Combining Multiscale Experimental and Computational Systems Pharmacological Approaches to Overcome Resistance to HER2-targeted Therapy in Breast Cancer

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ABSTRACT

The emergence of human epidermal growth factor receptor type-2 (HER2) therapy resistance in HER2-positive (HER2+) breast cancer (BC) poses a major clinical challenge. The primary mechanisms of resistance include aberrant activation of the HER2 and phosphatidylinositol-3-kinase/mammalian target of rapamycin (PI3K/mTOR) pathways. The existence of feedback loops in this pathway may engender resistance to targeted therapies such as everolimus, an mTOR inhibitor, resulting in a more aggressive form of refractory HER2+ BC. Here, we hypothesize that a triple and sequential combination therapy of paclitaxel, a potent cytotoxic agent, before concomitant administration of dasatinib, a SRC proto-oncogene nonreceptor tyrosine kinase (Src) family kinase inhibitor, with everolimus, restores sensitivity to treatment in refractory HER2+ BC. This was assessed by a combination of experimental and computational approaches. Quantitative systems pharmacological (QSP), pharmacokinetics (PK), and pharmacodynamics (PD) studies were conducted in static and three-dimensional and dynamic (3DD) cell culture systems using a HER2+ cell line resistant to HER2 therapy, JIMT-1. The dynamic responses in cellular viability and key signaling proteins in the HER2 and PI3K/Akt/mTOR pathways were measured upon treatments with single drugs, combinations, and appropriate controls. A QSP-PK/PD model was developed and used to optimize the sequence and interdose interval of the three agents in the combination. The proposed sequential combination therapy demonstrated strong cytotoxic effects in JIMT-1 cells, and our models predicted the usefulness of this combination over prolonged durations in the 3DD setting. Our combined experimental and QSP-PK/PD modeling approach may serve as a useful screening tool in predicting clinical efficacy of combination therapies in oncology. Nonetheless, further in vivo human xenograft tumor studies are warranted.

Introduction

Human epidermal growth factor receptor type-2 positive breast cancer (HER2+ BC) is characterized by an overexpression of the HER2 receptor on the cell surface in approximately 25% of all breast cancers. It has been associated with poor prognosis, a higher incidence of metastases, and a shorter overall survival as compared with most other BC subtypes (Loibl and Gianni, 2017). HER2-targeted therapies such as trastuzumab (Herceptin) and lapatinib (TYKERB) have demonstrated improved clinical outcomes in HER2+ metastatic BC, but innate and/or acquired treatment resistance may occur (Yarden, 2001; Pohlmann et al., 2009; Singh et al., 2014; Zhang et al., 2017). Resistance to HER2 therapy in HER2+ BC patients has become an important clinical unmet medical need, motivating the search for alternative treatment approaches to overcome resistance and prolong patients’ survival. Here, we propose to reorient and/or combat a difficult-to-treat BC that is refractory to HER2 therapy via a novel combination therapy comprising three agents with distinct but complementary mechanisms of action, including everolimus, dasatinib, and paclitaxel.

Everolimus is a small molecule inhibitor of the mammalian target of rapamycin complex 1 (mTORC1) protein complex in the phosphatidylinositol 3-kinase/AKT8 virus oncogene cellular homolog/mammalian target of rapamycin (PI3K/Akt/mTOR) pathway (Houghton, 2010), which is aberrantly activated in HER2-positive cancers (Wilks, 2015). Everolimus exerts its antitumor effects through mTORC1-mediated dephosphorylation of ribosomal protein S6 kinase-1 (S6K1) and eukaryotic translation initiation factor 4E-binding protein 1 (4E-BP1), causing signal blockade in the PI3K/Akt/mTOR pathway and inhibition of cellular proliferation (O’Brien et al., 2014). In contrast, the inhibition of mTORC1 releases a feedback activation loop mediated by insulin-like growth
factor receptor type-1 (IGF-1R) and the insulin receptor, which results in the activation of insulin receptor substrate-1 (IRS-1) and in turn activates Akt located upstream of mTORC1 (O'Reilly et al., 2006).

Thus, a second agent targeting a signaling protein upstream of Akt is needed to counterregulate this feedback activation loop (Yori et al., 2014). One such targeted small molecule agent is dasatinib (Araujo and Logothetis, 2010). Dasatinib is a multikinase inhibitor of SRC proto-oncogene nonreceptor tyrosine kinase (Src), a proto-oncogene from the Src family kinases (SKFs), located upstream of Akt. It is responsible for regulating multiple cellular growth pathways via the signaling proteins Akt, mitogen-activated protein kinase (MAPK), and signal transducer and activator of transcription 3 (STAT3) (Chang and Wang, 2013). Its over-activation has been implicated in HER2+ BC cells’ resistance to trastuzumab and lapatinib (De Luca et al., 2014; Jin et al., 2017). The dual inhibition of mTOR and SKFs in a mouse model of HER2+ BC efficaciously caused tumor regression via prevention of the Akt feedback activation loop, thus supporting the hypothesis that combination of everolimus with dasatinib may be successful at combating treatment resistance in HER2+ BC (Dehm and Bonham, 2004; Yori et al., 2014).

To further enhance the tumor inhibitory effects of everolimus and dasatinib, we selected paclitaxel as a standard cytotoxic agent. Paclitaxel cell-killing results from microtubule stabilization, leading to mitotic arrest and subsequently cancer cell death (Horwitz, 1994). In ovarian granulosa tumor cells, paclitaxel in combination with dasatinib or mTOR inhibitors showed a synergistic growth inhibitory effect (Haltia et al., 2017). Thus, the potent cytotoxic activity of paclitaxel mediated by the activation of apoptotic pathways increases the likelihood of achieving synergistic tumor cell-killing when used in combination with the proposed targeted cytostatic agents in refractory HER2+ BC.

In the present work, we sought to evaluate the efficacy of our proposed triple combination therapy. We conducted in vitro cell culture studies in two-dimensional (2D) static and three-dimensional dynamic (3DD) settings using JIMT-1, a HER2+ BC cell line resistant to trastuzumab and lapatinib (Köninki et al., 2010). Concentration–response, time-dependent cell-killing, and activity of key signaling proteins were examined upon exposure of JIMT-1 cells to single and combination therapies. A pharmacokinetic and pharmacodynamic (PK/PD) study was conducted using a 3DD cell culture system (Ho et al., 2004; Toriniwa and Kamiya, 2007; Ande et al., 2018).

A quantitative systems pharmacology (QSP) PK/PD model was developed, and it characterized well all the observed data. The developed QSP-PK/PD model served as an in silico tool for simulations of optimized dosing regimens and inter-dose intervals of the three agents that best desensitize (or overcome) resistance in HER2+ BC. Our strategy of combining experimental and computational modalities is promising and may enable predictions of the clinical efficacy of the proposed triple combination as well as other therapeutic strategies in oncology.

**Material and Methods**

**Drugs and Reagents**

Paclitaxel, everolimus, and dasatinib were purchased from Selleck Chemicals (Houston, TX). The JIMT-1 cell line was purchased from the American Type Culture Collection (ATCC, Manassas, VA). Cell culture reagents including Dulbecco’s modified Eagle’s medium (DMEM), sodium bicarbonate solution, and nonessential amino acids solution were purchased from Corning (Tewksbury, MA). FBS and cell counting kit-8 (CCK-8) were purchased from Sigma-Aldrich (St. Louis, MO). The biocinchonic acid (BCA) protein assay kit and protease inhibitor cocktail were obtained from Thermo Fisher Scientific (Waltham, MA). Crystal violet nuclear dye and the 3DD cell culture (BelloCell) system apparatus were purchased from Chemglass Life Sciences (Vineland, NJ). Caspase-3 colorimetric assay kit for assessing caspase-3 activity was purchased from Abcam (Cambridge, MA). The radioimmunoprecipitation assay (RIPA) buffer was obtained from Boston BioProducts, (Ashland, MA). Phosphorylated Akt (pAkt), Src (pSrc), and mTOR (pmTOR) protein assay kits were purchased from EMD Millipore (Billerica, MA). Quantitative protein assays were conducted using the MAGPIX multiplexing instrument from Luminex Corporation (Austin, TX). Colorimetric assays for cell viability and caspase-3 activity were performed using a microplate spectrophotometer (BioTek Instruments, Winooski, VT).

