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Examination of Urinary Excretion of Unchanged Drug in Humans and Preclinical Animal Models: Increasing the Predictability of Poor Metabolism in Humans

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Abstract

Purpose—A dataset of fraction excreted unchanged in the urine (fe) values was developed and used to evaluate the ability of preclinical animal species to predict high urinary excretion, and corresponding poor metabolism, in humans.

Methods—A literature review of fe values in rats, dogs, and monkeys was conducted for all Biopharmaceutics Drug Disposition Classification System (BDDCS) Class 3 and 4 drugs (n=352) and a set of Class 1 and 2 drugs (n=80). The final dataset consisted of 202 total fe values for 135 unique drugs. Human and animal data were compared through correlations, two-fold analysis, and binary classifications of high (fe ≥ 30%) versus low (<30%) urinary excretion in humans. Receiver Operating Characteristic curves were plotted to optimize animal fe thresholds.

Results—Significant correlations were found between fe values for each animal species and human fe ($p < 0.05$). Sixty-five percent of all fe values were within two-fold of human fe with animals more likely to underpredict human urinary excretion as opposed to overpredict. Dogs were the most reliable predictors of human fe of the three animal species examined with 72% of fe values within two-fold of human fe and the greatest accuracy in predicting human fe ≥ 30%. ROC determined thresholds of ≥ 25% in rats, ≥ 19% in dogs, and ≥ 10% in monkeys had improved accuracies in predicting human fe of ≥ 30%.

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Conclusions—Drugs with high urinary excretion in animals are likely to have high urinary excretion in humans. Animal models tend to underpredict the urinary excretion of unchanged drug in humans.

Keywords

Fraction excreted unchanged; poorly-metabolized drugs; animal models; renal clearance; BDDCS

INTRODUCTION

A significant aspect of preclinical drug development is understanding drug absorption, distribution, metabolism, and elimination, all of which are important in identifying lead candidates and potential first-in-human doses. The elimination pathway of a new molecular entity (NME) can help guide further steps in development. For instance, if a compound is likely to be administered to patients with renal dysfunction, it may be advisable to instead choose a candidate that is primarily eliminated via hepatic metabolism or biliary excretion. Thus, substantial efforts are taken to deduce if an NME is eliminated by metabolism, biliary excretion, or renal excretion. Consequently, numerous *in silico*, *in vitro*, and *in vivo* models have been developed to predict drug clearance and the elimination pathways of NMEs prior to first-in-human studies [1–15]. We have previously reported on *in silico* and *in vitro* approaches to predict when a drug will likely be metabolized versus being eliminated unchanged in the bile or urine [8, 10]. Herein, we explore how *in vivo* animal models may help elucidate the elimination route of an NME early in drug development.

Animal models including rodent species such as the rat, and non-rodent species such as the dog and monkey, are used extensively in preclinical studies to predict drug elimination and other pharmacokinetic parameters. Although much research has gone into developing allometric scaling equations and physiologically-based modeling techniques, many of the proposed prediction methods are complicated and require extensive species and drug data. In general, it is believed that drugs that undergo extensive metabolism in humans are difficult to scale using simple allometric scaling approaches [16–19]. This lack of predictive ability between animals and humans for extensively metabolized drugs likely stems from differences in metabolism due to differences in isoforms, expression, activities, and substrate specificities of drug metabolizing enzymes. In contrast, drugs with minimal hepatic metabolism and drugs predominately excreted renally are generally more amenable to allometric scaling [16, 19]. Furthermore, it is generally believed that there are fewer species differences in pharmacokinetics for drugs that are poorly metabolized [20]. Given that animals poorly predict extensive metabolism in humans, here we ask whether animal models can predict when a drug will likely have limited metabolism in humans and be eliminated through another route, namely urinary excretion of unchanged drug.

For this study, we utilized the Biopharmaceutics Drug Disposition Classification System (BDDCS) that categorizes drugs based upon their solubility and overall extent of metabolism in humans (Fig. 1). Solubility in BDDCS is defined by the United States Food and Drug Administration (US FDA) as the ability of the drug at its highest dose strength to completely dissolve in 250 ml of water over a pH range between 1 and 7.5 at 37°C [21].

Metabolism is defined as the overall extent of metabolism in humans. Class 1 and 2 drugs have an extent of metabolism $\geq 70\%$, whereas Class 3 and 4 drugs have $<70\%$ metabolism, but the great majority exhibit $<30\%$ metabolism [21, 22].

The extent of metabolism in BDDCS corresponds with the fraction of drug excreted unchanged in the urine or the bile. Class 1 and 2 drugs, which have high extents of metabolism, have correspondingly low amounts of drug excreted unchanged. Conversely, Class 3 and 4 drugs, which have low extents of metabolism, have corresponding high amounts of the drug excreted unchanged in the urine or the bile. With this in mind, it is reasonable to use extent of drug excreted unchanged as a marker for the extent of metabolism. In fact, the fraction of drug excreted unchanged in the urine (f_e) is easily obtained after administration of a drug intravenously to humans or animals. It should be noted, however, that the extent of biliary excretion of unchanged drug is difficult to experimentally determine in humans due to the invasive techniques needed for sample collection. Taken together, when Benet et al. assigned BDDCS classes to over 900 drugs, the percent excreted unchanged in the urine values in humans were utilized along with other data including known biliary excretion and extent of metabolism [22]. Almost all drugs assigned as either BDDCS Class 1 and 2 possess f_e values of $<30\%$ in humans [22]. The majority of drugs (84%) assigned to either Class 3 or 4 have a human f_e value of $\geq 30\%$ [22]. This means, however, that approximately 16% of the Class 3 and 4 drugs have a human f_e of $<30\%$ and are likely to have high biliary excretion in humans [22].

In this study, we examine if drugs with high urinary excretion in humans also have high urinary excretion in preclinical animal studies. To do this, we investigated drugs already identified to be poorly metabolized in humans (BDDCS Class 3 and 4 drugs) and conducted an extensive literature review of reported f_e values for the three animal species and compared them to human f_e values. Our dataset primarily focused on BDDCS Class 3 and 4 drugs since it is generally believed that animals, particularly small animals such as the rat, metabolize drugs to a greater extent in humans when compared on a weight-normalized basis [20]. In other words, it is generally believed that drugs that are extensively metabolized in humans (BDDCS class 1 and 2) are predominately extensively metabolized in animal models. Thus, we expected that BDDCS class 1 and 2 drugs would have low f_e values in animals. To verify this assumption, we conducted a smaller scale literature review of a set of 80 BDDCS Class 1 and 2 drugs. We focused only on urinary excretion rather than biliary elimination due to the difficulty in obtaining biliary values in humans. We recognize this is not a perfect representation since several Class 3 and 4 drugs are predominantly excreted unchanged in the bile and have very low f_e values. The developed dataset of f_e values was analyzed to explore the relationship of urinary excretion of drugs that are primarily poorly metabolized in humans with that of animals.

