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Recent Advances in the Ontogeny of Drug Disposition

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Abstract

Developmental changes that occur throughout childhood have long been known to impact drug disposition. However, pharmacokinetic studies in the pediatric population have historically been limited due to ethical concerns arising from incorporating children into clinical trials. As such, much of the early work in the field of developmental pharmacology was reliant on difficult-to-interpret *in vitro* and *in vivo* animal studies. Over the last two decades, our understanding of the mechanistic processes underlying age-related changes in drug disposition has advanced considerably. Progress has largely been driven by technological advances in mass spectrometry-based methods for quantifying proteins implicated in drug disposition, and *in silico* tools that leverage that data to predict age-related changes in pharmacokinetics. This review summarizes our current understanding of the impact of childhood development on drug disposition, particularly focusing on research of the past 20 years, but also highlighting select examples of earlier foundational research. Equally important to the studies reviewed herein are the areas that we cannot currently describe due to the lack of research evidence; these gaps provide a map of drug disposition pathways for which developmental trends still need to be characterized.

Keywords

developmental trajectory; developmental expression; ontogeny; drug biotransformation; drug transporters; absorption; renal excretion

Introduction

Over the past decades, many efforts have been made to predict age-related alterations in pharmacokinetics of drugs in the pediatric population. In addition to dedicated pharmacokinetic studies conducted in pediatric populations, extrapolations from investigations in adults have also been used to estimate dose-exposure relationships in children, including approaches based on changes in body size, body composition, body maturation, organ volume maturation. In addition, research studies utilizing juvenile animal

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models and postmortem human pediatric tissue have also provided insights into the disposition pathways underlying differences in pharmacokinetics in children relative to adults.

Accumulated evidence to date indicates that there is no single uniform pattern describing the developmental trajectory of all processes contributing to drug disposition. Rather, each physiologic process, including drug-metabolizing enzyme (DME) and transporter expression and function, has its own unique developmental trajectory. This reality makes predictions of drug exposure without any prior pediatric clinical pharmacokinetic experience complex. This challenge can be overcome by mechanistic modelling approaches, such as physiologically based pharmacokinetic (PBPK) models, which present an elegant way to combine a multitude of known age-dependent systems (i.e., physiological) related parameters with drug-related parameters in an attempt to accurately extrapolate and/or simulate drug exposure in children. This approach has successfully been used to simulate clinical studies for estimating drug dosing in the pediatric population and has contributed to the approval of pediatric dosing guidelines for valganciclovir and nilotinib by the United States Food and Drug Administration [12, 13]; more recent publications have illustrated to potential to infer drug-drug interaction potential in children based on adult data [1]. The extension of PBPK modeling and simulation to a wider array of drugs demands accurate systems-based parameters. To that end, a quantitative characterization of changes in the proteins and processes governing drug disposition (highlighted in Figure 1) is underway. Much progress has been made but still much more work lies ahead.

This review supplements past knowledge with select illustrative examples of some of the more important advances that have been made in describing age-related changes in physiological processes and DME/transporter expression, with a particular emphasis on developments from the past 20 years. It highlights the information gaps and limitations in our understanding of developmental trajectories of drug disposition pathways (mostly from post-conception to childhood period), and offers a roadmap towards future, more accurate mechanistic predictions of pediatric drug exposure in drug development, as well as in the hospital and outpatient setting.

Enteral Absorption

As with adults, most medications are administered orally to children, and the first organ of pharmacokinetic significance that drugs encounter is typically the stomach. The low pH environment of the stomach is favorable for the dissolution of weak bases, which constitute the majority of marketed drugs [2]. Amniotic fluid swallowed *in utero* results in a neutral gastric pH in children at birth, but the fasted pH of the stomach begins to decline thereafter [3]. While there is some debate over the exact timing, fasted gastric pH drops to values comparable to those seen in adults within the first few weeks of life [4-8]. However, because pH can increase substantially in the postprandial period, timing of meals may be an even greater determinant of gastric pH in neonates than age-related alterations in basal hydrochloric acid secretion [9, 10], an important fact considering the frequency of feeding by neonates. Elevated gastric pH, regardless of the underlying mechanism, has been proposed to explain the increased oral bioavailability of benzylpenicillin, an acid-labile drug,

in neonates. Higher gastric pH may also reduce the solubility of some poorly soluble weak bases and delay or reduce their subsequent absorption. This mechanism has been suggested to explain reduced or non-existent exposure to orally administered ketoconazole in neonates [11, 12]. Dramatically smaller stomach volumes, particularly in the first weeks of life, may further exacerbate impaired drug dissolution [13].

The pattern and rate at which the contents of the stomach are emptied into the small intestine (i.e. gastric emptying) can also influence drug absorption. While some evidence suggests that gastric emptying may be slower in pre-term infants and neonates, a more recent meta-analysis did not observe a significant effect of age (postnatal or gestational) on gastric emptying time [14]. However, as with pH, gastric emptying is determined by several factors, including the timing and composition of meals. Indeed, gastric emptying half-time of formula was found to be about 60% greater than that of breast milk in newborns [15]. For acid-labile drugs, increased residence time in the stomach could result in increased degradation. Additionally, because absorptive (e.g., uptake transporters) and restrictive processes (e.g., DMEs and efflux transporters) in the small intestine may be saturable, prolongation of the release of drug from the stomach into the small intestine may avert these processes from becoming overwhelmed and less efficient.

Following gastric emptying, drugs next enter the small intestine, the major site for the absorption of most orally administered medications. The general primacy of the small intestine in oral drug absorption principally derives from its expansive surface area resulting from numerous tissue folds, villi (i.e. multicellular finger-like projections) and an epithelial apical brush border [16]. While villi mostly mature by 20 weeks of gestation [17, 18], some evidence suggests villous surface area and density moderately increase in the first few months of life, a function of widening villi and crypt elongation [19].

Enterocyte height has also been shown to modestly increase (by 14%) from infancy into adulthood [20], suggesting the cells undergo a postnatal maturation process. It is difficult to predict the impact of changes in enterocyte height on drug absorption, but if microvillous length or brush border density are also subject to developmental changes in cellular morphology, then changes in absorptive surface area would be anticipated. Notably, breast milk versus formula feeding has not been shown to alter villous length or enterocyte height in infants [20]. Increases in intestinal absorptive surface area are also attributable to increasing diameter and length of the organ; the length of the small intestine increases from approximately 300 cm at term to around 600 cm in adulthood [21]. Collectively, the effect of age-related increases in small intestinal surface area on drug bioavailability have not been conclusively established, but they are expected to increase the fraction absorbed for some drugs whose absorption is dependent on passive partitioning across the intestinal epithelium.

Another important contributor to efficient absorption of drugs and nutrients is the extensive perfusion of the intestines. Once molecules cross the intestinal epithelium and enter the microvasculature, the high rate of villous blood flow rapidly draws the solutes away from the intestine and into the portal vein. This reduces partitioning of absorbed drug back into the enterocytes and ensures the maintenance of a favorable concentration gradient for absorption, with concentrations in the intestinal lumen exceeding microvascular drug

concentrations. Mesenteric blood flow velocity is decreased during the first week of life [22, 23], which may affect the rate and extent of absorption. This may be particularly relevant for acidic drug molecules that are frequently ionized under the pH conditions of the small intestine; normal pH ranges for the small intestine do not differ appreciably between children and adults [24, 25].

Small intestinal motility also has the capacity to impact oral drug absorption. Relatively delayed gastrointestinal transit time in infants has been posited as an explanation for reduced time to reach peak plasma concentrations (T_{max}) of cisapride in infants under 42 weeks compared to adults [26]. However, this interpretation is complicated by a simultaneous reduction in cisapride half-life, another potential contributor to the observed reduction in T_{max} . Furthermore, some reports challenge the idea that there are substantial age-related changes in small intestinal transit time [27-29], and a relatively recent meta-regression analysis found no significant increase in basal intestinal motility from the neonatal period to adulthood [30]. Interestingly, it has been reported that intestinal transit in preterm infants may be reduced but evidence is limited [27].