**Two-Dimensional (2D) or Static Cell Culture Experiments**

Concentration–response relationships were examined in vitro after exposure of JIMT-1 cells to paclitaxel, everolimus, and dasatinib, as described previously elsewhere (Ande et al., 2018). Caspase-3 activity in JIMT-1 cells was measured over a time course of 0, 6, 12, 24, 48, and 72 hours after exposure to 50 nM paclitaxel, everolimus, and dasatinib as single agents and combinations by use of a colorimetric caspase-3 assay kit (Abcam), as per the manufacturer’s instructions. Total and phosphorylated Src, Akt, and mTOR proteins were measured over a period of 0, 1, 3, 6, 12, 24, and 48 hours after exposure of JIMT-1 cells to single agents and combinations of agents by use of protein assay kits from EMD Millipore, as per the manufacturer’s protocols. Cell viability over a time course of 0, 24, 48, 72, and 96 hours was measured by use of the CCK-8 kit (Sigma-Aldrich) after exposure of JIMT-1 cells to the single agents as well as combinations.

**Three-Dimensional and Dynamic (3DD) Cell Culture Experiments**

A PK/PD study was conducted in a novel 3DD cell culture system (BelloCell; Supplemental Fig. 1) by exposing JIMT-1 cells to a triple combination of paclitaxel followed by sequential administration of dasatinib plus everolimus under dynamic conditions, as described previously elsewhere (Ande et al., 2018). Briefly, the 3DD system is an oscillating bioreactor that allows for high-population-density culture of cells over long periods of time (15–20 days). It is a fluid flow system that allows drug concentrations to be varied over time to mimic animal/human PK. Additionally, PD biomarkers can be sampled and measured without perturbing the system as such (Ho et al., 2004; Toriniwa and Kamiya, 2007).

In the present study, paclitaxel was administered as a 3-hour continuous infusion at a rate of 3.75 μg/minute to achieve a peak concentration of approximately 50 nM, based on a preliminary pilot study. On the following day, everolimus and dasatinib were administered into the system simultaneously with a constant concentration maintained at 50 nM for 72 hours, followed by a washout phase. PK samples were collected over a period of 96 hours starting from day 0 for measurement of paclitaxel concentrations in the system. Paclitaxel concentrations were quantified using high-pressure liquid chromatography–tandem mass spectrometry (LC-MS/MS). JIMT-1 cell viability was assessed every 24–48 hours throughout the duration of the study using a crystal violet nuclear dye counting kit (Chemglass Life Sciences).
a time course, upon exposure of JIMT-1 cells to paclitaxel, dasatinib, and everolimus as single agents and combinations. Model building was performed by characterization of protein dynamics and cellular responses after perturbation of protein activity in response to 1) the single agents paclitaxel (P), dasatinib (D), and everolimus (E); 2) dual combination therapy of dasatinib + everolimus (DE); and 3) triple combination therapy of paclitaxel + dasatinib + everolimus (PDE, simultaneous) and paclitaxel followed by dasatinib + everolimus (PDE, sequential), as depicted in Fig. 1. All measured proteins were characterized using turnover rate constants (system parameters) across all treatment arms, and protein perturbations due to various treatment regimens were characterized using transit compartment models with inhibition or stimulation coefficients (Sun and Jusko, 1998; Lobo and Balthasar, 2002), as applicable (drug-related parameters).

All mathematical modeling was performed using Monolix software version 2016R1 (Lixoft SAS, 2016).

**Single Agents.**

**Paclitaxel.** Model development for paclitaxel was initiated with pAkt being inhibited through the use of a precursor pool indirect response model (Sharma et al., 1998). Inhibition of the PI3K/Akt pathway is implicated in paclitaxel-mediated cell death in BC cells via activation of c-Jun N-terminal kinases (JNK), leading to activation of the apoptotic machinery (Sunters et al., 2006). Moreover, aberrant activation of this pathway is characteristic of HER2-therapy resistant BC cells, making it a key pathway for examination of protein activity perturbations.

Inhibition of Akt activity leads to the inhibition of its downstream protein mTOR via dephosphorylation, which in turn causes the inhibition of cell proliferation through inhibition of ribosomal S6K, as described previously. Inhibition of Akt activity was accounted for in the model through the inhibition of a hypothetical compartment, AktIc, upstream of Akt, which phosphorylates Akt (Chudasama et al., 2015; Vaidya et al., 2018). Akt protein activity, however, returns to its baseline after approximately 6 hours (Fig. 2). Therefore, a precursor pool based indirect response model was used to capture this trend, as depicted in the following equations:

\[
\frac{d(AktIc)}{dt} = \frac{K_{inh} \cdot (1 - (C_P \cdot I_P)) - K_{inh} \cdot Akt_{Ic}}{C_P} \quad \text{Akt}_{Ic}(0) = 1
\]

\[
\frac{d(pAKt)}{dt} = K_{Akt} \cdot Akt_{Ic} \cdot pAKt - K_{pAKt} \cdot pAKt \quad pAKt(0) = 1
\]

\[
\frac{dpAKt}{dt} = K_{pAKt} \cdot Akt_{Ic} \cdot pre_{pAKt} - K_{pAKt} \cdot pAKt \quad pAKt(0) = 1
\]

where, \(pre_{pAKt}\) and \(pAKt\) represent the precursor pool compartment and pAKt compartment, \(K_{inh}\) is the turnover rate constant for the inhibitory compartment AktIc, and \(K_{Akt}\) is the turnover rate constant for the precursor pool and Akt protein. \(C_P\) represents the paclitaxel concentration (50 nM), and \(I_P\) represents the coefficient for its inhibitory effect on cancer cells. All protein dynamic data were normalized to the no-treatment control arm. Therefore, homeostasis was maintained for the control protein dynamic data at a level of 1 unit under unperturbed conditions to satisfy the law of mass balance. The initial conditions for all protein compartments were set at 1.

Further, the inhibitory effect of pAKt on pmTOR was described through the following equations. Two transit compartments were able to adequately describe the delay in signaling between pAKt and pmTOR.
pmTOR proteins (Sun and Jusko, 1998; Lobo and Balthasar, 2002) as follows:

\[
\frac{dK_{M1}}{dt} = \frac{1}{\tau_{MP}} \cdot ((pAkt)^{S1P}) - K_{M1}; \quad K_{M1}(0) = 1
\]

(4)

\[
\frac{dK_{M2}}{dt} = \frac{1}{\tau_{MP}} \cdot (K_{M1} - K_{M2}); \quad K_{M2}(0) = 1
\]

(5)

\[
\frac{d(pre_{pmTOR})}{dt} = K_{mTOR} \cdot pre_{pmTOR} - K_{mTOR} \cdot pmTOR; \quad pmTOR(0) = 1
\]

(6)

\[
\frac{dpmTOR}{dt} = K_{mTOR} \cdot pmTOR - pre_{pmTOR} \cdot pmTOR; \quad pmTOR(0) = 1
\]

(7)

where \(K_{M1}\) and \(K_{M2}\) represent transit compartments, \(\tau_{MP}\) represents the mean transit time for the delay of paclitaxel-mediated signaling between pAkt and pmTOR, \(K_{mTOR}\) represents the turnover rate constant for pmTOR, and \(S_{TP}\) represents the coefficient for inhibition of mTOR activity due to paclitaxel.

In addition, caspase-3 (Cas3 in the equations), the executor of apoptosis, is activated in response to paclitaxel treatment. Its activity over time was captured well with three transit compartments as shown in eqs. 8-10, which led to the production of active caspase-3 described by a precursor pool indirect response model (Fig. 1). A negative retroregulation loop from the active caspase-3 compartment (Cas3) to the first transit compartment (\(K_{C1}\)) allowed to capture the tolerance phenomenon observed in the caspase-3 activity temporal profile (i.e., return to the baseline activity level for Cas3 while JIMT-1 cells are still exposed to paclitaxel).

\[
\frac{dK_{C1}}{dt} = \frac{1}{\tau_{CP}} \cdot \left(1 + \frac{(k_P \cdot C_{pC})^{S2P}}{C_{as3}^{S2P}}\right) - K_{C1}; \quad K_{C1}(0) = 1
\]

(8)

\[
\frac{dK_{C2}}{dt} = \frac{1}{\tau_{CP}} \cdot (K_{C1} - K_{C2}); \quad K_{C2}(0) = 1
\]

(9)

\[
\frac{dK_{C3}}{dt} = \frac{1}{\tau_{CP}} \cdot (K_{C2} - K_{C3}); \quad K_{C3}(0) = 1
\]

(10)

\[
\frac{d(pre_{Cas3})}{dt} = K_{as3} - K_{as3} \cdot pre_{Cas3} \cdot C_{as3}; \quad pre_{Cas3}(0) = 1
\]

(11)

\[
\frac{dCas3}{dt} = K_{as3} \cdot pre_{Cas3} - C_{as3} \cdot pre_{Cas3}; \quad pre_{Cas3}(0) = 1
\]

(12)

where \(k_P\) and \(S2P\) represent the slope and exponent for stimulatory effect of paclitaxel on caspase-3 activity, \(\tau_{CP}\) represents the mean
transit time for paclitaxel-mediated caspase-3 activation signaling, $K_{\text{mue}}$ represents the turnover rate constant for caspase-3 activity, and $S_{3P}$ represents the feedback coefficient for caspase-3 activity.

