

Improving the decision-making process in structural modification of drug candidates: reducing toxicity

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The rule of three, relating to activity–exposure–toxicity, presents the single most difficult challenge in the design and advancement of drug candidates to the development stage. Absorption, distribution, metabolism and excretion (ADME) studies are widely used in drug discovery to optimize this balance of properties necessary to convert lead compounds into drugs that are both safe and effective for human patients. Idiosyncratic drug reactions (IDRs; referred to as type B reactions, which are mainly caused by reactive metabolites) are one type of adverse drug reaction that is important to human health and safety. This review highlights the strategies for the decision-making process involving substructures that, when found in drugs, can form reactive metabolites and are involved in toxicities in humans; the tools used to reduce IDRs are also discussed. Several examples are included to show how toxicity studies have influenced and guided drug design. Investigations of reactive intermediate formation in subcellular fractions with the use of radiolabeled reagents are also discussed.

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▼ There is no doubt as to the value of predicting the potential toxicity of compounds as early as possible in the drug discovery process. Pharmaceutical companies are coming under increasing pressure to prove the long-term safety of their products more precisely, and to provide more data on them. Failure to address these concerns successfully causes companies to withdraw drugs from the market; this not only presents human health consequences, but also has a negative economic and public-relations impact on the pharmaceutical industry. Because of human health-safety concerns, a long list of drugs have been withdrawn from the market, the most recent example being Merck pulling Vioxx off the market after finding it doubled risks of heart attack and stroke after 18 months' use. Failures in the drug discovery process account

for a substantial part of the cost of drug development because many compounds are discarded after substantial investment owing to unforeseen toxicological effects.

One of the major challenges in drug discovery is to accurately predict which new drugs will be associated with a significant incidence of IDRs. An important consideration is that any screening process will produce false results, both positive and negative, and our goal must be to reduce or eliminate these, which will in turn lead to improved drug safety. The potential for IDRs can be minimized by appropriate structural modifications to the drug candidate in early discovery. Until recently, most of the optimization effort was directed toward the potency of the leads against the target of interest, and selectivity among subtypes, whereas the equally important aspects of toxicities were left to be addressed at the end of a potency optimization cycle, sometimes disqualifying the obtained candidates [1–8]. The ability to produce this information on potential toxicity early in the discovery phase has become increasingly important as a basis for judging whether a drug candidate merits further development. The effort to reduce IDRs during drug discovery has mostly been a combination of empirical methods and trial and error. This has led to an accrued interest in applying substructure analysis to the problem of toxicological predication, which is a process aimed at identifying the structural features that confer toxicological properties to molecules. One approach to this dilemma would be to thoroughly explore the structure requirements for *in vitro* pharmacological activity through combinatorial synthesis and identify the key structural features

that are essential for activity for each chemical series, and then attempt to improve the metabolism and toxicity properties through structure modifications to the regions of the molecule that have little or no impact on the desired activity. Thus one can maintain an optimal level of potency while introducing structural features that will improve the metabolism and toxicity characteristics.

Herein, we will discuss strategies to deal with reactive metabolites, and tools used to reduce them during the drug discovery process. Also, some of the chemical substructures that form reactive metabolites and are involved in toxicities in humans are discussed. Several examples from literature are included to show how toxicity studies have influenced drug design and strategies and have helped to facilitate improvements. Improved screening of reactive intermediate formation in subcellular fractions with the use of radiolabeled reagents is also discussed.

Reducing toxicity

One of the most important keys to successful drug design and development is a process of finding the right combination of multiple properties such as activity, toxicity and exposure. It is very important first to determine, and then to optimize, the exposure–activity–toxicity relationships or the rule of three for drug candidates, and thus their suitability for advancement to development. Toxicity problems, especially those which may only occur under unusual or idiosyncratic conditions during the late stages of drug development, are one of the most devastating surprises for pharmaceutical companies [9–13]. Variations in human drug metabolizing enzymes can produce subtle evidence of potential toxicity, or none at all, during pre-clinical safety studies. Such problems are also unlikely to show up in all but the largest clinical trials, but if the side effects are serious, can result in product withdrawal. There are indications that some substructures found in drugs can form reactive metabolites that are involved in toxicities in humans. These substructures include arylacetic and arylpropionic acids, aryl hydroxamic acids, oximes, anilines, anilides, hydrazines, hydrazides, hydantoins, quinones, quinone methides, nitroaromatics, heteroaromatics, halogenated hydrocarbons, some halogenated aromatics, chemical groups that can be oxidized to acroleins, and medium-chain fatty acids. Reactive metabolites are unstable, and are intermediates to more stable metabolites. Table 1 shows several examples of drugs that undergo metabolic activation and cause adverse reaction in humans, which have been withdrawn from the market or restricted in use with toxicity warnings. Clearly, a drug candidate that does, or might, metabolize to such substructures would increase the risk of failure or withdrawal.