In addition to the contents from the stomach, the small intestine also receives bile from the liver and digestive enzyme-rich secretions from the pancreas. Bile, a solution consisting of various lipids and surfactants (e.g. bile acids), aids in the dissolution and absorption of nutrients and lipophilic drugs. Much of the research related to the maturation of bile acid synthesis and secretion was conducted decades ago with the foundational research reviewed and contextualized by Murphy and Signer [31]. Rapid maturation of the processes governing bile acid synthesis and secretion occur in the first months of life with age-related effects being most evident in neonates and pre-term infants [32, 31]. Bile acids require a threshold concentration, ~1 to 2 mM under simulated *in vivo* conditions, to form the micelles necessary to aid in absorption of fats [31]. Studies in low birth weight infants and healthy neonates suggest bile acid concentrations in the duodenum are frequently below the critical micellar threshold concentrations [33, 34] and result in a disproportionate reduction in fat absorption for highly lipophilic compounds. Insufficient bile acid concentrations have been suggested to result in poor absorption of fat-soluble vitamins (summarized in the review by Murphy and Signer [31]), and pleconaril [35]. It is worth noting that bile salts are present in breast milk and may offset lower concentrations of endogenously produced bile acids in the neonatal duodenum [36, 37]. Further studies are required to determine whether breastfed pre-term and term neonates have a greater capacity to absorb poorly soluble lipophilic drugs than those who are formula fed. Following the neonatal period, total bile acid concentrations in the duodena reach those seen in adults [33, 31]. However, the proportions of specific bile acids are altered throughout infancy [32, 38, 39]. This is likely the result of both normal liver development and the maturation of the intestinal microbiome, which is responsible for bile acid deconjugation and the formation of secondary bile acids. In addition to affecting bile acid homeostasis, intestinal flora can also impact oral bioavailability through direct drug metabolism. Historical examples include the therapeutic bioactivation of sulfasalazine and the metabolic inactivation of digoxin [40-42], but more recent investigations reveal that a broad range of drugs are subject to presystemic biotransformation by gut microbiota [43]. Furthermore, it is not surprising that an individual's unique gut microbiome may contribute to inter-individual variability in the nature and extent of drug biotransformation

and clearance beyond that related to the host genome [44, 43]. Although rapidly occurring changes in the gut microbiome after birth and following perturbations associated with antibiotic use represent additional challenges to be considered, initial efforts are beginning to recognize the potential of pharmacokinetic modeling to incorporate the contribution of the intestinal microbiota to overall drug disposition [45, 46].

In addition to the intestinal microbiota, several host proteins support intestinal barrier function, including efflux transporters and DMEs. Cytochrome P450 3A4 (CYP3A4) is the most notable among these DMEs due to its high expression in the small intestine and broad substrate specificity for lipophilic drugs [47, 48]. Several studies have characterized the developmental trajectories of CYPs 3A4, 3A5 and 3A7 mRNA [49, 50], but data more closely related to activity are more relevant clinically. Two studies using immunoassay methodologies to quantify CYP3A4 protein in small intestinal biopsies demonstrated that low amounts of the enzyme are present at birth, but expression increases throughout early childhood [49, 50]. Conversely, CYP3A4 mRNA expression in the duodenum has been shown to decline with age [51, 50]. Delayed maturation of CYP3A4 in intestinal mucosa and liver accounts for the increased bioavailability of midazolam (by approximately 3-fold) in premature newborns relative to adults [52].

Relatively less is known about the developmental trajectories of other DMEs isoforms in the small intestine. The catalytic activity of CYP1A1 in biopsies from the small intestine of children appears to increase by approximately 3-fold on average from infancy to adolescence [53]. Intestinal expression of CES2 protein, as determined via immunoblotting, and mRNA expression have been shown to increase throughout infancy to near adult levels [50]. Conversely, some evidence suggests that the expression pattern for another DME, GSTA1, may decrease over childhood. In pediatric small intestinal biopsies, the glutathionylation rate of the GSTA1 substrate, busulfan, was 77% greater in 1 to 3 year old children than in those 9 to 17 years of age [54].

Working in concert with DMEs, efflux transporters in the apical membrane of intestinal enterocytes extrude drug molecules from the cytosol and cellular phospholipid bilayer. To-date, our knowledge of intestinal transporter protein ontogeny is mainly based on assessments of transporter gene transcription and transporter localization via immunohistochemistry. It is important to note that, while expression of transporter genes may be activated at birth, the functioning of the transporter and its contribution to drug absorption will depend on its protein expression and any additional post-translational modifications that may be required for proper membrane localization. Functional activity and specific membrane localization of transporters in cellular membranes is governed by complex cellular trafficking processes that are directed in part by glycosylation of the transporter proteins in the endoplasmic reticulum and Golgi apparatus [55, 56]. These processes are not necessarily captured in proteomic analysis of tissue homogenates or even plasma membrane fractions.

An array of apical efflux transporters exists in the small intestine. Notable transporters include permeability glycoprotein (P-gp), multidrug resistance protein (MRP) 2 and breast cancer resistance protein (BCRP). Owing to its wide substrate profile, P-gp is one of the

most broadly relevant efflux transporters in the human intestine. Expression of P-gp in enterocytes, as determined via immunohistochemical staining, is detectable after 12 weeks of gestation [57]. Data suggest that mRNA expression reaches adult levels at, or shortly after, birth and is marked by a considerable inter-individual variation [51, 58, 59]. The findings from mRNA studies are supported by the observation that the oral bioavailability of cyclosporine, a prototypical P-gp substrate, does not change from infancy to 18 years of age [60]. However, because cyclosporine is also a CYP3A4 substrate, interpretation of these findings is complicated and may conflict with observations of increasing CYP3A4 protein expression throughout early childhood [49]. Nevertheless, functional studies of another P-gp substrate, aliskiren, have similarly revealed its pharmacokinetic and safety profile to be comparable between children aged 6-17 years old and adults [61]. In the small intestine, MRP2 appears to have a similar developmental trajectory as P-gp; its mRNA levels are detected in neonatal tissue, appear constant through adulthood and are characterized by substantial inter-individual variation [59, 62, 63]. Lastly, protein expression and cellular localization of BCRP has been detected as early as 6 weeks of gestation and remain constant out to 28 weeks [57, 63].

Contrasting with efflux transporters, apical membrane bound transporters including peptide transporter 1 (PEPT1), organic cation transporter (OCT) 3, organic anion transporting polypeptides (OATP) 1A2 and OATP2B1 play a role in facilitating the uptake of drug molecules into the intestinal epithelium. In the case of OATP2B1, the anticipated impact of its ontogeny on the distribution of substrates is complicated by reports of basolateral localization which would presumably result in uptake into the intestinal epithelium from the blood [64]. Significantly higher mRNA levels (over 2-fold, as judged by the median values) of *SLCO2B1*, the gene encoding for OATP2B1, have been detected in neonates compared to adults [59], suggesting that levels decrease as children mature. On the other hand, investigations into small intestinal expression of *SLC15A1*, the gene encoding for PEPT1, revealed mRNA levels are comparable between neonates and older children, with tissues from the former exhibiting only marginally lower (0.8-fold) relative mRNA expression [65]. Specific apical localization of PEPT1 was also demonstrated in both neonatal and adult tissue [65, 66]. Some basolateral efflux transporters, such as MRP1, can theoretically work in conjunction with apical uptake transporters in the vectorial transit of drugs across the intestinal epithelium by extruding transporter-imported molecules from the cytosol into systemic circulation [67]. The limited data that describe MRP1 ontogeny come from immunoblotting tissue studies; at 7 weeks of gestation, expression is comparable to that observed in adult specimens [57].