The changes in protein activity were linked to JIMT-1 cellular response as follows:

$$\frac{dR}{dt} = (\text{pmTOR}^{S_{3P}}) \cdot k_g R - kd_P R.(\text{Cas}3 - 1); \quad R(0) = R_0$$  \hspace{1cm} (13)

where $R$ represents cell viability response, and $R_0$ represents initial number of cells at time 0. Because all data were normalized to the control arm, $R_0$ was equal to 1.

In the 2D experimental studies, JIMT-1 cells exhibited an exponential pattern in their growth over time under control conditions (no treatment). Therefore, $k_g$, the first-order growth rate constant, was used to quantify the JIMT-1 cellular proliferation rate. The protein signal from the pmTOR compartment (eq. 7) influenced the inhibition of JIMT-1 cell growth, and its effect was incorporated using the exponent $S_{4P}$. The $kd_p$ parameter represents the death rate constant for JIMT-1 cells and was used to stimulate JIMT-1 cells death driven by caspase-3 activity. The subscript “P” in the above set of equations stands for all paclitaxel-associated parameters.

**Dasatinib.** Protein modeling for dasatinib included the inhibition of its target protein pSrc via dephosphorylation, followed by the inhibition of its downstream proteins pAkt and pmTOR, as described by the following equations:

$$\frac{dp_{\text{pSrc}}}{dt} = k_{\text{src}} - k_{\text{src}} \cdot p_{\text{pSrc}} \cdot (1 - (C_{1D}, S_{1D})); \quad p_{\text{pSrc}}(0) = 1$$  \hspace{1cm} (14)

$$\frac{dp_{\text{Src}}}{dt} = k_{\text{src}} \cdot p_{\text{pSrc}} \cdot (1 - (C_{1D}, S_{1D})) - k_{\text{src}} \cdot p_{\text{Src}}; \quad p_{\text{Src}}(0) = 1$$  \hspace{1cm} (15)

$$\frac{dp_{\text{Akt}}}{dt} = k_{\text{Akt}} - k_{\text{Akt}} \cdot p_{\text{Akt}}; \quad p_{\text{Akt}}(0) = 1$$  \hspace{1cm} (16)

$$\frac{dK_{M1}}{dt} = \left(\frac{1}{\tau_{MD}}\right) \cdot (p_{\text{Akt}}^{S_{3P}} \cdot (1 - (C_{1D}, S_{1D})); \quad K_{M1}(0) = 1$$  \hspace{1cm} (17)

$$\frac{dK_{M2}}{dt} = \left(\frac{1}{\tau_{MD}}\right) \cdot (K_{M1} \cdot (1 - (C_{1D}, S_{1D})); \quad K_{M2}(0) = 1$$  \hspace{1cm} (18)

$$\frac{dp_{\text{pmTOR}}}{dt} = K_{\text{mtOR}} - K_{\text{mtOR}} \cdot p_{\text{pmTOR}} \cdot (1 - (C_{1D}, S_{1D})); \quad p_{\text{pmTOR}}(0) = 1$$  \hspace{1cm} (19)

$$\frac{dp_{\text{pmTOR}}}{dt} = K_{\text{mtOR}} \cdot K_{\text{M2}} \cdot p_{\text{pmTOR}} \cdot (1 - (C_{1D}, S_{1D}); \quad p_{\text{pmTOR}}(0) = 1$$  \hspace{1cm} (20)

$$\frac{dR}{dt} = (\text{pmTOR}^{S_{3P}}) \cdot k_g R; \quad R(0) = R_0$$  \hspace{1cm} (21)

A precursor pool-based indirect response model was used to capture pSrc inhibition under dasatinib treatment and to characterize the return to baseline phase after 9 hours of pSrc inhibition (Fig. 2). $K_{\text{src}}$ represents the turnover rate constant for pSrc, $C_{P}$ is the dasatinib concentration ($50 \, \text{nM}$), and $S_{1D}$ is the coefficient for inhibition of pSrc due to the dasatinib effect. $S_{2D}$ represents the coefficient for effect of pSrc on pAkt, wherein Akt activity is inhibited via stimulation of loss of pAkt due to inhibition of Src (Liao and Hung, 2010). The mTOR activity is then inhibited due to pAkt via two transit compartments, $K_{G}$ and $K_{M2}$, with $\tau_{MD}$ as the mean transit time and $S_{2D}$ as the coefficient of inhibition. The inhibition of mTOR activity drives the inhibition of JIMT-1 cellular response as shown in eq. 22. The subscript “D” stands for dasatinib-associated parameters, and all other terms have the usual notations described previously.

**Everolimus.** The final QSP model for everolimus integrated inhibition of the pmTOR protein, followed by a stimulatory feedback loop from pmTOR on the pAkt protein, in accordance with the reported literature and our observed pAkt activity data (Fig. 2). Notably, an increase in Src activity in response to everolimus treatment was also observed. This is in line with the finding that rapamycin, an mTORC1 inhibitor, causes phosphorylation and transactivation of the epidermal growth factor receptor (EGFR) pathway via Src activation in some cell lines, thus promoting cell survival (Chaturvedi et al., 2009). In addition, induction of IRS-1 and the release of feedback inhibition of the IGF-1R/Pi3K pathway cause Akt overactivation, which promotes cell growth in the presence of everolimus alone (O’Reilly et al., 2006). The model equations governing protein dynamics are as follows:

$$\frac{dp_{\text{prepmTOR}}}{dt} = K_{\text{mtOR}} - K_{\text{mtOR}} \cdot p_{\text{prepmTOR}} \cdot (1 - (C_E, S_{1E})); \quad p_{\text{prepmTOR}}(0) = 1$$  \hspace{1cm} (23)

$$\frac{dp_{\text{pmTOR}}}{dt} = K_{\text{mtOR}} \cdot p_{\text{prepmTOR}} \cdot (1 - (C_E, S_{1E})); \quad p_{\text{pmTOR}}(0) = 1$$  \hspace{1cm} (24)

$$\frac{dK_{S1}}{dt} = \left(\frac{1}{\tau_{SE}}\right) \cdot (p_{\text{pmTOR}}^{S_{3P}} \cdot (1 - (C_{1D}, S_{1D})); \quad K_{S1}(0) = 1$$  \hspace{1cm} (25)

$$\frac{dK_{S2}}{dt} = \left(\frac{1}{\tau_{SE}}\right) \cdot (K_{S1} - K_{S2}); \quad K_{S2}(0) = 1$$  \hspace{1cm} (26)

$$\frac{dK_{S3}}{dt} = \left(\frac{1}{\tau_{SE}}\right) \cdot (K_{S2} - K_{S3}); \quad K_{S3}(0) = 1$$  \hspace{1cm} (27)

$$\frac{dp_{\text{prepmSrc}}}{dt} = K_{\text{src}} - k_{\text{src}} \cdot p_{\text{prepmSrc}}; \quad p_{\text{prepmSrc}}(0) = 1$$  \hspace{1cm} (28)

$$\frac{dp_{\text{Src}}}{dt} = K_{\text{src}} \cdot p_{\text{prepmSrc}} - k_{\text{src}} \cdot p_{\text{Src}}; \quad p_{\text{Src}}(0) = 1$$  \hspace{1cm} (29)

$$\frac{dp_{\text{prepmAkt}}}{dt} = K_{\text{Akt}} - k_{\text{Akt}} \cdot p_{\text{prepmAkt}}; \quad p_{\text{prepmAkt}}(0) = 1$$  \hspace{1cm} (30)

$$\frac{dp_{\text{pmAkt}}}{dt} = K_{\text{Akt}} \cdot p_{\text{prepmAkt}} \cdot p_{\text{pmSrc}} \cdot p_{\text{pmTOR}}; \quad p_{\text{pmAkt}}(0) = 1$$  \hspace{1cm} (31)

$$\frac{dR}{dt} = \left(\text{pmTOR}^{S_{3P}}\right) \cdot k_g R; \quad R(0) = R_0$$  \hspace{1cm} (32)

where $C_E$ is the everolimus concentration ($50 \, \text{nM}$) and $S_{1E}$ is everolimus coefficient of inhibition on pmTOR. Feedback activation of pSrc due to pmTOR was driven by three transit compartments. The pmTOR activity drove the inhibition of the proliferation of JIMT-1 cells as represented in eq. 32. The subscript “E” denotes everolimus-associated model terms and parameters.