Considerations

To illustrate how to reduce or eliminate reactive metabolites, consider drug-induced adverse reactions, particularly idiosyncratic drug reactions (IDRs; referred to as type B reactions). Such reactions are a major issue because, given current techniques and approaches, they often go undetected until late in the process, or even after the drug has been released onto the market, and the consequences are disastrous for all concerned. IDRs mediated through a reactive metabolite can be associated with several mechanisms [10–13]. Currently there is no general approach or ‘one-size-fits-all’ screen that addresses idiosyncratic reactions, because of the difficulties in understanding the mechanisms of these reactions and in accurately predicting clinical results. Some of the strategies under consideration to improve our understanding of these mechanisms and to develop safer drugs include:

- Avoidance or flagging of chemical functional groups that are known to cause toxicity during drug design (e.g. aromatic and hydroxy amines, phenols, epoxides, acyl halides, acyl glucuronides, thiopenes, furans, fatty acid-like compounds, hydroxylated metabolites and quinines).
- Development of suitable *in vitro* and *in vivo* systems to elucidate the role of short-lived, potentially toxic metabolites in the pathogenesis of idiosyncratic toxicity.
- Identification of chemical functional groups that are associated with low or no toxicity, and development of more metabolically stable drugs to potentially avoid metabolic interactions.

Although there is no evidence that safer drugs will be identified by addressing the following questions in the drug discovery/development stages, it is considered that drugs without these potential liabilities may have a better safety profile:

- Does the candidate have the potential to form reactive metabolites based on chemical ‘structure-alerts’?
- Does the compound form reactive metabolites in liver, blood or skin tissue or cells?
- Is the binding of the drug > 50 pmol/mg of microsomal protein?
- Does the candidate form reactive intermediates that are able to ‘travel’ and react covalently with other tissues?
- What proteins are affected and what are the effects of the modified proteins?
- Which genes are affected? Could these affected genes generate a potential IDR?
- What cellular functions are affected by the reactive intermediate?
- Bioaccumulation in liver?
- Glutathione depletion?
- Drug-drug interactions?
- Ames and/or micronucleus positive responses?

It remains to be determined whether the answers to these questions will allow the pharmaceutical industry to reduce or eliminate IDRs. Because the major organs involved in IDRs are the liver, skin and bone marrow, preclinical approaches should consider these target organs to study the effects of reactive intermediates. Thus, a sound strategy should evaluate three major elements: reactive intermediate characterization, covalent binding and biological impact and/or function.

Key tools and strategies to improve drug safety

Many tools are in the exploratory stage, encompassing computational approaches and experimental assays to predict the formation of reactive metabolites *in vivo* and their role in IDRs [9]. For example, during *in vitro* testing, if significant protein binding is found, an attempt is made to discover the chemical basis for the binding so that it can be designed out of the structure. Another potential technique is to trap reactive intermediates by incubating them in human liver microsomes. To evaluate the biological effects of reactive intermediates initially, methods for cytotoxicity testing including tests for cell viability, membrane integrity, protein synthesis, DNA synthesis, glutathione [GSH] level, apoptosis, free radical production, lipid peroxidation, enzyme inhibition and other enzymatic activities due to oxidative stress are being developed for early drug discovery. Results suggest that these types of screens can be used to differentiate known toxicants from relatively safe drugs. Table 2 presents some of the current tools; below we will summarize the advantages and disadvantages of the current tools and relate them to the problems facing those in drug discovery and development, and attempt to synthesize these tools and strategies into an alternative strategy.

