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THE PROTON-COUPLED FOLATE TRANSPORTER: BIOLOGY AND THERAPEUTIC APPLICATIONS TO CANCER

by

SITA KUGEL DESMOULIN

DISSERTATION

Submitted to the Graduate School

of Wayne State University,

Detroit, Michigan

in partial fulfillment of the requirements

for the degree of

DOCTOR OF PHILOSOPHY

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Approved by:

Advisor

Date



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DEDICATION

This dissertation is lovingly dedicated to my family.

To my mother, Monica Kugel, whom I love and admire more than anyone else in the world. Your strength, integrity and enormous capacity to love are my permanent support and my life's inspiration.

To my wonderful bothers Kunal, Nitya and Harish, who bring a continuous source of pride and happiness to my life.

And lastly, to the memory of my father, Helmut Kugel (1938 -1992) who instilled in me a strong work ethic and the feeling of satisfaction that comes from doing your job well, no matter what that job is. His memory motivates me and reminds me daily of the importance of cancer research.



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LIST OF ABBREVIATIONS

Ade	Adenosine
AICAR	5-amino-4-imidazolecarboxamide ribonucleotide
AICARFTase	5-amino-4-imidazolecarboxamide ribonucleotide formyltransferase
AIRS	Aminoimidazole ribonucleotide synthase
АМРК	AMP-activated protein kinase
ALL	Acute lymphoblastic leukemia
AML	Acute myelogenous leukemia
AMT	Aminopterin
AFB	Anion-free buffer
APRT	Adenine phosphoribosyl transferase
CAIRS	Carboxyaminoimidazole ribonucleotide synthase
CBE	Cl ⁻ /HCO3 ⁻ exchanger
СНО	Chinese hamster ovary cells
CML	Chronic myelogenous
Cmpd	Compound
CK2	Casein kinase 2
DDATHF	6R diastereomer of 5,10-dideazatetrahydrofolate
dFBS	Dialyzed fetal bovine serum
DHF	Dihydrofolate
DHFR	Dihydrofolate reductase
DPBS	Dulbecco's phosphate-buffered saline
dTMP	Thymidylate



dUMP	Deoxyuridine monophosphate
EL	Extracellular loop
FCCP	Carbonylcyanide p-trifluoromethoxyphenylhydrazone
FITC	Fluorescein isothiocyanate
5-CHO-THF	5-formyl-tetrahydrofolate
FPGS	Folylpoly- γ -glutamate synthase
FR	Folate receptor
GAPDH	Glyceraldehyde-3-phosphate dehydrogenase
GAR	Glycinamide ribonucleotide
GARFTase	Glycinamide ribonucleotide formyltransferase
GARS	Glycinamide ribonucleotide synthase
GlpT	Glycerol-3-phosphate transporter
GPAT	Glutamine phosphoribosylpyrophosphate amidotransferase
НА	Hemagglutinin
HEPES	4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid
HFM	Hereditary folate malabsorption
HPLC	High performance liquid chromatography
HPRT	Hypoxanthine phosphoribosyl transferase
IC ₅₀	Fifty percent inhibitory concentration
IL	Intracellular loop
IMP	Inosine monophosphate
ІМРСН	Inosine monophosphate cyclohydrolase
LacY	Lactose permease



LMX	Lometrexol
МСТ	Monocarboxylate-H ⁺ efflux symporter
MEM	Minimal essential media
MES	4-morphilinopropane sulfonic acid
MeOH	Methanol
MRS	Magnetic resonance spectroscopy
MRI	Magnetic resonance imaging
mSHMT	Mitochondrial serine hydroxymethyltransferase
MTAP	Methylthioadenosine phosphorylase
MTHFD	5,10-methylene tetrahydrofolate dehydrogenase
MTHFR	5,10-methylene tetrahydrofolate reductase
MTHFS	Methenyl tetrahydrofolate synthase
MTX	Methotrexate
NCI	National Cancer Institute
ND	Not determined
NHE1	Na ⁺ /H ⁺ exchanger
NRF-1	Nuclear respiratory factor 1
NS	Non-specific
NSCLC	Non-small cell lung cancer
OATP	Organic anion transporting polypeptides
PABA	p-aminobenzoic acid
PAICS	Phosphoribosyl aminoimidazole carboxylase and phosphoribosyl
	aminoimidazole succinocarboxamide synthetase



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PCFT	Proton-coupled folate transporter
PDX	Pralatrexate
PET	Positron emission tomography
PG	Polyglutamate
pHLIP	pH (low) insertion peptide
PI	Propidium iodide
PIPES	Piperazine-N,N'-bis(2-ethanesulfonic acid)
PMX	Pemetrexed
PNGase	Peptide: N-Glycosidase
PRPP	Phosphoribosyl pyrophosphate
PVDF	Polyvinylidene difluoride
RFC	Reduced folate carrier
RTX	Raltitrexed
RT-PCR	Reverse transcription-PCR
RXRα	Retinoid X receptor-a
SAICARS	Succinylaminoimidazolcarboxamide ribonucleotide synthase
SAM	S-adenosylmethionine
SAR	Structure activity relationship
SCID	Severe combined immunodeficient
SEM	Standard error of the mean
TCA	Trichloroacetic acid
Thd	Thymidine
THF	Tetrahydrofolate



TMD	Transmembrane domain
TS	Thymidylate synthase
TSC2	Tuberous sclerosis complex 2
VDR	Vitamin D receptor
Vitamin D3	1,25-dihydroxyvitamin D3
WT	Wild-type
YFP	Yellow fluorescent protein
ZMP	5-amino-4-imidazolecarboxamide ribotide



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CHAPTER 1

INTRODUCTION

1.1 General Introduction.

Proliferating tumor cells have unique metabolic requirements characterized by enhanced cell-autonomous nutrient uptake and reorganization of metabolic pathways to support the biosynthesis of macromolecules needed for cell growth and division. This includes the folate-dependent *de novo* synthesis of purines and thymidylate for the synthesis of DNA and RNA.

Early observations made by Farber and colleagues established the importance of folate metabolism in cancer progression. Specifically, folic acid supplementation was found to stimulate leukemic cell growth and enhance disease progression among children with acute lymphoblastic leukemia (ALL) (Farber et al., 1947). Therefore, it was hypothesized that folic acid antagonists may inhibit or arrest the proliferation of cancer cells (Farber and Diamond, 1948). In collaboration with SubbaRow and colleagues of Lederle Laboratories, a series of folic acid analogs including aminopterin (AMT) and methotrexate (MTX) were synthesized. This collaboration signified one of the first examples of rational drug design in cancer drug discovery. When administered to children with ALL in 1948, these antifolates became the first drugs to induce remission in this malignancy (Farber, 1949; Farber and Diamond, 1948). Remarkably, MTX continues to achieve widespread clinical use as an essential component of multidrug regimens for treating ALL (Pui and Evans, 2006), lymphomas, and solid tumors worldwide (Jolivet et al., 1983; Monahan, 2001). Thus, targeting folate metabolism and nucleic acid synthesis has the potential to affect cancers arising from many different tissues. Unfortunately, the efficacy of MTX clinically is limited by a lack of tumor selectivity and the presence of de



novo and acquired resistance (Matherly et al., 2007). These limitations have led to decades of drug discovery efforts aimed at characterizing more effective antifolates.

The novel antifolate, pemetrexed (PMX) is one of the antimetabolites that were identified through these drug discovery efforts (Taylor et al., 1992). The FDA approval of PMX for the treatment of malignant pleural mesothelioma in 2004 (Hazarika et al., 2004) and non-small cell lung cancer (NSCLC) in 2008 (Cohen et al., 2009) and the concomitant discovery of the proton-coupled folate transporter (PCFT), the preferred cellular uptake route of PMX, by Goldman and colleagues in 2006 (Qiu et al., 2006) has caused a revival of interest in antifolates for cancer therapy (Goldman et al., 2010). This success has shaped a new therapeutic approach to rational folate analog design based on targeting delivery into the cancer cell by exploiting the tumor-specific expression and/or function of folate transporters. This strategy is expected to increase the tumor selectivity of these antimetabolites and enhance their therapeutic window.

This chapter will review the basic biology of PCFT as it relates to the therapeutic application of PCFT in tumor targeting. It will provide an overview of PCFT function, expression, and transcriptional regulation, as well as discuss structurally and functionally important amino acids and domains. The relationship of PCFT to other folate transporters and the consequences of PCFT mutations in human disease will be described. Finally, this chapter will begin to establish the feasibility of a treatment strategy that targets solid tumors based on PCFT-specific uptake of novel folate based analogs.

1.2 Folate Metabolism.

Folates designate the family of B9 vitamins that are essential cofactors necessary for various one-carbon transfer reactions in intermediary metabolism. Important among these reactions are critical steps in the *de novo* synthesis of thymidylate and purine nucleotide



biosynthesis, the regeneration of methionine from homocysteine, the interconversion of serine and glycine, and the catabolism of histidine and formic acid (Matherly and Goldman, 2003; Sirotnak and Tolner, 1999; Stokstad, 1990). The folate molecule consists of three structural components: a pteridine ring system, a p-aminobenzoic acid (PABA) and an L-glutamate moiety (Figure 1.1) (Assaraf, 2007; Zhao et al., 2009a). Mammalian cells are devoid of the metabolic enzymes necessary for folate biosynthesis. Thus, all folate requirements must be acquired through the diet (Matherly and Goldman, 2003; Sirotnak and Tolner, 1999). Within the mammalian cell, folates are converted to various one-carbon-substituted tetrahydrofolate (THF) cofactors with a one-carbon moiety at the N5 and/or N10 position at the oxidation level of methanol (5-methylTHF), formaldehyde (5,10-methyleneTHF) or formate (10-formylTHF or 5,10-methenylTHF). Additionally, folates undergo polyglutamylation by folylpoly- γ -glutamate synthase (FPGS) in which 2 to 8 linked glutamyl residues are added to the γ -carboxyl on PABA of the THF cofactor. Polyglutamates of THF cofactors are polyanions which are impermeable to the plasma membrane and hence are retained in cells, thus ensuring high levels of intracellular reduced folates (Figure 1.1) (Stokstad, 1990).

Carbon 3 of serine (derived from glycolytic intermediates) is the primary source of onecarbon units for cytoplasmic one-carbon metabolism (Davis et al., 2004), mainly through its conversion to formate in the mitochondria (Anguera et al., 2006; Barlowe and Appling, 1988; Barlowe and Appling, 1990; Garcia-Martinez and Appling, 1993; Gregory et al., 2000; Herbig et al., 2002; Kastanos et al., 1997; MacFarlane et al., 2008; Pasternack et al., 1994; Pasternack et al., 1996; Patel et al., 2003; Quinlivan et al., 2005; Tibbetts and Appling, 2010). The cytoplasmic and mitochondrial compartments are metabolically connected by transport of serine, glycine and formate across mitochondrial membranes. Once transported into the mitochondria, the one-





Figure 1.1 Structure of 5-methyl tetrahydrofolate and classical antifolates. 5-methyltetrahydrofolate (THF) is the major dietary form and the dominant folate found in blood. The folate molecule consists of a 6-methylpteridine moiety with A and B rings linked at carbon 6 by a methylene bridge to p-aminobenzoylglutamic acid. The N5 and/or N10 position can associate with a methyl (*Panel A*), formyl, methylene or methenyl one carbon moiety, which serve as onecarbon donors in biosynthetic reactions. THF undergoes polyglutamylation by folylpoly- γ glutamate synthase (FPGS) in which 2 to 8 linked glutamyl residues are added to the γ -carboxyl on PABA of the THF cofactor. *Panel B*, Antifolates are structural analogs of natural folates that inhibit folate-dependent enzymes. Antifolates inhibiting: dihydrofolate reductase (DHFR) are aminopterin (AMT), methotrexate (MTX), and praletrexate (PDX); thymidylate synthase (TS) are raltitrexed (RTX) and pemetrexed (PMX); β -glycinamide ribonucleotide formyltransferase (GARFTase) is lometrexol (LMX). PMX inhibition of 5-amino-4-imidazolecarboxamide ribonucleotide formyltransferase (AICARFTase) and MTX polyglutamate inhibition of TS and AICARFTase is not illustrated.



5

carbon unit from serine is transferred to THF in a reaction catalyzed by mitochondrial serine hydroxymethyltransferase (mSHMT), which generates 5, 10-methyleneTHF and glycine (reaction 1m) in Figure 1.2 (Tibbetts and Appling, 2010). In the mitochondria, 5,10methyleneTHF is converted into 10-formylTHF by the bifunctional MTHFD2 in embryonic tissue (Mejia and MacKenzie, 1985) or MTHFD2L in adult tissues (Bolusani et al., 2011). Bifunctional MTHFD2 has both 5,10-methyleneTHF dehydrogenase (reaction 2m) and 5,10methenylTHF cyclohydrolase (reaction 3m) activities. 10-formylTHF can then be converted by the monofunctional MTHFD1L 10-formylTHF synthetase into formate and reduced THF (reaction 4m) (Prasannan et al., 2003). Once exported into the cytoplasm, formate reacts with unsubstituted THF, facilitated by the 10-formylTHF synthetase activity of the cytoplasmic trifunctional enzyme C_1 -tetrahydrofolate synthase (referred to as MTHFD1) to produce 10formylTHF (reaction 4) (Hum et al., 1988; Paukert et al., 1977; Schirch, 1978; Smith et al., 1980; Thigpen et al., 1990). The formyl group of 10-formylTHF can be used in de novo purine nucleotide synthesis where it is donated to β -glycinamide ribonucleotide (GAR) and then 5amino-4-imidazolecarboxamide ribonucleotide (AICAR), which is catalyzed by GAR formyltransferase (GARFTase; reaction 5) and AICAR formyltransferase (AICARFTase; reaction 6), respectively. This leads to a net two carbon transfer from 10-formylTHF to C-2 and C-8 of the purine ring, regenerating unsubstituted THF (Hartman and Buchanan, 1959b; Smith et al., 1981; Smith et al., 1980). The 5,10-methenylTHF cyclohydrolase (reaction 3) and 5,10methyleneTHF dehydrogenase (reaction 2) activities of the cytosolic trifunctional MTHFD1 can also convert 10-formylTHF to 5,10-methenylTHF and subsequently 5,10-methyleneTHF (Hum et al., 1988; Paukert et al., 1977; Schirch, 1978; Smith et al., 1980; Thigpen et al., 1990), which can donate the one-carbon unit in the irreversible conversion of deoxyuridine monophosphate



(dUMP) to thymidylate (dTMP, a precursor to DNA), catalysed by thymidylate synthase (TS) (reaction **7** in the cytoplasm and **7n** in the nucleus) (Friedkin and Roberts, 1956; Phear and Greenberg, 1957). The resulting dihydrofolate (DHF) (Humphreys and Greenberg, 1958; McDougall and Blakley, 1960) is reduced by cytoplasmic DHFR to unsubstituted THF (reaction **8**). Alternatively, 5,10-methyleneTHF can be reduced in an irreversible reaction by 5,10-methyleneTHF reductase (MTHFR) to generate 5-methylTHF for entry into the methyl cycle (reaction **9**). 5-methylTHF can donate a one carbon unit in the B12-dependent regeneration of methionine from homocysteine, regenerating the THF, catalyzed by methionine synthase (reaction **10**) (Hatch et al., 1961). Methionine is a precursor for the synthesis of S-adenosylmethionine (AdoMet or SAM), a cofactor and methyl group donor for numerous methylation reactions, including the methylation of cytosine bases in DNA, histones, RNA, neurotransmitters, and other small molecules, phospholipids, and other proteins (Figure 1.2) (Lu, 2000).

1.3 Membrane Transport of Folates.

Due to the highly hydrophilic nature of folates and antifolates, three genetically distinct and functionally diverse transport systems are in place to facilitate their uptake into the cells of peripheral tissues.

1.3.1 Reduced Folate Carrier.

The reduced folate carrier (RFC; SLC19A1), a member of the Major Facilitator Superfamily of solute carriers, is a secondary active anionic exchanger and the major transport system for reduced folates ($K_t \sim 2-4 \mu M$) in mammalian cells and tissues at physiologic pH (Figure 1.2) (Goldman et al., 1968; Sirotnak et al., 1968). RFC has a very low affinity for folic acid and as the pH is decreased, the activity for reduced folates is diminished so that there is little





Figure 1.2 Folate transporters, folate metabolic pathways and intracellular enzyme targets of antifolates. Folate and antifolate transport across biological membranes is mediated by the reduced folate carrier (RFC), the proton-coupled folate transporter (PCFT) and the folate receptor (FR). Reactions 1-4 are in both the cytoplasmic and mitochondrial (m) compartments. Reactions 1 and 9 are also present in the nucleus (n). The numbered reactions are catalyzed by the following enzymes: 1, 1n and 1m, serine hydroxymethyltransferase (SHMT). In the mitochondria, reactions **2m** and **3m** are catalyzed by bifunctional MTHFD2 or MTHFD2L and 4m is catalyzed by monofunctional MTHFD1L. In the cytoplasm, reactions 4, 3 and 2: 10cyclohydrolase formvlTHF synthetase. 5,10-methenylTHF and 5,10-methyleneTHF dehydrogenase, respectively, are catalyzed by trifunctional C1-THF synthase in the cytoplasm (MTHFD1); 5, β -glycinamide ribonucleotide formyltransferase (GARFTase); 6, 5-amino-4imidazolecarboxamide ribonucleotide formyltransferase (AICARFTase); 7 and 7n, thymidylate synthase (TS); 8, dihydrofolate reductase (DHFR); 9, 5,10-methyleneTHF reductase (MTHFR); 10, methionine synthase. Aminopterin (AMT), methotrexate (MTX), praletrexate (PDX), raltitrexed (RTX), lometrexol (LMX), pemetrexed (PMX) (Figure 1.1), ONX-0801 (ONX), compound 3, compound 16 and compound 17 (Figure 3.1).



activity below pH 6.5. The human RFC gene is located on chromosome 21q22.3, and the gene structure appears to be conserved across species, with as many as six non-coding regions and alternative promoters (A1, A2, A, B, C, D and E) spanning 35 kb upstream from the major AUG translational start in coding exon 1, and five major coding exons with conserved intron-exon boundaries. This gives 15 distinct 5'untranslated regions fused to a common splice acceptor at position -49 and the same 1,776 bp coding sequence, which encodes a protein consisting of 591 amino acids (Flatley et al., 2004; Matherly et al., 2007; Payton et al., 2007; Whetstine et al., 2002a). Promoter activity has been confirmed for the 5' regions proximal to the A1/A2, A, B, C and D non-coding regions. Regulation of RFC gene expression is by both ubiquitous (e.g. Sp, USF) and tissue-specific (e.g., Ap2, C/EBp, Ikaros, GATA) transcription factors that, when combined, transactivate or repress transcription in response to tissue-specific stimuli. Additionally, promoter methylation, general architecture and chromatin structure have all been implicated in transcriptional regulation of RFC (Liu et al., 2004; Payton et al., 2005a; Payton et al., 2005b; Whetstine et al., 2002b).

Hydropathy plot analysis of the RFC amino acid sequence predicted a topological model of 12 transmembrane domains (TMDs) and both amino- and carboxyl termini oriented to the cytosol. This was confirmed by hemagglutin epitope insertion, scanning N-glycosylation mutagenesis, and scanning cysteine accessibility methods (Cao and Matherly, 2004; Ferguson and Flintoff, 1999; Liu and Matherly, 2002). RFC is N-glycosylated at an N-glycosylation consensus site in the first intracellular loop (IL1) between TMD1 and TMD2. A large loop domain connecting TMD6 and TMD7 is needed to provide appropriate spacing between TMD1-TMD6 and TMD7-TMD12 segments for optimal transport. Amino acids localized in TMD4, TMD5, TMD7, TMD8, TMD10 and TMD11 were implicated in forming the putative substrate-



binding pocket (Hou et al., 2005; Hou et al., 2006). This structure is consistent with crystal structures for the bacterial Major Facilitator Superfamily proteins, lactose permease (LacY) and glycerol-3-phosphate transporter (GlpT) (Abramson et al., 2003; Huang et al., 2003b). Like other Major Facilitator Superfamily transporters, RFC exists as a homo-oligomer; however, each monomer functions as an independent transport unit and is fully active (Hou and Matherly, 2009; Hou et al., 2010).

Various studies on transcriptional and protein expression levels showed that RFC is ubiquitously expressed in tissues where it participates in transporting folate cofactors into cells, thus suggesting its integral role in specialized tissues that are important for *in vivo* folate homeostasis. Immunohistochemical analysis demonstrated mouse RFC protein expression on the apical brush-border membrane of small intestine and colon, liver hepatocyte membranes, the apical surface of the choroid plexus, the basolateral membrane of renal tubular epithelium, and the apical membrane of cells lining the spinal canal (Wang et al., 2001b). Measuring transcriptional expression of RFC in 76 human tissues and tumor cell lines showed the highest levels in placenta and liver, with considerably higher levels in leukocytes, kidney, lung, bone marrow and small intestine, and low but detectable levels in heart and skeletal muscle (Whetstine et al., 2002a). In at least some tissues (e.g., small intestine), the rodent RFC is responsive to dietary folate availability such that under conditions of folate deficiency, increased levels of RFC transcripts and proteins are observed (Liu et al., 2005). However, as acidic pH in the gut decreases the transport activity of RFC, the significance of this increased expression in the gut is unclear.

1.3.2 Folate Receptor.



Folate receptors (FRs), often referred to as high affinity folate binding proteins, bind and transport folic acid, reduced folate, many antifolates and folate conjugates with a high affinity (Kd~0.1–1 nM). There are three isoforms of human FR, α , β , and γ , encoded by distinct genes (Elwood, 1989; Lacey et al., 1989; Ratnam et al., 1989; Sadasivan and Rothenberg, 1989; Shen et al., 1994; Shen et al., 1995), localized on chromosome 11q13.3-q13.5 (Ragoussis et al., 1992). The human FR isoforms are homologous, with 68~79% identical amino acid sequences and two (β and γ) or three (α) N-glycosylation sites (Roberts et al., 1998; Shen et al., 1997). FR α and β are cell surface glycosyl phosphatidylinositol (GPI)-anchored glycopolypeptides, while $FR\gamma$ lacks the signal for GPI-anchor attachment and is therefore a secretory protein with unknown function (Shen et al., 1995). Upon binding (anti)folates or folate-conjugates, FR internalizes them by a non-classical endocytic mechanism (Figure 1.2) (Rijnboutt et al., 1996; Sabharanjak and Mayor, 2004). In this process, folates bind to FRs at the cell membrane, invaginate and bud off to form vesicles that are internalized into the intracellular endosomal compartment. Release of the ligand from the receptor occurs with a decrease of pH in the endosome and exit from the intact vesicle occurs presumably by diffusion or a process that operates optimally at low pH (Kamen et al., 1988).

FR is predominantly expressed on the apical (luminal) surface of polarized epithelial cells where it is not in contact with circulating folate (Chancy et al., 2000). In normal tissues, FR α is expressed in the brush-border membrane of the choroid plexus, retinal pigment epithelium, proximal tubules in kidney, fallopian tubes, uterus and placenta (Elnakat and Ratnam, 2004). FR β expression in normal tissues is only found in placenta and hematopoietic cells (Ratnam et al., 1989). In normal bone marrow and peripheral blood cells, expression of FR β is restricted to myelomonocytic lineage such as mature neutrophils, and was reported to have little binding



function with folic acid (Pan et al., 2002; Reddy et al., 1999). The polarized expression of FR α and β serves to protect normal tissues from FR-targeted cytotoxic agents in the circulation given intravenously (Weitman et al., 1992). Overexpression of FR α was reported in several malignant tissues including non-mucinous adenocarcinomas of ovary, uterus and cervix and ependymal brain tumors (Elnakat and Ratnam, 2004), and was found to positively correlate with tumor grade and stage in ovarian tumors (Buist et al., 1995; Garin-Chesa et al., 1993; Veggian et al., 1989; Wu et al., 1999). The FR α overexpressed in malignant tissues was shown to retain the high affinity binding of folate (Ross et al., 1994; Weitman et al., 1992). Malignant expression of FR β is found in all chronic myelogenous leukemia (CML) cells and 70% of acute myelogenous leukemia (AML) cells, but not in ALL (Pan et al., 2002; Ross et al., 1999).

1.3.3 Proton-coupled Folate Transporter.

In addition to RFC and the FRs, a low-pH folate transport mechanism was observed in mammalian cells, but the carrier responsible for this transport activity remained elusive for more than three decades. The transporter that is the basis for this activity and the subject of this dissertation has been recently identified and characterized as a proton-coupled folate transporter (PCFT; SLC46A1) (Nakai et al., 2007; Qiu et al., 2006; Umapathy et al., 2007; Zhao and Goldman, 2007) (Figure 1.2. PCFT is a proton-folate symporter that functions optimally at acidic pH by coupling the uptake of folates with the flow of protons down their electrochemical concentration gradient. Although human PCFT shares only ~14% amino acid identity with human RFC, like RFC, it belongs to the Major Facilitator Superfamily (Zhao and Goldman, 2007; Zhao et al., 2009a). Strategies used to clone PCFT included database mining, using the conserved amino acid sequence of SLC19 family members, and screening of candidate mRNAs in cell lines where the RFC gene was deleted and low pH transport was either retained or



markedly decreased (Qiu et al., 2006). PCFT was initially reported to be a low-affinity heme transporter that is pH-independent (Shayeghi et al., 2005). Although PCFT may be capable of heme transport, its primary function appears to be absorption of folates at low pH. The ability of PCFT to transport folate under acidic conditions is important for folate homeostasis, as dietary folate absorption in the duodenum and upper jejunum occurs via PCFT (Inoue et al., 2008; Qiu et al., 2007).

1.4 Biology of the Proton-Coupled Folate Transporter.

1.4.1 PCFT Tissue Expression.

PCFT is localized to chromosome 17q11.2 in humans and the gene consists of five exons, and codes for a 459 amino acid protein with a predicted molecular mass of ~50 kDa. As mentioned above, the highest expression levels of PCFT in normal tissues were reported in the apical brush-border membrane along the proximal jejunum and duodenum, kidney, liver, placenta, spleen, and choroid plexus (Inoue et al., 2008; Qiu et al., 2006; Qiu et al., 2007; Urguhart et al., 2010). It has been hypothesized that PCFT may still play a role in folate uptake into tissues that do not experience low pH, though whether this is due to localized acidification or solely due to the high level of expression, combined with residual transport of 5-methylTHF at neutral pH, remains to be determined (Qiu et al., 2006). Delivery of folates to the central nervous system has been proposed to involve PCFT and FRa coupling in the choroid plexus, whereby PCFT exports folates from the acidic endocytic compartment created by FR α -mediated endocytosis (Zhao et al., 2009b) (Figure 1.2). For the maintenance of cerebrospinal fluid folate, the presence of one transporter is inadequate in the absence of the other; therefore, when either FR or PCFT is mutated in humans, the syndrome of folate deficiency manifests (Cario et al., 2009; Steinfeld et al., 2009).



A comprehensive examination of PCFT and RFC expression in malignant cell lines and tissues has not previously been performed, however, low pH transport of [³H]MTX was detected in human solid tumor cell lines from the National Cancer Institute (NCI) 60 tumor panel and other sources. In this study MTX influx at pH 5.5 was equal to, or greater than, MTX influx at pH 7.4 in 29 of 32 cell lines (Zhao et al., 2004b). These findings suggest that if the low pH transport can be attributed to PCFT-mediated uptake of MTX, designing therapeutics selective for PCFT uptake over RFC has the potential of increasing solid tumor selectivity of antifolates.

1.4.2 Regulation of PCFT Gene Expression.

Understanding the regulation and silencing of PCFT gene expression is important due to the physiologic and pharmacologic importance of PCFT. The PCFT minimal transcriptional regulatory region is localized between positions -42 and +96 (the transcriptional start site is +1) (Diop-Bove et al., 2009; Stark et al., 2009).

