the most likely damaging metabolite [125, 128, 129]. The principal reductases which catalyse this reductive bioactivation are cytochrome P450 and NADPH:cytochrome P450 reductase [126, 130].

More recent data from our laboratory have shown that SR 4233 may be metabolized by DT-diaphorase from the Walker 256 rat carcinoma to both two- and four-electron reduced products [127, 131]. Detailed characterization of the kinetics of this reduction demonstrated that SR 4233, like mitomycin C and CB 1954, does not appear to be a particularly good substrate for the purified Walker enzyme, the K_m and V_{max} being 1.2 mM and 8.6 nmol/min/ μ g protein, respectively [131]. However, the direct, obligatory two-, four- and, possibly, six-electron reduction of SR 4233 would bypass the formation of the one-electron reduced drug free radical, and DT-diaphorase may therefore provide an important cellular defense against this novel hypoxic cytotoxin.

Enzyme-directed bioreductive drug development

We have proposed that the selectivity of bioreductive anticancer agents could be enhanced not only by tumour hypoxia, but also by increased expression of key reductase enzymes in cancer cells [66, 100]. The relative role of DT-diaphorase and other enzymes in the activation of cancer drugs under normoxic versus hypoxic conditions, remains unclear, and is clearly complicated for mitomycin C [91, 99]. Nevertheless, we have further suggested that even greater selectivity could be achieved by tailor-making drugs to be activated specifically by DT-diaphorase or indeed other appropriate reductase enzymes [66].

DT-diaphorase from various sources is available in crystalline form [52, 132]. It has not yet been possible to obtain a high resolution X-ray structure although preliminary data have been reported [133]. Current efforts are therefore concentrating on a medicinal chemistry approach, i.e. determining the effects of manipulating various structural features of drug molecules on their ability to act as substrates for DT-diaphorase. These results can then be correlated with cytotoxicity data in DT-diaphorase rich and deficient cell lines, with and without enzyme inducers or inhibitors. Construction of an appropriate structure-activity data base might then allow a more rational drug design approach to be implemented. Such studies are in progress with analogues of AZQ, EO9, MMC and CB 1954.

The effect of replacing the carbamoyl ester ethyl groups in AZQ with alternative alkyl moieties has been studied by two groups. Work in our laboratory has shown that the order of reduction rates for the purified Walker rat tumour enzyme was di-*n*-butyl > di-methyl > di-*iso*-butyl > di-*n*-propyl = di-ethyl > di-*iso*-propyl > di-*sec*-butyl [134]. The order of cytotoxic potency in Walker cells was very comparable: di-*n*-butyl > di-methyl > di-ethyl > di-*n*-propyl > di-*iso*-butyl > di-*sec*-butyl > di-*iso*-propyl. Although the exact order was slightly different, a similar overall relationship was found between reduction by purified rat liver enzyme and cytotoxicity in HT-29 human colon carcinoma cells [135].

For EO9 analogues, replacement of the aziridine group with methyl aziridine markedly decreased both Walker enzyme reduction rate and cytotoxicity [134]. Aziridine ring opening to the hydroxyethylamino derivative essentially eliminated both properties. Replacement of aziridine by methoxy reduced the rate of DT-diaphorase metabolism only slightly, but lowered cytotoxicity considerably. Thus, the aziridine appears to contribute to cell killing by regulating DT-diaphorase activation and also through an enzyme-independent effect (presumably DNA cross-linking). For both the indoloquinone and the AZQ analogues, it appears that the rate of reduction is not a simple function of redox potential, or "electron affinity", and further studies are required to elucidate the major contributing factor(s). Structural variation also affects the pH-dependent metabolism of mitomycins by rat liver DT-diaphorase. Thus, mitomycins A and B which contain a 7-methoxy group were reduced at both pH 7.8 and 5.8, whereas mitomycin C was an inhibitor at neutral pH [101].

Major effects of structural modification on reduction by the Walker rat and human HepG2 cell DT-diaphorase have also been noted with CB 1954 analogues. As with EO9, the aziridine ring-opened derivative was a very inefficient substrate. However, no clearly predictable structure-activity relationship is yet emerging.

The observation that both CB 1954 and EO9 are much poorer substrates for the human vis-a-vis the rodent form may give a useful guide to the design of human-specific drugs [100, 118, 134]. This difference, which explains why human cells that express equivalent DT-diaphorase activity are much less sensitive to CB 1954, is probably related to the charge at amino acid 124 within the proposed substrate binding region [118]. This information could prove useful to new drug design. In fact, derivatives of both CB 1954 and EO9 with much improved performance for the human enzyme have now been found by screening against the latter enzyme [118, 134].

Future perspectives

A steady accumulation of data testifies to the increased expression of DT-diaphorase in tumour tissues from experimental animal models and patients. The regulatory mechanisms controlling the level of expression of DT-diaphorase genes are becoming clearer. The much higher levels of NQO₁ mRNA seen in human hepatocarcinoma [57] correlate with similar results in rodent models, where hypomethylation is a major factor. However, much further work needs to be done to characterize the molecular basis for changes in DT-diaphorase which occur in human cancers.