Of note, there was no increase in caspase-3 activity observed in response to the everolimus or dasatinib treatments, indicating a cytostatic effect of these two agents in JIMT-1 cells.

**Dual Combination Therapy of Dasatinib with Everolimus (DE).** The dual therapy model included components of the individual models for each agent in the combination with attenuation of the feedback activation loops due to counterregulatory mechanisms of dasatinib on everolimus. In addition, an active caspase-3 component was included in the model due to slight elevation in active caspase-3 expression observed with the dual combination (Fig. 3). The corresponding model equations are as follows:

$$\frac{dp_{\text{prepmTOR}}}{dt} = K_{\text{mtOR}} - K_{\text{mtOR}} \cdot p_{\text{prepmTOR}} \cdot (1 - (C_E, S_{1E})); \quad p_{\text{prepmTOR}}(0) = 1$$  \hspace{1cm} (33)

$$\frac{dp_{\text{pmTOR}}}{dt} = K_{\text{mtOR}} \cdot p_{\text{prepmTOR}} \cdot (1 - (C_E, S_{1E})); \quad p_{\text{pmTOR}}(0) = 1$$  \hspace{1cm} (34)

$$\frac{dp_{\text{pSrc}}}{dt} = K_{\text{src}} - K_{\text{src}} \cdot p_{\text{pSrc}} \cdot (1 - (C_{1D}, S_{1D})); \quad p_{\text{pSrc}}(0) = 1$$  \hspace{1cm} (35)
where $C_{DE}$ denotes concentration of dasatinib and everolimus (50 nM), and the subscript “DE” denotes dasatinib-everolimus–associated terms and parameters. $S1_{DE}$ is the coefficient for effect of pAkt on pmTOR in the presence of DE treatment, $k_{DE}$ and $S2_{DE}$ are the slope and exponent for activation of caspase-3, and $\tau_{CDE}$ is
the mean transit time for delay in active caspase-3 production. $S_{3DC}$ represents an exponent used for modulation of signaling intensity by amplification to compensate for attenuation of signal due to time delays required to characterize observed caspase-3 activity (Sun and Jusko, 1998; Mager and Jusko, 2001). $S_{4PDE}$ represents the coefficient of cell growth inhibition due to pmTOR with DE treatment, and $kd_PDE$ is the cell death rate constant for JIMT-1 cells with DE treatment.

**Triple Combination Therapy of Paclitaxel with DE.** QSP models were built to characterize the effect of PDE and PDE treatments on selected proteins and JIMT-1 cells. PDE refers to concomitant administration of paclitaxel with DE, whereas, PDE refers to paclitaxel administered 24 hours before DE. The final combination QSP models integrated components from the individual agent QSP models with attenuation of feedback activation loops on Src and Akt. The mathematical equations for PDE treatment are as follows:

\[
\frac{dp_{pAkt}}{dt} = K_{mtor} - K_{mtor} \cdot p_{pAkt} (1 - C_E \cdot S_{1E}) \cdot (pAkt^{S_{pAkt}}); \quad p_{pAkt}(0) = 1
\]

\[
\frac{dp_{src}}{dt} = K_{src} - K_{src} \cdot p_{src} (1 - (C_D \cdot S_{1D})); \quad p_{src}(0) = 1
\]

\[
\frac{dp_{Akt}}{dt} = K_{Akt} - K_{Akt} \cdot Akt_{Ic} \cdot Akt_{Ic} \cdot Akt_{Ic}; \quad Akt_{Ic}(0) = 1
\]

\[
\frac{dC_1}{dt} = \left( \frac{1}{r_{CPDE}} \right) \cdot \left( \frac{1}{(1 + (k_{DE \cdot C_{DE}}^{S_{pAkt}})) + (k_{P \cdot C_P}^{S_{pAkt}}))} \right) - K_{C_1}; \quad K_{C_1}(0) = 1
\]

\[
\frac{dC_2}{dt} = \left( \frac{1}{r_{CPDE}} \right) \cdot (K_{C_1} - K_{C_2}); \quad K_{C_2}(0) = 1
\]

\[
\frac{dC_3}{dt} = \left( \frac{1}{r_{CPDE}} \right) \cdot (K_{C_2} - K_{C_3}); \quad K_{C_3}(0) = 1
\]

\[
\frac{dK_{pAkt}}{dt} = K_{pAkt} - K_{pAkt} \cdot p_{pAkt}^{S_{pmTOR}} - K_{pAkt} \cdot p_{pAkt} \cdot p_{pAkt}^{S_{pmTOR}}; \quad p_{pAkt}(0) = 1
\]

\[
\frac{dK_{pSrc}}{dt} = K_{pSrc} - K_{pSrc} \cdot p_{pSrc} \cdot p_{pSrc} + p_{pSrc}; \quad p_{pSrc}(0) = 1
\]

\[
\frac{dK_{pSrc}}{dt} = K_{src} - K_{src} \cdot p_{src} \cdot p_{src} \cdot p_{src}; \quad p_{src}(0) = 1
\]

\[
\frac{dR}{dt} = (pmTOR^{S_{pAkt}}) \cdot k_R - kd_{PDE} \cdot R (cas_3 - 1); \quad R(0) = R_0
\]

where $S_{pAkt}$ represents the effect of pAkt on pmTOR and $S_{pSrc}$ represents the coefficient for feedback activation of pAkt due to pmTOR in the presence of PDE treatment. $S_{3DC}$ represents the coefficient of inhibition of cell growth due to mTOR activity, and $t_{PDE}$ represents the mean transit time for activation of caspase-3. The subscript "PDE" denotes paclitaxel + dasatinib + everolimus-associated terms and parameters.

The mathematical equations for the sequential combination P(DE) are as follows for time < 24 hours:

\[
\frac{d(Akt_{Ic})}{dt} = K_{Akt} \cdot Akt_{Ic} - K_{Akt} \cdot Akt_{Ic} \cdot Akt_{Ic}; \quad Akt_{Ic}(0) = 1
\]

\[
\frac{d(Akt_{Ic})}{dt} = K_{Akt} \cdot Akt_{Ic} - K_{Akt} \cdot Akt_{Ic}; \quad Akt_{Ic}(0) = 1
\]

\[
\frac{d(p_{pAkt})}{dt} = K_{Akt} \cdot Akt_{Ic} \cdot Akt_{Ic} \cdot pre_{pAkt}; \quad pre_{pAkt}(0) = 1
\]

\[
\frac{dK_{M1}}{dt} = \left( \frac{1}{r_{MP}} \right) \cdot (pAkt^{S_{pAkt}}) - K_{M1}; \quad K_{M1}(0) = 1
\]

\[
\frac{dK_{M2}}{dt} = \left( \frac{1}{r_{MP}} \right) \cdot (pAkt^{S_{pAkt}}) - K_{M2}; \quad K_{M2}(0) = 1
\]

\[
\frac{dC_1}{dt} = \left( \frac{1}{r_{CPDE}} \right) \cdot \left( \frac{1}{(1 + (k_{DE \cdot C_{DE}}^{S_{pAkt}})) + (k_{P \cdot C_P}^{S_{pAkt}}))} \right) - K_{C_1}; \quad K_{C_1}(0) = 1
\]
The schematic representation of the mathematical model for the protein signaling networks and cellular response is depicted in Fig. 1.

QSP Models for Protein Dynamics and Cellular Response in the 2D Cell Culture Setting

Protein Dynamics. The protein signaling networks and their impact on JIMT-1 cellular responses were established based on knowledge of the mechanisms of action of each single agent and combinations, and on the pattern of time-course profiles of measured proteins expression from JIMT-1 cells exposed to the various treatments in the 2D cell-culture setting. The established protein network models were used...
to drive cell viability of JIMT-1 cells for all tested treatment arms.