The benefits of consolidation and integration of new data describing the developmental trajectories of multiple processes involved in drug absorption are now being realized in the form of comprehensive PBPK absorption models for drugs like acetaminophen, theophylline and ketoconazole, but also illustrate that some knowledge deficits persist [68].

Distribution

Distribution is the reversible exchange of drug from one site in the body to another. These sites may reflect anatomical compartments, such as organs or tissues, or they may represent

mathematical “apparent” spaces such as those used in compartmental pharmacokinetic modeling (i.e. central and peripheral compartments). In either case, developmental changes in physiological process such as body fat/water composition, plasma protein homeostasis and drug transporter expression will impact the rate and extent of drug distribution. It is important to stress that changes in volume of distribution do not affect the overall exposure of drug in blood/plasma, however they can impact the shape of the concentration-time curve, effectively resulting in changed trough and peak drug blood/plasma concentrations.

Infants and neonates have larger total body-water space relative to their weight than older children or adults. As such, dosing strategies based upon proportional reductions in dose by weight for hydrophilic drugs may result in relatively reduced plasma concentrations in the very young. Notable examples include antibiotics such as linezolid and gentamicin [69, 70]. In the case of gentamicin, one study observed mean peak concentrations of 1.58, 2.03 and 2.81 $\mu\text{g}/\text{mL}$ in the 1.5-5, 5-10, and >10 year age groups, respectively, following a 1 mg/kg dose [70]. This may be clinically significant considering the established relationship between peak concentrations and efficacy/toxicity [71, 72]. It is also important to note that age-related changes in the renal clearance of gentamicin and linezolid, in addition to distributional phenomena, will also affect drug concentrations in infants.

Reductions in amounts of circulating plasma proteins (e.g. albumin and α 1-acid glycoprotein) and increased plasma concentrations of bilirubin (a competing ligand for albumin) in neonates and young infants may also reduce total concentrations of highly protein-bound drugs in circulation as a greater portion of drug molecules will partition out of the plasma [73, 74]. As a result, the fraction of unbound drug in plasma will increase and therapeutic drug monitoring approaches that rely on total concentrations may be misleading. Increased fraction unbound in the range of 2- to as much as 4-fold in neonates and infants has been observed for cyclosporine, diazepam, thiopental and sufentanil [75-77]. Complicating issues further is the fact that neonates possess relatively (up to 20-30%) higher hematocrit levels than adults [78, 79]. This has the potential to translate into increased blood concentrations for drugs that accumulate in erythrocytes. However, this may not necessarily be the case if uptake transporters or specific cellular binding proteins that may themselves be subject to maturation trends contribute to drug sequestration in the erythrocytes. Therapeutic drug monitoring approaches that rely upon whole blood rather than plasma measurements (e.g. cyclosporine) may be more challenging to interpret in this context, as the ratio of blood to free plasma concentrations may be impacted. Fortunately, hematocrit levels decline to adult levels within the first few weeks of life and drugs with whole blood monitoring are infrequently administered during this brief period [78, 79].

Changes in the expression and activity of transporters in the liver and kidneys may also influence the apparent volume of distribution (V_d) of substrate drugs as reviewed by Grover and Benet [80]. Furthermore, hepatic uptake transporters located in the sinusoidal membranes of hepatocytes may be of additional clinical significance as the liver is often a site of drug action, biotransformation and toxicity. However, due to issues of ethics and feasibility, experiments evaluating the ontogeny of transporter-mediated effects on drug disposition in children have been limited. Currently, our understanding of drug tissue

distribution is mainly based on findings from animal studies, *in vitro* systems or human tissues collected post-mortem.

Studies applying quantitative proteomic approaches or immunoblot analysis to characterize expression of OATP1B3 and OCT1 respectively have revealed that neonates and infants have significantly lower hepatic abundance of these transporters compared to older children (by 60 and 80% on average, respectively), who possess amounts comparable to adults [81, 82]. However, it is important to note that a complete understanding of the developmental trajectory for a given protein is dependent on a sufficient sample size for each age group or developmental stage. For example, a separate study that analyzed a greater number of pediatric liver samples, but using immunoblotting techniques, reported relatively high OATP1B3 expression at birth, which then declined for a period of time before increasing again over the preadolescent age range [83]. Caution also should be taken in interpreting these studies given that age-related changes in transporter activity are superimposed upon other sources of inter-individual variability (e.g. genetics, epigenetics, concomitant medications). For example, age-dependent changes in OATP1B1 expression are only evident in the carriers of the reference allele, but not when the ontogeny of hepatic OATP1B1 expression is analyzed in a combined (non-genotype stratified) manner [82]. Indeed, genetic variation has also been established to be a significant contributor to variability in morphine [84], simvastatin [85], pravastatin [86], and rosuvastatin exposure in children [87]. As for the transporters that shuttle drugs and metabolites out of the hepatocytes back into the blood compartment (i.e., MRP3, MRP4, OAT7), very little is known about their ontogeny. The expression of MRP3 was shown to increase by approximately 2-fold on average from neonates to adults [82], and is marked by significant inter-individual variability in all age groups. While dedicated pediatric pharmacokinetic studies describing the ontogeny of MRP3 substrates are missing, transporter proteomic data may inform the impact of MRP3 ontogeny on the disposition of 25-hydroxy-vitamin D₃ glucuronide, a metabolite of the prohormone and therapeutic agent 25-hydroxy-vitamin D₃ [88].

The blood-brain barrier is a gateway for passage of drugs and metabolites between vascular and neural compartments in the brain. Its permeability in the pediatric population could be assessed via measurements of brain extracellular fluid (ECF) drug concentrations, however such measurements are not usually performed due to relative brain ECF inaccessibility. Instead, drug concentrations in the cerebrospinal fluid (CSF) can be measured as a surrogate. One study evaluating CSF uptake of imipenem, a drug that predominantly transits passively across the blood-brain barrier [89], observed no difference in blood brain barrier permeability across the age range studied (4 months to 11 years of age)[90]. Because the central nervous system (CNS) is an important site of action for many drugs, age-related patterns in the expression of efflux transporters in the blood-brain and blood-CSF barriers may be of clinical importance. Given the limited availability of sufficient amount of human tissue to conduct quantitative proteomic investigations, the monitoring of radiolabeled compounds using positron emission tomography (PET) and the measurement of central pharmacodynamic responses have been proposed as potential means to characterize the ontogeny of P-gp in the blood brain barrier [91]. However, there are considerable practical challenges to conducting PET imaging studies in the pediatric population including requiring exposure to radiation and sedative drugs, which may be required to reduce the

movement of pediatric subjects while obtaining measurements [92]. As such, much of our current knowledge comes from antibody-based *in vitro* analyses.

A recent immunohistochemical study reported higher intensity staining of P-gp and BCRP, and decreased staining intensity of MRP1 and MRP2, in adults relative to children under 3 years of age [93]. While the results for P-gp and BCRP mirror findings from an earlier investigation, the observed trend for MRP1 ontogeny was reversed; the cellular localization pattern of all transporters evaluated in the earlier study was found to be similar to that of adults [94]. A third investigation into the developmental trajectory of P-gp in the brain demonstrated that infants between 3 to 6 months exhibit comparable levels of P-gp protein to adults, complicating our understanding of its ontogeny [95]. Nevertheless, for the neonate, it is possible that reduced expression of P-gp contributes to increased CNS exposure to morphine, a P-gp substrate, and may account for observations of greater morphine sensitivity in neonates compared to older infants and adults [96-98]. These findings may also be explained in part by developmental changes impacting systemic morphine disposition, such as reduced OCT1 expression [99, 63], contributing to reduced hepatic morphine uptake [100] and reduced UGT2B7-mediated glucuronidation [101]. However, greater apparent analgesia was observed in neonates under 10 days of age who were exposed to similar circulating concentrations of morphine as older infants [102]. This supports the hypothesis that age-related changes in systemic pharmacokinetics alone cannot fully account for differences in morphine sensitivity. Indeed, differences in distribution into the CNS, morphine pharmacodynamics or the perception of pain in the very young have all been posited as additional contributors to increased morphine sensitivity in the very young [102].

