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#### **Intestinal Efflux Transporters P-gp and BCRP Are Not Clinically Relevant in Apixaban Disposition**

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#### **Abstract**

**Purpose—**The involvement of the intestinally expressed xenobiotic transporters P-glycoprotein (P-gp) and Breast Cancer Resistance Protein (BCRP) have been implicated in apixaban disposition based on in vitro studies. Recommendations against co-administration of apixaban with inhibitors of these efflux transporters can be found throughout the literature as well as in the apixaban FDA label. However, the clinical relevance of such findings is questionable due to the high permeability and high solubility characteristics of apixaban.

**Methods—**Using recently published methodologies to discern metabolic- from transportermediated drug-drug interactions, a critical evaluation of all published apixaban drug-drug interaction studies was conducted to investigate the purported clinical significance of efflux transporters in apixaban disposition.

**Results—**Rational examination of these clinical studies using basic pharmacokinetic theory does not support the clinical significance of intestinal efflux transporters in apixaban disposition. Further, there is little evidence that efflux transporters are clinically significant determinants of systemic clearance.

**Conclusions—**Inhibition or induction of intestinal CYP3A4 can account for exposure changes of apixaban in all clinically significant drug-drug interactions, and lack of intestinal CYP3A4 inhibition can explain all studies with no exposure changes, regardless of the potential for these perpetrators to inhibit intestinal or systemic efflux transporters.

#### **Keywords**

apixaban; bioavailability; clearance; complex drug-drug interactions; mean absorption time

#### **INTRODUCTION**

Apixaban (Fig. 1) is an anticoagulant factor Xa inhibitor approved for a number of indications including stroke or blood clot prevention and treatment of deep vein thrombosis

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or pulmonary embolism [1]. Apixaban is primarily metabolized by cytochrome P450 (CYP) 3A4 (with minor contributions of other isoforms such as CYP 1A2, 2C8, 2C9, 2C19, and 2J2) [1]. The involvement of the intestinally-expressed efflux transporters P-glycoprotein (Pgp) and Breast Cancer Resistance Protein (BCRP) has also been suggested throughout the literature [2, 3], as well as in the apixaban Food and Drug Administration (FDA) label [1]. However, in vitro susceptibility to transporters does not always translate to clinically significant outcomes, and this is particularly true for high-solubility drugs that display high membrane permeability characteristics (i.e. Biopharmaceutics Drug Disposition Classification System (BDDCS) Class 1 drugs) [4] for which a significant degree of passive passage across biological membranes is achieved, potentially rendering any transporterassisted passage clinically insignificant. Thus, the purported clinically significant involvement of efflux transporters in the disposition of apixaban (BDDCS Class 1) is questionable. Understanding major contributors to drug disposition is critical in the clinical setting to allow for appropriate dosing and in particular, how to adjust dose based on disease state, due to pharmacogenomic variance, or in anticipation of a drug-drug interaction (DDI).

Clearance  $(CL)$  is a critical determinant of drug dosing regimens, as it is inversely related to drug exposure  $(AUC)$ ; area under the concentration-time curve) that ultimately is believed to drive the therapeutic efficacy and potential toxicity of a drug (Eq. 1)

$$
AUC = \frac{\text{F} \cdot \text{Dose}}{CL} \tag{1}
$$

where F denotes fractional bioavailability following an oral dose, and is assumed to be 1 for an intravenous (IV) dose. Characterization of the contributors to clearance pathways, i.e., metabolic enzymes and/or xenobiotic transporters, is crucial in anticipating potential changes in clearance due to DDIs or pharmacogenomic variance of metabolic enzymes or transporters. Our laboratory has thoroughly detailed and documented the expected changes in pharmacokinetic parameters for interactions involving purely metabolic enzymes [5, 6] versus xenobiotic transporters [7, 8]. Inhibition or induction of metabolic enzymes results in changes in CL and AUC that are directionally intuitive and translate to rational changes in mean residence time (*MRT*) and terminal half-life ( $t_{1/2, z}$ ), as volume of distribution ( $V_{\rm ss}$ ) remains unchanged for metabolic interactions [5, 6], as depicted in Eq. 2 [9]

$$
MRT = \frac{V_{ss}/F}{CL/F}
$$
 (2)

It is considered reasonable to predict strictly metabolic interactions based on in vitro studies [10] due to a strong understanding by the field of the metabolizing enzymes commonly implicated in drug metabolism, which is further bolstered by well-characterized clinical specificities of routinely used metabolic inhibitors and inducers [11].