A decline in pAkt and pmTOR expression levels was observed after treatment with paclitaxel, indicating a cell growth inhibitory effect, in addition to activation of caspase-3, leading to an apoptotic effect in JIMT-1 cells (Fig. 2). JIMT-1 cells treatment with dasatinib led to a decline in the expression level of its pharmacological target pSrc, and subsequently a decline in downstream pAkt and pmTOR expression levels (Fig. 2). Hence, pmTOR protein activity was used as the driver of the dasatinib inhibitory effect on JIMT-1 cell growth. For everolimus, a decline in pmTOR protein activity was observed in accordance with its mechanism of action, as represented in Fig. 2. Moreover, a feedback activation of pAkt was also observed in parallel, a phenomenon that is commonly observed in response to pmTOR inhibition in several tumor types through release of feedback inhibition from upstream tyrosine kinase signaling pathways (O’Reilly et al., 2006). In addition, we observed an increase in the expression levels of pSrc in response to everolimus treatment, which also contributed to an increase in pAkt protein expression and cell growth (Fig. 2). Notably, we did not observe any significant increase in caspase-3 activity for dasatinib or everolimus as single agents, indicating their cytostatic role in the HER2-therapy resistant JIMT-1 cell line.

Figure 3 depicts the temporal changes in the signaling protein levels compared with control for all examined combination therapies, including DE, PDE (simultaneous), and P(DE) (sequential). The dual and triple combination (DE, PDE, and P(DE)) model structures were built in a hierarchical manner by including components from the individual agents’ model structures. For example, the DE model was an integration of the dasatinib and everolimus single-agent models with suppression of the pSrc feedback activation loop and attenuation of the pAkt feedback activation loop when the two drugs were administered simultaneously. For the P(DE) sequential model, components of the paclitaxel model were included at times earlier than 24 hours, while components of the PDE model were used at times beyond 24 hours when DE treatment was administered.

In the DE combination arm, both pharmacological targets for dasatinib (pSrc) and everolimus (pmTOR) declined over time. Similarly, a decline to levels below the initial baseline value of the pAkt protein was observed, confirming the hypothesis that dasatinib counterregulates the feedback activation loop of pAkt upon inhibition of pmTOR by everolimus.

In the DE-perturbed protein model, components of the dasatinib and everolimus single-agents’ protein models were integrated and their parameters were fixed in the combination model to test their ability at capturing protein trends in the DE treatment arm. The only parameter that was estimated in this integrated model was the coefficient for effect of pAkt on pmTOR (S1DE), which was comparable with the corresponding coefficient in the everolimus single-agent model (S2E): 1.36 ± 0.46 versus 1.42 ± 0.11 (Table 1). This parameter was estimated and compared with the everolimus arm because the two transit compartments describing the delay in effect on pmTOR due to pAkt in the dasatinib model (K31 and K32) were eliminated in this model, as there was direct inhibition of pmTOR due to everolimus. Additionally, the feedback activation loop from pmTOR to pSrc was also eliminated in this model because the pSrc levels were comparable to the dasatinib single-agent arm (Figs. 2 and 3), indicating that dasatinib completely suppresses everolimus-mediated feedback activation of pSrc. The trends in protein dynamics for the DE arm were captured reasonably well, thus qualifying our dasatinib and everolimus single-agent models. Finally, a slight elevation in the activity of caspase-3 protein (apoptosis marker) was also observed in the DE dual treatment arm (Fig. 3), which contributed to cell death in our cell viability model, in conjunction with the growth inhibitory effect due to pmTOR.

The simultaneous (PDE) and sequential (P(DE)) combination treatment models invoked features of the single agents and DE dual therapy models. There was a decline in pSrc, pAkt, and pmTOR expression levels observed for both treatment arms, with distinct phases of protein signaling before and after 24 hours as reflected in our observed data and model fittings for the sequential treatment arm (Fig. 3). Moreover, active caspase-3 levels were elevated above baseline with a relatively larger magnitude as compared with the DE dual therapy (~1.5 times) and paclitaxel treatment alone (~1.2 times) for both triple-agent combinations (Figs. 2 and 3). Additionally, in the PDE treatment arm, the onset of caspase-3 activation was observed to be earlier (24 hours) in comparison with the DE and P(DE) treatment arms (48 hours; Fig. 3), due to the combined synergistic activity of all three agents simultaneously.

**Cellular Response.** The established models for protein networks were able to capture the observed data relatively well and were used as drivers to characterize JIMT-1 cell viability (cellular response) over time for the various treatment arms.

Figure 4 represents JIMT-1 cellular response to all treatment arms. For paclitaxel, almost 70% of cell killing from baseline was observed at 72 hours, indicating its significantly cytotoxic role in causing inhibition of cell growth and stimulation of cell death in JIMT-1 cells. A decline in the viability of JIMT-1 cells was observed in the dasatinib treatment arm as compared to the control arm as well. This was captured with an inhibitory effect of the pmTOR protein on cell growth through the model parameter S4D (eq. 22).

In contrast, JIMT-1 cell viability did not decline in the everolimus treatment arm as compared with control. This result suggests the existence of a feedback activation loop from pmTOR to pAkt via proteins of key cell survival and growth pathways (S6K, IGF-1R, PI3K, Src), which confers very weak sensitivity of JIMT-1 cells to everolimus.

For the DE treatment arm, we observed a higher magnitude of cell killing as compared with either agent alone, due to attenuation of the feedback activation loop of pAkt in the presence of this dual combination. However, 100% cell killing was not achieved, due to the predominantly cytostatic effect of this combination.

For both the triple combination arms (PDE and P(DE)), the cytotoxic effects reached 100% killing of JIMT-1 cells by 96 hours, indicating superior efficacy of the triple combination compared with the single-agent arms and to DE therapy. Not surprisingly, in the (PDE) arm, the DE treatment after paclitaxel administration led to a slight delay (of approximately 24 hours) in JIMT-1 cell death as compared with the PDE simultaneous treatment arm (Fig. 4).

The model parameters obtained from modeling all the observed data collected in the 2D cell culture setting are
<table>
<thead>
<tr>
<th>Parameter (Unit)</th>
<th>Definition</th>
<th>Estimate</th>
<th>Relative S.E. (% RSE)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Turnover of measured signaling proteins (h⁻¹)</td>
<td>Turnover rate constant for pSrc</td>
<td>0.257</td>
<td>17</td>
</tr>
<tr>
<td>$K_{src}$</td>
<td>Turnover rate constant for pAkt</td>
<td>3.37</td>
<td>94</td>
</tr>
<tr>
<td>$K_{Akt}$</td>
<td>Turnover rate constant for pmTOR</td>
<td>0.094</td>
<td>22</td>
</tr>
<tr>
<td>$K_{pmTOR}$</td>
<td>Turnover rate constant for active caspase-3</td>
<td>0.02</td>
<td>12</td>
</tr>
<tr>
<td>$K_{casp}$</td>
<td>Turnover rate constant for pAkt inhibitory compartment</td>
<td>0.708</td>
<td>26</td>
</tr>
<tr>
<td>$K_{inh}$ (h⁻¹)</td>
<td>Coefficient of pAkt inhibition by paclitaxel</td>
<td>0.173</td>
<td>9</td>
</tr>
<tr>
<td>$I_p$ (× 10⁻⁷ nM⁻¹)</td>
<td>Coefficient of pAkt inhibition by paclitaxel due to pmTOR</td>
<td>0.567</td>
<td>11</td>
</tr>
<tr>
<td>$I_{pdT}$ (× 10⁻¹ h⁻¹)</td>
<td>Coefficient of inhibition of pmTOR due to paclitaxel</td>
<td>1E-05</td>
<td>—</td>
</tr>
<tr>
<td>$S_1p$</td>
<td>Transit rate constant for activation of caspase-3 due to paclitaxel</td>
<td>0.697</td>
<td>16</td>
</tr>
<tr>
<td>$S_3p$</td>
<td>Slope for activation of caspase-3</td>
<td>1E-05</td>
<td>—</td>
</tr>
<tr>
<td>$S_2p$</td>
<td>Exponent for activation of caspase-3</td>
<td>0.445</td>
<td>18</td>
</tr>
<tr>
<td>$S_4p$</td>
<td>Feedback coefficient for active caspase-3</td>
<td>15.3</td>
<td>66</td>
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**Paclitaxel model parameters: 2D system**

