Data-Based Mathematical Modeling of Vectorial Transport across Double-Transfected Polarized Cells

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ABSTRACT:
Vectorial transport of endogenous small molecules, toxins, and drugs across polarized epithelial cells contributes to their half-life in the organism and to detoxification. To study vectorial transport in a quantitative manner, an in vitro model was used that includes polarized MDCKII cells stably expressing the recombinant human uptake transporter OATP1B3 in their basolateral membrane and the recombinant ATP-driven efflux pump ABCC2 in their apical membrane. These double-transfected cells enabled mathematical modeling of the vectorial transport of the anionic prototype substrate bromosulfophthalein (BSP) that has frequently been used to examine hepatobiliary transport. Time-dependent analyses of \(^{3}H\)-labeled BSP in the basolateral, intracellular, and apical compartments of cells cultured on filter membranes and efflux experiments in cells preloaded with BSP were performed. A mathematical model was fitted to the experimental data. Data-based modeling was optimized by including endogenous transport processes in addition to the recombinant transport proteins. The predominant contributions to the overall vectorial transport of BSP were mediated by OATP1B3 (44%) and ABCC2 (28%). Model comparison predicted a previously unrecognized endogenous basolateral efflux process as a negative contribution to total vectorial transport, amounting to 19%, which is in line with the detection of the basolateral efflux pump Abcc4 in MDCKII cells. Rate-determining steps in the vectorial transport were identified by calculating control coefficients. Data-based mathematical modeling of vectorial transport of BSP as a model substance resulted in a quantitative description of this process and its components. The same systems biology approach may be applied to other cellular systems and to different substances.

Vectorial transport of small molecules is an important process in polarized cells. Uptake across the basolateral membrane and efflux across the apical membrane domain of polarized cells contribute to the elimination and often detoxification of substances. In mammals, endogenous compounds and drugs are taken up from the blood into hepatocytes and subsequently effluxed mainly into bile. Several factors affect vectorial transport of small molecules. First, unidirectional transport does not occur at a sufficient rate in the absence of the respective transport proteins in the basolateral and apical membranes, as evidenced by studies in hereditary mutants lacking certain transport proteins (Jansen et al., 2001; Keppler et al., 2001; Schinkel and Jonker, 2003) or in cell lines stably transfected with cDNAs encoding transport proteins (Cui et al., 2001; Sasaki et al., 2002; Hagenbuch and Meier, 2004). Second, it is affected in the intact organism by blood flow, intravascular binding to proteins, and intracellular metabolism. To build a mathematical model of vectorial transport, we used a well defined cellular system developed previously (Cui et al., 2001). Polarized cells grown on filter membrane supports were stably transfected with cDNAs encoding the human uptake transporter for organic anions, OATP1B3 (König et al., 2000), and the human apical conjugate export pump ABCC2, also known as multidrug resistance protein 2 (MRP2) (Büchler et al., 1996). Such double-transfected cells exhibit transporter-mediated substrate flux from the basolateral to the apical compartment and, for most compounds, very little intracellular metabolism (Cui et al., 2001; Keppler, 2005; Letschert et al., 2005). Bromosulfophthalein (BSP) is a substrate for both transport proteins, OATP1B3 (König et al., 2000) and ABCC2 (Cui et al., 2001). Moreover, BSP is an established test compound for studies of hepatobiliary elimination in humans and animals (Wolkoff, 1994). Math-

ABBREVIATIONS: OATP1B3, human organic anion-transporting polypeptide, member 1B3; ABCC2, human ATP-binding cassette transporter, subfamily C, member 2; MRP2, multidrug resistance protein 2; BSP, bromosulfophthalein; MDCKII, Madin-Darby canine kidney cells strain II; Abcc4, canine ATP-binding cassette transporter, subfamily C, member 4; ABCC3, human ATP-binding cassette transporter, subfamily C, member 3; Endo\(_{\text{apical}}\), apical endogenous efflux transporter; Endo\(_{\text{bl}}\), basolateral endogenous efflux transporter; Endo\(_{\text{bl}}\)
Mathematical modeling was performed in this focused cellular system to mediate the vectorial transport of BSP. The same modeling approach can be applied to other polarized cellular systems and to a variety of different substances, thus opening the perspective of quantitative and predictive modeling and the understanding of vectorial transport systems.

Materials and Methods

Cell Culture and Cell Lines. MDCKII cells permanently expressing high levels of recombinant human OATP1B3 or OATP1B3 together with ABCC2 were cultured as described previously (Cui et al., 2001; Fig. 1).