The FDA has provided guidance on predicting clinically significant transporter interactions [10], however, such predictions are not as straightforward and are even more challenging when both enzymes and transporters are involved in drug disposition, i.e., in so-called "complex DDIs". We have recently thoroughly discussed how to appropriately predict

changes in exposure when transporters are involved using the Extended Clearance Model, which not only requires understanding of how transporter-mediated active influx and efflux intrinsic clearances will potentially change, but also requires estimation of passive diffusion and changes in metabolic and biliary elimination [12]. The methodologies employed to estimate each of these elimination processes are not trivial, and each requires a different set of experimental conditions. Further, the susceptibility of a drug to uptake or efflux transporters in vitro does not always translate to clinically significant in vivo involvement [4]. Additionally, validated clinical transporter probe substrates and inhibitors are lacking [11]; routinely-used inhibitors are often not specific and may have inhibitory potential towards both enzymes and transporters [13], and additional xenobiotic transporters are continuously emerging and suggested to be clinical relevant by the field [14–16]. Furthermore, clinically significant transporter interactions can affect  $V_{ss}$  for victim drugs [8] in addition to potential CL changes, resulting in counterintuitive changes in changes in MRT and  $t_{1/2,z}$  that are not necessarily opposite in magnitude of CL changes [7], further complicating pharmacokinetic predictions (Eq. 2). Thus, the challenge in predicting exposure changes for complex DDIs is beyond simply accurately estimating the contribution of metabolism versus transporters, is further complicated by the potential for enzymetransporter interplay, and is currently an area of significant efforts by the field [17, 18].

Oral dosing changes in  $F$  (due to altered absorption or first pass extraction) are often underemphasized as an important contributor in DDI-related exposure changes as compared to  $CL$  changes (Eq. 1). Discriminating changes in  $CL$  from changes in  $F$  has been believed not possible without also performing an IV DDI study to estimate changes in CL alone; however, most orally approved drugs have only been studied when orally administered. We have recently discussed that for low extraction ratio drugs, the minimal first pass elimination can indicate that changes in apparent clearance  $CL/F$ ) are primarily due to changes in  $CL$ alone [5]. Further, for purely metabolic interactions, knowledge that  $V_{ss}$  is unchanged can allow for estimation of F changes by examining the change in apparent volume of distribution ( $V_{ss}/F$ ), which can further be utilized to predict changes in CL alone [19]. For clinically significant intestinal transporter substrates, alteration of transporter activity or expression will result in significant changes in absorption rate and we maintain that such changes should always be used to implicate transporter involvement in vivo [20]. However, changes in absorption rate may not necessarily translate to changes in extent of absorption if there is still sufficient time for absorption to occur, an additional consideration that complicates pharmacokinetic predictions of intestinal transporter substrates.

Utilization of these guiding principles in analyzing clinical data of purported complex DDIs, such as examining changes in absorption rate or  $V_{ss}$ , can allow validation of the clinical significance of transporter involvement based on *in vitro* predictions. We have recently introduced these concepts [19, 20] in evaluating the apixaban-rifampin interaction [29] Here, we critically evaluate all published apixaban clinical DDI studies using the guiding principles mentioned above to investigate the purported clinical significance of P-gp and BCRP in apixaban disposition.

#### **MATERIALS AND METHODS**

To determine if intestinal transporter involvement is clinically significant in oral DDIs, changes in mean absorption time (*MAT*) or time to maximum concentration ( $t_{max}$ ) can be compared between the interaction versus control phase of clinical DDI studies [20]. For clinically significant intestinal transporter DDIs, inhibition would result in decreased MAT and  $t_{max}$ , and induction would result in increases in these values. Values of  $t_{max}$  are routinely reported, however, MAT values are less frequently reported and therefore were estimated by digitizing published pharmacokinetic concentration-time profiles using WebPlotDigitizer Version 4.2 (San Francisco, CA) and fitting resulting data to a 2-compartmental model with first-order absorption from the gut using WinNonlin Professional Edition Version 2.1 (Pharsight, Mountain View, CA) to estimate absorption rate  $(k_a; MAT = 1 / k_a)$ , as we have previously described [21]. If pharmacokinetic curves were not published, MAT was calculated using published  $t_{max}$  and  $t_{1/2,z}$  values using the single-dose relationship between the three parameters, as we recently described in detail [20]. It should be noted that  $t_{max}$ values are observed values and these values depend heavily on the sampling scheme employed by the clinical investigators. However, any such errors have much less impact on drugs with large  $t_{max}$  values such as apixaban (3–4 h) [1]. Recent simulations illustrating the impact of 15 min errors in MAT (which could occur due to minimal absorption phase sampling) for both a rapidly absorbed drug ( $MAT = 0.5$  h;  $t_{max} = 1.33$  h) and a less-rapidly absorbed drug ( $MAT = 2$  h;  $t_{max} = 3.2$  h) highlight that such errors have markedly less impact on drugs with larger  $t_{max}$  values [20].

Changes in *AUC*, CL/F,  $V_{ss}/F$ , MRT,  $t_{1/2,z}$  are reported as ratios of interaction to control, where ratios of AUC were dose-normalized. Percent AUC extrapolation is also examined as a potential indication of the accuracy of any parameters derived from  $AUC$ , with the understanding that high percent extrapolations are only indicative of inaccuracies if terminal half-life is not adequately captured. MRT was calculated using Eq. 3:

$$
MRT = \frac{AUMC}{AUC} - MAT \tag{3}
$$

where AUMC is area under the moment curve, and both AUC and AUMC are extrapolated to infinity since all clinical investigations were conducted for a single-dose of apixaban.  $V_{\rm sg}$ F is calculated using Eq. 2. Published clinical values are utilized in calculation of ratios in priority, with digitization utilized only to supplement any unreported parameters-ofinterest.

