Title: Pharmacokinetic and Pharmacodynamic Properties of Drug Delivery Systems

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    Absorption, Distribution, Metabolism, and Elimination (ADME)
    Biodistribution (BD)
    Drug Delivery Systems (DDSs)
    Enhanced Permeability & Retention (EPR)
    Gastrointestinal (GI)
    Intravenously (IV)
    Neonatal Fc Receptor (FcRn)
    Monoclonal Antibody (mAb)
    Reticuloendothelial System (RES)
    Pharmacodynamics (PD)
    Pharmacokinetics (PK)
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    Subcutaneously (SC)
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ABSTRACT

The use of drug delivery systems (DDSs) is an attractive approach to facilitate uptake of therapeutic agents at the desired site of action, particularly when free drug has poor pharmacokinetics/biodistribution (PK/BD) or significant off-site toxicities. Successful translation of DDSs into the clinic is dependent on a thorough understanding of the in vivo behavior of the carrier, which has for the most part been an elusive goal. This is, at least in part, due to significant differences in the mechanisms controlling pharmacokinetics for classical drugs and DDSs. In this review, we summarize the key physiological mechanisms controlling the in vivo behavior of DDSs, comparing and contrasting this with classical drugs, and describing engineering strategies designed to improve DDS PK/BD. In addition, we describe quantitative approaches that could be useful for describing PK/BD of DDSs, as well as critical steps between tissue uptake and pharmacologic effect.

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INTRODUCTION

Modern pharmacotherapy employs an expanded roster of distinct classes of therapeutic, prophylactic, imaging and other agents, ranging in size and complexity from diatomic gases, oxygen and nitric oxide, to cellular fragments and cells themselves – natural or modified chemically or genetically. In between these extremes, therapeutics can be divided into classical small drugs and biologicals or biotherapeutics such as proteins, nucleic acids and other biomolecules.

Both small molecules and biologicals have issues with delivery in the organism of a patient, from administration site to the desirable site of action. Accordingly, diverse drug delivery systems (DDSs: liposomes, nanocarriers, affinity drug conjugates and so on) are devised to enable or improve delivery of some of these agents. In addition, in some cases DDSs themselves have additional functions and even therapeutic action. In this review, we highlight critical factors that affect the behavior of DDS following injection into an organism. The majority of the work discussed focuses on liposomes, as these have been the most extensively studied DDS to date; however, the critical parameters affecting in vivo behavior are likely relevant to many types of DDS.

Each type of these agents - small drugs, biologicals and DDSs - has advantages and challenges, some of which outlined in Table 1. Here we attempt a comparative review of the main parameters of their behavior in the body, that we colloquially call pharmacokinetics (PK). PK is often defined simply as 'what the body does to the drug', and is typically described using four critical processes: absorption (A), distribution (D), metabolism (M), and elimination (E), or

ADME. The interactions between the drug molecule (or drug delivery system) and the body control the relative rates and efficiencies of each of these processes and body compartments involved.

While these processes are well understood and described for small molecule drugs and for many protein therapeutics, a thorough understanding of PK (and underlying mechanisms) is often lacking for DDSs. This is likely due to several reasons, including, but not limited to assay limitations, interspecies differences in processes controlling PK, and a smaller overall body of work on PK of drug delivery systems (DDS), particularly in the clinic. In this review, we discuss differences in ADME processes for small molecule drugs, protein biotherapeutics, and DDS. In addition, the key features of DDS that can be tuned to modulate PK and analysis of DDS PK will be discussed in detail.

ADME PROCESSES

One challenge in characterization of the in vivo behavior of DDS is the differences in mechanisms controlling PK and biodistribution compared with small molecule drugs and biologics. As the purpose of this review is not to provide a detailed description of the ADME of small molecules and biologics, but rather to highlight their differences with DDS, only a brief overview of mechanisms controlling their in vivo behavior will be provided (Figure 1, Table 2).

Absorption

For drugs administered via an extravascular route, the first barrier to reaching the site of action is absorption into the bloodstream, which can be controlled both by properties of the drug and of

the site of administration. For small molecule drugs, absorption most frequently occurs from the

gastrointestinal (GI) tract following oral administration. Briefly, following dosing, the dosage

form must disintegrate and the drug has to dissolve and permeate across the GI wall. The rate

and extent of this process can vary widely between drugs, although predictions can often be

made based on physicochemical properties of the drug molecule (Palm et al., 1997; Lipinski et

al., 2001). It should be noted; however, that interactions with transporters (Estudante et al.,

2013) and drug-metabolizing enzymes (Peters et al., 2016) in the GI tract can significantly

modulate the passive absorption profile that would be predicted using molecular descriptors.

On the other hand, in general, biologics are poorly absorbed following oral absorption, and as

such, are often administered intravenously (IV); however, subcutaneous (SC) dosing of protein

therapeutics has become more popular in recent years. Absorption from this space is generally a

slow process (hours – days), due to the pathway through the lymphatic system that most proteins

follow following SC dosing (Supersaxo et al., 1990; Bittner et al., 2018). While determinants of

the efficiency of SC administration for protein therapeutics are not as well-understood as oral

absorption of small molecules, it is appreciated that molecular properties of the protein (e.g. size,

charge), affinity for the neonatal Fc receptor (FcRn) (Deng et al., 2012; Zheng et al., 2012;

Richter et al., 2018), and addition of absorption enhancers to the formulation (e.g. buffer

components, hyaluronidase) can impact bioavailability (Fathallah et al., 2015; Bittner et al.,

2018).