In silico screens as filtering process

A promising new trend in early drug discovery is the collaboration between medicinal and computational chemists and drug metabolism scientists seeking to identify and eliminate potential toxic chemical groups. Structure–activity relationships are well-known as a means to identify several toxic end points. One way to improve screening for such potentially toxic compounds would be to increase the use of *in silico* testing methods at earlier stages in drug discovery [2,4,14,15]. Several programs such as TOPKAT, CASE/MULTI-CASE, DEREK, HazardExpert and OncoLogic are commercially available for the prediction of mutagenicity and carcinogenicity based on chemical structure. These available commercial systems for mutagenicity and/or carcinogenicity prediction differ in their specifics, yet most fall into two major categories. One is automated approaches that rely on the use of statistics for extracting

correlations between structure and activity. The others are knowledge-based expert systems that rely on a set of programmed rules distilled from available knowledge and human expert judgment. The advantages of *in silico* techniques include time and money savings, reduced use of laboratory animals, and the ability to rapidly screen large numbers of structures even before synthesis occurs. This high capacity improves prioritization in early discovery for toxicology testing and highlighting toxophores for easy identification. Because it might be difficult to avoid some of these functionalities in the design of new compounds, in some cases their presence should be considered as a ‘structural-alert’ for the drug metabolism scientist. In turn, studies can be conducted at an earlier stage to determine whether the compound in question undergoes metabolism at the site to generate a potentially toxic intermediate. However, *in silico* methods still cannot completely replace conventional toxicity testing. These systems are not designed or validated to screen for potential IDRs but could be useful as a first step in eliminating compounds with other potential toxic effects.

Trapping reactive intermediates

Direct detection of reactive intermediates has been proven difficult both *in vitro* and *in vivo*. The basic methods to trap reactive intermediates have been well established and recently have received interest for screening in a high-throughput manner in drug discovery [16]. For example, early methods to trap electrophiles have been designed to form glutathione (GSH) adducts, cyanide derivatives, nucleotide adducts, glucuronides, and albumin adducts. It is important to recognize that a compound may form one or several reactive intermediates. The difficulty arises in trying to assess which reactive intermediate could be responsible for certain toxic effects. For example, valproic acid, tamoxifen, and tolmetin might have competitive pathways for reactive metabolism. On the other hand, reactive intermediates might interact covalently and noncovalently with biomacromolecules as part of their potential mechanism for toxic reactions [17,18].

Electrophiles

Reactive electrophile screenings generated from *in vitro* experiments in several tissues (e.g. liver microsomes) have been designed to react with GSH and subsequent analysis of the GSH adducts by LC-MS [16]. Several types of reactive metabolites (epoxide, arene oxide, quinone, quinone imine, quinone methide, iminoquinone methide, nitroso, nitrenium ion, nitro reduction, nitro radical, iminium ion, free radical, S-oxidation, Michael acceptor, S-oxide, aliphatic aldehyde, or hydrolysis/acetylation) can be trapped in the