MATERIAL AND METHODS

Dataset

Fraction excreted unchanged in the urine (f_e) values for rats, dogs, and monkeys were searched in the biomedical literature for BDDCS Class 3 ($n=288$) and Class 4 ($n=64$) drugs that were assigned classification in our previously published datasets [22, 23]. In addition,

the literature was searched for a small subset of BDDCS Class 1 (n=41) and Class 2 (n=39) drugs [22, 23]. Drugs were included in the analysis even if they display known nonlinearities in their pharmacokinetics. The compound name was cross-referenced with the animal species type (i.e. rat, dog, monkey) and other search terms such as “pharmacokinetics” or “disposition” in a database search such as Pubmed. All original references of animal fe data were obtained and further inspected to ensure compliance with the below criteria. Human fe values for BDDCS Class 1 through 4 drugs were obtained directly from our previously published dataset [22] or searched in the literature.

Inclusion criteria were used to define acceptable parameters for data collection and to ensure consistent data reporting. Obtained fe values were only included in analysis for both animals and humans if the drug was administered intravenously and unchanged drug in the urine was measured. Oral data was not collected due the potential influence of bioavailability. The fraction eliminated as unchanged drug in the bile was not collected due to the difficulty in obtaining biliary values in humans. Studies that evaluated only total radioactivity were not included in the dataset. In some cases, the fe value was not listed but was estimated by dividing renal clearance by total body clearance. No restrictions were made regarding sex of the animal or the particular strain/breed of the animal. Monkey data were obtained from pharmacokinetic studies using either Cynomolgus monkeys, African green monkeys, rhesus monkeys, or pigtailed macaques.

Data analysis

Obtained fe values from animal models were compared to human fe values by: (1) correlation, 2) analysis of drugs within a two-fold error range, and (3) binary classifications with corresponding sensitivity and specificity analyses. All data were analyzed by Microsoft Excel (Microsoft Corporation, Redmond, WA, USA) or GraphPad Prism 7.02 (GraphPad Software, La Jolla, CA, USA).

Urinary excretion data from each animal species were plotted against human values. The normality of each animal model dataset was assessed by a D’Agostino & Pearson normality test. As rat and dog data were not normally distributed, but monkey data were, both Spearman and Pearson correlations were used to assess statistical significance of correlations between humans and all animal models. Spearman and Pearson correlation coefficients were also calculated. Additionally, human fe values were paired with collected fe values for each animal species and graphed using boxplots for each BDDCS class. Statistical differences in paired fe data between humans and each animal species for each BDDCS class were calculated through Wilcoxon matched-pairs signed rank tests. To complete the two-fold analysis, animal fe values were plotted against human fe values and the proportion of drugs that fell within and outside of a two-fold range was determined.

In addition to completing analyses of the continuous fe data, a binary classification approach was also used to assess how frequently a drug had high urinary excretion in both animals and humans. High urinary excretion in humans was defined as fe ≥ 30% to match the BDDCS thresholds of poor and extensive metabolism described above. Low urinary excretion in humans was defined as fe <30%. Two different thresholds for segregating high and low urinary excretion were utilized for animal fe data. For the first threshold,

collected animal fe data was classified to have either high urinary excretion (fe ≥ 30%) or low urinary excretion (<30%) and then compared to the same threshold in humans (Fig. 2). The second threshold assessed was determined by Receiver Operating Characteristic (ROC) curves to optimize the animal fe threshold to predict a human fe ≥ 30% or <30%. ROC curve generation for each animal species was completed using the ROCR package in R [24]. As further defined below, the true positive rate (sensitivity) was plotted against the false positive rate (1-specificity) for each continuous value of animal fe as a predictor of extent of human fe. The threshold that maximized the average between sensitivity and specificity was selected. Compounds were considered true positives (TP) if both the animal fe and human fe were ≥ 30% or ROC determined threshold. Compounds were considered false positives (FP) when animal fe was high but human fe was below the threshold. False negatives (FN) were compounds where animal fe was low but human fe was above the threshold. When both animal fe and human fe were low, the compounds were considered as true negatives (TN).

These binary classifications were evaluated by calculating sensitivity, specificity, accuracy, positive predictive value (PPV), and negative predictive value (NPV) (Equations 1 through 5). Sensitivity is the percent of positives (compounds with high fe in humans) that were correctly predicted by high fe in animals. Specificity is the percent of negatives (compounds with low fe in humans) that were correctly predicted by low fe in animals. Accuracy is the proportion of true results to all results. PPV is the percent of compounds with high fe in animals that are also high in humans. NPV is the percent of compounds with low fe in animals that are also low in humans.

$$\text{Sensitivity (\%)} = \frac{\text{true positives}}{\text{true positives} + \text{false negatives}} * 100\% \quad (\text{Equation 1})$$

$$\text{Specificity (\%)} = \frac{\text{true negatives}}{\text{true negatives} + \text{false positives}} * 100\% \quad (\text{Equation 2})$$

$$\text{Accuracy (\%)} = \frac{\text{true positives} + \text{true negatives}}{\text{true positives} + \text{true negatives} + \text{false positives} + \text{false negatives}} * 100\% \quad (\text{Equation 3})$$

$$\text{PPV (\%)} = \frac{\text{true positives}}{\text{true positives} + \text{false positives}} \quad (\text{Equation 4})$$

$$\text{NPV (\%)} = \frac{\text{true negatives}}{\text{true negatives} + \text{false negatives}} \quad (\text{Equation 5})$$

RESULTS

Dataset

Fraction excreted unchanged data for one or more animal species was collected for a total of 135 drugs. The drug name, BDDCS class, and fe value for each animal species are listed

in Table I. The dataset primarily included Class 3 (n=82, 60% of dataset) and Class 4 drugs (n=14, 11% of dataset). For many of the drugs, fe data were collected in more than one species. This allowed collection of 202 total fe values (38 values for Class 1 drugs, 21 values for Class 2 drugs, 121 values for Class 3 drugs, and 22 values for Class 4 drugs). The number of fe values obtained for each animal species and for each BDDCS class are listed in Table II. The rat was the most common animal model that reported fe followed by dog and monkey. A total of 103 drugs with rat fe values, 67 drugs with dog fe values, and 32 drugs with monkey fe values were found.