Finally, for DDS, absorption is not typically a process that is considered, as the efficiency of

uptake into the systemic circulation after extravascular delivery is very low. There have been

many preclinical investigations of oral delivery of nanoparticles; however, absorption is often low due to poor permeation across the GI wall. Following extravascular injection (e.g. SC or intramuscular) of DDS, bioavailability would likely be very low due to efficient uptake by resident immune cells in the lymph nodes collecting fluid draining from the injection site; however, this may be an efficient route of administration for local delivery (Kaledin et al., 1982).

Distribution

Following entry into the systemic circulation, the movement of drugs between blood and tissues is a critical factor controlling the efficacy and toxicities associated with therapy. As with absorption, distribution varies widely between drug classes both in kinetics and in mechanism. The distribution of small molecule drugs, in particular, may range from being confined to the plasma space to being distributed throughout the entire body. This variability can, in part be described using molecular descriptors and binding to plasma proteins (Poulin and Theil, 2002b; Poulin and Theil, 2002a). Distribution of small molecule drugs can be modulated by interactions with uptake and/or efflux transporters expressed in certain tissues (Giacomini et al., 2010).

The efficiency of distribution of protein therapeutics into tissues is highly dependent on the molecular weight of the protein, with smaller proteins entering tissues more efficiently than larger proteins, due to enhanced diffusion and improved permeation through paracellular pores (convective uptake) (Sarin, 2010). Additionally, tissue uptake can be increased via receptor-mediated transcytosis for proteins with high affinity for receptors such as the transferrin receptor (TfR) (Friden et al., 1991; Pardridge et al., 1991).

As most DDS are much larger than typical pores between endothelial cells, distribution is often limited to the vascular space (Allen et al., 1989), in the absence of specific pathologies or affinity for receptors. However, in tissues with larger endothelial pores (e.g. fenestrations in liver and spleen), tissue uptake via bulk fluid flow (convection) may be favorable. In a similar manner to biologics, DDS with affinity for receptors that undergo transcytosis may have enhanced tissue uptake at sites of target expression (Cerletti et al., 2000; Hatakeyama et al., 2004).

Metabolism/Elimination

As with the previous processes, elimination of drugs from the system occurs via different mechanisms and at different rates for various types of molecules. For small molecules, there are two primary routes of elimination. Renal clearance is controlled by the relative efficiencies of glomerular filtration, active secretion into the urine, and reabsorption (active and passive) from the tubules (Dave and Morris, 2015). Metabolic clearance, occurring primarily in the liver for most drugs, is dependent on recognition of the drug molecule by a drug-metabolizing enzyme (e.g Cytochrome P450). Following metabolism, the metabolite can be further metabolized, cleared via the bile ducts into the feces, or eliminated in the urine.

For peptides and small protein therapeutics, renal clearance may be significant when molecular weight is smaller than the glomerular filtration threshold (~ 60 kDa). However, for proteins that are not eliminated in the urine, catabolic breakdown can occur throughout the body, typically following uptake into the endo-lysosomal pathway. The efficiency of this breakdown can be enhanced if a protein with high affinity for an internalizing receptor is taken up via receptor-mediated endocytosis, in a process often referred to as target-mediated drug disposition (TMDD)

(Levy, 1994; Mager and Jusko, 2001a). For proteins containing an Fc region (e.g. mAbs and Fc fusion proteins), elimination may be blunted via interactions with the neonatal Fc receptor (FcRn), which protects IgG and albumin from degradation, allowing them to have long circulating half-lifes (~ 3 weeks in man) (Ghetie et al., 1996; Israel et al., 1996; Junghans and Anderson, 1996).

For drug delivery systems, the primary route of elimination is via tissues of the reticuloendothelial system (RES), such as the liver, spleen, bone marrow, and lung. These tissues contain large amounts of phagocytic cells (e.g. macrophages) that recognize nanoparticles as foreign bodies and efficiently remove them from the circulation. The efficiency of this pathway can be enhanced by opsonization of the nanoparticle by serum proteins (e.g. immunoglobulins and complement proteins), which cause more efficient recognition by phagocytes (Devine and Marjan, 1997). On the contrary, this clearance mechanism can be slowed by enhancing the 'stealthiness' of nanoparticles via approaches such as conjugation of polyethylene glycol (PEG) (Klibanov et al., 1990) (see **DDS Design Parameters**). Similar to targeted protein therapeutics, specific interactions with the receptors (TMDD) can be a significant route of elimination for targeted DDS.

PHYSIOLOGICAL FACTORS AFFECTING DDS PHARMACOKINETICS

In order to mechanistically describe the in vivo behavior of any drug (or drug carrier), understanding of how physiology may control disposition is critical. In this section, we will provide a high level overview of physiological processes that contribute to the ADME of DDS.

Cardiovascular System

Following systemic injection, drugs are immediately present in the bloodstream. While often described as a simple, well-mixed space in quantitative representations of pharmacokinetics, the cardiovascular system is in reality a dynamic space that significantly impacts PK. Almost immediately following injection, nanomaterials are typically coated with a layer of plasma proteins in a process referred to opsonization, or protein corona formation. While the exact determinant of the protein corona is highly complex, and likely specific to a given nanoparticle, species, and individual, it typically will include complement proteins and immunoglobulins, which lead to more efficient elimination of the particle by immune cells (Devine and Marjan, 1997; Yan et al., 2005).

In addition to the coating of nanoparticles by proteins, there is the potential for dynamic interactions between particles and blood cells (e.g. erythrocytes, platelets, leukocytes). While this is not an area that has been studied extensively, flow cytometry has been utilized to demonstrate rapid association of liposomes with erythrocytes and platelets in mice following IV injection (Constantinescu et al., 2003).