Table 1. Examples of chemical structures activating to produce toxic metabolites

| Chemical class | Bio-transformation | Toxic metabolite | Compound | | Biological effects | Refs |
|------------------------------|---------------------|--------------------|---------------------|-------------------------------|-------------------------------|---------|
| | | | Name | Clinical use | | |
| Quinone | Oxidation | Quinone-type | Tacrine | Alzheimer's disease | Hepatic toxicity | [47] |
| | | | Troglitazone | Treat Type II diabetes | Hepatic toxicity | [48,49] |
| | | | Minocycline | Antibiotics | Hepatic toxicity | [50] |
| | | | | | Lupus-like syndrome | |
| | | | Acetaminophen | Analgesic agent | Hepatic toxicity | [51] |
| | | | Aminosalicylic acid | Inflammatory bowel disease | Lupus-like syndrome | [52] |
| | | | | | Pancreatic toxicity | |
| | | | | | Hepatic toxicity | |
| | | | Amodiaquine | Treat malaria | Renal toxicity | [53] |
| | | | | | Hepatic toxicity | |
| | | | Phenytoin | Anticonvulsant | Agranulocytosis | [54] |
| | | | | | Drug-induced hypersensitivity | |
| | | | Carbamazepine | Anticonvulsant | Teratogenicity | [55] |
| | | | | | Teratogenicity | |
| | | | Vesnarinone | Phosphodiesterase r inhibitor | Agranulocytosis | [56] |
| Prinomide | Antiinflammatory | Agranulocytosis | [57] | | | |
| Estrogens | NSAID* | Breast cancer | [58] | | | |
| | | Uterine cancer | | | | |
| Tamoxifen | NSAID | Endometrial cancer | [59] | | | |
| Fluperlapine | Antipsychotic agent | Agranulocytosis | [60] | | | |
| Aryl nitro | Reduction | Nitroso | Tolcapone | Parkinson's disease | Liver toxicity | [61] |
| | | | Chloramphenicol | Antibiotic | Aplastic anemia | [62] |
| | | | | | Bone marrow toxicity | |
| | | | Dantrolene | Muscle relaxant | Liver toxicity | [63] |
| | | | Nimesulide | COX 2 inhibitors | Liver toxicity | [64] |
| Nitrogen-containing aromatic | Oxidation | Nitrenium ion | Clozapine | Antipsychotic agent | Agranulocytosis | [65,66] |
| | | | Liver toxicity | | | |
| | | Free radical | Aminopyrine | Painkiller | Myocarditis | [67] |
| | | | | | Agranulocytosis | |
| | | Dipyrrone | Painkiller | CNS toxicity | [68] | |
| Agranulocytosis | | | | | | |

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presence of either GSH or an equimolar mixture of *N*-acetyl-cysteine and *N*-acetyl-lysine. This method is relatively simple and rapid, and has been implemented for HTS to identify reactive metabolites generated by bioactivation with Phase I and Phase II enzymes [16,20–23]. A preliminary evaluation of this method was conducted using 20

commercially available compounds with known toxicological profiles in liver microsomes at substrate concentrations of 10 μ M [16]. The results indicated that the method is unlikely to produce false negative response because relatively safe compounds did not generate GSH conjugates, whereas eight of the ten compounds that are known to generate

Table 1. (continued)

| Chemical class | Bio-transformation | Toxic metabolite | Compound | | Biological effects | Refs |
|-------------------|----------------------------|-------------------------|-------------------|------------------------|---|---------|
| | | | Name | Clinical use | | |
| Aryl amines | Oxidation to hydroxylamine | Nitroso | Sulfamethoxazole | Antibacterial agent | Hepatotoxicity Agranulocytosis Lupus-like syndrome Skin rashes | [69] |
| | | | Dapsone | Antiparasitic | Agranulocytosis Flu-like syndrome Hemolytic anemia Methemoglobinemia | [70] |
| | | | Procainamide | Cardiac antiarrhythmic | Lupus-erythematosus Agranulocytosis Fever | [71] |
| | | | Nomifensine | Antidepressant | Hemolytic anemia Allergic reactions | [72] |
| | | | Sulfasalazine | Ulcerative colitis | Abnormal liver function Decreased blood counts Allergic reactions | [73] |
| | | | Aminoglutethimide | Breast cancer | Skin rashes Fever Agranulocytosis Thrombocytopenia Liver toxicity | [74] |
| | | | | | | |
| | | | | | | |
| | | | | | | |
| | | | | | | |
| Michael acceptors | Hydrolysis oxidation | Aldehyde Co-A conjugate | Felbamate | Anticonvulsant | Aplastic anemia Liver toxicity | [75,76] |
| | | | Terbinafine | Antifungal agent | Bone marrow toxicity Liver toxicity Skin rashes | [77] |
| | | | Valproic acid | Anticonvulsant | Liver toxicity | [78] |
| | | | Mianserin | Antidepressant | Agranulocytosis | [79] |
| | | | Leflunomide | Inflammatory arthritis | Liver toxicity Agranulocytosis | [80] |
| | | | | | | |
| Carboxylic acids | Glucuronidation | Acyl glucuronides | Diclofenac | NSAID | Liver toxicity Agranulocytosis | [81] |
| | | | Zomepirac | NSAID | Liver toxicity | [82] |
| | | | Ibuprofen | NSAID | Liver toxicity | [83] |
| | | | Bromfenac | NSAID | Liver toxicity | [84,85] |
| | | | Benoxaprofen | NSAID | Liver toxicity | [86] |
| | | | Indomethacin | NSAID | Bone marrow toxicity | [87] |