The promoter of the PCFT gene harbors a 1085-bp CpG island (nucleotides –600 through +485) and hence the extent of methylation is a possible mechanism of PCFT transcriptional control. Hypermethylation of the PCFT promoter was shown to be associated with low PCFT gene and protein expression in CCRF-CEM and Jurkat T-cell leukemia cell lines (Gonen et al., 2008) and a MTX-resistant HeLa cell line (R1) (Diop-Bove et al., 2009). In both cases, treatment with the DNA methyltransferase inhibitor, 5-aza-2'-deoxycytidine, resulted in substantial restoration of pH 5.5 transport and PCFT mRNA expression. Folate status can affect methylation of CpG islands of DNA and of histones through their requirement in vitamin-B12-dependent synthesis of methionine, a precursor of SAM (Stokstad, 1990). To this end, hypomethylation can accompany folate deficiency under some conditions (Wasson et al., 2006). Hence, control of PCFT expression through methylation provides an elegant method of altering



uptake in the face of folate excess or deficiency (Zhao et al., 2011a). Additionally, low dose 5aza-2'deoxycytidine treatment may restore PCFT-mediated transport of antifolates in patients with acquired resistance due to methylation of the PCFT promoter.

PCFT mRNA levels are also controlled by 1,25-dihydroxyvitamin D3 (vitamin D3), and expression of PCFT is increased in a dose-dependent fashion in Caco-2 cells *in vitro* and in duodenal rat biopsies *ex vivo* when treated with vitamin D3. Vitamin D receptor (VDR) heterodimerizes with retinoid X receptor- α (RXR α) in response to vitamin D3 and binds a VDR response element in the PCFT promoter region (-1694/-1680), increasing expression and therefore function of PCFT (Eloranta et al., 2009). This finding suggests that vitamin D3 supplementation could affect the bioavailability or toxicity of PCFT-targeted therapeutics in the clinic and may be an important consideration in the design of clinical trials.

Three adjacent putative binding sites for the nuclear respiratory factor 1 (NRF-1) transcription factor were identified in the PCFT minimal promoter. NRF-1 was found to bind and transactivate the human PCFT promoter leading to an increase in PCFT mRNA levels (Gonen and Assaraf, 2010). NRF-1 is a major regulator of mitochondrial biogenesis (Scarpulla, 2002; Scarpulla, 2006; Scarpulla, 2008; Scarpulla, 2011). Folates play an important role in mitochondrial integrity, and folate deficiency has been found to cause large mitochondrial deletions, cytochrome c dysfunction, membrane depolarization and superoxide overproduction (Chang et al., 2007). Interestingly, NRF-1 has been found to up-regulate the bi-directional transcription of glutamine phosphoribosylpyrophosphate amidotransferase (GPAT) (reaction 1) and phosphoribosylaminoimidazole carboxylase/phosphoribosylaminoimidazole succinocarboxamide synthetase (PAICS) (reaction **6** and **7**) which are both enzymes needed for *de novo* purine biosynthesis (Figure 1.5) (Brayton et al., 1994; Chen et al., 1997). Thus, NRF-1



may function to coordinate mitochondrial respiration-biogenesis with folate uptake, folate metabolism and *de novo* purine biosynthesis (Gonen and Assaraf, 2010).

1.4.3 Hereditary Folate Malabsorption.

Direct evidence that PCFT is responsible for low-pH transport and intestinal folate absorption came from the discovery that homozygous mutations in the coding region of the PCFT gene leads to the rare autosomal recessive disorder, hereditary folate malabsorption (HFM) (Atabay et al., 2010; Borzutzky et al., 2009; Geller et al., 2002; Lasry et al., 2008; Mahadeo et al., 2010; Mahadeo et al., 2011; Meyer et al., 2010; Min et al., 2008; Qiu et al., 2006; Shin et al., 2011; Shin et al., 2010; Zhao et al., 2007). HFM is characterized by the onset of macrocytic folate-deficiency, anemia, and failure to thrive within the first few months of life. This may be accompanied by hypoimmunoglobulinemia associated with infectious complications, most frequently *Pneumocyctis jiroveci* pneumonia. The syndrome is characterized by developmental delays, gait disorders, peripheral neuropathies, and, in the absence of adequate and timely treatment, seizures (Geller et al., 2002; Mahadeo et al., 2010). Loss of PCFT function leads to impaired intestinal folate absorption, resulting in severe folate deficiency and impaired transport of folates across the choroid plexus into the central nervous system, reflecting the important physiological functions of PCFT folate transport (Zhao et al., 2009a). The fact that subjects who are PCFT null develop severe folate deficiency indicates that RFC does not contribute significantly to folate absorption under these conditions (pH 5.8-6.0) despite its presence in the intestinal epithelium. Many insights into the structure and function of PCFT have been gained by mechanistically evaluating the HFM loss-of-function mutations (Figure 1.3; Figure 1.4; Table 1.1).





determined from published mutagenesis studies, are shown as *purple circles*. Amino acids mutated in patients with hereditary folate malabsorption (HFM) are shown as red and blue circles. GxxxG putative dimerization motifs are shown as yellow circles and glycosylated residues N58 and N68 are shown as green circles.

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Figure 1.4 Amino acid sequence alignment of PCFT homologs from different species.


	Reference	Shin etal, 2011	Zhao et al., 2007	Meyeretal., 2010	Min et al., 2008	Shinn etal., 2011;Atabay etal., 2010	Zhao et al., 2007	area at al. 0000	Latey 91 at 2008	Zhaoetal., 2007	Shin et al., 2010	Zhaoetal., 2007	Shin et al., 2011	Shin etal, 2011	Giu et al., 2006; Borzutzky et al., 2009; Mahadeo et al., 2011	Zhao et al., 2007			Mahadeo et al., 2010						Mahadeo et al., 2010			Zhao etal, 2007	Hou et al., 2011	
y of published PCFT mutations in subjects with the clinical diagnosis of hereditary folate malabsorption.	Transport substrate	QN	5-methylTHF	ND	5-methyITHF	Q	5-methyITHF	folic acid	MTX	5-methyITHF	MTX	5-methylTHF	XTM	MTX	5-methylTHF	5-methyITHF	5-methyITHF	Folic acid	5-formyITHF	MTX	PMX	5-methyITHF	Folic acid	5-formyITHF	MTX		PMX		5-methyITHF	MTX
	Transport	QN	no transport	ND	no transport	Ð	no transport	no transport	no transport	13% ofWT	no transport	no transport	no transport	no transport	no transport	no transport	no transport	no transport	no transport	no transport	no transport	no transport	no transport	no transport	no transport	~50% of	TN	† Imiux km = Vmax	3.5% of WT	~5% of WT
	Cell surface expression	QN	0	ND	0U	QN	01	9077	y 8	8	01	8	Q	ΩN	no intracellular	0U			same as WT						~50% ofWT				yes	yes
	Crude membrane expression	QN	8	ΠN	8	Ð	00	ци	ND	8	Iow MW PCFT	low	Ð	ΠN	low MW PCFT	low			same as WT				~50% ofWT				8	yes		
	Cells used for transfection	QN	WT HeLa	ND	R1-11 HeLa	QN	WT HeLa	C = MTVR0.15	VIN CO	WT HeLa	R1-11 HeLa	WT HeLa	R1-11 HeLa	R1-11 HeLa	HeLa	WT HeLa			R1-11 HeLa				R1-11 Hela				WT HeLa	R1-11 HeLa		
	Location of mutation	N-term	ELI	ELI	EL1	EL1	IL1	Ē	2	TMD4	TMD4	TMD8	TMD9	TMD9	TMD10 + IL5		•	TMD10		•					TMD10		Ele	3		
	Amino acid change	E9Gfs	G65Afs X25	C66Lfs X99	CeeX	N68Kfs^	R113S	Detroc	1130	G147R	D156Y	S318R*	A335D^	G338R	Y362_G389del			Bardw.				R37 60				DAGED	1071			
Table 1.1 Summary	Nucleotide change	17-18insC	194delG	194dupG	GC197-198AA	204-205delCCA	C337A	Taga	- 222/	G439C	G466T	C954G*	C1004A^	G1012C	G1082-1A splice acceptor site			C11 26 T					Gi 127A					C1974G	04/710	

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The first exon, particularly nucleotides encoding extracellular loop 1 (EL1) between the first and second transmembrane domains, has a high GC content, 65.8% (75% between residues 63 and 70), and is the most frequent site of PCFT mutations in subjects with HFM (Shin et al., 2011). There are five reported mutations. These include four frame-shifts: c.17-18insC, p.E9Gfs (Shin et al., 2011); c.194delG, p.G65Afs (Zhao et al., 2007); c.194dupG, p.C66Lfs (Meyer et al., 2010); and c.204-205delCC, p.N68Kfs (Atabay et al., 2010; Shin et al., 2011) and a stop codon (c.GC197AA; p.C66X (Min et al., 2008)) (See Table 1.1 for references describing various HFM mutations). These genetic alterations led to truncation of PCFT and loss of PCFT expression and function. Additionally, a number of residues identified in patients with HFM, (c.G439C, p.G147R in TMD4 (Zhao et al., 2007); c.G466T, p.D156Y in TMD4 (Shin et al., 2010); c.C954G, p.S318R in TMD8 (Zhao 2007); c.C1004A, p.A335D in TMD9 (Shin 2011) and c.G1012C, p.G338R in TMD9 (Shin 2011)) (Figure 1.3 and Table 1.1) when mutated lead to no or very low (13% of wild-type (WT) for G147R) levels of transport of either 5-methylTHF or MTX. Point mutations involving either Arg113 to serine (c.C337A, p.R113S (Zhao et al., 2007)) or cysteine (c.C337T, p.R113C (Lasry et al., 2008)) and either Arg376 to tryptophan (c.C1126T, p.R376W (Mahadeo et al., 2010)) or glutamine (c.G1127A, p.R376Q (Mahadeo et al., 2010)) have been found in two unrelated families with HFM. Characterization of these mutations suggested that mutation of Arg113 may affect binding and/or translocation of negatively charged folate substrates and mutation of Arg376 may affect proton binding and therefore modulates the folate-binding pocket in a substrate-dependent manner. Please see section 1.4.4.3 for a more in depth discussion of the importance of these residues for PCFT function. Interestingly, most point mutations associated with HFM occur in TMDs or at TMD junctions. TMD4 and 9 contain the most mutations (Figure 1.3) (Zhao et al., 2011b). The mutation c.G1082-1A is located in the



splice acceptor of intron 2 (intron 2/exon 3 boundary), causing skipping of exon 3 which creates a splice variant that results in deletion of 28 amino acids in TMD10 and IL5 (p.Y362_G389del). This mutation results in a protein with decreased stability and impaired trafficking to the cell membrane and was identified in eight unrelated families of Puerto Rican heritage (Borzutzky et al., 2009; Mahadeo et al., 2011; Qiu et al.). Finally, the residue Pro425 in the EL6 was found to be mutated (c.C1274G, p.P425R) in a family of Arab descent. This mutation only slightly impacted cell surface expression of PCFT, but function was 3.5-5% of WT (Shin et al., 2012; Zhao et al., 2007). Interestingly, combined WT and inactive mutant P425R PCFTs were targeted to the cell surface by surface biotinylation/Western blotting and confocal microscopy, and functionally exhibited a "dominant-positive" phenotype, implying positive cooperativity between monomers comprising oligomeric PCFT and functional rescue of mutant by WT PCFT (Hou et al., 2011) (see section 1.4.4.4).

A possible mechanism of resistance to antifolates selective for PCFT-mediated uptake may be loss of PCFT function; therefore a better understanding of the impact of mutations on PCFT structure and function could provide insight into possibly reversing future cases of resistance.

1.4.4 Structure and Function of PCFT.

1.4.4.1 Topology.

Based on hydropathy plot analysis, the membrane topology of PCFT is predicted to include twelve TMDs with the N- and C- termini directed into the cytoplasm (Figure 1.3) (Zhao and Goldman, 2007; Zhao et al., 2009a). Orientation of the N- and C- termini was validated by immunofluorescence analysis of HA-tagged PCFT. The loop domain between TMD1 and TMD2 was found to be extracellular since the two predicted N-glycosylation sites (Asn58,



Asn68) in this region are glycosylated (Figure 1.3). N-linked glycosylation at the above mentioned sites was validated by Peptide: N-Glycosidase (PNGase) F cleavage of the oligosaccharide, tunicamycin inhibition of N-linked glycosylation and site-directed mutagenesis of Asn58 and Asn68. Trafficking and function of PCFT was not affected by N-glycosylation status (Unal et al., 2008). In MDCK and Caco-2 cells, C-terminal-tagged yellow fluorescent protein (YFP) PCFT was functionally expressed at the apical membrane, which is different from the basolateral localization for RFC (Subramanian et al., 2008). Complete truncation of the PCFT C-terminal region had no significant effect on either apical cell surface targeting or transport function (Subramanian et al., 2008). A disulfide bond exists that is not important to function that links Cys66 in the first extracellular loop to Cys298 in the fourth extracellular loop (Zhao et al., 2010).

1.4.4.2 Transport Characteristics.

PCFT has similar affinities (K_t ~ 0.5-1.0 μ M) for reduced (5-methylTHF, 5-formylTHF) and oxidized (folic acid) folates at pH 5.5 and is stereospecific for 5-formylTHF (Zhao and Goldman, 2007). Folic acid and MTX uptake in *Xenopus laevis* oocytes was increased > 200 fold at pH 5.5 when injected with PCFT cRNA (Qiu et al., 2006; Qiu et al., 2007). Increased low-pH (pH 5.5) transport was also observed when PCFT cDNA was transiently transfected into HeLa cells or stably transfected into HepG2 cells (Zhao et al., 2008). When PCFT was silenced with interfering RNAs, the low-pH transport of Caco-2 was reduced by 80% (Qiu et al., 2006). PCFT transport activity was highest at the lowest pH (pH 5.5) and declined as the pH increased (pH 7.4). Uptake by PCFT conformed to Michaelis-Menten kinetics. The K_t increased and V_{max} decreased as the pH increased from pH 5.5 to pH 7.4 (Qiu et al., 2006; Zhao and Goldman, 2007). The activity of PCFT is not affected by removal of extracellular Na⁺, K⁺, Ca⁺², Mg⁺² or



Cl⁻ (Qiu et al., 2006). Dissipation of the transmembrane proton-gradient by carbonylcyanide ptrifluoromethoxyphenylhydrazone (FCCP) (a proton ionophore) (Qiu et al., 2006) and nigericin (a K^+/H^+ -exchanging ionophore) (Inoue et al., 2008) in *Xenopus* oocytes and HEK293 cells, respectively, reduced transport by PCFT. Studies in *Xenopus* oocytes have demonstrated that folate transport by PCFT is electrogenic, where there is a net translocation of positive charge as each negatively charged folate molecule is transported. Assuming that folates are bivalent anions, more than two protons must be co-transported with each folate molecule to account for the net transport of positive charge (Qiu et al., 2006; Qiu et al., 2007). Cellular acidification that accompanies folate transport into oocytes was measured, confirming proton coupling (Unal et al., 2009a). Conversely, in HEK293 cells, transport by PCFT was insensitive to membrane potential, suggesting potential-independent, non-electrogenic transport, although in either case there was still a requirement for an inwardly directed proton gradient (Inoue et al., 2008). PCFT functions even when there is no transmembrane pH gradient, based partly on the membrane potential. At pH 7.4, when the membrane potential is increased, folate-induced currents are increased (Qiu et al., 2006; Umapathy et al., 2007). At low pH, PCFT has also been found to have channel-like activities, where protons can flow uncoupled from the flow of folates (Mahadeo et al., 2010; Unal et al., 2009a). Anionic compounds, sulasalazine and pyrimethamine were found to be weak inhibitors of PCFT-mediated uptake with K_i values of 42.3 and 161.1 μ M, respectively. One could envision that the efficiency of intestinal folate absorption or the efficacy of orally administered PCFT-selective antifolates for cancer therapy would be affected in subjects administered these compounds (Inoue et al., 2008; Nakai et al., 2007; Urguhart et al., 2010). Hence, it is important to gain a better understanding of PCFT substrate affinity and



transport characteristics to create better PCFT substrates and avoid drug interactions during clinical administration.

1.4.4.3 Functionally Important Residues.

Functional analysis of HFM mutations and mutations generated by site-directed mutagenesis have identified residues that are important in PCFT structure and function.

Arg113 was found to be mutated in two unrelated families of Turkish (c.C337A, p.R113S) and Arab (c.C337T, p.R113C) descent by two independent investigators (Lasry et al., 2008; Zhao et al., 2007). The residue Arg113 is found in the highly conserved (Figure 1.4) IL1 motif D₁₀₉XXGRR₁₁₄ connecting TMD2 and TMD3 in PCFT (Table 1.1; Figure 1.3). When expressed in C5 MTXR^{0.15} CHO cells, R113C PCFT was expressed at the cell surface, but did not transport folic acid or MTX (Lasry et al., 2008). Similarly, when R113S PCFT was expressed in WT HeLa cells, no protein was found at the cell surface and no transport of 5methylTHF was detected (Zhao et al., 2007). Since the recently crystallized E coli GlpT shares several structural and functional characteristics with PCFT and is the closest structural homolog with 13.8% sequence similarity over 424 aligned amino acid residues (from a total of 459), GlpT was used as a template in a homology-based structural model to analyze the structure of the IL1. Homology modeling analysis predicted that the DXXGRR motif forms a β -turn whereas the cationic R113 residue of PCFT is completely buried in a putative hydrophobic cavity, the walls of which are made up of TMD1, TMD3, TMD4, and TMD6. It was suggested that R113 might possibly participate in the binding and/or translocation of negatively charged folate substrates (Lasry et al., 2008). Alanine mutagenesis across this stretch disrupted the β turn and resulted in endoplasmic reticulum retention with loss of transport (Subramanian et al., 2008).



Arg376 is a highly conserved residue (Figure 1.4) that has been found to be mutated in two unrelated families with HFM of Mexican (c.C1126T, p.R376W) (Mahadeo et al., 2010; Zhao et al., 2007) and Chinese (c.G1127A, p.R376Q) descent (Table 1.1; Figure 1.3). When expressed in R1-11 HeLa cells, R376W was expressed in crude membranes and localized to the membrane similar to WT; however, no transport of 5-methylTHF, 5-formylTHF, folic acid, MTX and PMX could be detected (Zhao et al., 2007). When explored more rigorously, it was found that a positive charge is favored at this residue. Interestingly, when this residue was mutated to a polar amino acid, as found in the HFM R376Q mutant, PMX transport activity was preserved at saturating concentrations (influx K_t increased and V_{max} decreased); however, no or very low transport of 5-methylTHF, 5-formylTHF, folic acid and MTX was detected. This mutant was expressed in crude membranes and localized to the membrane at levels 50% of WT. The data suggest that mutation of the R376 residue to glutamine impairs proton binding which, in turn, modulates the folate-binding pocket and depresses the rate of conformational alteration of the carrier, a change that appears to be, in part, substrate dependent (Mahadeo et al., 2010; Mahadeo et al., 2011).

Histidine has been shown to be critical for the function of some of the proton-coupled solute carriers (Fei et al., 1997; Lam-Yuk-Tseung et al., 2003; Metzner et al., 2008). There are ten His residues in PCFT; of these, His84, 247 and 281 are fully conserved across all species (Figure 1.4) and mutation of His281 and His247 to alanines caused loss of MTX transport function at pH 5.5 and pH 7.0. H247A (located in IL3) and H281A (located in TMD7) (Figure 1.3) were expressed to the same extent as WT, except the H247A mutant protein migrated faster by SDS PAGE than WT or H281A. This was not due to protein instability. Independent of changes in V_{max} , H247A had increased affinity for folic acid, 5-formylTHF and 5-methylTHF



compared to WT. The affinities for all the different substrates were very similar, which is in contrast to results for WT PCFT (Unal et al., 2009a). GlpT was used as a template in a homology-based structural model to analyze the role of His247 in PCFT function. The model predicted His247 to be localized in a highly electropositive region at the cytoplasmic opening to the water-filled translocation pathway. Additionally, the model predicted that His247 interacts with Ser172 and limits access of extracellular folate substrates, thus determining the selectivity of PCFT for folate. Ser172 mutated to alanine caused a similar change in influx K_t, as caused by the His247 mutation. Additionally, the mutant exhibited folate-independent proton transport or "slippage". Mutation of His281 to alanine produced a substantially different phenotype, characterized by increased influx K_t and maintenance of a selectivity profile similar to WT PCFT. The magnitude of the increase in folic acid transport as a function of pH was far less; however there was still folate-induced cellular acidification. Therefore, His281 is not needed in proton –coupling but protonation of this residue may result in increased binding of folate substrates (Unal et al., 2009a).

More rigorous evaluation of the HFM mutant, D156Y, revealed that Asp 156 is important for protein stability (Table 1.1; Figure 1.3) (Shin et al., 2010). Loss of stability was observed with a variety of polar, neutral, or positively charged mutants. However, stability and trafficking were preserved with a Gly (relatively polar) or, to a lesser extent, with Ser (polar) substitutions. All the residues that are point mutated in HFM are completely conserved across all the species analyzed, demonstrating their importance for expression and function of PCFT (Figure 1.4). Discovery and characterization of the D156Y mutation in HFM led to rigorous analysis of the other 6 conserved Asp residues in PCFT. Only one, Asp109, is shown to be required for function. No substitution, irrespective of charge or polarity preserved function, even conservative



substitutions. All of the Asp109 mutants were expressed and were detectable at the cell membrane at levels similar to WT, but no MTX transport was detected at high MTX concentrations and when the extracellular proton concentration was increased. This suggested that the loss of activity was not due to an increase in influx K_t , like the R376Q mutation, or that there was a decrease in affinity of a proton-binding site that allosterically alters the conformation of the folate-binding pocket, like the H281A mutation. Additionally, lack of activity at pH 7.4 excludes a role of this residue for proton-coupling. The Asp109 is found in IL1 like the R113S and R113C HFM mutations. When Asp109 was replaced with other amino acids (even glutamate), substrate either does not bind and/or the alternative-access mechanism of transport is impaired (Figure 1.3) (Shin et al., 2010).

Conserved, charged residues located in TMDs are preserved through evolution because they usually contribute by intramolecular interactions to the stabilization of transporter tertiary structure and are therefore important for function of the carrier (Zvelebil et al., 1987). The residue Glu185 when mutated to leucine or alanine resulted in loss of MTX transport at pH 5.5 due to a decrease in the influx V_{max} with no change in influx K_t . The preservation of a negative charge at position 185 is essential, since low pH transport was lost for all E185 substitutions regardless of charge and polarity except for the similarly charged E185D, which maintained a third of WT function. Unexpectedly, transport at pH 7.4 for the E185A mutant was comparable to that of WT. This suggests that Glu185 plays an important role in proton-coupling (Figure 1.3) (Unal et al., 2009b).

1.4.4.4 Oligomerization.

As mentioned previously, PCFT belongs to the Major Facilitator Superfamily of transporters. Since numerous Major Facilitator Superfamily proteins including LacS (Veenhoff



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(Hickman and Levy, 1988; Yin et al., 2000), and RFC (Hou and Matherly, 2009) have been reported to exist as oligomers (e.g., dimers, tetramers, etc.), and given the potential mechanistic and regulatory ramifications of such structures for PCFT, the oligomerization status was evaluated (Hou et al., 2011). The HFM mutation P425R (described in section 1.4.3 and Zhao et al. (2007)) was used in conjunction with an assortment of biochemical and molecular techniques to validate the existence of PCFT homo-oligomers. By protein cross-linking, oligomeric PCFT appeared to predominate over monomeric PCFT. On a non-denaturing blue-native-PAGE, dimeric PCFT was the most predominant species. HA and FLAG/His 10 epitope-tagged PCFT protein monomers co-localized to the plasma membrane. PCFT monomers associate when analyzed using Ni affinity chromatography. FRET was detected between two YPet and ECFPtagged PCFT monomers. Finally, co-expression of WT PCFT with P425R PCFT monomers led to a dominant-positive transport phenotype. This appeared to involve co-folding and increased surface trafficking of P425R PCFT to the cell surface, as reflected in increased surface levels of mutant PCFT protein by surface biotinylation and Western blotting, and by indirect immunofluorescence and confocal microscopy. Thus, not only does PCFT exist as a homooligomer but there is functional cooperation between PCFT monomers in facilitating transport of folate substrates (Hou et al., 2011). Interestingly, the PCFT primary structure includes GXXXG motifs in TMD2 (amino acids 93-97) and TMD4 (amino acids 155-159) (Figure 1.3), analogous to "dimerization motifs" implicated in the oligomerization of other amphipathic proteins, including, ABCG2 and OAT1 (Duan et al., 2011; Polgar et al., 2010). Additionally, a cluster of PCFT nonfunctional mutations have been found in TMD4 (G147R, D156Y and L161R), suggesting that this region may be important in oligomerization (Figure 1.3 and Figure 1.4). A



better understanding of the structural and regulatory determinants of PCFT oligomerization may lead to novel approaches for therapeutically rescuing functionally impaired PCFT mutants in HFM or that may arise as a form of resistance to PCFT-selective novel folate analogs, perhaps with PCFT peptidomimetics or small molecules.

1.5 The Role of Antifolates in Cancer Therapy.

1.5.1 Inhibition of *De Novo* Thymidylate Biosynthesis Pathway.

Antifolates that inhibit DHFR, such as the classic antifolates, AMT and MTX, and the newer generation antifolates, pralatrexate (PDX) and the non-polyglutamable PT523 (Figure 1.1 and 1.2), block the regeneration of unsubstituted THF from DHF. This causes a depletion of THF cofactors and the accumulation of DHF, resulting in cessation of one-carbon-dependent processes (Matherly et al., 1987a; Seither et al., 1989). AMT has a much higher binding affinity for RFC and FPGS than MTX and is therefore transported into the cell and metabolized to polyglutamates much more rapidly (Smith et al., 1996). This increases the activity of AMT clinically, but also increases the toxicity of the compound compared to MTX (Goldin et al., 1955). PDX was discovered through drug development efforts of F.M. Sirotnak and colleagues at Memorial Sloan Kettering Cancer Center and J. DeGraw and coworkers at the Southern Research Institute. They found that 10-deaza-AMT was more potent than MTX (Sirotnak et al., 1984) and that the 10-ethyl derivative of 10-deaza-AMT (edatrexate) had even better efficacy both preclinically and clinically (Beinart et al., 2007; Gralla, 1995; Schmid et al., 1985; Shum et al., 1988; Sirotnak et al., 1993; Vandenberg et al., 1993). Based on the finding of Jones et al. (1981) that the N-10-propargyl analog of 5,8-dideazafolic acid (CB 3717) possessed potent inhibitory activity against TS (discussed in more detail below), 10-propargyl-10-deaza-AMT (PDX) was synthesized and tested to evaluate the effect of the propargyl group on growth



inhibition. It was found that PDX had a 3-fold decreased affinity for DHFR and a 10-fold RFC transport advantage compared to MTX, resulting in 5-fold enhanced anti-proliferative activity (DeGraw et al., 1993; Sirotnak et al., 1998). In September 2009, the FDA approved the use of PDX for the treatment of relapsed, refractory peripheral T-cell lymphoma (Thompson, 2009). Since then, PDX has been evaluated clinically either alone or in combination with other agents in a wide range of malignancies with promising results (Azzoli et al., 2007; Marchi et al., 2010; Toner et al., 2006; Zain and O'Connor, 2010a; Zain and O'Connor, 2010b).

Raltitrexed (RTX; Tomudex) is a potent TS inhibitor and arose from rational drug design efforts of researchers from the Institute for Cancer Research and Astra Zeneca (Figure 1.1 and 1.2) (Calvert et al., 1980). Previous work demonstrated that 5,8-dideazafolic acid was a weak inhibitor of TS; sequential modification of this compound produced N10-propargyl-5,8dideazafolic acid or CB3717 (Calvert et al., 1986; Jones et al., 1981). In the initial phase I/II clinical trials, this drug had activity against ovarian, liver, and breast cancer but also resulted in troublesome hepatic toxicity and dose-limiting nephrotoxicity, which occurred in 70% of patients at doses greater than 450 mg/m²)(Jackman and Calvert, 1995). To try and reduce toxicity, efforts were made to make the compound more water soluble at physiological pH; this was achieved by removing the 2-amino group and synthesizing a 2-desamino-2-methyl compound (ICI 198583) (Jackman et al., 1991b). Finally, replacement of the para-aminobenzoate with a thiophene and introduction of a N10-methyl substituent produced ZD1694 or RTX (Jackman et al., 1996; Jackman et al., 1991a; Jackman et al., 1991c). RTX had reduced TS inhibition compared to CB3717 but showed enhanced cellular uptake by RFC and polyglutamylation, leading to more potent tumor growth inhibition both in vitro and in vivo (Gibson et al., 1993; Jackman et al., 1993; Jackman et al., 1991c). This drug discovery effort exemplifies the power of establishing



structure activity relationships (SAR) through careful cellular, biochemical and pharmacological evaluation to test each chemical modification. RTX was approved for clinical use outside the US for advanced colorectal cancer (Chu et al., 2003).