DDDs aggregation (or initially large size, usually >200-300 nm) leads to rapid mechanical and charge mediated entrapment in the microvasculature and clearing compartments. This may either impede delivery (Shuvaev et al., 2011b), or enable rather fortuitous accumulation in the vasculature of organs of interest (Myerson et al., 2016).

Reticuloendothelial System

It has been appreciated since the earliest studies of the in vivo disposition of liposomes that injected particles are rapidly taken up by the liver (Gregoriadis and Ryman, 1971; Gregoriadis and Ryman, 1972). The mechanism for this efficient clearance pathway in liver and other tissues of the RES (e.g. spleen, bone marrow, lung) is via phagocytic uptake of particles by cells accessible from the vascular space (e.g. hepatic Kupffer cells). This clearance pathway is saturable at doses of 0.1 – 10 mg lipid, and saturation of the primary RES organs by increasing doses of liposomes has been shown to lead to decreased uptake in liver, and shifting uptake to spleen (lower doses) and lung (higher doses) (Abra and Hunt, 1981; Souhami et al., 1981). In fact, pre-blocking of the RES with empty liposomes has been investigated as a strategy to improve circulation time (Ellens et al., 1982; Dave and Patel, 1986) and enhance uptake in target tissues (Sun et al., 2017; Liu et al., 2018). Additionally, Chow and colleagues have demonstrated that the saturability of the RES not only leads to redistribution to other tissues, but also allows for altered distribution within the liver, shifting uptake from Kupffer cells to hepatocytes (Chow et al., 1989).

Target Epitope Properties

Uptake of DDS at the desired site is often obtained via either active targeting or by taking advantage of pathological alterations in the target tissue and must out-compete elimination via the RES to achieve efficient uptake. In many cases, passive targeting of nanoparticles is carried out using pathological changes that lead to advantageous distribution in the site of injury. For example, in conditions such as inflammation and solid tumors, vascular leakiness is increased, which may lead to improved uptake into target tissues via bulk fluid flow. In the case of solid tumors, many studies have utilized this enhanced permeability and retention (EPR) effect in

mouse models to obtain delivery of drug into the tumor (Maeda et al., 2013); however, it should

be noted that the magnitude of the EPR effect is likely highly variable and may not exist in all

tumors (Wilhelm et al., 2016).

In the case of active targeting, selection of the target epitope can be critical in obtaining optimal

delivery to the desired site. While many targets are selectively upregulated in pathologies,

expression is still likely to occur in healthy tissues. The relative target expression in diseased

and healthy tissues is a critical parameter that defines drug targeting (Scherpereel et al., 2002;

Shuvaev et al., 2011b).

Additionally, a critical parameter in active targeting is the accessibility of the target, as this will

lead to drastically different concentrations of targeting ligand available to interact with target.

For example, for a target expressed constitutively on the surface of the vascular endothelium, the

entire concentration of affinity ligand in the bloodstream will be able to bind; however, if the

target is located at an extravascular site, then the relevant concentration will be that which has

extravasated into the tissue. This concentration will likely be folds lower than the concentration

within the bloodstream, due to generally poor uptake of particles into tissues, and the limiting

step in targeting may be tissue uptake, rather than target binding (Chacko et al., 2011; Howard et

al., 2014).

Finally, following binding of DDS to target molecules, it is possible that the DDS-target complex

will be internalized. In some cases, the features of DDS induce internalization even though the

DDS is anchored on cellular receptor normally not involved in internalization (Muzykantov,

2013; Han et al., 2015). In general, internalization of DDS is desirable, as most DDS release

drugs within the endo-lysosomal space. However, for chronic administration of DDS,

internalization of complex may lead to reduced target available on subsequent doses, leading to

diminished targeting and efficacy on later doses. While not demonstrated to date for

nanomedicines, this principle has previously been shown for mAbs (Meijer et al., 2002).

DDS DESIGN PARAMETERS

In order to reach the desired site of action, DDS must evade major clearance mechanisms (e.g.

RES uptake) and bypass distributional barriers to reach the desired site of action. The use of

DDS dates back nearly 50 years to early publications using liposomes as delivery vehicles

(Gregoriadis et al., 1971). Over this nearly half-century, a myriad of approaches has been

proposed to modulate the in vivo behavior of DDS, with varying degrees of success. In this

section, we will highlight some of the most commonly studied strategies for design of DDS,

mainly focusing on liposomes as a model DDS.

'Classical' Design Parameters

From the early days of liposome research, it has been appreciated that modulating the liposome

properties can lead to alterations in blood clearance (Juliano and Stamp, 1975). One parameter

that has been studied in detail for liposomes is the effect of size. Liu and colleagues performed a

detailed characterization of the PK and biodistribution of liposomes, and found that maximal

blood concentrations and minimal liver concentrations were observed for liposomes with in the

size range of 100 – 200 nm (Liu et al., 1992). This 'sweet spot' of liposome size has been

hypothesized to be due to efficient extravasation of small (diameter < 100 nm) liposomes in the

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liver, allowing for hepatocyte uptake, and rapid clearance of large (diameter ~ 500 nm)

liposomes by Kupffer cells and splenic macrophages (Rahman et al., 1982). In addition to size,

the impact of liposome charge has also received a great deal of investigation for its impacts on

PK and distribution. In their early work, Juliano and Stamp observed that cationic liposomes

were cleared more rapidly than anionic or neutral liposomes (Juliano and Stamp, 1975).