In addition to factors driving changes in gene transcription, it appears that developmental differences in post-translational factors may also contribute to developmental trajectories of transporter function. For example, age-dependent changes in the ratio of glycosylated OATP1B3 to total OATP1B3 protein concentrations have been reported in pediatric liver and could have functional consequences in terms of transporter activity [83]. Furthermore, decreased *N*-linked glycosylation of NTCP, MRP2 and OATPs 1B1, 1B3 and 2B1 have been reported in the presence of non-alcoholic fatty liver disease, with potential implications for altered disposition of drugs in obese (> 95th percentile for body mass index) children and adolescents as has been reported for pravastatin [86].

Hepatic Biotransformation

Enzymatic biotransformation is the major route of systemic elimination for approximately 75% of drugs [103], and hepatic biotransformation represents the primary site of metabolism for most drugs due to the high degree of blood perfusion and DME abundance in liver. Furthermore, due to direct blood flow from the intestines, the liver also contributes to first-pass metabolism wherein drug is cleared before ever reaching the systemic circulation. Because transdermal and subcutaneous administration bypasses hepatic first-pass metabolism, bioavailability by these routes is not affected by developmental changes in hepatic DME activity.

DMEs are classified as either Phase I enzymes that metabolize drug molecules via oxidation/reduction/hydrolysis or Phase II enzymes that conjugate polar substituents to substrates. From a developmental perspective, Phase I and Phase II DMEs have historically been classified according to three general developmental trajectories: Class I DMEs are most abundant in the fetus and decline after birth, Class II DMEs have relatively constant expression from gestation to adulthood, and Class III DMEs are expressed to a relatively low extent in fetal liver and increase after birth [104]. An overview of the ontogeny of Phase I DMEs (including the impact of additional factors such as pharmacogenetics, concurrent critical illness and other confounding factors) has been summarized in a recent review [105], and ontogeny functions have now been published for several CYPs and UGTs [106-109]. Multiple data types have been utilized for the characterization of DME and (and transporter) developmental trajectories, and not all are equally informative for accurate characterization of changes in drug clearance *in vivo* after birth. For example, changes in mRNA expression *in vitro* provide an assessment of developmental activation of DME gene expression, but do not necessarily translate in functional catalytic activity. Similarly, measurement of protein content by immunochemical or quantitative proteomic approaches provides a measure of protein content, but again does not necessarily equate with functional *in vitro* activity; for example, CYP apoprotein may be detected by either technique, but catalytic activity require the presence of a prosthetic heme group as well as an accessory oxidoreductase protein for electron transfer [110]. Extrapolation of enzyme activity *in vitro* to clearance *in vivo* is also not without challenges as data regarding the developmental trajectories of critical scaling factors, such as microsomal protein per gram of liver (MPPGL) or cytosolic protein per gram liver (CPPGL) derived from pediatric tissues, are extremely limited [105]. Recognizing these limitations, Upreti and Wahlstrom [109], conducted a comprehensive analysis of published *in vitro* and *in vivo* data relevant to CYP ontogeny and determined that similar developmental trajectories are derived from *in vitro* or *in vivo* data for CYP2A6, CYP2D6 and CYP2E1 (or differ only at very young ages), whereas the two data types generate quite different patterns for CYP1A2 and CYP3A4. CYP2C9 and CYP2C19 represent intermediate situations wherein the developmental trajectories are similar for *in vitro* and *in vivo* data at the extremes of age but are quite different between the ages of 0.5 and 10 years. They further observed that, in general, when differences between *in vitro* and *in vivo* trajectories are present, *in vivo* activity is greater than that observed *in vitro* and pediatric activity exceeds adult activity before returning to adult values during adolescence.

The analysis conducted by Upreti and Wahlstrom provides a comprehensive resource of literature describing CYP ontogeny, and reviewers are referred to that paper for references to the primary literature [109]. A summary of parameter estimates for a number of CYP and other DME isoforms in the liver is also provided in Table 1. Rather than recapitulate the findings from each study in detail, we will instead discuss some additional issues relevant to interpretation of ontogeny data. First, several exogenous factors may influence typical developmental trajectories. For example, formula feeding may accelerate developmental increases in CYP1A2 activity such that adult expression levels are achieved sooner in formula-fed infants compared to infants solely fed breast milk, as revealed by the latter group demonstrating >3-fold longer elimination half-life [111]. The effects of infant diet

were confirmed in a longitudinal phenotyping study conducted using caffeine as a probe [112]. Second, in *in vitro* studies where individual level data are provided, it is not unusual to observe considerable inter-individual variability (approximately 300-fold) in protein expression as has been reported for CYP2B6 [113], and this extensive inter-individual variability in protein content or activity may obscure modest increases in average protein expression with increasing age throughout childhood (CYP2B6 is considered invariant with age in the Upreti and Wahlstrom analysis). Indeed, the percentage of samples with detectable CYP2B6 protein has been reported to increase with postnatal age (from 64% in fetal samples to 95% in samples from children >10 years of age) [114], and after birth, protein expression of CYP2B6 steadily increases, reaching adult levels by age 1 [113]. These *in vitro* data are consistent with the developmental trajectory of efavirenz pharmacokinetics, a CYP2B6 substrate, in newborns [115].

Third, rapid increases in CYP2D6 expression and activity have been observed after birth. Studies relying on dextromethorphan and tramadol urinary metabolite ratios as probes of CYP2D6 activity have demonstrated that CYP2D6 phenotype is concordant with genotype after approximately two weeks of age [116, 117], but it does not necessarily follow that clearance of CYP2D6 substrates reaches adult values within that time frame. On the other hand, plasma data confirm that clearance of the CYP2D6 substrate, tramadol, increases rapidly after birth and that the clinical consequences of developmental changes in acquisition of CYP2D6 activity may be limited to premature newborns [118]. It has now become apparent that consideration of genetic variation is much more important than ontogeny as a factor contributing to variation in clearance of CYP2D6 substrates. Nevertheless, consideration of CYP2D6 ontogeny and genetic variation alone is insufficient to characterize the disposition of substrates like tramadol [119], and other as yet unknown factors must be identified to address the current limitations (e.g. under-prediction) of PBPK models to describe tramadol pharmacokinetics in children [120].

A final issue involves new knowledge regarding the developmental trajectories of CYP3A4 and CYP3A7. CYP3A4 expression and activity is characterized by a large degree of inter-individual variability, and genetic variation generally is not regarded to be clinically significant source of the observed variability [121]. As apparent from the ontogeny functions described above, expression of hepatic CYP3A4 protein follows the Class III DME pattern [122, 123], and ontogeny may represent a significant source of inter-individual variability in the clearance of compounds administered in the early postnatal period, such as midazolam, sildenafil and fentanyl. In contrast, CYP3A7, exhibits a Class I DME developmental trajectory with predominantly fetal expression that declines rapidly to very low or absent levels shortly after birth in most individuals, exceptions being individuals who possess the *CYP3A7*1C* allele, which has been associated with persistence of CYP3A7 protein expression in adulthood [124]. Although CYP3A7 shares a similar substrate profile with CYP3A4 and CYP3A5, it is generally less active towards prototypic CYP3A substrates such as midazolam [125]. Due to relatively high abundance, however, its role in the clearance of CYP3A substrates, especially in the most premature newborns, may be underappreciated. Transcription factors regulating CYP3A4 developmental expression, such as the pregnane X-receptor (PXR) and constitutive androstane receptor (CAR) also appear to be developmentally regulated [126], more recent data implicate age-dependent changes

in cytosine methylation of the *CYP3A7* and *CYP3A4* promoter regions as a mechanism for the “developmental switch” that occurs at birth. Increasing methylation of critical cytosine residues in *CYP3A7* promoter region is associated with decreased transcription and silencing of *CYP3A7* and the opposite scenario is true for *CYP3A4* [127].