Box plots of paired animal and human fe values arranged according to animal species and BDDCS classification are shown in Fig. 3. In comparison to human fe values, significantly lower fe values were found for rats ($p<0.05$), dogs ($p<0.05$), and monkeys ($p<0.005$) for the BDDCS Class 3 drugs in the dataset. Significantly lower fe values were also seen for dogs in comparison to humans for the BDDCS Class 4 drugs in the dataset ($p<0.05$). Values of fe were $<40\%$ for all species for Class 1 and 2 drugs.

Correlation analysis

Statistically significant correlations between animal fe values and human fe values were seen for rats ($p<0.0001$), dogs ($p<0.0001$), and monkeys ($p<0.0001$) when examining all drugs in the dataset. Spearman rho values of 0.817, 0.818, and 0.730 were calculated for rats, dogs, and monkeys, respectively. Pearson rho values of 0.819, 0.834, and 0.701 were calculated for rats, dogs, and monkeys, respectively.

Two-fold analysis

For the majority of drugs, animal fe values were within two-fold of human fe values (Fig. 4). As expected, fe values for BDDCS class 1 and 2 drugs were very low for both animals and humans, and thus, a greater proportion of Class 3 and 4 drugs fell within two-fold in comparison to Class 1 and 2 drugs (Table III). Of the BDDCS Class 3 and 4 drugs in the dataset, 81% of rat, 83% of dog, and 62% of monkey fe values were within two-fold of their human fe counterparts. BDDCS Class 3 and 4 drugs that fell outside of the two-fold range are listed in Table IV.

ROC curve analysis

ROC curve analysis was used to determine a fe threshold in animals that would predict 30% fe in humans. Optimized thresholds of 25% in rats, 19% in dogs, and 10% in monkeys were identified as potential thresholds to optimally predict a human fe of 30%. The area under the ROC curve for each animal species (rats=0.96, dogs=0.98, and monkey=0.98) was greater than the generally accepted cutoff of 0.8 indicating the fe in these animal species has a high discriminatory ability to predict extent of urinary excretion of parent drug in humans.

Binary classifications

The ability of animal models to properly classify human fe as $\geq 30\%$ or $<30\%$ is shown in Figure 5. Two thresholds for each animal species were evaluated: $\geq 30\%$ or $<30\%$ to directly match the cutoff in humans or a cutoff determined through ROC curve analysis (above).

Each animal species had a large number of drugs that had high urinary excretion in both animals and humans, which were classified as true positives. Very few drugs possessed a high urinary excretion in animals ($\geq 30\%$ or ROC determined threshold) but low urinary excretion in humans ($<30\%$); as a result, very few false positives were seen. In comparison, there were more false negatives for each animal species where the animal fe values were less than the threshold but human fe value was $\geq 30\%$. The vast majority of BDDCS Class 1 and 2 drugs in the dataset were classified as true negatives (low urinary excretion in both animals and humans).

Calculations of sensitivity, specificity, accuracy, PPV, and NPV for each animal model to properly classify human fe using both thresholds are shown in Table V. When using the $\geq 30\%$ threshold to directly match the cutoff in humans, high specificities were attained. In addition, all animal models possessed high positive predictive values (PPV) but low negative predictive values (NPV). When utilizing the ROC optimized thresholds of $\geq 25\%$ in rats, $\geq 19\%$ in dogs, and $\geq 10\%$ in monkeys, calculated sensitivities, accuracies, and NPVs improved for all three animal species.

DISCUSSION

Here, we report an extensive dataset of fe values for poorly metabolized, BDDCS Class 3 and 4 drugs, along with a smaller set of fe values for highly metabolized, BDDCS Class 1 and 2 drugs. These values were obtained for humans as well as three animal species commonly used in preclinical drug development. The collected fe values were utilized as a marker of extent of urinary excretion, suggestive of extent of metabolism since drugs that are highly metabolized (i.e., $\geq 70\%$ extent of metabolism) in humans generally have a fe $<30\%$ [21]. For drugs that are poorly metabolized in humans (i.e., $<70\%$ extent of metabolism), $\geq 30\%$ of the drug is likely eliminated unchanged in the urine or bile. It should be noted that within this study only urinary excretion data were collected due to the difficulty in collecting biliary data experimentally in humans.

A good relationship between animal fe and human fe was observed with statistically significant correlations found between the fe values of humans and each animal model ($r > 0.70$ for all species). Sixty-five percent of all animal fe values fell within two-fold of human fe values. Dogs were the most reliable predictors of the three species with the largest percentage of fe values within two-fold of human fe (72%), the highest correlation coefficients, and the greatest predictive accuracy (Table V). Interestingly, of the three species, monkeys were the poorest predictors of human fe. Monkeys had the lowest proportion of compounds within two-fold of the human values (53%) and exhibited the lowest correlation coefficients (~ 0.7). Monkeys further had a very low ROC determined fe cutoff (10%), potentially indicating that monkeys have substantially greater hepatobiliary elimination processes than humans.

Evaluation of physiochemical properties of BDDCS Class 3 and 4 drugs that fell within two-fold versus those that were outliers showed no major differences between the two groups of medications in terms of partition coefficient (log P), molecular weight, or water solubility (data not shown). Of the outliers noted in Table IV, two of drugs, dorzolamide and

mezlocillin, are known to display nonlinear pharmacokinetics. Differences in plasma protein binding between animals and humans as an explanation for the outliers was not explored due to the paucity of this published information.

As expected, human f_e was better predicted by animal models for Class 3 and 4 drugs than Class 1 and 2 drugs. The limited number of Class 1 and 2 drugs having animal f_e values within two-fold of the human f_e value is likely due to their very low f_e values. Such low f_e values are likely to produce differences greater than two-fold, but are not physiologically meaningful; for example, griseofulvin had a 0.3% f_e in humans and a 0.1% f_e in rats, a three-fold difference. It is plausible that predictions for Class 4 drugs were less accurate than Class 3 drugs due to the nature of Class 4 drugs, which are poorly soluble and poorly permeable. Nonetheless, the graphs in Fig. 4 suggest that it is much more common for animal data to underpredict f_e than overpredict f_e , likely due to greater metabolic disposition in animals, compared to humans.