* Non-steroidal anti-inflammatory drugs

Table 2. Approaches to help to screen for reactive metabolites

| Stage | Approaches | Comments |
|--------------------------|--|--|
| Presynthesis of compound | <i>In silico</i> methods/drug design/data mining. | Flag potentially toxic compounds. Alert to conduct toxicity evolution earlier. |
| Early drug discovery | Microsomal/CYP time-dependent inactivation. Reactive intermediate screens in human liver. | <i>In vitro</i> studies in subcellular fractions or purified enzymes. |
| Late drug discovery | Covalent binding. Oxidative stress. Hapten characterization. Reactive intermediate comparison (human versus preclinical species). | Cellular/subcellular/enzymatic or preliminary <i>in vivo</i> studies. Is the binding > 50 pmol/mg microsomal protein? |
| Preclinical development | Animal models/biomarkers. Proteomics/metabolomics/genomics. Reactive intermediate exposure in animal models. Prediction of species differences in exposure of reactive intermediates. | Available animal models have limited prediction rates of IDRs, but new tools may improve predictability. |
| Clinical development | Biomarkers/proteomics/genomics/metabolomics. Reactive intermediate exposure when considered relevant. | Hapten identification. mRNA. Immunotoxicity. Reactive metabolites (in blood, skin and liver). |

reactive metabolites resulted in positive responses. The two compounds that are known to generate reactive metabolites, but did not produce positive responses in the current assay, were valproic acid and phenytoin. The reason for this was that the formation of the valproic acid reactive metabolite (2,4-dieneVPA) requires P450-oxidation and β -oxidation catalyzed by a mitochondrial coenzyme A-dependent process, rather than microsomal enzymes [20–23]. The reactive metabolite of phenytoin could be a free radical instead of an epoxide which cannot form a stable GSH conjugate [24,26]. This method was further evaluated using 43 compounds as positive controls and 16 compounds as negative controls. The results indicated that 40 of 43 compounds tested gave positive results as expected from the literature. Those producing false negatives were felbamate, trimethoprim and sulfamethoxazole. The potential reason for this was a relatively low *in vitro* concentration used in the assay (100 μ M). On the other hand, all 16 of the compounds used as negative controls were found to be negative as expected, indicating that this method could be useful in determining the potential for a compound to form reactive intermediates. Although feasible for HTS, the strategy has limited applications to trap the most stable GSH adducts. Those unstable GSH adducts can spontaneously regenerate GSH and the reactive metabolite. A highly reactive metabolite can react with an active site residue of the enzyme that forms it and thus might not be trapped by

GSH. If the reactive metabolite is a free radical, it will most likely abstract a hydrogen atom from GSH rather than react with it. Alternative trapping reagents can be used for more reactive intermediates [27].

Free radicals

Techniques for trapping free radicals are well established. Free radicals resulting from reduction and oxidation can be trapped with spin-trapping reagents [27–29]. For example, a method for trapping free radicals was used on hydrazine analogs and their derivatives which are responsible for hemolytic and hepatotoxic events, presumably via the alkyl or aryl free radicals that oxidize essential cysteinyl residues in proteins or covalently react with biomacromolecules [30]. Another example is the bioactivation of phenytoin to a free radical species, proposed to be mediated by COX-1, that can be trapped with the spin trapping agent α -phenyl-*N*-t-butyl-nitrone (PNB) *in vitro* in embryo cell cultures [24–27]. The techniques to trap free radicals need further evaluation to develop high throughput methodology and their role in IDRs.

Iminium ion

Trapping iminium ions with cyanide is also a well-known technique [30]. The technique can be implemented as a screen for the detection of reactive iminium intermediates by trapping them with radiolabeled cyanide. With (S)-nicotine

as the reference compound, the extent of radiolabeled cyanide incorporated into the test compounds can be quantified. If compounds have higher cyanide incorporation than (S)-nicotine, it is considered indicative of the formation of iminium intermediates. However, the iminium ions can also form GSH adducts depending on their relative stability. For example, U-89843 incubated in liver microsomes formed N-acetylcysteinyl and GSH adducts in NADPH-supplemented rat liver microsomes supporting a bioactivation pathway potentially involving an iminium intermediate [31,32]. The reactive metabolites of DMP 406 and mianserin both reacted with a range of nucleophiles, but in many cases the reaction was reversible. The best nucleophile for trapping these reactive metabolites was cyanide [30]. These results suggest the potential need for a combination of trapping methods to evaluate the formation of reactive intermediates.