Antifolates that target TS (Matsui et al., 1996; Yin et al., 1997), and DHFR (Benigni et al., 1983; Lorico et al., 1988) decrease levels of deoxythymidine triphosphate (dTTP), which results in a "thymineless" death. The decreased dTTP levels cause misincorporation of deoxyuridine triphosphate (dUTP) in place of dTTP into newly synthesized DNA. The dUTP is recognized as incorrect and cycles of futile excision-repair ensue, ultimately leading to DNA strand breaks and cell death (Bronder and Moran, 2003).

1.5.2 Inhibition of *De Novo* Purine Biosynthesis Pathway.

Purines serve as building blocks of RNA and DNA; they regulate enzymatic activity as components of vitamins and cofactors, and mediate energy transfer in the cell (King et al., 1983). Most differentiated adult cells can satisfy their purine requirements through purine salvage mechanisms (Howell et al., 1981; Jackson and Harkrader, 1981; King et al., 1983; LeLeiko et al., 1983; Mackinnon and Deller, 1973). Conversely, proliferating cells, such as activated T-cells and tumor cells, require activation of *de novo* purine synthesis in order to meet the greater nucleotide demands for DNA and RNA synthesis (Denkert et al., 2008; Fairbanks et al., 1995; Howell et al., 1981; Jackson and Harkrader, 1981; Kondo et al., 2000). Inhibitors of *de novo* purine biosynthesis inhibit lymphocyte and tumor cell growth, which suggests that purine salvage pathways are insufficient to support nucleotide synthesis (Christopherson et al., 2002; Hovi et al., 1976). Interestingly, even though bone marrow progenitor cells and intestinal crypt cells are highly proliferative they rely principally on purine salvage for their purine demands. This is reflected in the high levels of purine precursors such as hypoxanthine (~7-11 μM, three to four



times higher than plasma levels) in these tissues, which can not only be salvaged but can also directly inhibit *de novo* purine biosynthesis (Howell et al., 1981; King et al., 1983; LeLeiko et al., 1983; Mackinnon and Deller, 1973).

Biosynthetically, adenosine and guanosine nucleotides are derived from inosine monophosphate (IMP), which is synthesized from phosphoribosyl pyrophosphate (PRPP) in both salvage and *de novo* synthesis of purines. PRPP is formed by PRPP synthetase which uses ATP to activate ribose-5-phosphate (made through the pentose phosphate shunt from glucose). In the salvage pathway, PRPP is used by either hypoxanthine phosphoribosyl transferase (HPRT) to convert guanine and hypoxanthine back into GMP and IMP, respectively, or by adenine phosphoribosyl transferase (APRT) to convert adenine back into AMP (Murray, 1971). While the salvage of purines is a one-step conversion, the *de novo* purine synthesis pathway consists of ten reactions catalyzed by 6 enzymes that convert PRPP into IMP, which is subsequently used to synthesize AMP and GMP (Figure 1.5). Synthesis of IMP occurs in the cytosol and requires five moles of ATP, two moles of glutamine, one mole of glycine, one mole of CO₂, one mole of aspartate and two moles of formate per mole of IMP. The enzymatic reaction and intermediates of the *de* novo purine biosynthesis pathway were largely characterized in seminal experiments by Buchanan and colleagues in avian models in the 1950s and 1960s (Hartman and Buchanan, 1959a). They have since been found to be conserved in species ranging from bacteria to humans.

The first reaction is the rate-limiting step and involves the conversion of PRPP into 5phosphoribosylamine by glutamine phosphoribosylpyrophosphate amidotransferase (GPAT), which entails replacement of the pyrophosphate of PRPP by the amide group of glutamine





Figure 1.5 De novo purine nucleotide biosynthesis pathway. The de novo purine nucleotide biosynthetic pathway from phosphoribosyl pyrophosphate (PRPP) to IMP is shown. The numbered reactions are catalyzed by the following monofunctional enzymes: 1, glutamine phosphoribosylpyrophosphate amidotransferase (GPAT); 4, formylglycinamide ribonucleotide synthase (FGAM synthetase); 8, adenylosuccinate lyase (ASL). Reactions 2, 3 and 5 are catalyzed by the trifunctional glycinamide ribonucleotide (GAR) formyltransferase (GARFTase) which contains GAR synthase (GARS; reaction 2), GAR formyltransferase (GARFTase; reaction 3) and 5-aminoimidazole ribonucleotide synthase (AIRS; reaction 5) activities. Reactions 6 and 7 catalyzed bifunctional phosphoribosylaminoimidazole are by the carboxylase/ phosphoribosylaminoimidazole succinocarboxamide synthetase (PAICS) enzyme, which



contains carboxyaminoimidazole ribonucleotide synthase (CAIRS; reaction 6) and 5aminoimidazole-4-(N succinylocarboxamide ribonucleotide synthase (SAICARS; reaction 7) activities. Reactions 9 and 10 are catalyzed by a bifunctional enzyme, 5-Amino-4imidazolecarboxamide ribonucleotide formyltransferase/ IMP cyclohydrolase (ATIC) that sequentially catalyzes the last two steps in the pathway for *de novo* synthesis of IMP. ATIC has 5-aminoimidazole-4-carboxamide ribonucleotide (AICAR) formyltransferase (AICARFTase; reaction 9) and inosine monophosphate cyclohydrolase (IMPCH; reaction 10) activities. There are two folate-dependent reactions (reaction 3 and 9) in which 10-formyl tetrahydrofolate serves as the one-carbon donor catalyzed by GARFTase and AICARFTase. 5-aminoimidazole-4carboxamide (AICA) and AICAR can be metabolized to AICAR monophosphate (ZMP) by either adenine phosphoribosyl transferase (APRT) or adenosine kinase (AK), thus circumventing the reaction catalyzed by GARFTase. For the *in situ* GARFTase assay, incorporation of [¹⁴C]glycine into [¹⁴C]F-GAR in the presence of azaserine is used as a direct measure of GARFTase activity.



(reaction 1). Subsequent steps involve three multifunctional enzymes: a trifunctional protein GARFTase, that has GAR synthase (GARS; reaction 2), GAR formyltransferase (GARFTase; reaction 3), and 5-aminoimidazole ribonucleotide synthase (AIRS; reaction 5) activities; a bifunctional phosphoribosylaminoimidazole enzyme, carboxylase/ phosphoribosylaminoimidazole succinocarboxamide synthetase (PAICS). that has carboxyaminoimidazole ribonucleotide synthase (CAIRS; reaction $\mathbf{6}$) and 5-aminoimidazole-4-(N succinylocarboxamide ribonucleotide synthase (SAICARS; reaction 7) activities; and a bifunctional enzyme, 5-Amino-4-imidazolecarboxamide ribonucleotide formyltransferase/ IMP cyclohydrolase (ATIC). that has 5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase (AICARFTase; reaction 9) and IMP cyclohydrolase (IMPCH; reaction 10) activities. The remaining steps are catalyzed by monofunctional enzymes, formylglycinamide ribonucleotide synthase (FGAM synthetase; reaction 4) and adenylosuccinate lyase (ASL; reaction 8). The formate that is used by GARFTase and AICARFTase to supply the number 2 and number 8 carbons of the purine ring is carried by THF in the form of 10-formylTHF (Hartman and Buchanan, 1959a; Hartman and Buchanan, 1959b).

In a continued effort to find other inhibitors of folate metabolism at sites other than DHFR, a "critical bond blocking" strategy was employed by a joint collaboration between E.C. Taylor at Princeton and a team of chemists at Eli Lilly led by Chuan (Joe) Shih. This effort resulted in the synthesis of the 6R diastereomer of 5,10-dideazatetrahydrofolate (DDATHF) or LMX (Figure 1.1), which is structurally identical to natural THF except the nitrogen atoms at positions 5 and 10 that participate in all of the one-carbon transfers are replaced by carbons (Moran et al., 1989; Taylor et al., 1985). LMX is transported into the cell by RFC (Westerhof et al., 1995), polyglutamylated by FPGS (Baldwin et al., 1991) and inhibits GARFTase leading to



ATP and GTP depletion (Figure 1.2) (Beardsley et al., 1989). Phase I clinical investigation of LMX found that without folic acid co-administration, LMX caused severe cumulative toxicity, with myelosuppression (anemia, thrombocytopenia and neutropenia) and mucositis being dose limiting (Ray et al., 1993). With folic acid co-administration, there was a reduction in the clinical toxicity, permitting a dose of greater than 10 times that in the absence of supplementation (Roberts et al., 2000a). It was thought that the delayed and cumulative toxicity may result from gradual release of LMX metabolites from the liver resulting in an extended γ -phase plasma half life (Taber et al., 1991). One hypothesis was that folate depletion increased the expression of FR and this was contributing to greater cellular uptake in the liver and hence greater toxicity of LMX (Mendelsohn et al., 1996; Pohland et al., 1994). Another hypothesis was that thrombocytopenia occurred because platelets have the highest requirement for ATP than any other cell of the body. It is delayed because of the long maturation time of megakaryocytes (which is probably further extended under conditions of purine shortage), and it may be irreversible because the polyglutamate forms of LMX turn over very slowly such that, once formed, they are effectively impossible to eliminate (Jackman, 1999). In an effort to reduce toxicity, second generation inhibitors were synthesized. LY309887 was designed to have lower FR β affinity (Wang et al., 1992), reduced polyglutamylation (Mendelsohn et al., 1996) and a 9fold increased affinity for GARFTase compared to LMX (Budman et al., 2001; Mendelsohn et al., 1999). Additionally, structure-based drug-design was used to design AG2034, which was based on the X-ray crystal structures of the E. coli GARFTase and of the GARFTase domain of the human enzyme. Like LY309887, preclinical enzyme inhibition studies showed that AG2034 was a potent inhibitor of GARFTase (Almassy et al., 1992; Boritzki et al., 1996). However, clinical evaluation of both these compounds demonstrated the same delayed, cumulative toxicity



as observed with LMX (Bissett et al., 2001; Boritzki et al., 1996; Budman et al., 2001; Kisliuk, 2003; Roberts et al., 2000b). Continued toxicity of these compounds, even with altered FR affinity, suggests that FR-mediated uptake in the liver is not a major determinant of toxicity and implies another transport-mediated process in the liver, most likely RFC (given the neutral pH microenvironment), that may be the true source of toxicity. Thus, GARFTase inhibitors with PCFT selectivity may have the potential of improving the efficacy and reducing the toxicity of antipurine antifolates in the clinic (Goldman et al., 2010).

GARFTase inhibitors block *de novo* purine synthesis, leading to a rapid decline in ATP and GTP pools (Beardsley et al., 1989; Boritzki et al., 1996; Chen et al., 1998; Pizzorno et al., 1991). Unlike TS and DHFR inhibitors, reduction of purine pools does not necessarily induce DNA strand breaks. There are two principle hypotheses as to how GARFTase inhibitors impact p53, cell cycle and cell death. The first proposed by Zhang et al. (1998a) states that reduction of ribonucleotide pools is sensed by p53, which then stabilizes and accumulates causing arrest at the G1 checkpoint and induction of cytostasis (Linke et al., 1996; Zhang et al., 1998a). Tumor cells lacking functional p53 or that have other defects in the G1 checkpoint are more sensitive to GARFTase inhibitors. Since 50% of human cancers lack a functional G1 checkpoint, GARFTase drugs may be selectively active towards these tumors while protecting normal cells with functional p53. Moran and colleagues demonstrated that the cytotoxic effects of agents that target de novo purine nucleotide biosynthesis are not dependent on p53 status since ribonucleotide depletion prevents full activation of p53. Due to low ATP and GTP pools, kinases cannot phosphorylate p53 leading to hypophosphorylated and hypoacetylated forms of p53. In these forms, p53 is capable of nuclear retention and binding to the p21 promoter, but remains in an inactive pre-initiation complex because of insufficient recruitment of chromatin-remodeling



complexes which prevent chromatin accessibility and transcriptional activation of the p21 gene. Lack of p21 induction prevents G1 arrest and allows for S-phase entrance of tumor cells; DNA replication in the face of low purine levels results in cytotoxicity to the cell regardless of p53 status (Bronder and Moran, 2002; Bronder and Moran, 2003). If these findings are accurate, characteristic growth inhibition by antipurine antifolates is not dependent on p53 status, thus increasing the potential of this drug to treat many different malignancies.

Another consideration involves the purine salvage pathway. In bone marrow mononuclear cells, physiologic levels of hypoxanthine inhibited *de novo* purine biosynthesis and the salvage pathway was preferentially used to synthesize purines (King et al., 1983). These findings may explain the low rates of *de novo* purine synthesis in bone marrow tissues and suggests that inhibitors of *de novo* purine synthesis will not be marrow toxic. Additionally, methylthioadenosine phosphorylase (MTAP) is an enzyme that releases adenine and methionine from methylthioadenosine formed during polyamine biosynthesis (Illei et al., 2003). Whereas MTAP has been reported to be abundantly expressed in normal tissues, in many solid tumors the MTAP gene is co-deleted with CDKN2A (encodes p16INK4A) (Illei et al., 2003). Thus, many solid tumors are deficient in purine salvage and functional purine salvage in normal tissues would theoretically protect cells from cell death caused by GARFTase inhibition, increasing tumor cell selectivity for GARFTase inhibitors (Bertino et al., 2011; Hori et al., 1996).

Recently, it was found that upon purine depletion, the human *de novo* purine biosynthetic enzymes colocalize in the cytoplasm to form a multienzyme complex called the "purinosome" (An et al., 2008). Purinosome formation is associated with an increased rate of purine biosynthesis. The formation of functional multienzyme complexes may produce efficient substrate channels that link the 10 catalytic active sites. Purinosomes are dynamically regulated



by inhibition of casein kinase 2 (CK2) (An et al., 2010b) and are spatially controlled by the matrix of microtubule filaments (An et al., 2010a). It will be important to determine the effect of *de novo* purine synthesis inhibitors on the formation and function of the purinosome. Interestingly, the trifunctional MTHFD1 which synthesizes 10-formylTHF through the ATPdependent condensation of formate and THF is not associated with the purinosome (An et al., 2008; An et al., 2010b). Recently, methenylTHF synthase (MTHFS), which catalyzes the irreversible and ATP-dependent conversion of 5-formylTHF to 5,10-methenylTHF was found to enhance purine biosynthesis by delivering 10-formylTHF to the purinosome in a cell cycle and SUMO-dependent fashion (Field et al., 2011). Furthermore, MTHFS expression has been found to be elevated in some tumors, which enhances *de novo* purine biosynthesis and confers partial resistance to antifolate purine synthesis inhibitors (Field et al., 2009; Field et al., 2006). Thus, MTHFS may be a modifier of GARFTase inhibitor efficacy and determining MTHFS expression in malignancies may be an important predictor of antipurine antifolate drug activity. Because of its importance of MTHFS in *de novo* purine biosynthesis, inhibitors have been designed for potential use in cancer therapy (Wu et al., 2009).

1.5.3 Mulitargeted Antifolate.

In order to meet FDA requirements of purity, efforts were made to eliminate the synthesis of both R and S diastereomers of DDATHF by eliminating the chirality at the 6-position of LMX. One strategy replaced the 5-deazapteridine ring of LMX with a pyrrolo[2,3-*d*]pyrimidine ring, resulting in LY231514 (PMX; Alimta) (Figure 1.1) (Taylor, 1993; Taylor et al., 1992). This structural alteration converted the sp3 center at C6 to sp2 geometry. Cell culture end-product reversal and enzymology experiments indicated that this compound potently inhibited TS and had weak inhibition of DHFR, GARFTase and AICARFTase (Figure 1.2) (Shih et al., 1997;



Taylor et al., 1992). PMX is rapidly transported across the cell membrane by both RFC and PCFT (Wang et al., 2004; Westerhof et al., 1995; Zhao et al., 2008), is highly polyglutamylated (best known substrate of FPGS) (Shih et al., 1997; Taylor et al., 1992) and is very sensitive to the cellular folate status (Taylor et al., 1992; Zhao et al., 2001b). The basis for this latter finding involves the inhibitory effects of physiological folates in cells on the polyglutamylation of antifolates at the level of FPGS (Andreassi and Moran, 2002) and at the level of drug binding their target enzymes. Recently, it was discovered by Moran and colleagues that AICARFTase inhibition by PMX causes a marked accumulation of the purine synthesis intermediate 5-amino-4-imidazolecarboxamide ribotide (ZMP) (Racanelli et al., 2009). ZMP is an AMP mimetic that is an activator of AMP-activated protein kinase (AMPK). Activation of AMPK causes phosphorylation of AMPK target proteins involved in initiation of cap-dependent translation, lipid synthesis and energy metabolism. Two such proteins are the tuberous sclerosis complex 2 (TSC2) and raptor (component of mTORC1 complex). AMPK phosphorylation in response to PMX exposure and ZMP accumulation leads to inhibition of mTOR signaling in colon and lung cancer cells (Racanelli et al., 2009; Rothbart et al., 2010). PMX was found to act synergistically with sorafenib (a multi-kinase inhibitor) to enhance tumor killing via the promotion of a toxic form of autophagy that leads to activation of the intrinsic apoptosis pathway (Bareford et al., 2011). As mentioned in the introduction, PMX in combination with cisplatin has been approved for the treatment of malignant pleural mesothelioma (Hazarika et al., 2004) and NSCLC (Cohen et al., 2009). Other phase II clinical trials have been recently completed or are underway to test the efficacy of this compound in a wide range of malignancies (Adjei et al., 2010; Karapanagiotou et al., 2009; Katirtzoglou et al., 2010; Krug et al., 2009; Martin et al., 2009; Matulonis et al., 2008; Patel et al., 2009a; Patel et al., 2009b; Paz-Ares et al., 2010; Pippen et al.,



2010; Simon et al., 2008). It will be interesting to determine why PMX has significant activity against lung carcinomas, which is unusual for an antifolate.

1.5.4 Polyglutamylation of Antifolates.

The above-mentioned antifolates with the exception of PT523 are substrates for polyglutamylation by FPGS. Polyglutamation of antifolates leads to augmentation of pharmacological activity through their sustained inhibition of THF-dependent enzymes, reflecting increased affinities for target enzymes, and abilities to inhibit enzymes that are poorly inhibited by monoglutamate antifolate forms (Goldman and Zhao, 2002; Hughes et al., 1999; Mendelsohn, 1999). For example, the crystal structure of GARFTase shows that the surface of the protein near the folate binding loop is either neutral or positively charged and, therefore, would provide a suitable surface for interaction with a polyglutamate tail. This may explain the increased affinity of polyglutamylated drugs such as LMX for GARFTase (Dahms et al., 2005; Similar explanations have been provided for other antifolates and Zhang et al., 2002). intracellular targets such as TS (Allegra et al., 1985). However, inhibition of DHFR by MTX is not in itself enhanced by polyglutamylation (Goldman and Matherly, 1985; Matherly et al., 1987b). Another important consequence of polyglutamylation involves sustained inhibition of intracellular targets since long chain polyglutamates of antifolates are poor substrates for influx or efflux transporters. Therefore, antifolates are retained by cells at high concentrations even after extracellular drug levels have been reduced due to clearance (Goldman and Matherly, 1985; Matherly et al., 1987b). It is interesting to note that polyglutamylation is important for selectivity of antifolates for tumor cells. Polyglutamates of MTX have been reported to accumulate more in tumor cells than in the bone marrow or intestinal cells, such that the metabolic effects of antifolates in normal cells tend to be relatively transient (Fry et al., 1983;



Koizumi et al., 1985). Yet, the effect on normal tissues such as myelosuppression and mucositis is still the dose-limiting factor in antifolate treatment.

1.5.5 Transport as a Determinant of Selectivity and Resistance.

Transport of antifolates by RFC, PCFT and FR is a very important determinant of drug activity and tumor selectivity. Since RFC is ubiquitously expressed and functional at the neutral pH surrounding most normal tissues, transport of antifolates by RFC into proliferating normal tissues is thought to be the cause of many drug-induced toxicities. The specificities of antifolates differ for the various folate uptake mechanisms. RFC can transport all the classic antifolates including MTX, AMT, PDX, RTX, LMX, and PMX with high affinities (Figure 1.2) (Matherly et al., 2007). MTX can be transported by PCFT, albeit to a lower extent than RFC (Zhao et al., 2008). PMX has a higher affinity for PCFT than RFC at low pH and is the best known substrate for PCFT yet described (Zhao and Goldman, 2007). PT523 is not a transport substrate for PCFT (Figure 1.2) (Zhao and Goldman, 2007). As mentioned in this section, it has been observed that the same or better growth inhibition could be obtained from an analog that had reduced affinity for its enzyme target but had greater substrate affinity and therefore uptake by RFC. Examples include PDX compared with AMT, and RTX compared with CB3717. This highlights the importance of concentrative antifolate uptake to provide sufficient (unbound) intracellular drug to sustain maximal inhibition of enzyme targets and for the synthesis of polyglutamates. The significance of transport-mediated uptake can also be demonstrated in cases of antifolate resistance where loss of RFC expression causes cells to become resistant to antifolates that depend on RFC for cellular uptake (Assaraf, 2007; Matherly et al., 2007; Zhao and Goldman, 2003).



Impaired RFC function is an important mechanism of resistance to MTX (Hill et al., 1979; Niethammer and Jackson, 1975; Sirotnak et al., 1968; Sirotnak et al., 1981) and other antifolates *in vitro*, and it may be associated with clinical resistance to this agent in the treatment of ALL (Belkov et al., 1999; Gorlick et al., 1997; Levy et al., 2003; Zhang et al., 1998b), osteosarcoma (Guo et al., 1999; Ifergan et al., 2003; Yang et al., 2003) and colorectal cancer (Wettergren et al., 2005), as well as primary central nervous system lymphoma (Ferreri et al., 2004). Impaired transport of antifolates into tumor cells in preclinical and clinical studies has been associated with quantitative and/or qualitative alterations in RFC expression and/or transport activity (Assaraf, 2007; Matherly et al., 2007; Zhao and Goldman, 2003). RFC function can be lost by methylation of a CpG island in the promoter between exons B and A (Worm et al., 2001), genomic deletion (Chattopadhyay et al., 2006; Ding et al., 2001; Zhao et al., 2004c), single point mutations within the open reading frame, mutation of the ATG start codon, insertions and frameshifts, truncated proteins, deletions, mutations resulting in RFC instability, and loss of RFC alleles due to translocations (Assaraf, 2007; Ding et al., 2001; Matherly et al., 2007; Rothem et al., 2002; Wong et al., 1999; Zhao and Goldman, 2003; Zhao et al., 1999). Treatment of a L1210 murine leukemia cell line with mutagen (ethylmethanesulfonate) followed by selection with MTX using 5-CHO-THF in the growth medium produced a spectrum of RFC mutations (Assaraf, 2007; Zhao and Goldman, 2003; Zhao et al., 1999). Two RFC point mutations (V104M and S46N) that led to MTX resistance but preserved PMX and LMX growth inhibition were identified. The first mutation, V104M in the third TMD of RFC had markedly impaired transport of MTX and 5-CHO-THF. Despite the fact that the cellular THF-cofactor pool was substantially decreased, growth was sustained, consistent with the low levels of folate required for normal growth (Zhao et al., 2000b). Cells with this mutation had collateral



sensitivity to LMX due to partial maintenance of LMX transport and contraction of the folate pools. A second mutation, S46N did not alter the influx Kt for MTX and the natural folates (Zhao et al., 1998). Rather, it produced a marked (40-fold) decrease in the V_{max} for MTX but a lesser (\sim 7–8-fold) decrease in the V_{max} for 5-CHO-THF. Sensitivity to PMX was partially preserved even though the THF-cofactor pools were similar to cells with wild-type RFC (Zhao et al., 2000a). The S46N mutation has also been identified in osteosarcoma patient samples from patients treated with MTX (Yang et al., 2003) and is therefore a clinically relevant mutation. Clinically, complete loss or functional alterations in RFC are rare since tumor cells need RFCmediated transport of reduced folates to maintain tumor growth; therefore most clinically occurring point mutations are similar to S46NN which have marked loss of carrier affinity and/or mobility towards MTX, while preserving THF cofactor transport. Similarly, reductions in RFC expression are observed; for example approximately 65% of osteosarcoma samples have decreased RFC expression at biopsy and 50% have reduced RFC expression in recurrent or metastatic disease (Guo et al., 1999). It has been shown that reduced RFC expression can be caused by CpG island promoter hypermethylation and transcriptional silencing due to loss of function of transcription factors that regulate the expression of RFC (Worm et al., 2001).

In addition to impaired transport, antifolate resistance can arise from reduced polyglutamylation (Drake et al., 1996; Li et al., 1992; Liani et al., 2003; Mauritz et al., 2002; McCloskey et al., 1991; McGuire and Russell, 1998; Pizzorno et al., 1989; Pizzorno et al., 1988; Pizzorno et al., 1995; Zhao et al., 2000c), decreased affinity of the drug for its folate dependent intracellular target due to mutation (Albrecht et al., 1972; Flintoff and Essani, 1980; Goldie et al., 1980; Haber et al., 1981; Jackson et al., 1976; McIvor and Simonsen, 1990; Melera et al., 1984; Melera et al., 1988; Miyachi et al., 1995; Srimatkandada et al., 1989), increased expression of the



enzyme target so that more drug is needed for the same level of inhibition (eg. DHFR (Alt et al., 1978; Dolnick et al., 1979; Horns et al., 1984; Jackson and Harrap, 1973; Mini et al., 1985; Nunberg et al., 1978; Trent et al., 1984; White and Goldman, 1981) and TS (Drake et al., 1996; Freemantle et al., 1995; Jackman et al., 1995; Kitchens et al., 1999; O'Connor et al., 1992; Sigmond et al., 2003; Tong et al., 1998; Wang et al., 2001a)) and increased expression and function of high capacity efflux pumps, such as MRPs that remove the antifolate from cells (Assaraf, 2006). Many of the antifolates that came after AMT and MTX were designed in an effort to reduce toxicity observed clinically, increase tumor selectivity and to circumvent some of the antifolate resistance mechanisms. This dissertation will highlight drug discovery efforts to find novel antifolates that are selective for PCFT-mediated uptake and that inhibit GARFTase and *de novo* purine nucleotide synthesis as a way to avoid selectivity and resistance problems. These compounds will also be tested in cells that are MTX resistant due to RFC loss to determine the impact of RFC function on antifolates that depend on PCFT for uptake.