This general tendency for animal models to underpredict the urinary elimination of parent drug in humans is highlighted by the lower ROC determined cutoffs that optimally identify high f_e in humans (i.e., $f_e \geq 25\%$ in rats, 19% in dogs, and 10% in monkeys instead of 30%). Regardless of which cutoff was used, the binary classifications of f_e data identified that a substantial proportion of drugs in the dataset were true positives indicating instances where both animals and humans had high urinary excretion (Fig. 5). These drugs would be expected to have poor metabolism in both animals and humans. Additionally, the majority of true negatives (e.g., drugs with low urinary excretion in both animals and humans) were BDDCS Class 1 and 2 drugs. Each animal model had few false positives (animal f_e threshold but human $f_e < 30\%$), but many true positives, resulting in high PPVs in all species ($>90\%$). This suggests that when high urinary excretion is found in a preclinical animal species, there is a strong likelihood that humans will also have a $f_e \geq 30\%$. A poor NPV was seen for the 30% threshold in animals, indicating that animal models tended to have lower f_e than humans for the same compounds, but NPV values improved for each animal species with the optimized ROC thresholds. This shift in the cutoff may indicate that even relatively low f_e values in animals (i.e., $f_e \geq 25\%$ in rats, 19% in dogs, and 10% in monkeys) are predictive of substantial renal elimination in humans and likely low extents of metabolism.

When both animal and human thresholds were set at 30% , the data illustrate high sensitivities between f_e values of animals and humans with the dog and rat (85% and 87% , respectively) having better sensitivities than the monkey (74%). Similarly, rats and dogs predicted human f_e more accurately (87% and 90% , respectively) compared to monkeys (81%). The high specificities calculated were likely the result of very few drug examples where the animal model had high urinary excretion but low urinary excretion in humans (i.e., false positives). When cutoffs of 25% in rats, 19% in dogs, and 10% in monkeys were used, sensitivities improved for each animal species (88% , 100% , and 96% in rats, dogs, and monkeys, respectively). The optimized thresholds also improved accuracies with the dog having the highest accuracy (97%), followed by the monkey (94%), and then the rat (88%).

To our knowledge, this is the first study to compare fraction excreted unchanged in the urine in animal models to that in humans as a method of predicting extent of metabolism in humans. Our results suggest that drugs with high urinary excretion in humans also often have high urinary excretion in animals. Since high urinary excretion ($f_e \geq 30\%$) is indicative of poor metabolism ($<70\%$), a drug with a f_e of $\geq 30\%$ in one or more preclinical animal species will likely have poor metabolism in humans, and therefore, be classified as a BDDCS Class 3 or 4 drug.

Other research groups have investigated the use of preclinical animal species to predict urinary excretion in humans with mixed conclusions. Only one study, to our knowledge, has attempted to compare f_e values of preclinical animal species with humans. That study by Fagerholm concluded that there are poor predictions of renal clearance between species including a poor correlation between rat and monkey f_e and human f_e [25]. This contradiction with our results likely stems from a much smaller dataset used by Fagerholm ($n=25$ drugs), whereas our dataset includes 137 drugs. Although the specific drug names included in the analysis are not listed, it appears that Fagerholm utilized a broad range of compounds versus our dataset that predominately included poorly permeable Class 3 and 4 drugs. Although Fagerholm concludes a poor correlation between animal and f_e data, the study goes on to suggest that correlations between f_e values in humans and animals is improved for drugs with high passive permeability, drugs with extensive tubular reabsorption, and/or drugs with high non-renal clearance. Further studies have explored interspecies scaling of urinary excretion amounts. A retrospective study of 13 antibacterial drugs found that the amounts of drug excreted into the urine or the feces was allometrically scalable between various preclinical animal models and humans with better predictions found for drugs with higher urinary excretion [26].

Prediction of clearance from preclinical animal species through allometric scaling has been investigated and reviewed in depth by numerous research groups [1, 2, 5, 6, 16–19, 27, 28]. There is general support in the literature that human pharmacokinetics is more easily predicted for renally eliminated drugs in comparison to those eliminated through metabolism, which aligns with the data presented herein. Briefly, Tang and Mayersohn found that systemic clearance was better predicted for drug excreted renally or in the bile in comparison to those eliminated by metabolism [18]. Similarly, Huh et al. investigated various allometric scaling approaches to predict human clearance using data from both small molecules and macromolecules and concluded that clearance in humans is well predicted for renally excreted drugs [17].

A number of studies have also specifically focused on the prediction of renal clearance from animal models. Mahmood determined that it was difficult to allometrically scale drugs that undergo active renal secretion and cautioned the interpretation of clearance parameters of renally secreted drugs [29]. It has been further suggested by Di et al. that interspecies allometric scaling of renal clearance may work better for drugs that undergo filtration with only limited active secretion and reabsorption [27]. The results presented here did not attempt to categorize drugs by their extents of active secretion or reabsorption or to identify if nonlinearities in these processes are possible explanations to any drug outliers. As the drugs evaluated in the dataset here were primarily BDDCS Class 3 and 4 drugs, one would

expect limited renal reabsorption due to the poor passive permeability of these compounds. It is possible that active secretion may be playing an important role for certain compounds. However, because actively secreted drugs tend to have underpredicted renal clearances in humans when allometrically scaled, one would still anticipate a drug to have high urinary excretion in humans if a drug is highly excreted into the urine in an animal model [29].

Considerable focus has also been placed on evaluating which preclinical animal species is most effective for allometric scaling in humans. Using various scaling approaches, Paine et al compared renal clearance predictions from rats and dogs and found the strongest correlation of human renal clearance with dogs [30]. Contrary to our results, other studies have shown monkeys to be better predictors of clearance in humans [2, 28]. This observation has been attributed to evolutionary similarity between monkeys and humans, as a result of similarities in transporters and drug metabolizing enzymes. In addition, it has been suggested that the monkey is the best of the preclinical animal species in predicting renal clearance no matter if a drug undergoes filtration, reabsorption, or active secretion in the kidney [27]. The *fe* data we report here indicate monkeys may underpredict urinary excretion to a greater degree than rats or dog. This result may be attributed to the small dataset of the monkey, which had the smallest dataset of the three animal species and consisted of only 32 drugs.