Ratios of change in  $MAT$  or  $t_{max}$  that indicated greater than 30% change (i.e. ratios outside of the range of 0.77 and 1.30) were considered to be potential evidence of a clinically significant intestinal transporter interaction. If MAT does not significantly change, it can be inferred that either xenobiotic transporters expressed in the intestine are not clinically significant determinants of apixaban disposition or that intestinal transporters are not inhibited or induced in that particular DDI [20].

A comprehensive literature search identified clinical apixaban DDI studies with the perpetrators atenolol [22], cyclosporine [23], diltiazem [24], enoxaparin [25], famotidine

[26], ketoconazole [24, 27], naproxen [28], rifampin [29], and tacrolimus [23]. In addition, a study with activated charcoal [30] and two studies investigating the influence of pharmacogenomic variance with respect to CYP3A5, P-gp and/or BCRP [31, 32] were identified and critically discussed to compliment the analysis of clinical DDI studies.

Inhibitory or induction-related specificities of each perpetrator were documented to assess potential alteration of CYP3A, P-gp and/or BCRP activity or expression based on a recent compilation of clinically recommended index inhibitors of drug metabolizing enzymes and drug transporters [11]. In addition, the inhibitory potential of perpetrator drug in the intestine and systemic circulation was investigated by considering the maximum perpetrator concentration in the gut  $[I_{gul}]$  or systemic circulation  $(C_{max})$  with respect to its half maximal inhibitory concentration ( $IC_{50}$ ) for CYP3A4, P-gp and BCRP. Values of [ $I_{gul}$ ] are estimated by considering perpetrator dose divided by the volume of water with which the perpetrator drug was dosed (and if unreported a standard value of 250 mL was utilized in calculations). Reported values of perpetrator  $C_{max}$  were utilized; however if unreported, these values were referenced from the literature for a similar perpetrator dosing scheme. Fraction unbound in plasma  $(f_{u,plasma})$  values were also tabulated to further contextualize systemic inhibitory potential based on unbound concentrations and were cited from reference [33] unless otherwise noted. Based on the FDA DDI Guidance, values of  $[I_{gul}] / IC_{50} > 10$  indicate a potentially significant intestinal interaction, and values of  $C_{max} > 0.1$  indicate a potentially significant systemic interaction [10].

The rifampin-apixaban DDI study was conducted following both oral and IV administration [29], therefore the recently published clearance versus bioavailability differentiation methodology for metabolic DDIs [19] was utilized to predict changes in CL versus F. This analysis from our previous publications [19, 20] is included for reference. Predicted changes in pharmacokinetic parameters were compared to actual changes based on IV dosing, and provided further insight into the hypothesis that the reported in vitro susceptibility to efflux transporters by apixaban may be clinically insignificant. In addition, predictions of changes in CL versus F were performed for all clinically significant DDIs to characterize the contribution of changes in F versus CL, and the major site of interaction (intestine versus liver), for each interaction.

#### **RESULTS**

Implicating intestinal transporter involvement in apixaban disposition proceeded via examination of changes in apixaban absorption rate in clinical DDIs, based on our recently published methodology to identify clinically significant intestinal transporter interactions [20]. Table I details the inhibitory specificities of the nine perpetrators investigated against CYP3A4, P-gp and BCRP, and summarizes the expected intestinal or systemic inhibitory outcomes based on calculations of  $[I_{gul}]$  or  $C_{max}$  divided by  $IC_{50}$ . Clinically significant alterations in intestinal efflux capacity (based on values of  $[I_{gul}]/IC_{50} > 10$ ) were expected for cyclosporine, diltiazem, ketoconazole, rifampin, and tacrolimus, and not expected or unknown for atenolol, enoxaparin, famotidine, and naproxen. Clinically significant inhibition of systemic efflux transporters based on values of  $C_{max}/IC_{50} > 0.1$  were expected for cyclosporine and diltiazem, however, consideration of unbound plasma systemic

concentrations ( $C_{max,u}$ ) of these inhibitors does not support systemic inhibitory potential, as unbound perpetrator concentrations are not sufficiently high. Based on multiple dosing of rifampin, clinically significant induction in both intestinal and systemic P-gp is expected.

Clinically insignificant DDI changes in pharmacokinetic parameters are presented in Table II (atenolol, cyclosporine, enoxaparin, famotidine, tacrolimus). Clinically significant DDIs are listed in Table III (diltiazem, ketoconazole, naproxen, rifampin). No changes in MAT values were observed for 10 of the 11 interactions studied, with ratios of interaction to control ranging from 0.92–1.12, indicating that intestinal transporters are not clinically significant in these DDIs with a number of potent inhibitors (and one inducer) of P-gp and/or BCRP. A modest prolongation of  $MAT$  and  $t_{max}$  was observed only for the diltiazem-apixaban interaction [24], with an *MAT* ratio of 1.38 and a  $t_{max}$  ratio of 1.33.