1.6 Hijacking the Acidic Tumor Microenvironment for Solid Tumor Targeting.

To maintain their rapid growth and proliferation, cancer cells have a higher need for energy and for biosynthesis of nucleotides than normal differentiated cells. This increased biosynthetic demand can be, in part, met by an altered metabolic program known as the Warburg effect or aerobic glycolysis in which cancer cells become highly glycolytic even in the presence of normal oxygen tension (Lunt and Vander Heiden, 2011). To avoid intracellular acidification, glycolytically-produced acid must be extruded from cells. This is achieved by increased expression and/or function of plasma membrane ion pumps and transporters such as H⁺-ATPases or vacuolar ATPases (Hinton et al., 2009; Martinez-Zaguilan et al., 1993; Sennoune et al., 2004), the Na⁺/H⁺ exchanger (NHE1) of the SLA9A family (Chiang et al., 2008; Kumar et al., 2009;



McLean et al., 2000; Miraglia et al., 2005), the monocarboxylate-H⁺ efflux symporter (MCT1 and MCT4) of the SLC9A family (Chiche et al., 2012; Kennedy and Dewhirst, 2010; Pinheiro et al., 2008a; Pinheiro et al., 2008b; Pinheiro et al., 2010), and the carbonic anhydrases CAIX and CAXII (Chiche et al., 2009; Ilie et al., 2011; Loncaster et al., 2001; Swietach et al., 2009; Wykoff et al., 2000), the Cl⁻/HCO3⁻ exchanger (CBE) (Alper, 2009) and Na⁺/HCO3⁻ cotransporter (NBC) (Boron et al., 2009). The increased activities of these transporters cause reversal of the normal intra-extracellular pH gradients, so that cancer cells produce significant acidification of the extracellular environment (acidic tumor microenvironment). Extracellular pH in tumor cells can be as low as $\sim 6.7-7.1$, while they maintain a normal or slightly alkaline intracellular pH of \geq 7.4. This is in comparison to normal differentiated adult cells which maintain an intracellular pH of ~7.2 and an extracellular pH of ~7.4 (Busco et al., 2010; Gallagher et al., 2008; Gillies et al., 2002; Stuwe et al., 2007; Webb et al., 2011). Acidification of the tumor environment is exacerbated by limited removal of glycolytic waste products due to poor perfusion, which is affected by tumor size and abnormal vascularization (Webb et al., 2011). The resultant H^+ - electrochemical gradient favors passive weak acid uptake by pH partition and, importantly, acts as a driving force for H⁺-coupled solute transport at the cancer cell plasma membrane. Additionally, the decrease in extracellular pH increases the affinity and broadens substrate specificity of pH-dependent transporters (Leuthold et al., 2009; Nozawa et al., 2004; Qiu et al., 2006; Rubio-Aliaga et al., 2003).

The targeted drug strategy that uses selective uptake of therapeutics into the tumor cell by H⁺-coupled transporters is novel but not unprecedented (Anderson and Thwaites, 2010). Aberrant H⁺-coupled di/tripeptide (PepT1 and PepT2) transport has been characterized in tumor cells and overexpression may be useful for targeting a number of experimental and clinical



anticancer substrates to tumor cells, including the photodynamic therapy and imaging agent 5aminolevulinic acid (Anderson et al., 2010) and the aminopeptidase inhibitor bestatin (Nakanishi et al., 2000). Prodrugs of floxuridine and cytarabine may also be transported by PepT1 (Sun et al., 2009). Additionally, the H⁺-coupled amino acid transporter PAT1 and the pH dependent OATPs could also be used for mediating uptake of anti-cancer drugs. PAT1 can also transport 5aminolevulinic acid (Anderson et al., 2010) and L-cycloserine (Anderson et al., 2004). Prominent low-pH transport activities have been observed for several organic anion transporting polypeptides (OATPs) (Leuthold et al., 2009); of these, only OATP1A2 is known to have MTX transport activity at low pH (Badagnani et al., 2006). Recently, OATP2B1 has been established as a low-affinity, but highly selective, low pH antifolate transporter demonstrating the critical role that pH, substrate, and substrate concentration can play in identifying the spectrum of activities of a transporter (Visentin et al., 2012).

This dissertation will focus on PCFT-mediated uptake of novel antifolates into the tumor cell by harnessing the proton gradient that exists in the tumor microenvironment as a therapeutic strategy.

CHAPTER 2

THE HUMAN PROTON-COUPLED FOLATE TRANSPORTER IS EXPRESSED AND FUNCTIONAL IN HUMAN SOLID TUMORS

2.1 Introduction.

The anionic nature of folates and antifolates precludes their diffusion across biological membranes. Therefore, three genetically distinct and functionally diverse transport systems are in place to facilitate uptake of these molecules into the cells of peripheral tissues. Two facilitative transporters, RFC and the newly discovered PCFT and two FR isoforms (α and β) mediate this uptake.

RFC is ubiquitously expressed in both normal and tumor tissues, with characteristic patterns of localization in intestine, hepatocytes, renal epithelial cells and choroid plexus, which suggest specialized roles in these tissues for folate homeostasis (Matherly and Goldman, 2003; Matherly et al., 2007; Zhao et al., 2009a). Indeed, given its widespread tissue expression, RFC is considered the major transport system for folates in mammalian cells and tissues.

FR α is predominantly expressed on the apical (luminal) surface of polarized epithelial cells where it is not in contact with circulating folate (Chancy et al., 2000). FR α is expressed in epithelial cells of the kidney, choroid plexus, retina, uterus, and placenta (Elnakat and Ratnam, 2004). Malignant tissue expression includes malignant pleural mesothelioma (Bueno et al., 2001) and adenocarcinomas of the cervix, uterus, and ovary (Elnakat and Ratnam, 2004). Importantly, FR α is overexpressed in up to 90% of ovarian cancers (Toffoli et al., 1997; Wu et al., 1999). Close associations were reported between FR α expression levels with grade and differentiation status of ovarian tumors (Buist et al., 1995; Garin-Chesa et al., 1993; Veggian et al., 1989; Wu et al., 1999). FR β is expressed in the thymus, spleen, placenta, and CD34+ human hematopoietic cells and is needed for normal myelopoiesis (Pan et al., 2002; Reddy et al., 1999).



Both acute and chronic myelogenous leukemias express FR β (Kamen and Smith, 2004; Salazar and Ratnam, 2007).

Human PCFT transcripts were reported to be highly expressed along the proximal jejunum, duodenum, kidney, liver, placenta, spleen and choroid plexus and, to a lesser extent, in the brain, testis and lung (Inoue et al., 2008; Qiu et al., 2006). Mouse PCFT transcripts were highly expressed in the duodenum, proximal jejunum, kidney, liver and to a lesser extent in the brain, skin, lung, stomach, and testis. Mouse PCFT protein was found on the apical brush-border membrane of the proximal jejunum and duodenum (Qiu et al., 2007). Direct evidence that this transporter is responsible for low-pH transport and intestinal folate absorption came from the discovery that homozygous mutations in the coding region of the PCFT gene leads to the rare autosomal recessive disorder HFM (Atabay et al., 2010; Borzutzky et al., 2009; Geller et al., 2002; Lasry et al., 2008; Mahadeo et al., 2010; Mahadeo et al., 2011; Meyer et al., 2010; Min et al., 2008; Qiu et al., 2006; Shin et al., 2011; Shin et al., 2010; Zhao et al., 2007). Loss of PCFT function leads to impaired intestinal folate absorption, resulting in severe folate deficiency, and impaired transport of folates across the choroid plexus into the central nervous system. Importantly this establishes the critical physiological functions of PCFT folate transport (Zhao et al., 2009a).

The discovery of PCFT may provide a novel transport route for antifolates into tumor cells. The ability of PCFT to utilize a proton gradient across the cell membrane to transport antifolates intracellularly may provide a new mechanism for tumor targeting, based on the acidic tumor microenvironments of solid tumors. To determine whether this approach is plausible, the therapeutic potential of PCFT as a means of selectively delivering antifolates into the tumor cell must be established. The expression of PCFT and how it compares to RFC and FR expression in



human malignancies is largely unestablished. In solid tumor cells, previous results have shown that MTX influx at pH 5.5 was equal to, or greater than, influx at pH 7.4 in 29 of 32 cell lines, including cell lines from the NCI60 cell line panel (Zhao et al., 2004b). However, it has yet to be established what the levels of PCFT are in these and other clinically relevant solid tumor cell lines. Further patterns of PCFT expression in tumor specimens have not been previously established. This chapter will focus on determining the level of PCFT expression in a wide range of solid tumor and leukemia cell lines. The expression of PCFT will be compared in tumor and normal tissues at the RNA, protein, and functional levels. Patterns of PCFT expression in both normal and tumor tissue will be compared to those for RFC and FR.

The findings presented in this chapter indeed establish that PCFT is expressed and functional in solid tumors and has restricted expression in normal tissues. Thus, PCFT could be used in conjunction with the acidic tumor microenvironment to efficiently deliver cytotoxic antifolates into the tumor cell.

2.2 Materials and Methods.

2.2.1 Chemicals and Reagents.

[3',5',7-³H]MTX (20 Ci/mmol) was purchased from Moravek Biochemicals (Brea, CA). Both labeled and unlabeled MTX were purified by HPLC prior to use (Fry et al., 1982). Other chemicals were obtained from commercial sources in the highest available purities.

2.2.2 Cell Culture.

The sources and cell culture conditions for the panel of human solid tumor and leukemia cell lines used for real-time RT-PCR assays of transcript levels for RFC and PCFT are summarized in Table 2.1. HeLa R1-11-RFC6 and R1-11-PCFT4 cells were derived from RFC- and PCFT-null R1-11 cells by stable transfection with HA-tagged pZeoSV2(+)-RFC and



pZeoSV2(+)-PCFT constructs, respectively (Zhao et al., 2008), and were gifts of Dr. I. David Goldman (Albert Einstein School of Medicine, Bronx, NY).

2.2.3 Real-time RT-PCR Analysis of RFC and PCFT Transcripts.

2.2.3.1 Origene cDNA Arrays of Tumor and Normal Tissue.

To expand the transporter expression profiles in normal and malignant human tissues we measured the levels of PCFT and RFC transcripts in a wide range of human normal and tumor tissues. We used arrays of normalized cDNAs from either 48 pathologist-verified normal tissues (e.g., adrenal, small intestine, liver, lung, ovary, etc.; "Human Major Tissue qPCR Array", Origene HMRT102) or 96 normalized cDNAs from pathologist-verified solid tumors and paired normal tissues ("TissueScan Oncology qPCR Array", Origene CSRT101). Real-time RT-PCR was performed in a 384 well plate format on a Roche LightCycler 480 using Universal Probes (Roche, Indianapolis, IN) and gene-specific primers. Details are included in Table 2.1. Transcript levels for PCFT and RFC genes were normalized to those for glyceraldehyde-3-phosphate dehydrogenase (GAPDH) and transcripts were quantified using the delta Ct method.

2.2.3.2 Solid tumor and Leukemia Cell Lines.

RNAs were isolated from a large variety of human cell lines including solid tumors (n=57) and leukemias (n=27) (Table 2.2) using TRIzol reagent (Invitrogen). cDNAs were synthesized using the Superscript reverse transcriptase III kit (Invitrogen) and purified with the QIAquick PCR Purification Kit (Qiagen). PCFT, RFC and FR α transcript levels were measured by real-time RT-PCR, which was performed using Universal Probes (Roche, Indianapolis, IN) and gene-specific primers. Details are included in Table 2.1. Transcripts were normalized to GAPDH and quantified by constructing external standard curves for each gene of interest. Standard curves were made by using serial dilutions of linearized templates, prepared by



Table 2.1 U	niversal Pro	bes and SYBR Green RT-PCR Primer Sequei	nces of Human	Genes		
	Gene	Primer Sequences	Probe	Size (bp)	Annealing (°C)	Gen Bank Accession
	PCFT	Upper: 5'-CTCATCCCGGCTGTTCTG-3' Lower: 5'-CTGGAACTCGAGGTGAGGAT-3'	89	60	60	NM_080669
Universal Probes	RFC	Upper: 5'-CAGTTCCTCGTGCCCATC -3' Lower: 5'-GGCAAGGAACGTGTTGACC -3'	37	93	60	U19720
	GAPDH	Upper: 5'-CTCTGCTCCTCCTGTTCGAC-3' Lower: 5'-GCCCAATACGACCAAATCC-3'	Catalog # 05190541001	119	60	
	PCFT	Upper: 5' -CCTCCGGCATCTTCAACTCACT Lower: 5'-CTCTGGGGAAACTGCTGGAAC	ICTA -3' CTC -3'	157	60	NM_080669
SYBR	RFC	Upper: 5' -GTGGAGAAGCAGGTGCCCGTG Lower: 5'-GGCAAAGAACGTGTTGACC	ЮАА -3' С -3'	174	64	U19720
Green	FRa	Upper: 5' -GACTGTGAGCAATGGTGGGAA Lower: 5'-TGTGGGGAAGTAGAGAGAAA	AGAT -3' AGGT -3'	141	60	AK223527
	GAPDH	Upper: 5' -AACGGGAAGCTTGTCATCAATG Lower: 5' -CGTGACCTGCTCCCGCGTGAA	igaaa -3' Agtt-3'	194	60	NM_002046

Table 2.2 Leuk	al-time PCR.				
CELL LINE	DISEASE	ORIGIN	SOURCE		
U937	AML	Macrophage?	ATCC		
CTS	AML M1	Peripheral blood	Fuse, A.		
Kasumi-1	AML M2	Peripheral blood	ATCC		
HL60	AML M2	Peripheral blood	ATCC		
MV4-11	AML M5	Peripheral blood	ATCC		
THP-1	AML M5	Peripheral blood	ATCC		
AML-193	AML M5	Peripheral blood	ATCC		
KG-1	AML M6	Bone marrow	ATCC		
KG-1a	AML M6	Bone marrow	ATCC		
K562 ¹	CML	Bone marrow	ATCC		
CMS	AML M7	Peripheral blood	Fuse, A.		
MEG-01	CML	Bone marrow	ATCC		
СМК	DS AML M7	Peripheral blood	DSMZ		
СМҮ	DS AML M7	Bone marrow	Fuse, A.		
697	BP-ALL	Bone marrow	DSMZ		
Nalm6	BP-ALL	Peripheral blood	DSMZ		
Uoc B4	BP-ALL	CSF	Findley, H.		
REH	BP-ALL	Unknown	ATCC		
CCRF-CEM ^{1,2}	T-cell ALL	Peripheral blood	ATCC		
MOLT4 ¹	T-cell ALL	Peripheral blood	DSMZ		
MOLT3	T-cell ALL	Peripheral blood	DSMZ		
HPB-ALL	T-cell ALL	Peripheral blood	DSMZ		
TALL-1	T-cell ALL	Bone marrow	DSMZ		
DND 41	T-cell ALL	Peripheral blood	DSMZ		
ALL-SIL	T-cell ALL	Peripheral blood	DSMZ		
Jurkat	T-cell ALL	Peripheral blood	ATCC		
TE-85	Osteosarcoma	Bone	Peterson, W.D.		
HTB166	Ewing's sarcoma	Bone	ATCC		
MCF-7 ^{1,2}	Adenocarcinoma	Breast	ATCC		
MDA-MB231 ^{1,2}	Adenocarcinoma	Breast	ATCC		
MDA-MB435 ^{1,2}	Adenocarcinoma/Melanoma	Breast/Skin?	ATCC		
$T-47D^1$	Ductal carcinoma	Breast	ATCC		
KB	Adenocarcinoma	Cervix	ATCC		
HeLa ²	Adenocarcinoma	Cervix	ATCC		
HCT-116 ^{1,2}	Colorectal adenocarcinoma	Colon	ATCC		
$SW-620^1$	Colorectal adenocarcinoma	Colon	ATCC		
HCT15 ^{1,2}	Colorectal adenocarcinoma	Colon	ATCC		
Caco-2	Colorectal adenocarcinoma	Colon	ATCC		
BCPC-3	Adenocarcinoma	Pancreas	ATCC		
UCVA-1	Adenocarcinoma	Pancreas	Peterson, W.D.		
786-O ^{1,2}	Renal cell adenocarcinoma	Kidney	ATCC		



ACHN ^{1,2}	Renal cell adenocarcinoma	Kidney	ATCC		
IGROV-1 ¹	Adenocarcinoma	Ovary	Ratnam, M.		
OVCAR-3 ^{1,2}	Adenocarcinoma	Ovary	ATCC		
SKOV-3 ¹	Adenocarcinoma	Ovary	ATCC		
HepG2 ²	Hepatocellular carcinoma	Liver	ATCC		
Hep3B ²	Hepatocellular carcinoma	Liver	ATCC		
Y79	Retinoblastoma	Eye, retina	ATCC		
SK-MEL5 ^{1,2}	Melanoma	Skin	ATCC		
SK-MEL-28 ¹	Melanoma	Skin	ATCC		
HTB139	Rabdomyosarcoma	Muscle	Peterson, W.D.		
SK-N-SH	Neuroblastoma	Brain	ATCC		
SK-N-BE	Neuroblastoma	Brain	ATCC		
SK-N-MC	Neuroepithelioma	Supraorbital area	ATCC		
HT1080	Fibrosarcoma	Connective tissue	ATCC		
PC-3 ^{1,2}	Adenocarcinoma	Prostate	ATCC		
DU-145 ^{1,2}	Carcinoma	Prostate	ATCC		
U 1650	Bronchoalveolar	lung	ATCC		
H1030	adenocarcinoma	lung	AICC		
H2122	Adenocarcinoma/NSCLC	lung	ATCC		
H2030	Adenocarcinoma/NSCLC	lung	ATCC		
H1573	Adenocarcinoma	lung	ATCC		
H1781	Bronchoalveolar	lung	ATCC		
111701	adenocarcinoma	lung	AICC		
H3255	Adenocarcinoma/NSCLC	lung	Gazdar, A.F.		
A549 ¹	Carcinoma	lung	ATCC		
CRI 5807	Bronchioalveolar carcinoma	lung			
CILLSOUT	/NSCLC	lung	ATCC		
CRL5872	Adenocarcinoma/NSCLC	lung	ATCC		
CRL5810 ^{1,2}	Adenocarcinoma/NSCLC	lung	ATCC		
CRL5800 ^{1,2}	Adenocarcinoma/NSCLC	lung	ATCC		
H596	Adenosquamous carcinoma	Lung	ATCC		
NCI-H460 ^{1,2}	Large-cell carcinoma	Lung	ATCC		
H69	SCLC	Lung	ATCC		
H446	SCLC	Lung	ATCC		
H226 ¹	Pleural mesothelioma	Pleura	ATCC		
H2373	Pleural mesothelioma	Pleura	Pass, H.I.		
H2452	Pleural mesothelioma	Pleura	Pass, H.I.		
H2461	Pleural mesothelioma	Pleura	Pass, H.I.		
H2591	Pleural mesothelioma	Pleura	Pass, H.I.		
H2595	Pleural mesothelioma	Pleura	Pass, H.I.		
H2714/HP-1	Pleural mesothelioma	Effusion	Pass, H.I.		

1 – Cell lines of NCI60 cell line panel

2 – Cell lines used in the report of (Zhao et al., 2004b)


amplification from suitable cDNA templates, subcloned into a TA-cloning vector (PCR-Topo; Invitrogen), and restriction digested.

2.2.4 Determination of PCFT Protein Expression Levels.

To determine whether transcript levels correlate with increased protein levels, PCFT and RFC protein levels in solid tumor cell lines and tissues were measured. Our laboratory has made human PCFT and RFC-specific (Hou et al., 2011; Wong et al., 1998; Wong et al., 1999) polyclonal antibodies specific for a carboxyl-termini PCFT peptide (CKADPHLEFQQFPQSP) or RFC (PEDSLGAVGPASLEQRQS) peptide. For PCFT, polyclonal antibody services at Invitrogen injected the peptide into rabbits with a hapten-conjugated carrier, after which they collected the bleeds and tested antibody specificity by ELISA. The serum was purified using a peptide affinity column synthesized from Affi-Gel 10 (BioRad, Richmond, CA) and the specific peptide, using pH 2.5 sodium citrate to elute the antibody. Specificity was validated by peptide competition in both western blot and immunohistochemistry experiments.

2.2.4.1 Western Blot Analysis of Solid Tumor Cell Lines.

For characterizing PCFT protein expression in solid tumor cell lines, sucrose-enriched plasma membranes were prepared by differential centrifugation. Briefly, cells were suspended in 10 mM Tris-HCl, pH 7.0, containing X1 protease inhibitor cocktail tablets (Roche, Indianapolis, IN), and disrupted with a Parr nitrogen cavitator (500 psi, 20 min). The homogenate was spun at 600 x g to remove cell debris and nuclei; the supernatant was centrifuged at 200,000 x g in a Beckman 70Ti rotor for 90 min. The membrane pellet was suspended in 600 µL of 10 mM Tris-HCl, pH 7.0, containing the protease inhibitor cocktail, and layered on a discontinuous sucrose gradient (2 mL 60% and 2.5 mL 20% sucrose in a SW55Ti rotor). Centrifugation was for 1 h at 58,000 x g. The 20%-60% interface containing plasma membranes was removed, diluted



approximately 10-fold with 10 mM Tris-HCl pH 7.0 (containing proteolytic inhibitors), and again centrifuged at 200,000 x g for 60 min to pellet the membranes (Matherly et al., 1991). Proteins were quantified with Folin-phenol reagent (Lowry et al., 1951). Membrane proteins were electrophoresed on 7.5% polyacrylamide gels in the presence of SDS (Laemmli, 1970) and electroblotted onto polyvinylidene difluoride membranes (PVDF) (Pierce, Rockford, IL) (Matsudaira, 1987). Immunoreactive PCFT and RFC were detected on membranes with the PCFT or RFC-specific polyclonal antibodies described above. An IRDye800CW-conjugated goat anti-rabbit IgG (Rockland, Gilbertsville, PA) was used as a secondary antibody, and the membranes were scanned with the Odyssey® Imaging System. Densitometry used Odyssey software (v 1.2) for quantitating levels of PCFT protein. PCFT levels were normalized to Na⁺/K⁺ ATPase protein levels (mouse antibody from Novus Biologicals, Littleton, CO) on Westerns.

2.2.4.2 Immunohistochemistry of Tumor and Normal Tissue Panels.

PCFT and RFC-specific peptide antibodies were used with immunohistochemistry to profile tissue/cellular distributions and transporter levels in commercially available paraffin tissue panels (US Biomax) of normal (FDA995) and malignant tissues (BCN961) from ovary, breast, prostate, liver, etc. Specificity was established with normal IgG and (as warranted) the addition of blocking peptide to the antibody mix. Panels included malignant tissues from a wide range of tumor types and normal tissue types including some samples with established expression of PCFT such as the duodenum, kidney, and liver. Immunohistochemistry was performed in collaboration with Mr. Larry Tait from the Karmanos Cancer Institute Imaging Core Facility.

2.2.5 Transport of [³H]MTX in Solid Tumor Cell Lines.



To determine the function of PCFT and RFC in the solid tumor cell lines, transport of 0.5 µM [³H]MTX was assayed in cell monolayers over 5 min at 37°C in 4-(2-hydroxyethyl)-1piperazineethanesulfonic acid (HEPES)-buffered saline (20 mM HEPES, 140 mM NaCl, 5 mM KCl, 2 mM MgCl₂, and 5 mM glucose) at pH 7.2 to determine RFC-mediated transport, or in 4morphilinopropane sulfonic (MES)-buffered saline (20 mM MES, 140 mM NaCl, 5 mM KCl, 2 mM MgCl₂, and 5 mM glucose) at pH 5.5 for determining transport by PCFT (Zhao et al., 2004b). Some transport experiments were performed in the presence of 20 nM folic acid to rule out uptake by the folate receptor. At the end of the incubations, transport was quenched with icecold Dulbecco's phosphate-buffered saline (DPBS), cells were washed 3 times with ice-cold DPBS, and cellular proteins were solubilized with 0.5 N NaOH. Levels of drug uptake were expressed as pmol/mg protein, calculated from direct measurements of radioactivity and protein contents of cell homogenates. Radioactivity was measured with a scintillation counter (Model LS6500; Beckman-Coulter, Fullerton, CA) and proteins were quantified using Folin-phenol reagent (Lowry et al., 1951). MTX was frequently used to characterize RFC and PCFT-mediated transport because it is commercially available, it is not metabolized over short intervals, and because of the ease and accuracy of influx determinations and distinguishing between free and tightly bound drugs within cells.

2.3 Results

2.3.1 Expression of RFC and PCFT in Human Normal and Tumor Tissue.

In order to determine the potential of targeting PCFT for drug uptake it was important to establish the expression of PCFT at both the transcript and protein levels in human normal and tumor tissues. For normal tissues, transcript levels for RFC and PCFT were measured by realtime RT-PCR of normalized Origene cDNA arrays from 48 pathologist-verified normal human



tissues. PCFT is expressed in most normal tissues, albeit at low levels. We measured high levels of PCFT mRNA in highly metabolic tissues such as the duodenum, kidney, liver, and the adrenal and pituitary glands (Figure 2.1, Panel A). This corroborated expression patterns observed in mouse tissues (Qiu et al., 2006). For RFC, expression was ubiquitous with the highest levels in tissues of the liver, lung, placenta, ovary and retina, and low in the heart and muscle. These findings were similar to mRNA expression patterns described by Whetstine et al. (2002a) in human tissues measured by northern blotting. The levels of PCFT at the transcript level were validated by immunohistochemical detection of PCFT protein using US Biomax tissue arrays of FDA approved human normal tissue and a polyclonal PCFT antibody. As demonstrated by realtime RT-PCR, the levels of PCFT protein were high in the duodenum (Figure 2.1, Panel B) and kidney (Figure 2.1, Panel C). Staining was specific since the signal could be competed out with a PCFT-specific peptide (data not shown) or when the secondary antibody was not included (data not shown). Overall, PCFT transcript and protein expression is more limited than RFC expression in normal tissues. For tumor tissues, RFC and PCFT transcripts were measured by real-time RT-PCR of normalized Origene cDNA arrays from multiple human primary tumors. Significant, albeit variable levels of PCFT transcripts were detected in all tumors tested. The expression pattern of PCFT in tumor tissue was similar to levels found in normal tissue, with liver tumors showing the highest levels (Figure 2.2, Panel A). Expression of RFC was high in the liver and lung, similar to the normal tissue expression pattern. Interestingly, the level of RFC was higher in both breast and colon tumors compared to normal tissue (Figure 2.2, Panel B). The continued clinical use of classical antifolates, which are substrates for RFC-mediated uptake, including MTX in breast cancer and RTX in colon cancer, may reflect the tumor-specific expression of RFC in these tissues. Patterns of transporter expression in primary tumors were





Figure 2.1 PCFT and RFC expression in human normal tissues. PCFT (*Panel A*) and RFC (*Panel D*) transcripts were measured using an Origene cDNA array of 48 pathologist-verified human normal tissue by real-time RT-PCR from total RNAs using a Roche480 Light-cycler and gene specific Universal probes and primers (Table 2.1). Transcript levels were normalized to GAPDH transcripts. Immunohistochemistry of US Biomax tissue arrays of human small intestine (*Panel B*) and kidney (*Panel C*) normal tissues stained with a polyclonal PCFT antibody. Experimental details are provided in the Materials and Methods.





Figure 2.2 PCFT and RFC expression in human normal and tumor tissues. PCFT (*Panel A*) and RFC (*Panel B*) transcripts were measured in an Origene cDNA array of pathologist-verified, breast, colon, kidney, liver, lung, ovary, prostate and thyroid human tumor tissue (n=6) cDNAs compared to paired normal tissues from the same patient (n=3) by real-time RT-PCR from total RNAs using a Roche480 Light-cycler and gene specific Universal probes and primers (Table 2.1). Transcript levels were normalized to β -actin transcripts. Immunohistochemistry of US Biomax tissue arrays of human ovarian (*Panel C*) and liver (*Panel D*) tumors stained with a polyclonal PCFT antibody. *Panel E*, the ratio of PCFT to RFC transcript levels. Experimental details are provided in the Materials and Methods.



confirmed by immunohistochemistry of tissue arrays probed with transporter-specific antibodies. Tissue arrays contained multiple cancer and adjacent tissues, single core per case, 16 types of common organs and were pathologically confirmed (bladder, brain, breast, colon, esophagus, kidney, liver, lung, lymph node, ovary, pancreas, prostate, rectum, skin, stomach and uterine cervix). Similar to real-time RT-PCR, the levels of PCFT protein were high in the ovarian and liver tumors (Figure 2.2, Panel C and D; respectively) compared to IgG control (data not shown), again reflecting PCFT transcript levels obtained from real-time RT-PCR. For the most part, PCFT levels are similar in both normal and tumor tissues at both the transcript and protein level.

The ratios of PCFT to RFC transcript expression in human normal and tumor tissues were determined. Thyroid, ovarian and liver tumors had higher tumor PCFT/RFC ratios compared to normal tissues (Figure 2.2, Panel E). The ratio of PCFT to RFC expression and function may represent a more important indicator of which tumor types will benefit from PCFT-selective antifolates. Functional RFC could transport reduced folates into the cell which would compete with the antifolate for binding to folate-dependent enzymes, thereby reducing the cytotoxicity of antifolates that depend on PCFT for cellular uptake (see Chapter 5).