Litzinger and colleagues demonstrated that cationic liposomes were rapidly taken up in the liver

(60% ID at 5 minutes), mainly in Kupffer cells (Litzinger et al., 1996). However, much like with

size, it has been hypothesized that there is a 'sweet spot' for cationic charge. In rats, it was

shown that liposomes with a zeta potential of ~15 mV had enhanced PK relative to those with

zeta potentials of -5 – +10 mV and > +25 mV. These results were hypothesized to be due to

balanced electrostatic interactions with erythrocytes (favoring circulation) and Kupffer cells

(favoring clearance) (Aoki et al., 1997).

Due to the observation that liposomes were primarily cleared by cells of the innate immune

system, several approaches were put forward to create 'stealth' liposomes, with natural abilities

to evade uptake by phagocytic cells. An early method proposed to extend liposome circulation

was to mimic the outer surface of a naturally long-circulating particle, erythrocytes, by including

sphingomyelin and ganglioside, G_{M1} in the liposome. This approach led to large increases in

blood and tumor uptake, with significant decreases in RES clearance (Gabizon and

Papahadjopoulos, 1988; Allen et al., 1989).

In the early 1990s, multiple groups observed that modifying lipids with PEG provided similar

evasion of RES clearance and extended circulation time (Klibanov et al., 1990; Allen et al.,

1991). This approach, termed PEGylation, was utilized in the development of the first approved

liposomal product, liposomal doxorubicin (Doxil). However, it has been observed that following

repeated injections of PEGylated liposomes, clearance and RES uptake were significantly

increased (Dams et al., 2000), which was shown to be due to formation of an antibody response

against PEG (Ishida et al., 2006; Wang et al., 2007).

'Modern' Design Parameters

In recent years, as the field has gained tighter control over the ability to reproducibly manipulate

nanomaterials, more intricate design features have been utilized to alter the pharmacokinetics of

DDS. Within the last 15 years, there have been several investigations of the impact of

nanoparticle shape on biodistribution and pharmacokinetics, dating to the observation that long,

worm-like, filomicelles have extended circulation time relative to spherical carriers (Geng et al.,

2007; Shuvaev et al., 2011a). Similarly, it has been shown for mesoporous silica nanoparticles

(MSN) (Huang et al., 2011) and for gold nanoparticles (Arnida et al., 2011) that an extended

(rod-like) configuration leads to extended blood circulation and reduced RES uptake. For

filomicelles, it was suggested that their hydrodynamic properties allowed them to better align

with blood flow and remain in circulation (Geng et al., 2007). While not exhaustive, these

examples highlight the potential for engineering of nanoparticle shape to modulate interactions

with clearance organs and prolong circulation.

With increasing interest in polymeric nanoparticles, there has been an increased ability to tune

not only size and shape, but also mechanical properties, creating 'soft' and 'hard' nanoparticles.

Anselmo and colleagues have used polymeric hydrogels to demonstrate that increased

nanoparticle flexibility led to extended circulation time in mice, and decreased uptake in several types of cells (macrophage, endothelial, tumor) (Anselmo et al., 2015). Similarly, Guo et al have shown that by tuning the elasticity of nanolipogels, uptake into tumor and RES organs could be controlled (Guo et al., 2018). Our group has also demonstrated that lysozyme-dextran nanogels were highly deformable and allowed for targeting of caveolar targets that were otherwise inaccessible to rigid particles of a similar size (Myerson et al., 2018), demonstrating the impact that particle flexibility could have not only on pharmacokinetics, but also on active targeting.

Targeted DDS Design Parameters

Instead of merely relying on passive uptake to guide delivery of DDS to their intended sites, active targeting using mAbs, antibody fragments, peptides, and small molecules has been extensively studied. By coating the surface of a particle with a targeting ligand, very high affinity and avidity for target epitopes can be achieved. It is possible that by modulating targeting ligand properties, the degree of uptake in the desired site of action can be controlled.

The most straightforward approach to modulating targeting properties would be to modify the density of targeting ligand coating on the nanoparticle. In the simplest scenario, it would be expected that by maximizing coating density, targeting to the desired site would be enhanced, which does appear to hold true in certain cases (Calderon et al., 2011). However, increased targeting ligand density could also lead to delivery to less desirable (e.g. off-target) sites or reduced sensitivity to changes in target expression (Zern et al., 2013).

Additionally, in the specific scenario where RMT is the desired outcocme, high avidity

nanoparticles have been shown to have reduced transcytosis, due to poor release from the

endothelial surface following exocytosis (Wiley et al., 2013). In general, caution should be

applied when tuning nanoparticle avidity, and in vivo experiments to assess the impact of

changes in avidity on targeting should be performed.

When selecting targeting ligands, the potential impact of the properties of the ligand on

pharmacokinetics and biodistribution should also be considered. Classically, mAbs have been

used to target nanoparticles, but with recent advances in molecular biology, the ability to make

antibody fragments (e.g. Fab, scFv, etc.) that can be conjugated to the surface of particles is

enhanced. By coupling full length mAbs to the surface of nanoparticles, the potential for

significant exposure of Fc fragments is present, potentially leading to increased immune-

mediated clearance (Koning et al., 2001). The clearance of liposomes displaying a high density

of Fc fragments was inhibited in mice by injection of an anti-Fc receptor (FcR) mAb,

demonstrating the potential role of FcR in the PK of immunoliposomes (Aragnol and Leserman,

1986). By using antibody fragments that do not contain an Fc fragment, enhanced delivery of

nanoparticle cargo to tumor was obtained in lymphoma (Cheng and Allen, 2008) and breast

cancer (Duan et al., 2018) models, which was hypothesized to be due to decreased Fc-dependent

clearance.