Table IV displays the ratios of change in IV and oral apixaban pharmacokinetics following multiple dosing of rifampin [29] that we previously reported [19, 20]. By assuming that this interaction is purely metabolic, and based on the recently published clearance versus bioavailability differentiation methodology [19], the observed 52% reduction in oral apixaban exposure following multiple dosing of rifampin was estimated to be a result of a 1.5-fold increase in CL and a 30% reduction in F. These estimates were compared to actual changes in CL and F based on the IV interaction data, indicating that the observed change in  $CL$  was 1.64-fold yielding a 24% reduction in F, supporting the accuracy of our method for predicting the differentiation of changes in clearance from changes in bioavailability for oral metabolic DDIs.

Although confirming IV data were not available for the remaining four clinically significant DDIs, Table V displays the predicted changes in CL versus F for these interactions with the assumption that all interactions are purely metabolic, based on the recently described CL versus F discrimination methodology [19]. Predicted changes in systemic CL were minimal, ranging from 0.77–1.04, while predicted changes in Franged from 1.43–1.79. Additionally, estimates of  $[I_{gut}]/IC_{50}$ ,  $C_{max}/IC_{50}$  and  $C_{max,u}/IC_{50}$  were calculated, suggesting that all four interactions are predicted to be primarily intestinal, rather than systemic.

In addition, a clinical study with activated charcoal dosed both 2 h and 6 h post apixaban oral dosing was identified [30], where no change in  $C_{max}$  or  $t_{max}$  was observed, however AUC and  $t_{1/2,z}$  decreased respectively to ratios of 0.49 and 0.40 (2 h dose) and to 0.71 and 0.37 (6 h dose).

Two pharmacogenomic studies were identified in which differences in apixaban disposition were investigated with respect to CYP3A5, P-gp and/or BCRP [31, 32]. The first study investigated apixaban disposition in patients with atrial fibrillation and acute stroke with respect to gene polymorphisms in CYP3A5 and ABCB1 (P-gp), concluding that these polymorphisms do not affect the pharmacokinetics of apixaban [31]. The second study investigated dose-normalized apixaban plasma trough concentrations in 70 measurements from 44 patients with atrial fibrillation [32]. The investigators concluded that P-gp pharmacogenomics did not impact plasma trough concentrations, however, patients with

either ABCG2 (BCRP) or CYP3A5 gene polymorphisms had higher plasma trough concentrations.

#### **DISCUSSION**

Discerning involvement of transporters versus metabolic enzymes is challenging, particularly because the susceptibility of drug to efflux or uptake transporters in vitro does not always translate to clinically significant in vivo involvement [4]. Further, following oral dosing DDIs, separating changes in CL or  $V_{ss}$  from F, as well as consideration of the impact of both  $CL$  and  $V_{ss}$  on MRT and half-life, makes discerning clinically significant transporter involvement a difficult task. Based on the recognition that significant intestinal transporter interactions will result in discernable changes in  $MAT$  (and therefore  $t_{max}$ ) [20], it is possible to implicate intestinal transporters in oral DDI studies, with no change indicating that intestinal transporters are not relevant. Apixaban  $t_{max}$  occurs approximately 3–4 h after oral dosing [1, 63], a value large enough to sensitively detect changes in absorption rate under standard pharmacokinetic sampling schemes [20].

No change in apixaban absorption rate was observed in 10 of 11 oral DDI studies with MAT ratios ranging from 0.92–1.12 (Tables II and III), which included perpetrator drugs with significant potential to inhibit P-gp and BCRP based on *in vitro* data (Table I). These results are consistent with the BDDCS class 1 designation of apixaban (high permeability, high solubility), which proposes that such drugs' high solubility characteristics allows very high concentrations of drug to passively diffuse, greatly overwhelming any transporter-mediated effects at clinically relevant concentrations [4]. It is noteworthy that the ketoconazoleapixaban interaction was conducted at both a clinically relevant dose (10 mg) and a microdose (25 μg), and thus it may be expected that for the lower dose, transporter effects can no longer be overwhelmed due to lower overall concentrations. However, in both studies no changes in  $MAT$  or  $t_{max}$  were observed, and the degree of changes in exposure and clearance were almost identical between both studies, indicating at both apixaban concentrations the interaction was primarily due to a process for which soluble concentrations are irrelevant; i.e., CYP3A4 inhibition. Although these results are striking, conclusions would be further strengthened if it were possible to examine patient data in order to calculate changes in  $MAT$  and  $t_{max}$  for each individual.