<table>
<thead>
<tr>
<th>Parameter (Unit)</th>
<th>Definition</th>
<th>Estimate</th>
<th>Relative S.E. (% RSE)</th>
</tr>
</thead>
<tbody>
<tr>
<td>$K_{inh}$ (h⁻¹)</td>
<td>Net growth rate constant for JIMT-1 cells</td>
<td>0.089</td>
<td>5</td>
</tr>
<tr>
<td>$I_p$ (× 10⁻¹ h⁻¹)</td>
<td>Death rate constant for JIMT-1 cells due to paclitaxel</td>
<td>0.123</td>
<td>3</td>
</tr>
<tr>
<td>$I_{pdT}$ (× 10⁻¹ h⁻¹)</td>
<td>Coefficient of pAkt inhibition by paclitaxel</td>
<td>0.181</td>
<td>2</td>
</tr>
<tr>
<td>$S_2p$</td>
<td>Coefficient of inhibition of pAkt due to pSrc</td>
<td>0.293</td>
<td>28</td>
</tr>
<tr>
<td>$S_3p$</td>
<td>Transit rate constant for effect of pAkt on pmTOR due to dasatinib</td>
<td>0.701</td>
<td>40</td>
</tr>
<tr>
<td>$S_4p$</td>
<td>Coefficient of inhibition of pmTOR</td>
<td>4.76</td>
<td>41</td>
</tr>
<tr>
<td>$S_1p$</td>
<td>Net growth rate constant for JIMT-1 cells</td>
<td>0.089</td>
<td>5</td>
</tr>
<tr>
<td>$S_4p$</td>
<td>Coefficient of dasatinib-mediated cell growth inhibition due to pmTOR</td>
<td>10.9</td>
<td>36</td>
</tr>
</tbody>
</table>

**Dasatinib model parameters: 2D system**

<table>
<thead>
<tr>
<th>Parameter (Unit)</th>
<th>Definition</th>
<th>Estimate</th>
<th>Relative S.E. (% RSE)</th>
</tr>
</thead>
<tbody>
<tr>
<td>$K_{inh}$ (h⁻¹)</td>
<td>Coefficient of pAkt inhibition by dasatinib</td>
<td>0.151</td>
<td>4</td>
</tr>
<tr>
<td>$I_p$ (× 10⁻¹ nM⁻¹)</td>
<td>Coefficient of effect of pAkt on pmTOR</td>
<td>1.42</td>
<td>8</td>
</tr>
<tr>
<td>$I_{pdT}$ (× 10⁻¹ h⁻¹)</td>
<td>Transit rate constant for feedback activation effect of pmTOR on pSrc</td>
<td>1</td>
<td>66</td>
</tr>
<tr>
<td>$S_2p$</td>
<td>Coefficient of feedback activation of pSrc due to pmTOR</td>
<td>7.27</td>
<td>65</td>
</tr>
<tr>
<td>$S_3p$</td>
<td>Coefficient of feedback activation of pAkt due to pmTOR</td>
<td>1E-05</td>
<td>—</td>
</tr>
<tr>
<td>$S_4p$</td>
<td>Coefficient of effect of pSrc due to pmTOR</td>
<td>1E-05</td>
<td>—</td>
</tr>
<tr>
<td>$S_1p$</td>
<td>Net growth rate constant for JIMT-1 cells</td>
<td>0.089</td>
<td>5</td>
</tr>
<tr>
<td>$S_4p$</td>
<td>Coefficient of everolimus-mediated cell growth inhibition due to pmTOR</td>
<td>0.001</td>
<td>—</td>
</tr>
</tbody>
</table>

**Everolimus model parameters: 2D system**

<table>
<thead>
<tr>
<th>Parameter (Unit)</th>
<th>Definition</th>
<th>Estimate</th>
<th>Relative S.E. (% RSE)</th>
</tr>
</thead>
<tbody>
<tr>
<td>$S_1p$ (× 10⁻¹ nM⁻¹)</td>
<td>Coefficient of pmTOR inhibition by everolimus</td>
<td>0.151</td>
<td>4</td>
</tr>
<tr>
<td>$S_2p$</td>
<td>Coefficient of effect of pAkt on pmTOR</td>
<td>1.42</td>
<td>8</td>
</tr>
<tr>
<td>$S_3p$</td>
<td>Transit rate constant for activation of caspase-3 due to dasatinib + everolimus (P+D+E)</td>
<td>0.996</td>
<td>2</td>
</tr>
<tr>
<td>$S_4p$</td>
<td>Transit rate constant for activation of caspase-3 due to dasatinib</td>
<td>1</td>
<td>66</td>
</tr>
<tr>
<td>$S_3p$</td>
<td>Exponent for activation of caspase-3</td>
<td>2.06</td>
<td>10</td>
</tr>
<tr>
<td>$S_4p$</td>
<td>Net growth rate constant for JIMT-1 cells</td>
<td>0.009</td>
<td>5</td>
</tr>
<tr>
<td>$S_1p$</td>
<td>Coefficient of D+E-mediated cell growth inhibition due to pmTOR</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>$S_4p$</td>
<td>Death rate constant for JIMT-1 cells due to D+E</td>
<td>0.124</td>
<td>10</td>
</tr>
</tbody>
</table>

**Dasatinib + everolimus model parameters: 2D system**

<table>
<thead>
<tr>
<th>Parameter (Unit)</th>
<th>Definition</th>
<th>Estimate</th>
<th>Relative S.E. (% RSE)</th>
</tr>
</thead>
<tbody>
<tr>
<td>$K_{inh}$ (h⁻¹)</td>
<td>Coefficient of effect of pAkt on pmTOR</td>
<td>1.36</td>
<td>34</td>
</tr>
<tr>
<td>$I_p$ (× 10⁻¹ nM⁻¹)</td>
<td>Transit rate constant for activation of caspase-3 due to dasatinib + everolimus (P+D+E)</td>
<td>0.996</td>
<td>2</td>
</tr>
<tr>
<td>$I_{pdT}$ (× 10⁻¹ h⁻¹)</td>
<td>Transit rate constant for activation of caspase-3</td>
<td>1</td>
<td>66</td>
</tr>
<tr>
<td>$S_2p$</td>
<td>Exponent for activation of caspase-3</td>
<td>2.06</td>
<td>10</td>
</tr>
<tr>
<td>$S_3p$</td>
<td>Net growth rate constant for JIMT-1 cells</td>
<td>0.009</td>
<td>5</td>
</tr>
<tr>
<td>$S_4p$</td>
<td>Coefficient of D+E-mediated cell growth inhibition due to pmTOR</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>$S_1p$</td>
<td>Death rate constant for JIMT-1 cells due to D+E</td>
<td>0.124</td>
<td>10</td>
</tr>
</tbody>
</table>

**Paclitaxel + dasatinib + everolimus model parameters: 2D system**

<table>
<thead>
<tr>
<th>Parameter (Unit)</th>
<th>Definition</th>
<th>Estimate</th>
<th>Relative S.E. (% RSE)</th>
</tr>
</thead>
<tbody>
<tr>
<td>$S_1p$</td>
<td>Coefficient of effect of pAkt on pmTOR</td>
<td>4.71</td>
<td>14</td>
</tr>
<tr>
<td>$S_2p$</td>
<td>Coefficient for feedback effect on pAkt due to pmTOR</td>
<td>1</td>
<td>—</td>
</tr>
<tr>
<td>$S_3p$</td>
<td>Transit rate constant for activation of caspase-3 due to paclitaxel + dasatinib + everolimus (P+D+E)</td>
<td>0.128</td>
<td>29</td>
</tr>
<tr>
<td>$S_4p$</td>
<td>Net growth rate constant for JIMT-1 cells</td>
<td>0.009</td>
<td>6</td>
</tr>
<tr>
<td>$S_1p$</td>
<td>Coefficient of P+D+E-mediated cell growth inhibition due to pmTOR</td>
<td>1</td>
<td>66</td>
</tr>
<tr>
<td>$S_4p$</td>
<td>Death rate constant for JIMT-1 cells due to P+D+E</td>
<td>0.786</td>
<td>3</td>
</tr>
</tbody>
</table>