2.3.2 Expression and Function of RFC and PCFT in Human Solid Tumor and Leukemia Cell Lines.

Following reports of a low pH transport activity in solid tumor cells lines and to find a solid tumor cell line model for our PCFT-targeted therapeutics, we turned our attention to establishing an expression profile for PCFT compared to RFC and FRs in a number of cell lines derived from human solid tumors and leukemias (Table 2.2). Transcript levels for PCFT along with RFC and FRs α and β were measured by real-time RT-PCR and normalized to levels of GAPDH. Our results demonstrated significant levels of PCFT transcripts in the majority of



human solid tumor cell lines of different origins (e.g., breast, prostate, ovarian, etc.) (Figure 2.3, Panel A), and uniformly low PCFT transcript levels in human leukemias, including both ALL and AML (Figure 2.3, Panel C). PCFT levels were highest in Caco-2 (colorectal) SKOV3 (ovarian), HepG2 (hepatoma), HeLa (cervical), and T47D (breast) cancer cells. RFC transcripts were detected in all leukemia and solid tumor cell lines with the exception of MDA-MB-231 breast cancer cells (reported to express very low RFC (Worm et al., 2001)) (Figure 2.3, Panel B and D). High levels of FR α were detected in a small subset of ovarian, cervical, and breast cancer cell lines and modest FR α levels were measured in ALL (mostly T-cell) sublines (data not shown). FR β transcripts were consistently low-to-undetectable in both solid tumors and leukemias, with the highest levels restricted to a small number of AML and T-cell ALLs (data not shown). The levels of human PCFT, RFC and FR transcripts in solid tumor and leukemia cell lines were published (Kugel Desmoulin et al., 2011). Real-time RT-PCR was repeated with SYBR green and gene-specific primers (Table 2.1), (experimental details are the same as in section 5.2.6) and identical results were obtained.

The level of PCFT and RFC protein expression was validated for ten solid tumor cell lines (HepG2, Hep3B, H596, CRL5810, H2595, HCT15, Caco-2, DU145, MDA-MB 321, SK-MEL5) and four control HeLa cell lines (R1-11-mock (no functional PCFT or RFC), R1-11-PCFT4 (R1-11-mock stably transfected with PCFT), HeLa (functional PCFT and RFC), R5 (HeLa cells that express PCFT but not RFC)) by isolating membrane fractions through differential centrifugation and sucrose gradients, followed by immunoblotting with PCFT and RFC-specific polyclonal antibodies. Relative PCFT and RFC protein levels paralleled levels of PCFT (Figure 2.4, Panel A) and RFC (Figure 2.4, Panel B) transcripts, as detected by real-time RT-PCR. There were some differences in protein sizes, which likely reflect post-translational





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Figure 2.3 PCFT and RFC transcript expression in human solid tumor and leukemia cell lines. PCFT (*Panel A and C*) and RFC (*Panel B and D*) transcripts were measured in 53 human solid tumor (*Panels A and B*) and 27 leukemia (*Panels C and D*) cell lines by real-time RT-PCR from total RNAs using a Roche480 Light-cycler and gene specific Universal probes and primers (Table 2.1). Transcript levels were normalized to GAPDH transcripts. Experimental details are provided in the Materials and Methods. A table summarizing the characteristics of the 53 tumor and 27 leukemia cell lines is also included in Table 2.2.





Figure 2.4 PCFT and RFC protein expression in human solid tumor cell lines. PCFT (*Panel A*) and RFC (*Panel B*). Pure membrane fractions were isolated using a Parr nitrogen cavitator at 500 psi for 20 min, differential centrifugation and sucrose gradients. Membrane proteins (25 μ g) were electrophoresed on 7.5% denaturing polyacrylamide gels and immunoblotted with polyclonal PCFT and RFC antibodies. Na⁺/K⁺ ATPase protein levels were used as loading controls. The characteristics of the 14 tumor cell lines are included in Table 2.2. Non-specific (NS) band.



modifications (e.g., glycosylation (Unal et al., 2008; Wong et al., 1998)). Finally, functional validation of transporter expression in solid tumor cell lines was determined by transport of [³H]MTX (Figure 2.5) at pH 5.5 for PCFT (Panel A), and at pH 7.2 for RFC (Panel B). Relative uptake of [³H]MTX somewhat paralleled transcript and protein levels for PCFT. More modest levels of transport were detected at pH 7.2, although the correlation with RFC protein was inexact. The reason for this is unclear. pH 5.5 (PCFT) to pH 7.2 (RFC) transport ratios ranged from ~2- to ~9-fold (Figure 2.5, Panel C), demonstrating broad spectrum and high-level PCFT to RFC membrane transport in clinically relevant human tumor cell lines, as previously reported (Zhao et al., 2004b).

2.4 Discussion

Our findings have established the expression patterns and pH-specific transport for PCFT in human solid tumor cell lines, primary tumors and normal tissues. We found that expression of PCFT transcripts and protein in normal tissues is more limited than for the ubiquitously expressed RFC, with high levels in the liver, kidney, and small intestine. In addition, a wide range of human solid tumor tissues and cell lines expressed PCFT transcripts and protein, and PCFT expression generally correlated with pH-dependent transport function. Goldman and colleagues measured low pH transport of MTX into human tumor cell lines (Zhao et al., 2004b). Our comprehensive analysis of PCFT expression and function identified PCFT as the low pH folate transporter responsible of MTX uptake at acid pH in solid tumor cell lines. While RFC protein was likewise detected in most of the tumor cell lines, transport was only modestly reflected in levels of RFC protein, suggesting the existence of previously unrecognized posttranslational regulatory mechanisms for RFC and/or an unknown non-RFC transport process at neutral pH. Finally, we have found the expression of PCFT to be very low in the bone marrow,





Figure 2.5 PCFT and RFC function in human solid tumor cell lines. Uptake of 0.5 μ M [³H]MTX was measured at 37°C for 5 min in cell monolayers at pH 5.5 (MES-buffered saline) (*Panel A*) or pH 7.2 (HEPES-buffered saline) (*Panel B*), and internalized [³H]drug was normalized to total protein. *Panel C*, the ratio of [³H]MTX uptake at pH 5.5 / pH 7.2 in WT and R5 HeLa cells. A table summarizing the characteristics of the 14 tumor cell lines is included in Table 2.2.

which would suggest that PCFT-targeted therapeutics may be less marrow toxic compared to antifolates presently in clinical use that rely on RFC-mediated uptake at neutral pH. It will be important to test normal hematopoietic stem cells to assess the impact of PCFT-selective analogs on this cell fraction.

The importance of PCFT expression in normal tissues to the development of drug toxicities will depend on transport function of PCFT in these tissues. Even though PCFT-mediated transport is maximal at low pH, transport is also detected at pH 7.4 in human cells and *Xenopus* oocytes that express PCFT. This residual PCFT function at pH 7.4 is thought to be driven by increases in membrane potential. Whether the level of PCFT-mediated transport at pH 7.4 in normal tissues is sufficient to cause dose-limiting toxicity of antifolates selective for PCFT mediated uptake remains to be determined. Additionally, there are instances of a localized acidic environment created by Na⁺/H⁺ exchangers at the basolateral membranes of the choroid plexus (Segal, 2000) and hepatocyte (Horne, 1993) which may contribute to uptake and toxicity in normal tissues generally thought to be at neutral extracellular pH.

PCFT expression is not static, as it has been found to be modulated by promoter methylation, vitamin D3 and the NRF-1 transcription factor. Hypermethylation of the PCFT promoter was shown to be associated with low PCFT protein expression in CCRF-CEM and Jurkat T-cell leukemia cell lines (Gonen et al., 2008) and a MTX-resistant HeLa cell line (R1) (Diop-Bove et al., 2009) and could represent a mechanism of resistance against drugs that use PCFT as their primary means of cellular entry. Nutritional status could also affect PCFT expression, as VDR heterodimerizes with RXRα in response to vitamin D3 and binds a VDR response element in the PCFT promoter region (-1694/-1680), increasing expression of PCFT (Eloranta et al., 2009). Interestingly, mouse PCFT transcript levels increased ~13-fold in the



proximal small intestine in mice fed folate-deficient versus folate-replete diets, consistent with the critical role that PCFT plays in intestinal folate absorption (Qiu et al., 2007). Interestingly, PCFT mRNA expression directly correlated with NRF-1 transcript levels in these tissues and was dependent on folate status (C. Cherian, unpublished observation), reaffirming the likely importance of NRF-1 in PCFT transcriptional control (Gonen and Assaraf, 2010). Thus, dietary increases or decreases in folate and vitamin D3 levels could affect expression of PCFT in normal tissues and could impact antifolate toxicity. The extracellular pH surrounding a cell may also have an effect on PCFT expression. For instance, treatment of patients with proton pump inhibitors, which increase extracellular pH, leads to decreased PCFT expression and folate deficiency due to reduced folate uptake from the gut (Urquhart et al., 2010). Of course, transcriptional control is most likely not the only mechanism of PCFT regulation. PCFT protein expression may also be stimulus controlled, such that decreased extracellular folate or decreased extracellular pH may induce cycling of PCFT from intracellular compartments to the cell surface in order to facilitate folate uptake. Indeed, PCFT protein has not only been found on the cell surface but also in intracellular compartments (Kugel Desmoulin et al., 2010b; Qiu et al., 2006), and PCFT has been proposed to aid in the exit of (anti)folate from acidic endosomes (Zhao et al., 2009b). It may be possible that the presence of intracellular PCFT may have particular regulatory significance.

This chapter has established PCFT expression in many solid tumor cell lines, but whether the level of expression and function is enough to transport a cytotoxic dose of antifolates that use this mechanism is still unknown. There is some indication that PCFT may facilitate PMX uptake and cytotoxicity toward solid tumor cell lines that express moderate levels of PCFT. PMX is a transport substrate for both RFC and PCFT-mediated uptake and is the best known substrate for



PCFT (Zhao and Goldman, 2007). Upon loss of RFC expression, when PCFT was the sole mechanism of PMX transport, uptake by PCFT was sufficient to maintain PMX cytotoxicity (Chattopadhyay et al., 2006; Zhao et al., 2004c) (See Chapter 5). Uptake of cytotoxic antifolates by RFC not only precludes selectivity, since RFC, as shown in this chapter as well as by Whetstine et al. (2002a) is expressed and functional in human normal tissues. However, its ability to transport antifolates into tumor cells may be compromised due to reduced transport activity at acidic pHs characterizing the tumor microenvironment. This suggests that designing drugs with greater affinity for PCFT and not the RFC has the potential to increase tumor selectivity without loss of drug activity (Kugel Desmoulin et al., 2011; Kugel Desmoulin et al., 2010b; Wang et al., 2010; Wang et al., 2011) (see Chapters 3 and 4). Due to the low activity of RFC at acidic pHs, tumor cells may favor overexpression of H⁺-coupled transporters, such as PCFT, in order to transport folates to meet their nutritional and metabolic requirements and to gain a competitive advantage in the acidic tumor microenvironment (Anderson and Thwaites, 2010). Hence, PCFT expression and function may increase in more advanced aggressive tumors, suggesting that antifolates selectively transported into tumor cells by PCFT would make better, more selective drugs that have the potential to improve therapy. Future studies should look at expression of PCFT with increasing tumor stage or grade.

To determine whether the therapeutic targeting of agents selective for PCFT uptake by utilizing tumor acidity to drive drug uptake will be successful, investigators will not only need to establish PCFT expression in tumors but also PCFT function. Further, the ability to measure tumor pH with accuracy, precision and high spatiotemporal resolution in experimental preclinical systems and in human beings will be very important for this therapeutic strategy (Zhang et al., 2010). Recent advances in optical imaging, PET radiotracers, and magnetic resonance



spectroscopy (MRS) and magnetic resonance imaging (MRI) have improved the ability to measure tumor pH. Optical techniques such as fluorescence ratio imaging spectroscopy and fluorescent lifetime imaging can be used to measure tumor pH. These methods use fluorescent probes that have varied fluorescent properties depending on local pH, which can be measured optically and converted to a pH distribution map. Positron emission tomography (PET)-based approaches use pH-sensitive PET radiotracers including the pH (low) insertion peptide (pHLIP) conjugated to ⁶⁴Cu (Vavere et al., 2009). pHLIP is a peptide that predominantly inserts across a lipid bilayer as a monomeric α -helix at an acidic extracellular environment but not at a normal physiological pH (Andreev et al., 2007; Fendos and Engelman, 2012). MRS methods are generally based on a difference in chemical shifts between pH-dependent and independent resonances; several isotopes have been evaluated for determination of tumor pH, such as ³¹P-MRS and ¹H-MRS with some success. There are still some limitations in spatial and temporal resolution (Gillies and Morse, 2005). Hyperpolarized ¹³C bicarbonate is a technique that uses ¹³C MRI and is based on transferring the polarization of unpaired electrons to neighboring nuclei by microwave irradiation of the sample (Hu et al., 2008). Finally, an alternative approach uses MRI and relies on agitating the relaxivity of water with pH-dependent relaxation agents (Aime et al., 1999; Garcia-Martin et al., 2006; Zhang et al., 1999). With the improvement of in vivo pH measurements, it may be possible to target treatment to those tumors that are more acidic, thus focusing therapy on the population of patients that will most benefit from PCFT-selective agents.



CHAPTER 3

THE IDENTIFICATION OF NOVEL ANTIFOLATES WITH PCFT-SELECTIVE UPTAKE

3.1 Introduction.

The activities of RFC, PCFT and FR folate transport systems toward antifolate substrates in tissues and tumors reflect their relative expression levels, along with their specificities for different antifolates and transport kinetics. With this said, antifolates selective for RFC, which include all classical antifolates presently approved by the FDA, can be envisaged to possess limited selectivity toward tumors over normal proliferative tissues such as bone marrow since these tissues all express RFC (Chapter 2 and Whetstine et al. (2002a)). The therapeutic approach of rational folate analog design that is based on targeting delivery into cancer cells by exploiting the tumor-specific patterns of expression and/or function of PCFT and FR may lead to more tumor-selective therapeutics. This approach is not entirely unprecedented, as recent efforts have focused on targeting FR as a means of delivering cytotoxic antifolates into the tumor cell. For instance, ONX0801 (previously BGC945) which is selectively transported by FRs and inhibits TS as its primary target (Gibbs et al., 2005; Theti et al., 2003) has recently been licensed by Onyx Pharmaceuticals and is currently in Phase I in the United Kingdom. Another approach links a variety of lipid soluble drugs, structurally unrelated to folates, to folic acid via a covalent bond. The complex binds FR on the cell surface, is endocytosed, the bond is broken in the reducing environment of the endosome, and the drug diffuses out of the endosome to inactivate its intracellular target. Several such agents have been designed. BMS-753493 is a molecule born from collaboration between scientists at Endocyte Inc. and Bristol Myers Squibb. It represents a folic acid conjugate that was constructed with a semi-synthetic analog of Epothilone A (a microtubule inhibitor). BMS-753493 is currently being evaluated for safety and efficacy in Phase



II clinical trials sponsored by Bristol Myers Squibb. EC-145 (Endocyte) is a desacetylvinblastine monohydrazide – folic acid complex (Reddy et al., 2007). A randomized Phase II trial is near completion in which EC-145 with Doxil was compared to Doxil alone for the treatment of platinum-resistant ovarian cancers (Dosio et al., 2010). Farletuzumab is a humanized MoAb with high affinity for FR α . Preclinical studies have demonstrated that farletuzumab mediates robust antibody-dependent cellular cytotoxicity and complement-dependent cytotoxicity *in vitro*, inhibits tumor growth in ovarian tumor xenografts, and displays a safe toxicology profile in non human-primates (Kalli, 2007; Smith-Jones et al., 2008). Farletuzumab has shown clinical efficacy in early phase trials as single agent and combination therapy with minimal drug-specific toxicity (Spannuth et al., 2010). The Phase III development plan in ovarian cancer patients includes combination chemotherapy studies in both platinum-sensitive (recently launched) and platinum-resistant (planned) recurrent disease (Bellati et al., 2011).

Based on the clinical successes of PMX, and in an effort to design novel antifolates with specificities other than RFC, our lab formed collaborations with Dr. Aleem Gangjee's group from Duquesne University. This cooperation has resulted in several novel series of compounds based on the chemical structure of PMX. These include: (i) 6-substituted pyrrolo[2,3-*d*]pyrimidine benzoyl antifolates with carbon bridge length variations of 1- to 6-carbons, compounds **1-6**, respectively (Deng et al., 2008; Kugel Desmoulin et al., 2010b) (Figure 3.1, Panel A); (ii) 6-substituted thieno[2,3-*d*]pyrimidine benzoyl antifolates with bridge length variations from 2-8 carbon atoms, compounds **7-13**, respectively (Deng et al., 2009) (Figure 3.1, Panel B); (iii) 6-substituted pyrrolo[2,3-*d*]pyrimidine antifolates with a thienoyl replacement for the benzoyl moiety and bridge length variations from 1-6 carbons, compounds **14-19**, respectively (Kugel Desmoulin et al., 2011; Wang et al., 2010; Wang et al., 2011) (Figure 3.1,



Panel C); and the (**iv**) 6-substituted pyrrolo[2,3-*d*]pyrimidine thienoyl regioisomers with a 4carbon bridge and different thienoyl ring substitutions (compounds **20-24**) (Wang et al., 2012) (Figure 3.1, Panel C).

The rationale behind the synthesis of the 6-substituted pyrrolo[2,3-d]pyrimidine benzoyl structures (group (i) above) (Figure 3.1, Panel A) is in part based on the finding that the 6-regio isomer of PMX (compound 2) was inactive against the growth of tumor cells expressing RFC in culture (Shih, 1993). Gangjee et al. postulated that a possible reason for its inactivity in culture could be that transposing the 5-ethylene bridge to the 6-position forces the benzoyl glutamic acid side chain in an orientation different from that required for optimal enzyme interaction and antitumor activity (Gangjee et al., 2005; Gangjee et al., 2004). They therefore elongated the ethylene bridge between the heterocycle and *para*-aminobenzoate with 3 (compound 3) or 4 (compound 4) methylene groups to allow greater conformational flexibility. Compounds 3 and 4 were both modest inhibitors of proliferation with CCRF-CEM leukemia cells (express RFC but no PCFT or FR) in the presence of micromolar concentrations of folic acid (Gangiee et al., 2005; Gangiee et al., 2004). Our laboratory found that the 6-substituted pyrrolo[2,3-d]pyrimidine benzoyl analogs were characterized by potent and selective substrate activities for FR α and FR β , and negligible substrate activity for RFC. Moreover, the intracellular enzyme target of the 6substituted pyrrolo[2,3-d]pyrimidine benzoyl antifolates was identified as GARFTase, the first folate-dependent reaction in the *de novo* purine nucleotide biosynthesis pathway (Deng et al., 2008).

The synthesis of 6-substituted thieno[2,3-*d*]pyrimidine benzoyl antifolates with bridge length variations (from 2-8 carbon atoms; compounds **7-13** respectively) (group (ii), above) (Figure 3.1, Panel B) was pursued to try to find a more potent analog and to understand the





Figure 3.1 Structures of novel antifolate drugs. Panel A, 6-substituted pyrrolo[2,3-d]pyrimidine benzoyl antifolates with carbon d]pyrimidine antifolates with a thienoyl replacement for the benzoyl moiety and bridge length variations from 1-6 carbons, compounds 14-19, respectively, and 6-substituted pyrrolo[2,3-d]pyrimidine thienoyl regioisomers with a 4-carbon bridge bridge length variations of 1- to 6-carbons, compounds 1-6, respectively. Panel B, 6-substituted thieno [2,3-d] pyrimidine benzoyl antifolates with bridge length variations from 2-8 carbon atoms, compounds 7-13, respectively. Panel C, 6-substituted pyrrolo[2,3-(compound **17**) and different thienoyl ring substitutions, compounds **20-24**, respectively.

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structural determinants of transport selectivity. Isosteric replacement of the pyrrolo ring with a thieno ring for this series provided an increase in ring size that more closely approximates the pteridine, 6-6 fused ring system of the natural cofactor. In addition, replacement of the NH of the pyrrole with an S also allows for comparison of the relative importance of a hydrogen bond donor (NH) with a hydrogen bond acceptor (S). Our laboratory found that the 6-substituted thieno[2,3-*d*]pyrimidine antifolate series was characterized by potent and selective substrate activities for FR α and FR β , and negligible substrate activities for RFC. Furthermore, the 6-substituted thieno[2,3-*d*]pyrimidine antifolates were found to target both GARFTase and AICARFTase (Deng et al., 2009).

The rationale for the synthesis of 6-substituted pyrrolo[2,3-*d*]pyrimidines with a thienoyl replacement for the benzoyl moiety and bridge length variations from 1-6 carbons antifolates (compounds **14-19**, respectively) (group (iii) above) (Figure 3.1, Panel C) came from the discovery and biochemical evaluation of RTX. RTX was synthesized by replacing the para-aminobenzoate of ICI 198583 (a precursor analog of RTX) with a thiophene and a N10-methyl substituent. This modification reduced TS inhibition compared to earlier analogs but enhanced cellular uptake by RFC and polyglutamylation leading to more potent tumor growth inhibition both *in vitro* and *in vivo*. Therefore, the rationale was that combining the chemical structures of the 6-substituted PMX with different carbon bridge lengths with the thienoyl group of RTX might give a more potent novel antifolate.

As an alternative approach for decreasing the distance between the bicyclic pyrrolo[2,3-d]pyrimidine and the L-glutamate portions, we systematically assessed the effects on cell proliferation for an expanded series of pyrrolo[2,3-d]pyrimidine thienoyl regioisomers of **17** with a 4-carbon bridge and thienoyl ring substitutions, 2',3' (**20**), 4',5' (**21**), 3',4' (**22**), 3',5' (**23**), and



2',4' (24) (group (iv) above) (Figure 3.1, Panel C). In analogs 20-24, the [1,2] substitution pattern on the thiophene forces the bicyclic scaffold and L-glutamate closer together than in the parent 3-atom bridge compound 16 which includes a [1,3] pattern on the thiophene ring.

This chapter will explore the potential of PCFT to selectively deliver cytotoxic antifolates for the chemotherapy of tumors. The transport activity profile for the earlier series of 6substituted pyrrolo[2,3-*d*]pyrimidine benzoyl antifolates (Deng et al., 2008) and 6-substituted thieno[2,3-*d*]pyrimidine benzoyl antifolates (Deng et al., 2009) will be expanded to include PCFT and the transport selectivity of the other novel series will be established. The potent antiproliferative activities of these compounds, attributable to inhibition of GARFTase and *de novo* purine biosynthesis, will be characterized. The goal is to establish a structure-activity relationship for compounds that are selective for PCFT-mediated uptake, have no RFC substrate activity and cause cell death through GARFTase inhibition at doses that are pharmacologically feasible. The findings presented here will establish that PCFT is an efficient means of delivering cytotoxic antifolate drugs and suggest that PCFT provides a unique opportunity to selectively target solid tumors with cytotoxic antifolates that are not substrates for the ubiquitously expressed RFC.

3.2 Materials and Methods.

3.2.1 Chemicals and Reagents.

[3',5',7-³H]MTX (20 Ci/mmol) and [³H]PMX (3.7 Ci/mmol) were purchased from Moravek Biochemicals (Brea, CA). Unlabeled MTX and (6 R,S)-5-formyl tetrahydrofolate (5-CHO-THF) were provided by the Drug Development Branch, National Cancer Institute, Bethesda, MD. Both labeled and unlabeled MTX were purified by HPLC prior to use (Fry et al., 1982). The sources of the antifolate drugs were as follows. RTX [*N*-(5-[*N*-(3,4-dihydro-2-



methyl-4-oxyquinazolin-6-ylmethyl)-N-methyl-amino]-2-thenoyl)-L-glutamic acid] was obtained from AstraZeneca Pharmaceuticals (Maccesfield, Cheshire, England); LMX (5,10dideaza-5,6,7,8-tetrahydrofolate) and PMX (Alimta) were from Eli Lilly and Co. (Indianapolis, IN); GW1843U89 [(S)-2-(5-(((1,2-dihydro-3-methyl-1-oxo-benzo(F) quinazolin-9-yl) methyl) amino)1-oxo-2-isoindolinyl) glutaric acid] was from the GlaxoWellcome-SmithKline Co. (Research Triangle Park, NC); and N^{alpha}-(4-amino-4-deoxypteroyl)-N^{delta}-hemiphthaloyl-Lornithine (PT523) was a gift of Dr. Andre Rosowsky (Boston, MA). Restriction and modifying enzymes were purchased from Promega (Madison, WI). Other chemicals were obtained from commercial sources in the highest available purities. Synthesis and properties of the 6-substituted pyrrolo[2,3-d]pyrimidine benzoyl antifolate compounds **1-6** (1-6 methylene groups in the bridge region connecting the pyrrolo[2,3-d]pyrimidine moiety to para-aminobenzoate) were described (Deng et al., 2008; Kugel Desmoulin et al., 2010b). Synthesis and properties of the 6-substituted thieno[2,3-d]pyrimidine antifolate with bridge variations from 2-8 carbon atoms (compounds 7-13) were described (Deng et al., 2009). Synthesis and properties of pyrrolo[2,3-d] pyrimidine thienoyl antifolate compounds **14-19** (1-6 methylene groups in the bridge region connecting the pyrrolo[2,3-d]pyrimidine moiety to *para*-aminobenzoate) were described (Kugel Desmoulin et al., 2011; Wang et al., 2010). Finally, synthesis and properties of 6-substituted pyrrolo[2,3d pyrimidine thienoyl regioisomers with a 4-carbon bridge and different thienoyl ring substitutions (compounds **20-24**) were described (Wang et al., 2012).

3.2.2 Cell Culture.

Novel antifolate preliminary screening was performed in sublines derived from PCFT-, RFC-, and FR-null MTXRIIOua^R2-4 (R2) Chinese hamster ovary (CHO) cells (Flintoff and Nagainis, 1983), a gift from Dr. Wayne Flintoff (University of Western Ontario, London,



Ontario, Canada). R2 cells were cultured in alpha-minimal essential media (MEM) supplemented with 10% bovine calf serum (Invitrogen, Carlsbad, CA), 100 units/mL penicillin, 100 μ g/mL streptomycin, and 2 mM L-glutamine at 37°C with 5% CO₂. PC43-10 and R2/PCFT4 cells are R2 cells stably transfected with human RFC (Wong et al., 1995) or human PCFT (Kugel Desmoulin et al., 2010b), respectively. Generation of R2/PCFT4 cells is described below. Both cell lines were cultured in complete alpha-MEM medium plus 1 mg/mL G418. Using LookOutTM, a PCR-based *Mycoplasma* detection kit from Sigma Chemical Company (St. Louis, MO), cell lines were periodically determined to be free of *Mycoplasma*.

3.2.3 Preparation of a Myc-His6-tagged Human PCFT Construct and Generation of Stable Transfectants.

Total RNA from wild type HeLa cells was reverse transcribed and PCR amplified with EasyA proof-reading polymerase (Agilent Technologies, La Jolla, CA) using the following primers: 5'-AACTC **GGA TCC** gca cat gga ggg gag cgc gag cc-3'; and 5'-AACTC **GGT ACC** ggg gct ctg ggg aaa ctg ctg gaa ctc ga-3' (bold capitals designate the BamHI and KpnI restriction sites, respectively). The 1403 bp amplicon was subcloned into pCDNA3.1 (Invitrogen) in-frame with a Myc-His6 sequence inserted at the C-terminal amino acid 466 (hereafter designated PCFT^{Myc-His6}/pCDNA3.1). The construct was confirmed by automated DNA sequencing at the Wayne State University Sequencing Core.

R2 cells were transfected with PCFT^{Myc-His6}/pCDNA3.1 by electroporation (200 V, 1000 μ F capacitance). After 24 h, the cells were cultured in the presence of G418 (1.5 mg/mL). Stable clones were selected by plating for individual colonies in the presence of 1.5 mg/mL G418. Colonies were isolated, expanded and screened for expression of PCFT^{Myc-His6} protein by Western blotting and transport assays at pH 5.5 (see below). One clone (R2/PCFT4) was



selected for further study. Vector control R2 cells (R2/VC) transfected with empty pCDNA3.1 were also prepared and used as a negative control.