The diltiazem-apixaban DDI resulted in a 1.38-fold change in MAT and a 1.33-fold change in  $t_{max}$ , both values that are very close to our cutoff of 1.30 but suggesting a potentially significant intestinal transporter interaction. If this result was truly reflective of inhibition of P-gp, then it would be expected that other P-gp inhibitors, in particular more potent inhibitors, should also show similar changes in absorption rate. The diltiazem estimate of  $[I_{gut}]/IC_{50}$  for P-gp ranges from 19.6 to 694 and is not markedly different from estimates for cyclosporine (53.9–450), ketoconazole (298–4630 and 746–11,600), and tacrolimus (29.6– 37.7). Ketoconazole also significantly inhibits intestinal BCRP, with  $[I_{gul}] / IC_{50}$  estimates of 251 and 628 for both studies. It is possible that non-transporter mediated changes in absorption rate may be responsible for these results, such as changes in pH or gastric emptying by the perpetrator drug diltiazem. However, apixaban does not contain ionizable groups, and thus potential changes in gastric pH by diltiazem should not alter apixaban

solubility or absorption, and this hypothesis was nicely confirmed in the famotidine study, where changes in gastric pH had no effect on apixaban pharmacokinetics [26]. Further, changes in gastric emptying by diltiazem are not expected [64], therefore perhaps this outcome is related to limitations associated with utilizing published average pharmacokinetic profiles, as such graphical representations do not necessarily represent any single subject within the study. The study authors indicate diltiazem had no effect on  $t_{max}$ [24], however since we only had access to published median  $t_{max}$  values our calculated  $t_{max}$ ratio was 1.33. Thus, we again highlight that conclusions from utilization of our methodology [20] will be strengthened if absorption rate is calculated for each individual in the study. It should also be recognized that  $t_{max}$  is influenced by both absorption rate and elimination rate parameters, and we have recently published the single dose and steady-state mathematical relationships for reference [20]. Therefore, implicating intestinal transporter involvement based on  $t_{max}$  ratios alone may mislead an investigator, such as in the atenolol or famotidine results where  $t_{max}$  ratios are 1.33 and 0.67, respectively, while the respective MAT ratios of 1.07 and 1.03 show no change in absorption rate.

As intestinal efflux transporter involvement is unlikely to contribute to apixaban bioavailability, we further investigate the potential involvement of systemic P-gp/BCRP inhibition to affect apixaban disposition. Examination of the inhibitory potential of perpetrators associated with clinically insignificant DDIs (Table II) reveals that only cyclosporine had the potential to inhibit systemic P-gp with a calculated  $C_{\text{max}}/IC_{50}$  value of >0.39 and a  $C_{\text{max},\text{u}}/IC_{50}$  value of >0.027 (based on values presented in Table I), yet no change in apixaban exposure was observed. Of the clinically significant inhibitory DDIs, only diltiazem was expected to achieve systemic concentrations capable of inhibiting P-gp, with similar  $C_{\text{max}}/IC_{50}$  values of >0.17 and  $C_{\text{max},u}/IC_{50}$  of >0.023, highlighting when compared to cyclosporine that the observed diltiazem AUC ratio of 1.4 is likely not due to inhibition of P-gp. Further, significant transporter interactions are expected to result in marked changes in  $V_{ss}$  of victim drug [7, 8], however changes in  $V_{ss}$  in the IV rifampinapixaban DDI were minimal (ratio 0.87) (Table IV). Purely metabolic DDIs do not affect the  $V_{ss}$  of victim drug [5, 6], thus following oral dosing it is possible to estimate the relative change in CL versus F by attributing the observed change in  $V_{\text{ss}}/F$  to F alone [19]. Table IV demonstrates that utilization of this methodology for the oral interaction data results in remarkably accurate predictions of CL versus F change, further supporting that for an interaction with a potent inducer of CYP3A4 and P-gp, apixaban is primarily susceptible to alterations in metabolic enzymes rather than transporters.

Examination of the clinically significant DDIs listed in Table III show that in general, changes in CL/F were similar in magnitude to  $V_{ss}/F$ , resulting in unchanged MRT and  $t_{1/2,z}$ , suggesting that these significant DDIs are primarily due to changes in  $F$ . Table V utilizes the  $CL$  versus F differentiation methodology [19] to predict the extent of change in  $CL$  and F to understand if the observed exposure changes are primarily due to an intestinal or systemic effect. Based on this analysis, predicted changes in systemic  $CL$  were minimal  $(0.77-1.04)$ whereas predicted changes in  $F$  ranged from 1.43–1.79. These results suggest that these significant exposure changes are primarily driven by intestinal interactions, and taken together with the unchanged absorption rates associated with these interactions, we conclude intestinal CYP3A4 is responsible for all significant apixaban DDIs. This conclusion is

further rationalized by examining the intestinal versus systemic CYP3A4 inhibitory potential listed in Table V, as all four perpetrators have  $[I_{gul}]/IC_{50}$  values greater than 10, however,  $C_{\text{max,u}}/IC_{50}$  is only greater than 0.1 for diltiazem.