Immunofluorescence Microscopy. MDCKII cells were grown on ThinCert membrane inserts (diameter, 6 mm; pore size, 0.4 µm; pore density, 1 × 10^6/cm^2; Greiner Bio-One, Frickenhausen, Germany; Letschert et al., 2005) for 3 days at confluence and induced with 10 mM sodium butyrate for 24 h to enhance the expression of recombinant proteins (Cui et al., 1999). Fixation and permeabilization were performed as described previously (Cui et al., 2001). OATP1B3 was detected by the antiserum SKT (König et al., 2000), and ABCC2 was detected by the antiseraum EAG (Cui et al., 1999), and canine Abcc4 was detected by the purified antiseraum SNG (Rius et al., 2003). Nuclei were stained with propidium iodide. Confocal laser scanning microscopy was performed with an LSM 510 META apparatus (Carl Zeiss, Jena, Germany).

Transport Studies. [3H]BSP (0.5 TBq/nmol) was obtained from Hartmann Analytic (Braunschweig, Germany) (Cui et al., 2001). MDCKII cells were grown on ThinCert membrane inserts (diameter, 24 mm; pore size, 0.4 µm; pore density, 1 × 10^6/cm^2; Greiner Bio-One) for 3 days at confluence and induced with 10 mM sodium butyrate for 24 h (Cui et al., 1999). The cells were washed in prewarmed (37°C) transport buffer (142 mM NaCl, 5 mM KCl, 1 mM KH_2PO_4, 1.2 mM MgSO_4, 1.5 mM CaCl_2, 5 mM glucose, and 12.5 mM HEPES, pH 7.3). The [3H]labeled substrate was dissolved in transport buffer and added to the basolateral compartment (1.5 ml) at the concentration indicated. After incubation at 37°C, radioactivity in the apical compartment (1.0 ml) was measured by sampling of aliquots from the apical compartment. Cells were washed twice with ice-cold transport buffer containing 0.5% bovine serum albumin and three times with ice-cold transport buffer. Intracellular radioactivity was determined after lysing the cells with 0.2% sodium dodecyl sulfate.

For preloading studies, cells were washed after incubation at 37°C with the labeled substrate as described above. Subsequently, cells were further incubated at 37°C with transport buffer (1.0 ml in the basolateral and 1.0 ml in the apical compartment) in the absence of labeled substrate, and radioactivity was determined as described above.

The paracellular leakage was determined by the addition of 1 µM [3H]inulin (BIOTREND, Köln, Germany) to the basolateral compartment and measurement of the radioactivity appearing in the apical compartment. The paracellular leakage was less than 2% of the radioactivity added for all MDCKII cell clones examined in this study.

Numerical Analysis. Ordinary differential equations were derived from the model depicted in Fig. 2 by assuming Michaelis-Menten kinetics in the linear regime, the kinetic behavior of the transporters OATP1B3 (König et al., 2000) and ABCC2 (Cui et al., 1999) has been characterized, and Michaelis-Menten constants were determined. The equations were integrated by ODESSA (Leis and Kramer, 1988,a,b). To ensure that we could identify all parameters while performing the multieperiment fit, we used a penalized likelihood as cost-function for parameter estimation. This likelihood includes prior knowledge of the parameter distribution (see Supplemental Data). The resulting cost-function was minimized using an optimization routine of the Gauss-Newton type (Hanson and Haskell, 1982; Peifer and Timmer, 2007). Because measurement errors show a linear dependence on the estimated mean value, we re-estimated the standard deviations by applying a linear error model to minimize the fluctuations in the estimated standard deviations (see Supplemental Data).

Results

The Cell System. MDCKII cells were grown in a polarized fashion on filter membrane supports, and transport of BSP, a substrate for both OATP1B3 and ABCC2, was studied in this system. The expression and sorting of the transport proteins were confirmed by immunofluorescence and confocal laser scanning microscopy (Fig. 1). The cell line represents an improved version of the double-transfectant described previously (Cui et al., 2001).

MDCKII cells were also analyzed for the expression and localization of endogenous transport proteins, as suggested by the mathematical modeling. Endogenous canine Abcc4 was localized to the basolateral membrane of the MDCKII cells (Fig. 1E). Thus, this endogenous basolateral efflux pump functions in addition to the recombinant human transport proteins. ABCC4 has a broad substrate specificity (Kruh et al., 2007) that includes BSP (data not shown). The influxes, effluxes, and concentration pools are summarized in Fig. 2.