The results presented here have several limitations. First, the dataset was constructed primarily from drugs already identified to have poor metabolism in humans (BDDCS Class 3 and 4 drugs) and may not be fully representative of the distribution of BDDCS classifications of NMEs. To minimize this limitation, we included a literature review of a small set of BDDCS Class 1 and 2 drugs. Of the *fe* values collected for Class 1 and 2 drugs, all but one drug, sumatriptan (rat *fe*=39.5%, dog *fe*=35.7%, human *fe*=22%), had low urinary excretion in both animals (<30%) and humans (<30%). Second, our dataset was limited to the published literature. As preclinical pharmacokinetic studies are not always published, our dataset may be missing key urinary excretion values that may impact our findings. Third, we focused only on urinary excretion and did not include biliary excretion due to the difficulty in finding such reliable references. Additionally, due to the retrospective nature of this dataset, it only includes mean data from the original experimental studies and not a measure of variability. Also, drugs were included in the dataset even if they exhibit known nonlinearities in their pharmacokinetics, which may impact interpretation of this analysis for those drugs. Finally, we did not investigate the role of filtration, active secretion, or reabsorption for drugs in this dataset nor did we make attempts to categorize the drugs by other parameters that may influence urinary excretion such as fraction unbound.

The results of this study provide another level of evidence, in addition to *in silico* and *in vitro* approaches, to determine the elimination pathway of an NME early on in development. Due to the high correlation between intestinal permeability rate and extent of metabolism, *in vitro* measures of passive membrane permeability including the use of parallel artificial membrane permeability assays (PAMPA), Caco-2 cells, and MDCK cells can be used to predict extent of metabolism [31–33]. Furthermore, a number of *in silico* tools have been published that attempt to predict a drug's permeability and/or elimination pathway based on physicochemical properties such as molecular weight, log P, polar surface area, and

others [10, 34–37]. In general, compounds that exhibit high permeability rate *in vitro* or *in silico* are very likely to be metabolized. While compounds with low permeability rates are expected to be eliminated as unchanged drug, a substantial fraction of drugs with relatively low permeability rates *in vitro* or *in silico* are actually metabolized [10]. These drugs with an “intermediate” permeability rates are especially difficult to predict with just *in vitro* or *in silico* data and could benefit from *in vivo* studies in preclinical species to further inform elimination mechanisms. Thus, an evaluation of urinary excretion in animal models may be useful in identifying which compounds are likely renally eliminated in humans (i.e., lack metabolism), and which are likely eliminated by a hepatic route (i.e., metabolism or biliary excretion). Overall, the results presented here suggest urinary excretion data in preclinical species may be helpful to confirm elimination route and the BDDCS classification suggested with *in silico* and *in vitro* models. Having *in silico*, *in vitro*, and *in vivo* evidence of BDDCS classification provides additional reassurance of the likely extent of metabolism in humans.

CONCLUSIONS

A dataset of animal and human f_e values was constructed and evaluated to determine the ability of preclinical animal species to inform when an NME will have high urinary excretion and corresponding poor metabolism in humans. Paired f_e values between animals and humans indicate that rats and monkeys have significantly lower f_e values than humans for Class 3 drugs, while dogs have significantly lower f_e values than humans for both Class 3 and 4 drugs. Statistically significant correlations were found between each animal species (rat, dog, and monkey) and human f_e . In addition, a high frequency of Class 3 and 4 drugs had animal and human f_e values within a two-fold range. Drugs with animal f_e values outside of a two-fold range of human f_e values were more likely to underpredict as opposed to overpredict human f_e . Alignment between animal and human data was seen when f_e values were classified as high ($f_e \geq 30\%$) or low ($f_e < 30\%$). ROC curve analysis suggests thresholds of 25% in rats, 19% in dogs, and 10% in monkeys may better predict when human f_e values of $\geq 30\%$ or $< 30\%$. High PPVs indicate that when an animal demonstrates high urinary excretion of a drug, high renal excretion of that drug in humans is likely. As high urinary excretion of unchanged drug is a marker for low extent of metabolism, this study indicates that high urinary excretion in animal models is suggestive of poor metabolism in humans and likely classification as a BDDCS Class 3 or 4 drug. Overall, this study provides an additional piece of evidence for predicting elimination pathways early on in drug development that could supplement current *in silico* and *in vitro* approaches.

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Data availability statement:

All data generated or analyzed during this study are included in this article.

ABBREVIATIONS:

BDDCS	Biopharmaceutics Drug Disposition Classification System
fe	fraction excreted unchanged in the urine
FN	false negative
FP	false positive
NME	new molecular entity
PPV	positive predictive value
NPV	negative predictive value
ROC	Receiver Operating Characteristic
TN	true negative
TP	true positive
US FDA	United States Food and Drug Administration

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	High solubility	Low solubility
Extensive metabolism	<u>Class 1</u> High solubility Extensive metabolism	<u>Class 2</u> Low solubility Extensive metabolism
Poor metabolism	<u>Class 3</u> High solubility Poor metabolism	<u>Class 4</u> Low solubility Poor metabolism

Fig. 1:
The Biopharmaceutics Drug Disposition Classification System (BDDCS) as proposed by Wu and Benet (21).

		Animal fe values	
		<30% or <ROC threshold	≥30% or ≥ROC threshold
Human fe values	≥30%	False negatives (FN)	True positives (TP)
	<30%	True negatives (TN)	False positives (FP)

Fig. 2:

A binary classification approach was used to determine how often low or high urinary excretion in animals aligned with low or high urinary excretion in humans. Two fe thresholds were used for each animal species: 30% or <30% to directly that match that in human, or thresholds optimized through Receiver Operating Characteristic (ROC) curves.