DESIGN OF IN VIVO STUDIES

Quantitatively accurate, objective, and methodologically reliable characterization of carrier

behavior in vivo (both PK and biodistribution (BD)) is necessary. Non-specific PK/BD

influence DDS in many ways, and may ultimately override a proposed targeting mechanism.

Without knowledge of PK/PD, data obtained from animal models are of limited translation

value, as lack of knowledge of these parameters may lead to erroneous interpretation of the

mechanism(s) of delivery and effect. Therefore, it is critical to define the relative contributions

of the designed targeting mechanism and other factors in delivery and effects of DDS.

Interaction with components of the blood may lead to uptake by blood cells, aggregation,

opsonization, degradation, or other alterations to DDS, which may alter PK/PD differentially in

normal vs. diseased organisms. Additionally, drugs and biologically active components of the

DDS may affect PK/PD. To account for all of these scenarios, the following formulations should

be tested in vivo:

- (A) Targeted vs. untargeted (coated by inactive ligand) carriers. Pristine characters are
  not a proper comparison group, as they may have different size, charge, and surface
  properties.
- (B) Naïve animals vs. animal model(s) of disease.
- (C) Empty vs. drug-loaded DDS.

Available methodologies to study PK vary, and no single method is sufficient to address all

potential questions related to in vivo behavior. By tracing DDS labeled with optical probes,

localization within the tissue at the microscopic level at post-mortem and macroscopically in real

time in sufficiently transparent sites is feasible (Pollinger et al., 2013). However, optical

methods are subjective, relatively low throughput, and difficult to analyze quantitatively.

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The use of molecular imaging approaches such as positron emission tomography (PET), single-photon emission computed tomography (SPECT), and magnetic resonance imaging (MRI) is insufficient to analyze sub-tissue localization, but these clinically useful technologies allow for real-time imaging of isotope-labeled components of DDS (Danilov et al., 1989; Rossin et al., 2008; Brinkhuis et al., 2012; Zern et al., 2013) at a macroscopic level, with the ability for quantitative approximation of the intensity of a signal from a region of interest (partially subjective).

Labeling of a DDS may alter PK/PD features and lead to artifacts due to dissociation of the labeled component from the DDS. To mitigate this, ideally, both the drug cargo and carrier (but not targeting moiety) should be stably traced by conjugated labels (Simone et al., 2012). Direct measurement of the isotope level in drawn blood samples and tissue specimens post-mortem is arguably the most reliable approach for PK studies (Danilov et al., 1991; Muzykantov et al., 1991; Muzykantov et al., 1996; Muzykantov et al., 1999; Shuvaev et al., 2011a; Pan et al., 2013). It allows for accurate, quantitative analysis of key parameters of PK, targeting, and biodistribution, including: percent of injected dose (%ID) in tissues, localization ratio (LR, or ratio of %ID per gram of tissue to that in blood), and immunospecificity index (ISI, or ratio of LR for targeted vs. untargeted formulations) (Muzykantov et al., 1995; Muzykantov et al., 1996).

It is critical that PK/BD data be normalized to the injected dose of DDS. Using the concentration in the first blood draw as 100 %ID is not acceptable, as a significant fraction of DDS may be eliminated within seconds. This can lead to artifacts in blood and tissue concentrations when analyzing PK/BD data (Figure 2).

A useful approach to increase the throughput of PK/BD studies would be to inject in the same

animal a mixture of both targeted and untargeted formulations labeled by different isotopes.

This can help to minimize individual variability and significantly reduce efforts. However,

caution should be taken to not administer a cumulative dose of DDS that would lead to saturation

of non-specific clearance processes (e.g. RES uptake).

QUANTITATIVE DESCRIPTIONS OF DDS PHARMACOKINETICS

'Non-Mechanistic' Approaches

For simple comparison of the blood kinetics of DDS formulations, simple, non-mechanism-

based approaches are often sufficient. The simplest of these, termed non-compartmental analysis

(NCA), simply utilizes values that can be extracted from the concentration vs. time curve to

characterize the PK of drugs (Figure 3a). Common parameters that are obtained from NCA

include the terminal half-life ($t_{1/2}$), volume of distribution (V_{ss}, V_d), clearance (CL), area under

the curve (AUC), and mean residence time (MRT). This approach is useful for obtaining

estimates of parameters related to drug exposure and distribution. In order to obtain further

description of the concentration vs. time curve, simple mammillary models can be used (Figure

3b). Briefly, these models link compartments representing volumes in rapid and slow

equilibrium with the blood stream via distributional clearance terms (CL_D) and assume all

elimination occurs from the central compartment (in rapid equilibrium with blood). These

models can be used with either linear or non-linear (saturable) clearance kinetics. While there

have been many models proposed for liposomes, many of them are used to describe the kinetics

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of the loaded and free cargo, as opposed to the particle (Harashima et al., 1999; Hempel et al., 2003; Fetterly et al., 2008). However, there are several examples of models proposed to describe the PK of the particle in rodents (Kume et al., 1991; Palatini et al., 1991; Decker et al., 2013), suggesting the potential utility of simple, mammillary models in describing the PK of DDS.

Mechanism-Based Modeling

In order to make meaningful extrapolations from modeling analyses, some degree of mechanism should be included in the model. Simple TMDD models can be developed via inclusion of parameters related to target binding, expression, and turnover in a mammillary model structure is a common approach used to describe non-linear PK of targeted therapeutics (e.g. mAbs) (Mager and Jusko, 2001a). To date, there have been no descriptions of the use of TMDD models for DDS in a mammillary model; however, with the large number of studies of targeted liposomes, this model structure could potentially be useful for those seeking to characterize target-specific parameters without needing to build a physiologically-based model.