Uptake and Efflux Transport in Polarized Cells. To acquire data, several sets of transport experiments were performed. Vectorial transport of labeled BSP was measured over 60 min at high (10 µM; Fig. 3) and low (10 nM; Fig. 4) concentrations. The intracellular content of labeled BSP was significantly higher in MDCKII cells expressing...
Radioactivity inside the cells (intracellular content, x) chamber (apical amount, x) data.

At least once. The solid lines result from the mathematical modeling of the measured points with error bars represent mean values, given as nanomoles per milligram of cellular protein ± S.D., from a triplicate determination reproduced independently at least once. The solid lines result from the mathematical modeling of the measured data.

recombinant OATP1B3 than in the control MDCKII cells (Figs. 3 and 4, bottom), indicating that OATP1B3 is responsible for the uptake and intracellular accumulation of BSP. The release of BSP into the apical chamber was mainly detected in cells expressing recombinant OATP1B3 together with ABCC2 (Figs. 3 and 4, top), indicating that ABCC2 in the apical membrane efficiently mediates the efflux of BSP.

To assess the contributions of endogenous transport processes, the cells were preloaded (Fig. 5) by adding 3H-labeled BSP to the basolateral chamber for 30 min. After this preloading time, the amounts of radioactivity effluxed into the apical chamber and into the basolateral chamber (basolateral amount), as well as radioactivity accumulated inside the cells, were determined. BSP was strongly accumulated in cells expressing OATP1B3 and, to a lesser extent, in cells expressing OATP1B3 together with ABCC2 (Fig. 5, middle). The MDCKII cells expressing recombinant OATP1B3 and ABCC2 showed the highest efflux of BSP into the apical chamber (Fig. 5, top). However, the major BSP efflux into the basolateral chamber was observed in the cells that had reached the highest intracellular content (Fig. 5, bottom). This efflux is most probably mediated by the endogenous (canine) Abcc4 of the MDCKII cells (Fig. 1E).

The Mathematical Model. Our model incorporated the effects of several transport factors. First, as can be seen from measurements in MDCKII control cells (Figs. 3 and 4), there was a small but significant increase of BSP in the intracellular compartment and in the apical chamber. This observation suggests the existence of an endogenous basolateral uptake transporter (Endoin-bl in Fig. 2) as well as an apical endogenous efflux pump (Endoex-cap in Fig. 2). Second, preloading experiments (Fig. 5) indicated the existence of a basolateral efflux pump (Endoex-bl in Fig. 2). Third, based on [3H]inulin transport experiments, we observed a low rate (less than 1% of total transport) of paracellular leakage (data not shown), which was also included in our model. Fourth, to determine the amount of [3H]BSP that bound to cytosolic proteins, we separated the cytosolic protein fraction by centrifugation at 20,000 g and measured the amount of radioactivity in the resulting supernatant. We found that approximately 86% of the BSP bound to intracellular macromolecules. To account for this binding, we added intracellular binding sites to the model (x_b in Fig. 2). Fifth, control experiments without any cultured cells showed a significant amount of BSP bound nonspecifically to the filter membrane support. This binding was also included in the model (x_b in Fig. 2). Finally, the intracellular content of BSP is approximately 7 times greater for the cells expressing recombinant OATP1B3 than for the control cells when determined at 60 min (Fig. 3). If transcellular diffusion played a significant role, the apical amount of BSP should be much greater for the OATP1B3-expressing cells than for the control cells. Thus, transcellular diffusion seems to be negligible and therefore was not factored into the model.

Assuming Michaelis-Menten kinetics in the linear regime, we derived the ordinary differential equations (Table 1) from the model shown in Fig. 2. This procedure is in accordance with similar modeling approaches (Liu and Pang, 2006; Turncliff et al., 2006). The rates of BSP uptake into cells may vary somewhat between different sets of experiments depending on the expression level of OATP1B3. Accordingly, we fitted our model to the data from all of the experiments of the present study by maximizing a penalized likelihood (Good and Gaskins, 1971) as explained in Supplemental Data. The penalized likelihood was introduced to ensure that we could identify...
all parameters for the multieperiment fit (see Supplemental Data). Results of the fits are shown in Figs. 3 through 5.

We found it necessary to include the endogenous transporters in the model. We compared the complete model (Fig. 2) to models lacking selected endogenous transport processes. Each of the smaller models yielded a significantly worse fit of the data than the complete model (see Supplemental Data).