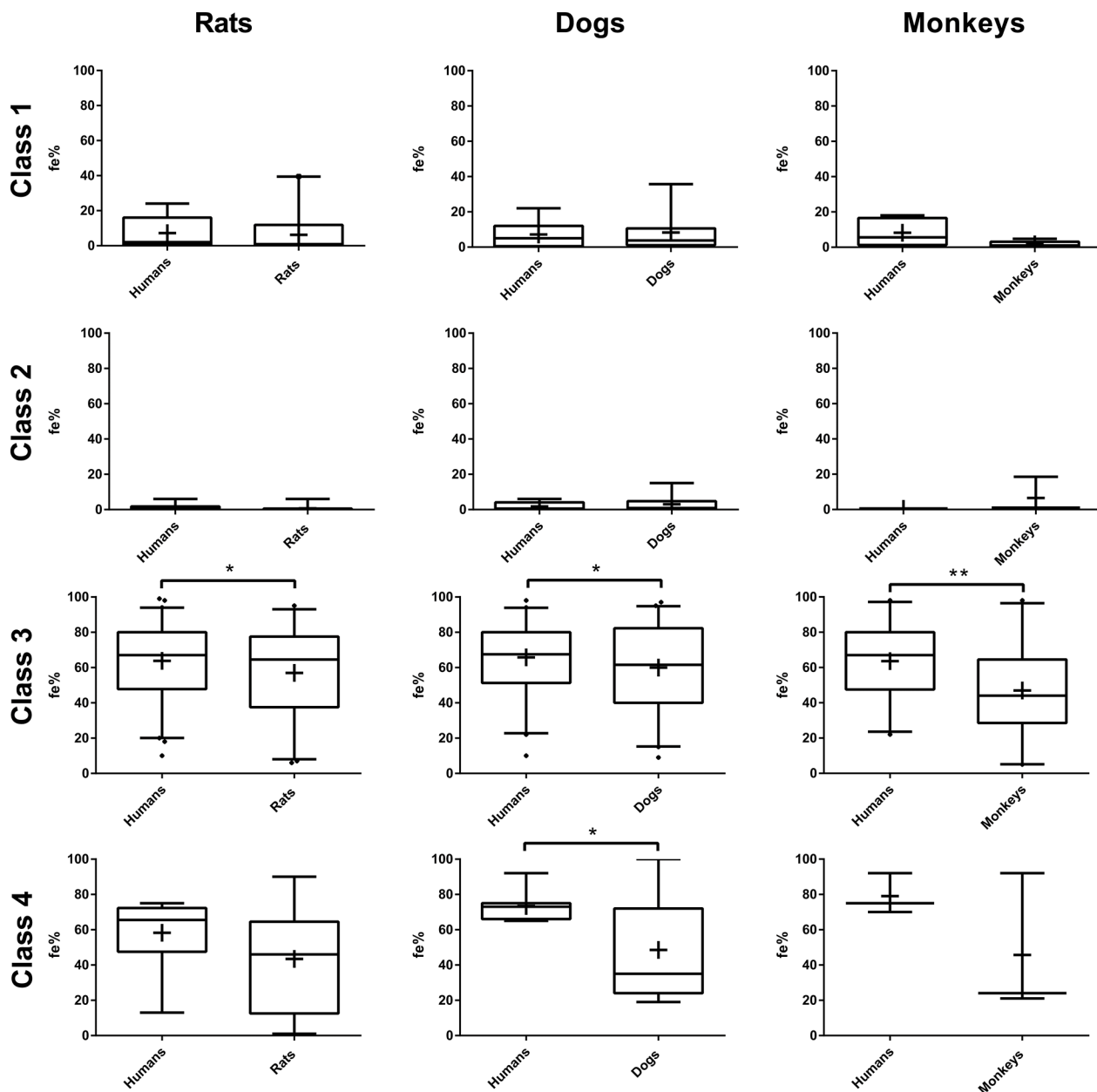


Fig. 3: Box plots of the fraction excreted unchanged in the urine (fe) values in humans that were paired to each animal species arranged by BDDCS class. The center line represents the median, the plus sign indicates the mean, the box itself denotes the interquartile range, the whiskers indicate the 5th and 95th percentiles, and the dots represent values outside the 5th and 95th percentiles. * $p < 0.05$, ** $p < 0.005$.

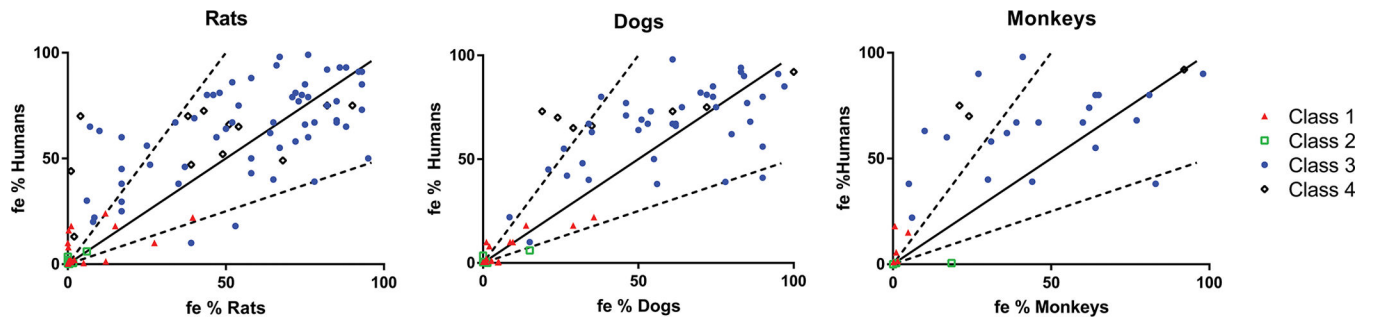


Fig. 4: Plots of rat, dog, and monkey fe values versus human fe values. The solid line denotes the line of unity while the dashed lines indicate an area within two-fold range.

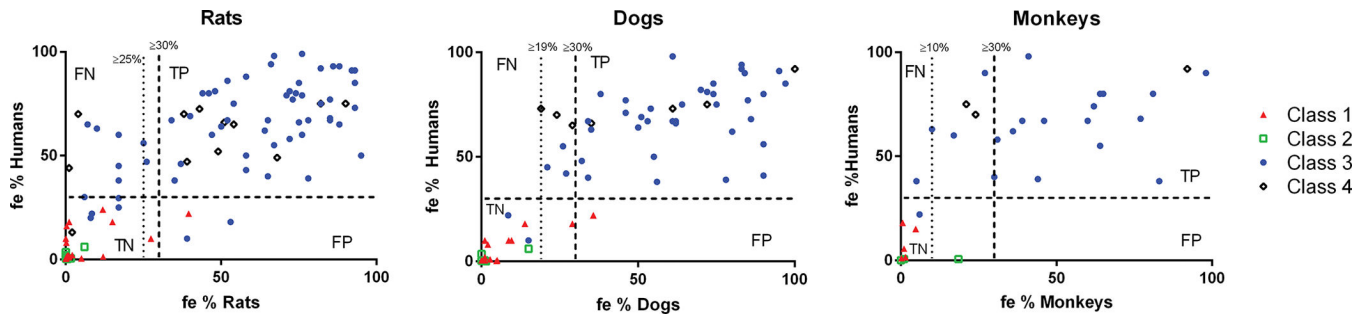


Fig. 5.
: Binary classification analysis of fe values from rat, dog, and monkey models versus human fe values. The dotted lines indicate fe thresholds in both the animal models and humans.