A more elegant, and possibly predictive, approach to describe the in vivo behavior of DDS would be to build pharmacokinetic models including some degree of physiological relevance. One such example, semi-physiologically pharmacokinetic modeling, adds a tissue of interest onto a mammillary model (Figure 3b). This tissue is described using physiologically relevant volumes and flow rates, and is used to describe the tissue concentration vs. time profile of drug. This approach was used previously to describe the blood, liver, and tumor PK of radiolabeled liposomes, detected by positron emission tomography (PET) imaging (Qin et al., 2010), and more recently to describe the processes controlling tumor exposure to nanoparticle-encapsulated

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drugs (Benchimol et al., 2019). In addition, we have recently used a semi-physiologic model to describe the pharmacokinetics of vascular targeted nanocarriers in a mouse model of acute-respiratory distress syndrome (ARDS). Using this model, we were able to predict the heterogeneous distribution of nanocarriers across the lung and support experimental hypotheses regarding the mechanisms controlling lung distribution (Brenner et al., 2017).

The 'gold standard' for prediction of drug behavior in an in vivo setting is the full physiologically-based pharmacokinetic (PBPK) model, which has been widely applied both for small molecules (Jones et al., 2015; Sager et al., 2015) and for biologics (Wong and Chow, 2017; Glassman and Balthasar, 2018). Briefly, these models include all tissues of the body, and are parameterized with physiologically-relevant values (e.g. blood flow, tissue volume, receptor expression, etc.). To date, there have been several reviews describing the potential utility of PBPK in nanomedicine; however, there are relatively few examples of applications of this approach (Li et al., 2010; Yang et al., 2010; Moss and Siccardi, 2014; Li et al., 2017; Yuan et al., 2019). Kagan and colleagues were among the first to demonstrate the use of PBPK for DDS. In their paper, they considered the blood and tissue PK of AmBisome (liposomal amphotericin) in mice, rats, and man, and ultimately used their model to predict the clinical PK of AmBisome over a multiple-dosing regimen. Key features of their model include: (1) dual-level modeling of encapsulated and released drug, (2) consideration of saturable uptake by phagocytic cells of the RES, and (3) interspecies scaling to predict the clinical behavior of liposomal drug (Kagan et al., 2014). More recently, Carlander and colleagues have proposed an extension to the model developed by Li for PEGylated polyacrylamide nanoparticles (Li et al., 2014) in order to consider several types of nanomaterials (polyacrylamide, gold, TiO_2). In this model, the authors

considered saturable uptake by phagocytic cells in all tissues of the body, potentially providing a

platform that could be used to describe the redistribution of nanoparticles from liver and spleen

at doses that would saturate RES clearance (Carlander et al., 2016). Further development of

PBPK models incorporating critical determinants of DDS disposition would be desirable for

prediction of the behavior of DDS in pathologies or for optimization of dosing regimens.

PHARMACODYNAMICS OF DDS

Beyond merely understanding what the body does to the DDS (e.g. pharmacokinetics), it is just

as important to characterize what the DDS does to the body (e.g. pharmacodynamics). This

generally is a less well-understood process; however, by delineating the key steps required to

move from uptake into tissues into therapeutic effect, one can gain an appreciation for the

complexity of the underlying mechanisms, and potentially gain insights into the kinetics of each

individual step (Figure 4).

Following uptake into the tissue of interest, the journey of a DDS (and its cargo) is not complete.

While merely understanding total tissue concentrations, or concentrations in a pathologically

altered region of tissue, may be sufficient to generate a dose-response relationship, the

pharmacologically relevant concentration is likely to be within a subset of that space. For most

DDS, the site of action is within the intracellular space of a target cell (e.g. tumor cell).

Therefore, following extravasation into the target tissue, the first critical processes are binding

(generally rapid for highly avid particles) to and internalization by target cells (dependent on

target epitope). For the therapeutic payload (cargo) to reach its intracellular destination, release

of drug should occur from the DDS within the endo-lysosomal route, often via breakdown of the

particle, allowing the payload to diffuse to its target organelle and elicit a pharmacologic effect.

From this simplified schematic of DDS processing and drug release, it becomes apparent that a

critical step in the pharmacodynamics of drugs loaded into DDS is the release from the particle.

For most delivery systems, drug release is optimally slow in the circulation, and rapid inside of

target cells. In general, burst release from the particle within the endo-lysosomal space is ideal

for molecules that are stable within this harsh environment, while for macromolecules (e.g

proteins and nucleic acids), release into the cytoplasm would be desirable.

In order to tune release within intracellular compartments, several strategies have been proposed,

including: (1) incorporation of pH-sensitive lipids into the bilayer, which destabilize the

liposome at acidic pH and/or induce fusion with the endosomal membrane (Connor and Huang,

1985; Straubinger et al., 1985; Connor and Huang, 1986), (2) incorporation of endosomal escape

peptides (Parente et al., 1988; Mandal and Lee, 2002; Kakimoto et al., 2009) or lipids (Du et al.,

2014; Sabnis et al., 2018) into the nanoparticle to facilitate cytoplasmic release, or (3) reliance on

natural breakdown of the liposome in the harsh lysosomal environment. Each of these methods

may provide different kinetics and efficiencies of release of therapeutic payload into the cell,

potentially leading to differential kinetics of pharmacologic effect.

In general, these transduction steps between delivery to target cells and pharmacologic effect are

hidden away in a 'black box', due to poor understanding of the kinetics of each individual step.