3.2.4 Gel Electrophoresis and Western Blotting.

For characterizing PCFT and RFC protein expression in R2/PCFT4 and PC43-10 cells, respectively, crude plasma membranes were prepared by differential centrifugation. Briefly, cells were suspended in 10 mM Tris-HCl, pH 7.0, containing X1 protease inhibitor cocktail tablets (Roche, Indianapolis, IN), and disrupted with a probe sonicator. The cell homogenate was centrifuged (600 x g, 10 min) to remove cell debris and nuclei; the supernatant was then centrifuged at 200,000 x g (48,000 rpm) in a Beckman TL100 ultracentrifuge for 30 min. The particulate fraction was solubilized in 10 mM Tris-HCl (pH 7) with 2% SDS in the presence of proteolytic inhibitors and proteins were quantified with Folin-phenol reagent (Lowry et al., 1951). Membrane proteins were electrophoresed on 7.5% polyacrylamide gels in the presence of SDS (Laemmli, 1970) and electroblotted onto PVDF (Pierce, Rockford, IL) (Matsudaira, 1987). PCFT^{Mye-His6} protein was detected with monoclonal Myc-specific mouse antibody (Covance, Berkeley, CA) and secondary IRDye800CW-conjugated antibody (Rockland, Gilbertsville, PA). Detection of immunoreactive proteins used the Odyssey® Infrared Imaging System (LI-COR, Lincoln, NE).

3.2.5 Indirect Immunofluorescence and Confocal Microscopy.

For confocal microscopy, R2/PCFT4 and R2/VC CHO cells were plated in Lab-Tek[®]II chamber slidesTM (Nalge Nunc International, Naperville, IL). Cells were fixed with 3.3% paraformaldehyde (in DPBS), permeabilized with 0.1% Triton X-100 (in PBS), and stained with monoclonal Myc-specific mouse antibody (Covance) and Alexa Fluor[®] 488 donkey anti-mouse IgG (H+L) secondary antibody (Molecular Probes, Eugene, OR). Slides were visualized with a



Zeiss laser scanning microscope 510 using a 63x water immersion lens, and exactly the same parameter setting for all samples. Confocal analysis was performed at the Imaging Core of the Karmanos Cancer Institute.

3.2.6 Transport Assays.

The expression and function of PCFT and RFC in R2/PCFT4, R2/VC, PC43-10 and R2 cell lines was validated by measuring pH-dependent transport of 0.5 µM [³H]MTX over 2 min at 37°C in cell suspensions. Briefly, three days before transport experiments, cells grown in monolayers, under G418 selection, were transferred to Cytostir spinners and maintained in suspension at densities of 2-5 x 10^5 cells/mL. Cells were collected by centrifugation, washed with DPBS, and the cell pellets (~2 x 10^7 cells) were suspended in 2 mL of either [³H]MTX containing HEPES-buffered saline (20 mM HEPES, 140 mM NaCl, 5 mM KCl, 2 mM MgCl₂, and 5 mM glucose) at pH 6.8 or 7.2, or in MES-buffered saline (20 mM MES, 140 mM NaCl, 5 mM KCl, 2 mM MgCl₂, and 5 mM glucose) at pH 5.5, 6.0, or 6.5 (Zhao et al., 2004b). At the end of the incubations, transport was quenched with ice-cold DPBS, cells were washed 3 times with ice-cold DPBS, and cellular proteins were solubilized with 0.5 N NaOH. Levels of drug uptake were expressed as pmol/mg protein, calculated from direct measurements of radioactivity and protein contents of the cell homogenates. Radioactivity was measured with a scintillation counter (Model LS6500; Beckman-Coulter, Fullerton, CA) and proteins were quantified using Folin-phenol reagent (Lowry et al., 1951).

To determine [³H]MTX and [³H]PMX kinetic constants for PCFT in R2/PCFT4 cells (K_t and V_{max}), transport rates were measured at pH 6.8 and pH 5.5, as described above, using substrate concentrations from 0.04 to 5.0 μ M. K_t and V_{max} values were determined from Lineweaver-Burke plots. Inhibition of RFC transport by unlabeled antifolates (reflecting



transport by the carrier) was measured in PC43-10 cells over 2 min at 37°C in Hank's balanced salts solution (pH 7.2) with 0.5 μ M [³H]MTX and 10 μ M inhibitor. For PCFT, inhibition of transport was determined from pH 5.5 to 7.2 in the above MES- and HEPES-buffered saline over 2 min at 37°C with 0.5 μ M [³H]MTX and 10 μ M inhibitors. K_is for PCFT were calculated from Dixon analysis, by plotting reciprocal transport velocities measured over a range (1-5 μ M) of inhibitor concentrations and 0.5 μ M [³H]MTX at pH 5.5 and pH 6.8. K_i values were calculated from the slopes, K_t and V_{max} values for MTX, and the concentration of [³H]MTX, using the equation K_i=K_t/(V_{max})(slope)(S).

3.2.7 Electrophysiology Experiments.

Electrophysiology experiments were performed in collaboration with Dr. Michael Romero (Mayo Clinic, Rochester, MN). *Xenopus* oocytes were used to assess currents associated with transport of the antifolate substrates. PCFT cRNA (50 nL of $0.5 \ \mu g/\mu L$, i.e., 25 ng) or water (50 nL) was injected into stage V/VI oocytes and electrophysiological measurements were made 3-5 days later (Unal et al., 2009a). Oocytes were voltage clamped to -90 mV to maximize folateinduced currents, a technique that was previously utilized in studies on the divalent metal transporter, DMT1 (Gunshin et al., 1997; Mackenzie et al., 2006) and PCFT (Unal et al., 2009a). Oocyte solutions were adjusted to pH 5.5 using MES. During these experiments, oocytes were continuously superfused with solution (with and without antifolates as indicated) at 5 mL/min.

3.2.8 Proliferation and Colony-forming Assays.

For growth inhibition assays, R2/PCFT4 CHO cells were plated in 96 well culture dishes (2500 cells/well, respectively; total volume of 200 μ L medium) with a broad concentration range of drugs. The drugs were dissolved in DMSO such that after dilution the DMSO concentration did not exceed 0.5%. The medium was folate-free RPMI 1640 (pH 7.2) supplemented with 10%



dialyzed fetal bovine serum (dFBS) (Invitrogen), 2 mM L-glutamine, 100 units/mL penicillin and 100 µg/mL streptomycin (hereafter referred to as complete folate-free RPMI 1640 media), containing 25 nM 5-CHO-THF. Cells were routinely incubated for up to 96 h, and metabolically active cells (a measure of cell viability) were assayed with CellTiter-Blue[™] cell viability assay (Promega). Fluorescence was measured (590 nm emission, 560 nm excitation) with a Molecular Devices fluorescence plate reader. Data were exported from Softmax Pro software to an Excel spreadsheet for analysis and determinations of $IC_{50}s$, corresponding to drug concentrations that result in 50% loss of cell growth. In some experiments, the protective effects of adenosine (60 μ M), thymidine (10 μ M), and 5-amino-4-imidazolecarboxamide (AICA) (320 μ M) were tested to validate the intracellular targeted pathways and enzymes for the cytotoxic antifolates. Growth inhibition assays for the PC43-10 CHO were routinely performed in regular RPMI 1640 (pH 7.2) supplemented with 10% dFBS (Invitrogen), 2 mM L-glutamine and 100 units/mL penicillin and 100 µg/mL streptomycin (hereafter referred to as complete RPMI 1640 media), although for a few experiments PC43-10 cells were cultured exactly as for the R2/PCFT4 cells. To follow changes in pH accompanying cell outgrowth, cells were seeded into T75 flasks, using the same media, cell number to volume ratio, and incubation times as for the cytotoxicity assays. Media pH values were measured daily with an Orion 2 Star benchtop pH meter.

For colony-forming assays, R2/PCFT4 cells (500 cells) were harvested in log-phase and plated into 60 mm dishes in complete folate-free RPMI 1640 medium, supplemented with 25 nM 5-CHO-THF and allowed to adhere for 48 h. For continuous drug exposures, R2/PCFT4 cells were then treated with increasing concentrations of drugs and colonies were allowed to outgrow for 10 days. At the end of the incubations, the dishes were rinsed with DPBS, 5% trichloroacetic acid (TCA), and borate buffer (10 mM, pH 8.8), followed by 1% methylene blue (in borate



buffer; 30 min). The dishes were again rinsed with borate buffer, and colonies were counted for calculating percent colony formation relative to the DMSO control.

To test the reversibility of compound **3** drug effects, as reflected in inhibition of colony formation over time, R2/PCFT4 cells were harvested in log phase and 500 cells were plated, allowed to adhere for 48 h, then cultured in the presence or absence of 1 μ M antifolate compounds and thymidine (10 μ M) plus adenosine (60 μ M) for 2, 4, 8, 24, or 48 h, before rinsing with DPBS and adding medium with or without thymidine (10 μ M) plus adenosine (60 μ M). The dishes were incubated for 10 days, and colonies were counted, as described above, for calculating percent colony formation compared to control.

3.2.9 In situ Assays for GARFTase.

Incorporation of $[{}^{14}C(U)]$ glycine into $[{}^{14}C]$ formyl GAR as an *in situ* measure of endogenous GARFTase activity in R2/PCFT4 cells was performed using a modification of published methods (Beardsley et al., 1989; Deng et al., 2008). For these experiments, R2/PCFT4 cells were seeded in 5 mL of complete folate-free RPMI 1640 plus 25 nM 5-CHO-THF in T25 flasks at a density of 2 x 10⁵ cells per flask. After 48 h, antifolate inhibitor or DMSO (control) was added to the culture medium and the cells were incubated for another 15 h after which the pH of the media was determined with an Orion 2 Star benchtop pH meter. Cells were washed twice with DPBS and resuspended in 5 mL folate-free, L-glutamine-free RPMI 1640 (Sigma) plus penicillin-streptomycin, 10% dFBS, 0.46 g/L NaHCO₃ and 1.21 g/L NaCl medium, with or without 0.5-100 nM antifolate and azaserine (4 μ M final concentration), and incubated for 30 min. L-glutamine (2 mM final concentration) and [14 C]glycine (final specific activity, 0.1 mCi/L) were added, followed by incubation at 37° C for 8 h, after which time cells were trypsinized and washed twice with ice-cold DPBS. Cell pellets were treated with 2 mL of 5%



TCA at 0° C. Cell debris was removed by centrifugation, samples were solubilized in 0.5 N NaOH and assayed for protein contents (Lowry et al., 1951). The supernatants were extracted twice with 2 mL of ice-cold ether to remove the TCA. The aqueous layer was passed through a 1 cm column of AG1x8 (chloride form), 100-200 mesh (BioRad), washed with 10 mL of 0.5 N formic acid, followed by 10 mL of 4 N formic acid, and eluted with 8 mL of 1 N HCl solution. The elutants were collected as 1 mL fractions and determined for radioactivity.

3.2.10 Determination of Intracellular ATP/GTP Levels.

For analysis of ATP and GTP levels following antifolate treatments, R2/PCFT4 cells were seeded in 10 mL of complete folate-free RPMI 1640 plus 25 nM 5-CHO-THF in T75 flasks at a density of 7 x 10⁵ cells per flask. After 48 h, antifolates or DMSO (control) were added to the culture medium. After another 24 h, the cells were trypsinized and washed (2x) with ice-cold DPBS, with a final additional wash with ice-cold DPBS containing 1 mM EDTA. The final cell pellet (2-5 x 10⁶ cells) was resuspended in 100 µL of 155 mM NaCl containing 1 mM EDTA and 100 µL of ice-cold 0.6 M TCA was added drop-wise while vortexing. Samples were incubated 10 min on ice with occasional mixing, and then centrifuged (14,000 rpm, 5 min). The supernatant was removed, whereas the protein pellet was solubilized in 0.2 mL of 0.5 N NaOH for protein determinations. Tri-n-octylamine (0.5 M) in trichlorotrifluoroethane (Freon) (1 mL) was added to the supernatant and the mixtures vortexed and incubated for 20 min on ice. Samples were centrifuged and the freon amine (lower) layer was discarded. One mL of methylene chloride was added to the upper layer, followed by mixing, incubation (ice, 10 min), centrifugation, and removal of the organic (lower) layer. Samples were stored at -80°C until analysis. Intracellular adenosine and guanosine triphosphates were measured by a modification of the HPLC method of Huang et al. (2003a). The chromatography system consisted of a Varian



9010 ternary gradient pump, a 9050 variable wavelength detector, and a Varian Star 5.3 data handling system. A 50 µL injection loop was used. The analytical column was a Waters Symmetry C₁₈ (5 µm, 150 x 4.6 mm) equipped with a Waters Novapak phenyl pre-column (Waters, Milford, MA). The detection wavelength was set at 254 nm. The flow rate was 1 mL/min. The gradient elution was as follows: 0-30 min at 60% A/40% B; 30-50 min linear at 1%/min to 40% A/60% B; and 50-60 min at 40% A/60% B. Buffer A was comprised of 10 mM tetrabutylammonium hydroxide, 10 mM KH₂PO₄ and 0.25% methanol (MeOH); the pH was adjusted to 6.9 with 1 N H₃PO₄. Buffer B consisted of 5.6 mM tetrabutylammonium hydroxide, 50 mM KH₂PO₄ and 30% MeOH; the pH was adjusted to 7.0 with 1 N KOH. Both solutions were freshly prepared before each experiment and degassed. External standards were used for each assay to construct a standard curve from which cellular levels were calculated. Standards ranged from 0-75 µM for ATP and 0-30 µM for GTP in the initial mobile phase. Variations between standards were 5% or less. Extraction efficiencies were established by adding known amounts of ATP and GTP standards (200 and 50 µM, respectively) to a control sample prior to extraction.

3.3 Results.

3.3.1 Generation of PCFT Stable Transfectants in Transport-impaired CHO Cells.

As part of our larger drug discovery endeavor to establish pharmacophores for all the major folate transporters and to develop transporter-specific drugs, we previously generated novel sublines derived from the RFC, FR-, and PCFT-null MTXRIIOua^R2-4 CHO cells (hereafter, simply R2) that ectopically express human RFC protein (designated PC43-10; Figure 3.2, Panel A and E) (Wong et al., 1995) and human FRs (designated RT-16).





Figure 3.2 Characterization of PCFT protein expression, membrane localization and pHdependent transport in R2/PCFT4 and R2/VC cells. *Panel A*, Western blot analysis of RFC in PC43-10 and R2 cells. *Panel B*, human PCFTMyc-His6 in R2/PCFT4 and R2/VC cells. Membrane fractions (10 μ g) were analyzed by SDS-PAGE and immunoblotting with human RFC and PCFT polyclonal antibody. *Panel C*, Immunofluorescence of R2/PCFT4 and R2/VC cells. Cells were fixed with paraformaldehyde, permeabilized with Triton X-100, stained with anti-myc antibody and visualized using confocal microscopy. *Panel D*, PCFT transport activity in R2/PCFT4 and R2/VC cells was assessed by measuring uptake of 0.5 μ M [³H]MTX at 37°C for 2 min at pH 5.5 or 6.0 in MES-buffered saline, and at 6.5, 6.8, or 7.2 in HEPES-buffered saline. Internalized [³H]MTX was normalized to total protein and expressed as a percent of the transport activity at pH 5.5. *Panel E*, RFC transport activity in PC43-10 and R2 cells was determined by measuring uptake of 0.5 μ M [³H]MTX at 37°C for 2 min at pH 5.5 or 6.0 in MESbuffered saline, and at 6.5, 6.8, or 7.2 in HEPES-buffered saline. As above, internalized [³H]MTX was normalized to total cellular protein and expressed as percent transport at pH 7.2. Transport results are presented as mean values ± standard errors from 6 experiments.



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More recently, we generated another R2 subline (R2/PCFT4) that expressed human PCFT (Deng et al., 2009; Kugel Desmoulin et al., 2010b). R2/PCFT4 cells were made by electroporating R2 CHO cells with a Myc-His6-tagged human PCFT (PCFT^{Myc-His6}) cDNA construct. Stable transfectants were selected with G418. Clones were isolated, expanded, and screened by Western blotting. The clonal R2/PCFT4 subline was established that expressed a high level of PCFT^{Myc-His6} protein (Figure 3.2, Panel B).

By indirect immunofluorescence staining with Myc-specific antibody and Alexa Fluor488-tagged secondary antibody, PCFT^{Myc-His6} protein was targeted predominantly to the cell surface of R2/PCFT4 cells with some intracellular staining compared to R2/VC (Figure 3.2, Panel C). Expression of PCFT^{Myc-His6} protein was accompanied by substantial [³H]MTX transport at pH 5.5 during 2 min over the low level measured in vector control R2/VC cells (Figure 3.2, Panel D). Transport at pH 7.2 was ~14% of that at pH 5.5 and at pH 6.8 transport increased to ~35% of that at pH 5.5. For RFC-expressing PC43-10 cells, [³H]MTX transport was active at pH 7.2 as reported (Wong et al., 1995), then fell with decreasing pH and was essentially indistinguishable from the residual low level in R2 cells at pH 5.5 (Figure 3.2, Panel E).

We measured the kinetics for [³H]MTX and [³H]PMX transport in R2/PCFT4 cells over a range of concentrations at pH 5.5 and pH 6.8. Data were analyzed by Lineweaver-Burke plots and are summarized in Table 3.2. Results for MTX showed a 16-fold decrease in K_t and a 2.3-fold increase in V_{max} when the pH was decreased from 6.8 to 5.5, whereas for PMX, the K_t and V_{max} changed 3.7-fold and 4.6-fold respectively. V_{max}/K_t values, a reflection of overall transport efficiency, were calculated for [³H]MTX and [³H]PMX and were 37-, 17-fold higher, respectively, at pH 5.5 than at pH 6.8.



Table 3.1 Growth inhibition by antifolate drugs toward PCFT- and RFC stable R2 CHO and HeLa transfectants. Growth inhibition was measured by a fluorescence (Cell Titer-BlueTM)-based assay after 96 h of exposure to a range of inhibitor concentrations. Results are presented as 50% inhibitory concentrations (IC₅₀s) (in nMolar) \pm standard errors from >3 experiments. ND, not determined.

Drug	R2/PCFT4	R2/VC	PC43-10	R2	R1-11- RFC6	R1-11- PCFT4
MTX	120.5 ± 16.8	>1000	12 ± 1.1	216 ± 9	35.7±7.1	218.2 (15.1)
GW1843U 89	>1000	>1000	11 ± 3.3	>1000	ND	ND
LMX	38.6 ± 5.0	>1000	12 ± 2.3	>1000	36.1±9.9	278.3±26.2
PMX	13.2 ± 2.4	974.0 ± 18.1	138 ± 13	894 ± 93	81.7±5.5	59.3±7.4
PT523	>1000	>1000	1.53 ± 0.16	>1000	3.19±0.4	>1000
RTX	99.5 ± 11.4	>1000	6.3 ± 1.3	>1000	ND	ND
1	>1000	>1000	>1000	>1000	ND	ND
2	>1000	>1000	>1000	>1000	ND	ND
3	23.0 ± 3.3	>1000	648.6 ± 38.1	>1000	>1000	155.0±12.9
4	212.9 ± 28.0	>1000	>1000	>1000	ND	ND
5	>1000	>1000	>1000	>1000	ND	ND
6	>1000	>1000	>1000	>1000	ND	ND
7	>1000	>1000	>1000	>1000	ND	ND
8	>1000	>1000	>1000	>1000	ND	ND
9	>1000	>1000	>1000	>1000	ND	ND
10	>1000	>1000	>1000	>1000	ND	ND
11	>1000	>1000	>1000	>1000	ND	ND
12	>1000	>1000	>1000	>1000	ND	ND
13	>1000	>1000	>1000	>1000	ND	ND



Table 3.1 Growth inhibition by antifolate drugs toward PCFT- and RFC stable R2 CHO and HeLa transfectants. Growth inhibition was measured by a fluorescence (Cell Titer-BlueTM)-based assay after 96 h of exposure to a range of inhibitor concentrations. Results are presented as 50% inhibitory concentrations (IC₅₀s) (in nMolar) \pm standard errors from >3 experiments. ND, not determined.

Drug	R2/PCFT4	R2/VC	PC43-10	R2	R1-11- RFC6	R1-11- PCFT4
14	291 ± 71	>1000	>1000	>1000	ND	ND
15	135 ± 18	>1000	>1000	>1000	ND	ND
16	3.34 ± 0.26	288 ± 12	101.0 ± 16.6	273.5 ± 49.1	>1000	28.2 ± 7.0
17	43.4 ± 4.1	>1000	>1000	>1000	>1000	99.2 ± 20.2
18	101.4 ± 17.9	>1000	>1000	>1000	ND	ND
19	>1000	>1000	>1000	>1000	ND	ND
20	>1000	>1000	>1000	>1000	ND	ND
21	>1000	>1000	>1000	>1000	ND	ND
22	>1000	>1000	>1000	>1000	ND	ND
23	41.5 ± 13.09	>1000	>1000	>1000	ND	ND
24	63.8 ± 16.23	>1000	>1000	>1000	ND	ND
Table 3.2. Kinetic constants for PCFT - CHO. Kinetic constants for MTX $(K_t \text{ and } V_{max})$ and PMX $(K_t \text{ and } V_{max})$ were determined with [³H]MTX and [³H]PMX respectively, and calculated from Lineweaver Burke plots with R2/PCFT4 cells. K_i values were determined by Dixon plots with [³H]MTX as substrate and a range of inhibitor concentrations in R2/PCFT4 cells. Results are presented as mean values <u>+</u> standard errors from 3 experiments.

Substrate	Parameter	pH 5.5	pH 6.8
MTX	$K_t(\mu M)$	0.280 ± 0.022	4.52 ± 0.19
	V _{max} (pmol/mg/min)	31.23 ± 4.31	13.72 ± 2.26
	V _{max} / K _t	111.5	3.0
PMX	$K_t (\mu M)$	0.15 ± 0.03	0.56 ± 0.12
	V _{max} (pmol/mg/min)	32.32 ± 6.49	7.06 ± 1.39
	V _{max} / K _t	215.5	12.6
Compound 3	$K_i(\mu M)$	0.223 ± 0.017	4.07 ± 0.339
Compound 16	$K_i(\mu M)$	0.1278 ± 0.0054	1.816 ± 0.0704
Compound 17	$K_i(\mu M)$	0.132 ± 0.009	1.954 ± 0.024
Compound 18	$K_i(\mu M)$	0.100 ± 0.012	2.234 ± 0.203
Compound 23	$K_i^{}(\mu M)$	0.386 ± 0.095	28.12 ± 5.31
Compound 24	$K_i^{}(\mu M)$	0.424 ± 0.112	30.70 ± 8.53
PMX	$K_i(\mu M)$	0.0960 ± 0.012	1.54 ± 0.17
LMX	$K_i(\mu M)$	0.249 ± 0.013	12.30 ± 0.96

Thus, as previously reported, transport by PCFT shows extraordinary pH dependence with the greatest activity at acidic pH. Further, the impact of pH on kinetic parameters for PCFT membrane transport varies with different transport substrates (Zhao et al., 2009a).

3.3.2 Chemosensitivities to Classical Antifolate Inhibitors and Identification of Novel Antifolates with PCFT Selectivity over RFC.

We screened R2/PCFT4 and PC43-10 cells for growth inhibition in the continuous presence of established antifolates including MTX, GW1843U89, LMX, PMX, PT523 and RTX. Growth inhibition results for PC43-10 were compared to those for R2 cells and R2/PCFT4 results were compared to R2 cells transfected with empty pCDNA3.1 vector (R2/VC) (Deng et al., 2009; Kugel Desmoulin et al., 2010b) (Table 3.1). Assays were performed at pH 7.2 in complete RPMI 1640 (for RFC-expressing PC43-10 and R2), or in complete folate-free RPMI 1640 supplemented with 25 nM 5-CHO-THF (for R2/PCFT4 and R2/VC cells). For most of the antifolates, drug sensitivities, as reflected in decreased IC₅₀s for inhibition of growth over 96 h, were increased in both R2/PCFT4 and PC43-10 cells over respective controls (Table 3.1). With RFC-expressing PC43-10 CHO cells, sensitivities to the classical antifolates were significantly increased (from 6.5-fold for PMX to >159-fold for RTX) over R2 cells. Likewise, R2/PCFT4 cells were sensitive to the classical inhibitors (>8.3- to 74-fold, compared to negative controls). Neither GW1843U89 nor PT523 showed any activity toward R2/PCFT4 cells. Since PCFT is optimally active at acidic pHs (Figure 3.2, Panel D), we measured the changes in media pH during the interval of drug exposure. Over 96 h, the pH of the media decreased linearly and reached pH 6.7 to 6.9 by day 4 (data not shown). Thus, at extracellular pHs approximating those associated with solid tumor microenvironments, several of these classical agents appeared to be substrates for PCFT in R2/PCFT4 cells, as reflected in patterns of growth inhibition. PT523 and



GW1843U89 were completely selective toward RFC over PCFT. Only PMX showed any indication of selective activity toward PCFT over RFC, (i.e., 74-fold increased activity for R2/PCFT4 cells versus 6.5-fold for the PC43-10 cells, compared to respective negative controls). However, this was incomplete; i.e., PMX was appreciably active toward both PCFT- and RFC-expressing cells.

Initial testing of the 6-substituted pyrrolo[2,3-*d*]pyrimidine benzoyl antifolate series as inhibitors of growth in the isogenic CHO sublines, revealed that compounds **1**, **2**, and **4-6** were all completely inert toward PC43-10 cells, establishing a lack of RFC transport activity for this series (Table 3.1). The 3-carbon analog of this series, compound **3**, showed a low level activity toward PC43-10 cells. Compounds **3** and **4** were active toward PCFT-expressing R2/PCFT4 cells, and **3** was more potent than **4** by ~9-fold (IC₅₀s of ~23 and ~213 nM, respectively). Conversely, compounds **1**, **2**, **5**, and **6** were completely inactive (Table 3.1). This result with compounds **3** and **4** is the first identification of an antifolate with selectivity for PCFT-mediated uptake with no or very little substrate activity for RFC (Deng et al., 2008; Kugel Desmoulin et al., 2010b).

The 6-substituted thieno[2,3-*d*]pyrimidine benzoyl antifolate series exhibited a different substrate specificity than compounds **3** and **4** when growth inhibition was measured in the CHO sublines. Compounds **8** and **9** were characterized by potent and selective substrate activities for FR α and FR β (**8** = **9** > **10** > **11**) (data not shown) and negligible substrate activities for both RFC and PCFT (Table 3.1) (Deng et al., 2009; Kugel Desmoulin et al., 2010b). The most potent analogs of the series, compounds **8** and **9**, with 3- and 4-methylene groups in the bridge region, respectively, showed activities similar to those for the most active classical inhibitors, LMX and RTX, toward FR-expressing cells, but were somewhat more active than either PMX or MTX.



The finding of FR- but not PCFT selectivity for this series is particularly interesting given the report of possible direct functional coupling between these transport systems (Zhao et al., 2009b). Our results with 6-substituted thieno[2,3-*d*]pyrimidine benzoyl antifolate substrates for FR establish that, should FR-PCFT coupling occur, this must not be obligatory.

Growth Inhibition of the 6-substituted pyrrolo [2,3-d] pyrimidine thienoyl antifolate series in the isogenic CHO cell line panel found that while 14, 15 and 17-19 were inert toward RFCexpressing PC43-10 cells and R2 cells up to 1000 nM drug, compound 16 showed evidence of a non-FR, non-PCFT cellular uptake process at higher drug concentrations (seemingly in part mediated by RFC and also by a non-RFC uptake mechanism), although substantial FR- and PCFT-selectivity over RFC (as reflected in relative IC_{50} s) was nonetheless preserved (Table 3.1). Of the pyrrolo[2,3-d] pyrimidine thienoval antifolates, **16** (3-carbon bridge) and **17** (4-carbon bridge) are the most potent agents toward PCFT-expressing R2/PCFT4 cells. Compounds 16, 17 and 18 showed a high level of PCFT-targeted activity, for PCFT-expressing R2/PCFT4 cells with IC_{50} s of 3.34, 43 and 101 nM, respectively (Table 3.1). Activity substantially declined for compounds 14 and 15 with 1- and 2-carbon bridge lengths, respectively, and compound 19 was completely inert. Compound 16 was more active than the classic agents and was likewise more so than compound 17. This was most impressively reflected in the ~11-fold decrease in IC_{50} (~3 nM) toward PCFT-expressing R2/PCFT4 cells with 16 compared to 17 (Kugel Desmoulin et al., 2011; Wang et al., 2010; Wang et al., 2011).