It is noteworthy that the cyclosporine and tacrolimus DDI studies did not result in clinically significant changes in exposure [23], given their potential to inhibit intestinal CYP3A4. It is possible that since the aim of this DDI study was to examine the impact of clinically relevant systemic cyclosporine and tacrolimus concentrations achieved in transplant patients on apixaban disposition, the oral dosing of these perpetrators was not necessarily at the same time as apixaban dosing. This aspect was not clearly described within the methods, however the study design scheme published within that article [23] does indicate there was some amount of time between dosing of perpetrator and apixaban. Thus, we hypothesize the true intestinal perpetrator concentrations may be much lower than we report in Table I.

The impact of activated charcoal was also investigated, where activated charcoal was dosed during the absorption phase of apixaban (2 h after dosing) and after apixaban absorption was complete (6 h after dosing) [30]. Activated charcoal is often used in situations of drug overdose, as drug is adsorbed on to activated charcoal in the intestine thus reducing extent of absorption. Activated charcoal studies can also be utilized to investigate the potential of a drug to undergo enterohepatic recycling, as reabsorption of drug is prevented after biliary excretion into the intestine. Between the 2 h and 6 h doses of activated charcoal, AUC decreased with ratios of 0.49 and 0.71, respectively, while  $t_{I/2, z}$  decreased similarly with ratios of 0.40 and 0.37, respectively. The differential changes in  $AUC$  with respect to dosing time support the expected outcome that a larger decrease in F would be observed when activated charcoal was dosed during the apixaban absorption phase. The modest reduction in exposure associated with the 6 h dose of activated charcoal  $(AUC$  ratio of 0.71) is not likely due to prevention of enterohepatic recirculation by activated charcoal, as biliary excretion is a minor elimination pathway [65] and none of the pharmacokinetic profiles in any investigated study displayed the characteristic secondary peaks commonly associated with enterohepatic recirculation. Thus, the study authors hypothesize that apixaban undergoes enteroenteric recycling (recycling between systemic circulation and intestinal lumen via passive diffusion) that is prevented when apixaban is adsorbed on to activated charcoal. This may explain the observed similar reduction in  $t_{1/2,z}$  for both the 2 h and 6 h doses, as there may be an increase in extent of direct apixaban elimination into the feces via the intestine when activated charcoal is present. We agree that further mechanistic studies are warranted, however, these results underscore the potential bidirectional ability of apixaban to cross intestinal membranes between gut lumen and systemic circulation via passive diffusion, further countering the hypothesis that apixaban is susceptible to the action of transporters.

We identified two pharmacogenomic studies in which CYP3A5, P-gp and/or BCRP pharmacogenomics were investigated. The first study concluded that differences in CYP3A5 and P-gp pharmacogenomics do not affect the pharmacokinetics of apixaban [31]. The second study investigated BCRP pharmacogenomics in addition to CYP3A5 and P-gp. Pharmacokinetic parameters were not assessed, however, investigators associated pharmacogenomics with dose-normalized trough concentration measurements taken 10–14 h post apixaban dosing, for 70 measurements from 40 patients. The investigators concluded

that BCRP and CYP3A5 pharmacogenomics, but not P-gp pharmacogenomics, impacted dose-normalized trough concentrations. However, it is unclear if these results accounted for the differences in sampling time between individuals in each group, or even with respect to multiple samples from the same individual. Thus, we reserve any conclusions related to apixaban pharmacogenomics and suggest further research is warranted.

#### **CONCLUSIONS**

Throughout the literature [66–69], and even in the apixaban FDA label [1], authors routinely cite the clinically significant DDI studies listed in Table III as evidence that P-gp and/or BCRP is a clinically significant determinant of apixaban disposition, confirming results of in vitro transporter studies [2, 3]. However, rational examination of these clinical studies using basic pharmacokinetic theory simply does not support the clinical significance of efflux transporters in apixaban disposition. These conclusions are not limited to the involvement of intestinal efflux transporters (based on changes in absorption time) for P-gp and BCRP, there is also little evidence that these transporters are clinically significant determinants of systemic clearance. Inhibition or induction of intestinal CYP3A4 can account for exposure changes of apixaban in all clinically significant DDIs, and lack of intestinal CYP3A4 inhibition can explain all studies with no exposure changes, regardless of the potential for these perpetrators to inhibit intestinal or systemic efflux transporters.

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#### **ABBREVIATIONS**





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**Fig. 1.**  Chemical structure of apixaban.

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### **Table I**

Inhibitory Potential of Perpetrator Drugs from Apixaban Drug-Drug Interaction Studies for Metabolic Enzymes (CYP3A4) and Xenobiotic Transporters Inhibitory Potential of Perpetrator Drugs from Apixaban Drug-Drug Interaction Studies for Metabolic Enzymes (CYP3A4) and Xenobiotic Transporters (P-gp and BCRP) Reported to be Clinical Determinants of Apixaban Disposition (P-gp and BCRP) Reported to be Clinical Determinants of Apixaban Disposition



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Systemic

a

 $I$ gud values are calculated by perpetrator dose divided by volume of water utilized in each clinical study. If unreported, the standard volume of 250 mL was assumed

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 $b_{\mu,plasma}$  values are referenced from Lombardo et al. [33] unless otherwise noted  $f_{U,p}$ lasma values are referenced from Lombardo et al. [33] unless otherwise noted