The continuing reports of high levels of expression of DT-diaphorase in human tumours strengthen the case for increasing efforts to design improved anticancer drugs for activation by the enzyme. Results with AZQ, MMC, EO9 and CB 1954 support the view that high DT-diaphorase levels can confer a selective tumour cell killing by these agents, although other sensitivity and resistance genes are certainly involved in the overall pattern of response.

We are not yet in a position to design improved bioreductive drugs from first principles. The ongoing elucidation of structure-activity relationships for bioreduction and cytotoxicity are giving us a hint of some of the molecular features which are either advantageous or disadvantageous. We are now aware that bioreduction can lead to pH-dependent enzyme inactivation. Indeed, those interested in designing irreversible inhibitors of enzymes would see some of our currently available agents as excellent candidates for mechanism-based inhibitors, and it is perhaps surprising that this is not a bigger problem.

In the cancer clinic, use of DT-diaphorase-activated drugs is currently restricted to MMC and AZQ. The balance of opinion suggests that high enzyme activity is likely to be a predictive factor. However, the pharmacological significance for MMC is undermined by the low pH requirement. Current thinking is moving away from an acidic intracellular milieu in tumours, favouring instead the view that the low pH is restricted to the extracellular fluid. Recent magnetic resonance spectroscopy studies suggest that human brain tumours have a slightly alkaline pH. However, local intracellular acidic environments may exist. It is probably advantageous that activation of AZQ and the developmental indoloquinone EO9 is not pH dependent within the normal physiological range.

Very few data are available as regards the role of DT-diaphorase in the control of tumour response *in vivo*. The recent correlation between EO9 response and enzyme activity in mouse colon carcinomas [110] has suggested the potential value of further work in this area. Moreover, we recommend clinical studies correlating tumour response to EO9 with DT-diaphorase activity. Similar clinical studies with AZQ in brain tumours might be considered.

One of the factors which may complicate any simple relationship between DT-diaphorase activity and drug sensitivity is the participation of additional bioreductive enzymes. This requires greater attention, including *in vivo* mechanistic studies. The relative involvement of one-electron donating enzymes needs to be established, especially, for example, the degree of competition between DT-diaphorase and cytochrome P450 reductase.

Another controversial issue is the comparative role of DT-diaphorase under hypoxic versus normoxic conditions. The classical work from Sartorelli and co-workers [84, 92, 93] suggested that the enzyme bioactivates mitomycin C under hypoxia but is protective in air. Similar studies need to be performed with other bioreductive agents. As mentioned earlier, the above experiments were highly dependent on the use of dicoumarol as a specific DT-diaphorase inhibitor. However, because of its lack of specificity, additional model systems should be used in future studies. These include naturally occurring high and low DT-diaphorase expressing lines (for example, HT-29 and BE cells); cell lines treated with inducers of DT-diaphorase; cells with induced resistance which express altered enzyme levels; and low DT-diaphorase expressing lines which have been transfected with the relevant gene under the control of the appropriate promoter.

It is also essential to continue studies aimed to

elucidate the mechanism of resistance to bioreductive anticancer agents. Of particular interest would be the possibility of selecting for cells with down-regulated, mutated or deleted DT-diaphorase. This could be conducted with MMC, AZQ, EO9 and CB 1954. However, a previous study with MMC resistance revealed a down-regulation of P450 reductase with no change in DT-diaphorase [136]. Connections with multidrug resistance also require clarification.

Should clinical resistance to certain bioreductive drugs prove to involve reduced expression of DT-diaphorase, we can imagine an attractive strategy to exploit the new enzyme profile. This would involve treating the resistant tumour with an agent which is detoxified by DT-diaphorase. At the moment, the best potential candidate for this would be the benzotriazine-di-N-oxide SR 4233. The converse might also apply. Thus, an agent like SR 4233 might induce resistance via up-regulation of DT-diaphorase and one could then treat the resistant tumour with DT-diaphorase-activated drugs. Possibilities also exist for selective induction or inhibition of DT-diaphorase in tumour versus normal cells. Another neglected area is the involvement of DT-diaphorase in the sensitivity or resistance of normal tissues to bioreductive agents. Such analyses may decipher why MMC is myelosuppressive while the indoloquinone EO9 is not.

As in other areas of biochemical pharmacology and toxicology, much work remains to be conducted on the roles of DT-diaphorase in cancer chemotherapy. It seems likely that the next few years will see further substantial advances in our understanding of the mechanism of drug action, together with the results of clinical studies correlating enzyme activities with drug response and the design of improved agents for activation by the human forms.

Note added in proof. A recent study shows that the anthraquinone-based antitumour agents mitoxantrone, daunorubicin and ametantrone are substrates for rat liver DT-diaphorase; the reaction can generate superoxide anions, hydrogen peroxide and hydroxyl radicals, probably by slow auto-oxidation of the corresponding hydroquinones [137].

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