**Paclitaxel + (dasatinib + everolimus) sequential treatment model parameters: 2D system**

<table>
<thead>
<tr>
<th>Parameter (Unit)</th>
<th>Definition</th>
<th>Estimate</th>
<th>Relative S.E. (% RSE)</th>
</tr>
</thead>
<tbody>
<tr>
<td>$S_1p$</td>
<td>Coefficient for feedback effect on pAkt due to pmTOR</td>
<td>0.0943</td>
<td>17</td>
</tr>
<tr>
<td>$S_2p$</td>
<td>Coefficient of effect of pAkt on pmTOR</td>
<td>1.01</td>
<td>27</td>
</tr>
<tr>
<td>$S_3p$</td>
<td>Net growth rate constant for JIMT-1 cells</td>
<td>0.009</td>
<td>6</td>
</tr>
<tr>
<td>$S_4p$</td>
<td>Coefficient of paclitaxel-mediated cell growth inhibition due to pmTOR (before 24 h)</td>
<td>1</td>
<td>66</td>
</tr>
<tr>
<td>$S_3p$</td>
<td>Coefficient of PDE mediated cell growth inhibition due to pmTOR (after 24 h)</td>
<td>1</td>
<td>66</td>
</tr>
<tr>
<td>$S_4p$</td>
<td>Death rate constant for JIMT-1 cells due to paclitaxel (before 24 h)</td>
<td>0.774</td>
<td>4</td>
</tr>
<tr>
<td>$S_4p$</td>
<td>Death rate constant for JIMT-1 cells due to PDE (after 24 h)</td>
<td>0.124</td>
<td>10</td>
</tr>
</tbody>
</table>
summarized in Table 1. The parameters for all models (single and combination therapies) were estimated with reasonable precision. Certain parameters in the models were fixed to improve model stability. For example, coefficients for the effect of certain proteins on others were fixed to 1, as direct/inverse proportionality (as applicable) was sufficient to characterize these effects. Fixing these parameters did not have any significant impact on model performance as it did not change parameter estimates, nor did it compromise the precision of the remaining estimated parameters. In the case of everolimus treatment, because it had practically no effect on JIMT-1 cell viability, the inhibitory coefficient for cell growth due to mTOR protein activity ($S_{6E}$) was fixed to a very low value of 0.001 (Table 1), as identified from trial and error. No change in the effect on cell growth inhibition was observed at magnitudes lower than this. Overall, the established models could adequately capture the observed data, with reasonable precision on parameter estimates.

**TABLE 1—Continued**

<table>
<thead>
<tr>
<th>Parameter (Unit)</th>
<th>Definition</th>
<th>Estimate</th>
<th>Relative S.E. (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>$\lambda_0$ ($\times 10^{-2}$ h$^{-1}$)</td>
<td>Rate constant for exponential growth of JIMT-1 cells</td>
<td>0.77</td>
<td>5</td>
</tr>
<tr>
<td>$\lambda_1$ (h$^{-1}$)</td>
<td>Rate constant for linear growth of JIMT-1 cells</td>
<td>7.41</td>
<td>59</td>
</tr>
<tr>
<td>$c_p$</td>
<td>Switching factor between exponential and linear growth</td>
<td>2$^{0.74}$</td>
<td>—</td>
</tr>
<tr>
<td>$\beta_p$ (h$^{-1}$)</td>
<td>Coefficient for JIMT-1 growth inhibition due to pmTOR (before 24 h)</td>
<td>1</td>
<td>23</td>
</tr>
<tr>
<td>$\beta_{PD}$ (h$^{-1}$)</td>
<td>Death rate constant for JIMT-1 due to caspase-3 activity (before 24 h)</td>
<td>0.132</td>
<td>3</td>
</tr>
<tr>
<td>$\beta_{PD}$ ($\times 10^{-1}$ h$^{-1}$)</td>
<td>Coefficient for JIMT-1 growth inhibition due to pmTOR (after 24 h)</td>
<td>1</td>
<td>23</td>
</tr>
<tr>
<td>$\beta_{PD}$ (h$^{-1}$)</td>
<td>Death rate constant for JIMT-1 due to caspase-3 activity (after 24 h)</td>
<td>0.841</td>
<td>3</td>
</tr>
</tbody>
</table>

aCoefficients were fixed to 1 to indicate a direct/inverse proportionality (as applicable) to the actual magnitude of the activity of a particular protein, without the need of a power coefficient.
bSlopes (proportionality constants) were fixed to 1 as the exponents used to characterize activation of caspase-3 due to drug concentrations alone were sufficient.
cCoefficient fixed to a relatively low magnitude to indicate minimal effect of activity of a protein. Any decrease in magnitude of this coefficient did not have an impact on model fittings.
dFixed factor to allow for a smooth switch from exponential to linear cell growth (Magni et al., 2006).

Fig. 4. Time course of cellular viability response after continuous exposure of JIMT-1 cells to treatments with paclitaxel (50 nM), dasatinib (50 nM), everolimus (50 nM), DE (50 nM each), PDE (50 nM each), and P(DE) (50 nM each). Black circles represent observed data under control conditions, and red circles represent observed data under treatment conditions. Solid lines represent model fittings.
QSP and PK/PD Models for Cellular Responses in the 3DD Cell Culture Setting

Figure 5 depicts the time-course profiles of JIMT-1 cell viability in the 3DD cell culture setting for actual measurements and model fittings of control and P(DE) treatment arms, along with simulated response profiles for various dosing regimens of single and combination therapies. A hybrid exponential and linear cell growth model could adequately describe the growth of JIMT-1 cells in the absence of treatment in the 3DD system, whereas in a 2D cell culture setting, an exponential model was sufficient to characterize JIMT-1 cell growth. The rate constants for the exponential cell growth in 2D and 3DD settings were similar in magnitude and determined at 0.009 versus 0.008 hour⁻¹ in 2D versus 3DD (Table 1). This result supports at least in part the translatability of findings for JIMT-1 cells from a 2D to 3DD cell culture setting.

Furthermore, the time-course of JIMT-1 cells viability in the 3DD cell culture system was reasonably captured for both treatment arms, control and sequential triple combination, using our established protein network model as a driver for JIMT-1 cellular response (black and red solid lines). The coefficients for inhibition of cell growth due to mTOR activity and stimulation of cell death due to caspase-3 activity in the 2D and 3DD systems for the sequential treatment arm (Table 1) were compared. The cell growth inhibition and cell death coefficients were not significantly different between the two settings (with ratios of 1 and 1.07, respectively), indicating translatability of our 2D QSP models to the 3DD system. These ratios were used as scaling factors to simulate the time-course profiles of JIMT-1 cells viability in the 3DD setting for the remaining treatment arms.

The dasatinib (green) and everolimus (blue) treatment arms demonstrated a marginal decrease in JIMT-1 cell viability from the control, mainly due to their cytostatic effects, whereas the DE treatment arm (orange) showed significantly higher cell killing than either agent alone. The simulated time-course profiles of JIMT-1 cell killing were more noticeable in the single-agent paclitaxel treatment arms when it was administered at a concentration regimen mimicking dasatinib and everolimus (50 nM for 72 hours followed by washout; yellow) and administered as per the 3DD experimental study design (3-hour short-term infusion; pink).

A comparison of the simulated response of JIMT-1 cells to PDE (purple dashed) and P(DE) (red dashed) treatments with all three drugs administered at the same dose levels (50 nM for 72 hours followed by washout) showed a comparable magnitude of cell killing (~1.2-fold greater maximum cell killing with the PDE simultaneous arm as compared with the P(DE) sequential arm), with a cell response approaching similar magnitudes at later time points (beyond ~200 hours). This was an expected finding as the sequential combination causes a delay in onset of JIMT-1 cell death due to dose staggering, as opposed to the simultaneous regimen with all three agents exerting cytostatic and/or cytotoxic effects through distinct mechanisms of action at the same time. A similar phenomenon was also observed in the 2D system (Fig. 4), thus corroborating our findings from the 3DD simulations and providing confidence in our scaled-up QSP-PK/PD model. Moreover, these results suggest potential for dose staggering of P and DE while achieving similar efficacy as that of the PDE simultaneous treatment arm in HER2-therapy resistant BC.

Figure 6 depicts the simulated responses of JIMT-1 viability for various treatment schedules (Fig. 6A) and over a long-term treatment period of 50 days (Fig. 6B). The additional simulated treatment schedules included P(DE) sequential treatment with interdose intervals of 24, 48, 72, 96, and 120 hours, with all three drugs administered at the same dose levels (50 nM for 72 hours followed by washout), and PDE and P(DE) (24-hour interval) treatment combinations at half-dose levels (25 nM for 72 hours followed by washout). A slight delay was observed in the time to tumor regrowth (TTR) of tumor cells in the P(DE) regimen for the intervals of 48 and 72 hours (Fig. 6A, green and yellow dashed profiles) as compared with the PDE simultaneous regimen (purple dashed profile) although the magnitude of tumor cell killing was comparable. Beyond interdose intervals of 72 hours, however, the P(DE) sequential treatment regimens were not as efficacious as the simultaneous PDE regimen (96-hour interval; blue dashed profile and 120-hour interval; orange dashed profile), indicating almost complete washout of paclitaxel before DE administration and thus minimizing overlapping synergistic effects of the three agents. Nonetheless, the TTR was significantly delayed as compared with paclitaxel or DE treatment alone. Notably, despite reduction in the dose levels by half, the PDE and P(DE) triple combinations had significantly higher efficacy in JIMT-1 cells as compared with the single- and dual-agent arms (black and gray dashed profiles).