Finally, 6-substituted pyrrolo[2,3-*d*]pyrimidine thienoyl regioisomers with 4-carbon bridge lengths and with contiguous thiophene substitutions [2'3' (20); 4'5' (21); 3'4'(22)] were completely inactive toward the RFC- and PCFT-expressing CHO sublines (Table 3.1). Compounds 23 and 24 were likewise inert toward PC43-10 cells, although both compounds



inhibited proliferation of R2/PCFT4 cells (IC₅₀s of 41.5 and 63.8 nM for **23** and **24**, respectively), essentially equivalent to compound **17** (IC₅₀ of 43.4 nM) (Table 3.1). This establishes cellular uptake of compounds **23** and **24** by PCFT. Drug sensitivities for **23** and **24** with R2/PCFT4 cells exceeded those for MTX and RTX, and were comparable to those for LMX. However, **23** and **24** were less potent than PMX (~3- and ~5-fold, respectively) and **16** (~12- and ~19-fold, respectively). None of the 6-substituted pyrrolo[2,3-*d*]pyrimidine regioisomers (**17** and **20-24**) had any impact on proliferation of R2 or R2/VC cells (Wang et al., 2012).

Since nucleoside salvage mechanisms circumvent biosynthetic requirements for reduced folates and growth inhibitory effects of classical antifolates such as MTX, we tested excess adenosine and thymidine for their capacities to abolish the growth inhibitory effects of the most potent analogs (compounds 3, 16 and 17). Results were compared to those for PMX, reported to act as an inhibitor of both purine nucleotide biosynthesis primarily at TS and AICARFTase and less so at GARFTase (Racanelli et al., 2009; Shih and Thornton, 1999), and for LMX, an established inhibitor of GARFTase (Beardsley et al., 1989; Mendelsohn et al., 1999; Moran et al., 1989). Whereas thymidine (10 μ M) also protected R2/PCFT4 cells from the growth inhibitory effects of low concentrations (<50 nM) of PMX, at higher PMX concentrations, protection was incomplete with thymidine either in the presence or absence of AICA (320 µM) (Figure 3.3, Panel A), which is metabolized to AICAR (circumvents drug effects at GARFTase). Adenosine (60 µM) could not circumvent effects of PMX. However, growth inhibition by PMX was completely reversed by adenosine combined with thymidine. Analogous results were previously described for nucleoside protection from the inhibitory effects of PMX for CCRF-CEM cells (Racanelli et al., 2009). In contrast, for LMX and compounds 3, 16 and 17





Figure 3.3 Protection of R2/PCFT4 cells from growth inhibition by PMX, compounds 3, 16 and 17 in the presence of nucleosides and 5-amino-4-imidazole (AICA). Proliferation inhibition was measured for R2/PCFT4 cells over a range of concentrations of PMX (*Panel A*), LMX (*Panel B*), 3 (*Panel C*), 16 (*Panel D*) or 17 (*Panel E*), as shown, in complete folate-free RPMI 1640 with 25 nM 5-CHO-THF, in the presence or absence of adenosine (60 μ M) or thymidine (10 μ M), or AICA (320 nM). Cell densities were measured with CellTiter-BlueTM fluorescence dye and a fluorescence plate reader. Results were normalized to cell density in the absence of drug. Results shown are representative data of experiments performed in triplicate.



(Figure 3.3, Panels B-D), growth inhibition was abolished by either adenosine or AICA alone. These results establish *de novo* purine nucleotide biosynthesis as the targeted pathway for compounds **3**, **16** and **17** and GARFTase as the principal intracellular enzyme target, analogous to LMX (Beardsley et al., 1989).

Cytotoxicity assays were extended to include colony-forming assays. Colony-forming assays were performed in which R2/PCFT4 cells were continuously exposed to a range of concentrations of compounds **3**, **16**, **17**, PMX, or LMX for 10 days (Figure 3.4, Panels A-E). Colonies were scored by counting visible colonies after 10 days and are presented as a percent of the vehicle control. Composite results are presented as mean values \pm standard errors from 3 experiments (Panel E). As an inhibitor of colony-formation, compounds **3** (Panel B), **16** (Panel C) and **17** (Panel D) gave IC₅₀s of 17.14 \pm 0.74 nM (SEM), 1.41 \pm 0.03 nM and 27.17 \pm 2.89 nM, respectively, whereas IC₅₀s for PMX (Panel A) and LMX were 4.94 \pm 0.48 nM and 29.70 \pm 0.59 nM, respectively.

To establish the time-dependent requirements for loss of clonogenicity upon exposure to compound **3**, LMX, or PMX, R2/PCFT4 cells were exposed to the drugs (each at 1 μ M) for different times (2, 4, 8, 24, 48, and 72 h), after which drug was removed and cells were incubated in the presence or absence of adenosine (60 μ M) and thymidine (10 μ M). A parallel incubation was performed in which cells were treated with drugs and nucleosides, after which drugs were removed and cells incubated in the presence of adenosine and thymidine. Colonies were counted after 10 days, with results compared to those for the untreated vehicle (DMSO) control. Nucleoside protection, both during and after drug treatments, completely protected R2/PCFT4 cells from loss of colony formation. When cells were treated during the initial incubation with antifolates *without nucleoside protection*, colony formation was significantly inhibited whether







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Figure 3.4 Inhibition of colony formation. R2/PCFT4 cells were plated into 60 mm dishes at a density of 500 cells per dish in the presence or absence of different concentrations of PMX (*Panel A*), **3** (*Panel B*), **16** (*Panel C*) or **17** (*Panel D*) from 1 to 100 nM. Colonies were scored by counting visible colonies after 10 days and are presented as a percent of the vehicle control. Results are presented as mean values \pm standard errors from 3 experiments (*Panel E*).



or not nucleosides were included after the drug was removed (Figure 3.5). The difference between these two conditions established a time-requirement for *irreversible* drug effects resulting in loss of clonogenicity and ranged from greater than 4 h for PMX (Figure 3.5, Panel A) and compound **3** (Panel C), to greater than 8 h for LMX (Panel B). For all drugs thereafter, there was a progressive diminution of the protective effects such that by 48-72 h, loss of colony formation was essentially complete. For compound **3** treatments, a visual representation of the stained colonies has been included to demonstrate the time-dependent irreversible drug effects (Panel D).

3.3.3 PCFT-selective Transport Characteristics for Compounds 3, 16 and 17.

Growth inhibition results (Table 3.1) strongly suggested selective membrane transport by PCFT and not RFC for compounds **3**, **16** and **17**. For further confirmation, we tested these compounds (10 μ M) as direct competitors for inhibition of PCFT-mediated uptake of [³H]MTX (0.5 μ M) in R2/PCFT4 cells from pH 5.5 to 7.2, and compared the results to those for PMX and PT523, established RFC substrates. A parallel experiment was performed with PC43-10 cells to assess the inhibitory effects of compounds **3**, **16** and **17** (10 μ M) on RFC-mediated [³H]MTX uptake (at pH 7.2), compared to other established RFC transport substrates. As shown in (Figure 3.6, Panel A), with R2/PCFT4 cells, compounds **3**, **16** and **17** were potent inhibitors of PCFT transport, only slightly less so than PMX and with substantially increased potencies at pH values less than 7.2. As expected (Zhao and Goldman, 2007), PT523 did not inhibit [³H]MTX uptake at any pH for R2/PCFT4 cells. For RFC-expressing PC43-10 cells at pH 7.2, PT523, PMX, RTX, LMX, and 5-CHO-THF all potently inhibited [³H]MTX transport (Figure 3.6, Panel B). However, compounds **3**, **16** and **17** were *essentially inert* as inhibitors of RFC.





Figure 3.5 Time dependence for loss of clonogenicity in R2/PCFT4 cells treated with PMX, LMX and compound 3. R2/PCFT4 cells were plated into 60 mm dishes at 500 cells per dish and allowed to adhere for 48 h, after which cells were treated with or without 1 μ M drug in the presence or absence of adenosine (60 μ M) and thymidine (10 μ M) for 2, 4, 8, 24 and 48 h. Following drug treatment, cells were washed with DPBS and resuspended with drug-free media with or without adenosine (60 μ M) and thymidine (10 μ M) protection. Colonies were enumerated after 10 days and results are presented as a percent of vehicle control. *Panel A*, PMX. *Panel B*, LMX. *Panel C*, Compound 3. *Panel D*, Representative image of dishes that were counted to produce *Panel C*. Results are presented as mean values \pm standard errors from 3 experiments. Abbreviations: Ade, adenosine; Thd, thymidine.



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Figure 3.6 Competitive inhibition of PCFT and RFC transport of [³H]MTX. *Panel A*, R2/PCFT4 cells ectopically expressing PCFT but no FR or RFC were assayed for [³H]MTX transport in the presence of 10 μ M PMX, compounds 3, 16, 17 and PT523 at pH 5.5-7.2. *Panel B*, R2 cells (vector) expressing no RFC, PCFT or FR and PC43-10 cells expressing RFC but no PCFT or FR were assayed for [³H]MTX transport in the presence of 10 μ M compounds 3, 16, 17 and PT523, PMX, RTX, LMX, or 5-CHO-THF at pH 7.2. Results are presented as mean values \pm standard errors from >3 experiments.



We used Dixon analysis at pH 5.5 and pH 6.8 with R2/PCFT4 cells and [³H]MTX to calculate K_is for PCFT competitors including compounds **3**, **16**, **17**, PMX and LMX (Table 3.2). Transport of 0.5 μ M [³H]MTX was measured over a range of inhibitor concentrations. The relative affinities of our lead compounds to PCFT were similar to PMX and are as follows: PMX < **17** < **16** < **3** < LMX. K_i values increase 14-18 fold at pH 6.8 for all compounds except LMX which had a 50-fold increased K_i at pH 6.8. For PMX, the K_is closely approximated the K_ts recorded with [³H]PMX.

To confirm that compounds **3**, **16**, and **17** are transported by PCFT, electrophysiological studies were performed in *Xenopus* oocytes injected with PCFT cRNA. Uptake was assessed in oocytes clamped to -90 mV at a bath pH of 5.5. A substrate concentration of 5 μ M was used, which is saturating for 5-CHO-THF and PMX. These experiments show that the currents induced by compounds **3**, **16** and **17** were comparable to that produced by 5-CHO-THF (Figure 3.7).

3.3.4 Identification of *de novo* **Purine Nucleotide Biosynthesis and GARFTase as Primary** Cellular Targets for Compounds 3, 16 and 17.

Our protection studies further identified *de novo* purine nucleotide biosynthesis as the primary targeted pathway following PCFT transport of the 6-substituted pyrrolo[2,3-*d*]pyrimidine –benzoyl (**3**) and –thienoyl antifolates (**16** and **17**). To confirm the inhibition of purine nucleotide biosynthesis by compounds **3**, **16** and **17**, we measured ATP and GTP pools by HPLC in R2/PCFT4 cells for compounds **3**, **16** and **17**. For compound **3**, cells were treated with increasing concentrations for 24 h and results were compared to those of LMX; results are shown as a percentage of control ATP and GTP levels (Figure 3.8, Panel A). Additionally, cells were treated with 1 µM of **16** and **17** for 24 h at pH 6.8, and results were compared to those for LMX and PMX (both at 1 µM) (Figure 3.8, Panel B). GTP and ATP pools





Figure 3.7 Electrophysiology studies of antifolate transport by PCFT in *Xenopus* oocytes. Substrate-induced currents (nA) were recorded in individual oocytes injected with wild type PCFT and voltage clamped to a holding potential (*V*h) of -90 mV. Oocytes were perfused with ND90 solution at pH 5.5 with 5-CHO-THF followed by compounds 3, 17 and 16. For all substrates, concentrations were maintained at a level of 5 μ M.



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Figure 3.8 Intracellular ATP levels and *in situ* GARFTase inhibition in R2/PCFT4 cells treated with compounds 3, 16, 17, LMX, and PMX. *Panel A*, for analysis of ATP levels, cells were treated with various concentrations of compounds 3 or LMX for 24 h. Nucleotides were extracted and ATP pools were determined by a modification of the HPLC method of Huang et al. (2003a). Details are provided in the Materials and Methods. *Panel B*, R2/PCFT4 cells were treated with 1 μ M 17, 16, PMX, or LMX, or solvent (0.5% DMSO for 3, 16 and 17, H₂O for PMX and LMX) for 24 h. Cells were washed, and nucleotides were extracted and analyzed by HPLC. Results are shown for percentage control ATP after the drug treatments. *Panel C*, GARFTase activity and inhibition were evaluated *in situ* with R2/PCFT4 cells. Accumulation of [¹⁴C]formyl GAR from [¹⁴C]glycine was measured in R2/PCFT4 cells treated with the antifolates. The production of [¹⁴C]formyl GAR was calculated as a percent of vehicle control over a range of antifolate concentrations. Results are presented as the mean values (standard errors from 3 experiments. Methodologic details are described in the Experimental Procedures section. IC₅₀s were as follows: 0.97 nM, 3; 0.69 nM, 16; 1.96 nM, 17; 31.5 nM LMX; and 7.3 nM, PMX.



were severely depleted (approximately 50 and 75%, respectively) during a 24 h exposure of R2/PCFT4 cells to 1 μ M of either compound **3** or LMX. For ATP pools, IC₅₀ values of 58 and 166 nM were measured for compound **3** and LMX, respectively (Figure 3.8, Panel A). For GTP pools, IC₅₀ values were 441 and 579 nM, respectively (data not shown). Treatment of R2/PCFT4 cells with either 1 μ M **16** or **17** for 24 h resulted in profound depletion of ATP pools (90%), which exceeded the decrease resulting from treatment with LMX (76%). PMX treatment, on the other hand only minimally impacted ATP pools (17%) (Figure 3.8, Panel B). Similar results were reported by Chen et al. (1998).

To confirm GARFTase inhibition and to provide a metabolic "read-out" for PCFT transport of compounds **3**, **16** and **17** in R2/PCFT4 cells, we used an *in situ* assay for GARFTase. GARFTase catalyzes formylation of the glycine-derived nitrogen of GAR, producing formyl GAR with 10-formyl THF as the one-carbon donor. The *in situ* GARFTase assay measures incorporation of [¹⁴C]glycine into [¹⁴C]formyl GAR in the presence of azaserine (4 μ M) (Beardsley et al., 1989; Deng et al., 2008). Modifications were made in the original protocol to measure GARFTase inhibition under pH conditions which permitted PCFT transport. Briefly, R2/PCFT4 cells were cultured for 48 h in complete folate-free media supplemented with 25 nM 5-CHO-THF. The 48 h incubation allowed the cells to adhere and the pH of the culture media to decrease to ~6.9 accompanying cell growth. Cells were then treated for 15 h with or without a range of concentrations of compounds **3**, **16** and **17**, or with PMX or LMX, after which cells were washed, resuspended in complete L-glutamine- and folate-free medium with or without drug and then treated with azaserine for 30 min, after which L-glutamine and [¹⁴C]glycine were added. After an additional 8 h, cells were washed, proteins were precipitated with TCA, and the



supernatants were ether-extracted and fractionated on anion exchange columns so that $[^{14}C]$ formyl GAR could be measured and IC₅₀s calculated.

Our results demonstrate that PMX, LMX, and compounds **3**, **16** and **17** all inhibited [¹⁴C]formyl GAR accumulation in R2/PCFT4 cells at ~pH 6.9 when PCFT is the *sole* mode of antifolate drug delivery (Figure 3.8, Panel C). Compound **16** was by far the most potent of these drugs with an impressive IC₅₀ for GARFTase inhibition of 0.69 nM. Relative drug sensitivities for the other lead compounds and classic antifolates were as follows, IC₅₀s (in nM) are in parentheses: **3** (0.97) > **17** (1.96) > PMX (7.3) > LMX (31.5). The most potent inhibitors were compounds **3** and **16**, suggesting that the chain length of the bridge region is an important determinant of GARFTase inhibition regardless of whether the compound is a pyrrolo[2,3-*d*]pyrimidine –benzoyl or –thienoyl. GARFTase inhibition is the ultimate determinant of growth inhibition, with the IC₅₀s following the same trend, **16** > **3** > **17** (Table 3.1).

3.4 Discussion.

Chemotherapy activity of classic antifolates has traditionally been interpreted in terms of their active membrane transport into tumors by RFC (Matherly et al., 2007). Furthermore, impaired membrane transport due to loss or mutations of RFC was reported to result in antifolate resistance (Assaraf, 2007; Matherly et al., 2007; Zhao and Goldman, 2003). However, after reports of a novel low-pH transporter termed PCFT (Nakai et al., 2007; Qiu et al., 2006; Zhao and Goldman, 2007) and the recognition that PCFT is expressed and functional in human solid tumors (Chapter 2) and can efficiently transport cytotoxic antifolates, such as MTX, at pH values approximating those of solid tumors (Chapter 2), it becomes necessary to examine the possibility that PCFT could represent an important mode of chemotherapy drug transport.



Because most cultured cells endogenously express more than one folate transport system (Chapter 2), to explore the role of PCFT in delivery of cytotoxic antifolates, we engineered the R2/PCFT4 CHO subline from PCFT-, RFC-, and FR-null R2 cells to express PCFT without either RFC or FRs. R2/PCFT4 cells exhibited optimal transport activity at acidic over neutral pHs, reflecting high-affinity transport of substrates with decreasing pH. The impact of pH on transport by PCFT was substantially different between (anti)folate substrates. By growth inhibition assays, R2/PCFT4 cells were sensitive to classic antifolates, including MTX, RTX, PMX, and LMX, suggesting their membrane transport by PCFT; PMX was the most active transport substrate and neither GW1843U89 nor PT523 was growth inhibitory. Although PCFT exhibits limited transport at neutral pH typical of culture media, transport of these cytotoxic antifolates by PCFT was enhanced by the progressively decreasing pH that accompanies cell outgrowth. PMX is a 5-substituted pyrrolo[2,3-d] pyrimidine benzoyl analog and is the best substrate previously described for PCFT (Zhao and Goldman, 2007). Because PMX was a potent inhibitor of R2/PCFT4 cell growth, we compared the growth inhibitory effects of a number of structurally related 6-substituted pyrrolo or thieno[2,3-d]pyrimidine benzoyl or thienoyl antifolates with bridge lengths from one to eight methylenes (depending on the drug series) as inhibitors of R2/PCFT4 cell proliferation.

The 6-substituted pyrrolo[2,3-*d*]pyrimidine with a –benzoyl B ring and three methylenes (compound **3**) or a -thienoyl B ring and three or four methylenes (compounds **16** and **17**, respectively) were potent inhibitors of R2/PCFT4 cell growth or clonogenicity. Additionally, these compounds were essentially inert toward RFC-expressing PC43-10 cells, thus establishing these analogs as our lead compounds for future studies. It is noteworthy that compounds **3**, **16** and **17** all selectively inhibited transport of [³H]MTX by PCFT with potencies only slightly less



than that for PMX, as reflected in K_i values, and with nearly identical pH dependencies. After microinjection of PCFT cRNA into *X. laevis* oocytes, perfusion with a saturating concentration of compounds **3**, **16** and **17** elicited a current, confirming that these compounds are electrogenically transported by PCFT. Collectively, these results establish that the cytotoxic 6substituted pyrrolo[2,3-*d*]pyrimidine –benzoyl compound **3** and –thienoyl compounds **16** and **17** are *bona fide* transport substrates for PCFT, essentially on par with PMX. However, unlike PMX, compounds **3**, **16**, and **17** have nominal transport activity with RFC.

Compound **3** was previously reported to be cytotoxic toward cells that express high levels of FR α , reflecting inhibition of GARFTase, the trifunctional enzyme that catalyzes the second, third, and fifth reactions of *de novo* purine nucleotide biosynthesis, including the first folatedependent step (Deng et al., 2008). Consistent with primary inhibition of GARFTase after transport by PCFT, both adenosine and AICA protected R2/PCFT4 cells from growth inhibition by compounds **3**, **16** and **17**. By an *in situ* GARFTase assay, which measures [¹⁴C]glycine incorporation into formyl GAR, compounds **3**, **16** and **17** were disproportionately inhibitory, with IC₅₀ values less than 1 nM, far lower than the IC₅₀ for LMX. Although PMX is primarily an inhibitor of TS and was recently reported to inhibit AICARFTase in CCRF-CEM cells (Racanelli et al., 2009), in R2/PCFT4 CHO cells, appreciable GARFTase inhibition was detected, albeit less than that for compounds **3**, **16** and **17**.

These results describe the first PCFT-selective antifolates and establish that PCFT is a surprisingly efficient means of cytotoxic drug delivery. The much higher concentrations of compounds **3**, **16** and **17** needed to inhibit colony formation and cell proliferation, or to significantly suppress ATP/GTP pools versus those required to inhibit GARFTase in cells, must reflect the nature of the enzyme target and requirement for sustained inhibition of GARFTase



and *de novo* purine biosynthesis for cell killing. Indeed, sustained exposures to GARFTase inhibitors were required to irreversibly inhibit colony formation of R2/PCFT4 cells, although an analogous time-dependence was obtained with PMX. Similar results were previously reported when comparing effects on clonogenicity of GARFTase inhibition by LMX versus TS inhibition by RTX in WiDr colonic carcinoma cells (Smith et al., 1993). The higher concentrations of LMX over compound 3 needed to inhibit GARFTase in cells relative to those required to manifest cytotoxicity provide further evidence that GARFTase inhibition is not limiting to cell killing. The decreased GARFTase inhibition for LMX in R2/PCFT4 cells probably reflects its reduced transport by PCFT compared with compound **3**, although factors such as differences in the extent of polyglutamate synthesis may also contribute. High-level substrate activity was previously reported for compound 3 for human FPGS (Gangjee et al., 2004); however compounds 16 and 17 have not been directly tested. The delay in irreversible drug effects upon inhibition of GARFTase may reflect salvage of purines generated from breakdown of nucleic acids (Bronder and Moran, 2002; Smith et al., 1993). Accordingly, the delay for irreversible cell death by GARFTase inhibitors may be substantially shortened in cells that have defects in purine salvage, increasing dependence on *de novo* purine synthesis. For instance, deletions of MTAP have been described in human malignancies, including ~70% of pleural mesotheliomas (Illei et al., 2003) and 38% of NSCLC (Schmid et al., 1998). On this basis, GARFTase inhibitors such as compounds 3, 16, and 17 may show far greater potencies in MTAP-deficient tumors, especially if there are high levels of PCFT.

It will be interesting to determine whether the ATP depletion caused by GARFTase inhibitors will lead to an increase in NRF-1, upregulation of PCFT transcription and enhanced



activity of the drug in tumor cells. Conversely, there could be an upregulation of *de novo* purine biosynthesis enzyme expression and subsequent resistance to GARFTase inhibitors.

Finally, the present results, combined with earlier studies of 6-substituted pyrrolo- and thieno[2,3-d]pyrimidine antifolates (Deng et al., 2009; Wang et al., 2010) begin to establish a structure activity relationship for PCFT-selective antifolates and shed light on the impact of both aromatic ring systems and the length of the bridge domain on transport by PCFT versus other folate transporters. Thus, antifolates with thieno[2,3-d]pyrimidine and benzoyl rings (designated A and B rings, respectively) (Figure 3.1) are effective transport substrates for FRs but not for RFC or PCFT, with optimal activity for the 3- and 4-carbon bridge analogs (Deng et al., 2009). Replacement of the thieno [2,3-d] pyrimidine A ring with a pyrrolo [2,3-d] pyrimidine system favors binding and transport by both PCFT and FRs, regardless of whether the B ring is a benzoyl (3) or thiophene (16 and 17). For the pyrrolo[2,3-d] pyrimidine -benzoyl and -thienoyl series, decreasing the bridge lengths between the bicyclic scaffold and L-glutamate from 8- to 4carbons (4 and 17) substantially increased the antiproliferative activities of the analogs, reflecting transport by PCFT. Further decreasing the bridge length of these compounds from 4to 3-carbons (3 and 16) increased drug potencies; however, this appeared to be accompanied by some loss of absolute transporter specificity for PCFT over RFC. Decreasing the bridge length to 1- or 2-carbons caused complete loss of activity.

In conclusion, we document PCFT-selective transport over RFC for the potent 6 substituted pyrrolo[2,3-*d*]pyrimidine -benzoyl and -thienoyl antifolate series, particularly compounds **3**, **16** and **17**. Our results strongly suggest the therapeutic potential of PCFT for targeting drugs to tumors. The notion of PCFT drug targeting is appealing given the acidic pH optimum for this system and the low pH microenvironment of many solid tumors (Anderson and



Thwaites, 2010; Helmlinger et al., 1997; Webb et al., 2011). For drugs such as compounds **3**, **16** and 17 which exhibit PCFT selectivity over RFC, tumor selectivity would be enhanced because transport by PCFT would be extensive under the low pH conditions in solid tumors yet should be limited at neutral pH typical of most normal tissues. This would result in significantly lower toxicity. Although compounds 3, 16 and 17 are also cytotoxic toward FR-expressing cells (Deng et al., 2008), given the frequent association of FRs with malignant cells (Chapter 2) (Elnakat and Ratnam, 2004), this may serve to broaden potential therapeutic applications of this drug platform. Our drug discovery efforts are currently focused toward identifying PCFT-specific agents without transport by FR or RFC to test this. Validation of these concepts will undoubtedly depend on establishing cytotoxicity of 3, 16 and 17 in human solid tumor cell lines with endogenous levels of PCFT (~10 fold lower than levels found in R2/PCFT4 cells) delivered at pHs that resemble the solid tumor microenvironment (pH 6.8), determining whether these novel analogs are polyglutamylated and establishing their affinities for FPGS, identifying the effects of the analogs on the cell cycle and the mechanisms of cell death. Further, it will be important to establish *in vivo* activity of the drugs against transplanted tumors that express PCFT as the sole means of drug delivery and also determining the impact of functional RFC on the pharmacology of these drugs. These questions will be studied in Chapters 4 and 5 of this dissertation.



CHAPTER 4

SOLID TUMOR TARGETING BY PCFT-MEDIATED UPTAKE OF NOVEL ANTIFOLATES **4.1 Introduction.**

PCFT transport function may be enhanced in many solid tumors by the acidic pH of the tumor microenvironment, which has been reported to reach as low as pH 6.2 to 6.8 (Helmlinger et al., 1997; Webb et al., 2011). Intracellular pH is normally alkaline, which creates a substantial transmembrane pH gradient directed *intra*cellularly (Fais et al., 2007). Clearly, harnessing this proton-motive gradient to transport cytotoxic antifolates into tumor cells by PCFT offers a uniquely attractive mechanism of therapeutic targeting solid tumors. Importantly, as described in Chapter 2, PCFT is expressed and is functional in a wide range of human solid tumor cell lines. PCFT expression was confirmed in primary human tumors. For tumor targeting of cytotoxic drugs via FR or PCFT, ideally, therapeutic agents are specifically transported by FRs and/or PCFT and not by RFC (Deng et al., 2008; Deng et al., 2009; Gibbs et al., 2005; Hilgenbrink and Low, 2005; Kugel Desmoulin et al., 2010b; Salazar and Ratnam, 2007; Wang et al., 2010). This strategy is necessary because antifolate membrane transport by RFC precludes tumor selectivity, in that RFC is expressed in both normal and tumor cells, and RFC transport is optimal at neutral pH characterizing most normal tissues (Matherly et al., 2007; Zhao and Goldman, 2003). Indeed, a major obstacle in implementing this approach has been a lack of FR- or PCFT-selective agents, since all of the clinically useful antifolates with significant FR- and PCFT substrate activity (e.g., MTX and PMX) are also transported by RFC (Matherly et al., 2007). In Chapter 3, we described a novel 6-substituted pyrrolo[2,3-d]pyrimidine antifolate with a thienoyl-for-benzoyl B ring replacement and a bridge length of four carbons (compound 17) (Figure 3.1, Panel C) (Kugel Desmoulin et al., 2011; Wang et al., 2010). Cellular uptake of compound 17 by FR α and PCFT



was substantial in the absence of its membrane transport by RFC, resulting in potent antitumor activity *in vitro* because of its inhibition of GARFTase in *de novo* purine nucleotide biosynthesis.