 $C_{\text{max}}$  values are associated with maximum concentration of perpetrator drug reported in original clinical study, however, if unreported the value was referenced from a comparable study with a similar dosing scheme dosing scheme  $\ddot{\phantom{0}}$ 

 $d$  pixaban-relevant intestinal (I) and/or systemic (S) inhibitory potential is indicated; [ $I$ gud]/C50>10 indicates intestinal inhibitory potential and  $C_{\text{max}}$ /C500-0.1 indicates systemic inhibitory potential,  $C_{\text{max}}/IC_50$  1 indicates systemic inhibitory potential, Apixaban-relevant intestinal (I) and/or systemic (S) inhibitory potential is indicated;  $|I_{g\bar{u}}d/ICS0>10$  indicates intestinal inhibitory potential and with recognition that unbound plasma concentrations may further diminish systemic inhibitory potential with recognition that unbound plasma concentrations may further diminish systemic inhibitory potential

Referenced  $C_{\text{max}}$  is associated with a single dose of 100 mg cyclosporine, and likely underpredicts the true  $C_{\text{max}}$  within this study Referenced  $C_{max}$  is associated with a single dose of 100 mg cyclosporine, and likely underpredicts the true  $C_{\text{max}}$  within this study

Referenced  $C_{\text{max}}$  is also associated with a steady-state 360 mg PO dose, however, this study utilized an extended release formulation of dilitazem and thus may underpredict the true  $C_{\text{max}}$  within this Referenced  $C_{max}$  is also associated with a steady-state 360 mg PO dose, however, this study utilized an extended release formulation of diltiazem and thus may underpredict the true  $C_{\text{max}}$  within this study

 ${}^g$ Utilized average molecular weight of 4500 g/mol to calculate [Igurd and Cmax; Cmax is associated with a pharmacodynamic measurement from a 40 mg subcutaneous dose  $C_{\text{max}}$ ;  $C_{\text{max}}$  is associated with a pharmacodynamic measurement from a 40 mg subcutaneous dose  ${}^E$ Utilized average molecular weight of 4500 g/mol to calculate [ $I$ gut] and

 $h$  iffering  $U_g$ ud values between studies for the same ketoconazole dose are due to the latter study using only 100 mL to dose PO ketoconazole versus the standard value of 250 mL Differing  $|I_{gul}$  values between studies for the same ketoconazole dose are due to the latter study using only 100 mL to dose PO ketoconazole versus the standard value of 250 mL

Referenced  $C_{\text{max}}$  is associated with a single dose of 5 mg tacrolimus, and likely underpredicts the true  $C_{\text{max}}$  within this study Referenced  $C_{\text{max}}$  is associated with a single dose of 5 mg tacrolimus, and likely underpredicts the true  $C_{\text{max}}$  within this study



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Clinically Insignificant Changes in Pharmacokinetic Parameters (Expressed as Ratios of Interaction / Control) in Drug-Drug Interaction (DDI) Studies Clinically Insignificant Changes in Pharmacokinetic Parameters (Expressed as Ratios of Interaction / Control) in Drug-Drug Interaction (DDI) Studies È the Victim  $\ddot{\phantom{0}}$  $\therefore$ 



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Pharmacokinetic values reported in the table are based on published average values, unless otherwise noted Pharmacokinetic values reported in the table are based on published average values, unless otherwise noted

MRT, mean residence time; P-gpy Opprotein; PO, oral administration; S, Systemic; Imax time to maximal concentration; 11/2,z, terminal half-life; V<sub>SS</sub>/F, apparent volume of distribution at steady state AUC, area under the curve; BCRP, Breast Cancer Resistance Protein; Con, control; CL/F, apparent clearance; CYP, cytochrome P450; DDI, drug-drug interaction; I, Intestine; MAI, mean absorption time; AUC, area under the curve; BCRP, Breast Cancer Resistance Protein; Con, control; CL/F, apparent clearance; CYP, cytochrome P450; DDI, drug-drug interaction; I, Intestine; MAT, mean absorption time;  $V_{SS}/F$ , apparent volume of distribution at steady state S, Systemic;  $t_{\text{max}}$  time to maximal concentration;  $t_{1/2,z}$ , terminal half-life; MRT, mean residence time; P-gp, P-glycoprotein; PO, oral administration;

a Interaction phase was  $n = 14$  Patios are calculated by digitization of published average plasma concentration-time profiles and performing non-compartmental and/or compartmental analysis Ratios are calculated by digitization of published average plasma concentration-time profiles and performing non-compartmental and/or compartmental analysis

 $^{\prime}CL/F$  was calculated using known dose, reported  $AUC$  and Eq. 1  $\mathcal{C} L$ /F was calculated using known dose, reported  $AUC$  and Eq. 1  $d_{\rm{slubjects}}$  were the same for the cyclosporine and tacrolimus DDI studies Subjects were the same for the cyclosporine and tacrolimus DDI studies