Figure 6B represents simulated JIMT-1 cell growth profiles over a longer period of time (50 days), until all growth curves became nearly parallel to one another. The calculated TTR of tumor cells exposed to the various dosing regimens is summarized in Table 2. The individual agents dasatinib, everolimus, and paclitaxel and the dual-agent (DE) treatment arm had a relatively shorter TTR as compared with the PDE triple combination regimens. The P(DE) treatment arms with 48 and 72 hours interdose intervals showed the longest TTR.
without loss of efficacy as compared with the PDE treatment, suggesting a synergistic effect of all three agents in this time window. Moreover, a reduction in dose levels by half in the triple combinations yielded significantly higher efficacy in JIMT-1 cells as compared with the single agents, further corroborating the synergistic effect of these three drugs in overcoming resistance to HER2 and mTOR therapies in BC.

Discussion

HER2+ BC represents 25% of all BC cases and is associated with poor prognosis, high incidence of metastases, and low survival rates (Slamon et al., 1987; Burstein, 2005; Kennecke et al., 2010). Despite improved treatment outcomes with HER2-targeted therapies such as trastuzumab and lapatinib, innate and acquired resistance to therapy remains a major unmet medical need (Pohlmann et al., 2009; Arteaga et al., 2011; Zhang et al., 2017). Here, we propose the use of a triple combination therapy comprising two targeted small-molecule agents, dasatinib and everolimus, in combination with the standard cytotoxic agent paclitaxel to overcome resistance to HER2 therapy in HER2+ BC.

Dasatinib and everolimus are inhibitors of Src and mTOR, two key signaling proteins of the PI3K/Akt/mTOR pathway, downstream of several transmembrane tyrosine kinase receptors involved in cell growth and proliferation. The overactivation of Src and mTOR proteins has been implicated in nearly 50% of HER2+ BC cases (Yori et al., 2014). This medical challenge presents an opportunity for achieving enhanced cytostasis through dual inhibition of these proteins. Moreover, preclinical studies with HER2+ BC cell lines and animal models have showed the benefit of dual inhibition of Src and mTOR at intensifying cell-growth inhibition (Park et al., 2012; Yori et al., 2014). Taking into account the benefit of combining dasatinib and everolimus treatment of enhanced cell-growth inhibition, we also added a third agent to the combination, paclitaxel, as an inducer of apoptosis to augment the overall cytotoxic effect of our combination therapy.

In the present work, we tested the potential of our proposed triple combination therapy at overcoming resistance to HER2 therapy in the HER2-therapy resistant cell line JIMT-1. A combined experimental and computational QSP approach was successfully applied for control, single, and combination therapies, where temporal changes in molecular (protein signaling) and cellular responses were measured in 2D and 3D cell culture systems and were successfully characterized with QSP models.

In the 2D in vitro setting, dasatinib as a single agent demonstrated a cytostatic effect through inhibition of the activity of Src protein followed by a decline in the Akt and mTOR protein activities, which led to inhibition of JIMT-1 cellular growth. Everolimus as a single agent, was inefficacious at inhibiting JIMT-1 cell growth at the concentrations tested, likely due to feedback activation of Src and Akt protein activities. Similar results have been previously reported on the weak sensitivity of JIMT-1 cells to everolimus (Dragowska et al., 2011). The combination of both agents successfully suppressed this feedback activation loop, leading to a much higher cytostatic effect than either agent alone. This was an expected finding because both agents target proteins in the aberrantly activated Akt/mTOR pathway in HER2-resistant BC cells through distinct mechanisms of action that are also complementary to each other. Moreover, a study reported on other BC cell lines having feedback activation of Akt, yielded similar results upon treatment with a combination of dasatinib and rapamycin, an mTOR inhibitor (Yori et al., 2014).

The single agent paclitaxel showed both cytostatic and cytotoxic effects on JIMT-1 cells. This result is consistent with the mechanism of action of paclitaxel, causing microtubule disarray and cell cycle arrest followed by apoptosis (Horwitz, 1994; Wang et al., 2000). Furthermore, the cytostatic effect due to paclitaxel can also be attributed to inhibition of the central cellular signaling and growth protein Akt via dephosphorylation, as observed with our experimental data.
(Fig. 2) and in accordance with literature findings (MacKeigan et al., 2002; Sutters et al., 2006).

In the 2D setting, both triple combinations PDE (simultaneous) and P(DE) (sequential) showed strong cytotoxic effects on JIMT-1 cells, reaching 100% cell killing at 96 hours. Despite these comparable cytotoxicity effects of PDE and P(DE), only P(DE) was further examined in our novel 3DD cell culture system (Ande et al., 2018). The rationale was 2-fold. First, prior treatment with paclitaxel is hypothesized to be particularly useful in the in vivo and/or clinical setting due to its tumor priming effect, through which it allows penetration of targeted agents and nanomedicines into the inner layers of solid tumors (Lu et al., 2007). Second, dose staggering of paclitaxel and the DE combination may provide a clinical safety benefit by reducing the occurrence and/or intensity of potential common adverse events of these drugs, particularly hematologic toxicities such as neutropenia and thrombocytopenia (Fornier et al., 2011; Ocana et al., 2017; Toi et al., 2017).

Our experimental results in the 3DD cell culture system showed that P(DE) treatment substantially blocked (8.5-fold compared with control) the growth of JIMT-1 cells in a durable manner lasting beyond cessation of therapy (up to 15 days). The latter result would not be possible to obtain from a 2D cell culture experiment due to the relatively short maximum duration of study design (~5 days) in this setting. Hence, our novel 3DD cell culture system presents several advantages over the traditional 2D cell culture system. First, it allows serial sampling of cells over a relatively long period of time (2 or more weeks) for measurement of cellular response without significant perturbations in the system. Second, the system provides a three-dimensional environment for the growth of adherent cells, which is closer to an in vivo tumor environment than a standard 2D cell culture system. Third, it permits flexibility in adjusting the drugs’ dosing regimens to mimic animal or human PK of drugs. This was used in our 3DD experiments where the PK of paclitaxel was simulated along with a constant exposure to DE combination therapy. The subsequently measured PK and JIMT-1 cellular responses were well characterized with our scaled up QSP-PK/PD model.

The calculated scaling factors (from 2D to 3DD) and the initial JIMT-1 growth rate constants indicated similarities between both systems and supported translation and applicability of our QSP models from the 2D setting to the 3DD setting. Our simulations of the simultaneous (PDE) and sequential (P(DE)) triple combinations (interdose intervals: 24, 48, and 72 hours) in the 3DD setting demonstrated similar magnitudes of cytotoxic effects, albeit with a slight delay in the onset of tumor cells regrowth for the P(DE) treatment as predicted by our long-term model simulations, thus providing an opportunity for dose staggering of P and DE. Moreover, despite dose reduction of the triple combinations, significant efficacy against JIMT-1 cells was retained, as suggested by our model simulations, corroborating the synergistic effect of all three agents. The synergism can be largely attributed to DE-mediated targeted inhibition of the crucial PI3K/Akt/mTOR axis, which is aberrantly activated in HER2-therapy resistant BC, making the cells particularly susceptible to this treatment combination. Furthermore, this can provide opportunities to reduce individual dose levels for all three agents when used in combination, minimizing potential occurrence of overlapping side effects.

In summary, the superior efficacy of our proposed triple combination therapy of paclitaxel with dasatinib and everolimus at overcoming resistance to HER2-targeted therapies in BC is established in vitro. Our novel 3DD cell culture system allowed us to mimic the PK of the three agents, which influenced the dynamic changes in protein signaling and cellular responses of JIMT-1 cells. The final established QSP-PK/PD models were able to characterize cell viability in the 3DD system relatively well under the given treatment conditions, and were able to predict cellular responses to various other dosing regimens over a relatively long period of time. Thus, our approach of combining the use of our novel
3DD cell culture system with the aid of QSP-PK/PD as a mathematical modeling and simulation tool has potential application for the screening of successful combination therapies in oncology and may serve as a surrogate for animal studies that may not be feasible in some cases and/or might not be representative of human systems.

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Authorship Contributions

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Contributed new reagents or analytic tools: Vaidya, Ande, Ait-Oudhia.

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