While CYPs are recognized as the most broadly important DMEs, around 25% of metabolically eliminated drugs are subject primarily to non-CYP mediated biotransformation [103]. Notable non-CYP Phase I DMEs include carboxylesterases (CESs), flavin-containing monooxygenases (FMOs), dehydrogenases and aldehyde oxidase, and data describing the developmental trajectories of these pathways have been published in recent years.

Both CES1 and CES2 are expressed in the liver, with CES1 being the more abundantly expressed isoform. In two separate studies, each relying on a different method of protein quantitation (immunoblotting and mass spectrometry), expression of both CES1 and CES2 were observed to be considerably lower in liver tissue isolated from neonates relative to older subjects [128, 129]. While the absolute expression of CES1 and CES2 varied between the two studies, the developmental trajectories were similar. Supporting these findings was an *in vitro* study that observed oseltamivir, a CES1 substrate, was hydrolyzed by S9 fractions of neonatal liver tissue with less efficiency than S9 fractions of tissue from older infants [130]. Further refinement of our understanding in CES ontogeny throughout childhood may provide particular benefit in the dosage selection for the CES1 substrate methylphenidate in attention deficit disorders [131].

Biotransformation of another common attention deficit disorder medication, amphetamine, is partially mediated by another non-CYP DME, FMO3 [132]. The FMO3 isoform is largely absent in the fetal liver; expression increases after birth and is detectable in most children by age 2, with adult levels achieved around age 11 [133]. The postnatal ontogeny of FMO3 has been described using a sigmoid E_{\max} model [134]; parameter estimates are provided in Table 1. Somewhat analogous to the switching that occurs between *CYP3A4* and *CYP3A7* following birth, another FMO isoform, FMO1, is expressed in the fetus, declines soon after birth, and is generally undetectable in the adult liver [133].

Other Phase I enzyme families are of generally less importance in drug metabolism to date, but developmental trajectories for some pathways have been characterized to an extent. Relative aldehyde oxidase (AO) activity in children has been estimated from the urinary ratio of pyridine to 1-methylnicotinamide, and is reported to be only 10 to 15% of adult activity in neonates. Adult levels of activity have been observed by one year of age [135]. A small investigation into protein expression of AO, applying immunoblotting methods to liver tissue, yielded findings that are generally consistent with the *in vivo* activity data [136]. Using targeted proteomic approaches, protein abundance data for alcohol and aldehyde dehydrogenases has also been characterized. Protein abundances in the liver increase from the neonatal period into early childhood for ADH1A, ADH1B, ADH1C, and ALDH1A1 by 3-, 8-, 146-, and 3-fold, respectively. Interestingly, expression of ADH1A expression then declines approximately 40% from early childhood levels by adulthood [137]. Ontogeny functions are presented in Table 1.

Encouraged by recent advances in targeted proteomics and a renewed appreciation for their role in the disposition of drugs, more efforts have been directed towards characterizing the ontogeny of Phase II DMEs. Phase II biotransformation activities are mediated by uridine 5'-diphospho-glucuronosyltransferases (UGTs), sulfotransferases (SULTs), glutathione S-transferases (GSTs) and N-acetyltransferases (NATs). Each of these enzyme families is known to have multiple isoforms with unique developmental trajectories. Ontogeny for key Phase II enzymes in the liver can also be found in Table 1.

Perhaps most well described of these enzymes in the pediatric population is UGT1A1, which is involved in the metabolism of both exogenous (e.g., acetaminophen, ibuprofen, warfarin) and endogenous compounds (e.g., bilirubin). According to a recent targeted proteomic analysis, protein abundance of UGT1A1 is low at birth but reaches adult levels in early childhood, effectively resulting in approximate 8-fold increase in protein expression [99]. This finding is in general agreement with observations that UGT1A1 activity is lower in the newborn liver but increases quickly with adult levels achieved in early childhood [106, 138]. However, it is notable that one study did not observe age-related changes in the expression of UGT1A1, nor for the closely related UGT1A6 isoform, when immunoblotting methods were used to determine protein abundance [138]. Other UGT1A isoforms were measured by Bhatt *et al.* using targeted proteomic methods; UGT1A4, 1A6 and 1A9 protein expression was respectively 55-, 35- and 33-fold greater in adult liver tissue compared to that of neonates and enzymatic activity generally followed the protein expression pattern [99].

Involved in the metabolism of morphine, naloxone and mycophenolic acid, UGT2B7 also demonstrates differential expression and activity with age. Protein expression gradually, but substantially (~8-fold), increases from the neonatal period into adulthood [99]. A similar developmental trajectory was observed for UGT2B15 with protein expression increasing by 3-fold from the neonatal period to adulthood [99]. A separate targeted proteomic study by Bhatt *et al.* observed limited UGT2B17 protein expression in children younger than 9 years old, with approximately 10-fold increase in expression from 9 years of age to adulthood [139]. It is notable that while Bhatt *et al.* observed generally concordant trends between protein expression of the investigated UGT isoforms and enzymatic activity, the age-related activity trends observed by Badée *et al.* using different probe substrates frequently do not align with the targeted proteomic data from the other studies. Badée *et al.* also investigated the ontogeny of enzyme activity for two UGT isoforms, UGT2B4 and UGT2B10, that were not evaluated in the Bhatt *et al.* targeted proteomic studies; these two enzymes appeared to have a moderately (up to 2-fold) greater enzyme activities in early childhood relative to adulthood [106]. Sulfotransferases (SULTs) represent another important enzyme family involved in Phase II metabolism. In addition to their role in xenobiotic metabolism, a number of endogenous molecules are substrates for SULTs and their importance in fetal development has long been recognized [140-142]. Notably, the sulfonation rates for dopamine and estradiol, markers of SULT1A3/4 and SULT1E1 respectively, are greater in fetal relative to adult liver tissue [143]. While SULT1A3 protein expression remains constant from birth to 70 years, expression of SULT1E1 was shown to decline from birth into adulthood. Protein expression of SULT1A1, SULT1B1 and SULT2A1 in liver cytosol samples from neonates was 24, 19, and 38% of the adult levels. Notably, SULT1A1 and

SULT2A1 showed highest protein expression in early childhood (between 1 to 6 years of age), followed by a decrease thereafter [144]. The importance of the decrease in SULT1A1 activity and concurrent increase in UGT1A6 expression with increasing age are illustrated by the developmental shift in acetaminophen conjugation wherein the sulfonated metabolite is primarily formed in newborns but the glucuronide metabolite predominates in adults [145]. It is important to note that because SULT1A1 is relatively less efficient at catalyzing its respective reaction, newborns and young infants have a longer acetaminophen half-lives than do older children and adults [145], an observation that now can be captured using contemporary PBPK models that take SULT and UGT ontogeny into consideration [146, 144].

GSTs are Phase II enzymes involved in metabolism of cisplatin, busulfan and endogenous compounds such as leukotrienes and prostaglandins [147]. Targeted proteomic data describing GST ontogeny is limited. Results obtained using immunohistochemistry and radioimmunoassays have revealed hepatic GSTA1 and GSTA2 are detectable as early as 10 weeks gestation and expression levels increase by 1.5 and 4-fold respectively to adult levels by early childhood [148, 149]. While GSTM expression is low during gestation, it rapidly increases (by approximately 5-fold) after birth, and hepatic levels of GSTM in neonates and infants approximate that of adults. On the other hand, GSTP1 expression is highest in fetal liver samples (10-22 weeks gestational age), followed by a reduction in expression during the second and third trimesters [148, 149]. While neonates continue to express up to 4-5 fold less GSTP1 protein relative to fetus, this protein becomes absent in the adult liver [148, 149].

Renal and Biliary Excretion

The kidneys are the primary organs through which xeno- and endobiotic excretion occurs. Three major processes dictate clearance of drugs via the kidney: passive filtration through the glomerulus, secretion (passive and active) in the proximal tubule, and/or reabsorption (passive and active) in the proximal or distal tubule. Although nephron development is complete by 36 weeks of gestation [150], the maturation of the kidneys continues further into childhood. At birth, the kidneys contain the same number of nephrons as in adults (approximately 1,000,000 per kidney); however age-related differences in anatomy, morphology and functionality can readily be observed [151]. Although premature infants have some capacity to form new nephrons after birth, there is concern that individuals born preterm may not ultimately achieve similar amounts of nephrons to individuals born at term [152, 153]. Between birth and 12 years of age, the kidneys almost double in length and correspondingly increase in weight. On a structural level, it can be observed that the average diameter of a glomerulus in a newborn is approximately one-third of the adult. In the first 3 months after birth, the radius of small pores in the glomerulus increases by approximately 25%, with accompanying increase in proportion of large pores relative to small pores [154, 155]. A noticeable development of proximal tubules also occurs; the average length of proximal tubules at birth is approximately 10% of that of an average adult. The variability in the length of proximal tubules is also greater at birth, with over an 11-fold difference between the shortest and longest measured proximal tubule in tissue samples, as compared to the approximately 2-fold variability observed in adults [156].

The age-dependent changes in kidney structure described above are, not surprisingly, accompanied with changes in kidney functioning. Glomerular filtration rate (GFR) increases abruptly after birth and continues to increase until the child's growth is complete. When standardized to a body weight of 70 kg using an allometric power model with a coefficient of 0.75, the GFR at 1 year of age is predicted to be at 90% of the adult GFR value, which is estimated at 121.2 mL/min [157]. It is important to note that, relative to healthy newborns, premature newborns display significantly reduced GFR that follows its own developmental trajectory [158]. With respect to tubular reabsorption, newborns have much lower urine concentrating ability (600 mOsm/kg water), a value that increases slowly to 900 mOsm/kg water during the first month of life, and reaching 1200 mOsm/kg in adolescence [158]. Renal clearance of drugs is generally reduced in the young, and especially in pre-term infants. For example, fluconazole half-life is over 3-fold longer in premature than in term infants [159]. Similarly, multiple studies over the past 15 years have demonstrated that vancomycin and amikacin clearances are reduced in premature infants and increase with postnatal age; evidence suggests that clearance of these compounds can serve as a proxy for the ontogeny of GFR [160-162].

Age-dependent changes in clearance of *p*-amino hippurate (PAH), a substrate for renal transport and a prototypical marker of renal plasma flow, have also been well documented. Immediately after birth, plasma clearance of PAH is low and then steadily increases to values comparable to adults around 2 years of age [163, 164]. To date, it is unclear whether this is a result of increasing plasma flow to the kidney, age-dependent changes in the expression of relevant transporters (e.g. basolateral uptake OAT1/3 and apical efflux MRP2/4), or a combination of both factors.

Recently, age-dependent changes in expression of transporters localized on the basolateral and apical membranes of proximal tubule epithelial cells have been characterized in pediatric tissues using targeted proteomics. The expression of basolateral uptake (OAT1, OAT3 and OCT2) and apical efflux (P-gp) transporters were significantly lower in term newborns and infants compared to children, adolescents and adults. A sigmoid E_{\max} model was fit to the relative expression data and provided Age_{50} values of 20, 31, 4.4, and 4.0 weeks post-natal age for OAT1, OAT3, OCT2 and P-gp respectively [165]. Expression of other apical efflux transporters (MATE1, MATE2-K, BCRP, MRP2 and MRP4) was consistent throughout the investigated age continuum [165]. The importance of understanding and integrating transporter ontogeny into PBPK models for renally eliminated drugs was illustrated in a recent *in silico* study. Including or excluding maturation trends for transporters involved in active tubular secretion predicted substantially different renal clearance values for several hypothetical drugs assessed, and these differences were most pronounced in children less than 2 years of age [166]. Based on these findings, it should be possible to hypothesize which medications (i.e. substrates of these transporters) may be subject to age-dependent changes in renal clearance and identify suitable candidate drugs for prospective pharmacokinetic studies to evaluate the clinical significance of these maturation trends.

In addition to the kidney, the liver is also capable of mediating the secretion of drug molecules. In general, hepatic excretion of drugs and metabolites into the bile is enabled by

some of the same properties that permit drug excretion in the renal proximal tubules. Tight junctions in the biliary canaliculi, countercurrent blood flow, expression of drug transporters and osmotic gradients favor the biliary excretion of drugs and metabolites [167]. Recent investigations using targeted proteomic techniques have offered some clearer insight into the maturation of drug transporters in the hepatic canalicular membrane. According to recent targeted proteomic data, expression of P-gp in neonates, infants, children (1-12 years) and adolescents (>12 to 16 years) were approximately 30, 40, 70 and 75% that of adult values. A sigmoid E_{\max} model was also fit to the protein abundance data (parameter estimates provided in Table 1) and seemed to reasonably describe the developmental trajectory of hepatic P-gp expression. Mean abundances of other canalicular efflux transporters including MRP2, BCRP and MATE1 were not significantly different across the same 4 age groups [82]. A separate study employing targeted proteomics, but extending the analysis to fetal samples, also observed no significant changes in BCRP and P-gp expression from birth to adulthood. However, expression of P-gp was ~2-fold less in fetal livers compared to those of adults, and MRP2 expression was ~3-fold greater in adults than in the fetus or term infants under 18 weeks of age [168].

Bile acids are synthesized in hepatocytes from cholesterol by CYP isoforms and are exported across the canalicular membrane by transporters, most notably the bile salt salt exporter pump (BSEP). Other transporters also play a role in bile acid homeostasis including the apical sodium bile acid transporter (ASBT) and the heteromeric organic solute transporters (OSTs) that are involved with the vectorial reabsorption of bile acids from the ileum and directly from the bile ducts [167, 169]. While these are not typically considered drug transporters *per se*, their effects on canalicular bile acid concentrations have the potential to impact hepatobiliary secretion of drugs. Two relatively recent proteomics studies demonstrated modest but non-significant trends of progressively increasing BSEP expression after birth [82, 168]. However, one of these studies also evaluated fetal tissue and demonstrated a statistically significant greater abundance of BSEP in the livers from term infants and adults compared to fetal livers [168]. Unfortunately, interpreting the ontogeny of bile acid transporters in terms of quantitative estimations of their impact on pharmacokinetics is challenging given their indirect relationship with drug disposition.