**Rate-Determining Steps in Vectorial Transport.** Based on our model (Fig. 2), we calculated the contribution of each transport process to the total amount of BSP transported into the apical chamber. The largest amount of BSP was transported by the recombinant uptake transporter OATP1B3, followed by the recombinant apical efflux pump ABC2, the endogenous efflux pump Endoex-ap, and paracellular BSP transport to the total amount of BSP transported into the apical chamber (basolateral amount, $x_1$), inside the cells (intracellular content, $x_3 + x_4$), and in the apical chamber (apical amount, $x_5$) were determined. Data points with error bars represent mean values, given as nanomoles per milligram of cellular protein ± S.D., from a triplicate determination reproduced independently at least once, and solid lines were derived from the mathematical modeling of the data.

**Mathematical Modeling of Vectorial Transport.** Based on our model (Fig. 2), we calculated the contribution of each transport process to the total amount of BSP transported into the apical chamber. The largest amount of BSP was transported by the recombinant uptake transporter OATP1B3, followed by the recombinant apical efflux pump ABC2, the endogenous efflux pump Endoex-ap, and paracellular BSP transport to the total amount of BSP transported into the apical chamber (basolateral amount, $x_1$), inside the cells (intracellular content, $x_3 + x_4$), and in the apical chamber (apical amount, $x_5$) were determined. Data points with error bars represent mean values, given as nanomoles per milligram of cellular protein ± S.D., from a triplicate determination reproduced independently at least once, and solid lines were derived from the mathematical modeling of the data.

**Ordinary differential equations deduced from the model by assuming linearized Michaelis-Menten kinetics**

Here, $x_1$ is the basolateral amount and $x_5$ is BSP bound nonspecifically to the filter membranes. Unbound intracellular BSP is denoted by $x_3$, whereas $x_4$ is BSP bound to intracellular-binding proteins and $x_5$ is the apical amount of BSP. The rate constants $p_1$ and $p_3$ for OATP1B3 and ABC2, as well as $p_5$ for Endoex-ap and Endoex-bl and Endoex-bl, are proportional to the respective concentrations of the transporters. $V_{bd}$ and $V_{ap}$ denote the volume of the basolateral and the apical chamber, respectively.

**Differential Equations**

$$\begin{align*}
1) \frac{dx_1}{dt} &= -p_1 x_1 - p_3 x_1 + p_3 x_3 - p_5 x_1 (p_4 - x_2) + p_3 x_2 - p_3 \left( \frac{x_1}{V_{bd}} - \frac{x_5}{V_{ap}} \right) \\
2) \frac{dx_2}{dt} &= p_3 x_1 (p_4 - x_2) - p_3 x_2 \\
3) \frac{dx_3}{dt} &= p_3 x_3 - p_3 x_3 + p_3 x_1 - p_5 x_1 (p_4 - x_2) + p_3 x_2 \\
4) \frac{dx_4}{dt} &= p_3 x_4 (p_4 - x_2) - p_3 x_4 \\
5) \frac{dx_5}{dt} &= p_3 x_5 + p_3 x_5 + p_3 \left( \frac{x_1}{V_{bd}} - \frac{x_5}{V_{ap}} \right) 
\end{align*}$$

Endoex-bl with approximately 19% (Fig. 6B). The endogenous transporters Endoin-bl and Endoex-bl and paracellular BSP transport together account for less than 10% of the total transport. Since the endogenous efflux pump Endoex-bl (probably Abcc4) transports BSP back into the basolateral chamber, its contribution to the total amount of BSP transported into the apical chamber is actually negative.

Control coefficients have frequently been used in metabolic control analysis to quantify the contribution of a given enzyme to the steady-state flux of metabolites (Schuster and Heinrich, 1992; Conradie et al., 2006). In this analysis, the fractional change of the steady-state flux of a metabolite $\nu$ is related to the fractional change of an enzyme activity $v_j$, defined as $C'_{ij} = \frac{\partial J}{\partial J_i}$. For our system, we calculated the relationship of the fractional change of the total flux into the apical chamber, $J = \frac{dx_5}{dt}$, to the fractional change of each transport process in our model (Fig. 7). Since the rate for each transport process in our model is linear and has the form $v_j = p_j x$, the normalized control coefficients read:

$$C'_{ij} = \frac{p_i}{J} \frac{\partial J}{\partial x_j}$$

where $p_i$ is the parameter controlling transport process $j$. The resulting control coefficients for the double-transfected and MDCKII control cells are depicted in Fig. 7.

For the double-transfected cells, the control coefficients of OATP1B3 and ABC2 were the dominant transport processes and were rate-determining in our system. This agrees with the fact that each of the single-transfected cells (i.e., OATB1B3 cells or ABC2 cells; Cui et al., 2001) exhibit significantly less total vectorial transport than the double-transfected cells. For control cells, on the other hand, the control coefficient of the endogenous transporters Endoex-bl and Endoex-ap, as well as the paracellular flow, are the main processes. The comparison of the control coefficients of the parental cells with the control coefficients of the double-transfected cells shows that the rate-determining step in vectorial transport clearly depends upon the expression level of the respective transport proteins.