Table 1:

Animal and human fe values collected through the literature review.

Compound Name	BDDCS Class	% Excreted Unchanged in Urine in Humans	% Excreted Unchanged in Urine in Rats	% Excreted Unchanged in Urine in Dogs	% Excreted Unchanged in Urine in Monkeys	References
Acamprosaic Acid	3	50	95			[22, 38]
Acetaminide; N-Acetyl Procainamide	3	81	72			[22, 39]
Acrivastine	3	67		34		[22, 40]
Almotriptan	3	40			30	[22, 41]
Amoxicillin	3	86	52			[22, 42]
Ampicillin	3	88	58			[22, 42]
Atenolol	3	94	66	83		[22, 43, 44]
Aztreonam	3	68	85	86	77	[22, 45]
Benazeprilat	3	18	53			[22, 46]
Betamipron	3	98	67	61	41	[22, 47]
Bisoprolol Fumarate	3	63	10	35	10	[22, 48]
Captopril	3	38		56 ^a	83 ^a	[22, 49]
Carboplatin	3	77	85	46		[22, 50, 51]
Cefazolin	3	80	74	90	81	[22, 52]
Cefmetazole Sodium	3	80	46	74	64	[22, 46, 52]
Cefodizime	3	80	44	38	65	[22, 53]
Cefotetan	3	67	52	53	60	[22, 52]
Ceftazidime	3	85	93	97		[22, 42]
Ceftizoxime	3	93	86			[22, 46]
Cephalixin	3	91	92			[22, 54]
Cephapirin	3	48		32		[22, 55]
Cidofovir	3	90			98	[22, 56]
Cimetidine	3	62	64 ^c	80	36	[22, 57, 58]
Clofarabine	3	55	67			[22, 59]
Dactinomycin (Actinomycin D)	3	10		15		[22, 60]

Compound Name	BDDCS Class	% Excreted Unchanged in Urine in Humans	% Excreted Unchanged in Urine in Rats	% Excreted Unchanged in Urine in Dogs	% Excreted Unchanged in Urine in Monkeys	References
Dexrazoxane	3	42		²⁷ <i>b</i>		[22, 61]
Didanosine	3	55			64	[22, 62]
Digoxin	3	60	17		17	[22, 63, 64]
Disopyramide	3	55		26		[22, 65]
Dorzolamide Hydrochloride	3	10	39			[22, 66]
Doxycycline	3	41		90		[22, 67]
Enalaprilat	3	60	76			[22, 46]
Ertapenem Sodium	3	38	17		5	[22, 68]
Famotidine	3	67	65	61	39	[22, 58, 69, 70]
Fexofenadine	3	25	17			[22, 71]
Fluconazole	3	75	82	64		[22, 42]
Gentamicin Cl Sulfate	3	91	93	95		[22, 42]
Ipratropium Bromide	3	50	58	55		[22, 72]
Kanamycin A	3	90		84		[22, 73]
Ketorolac	3	58			31	[22, 74]
Lamivudine	3	67	⁷⁸ <i>a</i>		46	[22, 75, 76]
Levetiracetam	3	66	75	62		[22, 77]
Levofloxacin	3	74			62	[22, 78]
Metformin	3	99	76			[22, 79]
Methotrexate	3	81	48	⁷² <i>b</i>		[22, 80–82]
Methyldopa	3	40		34		[22, 83]
Mezlocillin	3	45	17			[22, 84]
Moxifloxacin Hydrochloride	3	22	8.4	8.5	6	[22, 85]
Nadolol	3	73	93			[22, 86]
Neostigmine	3	67		62		[22, 87]
Ofloxacin	3	64	50	50		[22, 42]
Olmесartan	3	43	58			[22, 46]

Compound Name	BDDCS Class	% Excreted Unchanged in Urine in Humans	% Excreted Unchanged in Urine in Rats	% Excreted Unchanged in Urine in Dogs	% Excreted Unchanged in Urine in Monkeys	References
Pamidronate Disodium	3	46	37			[22, 88]
Pancuronium Bromide	3	67	85			[22, 89]
Peprinine	3	92	82	83		[23, 90]
Penicillamine	3	45		21		[22, 91]
Penicillin G, Benzylpenicillin	3	79	71			[46, 92]
Pipecuronium Bromide	3	39		78		[22, 93]
Piperacillin	3	71		46		[22, 42]
Pramipexole	3	90			27	[22, 94]
Pravastatin	3	47	26			[22, 46]
Procainamide	3	67	34			[22, 39]
Pyridostigmine	3	85		74		[22, 87]
Rantidine	3	69	40	51		[95-97]
Rosuvastatin Calcium	3	30	6			[22, 46]
Sitafloxacin	3	75	54	75		[22, 98]
Sotalol	3	85	75			[22, 99]
Stavudine	3	39	78		44	[22, 100, 101]
Tazobactam Sodium	3	77	73	85		[22, 102]
Temocaprilat	3	29.5	17			[22, 46]
Tenofovir Disoproxil	3	82		70		[22, 103]
Terbutaline	3	56	25	90		[22, 104, 105]
Tetracycline	3	58	72			[22, 106]
Tiludronic Acid	3	60	47 ^d			[22, 107]
Tirofiban Hydrochloride	3	65	7			[22, 108]
Tobramycin	3	93	88			[22, 42]
Tocamide	3	38	35			[22, 108]
Topotecan	3	40	65			[22, 109]
Vancomycin	3	79	76 ^b			[22, 110]
Vecuronium Bromide	3	20	8			[22, 89]