Reactive oxygen species

It has been proposed that some IDRs might be the result of oxidative stress – increases in the intracellular levels of reactive oxygen species (ROS) [33–36]. Generally, ROS are generated as byproducts from cellular metabolism, primarily in the mitochondria. When the production of ROS exceeds the antioxidant capacity of the cell, cellular macromolecules such as lipids, proteins and DNA can be damaged. To prevent oxidative stress under normal physiological conditions, these free radicals are neutralized by an elaborate antioxidant defense system consisting of enzymes (e.g. catalase, superoxide dismutase and GSH peroxidase), and numerous non-enzymatic antioxidants (e.g. vitamins A, E and C, GSH, ubiquinone and flavonoids) [37–39]. GSH-associated metabolism is a major mechanism for cellular protection against agents or reactive intermediates. It has been reported that several mechanisms could contribute to cell death associated with oxidative stress, which can be summarized in three steps [40]. The first stage is the recognition of stress by sensitive protein(s), (e.g. the depletion of GSH), mitochondrial damage, inactivation of critical cellular functions, activation of transcription factors, defense gene expression, protein expression, protein function, and release of pro-inflammatory cytokine. The second stage is the subsequent activation of cellular defenses through Phase II metabolism enzymes [e.g. uridine diphosphate-glucuronyltransferase (UDP-GT), GSH-related enzymes (e.g. glutathione S-transferase (GST)], heat shock proteins (e.g. Hsp72), antioxidants and cell cycle inhibitors. At stage three, the cells of tolerant individuals are able to dynamically protect themselves from continued stress, but the cells of susceptible individuals might not be able to do so, leading to premature apoptotic death. Some

strategies of antioxidative defence are: the transition metals can be inactivated by chelating proteins (e.g. ferritin); and ROS can be reduced enzymatically (e.g. by the glutathione peroxidase) or non-enzymatically by antioxidants (e.g. by vitamin E, vitamin C and glutathione).

Biological markers

Biological markers (biomarkers) can be measured and quantified, providing useful information for a wide range of clinical and pre-clinical uses [41–43]. Some potential examples of biological parameters that can be measured include: concentration of specific enzyme(s) and/or specific hormones; specific gene phenotype distribution in a population; the presence of biological substances that are useful as indicators for health and physiology related assessments such as disease risk, psychiatric disorders, environmental exposure and its effects; disease diagnosis; metabolic processes; substance abuse; pregnancy; cell-line development; and epidemiologic studies. These and other parameters can be used to identify a toxic effect in an individual organism and can be used to extrapolate between species. Biomarkers can serve to confirm diagnoses, monitor treatment effects or disease progression, and predict clinical results.

Biomarkers are clearly indicated as having important roles in drug development for several situations, such as their ability to provide a rational basis for selection of lead compounds, as a help in determining the ability to work toward qualification and use as a surrogate endpoint. Changes in a biomarker can provide useful indicators for pathophysiology, which in turn are important in identifying a suitable therapeutic target. For example, the association of elevated serum cholesterol levels with an increased incidence of coronary heart disease provides an underlying rationale for developing drugs that lower cholesterol by inhibiting 3-hydroxy-3-methylglutaryl coenzyme A reductase. Thus, total cholesterol is a good example of a clinical biomarker that has been qualified for use as a surrogate endpoint [44,45].

Biomarkers are also important to the preclinical assessment of the potential benefits and harmful effects of a new drug candidate. Screening tests in animals using biomarkers, such as reduction of blood pressure, provide important demonstration that a compound is able to produce the intended therapeutic activity in patients. By measuring blood levels during adverse events, such as seizures, in animal toxicology studies can help guide the design of dose-escalation studies in humans and serve as a surrogate for preventing or reducing the likelihood of similar adverse events in humans.

Biomarkers for potential toxicity play an equally important role. For example, a drug found to prolong the QT

interval in animals might warn of potential cardiovascular risk in subsequent clinical studies. Also, biomarkers could be glutathione conjugates and/or glutathionylated or oxidized proteins detectable both *in vitro* and *in vivo*. Biomarkers of oxidative stress involving gene/protein expression at least require a whole-cell system. It is highly unlikely that a single compound/gene/protein/function will be an effective biomarker; however, combinations of these might prove more successful. Several potential biomarkers of oxidative stress can be monitored to evaluate the potential toxic effects of drugs. Drugs that undergo redox cycling or form free radicals can generate toxic effects through oxidative stress without forming covalent adducts with biomolecules. This suggests that certain groups of compounds can be screened out in the drug design. The potential advantage of an oxidative stress biomarker is that it can be monitored during *in vitro* and/or *in vivo* studies.

Pharmacokinetic–pharmacodynamic studies using biomarkers can be particularly useful; for example, one such study showed good correlation between the hypotensive effects of an antiarrhythmic drug in dogs and humans. One shortcoming is that most biomarkers, used singly, are unlikely to capture all the effects of a drug, and thereby fulfill the most stringent criterion for a surrogate endpoint, although by using several of them in combination, it is more likely, and desirable, to produce evidence which is consistent enough to point in a particular direction.

Promising strategies

Because thousands of compounds must be screened in a typical pharmaceutical industry setting, it is almost impossible, and very expensive, to have all of them radiolabeled. Using radiolabeled reagents such as GSH and KCN is easier and more cost-effective to obtain an accurate measurement of adduct formation [46]. The reactive intermediates might be formed in other subcellular fractions such as liver S9, mitochondria, and cytosol, and thus, screening for reactive intermediates in these fractions will minimize false negatives. As an example, valproic acid forms reactive metabolites in subcellular mitochondria, as explained above. We have compared *in vitro* cellular and subcellular models for identifying drug candidates with the potential to produce reactive metabolites. For purposes of evaluating these models, six known compounds currently in the clinic with dose limitations due to hepatotoxicity were selected. Labetalol, Acetaminophen, Niacin, Iproniazid, 8-Hydroxyquinoline, and Isoniazid were incubated separately with human liver mitochondria, S9, microsomes, cytosol and hepatocytes. LC-QTOF-MS methods were used to elucidate metabolic profiles of selected compounds. The Phase II metabolites

were in good agreement with previously published results. Without supplementation of reagents in subcellular fractions, Phase II metabolites were not detected. Hepatocytes also formed GSH conjugates but the relative abundance was lower, indicating that the best model to identify potential reactive metabolites involves the subcellular fractions [46]. Using the results for Acetaminophen, for example, when reactive intermediates are produced, they can be trapped by GSH, whereas in the case of Labetalol no reactive intermediates were produced and subsequently no GSH adducts were detected. Studies should be done to improve our knowledge of, and hence techniques used for, screening with the use of radiolabeled reagents, which would give an accurate measurement of the amount of reactive intermediates [46]. Also, reactive intermediate formation in subcellular fractions should be investigated, which will aid in reducing false results [46].

Conclusions

We have discussed strategies and tools to enable researchers in the pharmaceutical industry to design drugs that are safer and more robust for humans. Structural information on metabolites is a great help in enhancing as well as streamlining the process of developing new drug candidates, which in turn has great value in several important aspects of drug discovery and development. By improving our ability to identify helpful and harmful metabolites, suggestions for structural modifications will optimize the likelihood that other compounds in the series are more successful. *In silico* and *in vitro* techniques are available to screen compounds for key ADME characteristics, which, when applied within a rational strategy, can make a major contribution to the design and selection of successful drug candidates. Screening for reactive intermediates with the use of radiolabeled reagents as has been discussed, which would give an accurate measurement of the amount of reactive intermediates.

These efforts will be aided by continued improvement and expansion of cooperation and dialogue among the disciplines involved in the entire process, especially between medicinal chemistry and drug metabolism to develop strategies to facilitate better and more-focused decision making throughout the drug discovery process. It is worth stating that drug safety should be further investigated by pharmaceutical companies to conduct post-marketing studies, which are required by the FDA when a safety question arises during the pre-approval period.

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