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Pharmacokinetic curves were not published, thus neither V<sub>SS</sub> nor MRT could be calculated. However, MAT was calculated by utilization of the single dose relationship between reported Imax and 11/2,2 V<sub>SS</sub> nor MRT could be calculated. However, MAT was calculated by utilization of the single dose relationship between reported  $t_{\text{max}}$  and  $t_{1/2,z}$  Pharmacokinetic curves were not published, thus neither as previously described [20] as previously described [20]

fInteraction phase was  $n = 19$ 



**Table III**

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*MRT*, mean residence time; *P-gp*, P-glycoprotein; *PO*, oral administration; *S*, Systemic; *t<sub>max</sub>* time to maximal concentration;  $t/2z$ , terminal half-life; *V<sub>SS</sub>F*, apparent volume of distribution at steady state  $\ddot{\cdot}$ AUC, area under the curve; BCRP, Breast Cancer Resistance Protein; Con, control; CL/F, apparent clearance; CYP, cytochrome P450; DDI, drug-drug interaction; I, Intestine; MAT, mean absorption time;  $V_{SS}$ F, apparent volume of distribution at steady state S, Systemic;  $t_{\text{max}}$ , time to maximal concentration;  $t_{1/2,z}$  terminal half-life; MRT, mean residence time; P-gp, P-glycoprotein; PO, oral administration;

Aatios are calculated by digitization of published average plasma concentration-time profiles and performing non-compartmental and/or compartmental analysis Ratios are calculated by digitization of published average plasma concentration-time profiles and performing non-compartmental and/or compartmental analysis

b Control phase was  $n = 17$   $^{\prime}CL$  /F was calculated using known dose, reported  $AUC$  and Eq. 1  $\mathcal{C}L$  F was calculated using known dose, reported  $AUC$  and Eq. 1

 $d_{MAT\text{ was calculated by utilization of the single dose relationship between reported  $t_{HJZX}$  and  $t_{1/2,7/2,8}$  as previously described [20]$ MAT was calculated by utilization of the single dose relationship between reported  $t_{max}$  and  $t_1/2$ , z as previously described [20]

 $e$  <br> Interaction phase was  $\rm n=18$ Interaction phase was n = 18



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Utilization of the Sodhi and Benet [19] Methodology to Discriminate Clearance from Bioavailability Changes for Orally Dosed Apixaban (Victim) and Utilization of the Sodhi and Benet [19] Methodology to Discriminate Clearance from Bioavailability Changes for Orally Dosed Apixaban (Victim) and Rifampin (Perpetrator) from the Study of Vakkalagadda et al. [29] Rifampin (Perpetrator) from the Study of Vakkalagadda et al. [29]



AUC, area under the curve; CL, clearance; CL/F, apparent clearance; DDI, drug-drug interaction; F, bioavailability; V<sub>SS</sub>, volume of distribution at steady state; V<sub>SS</sub>F, apparent volume of distribution at  $V_{SS}/F$ , apparent volume of distribution at  $V_{SS}$ , volume of distribution at steady state; F, bioavailability;  $AUC$ , area under the curve;  $CL$ , clearance;  $CLF$ , apparent clearance; DDI, drug-drug interaction; steady state

a Ratios are calculated by digitization of published average plasma concentration-time profiles and performing non-compartmental and/or compartmental analysis Ratios are calculated by digitization of published average plasma concentration-time profiles and performing non-compartmental and/or compartmental analysis



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## **Table V**

F (Expressed as Ratios of Interaction / Control) in Clinically Significant Drug-Drug Interactions (DDIs) with Apixaban Estimated Changes in CL versus F (Expressed as Ratios of Interaction / Control) in Clinically Significant Drug-Drug Interactions (DDIs) with Apixaban as the Victim Drug Hillizing the Methodology of Sodhi and Benet [19] as the Victim Drug, Utilizing the Methodology of Sodhi and Benet [19] Estimated Changes in CL versus



AUC, area under the curve; BCRP, Breast Cancer Resistance Protein; Con, control; CL, clearance; CLF; apparent clearance; CYP, cytochrome P450; DDI, drug-drug interaction; F, bioavailability; I, Intestine; P-gp, P-glycopro F, bioavailability; I, AUC, area under the curve; BCRP, Breast Cancer Resistance Protein; Con, control; CL, clearance; CL/F, apparent clearance; CYP, cytochrome P450; DDI, drug-drug interaction;  $V_{SS}/F$ , apparent volume of distribution at steady state  $V_{SS}$ , volume of distribution at steady state; S, Systemic; Intestine; P-gp, P-glycoprotein; PO, oral administration;

Aatios are calculated by digitization of published average plasma concentration-time profiles and performing non-compartmental and/or compartmental analysis Ratios are calculated by digitization of published average plasma concentration-time profiles and performing non-compartmental and/or compartmental analysis

 $^bCLF$  was calculated using known dose, reported  $AUC$  and Eq. 1  $\overline{CL/F}$  was calculated using known dose, reported  $AUC$  and Eq. 1

 $c_{\mbox{Control phase was}\;n=17}$ Control phase was n = 17