With this level of knowledge, the best case scenario for describing pharmacodynamics would be

to link an estimated total or receptor bound target tissue concentration to a therapeutic outcome using a signal transduction model (Sun and Jusko, 1998; Mager and Jusko, 2001b; Lobo and Balthasar, 2002). However, in order to open this 'black box' of transduction compartments, recent developments in cellular pharmacokinetic/pharmacodynamic models could be repurposed in nanomedicine, leveraging in vitro cellular processing data to predict in vivo effects following receptor binding. In particular, models developed for antibody-drug conjugates (ADC) could be of particular utility, as they consider similar processes as would be required for nanoparticle-based DDS (Cilliers et al., 2016; Singh et al., 2016; Singh and Shah, 2017).

CONCLUSIONS

Successful use of drug delivery systems in clinical medicine has been hampered by poor understanding of the mechanisms controlling pharmacokinetics and biodistribution, as well as the kinetics of each of these processes. In this review, we have provided an overview of critical differences in ADME processes for small molecule drugs, protein therapeutics, and DDS, focusing in on the physiological mechanisms relevant for DDS. By understanding the interplay between the organism and the DDS, engineering strategies can be applied to the drug carrier to modulate the efficiency of various ADME processes. Well-designed PK/BD studies for DDS coupled with quantitative approaches for describing PK can be useful in predicting the pharmacologic effect (pharmacodynamics), and ultimately allow for design of better drug delivery systems.

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P.M.G. and V.R.M. contributed to the writing and editing of the manuscript.

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FOOTNOTES

FIGURE LEGENDS

Figure 1: Mechanisms controlling the behavior of small molecule drugs (left), protein therapeutics (center), and drug delivery systems (right) in blood (top) and in eliminating organs (bottom).

Figure 2: Apparent pharmacokinetics for a theoretical DDS with a terminal half-life of 6 hours when normalizing to injected dose (blue), blood concentration 1 (orange), 5 (grey), or 10 (yellow) minutes post-injection for a DDS with 50% of injected dose eliminated in 1 (a), 5 (b), 10 (c), or 30 (d) minutes.

Figure 3: Pharmacokinetic data analysis. (a) Sample concentration vs. time curve showing calculations for select parameters derived using non-compartmental analysis. (b) Pharmacokinetic model structure for a simple 2-compartment mammillary (grey) and a semi-physiologic (blue + grey) model.

Figure 4: Transduction steps between DDS arrival in system and pharmacologic effect. (1a) Extravasation via endothelial pores into tissue interstitium, (1b) Transendothelial uptake into the interstitium, (2) Diffusion within the interstitial space, (3) Binding to target epitope, (4) Internalization into endosomes and sub-cellular sorting, and (5) Drug release into cell allowing for pharmacologic activity.

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Table 1: Comparison of features of small molecule drugs, biotherapeutics proteins, (BTP)

and multimolecular drug delivery systems (DDSs)

|	Small molecules	Proteins	DDSs
Size	<5 kD	10-300 kD	Above 1000 kDa
	< 1nm	1-10nm	10-1,000 nm
Advantages	Stability		Multifunctional
	Utility	Precision	High Drug Load
	Low Cost	Catalytic Power	Controlled Release
	Quality Control	Natural Activity	Regulation of PK/BD
	High Purity	Targeting	Delivery of Nucleic Acids
	Routes of Administration		Targeting
Challenges			As for Proteins
		High Cost	RES Overload
	Off-Target Effects	Parenteral Routes	Host Defense Reactions
	Limited Efficacy	Immunological Issues	
	Limited Mechanisms	Precise Delivery Needed	Biological Barriers