Compound Name	BDDCS Class	% Excreted Unchanged in Urine in Humans	% Excreted Unchanged in Urine in Rats	% Excreted Unchanged in Urine in Dogs	% Excreted Unchanged in Urine in Monkeys	References
Xamoterol	3	73		54		[23, 111, 112]
Zalcitabine	3	65	88			[22, 113]
Acyclovir	4	75	90	72 ^b	21 ^c	[22, 114–116]
Candesartan	4	52	49			[22, 46]
Cefditoren	4	70	4			[22, 117]
Cefprozil	4	73		61		[22, 118]
Chlorothiazide	4	92		100	92	[22, 119, 120]
Ciprofloxacin	4	65	54	29		[22, 121, 122]
Fleroxacin	4	72.5	43	19		[22, 123]
Furosemide	4	66	51 ^e	35		[22, 124–126]
Medroxyprogesterone Acetate	4	44	1			[22, 127]
Meropenem	4	70	38	24	24	[22, 128]
Nitrofurantoin	4	47	39			[22, 129]
Sulfisoxazole	4	49	68			[22, 130]
Valsartan	4	13	2			[22, 46]
Vitamin B2 (Riboflavin)	4	75	82			[22, 131]
Acebutolol	1	10	27.4 ^{d,e}			[22, 132]
Amitriptyline	1	1	0.847 ^b		0.2	[22, 64, 133]
Caffeine	1	1		2.76		[22, 134]
Chlorpheniramine	1	10		1.1		[22, 135]
Chlorpromazine	1	0.5	0.02 ^{d,e}	1		[22, 136–138]
Desipramine	1	2	2.1			[22, 139]
Diazepam	1	0.5	0 ^a	0		[22, 137, 140]
Diltiazem	1	2	0.74	1.1 ^{d,e}		[22, 141, 142]
Enalapril	1	10	0	9.6		[22, 143]
Imipramine	1	1.5	1.2			[22, 144]

Compound Name	BDDCS Class	% Excreted Unchanged in Urine in Humans	% Excreted Unchanged in Urine in Rats	% Excreted Unchanged in Urine in Dogs	% Excreted Unchanged in Urine in Monkeys	References
Levodopa	1	0.5		1.082 ^b		[22, 145]
Lidocaine	1	8	0.2	2		[22, 146]
Metoprolol	1	10		8.68		[22, 147]
Midazolam	1	5.6			1	[22, 64]
Phenobarbital	1	24	11.9 ^{a,c}			[22, 137, 148, 149]
Prazosin	1	0.5	5	5		[22, 150]
Prednisolone	1	16	0.29			[22, 151]
Propranolol	1	0.25	0.196 ^e	4.8		[22, 152–154]
Propylthiouracil	1	1.28	12			[155, 156]
Quinidine	1	18	1.101 ^{a,e}	29	0.6	[22, 64, 137, 157–159]
Sumatriptan	1	22	39.5 ^d	35.7 ^d		[22, 160]
Tamoxifen	1	0.5	0			[22, 161]
Theophylline	1	18	15 ^e	13.85 ^e		[22, 148, 162–164]
Timolol	1	15			4.8	[22, 64]
Verapamil	1	1.5	0.306		1.5	[22, 64, 165]
Buspirone	2	0.1	0.5 ^d			[22, 166]
Carbamazepine	2	0.5	0.514		1	[22, 167, 168]
Diclofenac	2	0.5	0.1			[22, 169]
Diflunisal	2	6	6 ^{b,e}	15		[22, 170, 171]
Domperidone	2	0		1.4		[22, 172]
Griseofulvin	2	0.3	0.1	0		[22, 173]
Ibuprofen	2	0.5	0	0.765	18.5	[22, 64, 174, 175]
Ketoprofen	2	0.5	1.7			[22, 176]
Nifedipine	2	0.01			0.057	[22, 64]

Compound Name	BDDCS Class	% Excreted Unchanged in Urine in Humans	% Excreted Unchanged in Urine in Rats	% Excreted Unchanged in Urine in Dogs	% Excreted Unchanged in Urine in Monkeys	References
Phenytoin	2	2	0 ^a			[22, 137]
Ritonavir	2	3.5	0	0		[22, 177]
Tacrolimus	2	0.5	0.0073	1		[22, 178, 179]
Terfenadine	2	0	0			[22, 180]
Warfarin	2	1	0 ^a			[22, 137]

^a Calculated from ratio of CL_{renal} and CL_{total} values.

^b Calculated as an average *f_e* following multiple doses.

^c Calculated as an average *f_e* following administration to male and female animals.

^d Calculated as an average *f_e* following administration to different aged animals.

^e Average calculated between multiple reports of *f_e*.

Table II:

Summary of fe data collected for each animal species arranged by BDDCS classification.

BDDCS class	Number fe values obtained			All animal species
	Rat	Dog	Monkey	
All drugs	103	67	32	202
Class 1 drugs	19	14	5	38
Class 2 drugs	12	6	3	21
Class 3 drugs	60	40	21	121
Class 4 drugs	12	7	3	22

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Table III:

Summary of the number and percentage of drugs with animal fe values within a two-fold range of human fe values arranged by animal species and BDDCS class.

BDDCS Class	Rat	Dog	Monkey	All animal species
All drugs	67 (65%)	48 (72%)	17 (53%)	132 (65%)
Class 1 drugs only	6 (32%)	7 (50%)	1 (20%)	14 (37%)
Class 2 drugs only	3 (25%)	2 (33%)	1 (33%)	6 (29%)
Class 3 drugs only	49 (82%)	35 (88%)	14 (67%)	98 (81%)
Class 4 drugs only	9 (75%)	4 (57%)	1(33%)	14 (64%)

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Table IV:

BDDCS Class 3 and 4 drugs with a greater than two-fold difference in human and animal fe (outliers).

Rat fe data		Dog fe data		Monkey fe data	
Drug class	Drug name	Drug class	Drug name	Drug class	Drug name
3	Benazeprilat	3	Cefodizime	3	Betamipron
3	Bisoprolol Fumarate	3	Disopyramide	3	Bisoprolol Fumarate
3	Digoxin	3	Doxycycline	3	Captopril
3	Dorzolamide HCl	3	Moxifloxacin HCl	3	Digoxin
3	Ertapenem Sodium	3	Penicillamine	3	Ertapenem Sodium
3	Mezlocillin	4	Ciprofloxacin	3	Moxifloxacin HCl
3	Moxifloxacin HCl	4	Fleroxacin	3	Pramipexole
3	Rosuvastatin Calcium	4	Meropenem	4	Acyclovir
3	Terbutaline			4	Meropenem
3	Tirofiban HCl				
3	Vecuronium Bromide				
4	Cefditoren				
4	Medroxyprogesterone acetate				
4	Valsartan				

Table V:

Performance of binary classifications of fe thresholds for each animal species to properly classify human fe as 30% or <30% for all BDDCS Class 1, 2, 3, and 4 drugs in dataset.

	Rat		Dog		Monkey	
	30%	25%	30%	19%	30%	10%
Sensitivity	85%	88%	87%	100%	74%	96%
Specificity	92%	89%	95%	91%	100%	89%
Accuracy	87%	88%	90%	97%	81%	94%
PPV	95%	93%	98%	96%	100%	96%
NPV	78%	81%	78%	100%	60%	89%

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