Discussion and Vision for the Future

Knowledge of age-dependent changes in various physiological processes relevant to drug disposition from birth to adulthood, especially developmental trajectories of enzymes and transporters, has greatly expanded over the past 2 decades as summarized in a recent comprehensive review [170]. This new knowledge has led to an increasing number of new applications impacting regulatory and clinical decision-making processes, such as initial dose selection for pediatric clinical trials [171], extrapolation of a model developed for one compound to other compounds metabolized by the same elimination pathway ([172], potential for drug-drug interactions [173, 1], and pediatric regulatory approvals [174]. Particularly interesting are the use of population PK approaches to improve the quality of PBPK models [175] and the use of PBPK modeling and simulation to identify covariates that can be used to improve the quality of population PK models ([176], with further potential application for model-informed precision dosing ([177]). Despite these

advances, critical gaps in our understanding remain; several challenges and opportunities are summarized below:

1. Characterization of developmental trajectories for key scaling factors used in PBPK models. A model has been published characterizing the change in liver volume between birth and 18 years of age, and the pediatric model also predicts liver volume in adults with precision and accuracy that exceeds almost all published adult models [178]. In contrast, as indicated earlier data regarding the developmental trajectory of MPPGL for scaling *in vitro* intrinsic clearance of unbound drug to hepatic clearance (CL_H) are extremely limited, consisting of only include only five samples with ages between 2 and 13 years of age ([179]. Similarly, the CPPGL value used for pediatric extrapolations is derived from adult tissues as no corresponding value for the pediatric age range is currently available. Unpublished data from our group indicate that MPPGL values vary little with increasing postnatal age, but absolute values are dependent on tissue source (flash frozen or perfused *versus* autopsy tissue; manuscript in preparation).
2. Developmental trajectories for unknown unknowns. A challenge for the future is to identify additional factors, currently unknown or poorly understood, with the potential to modulate known developmental trajectories of processes governing drug disposition. Examples include accessory proteins and co-factors for DMEs, such as cytochrome P450 oxidoreductase, uridine diphosphate glucuronic acid [180] and enzymes catalyzing the biosynthesis of 3'-phosphoadenosine 5'-phosphosulfate (PAPS), and glycosyltransferases involved in glycosylation and membrane localization of transporters.
3. Leveraging intensive opportunistic sampling to characterize developmental trajectories of biotransformation pathways at the individual level *in vivo*. Existing developmental trajectories, especially those derived from *in vitro* data, are derived from a single time point (age) from an individual sample. Much more valuable information could be gained from multiple samples collected longitudinally in each patient. A brief report describing patterns of indomethacin acylglucuronide formation and *O*-demethylation in individual patients in a neonatal intensive care setting illustrate the potential for comprehensive urine collections, albeit labor intensive (collection of all diapers up to at least 7 days after the last dose of drug and binned into 12-hour intervals), to provide novel insights into the acquisition of drug biotransformation activity after birth. In this study we found that study participants could be assigned to one of three patterns of cumulative acylglucuronidation/*O*-demethylation excretion in urine, with a higher percentage of the administered dose being recovered in newborns in whom *O*-demethylation was the predominant biotransformation pathway [181]. More importantly, these insights would not have been gained if we had limited our collection interval to a more common protocol of 24-hour collections. One would expect that similar intensive sampling using discarded plasma samples and dried blood spots collected with routine clinical blood draws will provide an equally rich dataset for characterization of developmental trajectories *in vivo*,

especially the degree of inter-individual variability in the rate and extent of the trajectories and the impact of systemic exposure and clinical response.

4. Use of endogenous biomarkers of DME and transporter activity in longitudinal studies and opportunistic sampling protocols further characterize developmental trajectories of important clearance pathways. In a recently published paper, Smits *et al*/summarized available data regarding CYP3A and OATP1B1/3 biomarkers in healthy term and preterm infants [182], and a potential biomarker of CYP2D6 activity has been described in a pediatric study [183]. Although available sample volumes may limit application of newer technologies like exosome-based liquid biopsies ([184] in opportunistic sampling protocols involving extremely young patients, incorporation of biomarker data holds considerable potential for creation of avatars of actual patients and clinical application of a pediatric version of the “virtual twin” approach [185].
5. Use of disease-/patient population-specific data. Scaling factors, such as liver mass, utilize estimates of height and weight derived from growth curves derived from “normal” developing males and females. Patients with conditions like cerebral palsy, anorexia nervosa, and obesity, among others, may not necessarily demonstrate typical growth trajectories. Preliminary data indicate that growth patterns for children with type 2 diabetes mellitus differ from those presented in Center for Disease Control and Prevention growth charts [186]. The implications for PBPK modeling and simulation remain to be determined.
6. Developmental trajectories for targets of drug action. The focus of this paper has been the ontogeny of processes governing drug disposition, but knowledge of the developmental trajectories of receptors, neurotransmitter re-uptake pumps, ion channels and other drug targets is critically important as the next step to ensure safe and effective use of medications throughout the age continuum. In the simplest sense, the risk benefit ratio for a medication will be unacceptable if the presumed target mediating the therapeutic response is not expressed at the age/developmental stage that a medication is administered, and further investigation in this area is of critical importance for the future.
7. Establishing the relationship between systemic drug exposure and therapeutic response as a function of drug target expression. This issue directly follows from the issue above, and in our opinion represents a major opportunity for the next generation of pediatric clinical pharmacology investigators. Analogous to the strategy of administering the same dose of medication or phenotyping probe to a study population and investigating the pharmacogenetic or developmental factors contributing to the observed variability in systemic exposure/clearance or other measure of drug disposition phenotype, a study design to identify genetic and developmental factors contributing a drug/therapeutic response requires administration of the same systemic exposure to the study cohort. In this context, there will be a need for tools to individualize dose and minimize inter-individual variability in systemic exposure so that the confounding effects of exposure on drug response can be reduced. More specifically, relevant signals will be

easier to detect if noise related to poor response due simply to low/inadequate systemic exposure can be eliminated. The concept of concentration-controlled clinical trials is not new, having been proposed by Carl Peck and colleagues in the early 1990s [187] and discussed further over the years [188], largely in the context of clinical trials conducted for regulatory purposes; the application we propose is somewhat different – as a means to identify important genetic and developmental factors influencing the exposure-response relationship in pediatrics, and advances in PK modeling made over the past 30 years now lead to considerable optimism for meaningful progress in this area in the foreseeable future.

Future advances should involve collaboration between the academic, regulatory, clinical and industry communities, with the data generated by these endeavors freely accessible in a centralized global repository. Similar databases have been proposed by the FDA and other researchers [189]. Such a repository would facilitate the continual development of ever more refined population PK, PBPK and hybrid models optimally developed and prospectively validated for the specific intended purpose providing a better understanding of the sources of variability in drug exposure throughout childhood with the objective of optimizing treatment for children of all ages.

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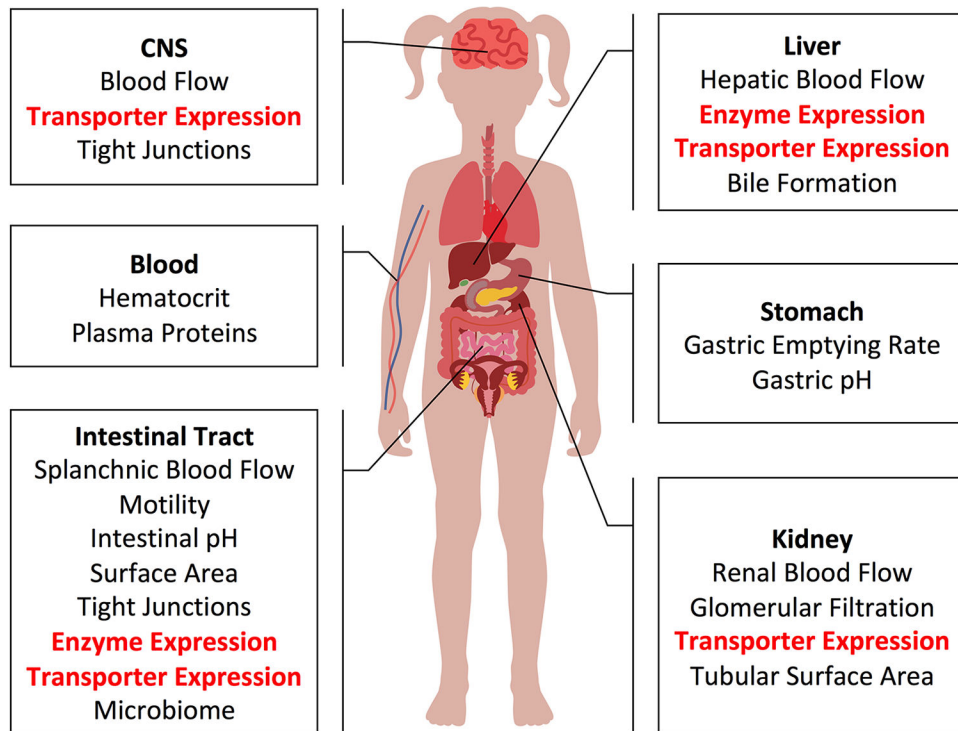


Figure 1. Processes governing drug disposition that may change through childhood developments. Areas in which LC-MS/MS protein quantification have provided substantial new information have in the last 10 years are highlighted in red.

Table 1. Published Sigmoid E_{\max} Models Describing Drug Metabolizing Enzyme and Transporter Ontogenies in the Liver

Enzyme or Transporter	Source	Data Type	Birth		Adult		Age ₅₀ (y)	Exp or h	Age Cap (y)	Reference Number
			E_0 (pmol/mg)	F_{birth}	Max (pmol/mg)	$F_{\text{adult or } F_{\text{max}}}$				
ADH1A	<i>in vitro</i>	Protein-QP	ND		426		0.842	0.84		[137]
ADH1B	<i>in vitro</i>	Protein-QP	1822		5220		0.775	40.6		[137]
ADH1C	<i>in vitro</i>	Protein-QP	21		2598		1.03	2.1		[137]
ALDH1A1	<i>in vitro</i>	Protein-QP	209		394		0.900	244		[137]
CES1	<i>in vitro</i>	Protein-QP ^e		0.20		1	1.10	0.56		[128]
	<i>in vitro</i>	Protein-IR		0.01		1.0	5.2	0.5		[109]
	<i>in vivo</i>	Activity		0.16		1.5	0.20	2.0	10.0 ^d	[109]
CYP1A2	<i>in vitro</i>	Hybrid ^h		0.08		1.05	1.69	1.1		[108]
	<i>in vivo</i>	Activity		0		1.6	1.05 ^g	5.7	3.76 ^{d,g}	[107]
	<i>in vitro</i>	Protein-IR		0.01		1.0	0.02	1.8		[109]
CYP2A6	<i>in vivo</i>	Activity		0.15		1.1	0.04	0.8		[109]
	<i>in vitro</i>	Hybrid ^h		0.1		1	1	1		[108]
CYP2B6	<i>in vitro</i>	Protein-IR		1.0		1.0	ND	ND		[109]
	<i>in vivo</i> ^f	Activity		1.0		1.0	ND	ND		[109]
	<i>in vitro</i>	Hybrid ^h		0.3		1	0.02	1		[108]
CYP2C8	<i>in vitro</i>	Protein-IR/mRNA		0.03		1.0	0.02	1.3		[109]
	<i>in vivo</i>	Activity		0.15		2.7	0.15	4.0	0.5 ^d	[109]
	<i>in vitro</i>	Hybrid ^h		0.17		1	0.016	0.53		[108]
CYP2C9	<i>in vitro</i>	Protein-IR		0.01		1.0	0.02	1.2		[109]
	<i>in vivo</i>	Activity		0.01		2.2	0.01	1.2	0.3 ^d	[109]
CYP2C19	<i>in vitro</i>	Hybrid ^h		0.3		1	0.28	2.44		[108]

Enzyme or Transporter	Source	Data Type	Birth		Adult		Age ₅₀ (y)	Exp or h	Age Cap (y)	Reference Number
			E ₀ (pmol/mg)	F _{birth}	Max (pmol/mg)	F _{adult} or F _{max}				
CYP2D6	<i>in vitro</i>	Protein-IR		0.11			0.21	1.5		[109]
	<i>in vivo</i>	Activity		0.16			0.30	2.0	0.8 ^d	[109]
CYP2E1	<i>in vitro</i>	Hybrid ^h		0.036			0.1	1		[108]
	<i>in vitro</i>	Activity		0.07			0.02	2.6		[109]
CYP3A	<i>in vivo</i> ^f	Activity		1.00			ND	ND		[109]
	<i>in vitro</i>	Hybrid ^h		0.086			0.226	0.496		[108]
CYP3A4/5	<i>in vitro</i>	Protein-IR		0.03			0.14	0.6		[109]
	<i>in vivo</i>	Activity		0.05			0.10	1.3	2.5 ^d	[109]
CYP3A4	<i>in vitro</i>	Hybrid ^h		0			0.66	0.78		[108]
	<i>in vitro</i>	Protein-IR		0.10			6.30	0.7		[109]
CYP3A5	<i>in vivo</i>	Activity		0			2.07 ^g	3.9		[107]
	<i>in vitro</i>	Protein-IR/QP		1.0			1.0	1.0		[109]
FMO3	<i>in vitro</i>	Protein-QP	1.75		31.22		0.80	0.49		[134]
SULT1A3	<i>in vitro</i>	Protein-QP		85.26			0.9094	166.5		[144]
SULT1B1	<i>in vitro</i>	Protein-QP		37.75			0.9092	166		[144]
UGT1A1	<i>in vitro</i>	Protein-QP		0.27			7.5	0.5		[99]
UGT1A4	<i>in vitro</i>	Activity		0.235			0.502	2.77		[106] ^a
	<i>in vitro</i>	Protein-QP		0.01			3.6	0.9		[99]
UGT1A6	<i>in vitro</i>	Protein-QP		0.03			10.3	0.6		[99]
UGT1A9	<i>in vitro</i>	Protein-QP		0			8.2	0.5		[99]
UGT1A9/2B7	<i>in vitro</i>	Activity		0			2.18	0.063		[106] ^a
UGT2B7	<i>in vitro</i>	Protein-QP		0.02			2.6	0.4		[99]
UGT2B17	<i>in vitro</i>	Activity		0.612			17.4	40.6		[106] ^a
	<i>in vitro</i>	Protein-QP	0.11		1.31		13.5	7.5		[139]

Enzyme or Transporter	Source	Data Type	Birth		Adult		Age ₅₀ (y)	Exp or h	Age Cap (y)	Reference Number
			E ₀ (pmol/mg)	F _{birth}	Max (pmol/mg)	F _{adult} or F _{max}				
			M ^b 0.10		M ^b 1.75		M ^b 13.6	M ^b 14.9		
			F ^b 0.05		F ^b 0.65		F ^b 10.7	F ^b 1.8		
OCT1	<i>in vitro</i>	Protein-QP	0.58		3.98		0.47	0.92		[82] ^c
OATP1B3	<i>in vitro</i>	Protein-QP	0.50		1.14		0.58	4.87		[82] ^c
P-gp	<i>in vitro</i>	Protein-QP	0.15		0.41		2.94	0.78		[82] ^c

Significant figures provided as they are presented in respective source material. Protein-QP and -IR refer to protein expression as determined by quantitative proteomics and immunoreactive methods respectively.

^aDevelopmental trajectories for UGT 1A1, 1A3, 1A6, 1A9, 2B4, 2B7, 2B10 and 2B15 activities described in reference by one-phase decay equations

^bData also presented separately for males (M) and females (F)

^cExpression of BCRP, MRP2, BSEP, MATE1 not influenced by age

^dOntogeny equation applicable up to an age cap due to average adult clearance not representing maximum clearance.

^eRepresents collective expression of both microsomal and cytosolic protein

^fUpreti et al state “*in vivo* data used to verify, but not develop. *in vivo* ontogeny”

^gP Refers to postmenstrual age

^hOntogeny models from this were collectively developed from both *in vitro* expression and activity data but specific use of expression and/or activity data unclear for specific isoforms