Table 2: Comparison of mechanisms controlling pharmacokinetic processes

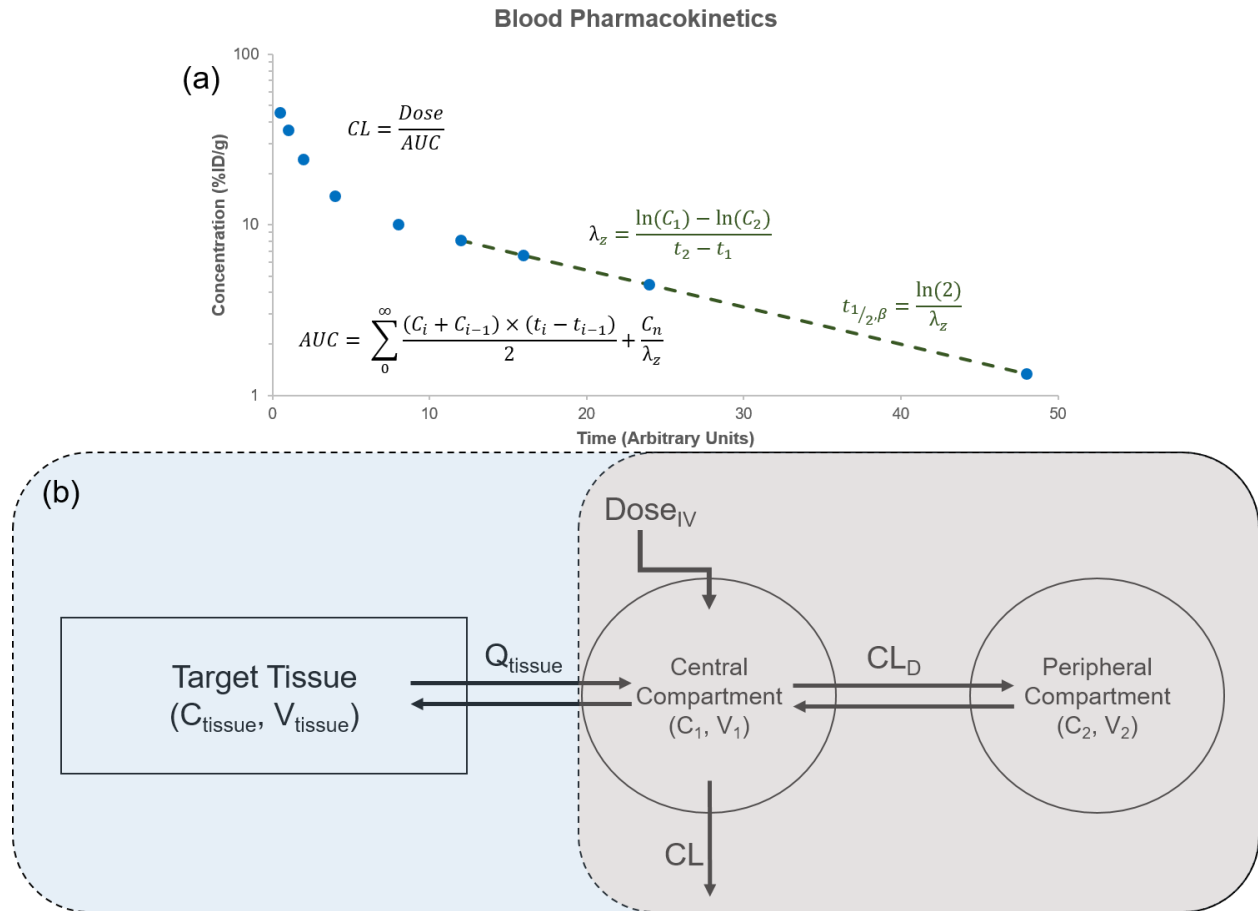| Drug Class	Absorption	Distribution	Metabolism/Elimination
Small Molecules	Gut Wall Permeability Active Transport Drug Metabolism	Plasma Protein Binding Diffusion Active Transport	Renal Filtration Active Transport Drug Metabolism
Biologics	Lymph Flow FcRn Binding	Diffusion Bulk Fluid Flow	Renal Filtration Intracellular Catabolism Target-Mediated Clearance
Nanoparticles	N/A	Bulk Fluid Flow	Reticuloendothelial System Target-Mediated Clearance
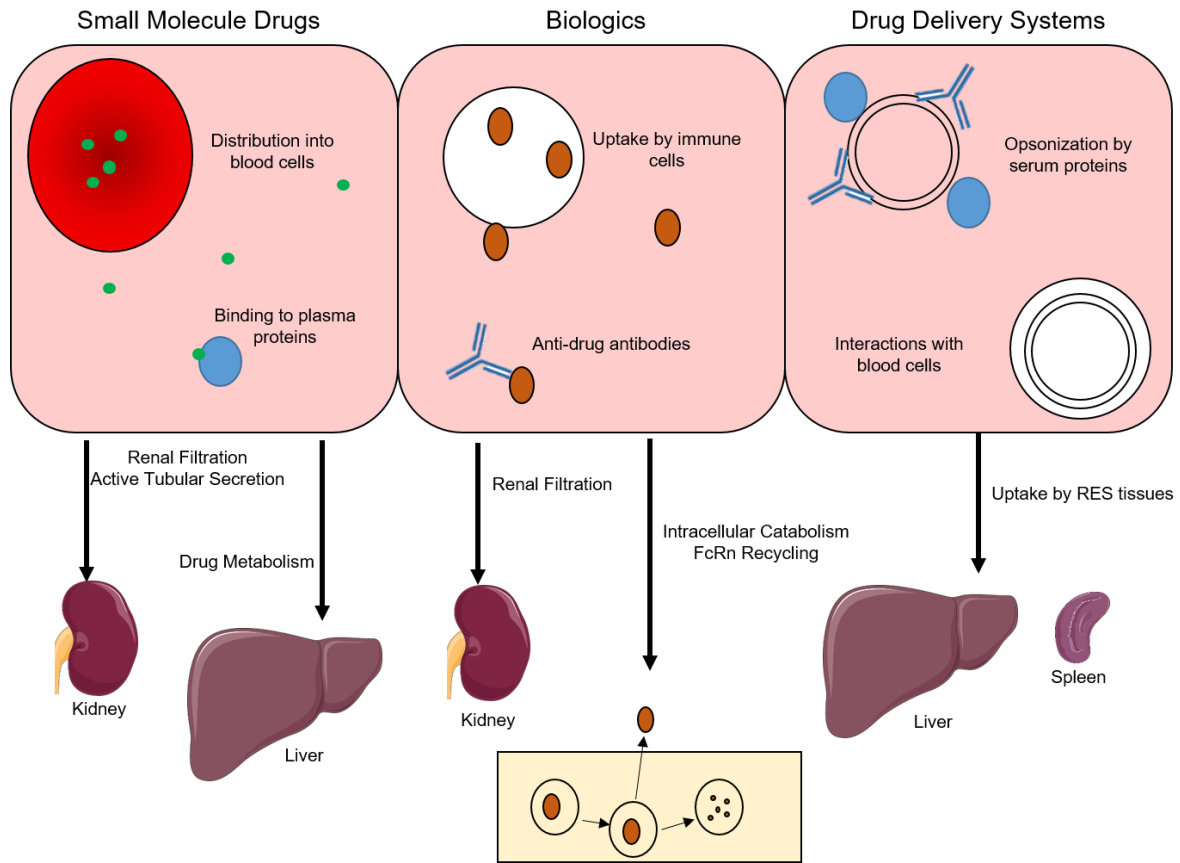
Figure 1

Figure 2

Figure 3:

Figure 4: