

Prodrug Design by Computation Methods: A New Era

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Introduction

Prodrugs, soft drugs, targeted drugs, and metabolites of drugs are common terms that are used in the pharmaceutical field. The term “prodrug” was first introduced by Albert to signify pharmacologically inactive chemical moieties that can be used to temporarily alter the physicochemical properties of drugs in order to increase their usefulness and decrease their associated toxicity [1]. The use of the term usually implies a covalent link between a drug and a chemical moiety. Generally, prodrugs can be enzymatically or chemically converted in vivo to provide the parent active drug to exert a therapeutic effect. Ideally, the prodrug should be converted to the parent drug as soon as its goal is achieved, followed by the subsequent rapid elimination of the released linker group [2-5].

On the other hand, soft drugs (antedrugs) are drugs that are readily degraded to inactive derivatives to prevent or reduce activity. Targeted drugs are drugs or prodrugs that exert their biological action only in specific cells or organs such as in the administration of omeprazole and acyclovir. The active metabolite term refers to the degradation of the drug by the body into a modified form that has a biological effect. Usually these effects are similar to those of the parent drug but are weaker yet still significant. Examples of such metabolites are 11-hydroxy-THC and morphine-6-glucuronide. In certain drugs, such as codeine and tramadol, the corresponding metabolites are more potent than the parent drug (morphine and O-desmethyltramadol respectively) [6-8].

The rationale behind the use of prodrugs is to optimize the Absorption, Distribution, Metabolism, and Excretion properties (ADME). In addition, the prodrug strategy has been used to increase the selectivity of drugs for their intended target. Development of a prodrug with improved properties may also represent a life-cycle management opportunity. Unfortunately, prodrugs are often considered only when problems are encountered with the parent drug. The design of an appropriate prodrug should be considered in the early stages of preclinical development and should not be viewed as a last resort.

Modifying the ADME properties of the parent drug requires a comprehensive understanding of the physicochemical and biological behavior of the drug candidate. Although prodrug design is very challenging, it can still be more feasible and faster than searching for an entirely new biologically active molecule with suitable ADME properties. The prodrug approach is becoming more popular and successful. To date, prodrugs comprise around 10% of the world's marketed medications and 20% of all small molecular medications approved between 2000-2008 [9,10].

The prodrug approach is a very versatile strategy to increase the utility of biologically active compounds, because one can optimize any of the ADME properties of potential drug candidates. In most cases, prodrugs contain a promoiety (linker) that is removed by an enzymatic or chemical reaction, while other prodrugs release their active drugs after molecular modification such as an oxidation or reduction reaction. The prodrug candidate can also be prepared as a double prodrug, where the second linker is attached to the first promoiety linked to the parent

drug molecule. These linkers are usually different and are cleaved by different mechanisms. In some cases, two biologically active drugs can be linked together in a single molecule called a codrug. In a codrug, each drug acts as a linker for the other [9,10]. The prodrug approach has been used to overcome various undesirable drug properties and to optimize clinical drug application. Recent advances in molecular biology provide direct availability of enzymes and carrier proteins, including their molecular and functional characteristics. Prodrug design is becoming more elaborate in the development of efficient and selective drug delivery systems. The targeted prodrug approach, in combination with gene delivery and controlled expression of enzymes and carrier proteins, is a promising strategy for precise and efficient drug delivery and enhancement of the therapeutic effect.

The prodrug design can be utilized in the following: (1) improving active drug solubility and consequently bioavailability; dissolution of the drug molecule from the dosage form may be the rate-limiting step to absorption [10]. It has been reported that more than 30% of drug discovery compounds have poor aqueous solubility [11]. Prodrugs are an alternative way to increase the aqueous solubility of the parent drug molecule by improving dissolution rate via attached ionizable or polar neutral functions, such as phosphates, amino acids, or sugar moieties [2,5,10,12]. These prodrugs can be used not only to enhance oral bioavailability but also to prepare parenteral or injectable drug delivery; (2) increasing permeability and absorption; membrane permeability has a significant effect on drug efficacy [13]. In oral drug delivery, the most common absorption routes are unfacilitated and largely nonspecific passive transport mechanisms. The lipophilicity of poorly permeable drugs can be enhanced by hydrocarbon moiety modification. In such cases, the prodrug strategy can be an extremely valuable option. Improvement of lipophilicity has been the most widely investigated and successful field of prodrug research. It has been achieved by masking polar ionized or non-ionized functional groups to enhance either oral or topical absorption [14]; (3) modifying the distribution profile; before the drug reaches its physiological target and exerts the desired effect, it has to bypass several pharmaceutical and pharmacokinetic barriers.

Today, one of the most promising site-selective drug delivery strategies is the prodrug approach that utilizes target cell- or tissue-specific endogenous enzymes and transporters. One of the few examples that were designed to increase the efficiency of a drug by accumulation into a specific tissue or organ is the antiparkinson agent

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L-DOPA. Because of its hydrophilic nature, the neurotransmitter dopamine is not able to cross the blood-brain barrier and distribute into brain tissue. However, the prodrug of dopamine, L-DOPA, enables the uptake and accumulation of dopamine into the brain via the L-type amino acid transporter 1 [2,15]. After L-type amino acid transporter 1-mediated uptake, L-DOPA is bioactivated by aromatic L-amino acid decarboxylase to hydrophilic dopamine, which is concentrated in dopaminergic nerves. Because L-DOPA is extensively metabolized in the peripheral circulation, DOPA decarboxylase inhibitors (carbidopa, benserazide, methyl dopa) and/or catechol-O-methyltransferase inhibitors (entacapone, tolcapone, nitecapone) are co-administered with levodopa to prevent the unwanted metabolism [16,17]; (4) prevent fast metabolism and excretion; the first-pass effect in the gastrointestinal tract and liver may greatly reduce the total amount of active drug reaching the systemic circulation and consequently its target. This problem has been overcome by sublingual or buccal administration or by controlled release formulations. Fast metabolic drug degradation can also be prevented by a prodrug strategy. This is usually done by masking the metabolically labile but pharmacologically essential functional group(s) of the drug. In the case of the bronchodilator and β_2 -agonist terbutaline, sustained drug action has been achieved by converting its phenolic groups, which are susceptible to fast and extensive first pass metabolism, into bis-dimethylcarbamate. The prodrug bambuterol is slowly bioactivated to terbutaline predominantly by nonspecific butyrylcholinesterase outside the lungs [18-20]. As a result of the slower release and prolonged action, once-daily administration of bambuterol provides relief of asthma with a lower incidence of adverse effects than terbutaline [21]; (5) reducing toxicity; adverse drug reactions can change the structure or function of cells, tissues, and organs and can be detrimental to the organism. Reduced toxicity can sometimes be accomplished by altering one or more of the ADME barriers but more often is achieved by targeting drugs to desired cells and tissues via site-selective drug delivery. A successful site-selective prodrug must be precisely transported to the site of action, where it should be selectively and quantitatively transformed into the active drug, which is retained in the target tissue to produce its therapeutic effect [2,22]. The ubiquitous distribution of most of the endogenous enzymes that are responsible for bioactivating prodrugs diminishes the opportunities for selective drug delivery and targeting. Therefore, exogenous enzymes are selectively delivered via antibody-directed enzyme prodrug therapy or as genes that encode prodrug activating enzymes. This approach is particularly used with highly toxic compounds such as anticancer drugs to reduce the toxicity of the drugs at other sites in the body [23,24].

There are two major challenges facing the prodrug approach strategy: (a) hydrolysis of prodrugs by esterases; the most common approaches for prodrug design are aimed at prodrugs undergoing *in vivo* cleavage to the active parent drug by catalysis of hydrolases such as peptidases, phosphatases, and carboxylesterases [14]. The less than complete absorption observed with several hydrolase-activated prodrugs of penicillins, cephalosporins, and angiotensin-converting enzyme inhibitors highlights yet another challenge with prodrugs susceptible to esterase hydrolysis. These prodrugs typically have bioavailabilities of around 50% because of their premature hydrolysis during the absorption process in the enterocytes of the gastrointestinal tract [14]. Hydrolysis inside the enterocytes releases the active parent drug, which in most cases is more polar and less permeable than the prodrug and is more likely to be effluxed by passive and carrier-mediated processes back into the lumen than to proceed into blood, therefore limiting oral bioavailability; (b) bioactivation of the prodrug

by cytochrome P450 enzymes. The P450 enzymes are superfamily enzymes that account for up to 75% of all enzymatic metabolisms of drugs, including several prodrugs. There is accumulating evidence that genetic polymorphisms of prodrug-activating P450s contribute substantially to the variability in prodrug activation and thus to the efficacy and safety of drugs using this bioactivation pathway [25,26].

Bioconversion of prodrugs is perhaps the most vulnerable link in the chain, because there are many intrinsic and extrinsic factors that can influence the process. For example, the activity of many prodrug activating enzymes may be decreased or increased due to genetic polymorphisms, age-related physiological changes, or drug interactions, leading to adverse pharmacokinetic, pharmacodynamic, and clinical effects. In addition, there are wide interspecies variations in both the expression and function of the major enzyme systems activating prodrugs, and these can pose challenges in the preclinical optimization phase. Nonetheless, developing a prodrug can still be a more feasible and faster strategy than searching for an entirely new therapeutically active agent with suitable ADMET properties.

An ideal drug candidate needs to have specific properties, including chemical and enzymatic stability, solubility, low clearance by the liver or kidney, permeation across biological membranes, potency, and safety.

The conversion of a prodrug to the parental drug at the target site is crucial for the prodrug approach to be successful. Generally, activation involves metabolism by enzymes that are distributed throughout the body [14,27,28]. The major problem with these prodrugs is the difficulty in predicting their bioconversion rates, and thus their pharmacological or toxicological effects. Moreover, the rate of hydrolysis is not always predictable, and bioconversion can be affected by various factors such as age, health conditions and gender [29-31].

The novel prodrug approach to be reported in this editorial implies prodrug design based on enzyme model (mimicking enzyme catalysis) that has been utilized to understand how enzymes work. The tool used in the design is a computational approach consisting of calculations using molecular orbital and molecular mechanics methods and correlations between experimental and calculated values of intra molecular processes that were used to understand the mechanism by which enzymes might exert their high rates catalysis. In this approach, no enzyme is needed for the catalysis of the intra conversion of a prodrug to its parent drug. The release of the drug from the corresponding prodrug is solely dependent on the rate limiting step for the intra conversion reaction.

In the past few decades, the use of computational chemistry for calculating physicochemical and molecular properties has been a progressive goal of organic, organometallic, inorganic, and pharmaceutical chemists. Thermodynamic and kinetic energy-based calculations for biological systems that have pharmaceutical/medicinal interest are a great challenge to the medical community. Nowadays, quantum mechanics such as *ab initio*, a semi-empirical and Density Functional Theory (DFT), and Molecular Mechanics (MM) are increasingly being utilized and widely accepted as tools that provide structure-energy calculations for the prediction of potential drugs and prodrugs [32].

The *ab initio* molecular orbital methods (quantum mechanics) such as HF, G1, G2, G2MP2, MP2 and MP3 are based on rigorous utilization of the Schrodinger equation with a number of approximations. Use of the *ab initio* method is restricted to small systems that do not have more than thirty atoms due to the extreme cost of computation time

[33-35]. MINDO, MNDO, MINDO/3, AM1, PM3 and SAM1, are semi-empirical methods based on the Schrodinger equation with the addition of terms and parameters to fit experimental data and have afforded vast information for practical application [36-39]. Calculations of molecules exceeding 50 atoms can be done using such methods. Density functional theory (DFT) is a semi-empirical method used to calculate structures and energies for medium-sized systems of biological and pharmaceutical interest and is not restricted to the second row of the periodic table [40]. Contrary to quantum mechanics, molecular mechanics is a mathematical approach used for the computation of structures, energy, dipole moment, and other physical properties, and is widely used in calculating many diverse biological and chemical systems such as proteins, large crystal structures, and relatively large solvated systems. However, this method is limited by the determination of parameters such as the large number of unique torsion angles present in structurally diverse molecules [41].

Recently we have been investigating the mechanisms for some intramolecular processes that have been used to gain a better understanding of enzyme catalysis and have been exploited for design of novel prodrug linkers [42-60]. Using molecular mechanics, DFT, and *ab initio* methods, we studied various intramolecular processes in order to assign factors affecting the rate-determining step. Among these processes are the following: (1) proton transfer between two oxygen in Kirby's acetals [61] and proton transfer between nitrogen and oxygen in Kirby's enzyme models [61]; (2) intra molecular acid-catalyzed hydrolysis in Kirby's maleamic acid amide derivatives [61]; (3) proton transfer between two oxygen in rigid systems as investigated by Menger [62-65] arriving at the following conclusions: (i) rate accelerations in intra molecular processes are a result of both entropy and enthalpy effects. In intra molecular cyclization processes where enthalpic effects were predominant, steric effects were the driving force for the acceleration, whereas proximity orientation was the determining factor in the case of proton transfer reactions. (ii) The distance between the two reacting centers is the main factor that determines whether the reaction type is intermolecular or intra molecular. In the cases where the distance exceeded 3 Å, an intermolecular engagement was preferred due to the involvement of a water molecule (solvent), whereas an intra molecular engagement prevailed when the distance between the electrophile and nucleophile was less than 3 Å. (iii) The efficiency of proton transfer between two oxygen and between nitrogen and oxygen in Kirby's enzyme models is attributed to relatively strong hydrogen bonding in the products and the transition states leading to them.

The information from our studies on enzyme models was used to design an efficient chemical moiety to be utilized as a prodrug linker with the potential to release the parent drug in a slow or fast manner. Unraveling the mechanism of Kirby's enzyme model (proton transfer in acetals) has led to the design of prodrugs of aza-nucleoside derivatives for the treatment of myelodysplastic syndromes, where the prodrug linker (the acetal moiety) was linked to the hydroxyl group of the nucleoside moiety [66]. In addition, prodrugs of the pain killer paracetamol that are capable of masking the bitter taste of the parental drug were also designed such that the linker is covalently linked to the phenolic group of paracetamol, which is believed to be responsible for the bitter taste of the drug [67].

Different linkers were also investigated for the design of several prodrugs that might be efficient in releasing their corresponding parent drugs at various rates that are dependent on the nature or the structural features of the linkers. Selected examples of these prodrugs include the anti-Parkinson's agent dopamine [68], anti-viral agent acyclovir [69], anti-malarial agent atovaquone [70], antihypertensive atenolol

[71], antibacterial cefuroxime [72], anti-psoriasis monomethyl maleate [73], and the anti osteoporosis agents raloxifene and alendronate [74]. Successful synthesis of most of the prodrugs mentioned above was reached and in vitro kinetic results at different pH values have shown promising results for obtaining novel prodrugs that might have enhanced dissolution, membrane penetration, and thus better bioavailability than their corresponding drugs.

In the past, the prodrug approach was viewed as a last resort after all other methods were exhausted. Nowadays, the prodrug approach is being considered in the very early stages of the drug development process. While the classic prodrug approach was focused on altering various physicochemical parameters, the modern computational approach considers using a design of linkers with drugs that have poor bioavailability to release the parent drugs slowly and thus improve their bioavailability. With the possibility of designing prodrugs with different linkers, the rate of release of the parental drugs can be controlled. In addition, since the linkers used in the studies described above are relatively small, it is expected that the prodrugs themselves might have considerable biological effects before intraconversion to their parent drugs. The future of prodrug technology is exciting and yet challenging. Advances must be made in understanding the chemistry of many organic reactions that can be effectively utilized to enable the development of even more types of prodrugs. The understanding of organic reaction mechanisms of certain processes, particularly intramolecular reactions, will be the next major milestone in this field. It is envisioned that the future of prodrug technology holds the ability to create safe and efficacious delivery of a wide range of active small molecules and biotherapeutics.

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