**Discussion**

Vectorial transport across polarized cells controls the half-life of many endogenous and xenobiotic substances in the mammalian or-
compartment. The parameters of the mathematical model described herein for the vectorial transport of BSP in double-transfected polarized cells were determined by maximizing a penalized likelihood (Good and Gaskins, 1971) as explained in detail in Supplemental Data. This approach provides new qualitative and quantitative insights into the components and dynamic behavior of vectorial transport. In particular, the role of endogenous transport processes was recognized and quantified in addition to the role of the transfected recombinant transporters OATP1B3 and ABCC2.

In this study, our data-based mathematical modeling was supported by application of an in vitro cell culture system that allowed quantitative analyses of a labeled model substance in different compartments at various time points. In several aspects, this biological system with double-transfected polarized cells (Fig. 1) resembles human hepatocytes and the vectorial transport of many substances, including BSP, from the blood circulation into bile (Keppler, 2005).

The model shows excellent agreement with the experimental data. The optimal fit of the model was achieved by maximizing a penalized likelihood (Good and Gaskins, 1971) and required the inclusion of endogenous transport processes of the MDCKII cell, in addition to the stably expressed recombinant human transporters OATP1B3 and ABCC2. The role of endogenous transport proteins in the MDCKII cells was addressed by preloading experiments, which enabled quantitative measurements of efflux from the cells into the apical and basolateral chambers. The excellent agreement of the model with the experimental data indicates that transepithelial diffusion was not required as an additional parameter, at least in the case of the hydrophobic BSP. A similar modeling approach could be taken with the introduction of other recombinant transport proteins, such as uptake mediated by OATP2B1 and the efflux pump ABCB2 (Kopplow et al., 2005) or the sodium-dependent bile acid uptake transporter NTCP and the efflux pump ABCB11 (Mita et al., 2006).

As expected, the greatest contributions to the transport of BSP came from recombinant OATP1B3 and ABCC2 (44 and 28% of total transport, respectively). Surprisingly, endogenous basolateral efflux, designated Endoex-bl, amounted to 19%, which is in line with the significant amount of the endogenous protein Abcc4 in the basolateral membrane. In hepatocytes, basolateral efflux pumps, including ABCC3 and ABCC4, also play an important role in overall transport of small molecules (Kius et al., 2003). The basolateral efflux in the MDCKII cells was initially indicated by model comparison, leading to the best fit with the experimental data. This efflux was verified and further quantified by preloading experiments. Notably, all other processes integrated into our model together amount to less than 10% of the transport. This small contribution is in accordance with the normalized control coefficients for the fluxes in the double-transfected cells. Thus, variations in the activity of OATP1B3 or ABCC2 have the greatest effect on total flux. Since the control coefficients for OATP1B3 and ABCC2 are similar, a rate-determining step cannot be singled out in this cellular system. This will be different when the activity of one of the six processes described in our model is significantly changed, as can be seen for the control coefficients of the MDCKII control cells where other partial processes dominate total vectorial flux.

In conclusion, the polarized cell system for studies on vectorial transport (Cui et al., 2001; Sasaki et al., 2002) was successfully used for data-based mathematical modeling and resulted in the quantification of individual transport steps in a complex system. This quantitative modeling greatly expands the mostly qualitative previous knowledge on the vectorial transport of endogenous and xenobiotic substances. Accordingly, predictions can be made for the time course of transport and for the relative contribution of single transport steps.
to the overall transport. The calculation of control coefficients enabled the identification of rate-determining single steps in overall vectorial transport. Moreover, the modeling approach in this study has been useful for the identification of previously unexpected partial processes, such as the quantitatively important basolateral efflux (Endoex-bl). This additional transport process is well explained by the detection of endogenous Abcc4 in the MDCKII cells. The inclusion of this process was necessary to obtain excellent agreement between the experimental data and the mathematical model. Thus, data-based quantitative mathematical modeling led to new qualitative as well as quantitative insight into the biological system. In this study, we focused on BSP as a well known model substance for the analysis of hepatobiliary elimination. However, this modeling approach may be applied to other substances, e.g., cholecystokinin octapeptide CCK-8, the vectorial transport of which has been characterized recently (Letschert et al., 2005), and other polarized cellular systems, such as quadruple-transfected MDCKII cells (Kopplow et al., 2005).

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References


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