This chapter will focus on directly testing the capacity of PCFT to deliver a cytotoxic dose of compound **17** under conditions relevant to the solid tumor microenvironment. Characteristics of drug transport, polyglutamylation, GARFTase inhibition, ATP levels, cell cycle analysis and mechanism of cell death will be evaluated in human solid tumor cell lines that have modest endogenous levels of PCFT. Drug treatments will be studied at pHs that are similar to those surrounding many solid tumors (pH 6.8), or performed *in vivo* where a true acidic tumor microenvironment can be created by the growing tumor (Raghunand et al., 1999). This chapter describes such experiments with compound **17** to establish the feasibility of selectively targeting chemotherapy to human solid tumors based upon drug membrane transport by PCFT. The majority of this work has been published (Kugel Desmoulin et al., 2011).

4.2 Materials and Methods.

4.2.1 Chemicals and Reagents.

 $[3',5',7^{-3}H]MTX$ (20 Ci/mmol), $[^{3}H]PMX$ (2.5 Ci/mmol), and custom-radiolabeled $[^{3}H]$ compound **17** (1.3 Ci/mmol) were purchased from Moravek Biochemicals (Brea, CA). (6*R*,*S*)-5-formyl tetrahydrofolate (5-CHO-THF) was provided by the Drug Development Branch, National Cancer Institute (Bethesda, MD). PMX [*N*-(4-[2-(2-amino-3,4-dihydro-4-oxo-7H-pyrrolo[2,3-*d*]pyrimidin-5-yl)ethyl] benzoyl)-L-glutamic acid] (Alimta) was provided by Eli Lilly and Co. (Indianapolis, IN). Synthesis and properties of the 6-substituted pyrrolo[2,3-*d*]pyrimidine thienoyl antifolate compound **17** were described previously (Kugel Desmoulin et al., 2011; Wang et al., 2010). Other chemicals were obtained from commercial sources in the highest available purities.



4.2.2 Cell Culture.

To determine the efficacies of the novel antifolates in human solid tumor cell lines, RFC-/PCFT-null HeLa (R1-11) sublines were obtained from Dr. I. David Goldman (Albert Einstein School of Medicine, Bronx, NY). R1-11-RFC6 and R1-11-PCFT4 cells were derived from R1-11 cells by stable transfection with HA-tagged pZeoSV2(+)-RFC and pZeoSV2(+)-PCFT constructs, respectively. Cells were maintained in regular RPMI 1640 medium supplemented with 10% fetal bovine serum (Invitrogen, Carlsbad, CA), 100 units/mL penicillin, 100 µg/mL streptomycin, 2 mM L-glutamine and 0.1 mg/mL zeocin (Invitrogen, Carlsbad, CA) at 37°C with 5% CO₂. Characteristics of the HeLa sublines were described previously (Zhao et al., 2008). Additionally, HepG2 cells were purchased from ATCC and were routinely grown in Eagle's MEM (Invitrogen, Carlsbad, CA) supplemented with 10% fetal bovine serum (Thermo Fisher Scientific, Waltham, MA), 100 units/mL penicillin, 100 µg/mL streptomycin and 2 mM Lglutamine.

4.2.3 Real-time RT-PCR Analysis of RFC, FRα, and PCFT Transcripts.

For characterizing human PCFT, RFC and FRα transcript levels, RNAs were isolated using TRIzol reagent (Invitrogen, Carlsbad, CA) according to the manufacturers instructions, from the HepG2 human hepatocellular carcinoma cell line, the IGROV1 human ovarian adenocarcinoma cell line, engineered R1-11 HeLa sublines (R1-11 mock, R1-11-RFC6, and R1-11-PCFT4) and *in vivo* HepG2 tumor samples (see section 4.2.10 for trial information). For isolation of RNA from HepG2 tumor *xenografts*, dry ice was used to ensure that the snap-frozen tumors remained cold to prevent RNase degradation of tumor RNA. Tumors were cut into thin sections using an ice cold razor blade. Tumor fragments were transferred into a microcentrifuge tube containing 1 mL TRIzol (Invitrogen) and quickly homogenized using a Kontes pellet pestle motor and



RNAase-free pellet pestle (Sigma-Aldrich, St. Louis, MO). The tumor fragments, resuspended in TRIzol (Invitrogen), were vortexed, pelleted by microcentrifugation and homogenized until all solid tumor fragments were solubilized. The remaining protocol for RNA isolation was the same as above. cDNAs for all samples were synthesized using random hexamers, RNase inhibitor, and MuLV reverse transcriptase and purified with the QIAquick PCR Purification Kit (Qiagen). Real-time RT-PCR was performed on a Roche LightCycler 1.2 (Roche, Indianapolis, IN) with gene-specific primers (Table 2.1) and FastStart DNA Master SYBR Green I enzyme reaction mix (Roche), as described (Ge et al., 2007). Transcript levels for human PCFT, RFC and FR α were normalized to those for GAPDH. External standard curves were constructed for each gene of interest using serial dilutions of linearized templates, prepared by amplification from suitable cDNA templates, subcloning into a TA-cloning vector (PCR-Topo; Invitrogen), and restriction digestions.

4.2.4 Proliferation and Colony-forming Assays.

For growth inhibition assays, R1-11-PCFT4, R1-11-RFC6 HeLa, and HepG2 cells were cultured in complete folate-free RPMI 1640 medium, pH 7.2, supplemented with 25 nM 5-CHO-THF, for at least 2 weeks prior to the experiment (folate-depleted). Cells were plated in 96-well culture dishes (5000 cells/well; 200 μ L/well) in the above medium with a broad concentration range of drugs (depending on the compound, drug dilutions were in DMSO or water with appropriate vehicle controls); cells were incubated for up to 96 h at 37°C in a CO₂ incubator. Metabolically active cells (a measure of cell viability) were assayed with CellTiter-BlueTM cell viability assay (Promega, Madison, WI) and a fluorescent plate reader (emission at 590 nm, excitation at 560 nm) for determining IC₅₀ values, corresponding to drug concentrations that result in 50% loss of cell growth. For colony-forming assays, folate-depleted R1-11-PCFT4 cells



(500 cells) in log-phase were plated into 60-mm dishes in complete folate-free RPMI 1640 medium, pH 7.2, supplemented with 25 nM 5-CHO-THF and allowed to adhere for 48 h. Cells were then treated with compound **17** or PMX in the above media, supplemented with 25 mM PIPES and 25 mM HEPES (complete buffered folate-free RPMI 1640 medium) to maintain the pH at 6.8. After 16, 24, or 48 h, cells were rinsed with DPBS, and then incubated in drug-free, complete folate-free RPMI 1640 medium, supplemented with 25 nM 5-CHO-THF, pH 7.2. Cells were allowed to outgrow for 12 days, at which time the dishes were rinsed with DPBS, 5% TCA, and borate buffer (10 mM, pH 8.8), followed by 1% methylene blue (in borate buffer). The dishes were again rinsed with borate buffer, and colonies were counted for calculating percentage colony formation relative to the DMSO controls.

4.2.5 Transport Assays.

For comparison of PCFT transport activities in R2/PCFT4 and R1-11-PCFT4 cells, PCFT transport activities in R2/VC, R2/PCFT4, R1-11-mock and R1-11-PCFT4 cells were assessed in cell monolayers by measuring uptake of 0.5 μ M [³H]MTX at 37°C for 5 min at pH 7.2 in HEPES-buffered saline (20 mM HEPES, 140 mM NaCl, 5 mM KCl, 2 mM MgCl₂, and 5 mM glucose), or at pH 5.5 in MES-buffered saline (20 mM MES, 140 mM NaCl, 5 mM KCl, 2 mM MgCl₂, and 5 mM glucose) (Zhao et al., 2004b). To determine the pH-dependent transport of [³H]compound **17** and [³H]PMX (both at 0.25 μ M) in R1-11-PCFT4, R1-11-mock, and HepG2 cells, uptake was assayed at 37°C in cell monolayers over 2 to 30 min at 37°C in complete buffered folate-free RPMI 1640 (pH 5.5, 6.8, and 7.2). At the end of the incubations, transport was quenched with ice-cold DPBS, cells were washed three times with ice-cold DPBS, and cellular proteins were solubilized with 0.5 N NaOH. Levels of drug uptake were expressed as picomoles per milligram of protein, calculated from direct measurements of radioactivity and



protein contents of cell homogenates. Proteins were quantified using Folin-phenol reagent (Lowry et al., 1951). For PCFT transport kinetic analyses, R1-11-PCFT4 cells were grown in suspension using spinner flasks at densities of 2 to 5 X 10^5 cells/mL. Cells were collected by centrifugation, washed with DPBS, and suspended (at 1.5 X 10^7 cells) in 2 mL of transport buffer (below) for cellular uptake assays. To determine [³H]compound **17** and [³H]PMX kinetic constants for PCFT (K_t and V_{max}), initial uptake rates were measured at 37°C over 2 min in HEPES-buffered saline at pH 6.8, or in MES-buffered saline at pH 5.5 (Zhao et al., 2004b), using substrate concentrations from 0.04 to 5 μ M. K_t and V_{max} values were determined from Lineweaver-Burk plots.

4.2.6 HPLC Analysis of Polyglutamyl Derivatives of Compound 17 and PMX.

Folate-depleted R1-11-PCFT4 and HepG2 cells were grown in complete folate-free RPMI 1640 medium, supplemented with 25 nM 5-CHO-THF. Cells were washed with DPBS and incubated in complete buffered folate-free RPMI 1640 medium, pH 6.8, with 1 μ M [³H]compound **17** or [³H]PMX at 37°C in the presence of 60 μ M adenosine, or 60 μ M adenosine plus 10 μ M thymidine, respectively. After 16 h, cells were washed three times with ice-cold DPBS, then scraped mechanically into 5 mL of ice cold DPBS, pelleted, and flash-frozen. The cell pellets were resuspended into 0.5 mL of 50 mM sodium phosphate buffer, pH 6.0, and 100 mM 2-mercaptoethanol, including unlabeled compound **17** (or PMX) and MTX-diglutamate, – triglutamate, and –tetraglutamate standards (Schircks Laboratories, Jona, Switzerland) (50 μ M each). A portion (50 μ L) was used to determine total [³H]compound **17** or PMX (in picomoles per milligram of protein). Proteins were measured by the Bio-Rad protein assay (Bio-Rad Laboratories, Richmond, CA). The remaining extract was boiled (10 min), the supernatant containing radiolabeled compound **17** (or PMX) and its metabolites was centrifuged, then (250



µL) injected into a Waters 4 µm Nova-Pak C-18 column (3.9 X 150 mm) with a Nova-Pak 4 µm C-18 guard column. A Varian 9012 ternary gradient-programmable pump was used for gradient development, and a 9050 Varian UV/Vis detector set to 313 nm was used for detection of compound 17, PMX, or MTX polyglutamate standards. HPLC analysis involved a binary gradient. Mobile phase A consisted of 100 mM sodium acetate at pH 5.5; mobile phase B consisted of 100% acetonitrile. The flow rate was set at 1.6 mL/min. The gradient consisted of 100% A from 0 to 5 min, then 85% A/15% B from 5 to 27.5 min. Fractions were mechanically collected every min for the first 10 min and then every 10 s for the duration of the run. Radioactivity of the fractions was measured with a scintillation counter. Intracellular levels of radiolabeled compounds are expressed as picomoles per milligram of protein, based on calculated percentages in the peaks from the HPLC chromatogram and total picomoles per milligram of cellular [³H]antifolate. To confirm the identities of the early-eluting peaks as polyglutamate metabolites of compound 17, samples were hydrolyzed to their parent drug forms by an overnight treatment at 32°C with a preparation of partially purified chicken pancreas conjugase in 0.5 mL of 0.1 M sodium borate, pH 7.8, containing 10 mM 2-mercaptoethanol (Matherly et al., 1985). Samples were deproteinized by boiling (5 min), then analyzed by HPLC.

4.2.7 In situ GARFTase Enzyme Inhibition Assay.

Incorporation of $[^{14}C(U)]$ glycine into $[^{14}C]$ formyl GAR as an *in situ* measure of endogenous GARFTase activity in folate-depleted R1-11-PCFT4 cells at pH 6.8 was performed using a modification of published methods (Beardsley et al., 1989; Deng et al., 2008; Kugel Desmoulin et al., 2010b). For these experiments, R1-11-PCFT4 cells were seeded in 5 mL of complete folate-free RPMI 1640 medium plus 25 nM 5-CHO-THF in 60 mm dishes and allowed to adhere overnight. Cells were washed twice with DPBS and resuspended in 5 mL of complete



buffered folate-free RPMI 1640 medium, pH 6.8, and 25 nM 5-CHO-THF. Antifolate inhibitor or an equivalent amount of vehicle (e.g., DMSO) ("control") was added to the culture medium, and the cells were incubated for another 16 h. Cells were washed twice with DPBS and resuspended in 5 mL of complete folate-free, L-glutamine-free RPMI 1640 medium/10% dFBS plus 25 mM PIPES/25 mM HEPES, pH 6.8, and 25 nM 5-CHO-THF, with or without 0.5 to 100 nM antifolate and azaserine (final concentration, 4μ M), and incubated for 30 min. L-Glutamine (final concentration, 2 mM) and $[^{14}C]$ glycine (final specific activity, 0.1 mCi/L) were added, followed by incubation at 37°C for 8 h, after which time cells were washed three times with icecold DPBS and trypsinized. Cell pellets were suspended in 2 mL of 5% TCA at 0°C. Cell debris was removed by centrifugation; samples were solubilized in 0.5 N NaOH and assayed for protein contents (Lowry et al., 1951). The supernatants were extracted twice with 2 mL of ice-cold ether. The aqueous layer was passed through a 1 cm column of AG1x8 (chloride form, 100–200 mesh) (BioRad Laboratories, Hercules, CA), washed with 10 mL of 0.5 N formic acid, followed by 10 mL of 4 N formic acid, and eluted with 8 mL of 1 N HCl solution. The elutants were collected as 1 mL fractions and determined for radioactivity.

4.2.8 Determination of Intracellular ATP levels.

For analysis of ATP levels after antifolate treatments, R1-11-PCFT4 cells were seeded in 10 mL of complete buffered folate-free RPMI 1640 medium, pH 6.8, and 25 nM 5-CHO-THF. After 24 h, 10 μ M compound **17** or DMSO (final concentration, 0.5%) (control) was added to the culture medium. Cells were incubated for an additional 24 to 72 h, after which they were trypsinized and washed twice with ice-cold DPBS. Nucleotides were extracted and ATP levels quantitated by HPLC exactly as described in Chapter 3 (Kugel Desmoulin et al., 2010b).

4.2.9 Assessment of Apoptosis and Cell Cycle Distribution.



R1-11-PCFT4 cells were treated with 10 µM compound 17 for 48 h at pH 6.8 in complete buffered folate-free RPMI 1640 medium, pH 6.8, and 25 nM 5-CHO-THF. Cells were trypsinized, pelleted, and washed once with ice-cold DPBS. Samples were divided so that the cell cycle profile and apoptosis analysis could be performed on the same sample. The amount of apoptosis was measured by staining cells with fluorescein isothiocyanate (FITC)-conjugated annexin V and propidium iodide (PI) with the apoptotic cells determined using the CELL LAB ApoScreen Annexin V-FITC Apoptosis Kit (Beckman Coulter, Fullerton, CA), as recommended by the manufacturer. Cells were analyzed for the presence of viable (annexin V and PI), early apoptotic (annexin V⁺ and PI), and late apoptotic/necrotic (annexin V⁺ and PI) cells by flow cytometry. To determine compound 17 concentration-dependent effects on cell cycle progression, R1-11-PCFT4 cells (10^6) were treated with 0, 0.5, 1, 5, and 10 μ M compound 17 in complete buffered folate-free RPMI 1640 medium, pH 6.8, and 25 nM 5-CHO-THF for 48 h. Cells (10^6) were fixed in ethanol (at least 1 h), then stained by resuspension in 0.5 mL of DPBS containing 50 µg/mL PI and 100 µg/mL RNase type I-A (Sigma Aldrich, St. Louis, MO). The cells were analyzed by flow cytometry for determining the percentage of cells in each phase of the cell cycle. Flow cytometry was performed at the Karmanos Cancer Institute Imaging and Cytometry Core using the BD FACSCanto II operated with BD FACSDiva software (v6.0) (BD Biosciences, San Jose, CA). In each experiment, 2 X10⁴ cells were assessed for apoptosis and cell cycle distribution. Data were analyzed with the FlowJo software (ver. 7.6.1; Tree Star, Inc, Ashland, OR).

4.2.10 In vivo Efficacy Study of Compound 17 in HepG2 Xenografts.

Cultured HepG2 human hepatoma tumor cells were implanted subcutaneously ($\sim 10^7$ cells/flank) to establish a solid tumor xenograft model in female ICR SCID mice (National



Institutes of Health DCT/DTP Animal Production Program, Frederick, MD). For the efficacy study, mice were 8 weeks old on day 0 (tumor implant) with an average body weight of 17.6 g. Mice were provided food and water *ad libitum*. Study mice were maintained on either a folate deficient diet (Harlan-Teklad, Madison, WI) or a folate-replete diet (autoclavable mouse breeder diet) starting 16 days before subcutaneous tumor implant to ensure serum folate levels would approximate those of humans. Folate serum levels were determined before tumor implantation and after the study with a Lactobacillus casei bioassay (Varela-Moreiras and Selhub, 1992). The animals were pooled and implanted bilaterally subcutaneously with 30- to 60-mg tumor fragments by a 12-gauge trocar and again pooled before unselective distribution to the various treatment and control groups. Chemotherapy was begun 4 days after tumor implantation, when the number of cells was relatively small $(10^7 - 10^8 \text{ cells}; \text{ before the established limit of palpation}).$ Tumors were measured with a caliper two or three times weekly. Mice were sacrificed when the cumulative tumor burden reached 1500 mg. Tumor weights were estimated from two dimensional measurements [i.e., tumor mass (in milligrams) = $(ab^2)/2$, where a and b are the tumor length and width in millimeters, respectively]. For calculation of end points, both tumors on each mouse were added together, and the total mass per mouse was used. The following quantitative end points were used to assess antitumor activities: 1) T/C and T - C (tumor growth delay) [where T is the median time in days required for the treatment group tumors to reach a predetermined size (e.g., 500 mg) and C is the median time in days for the control group tumors to reach the same size; tumor free survivors are excluded from these calculations]; and 2) calculation of tumor cell kill $[\log_{10} \text{ cell kill total } (\operatorname{gross}) = (T - C)/(3.32)(Td)$, where (T - C) is the tumor growth delay, as described above, and Td is the tumor volume doubling time in days, estimated from the best fit straight line from a log-linear growth plot of control group tumors in



exponential growth (100- to 800-mg range)]. With the exception of the xenograft model, these methods are essentially identical to those described previously (Wang et al., 2010).

4.3 Results.

4.3.1 Effects of Compound 17 on Cell Growth Inhibition and Colony Formation in HeLa and HepG2 Human Tumor Sublines.

In Chapter 3, studies established that the novel pyrrolo[2,3-d]pyrimidine thienoylantifolate compound 17 (Figure 3.1 and Table 3.1) was a potent (nanomolar) inhibitor of proliferation of a R2/PCFT4 CHO subline engineered to express PCFT in the absence of other folate transporters (RFC and FRs) and to inhibit [³H]MTX transport by PCFT (Figure 3.6, Panel A). Conversely, the data strongly suggested that compound 17 was not transported by RFC in a CHO subline similarly engineered to exclusively express human RFC. To begin to establish the therapeutic potential of PCFT as a selective approach for chemotherapy drug delivery to human solid tumors, we used isogenic HeLa sublines derived by stable transfections of RFC- and PCFTnull R1-11 HeLa cells, designated R1-11-PCFT4 (express physiologic levels of PCFT in the absence of RFC, as measured by real-time RT-PCR) and R1-11-RFC6 (engineered to express RFC without PCFT), (Zhao et al., 2008) (Figure 4.1, Panel A and B). Low levels of FR α were detected in all the R1-11 sublines (Panel C). As a tumor prototype with endogenous PCFT expression, we used HepG2 cells established from our tumor cell line screen to express significant levels of PCFT and RFC (Figure 2.3, Panels A and B) without FR α (expression levels for PCFT and RFC in HepG2 cells are compared with those for the R1-11 sublines in Figure 4.1, Panel A-C). We measured inhibition of cell proliferation by compound 17 and results were compared with those for PMX. PMX inhibited cell growth in both the R1-11-PCFT4 and R1-11-RFC6 lines with IC₅₀ values (mean \pm S.E.M.) of 59.3 \pm 7.37 and 81.7 \pm 5.49 nM, respectively



(Figure 4.2, Panel A), demonstrating its lack of specificity for PCFT over RFC despite its high PCFT substrate activity (Kugel Desmoulin et al., 2010b; Zhao et al., 2008). Conversely, compound 17 inhibited cell growth in R1-11-PCFT4 cells (IC₅₀, 99.2 \pm 20.2 nM) but not R1-11-RFC6 (Figure 4.2, Panel B), indicating selective PCFT transport. The decreased (~2-fold) sensitivity in the R1-11-PCFT4 cells versus R2/PCFT4 CHO cells (Table 3.1) probably reflects differences (~10-fold) in PCFT transport activity at pH 5.5 between these engineered sublines (Figure 4.1, Panel D). In HepG2 cells, both PMX (IC₅₀, 40.63 \pm 4.52 nM) and compound 17 $(IC_{50}, 227.50 \pm 8.98 \text{ nM})$ were growth inhibitory (data not shown). The decreased sensitivity to compound **17** for HepG2 cells compared with R1-11-PCFT4 cells probably reflects the presence of RFC in HepG2 cells. Although not active for transport with compound 17, RFC still transports folates and elevates intracellular folate pools, resulting in decreased cytotoxic drug effects on this basis (see Chapter 5). Proliferation assays were extended to include colony-forming assays, in which R1-11-PCFT4 cells were exposed to a range of concentrations (1-10 µM) of PMX (Figure 4.2, Panel C) or compound 17 (Panel D) for 16, 24, or 48 h. Drug exposures were performed at pH 6.8, after which drugs were removed and colonies allowed to outgrow for 12 days. As an inhibitor of colony formation, PMX and compound 17 showed both concentration- and timedependence, although this effect was more pronounced for compound 17, and PMX was more active at 16 h for the lower drug concentrations. Despite the latter activity, the maximum extent of inhibition after 48 h at 10 μ M drug was greater for compound **17** (95%) than for PMX (87%). Collectively, these results demonstrate that compound 17, like PMX, is cytotoxic toward cells that express PCFT, and under acidic conditions (pH 6.8) achievable in solid tumors. Unlike PMX, compound 17 is selectively active toward cells expressing PCFT and is inactive toward cells expressing exclusively RFC.





Figure 4.1 Characterization of folate transporter expression in solid tumor, HeLa, CHO sublines and HepG2 *in vivo* tumor samples. RT-PCR was used to measure: *Panel A*, PCFT; *Panel B*, RFC; and *Panel C*, FR α transcript levels. The cell lines included R1-11 sublines, IGROV1 and HepG2 cells and HepG2 tumors from the *in vivo* efficacy trial treated with compound 17 or untreated. RNAs were isolated using TRIzol reagent, cDNAs were synthesized using random hexamers and RT-PCR was performed using SYBR green and gene-specific primers (primer sequences are reported in Table 2.1). Transcript levels were normalized to GAPDH. *Panel D*, PCFT transport activities in R2/VC, R2/PCFT4, R1-11-mock and R1-11-PCFT4 cells were assessed in cell monolayers by measuring uptake of 0.5 μ M [³H]MTX at 37°C for 5 min at pH 5.5 or 7.2 in MES-buffered saline, and at 7.2 in HEPES-buffered saline. Internalized [³H]MTX was normalized to total protein.



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Figure 4.2 Compound 17 and PMX growth inhibition and inhibition of colony formation in R1-11 sublines. *Panels A and B*, Growth inhibition curves for folate-depleted R1-11-PCFT4 and -RFC6 cells treated with PMX (*Panel A*) or compound 17 (*Panel B*) for 96 h are shown. *Panels C and D*, R1-11-PCFT4 cells were plated in 60 mm dishes at a density of 500 cells per dish and allowed to adhere overnight. Cells were treated at pH 6.8 in the presence or absence of different concentrations of PMX (*Panel C*) or compound 17 (*Panel D*) from 0 to 10 μ M for 16, 24 and 48 h, followed by removal of drug. Plates were scored by counting visible colonies after 12 days (by staining with methylene blue) and presented as a percent of vehicle control.



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4.3.2 Transport Characteristics for [³H]Compound 17 in HeLa R1-11-PCFT4 and HepG2 Cells.

To directly measure PCFT membrane transport of the cytotoxic antifolates into HeLa R1-11-PCFT4 and HepG2 cells, we used radiolabeled compound **17** and PMX. For R1-11-PCFT4 cells, uptake of [3 H]compound **17** (0.25 μ M) was time- and pH dependent with maximum drug accumulation at pH 5.5 (Figure 4.3, Panels A–C). Uptake in R1-11-PCFT4 cells exceeded that of its PCFT-null isogenic counterpart (R1-11-mock transfectant), unequivocally establishing transport of compound **17** by PCFT. A modest time-dependent uptake in the PCFT null R1-11mock transfected subline was particularly obvious at 30 min and probably reflects the presence of low levels of FR in these cells (Figure 4.1, Panel C).

We compared the uptake of [³H]PMX with that of [³H]compound **17** in HepG2 cells (Figure 4.3, Panel D and E). For compound **17**, pH-dependent uptake in HepG2 cells showed a profile (despite the ~2-fold increased net uptake) similar to that of R1-11-PCFT4 HeLa cells. Net uptake of [³H]PMX exceeded that of [³H]compound **17** in HepG2 cells by ~50 to 100% and showed a greater uptake fraction at neutral pH, most likely due to the presence of RFC in HepG2 cells (Figure 4.1, Panel B).

We measured transport kinetics over 2 min for [³H]compound **17** and [³H]PMX in R1-11-PCFT4 cells using a range of drug concentrations at pH 5.5 and 6.8 (Table 4.1). The data show nearly identical *K*t values for compound **17** and PMX at pH 5.5 and only modest (within ~40%) differences in V_{max} . Increases in both K_t (increased ~300- to 400-fold, respectively, compared with values at pH 5.5) and V_{max} values (~70% increased) were observed at pH 6.8. V_{max}/K_t ratios for compound **17** and PMX were similar (within ~2-fold) at both pH 5.5 and pH





Figure 4.3 pH- and time-dependent transport of compound 17 and PMX into R1-11-PCFT4 and HepG2 cells. *Panels A-D*, Direct PCFT transport activity of compound 17 and *Panel E*, PMX in R1-11-PCFT4 (*A-C*) and HepG2 (*D and E*) cells was assessed by measuring uptake of 0.25 μ M [³H]compound 17 or [³H]PMX over 2-30 min at 37°C in complete folate-free RPMI 1640 (pH 5.5, 6.8 and 7.2), supplemented with 10% dFBS, and 25 mM HEPES/25 mM PIPES. Internalized [³H]compound 17 and [³H]PMX were normalized to total protein and expressed as pmol/mg protein.



Table 4.1 Kinetic constants for PCFT – R1-11-PCFT4. Kinetic constants for PMX (K_t and V_{max}) and compound 17 (K_t and V_{max}) were determined with [³H]PMX and [³H]compound 17, respectively, and calculated from Lineweaver Burke plots with R1-11-PCFT4 cells. Results are presented as mean values <u>+</u> standard errors from 3 experiments.

Substrate	Parameter	рН 5.5	рН 6.8
	$K_{t}\left(\mu M\right)$	0.03 ± 0.003	4.43 ± 0.253
PMX	V _{max} (pmol/mg/min)	1.27 ± 0.023	2.18 ± 0.317
	V _{max} / K _t	42.3	0.49
	$K_t \left(\mu M \right)$	0.02 ± 0.013	5.91 ± 1.36
Compound 17	V _{max} (pmol/mg/min)	1.76 ± 0.154	3.08 ± 0.451
	V _{max} / K _t	88	0.52



6.8. These results establish that for both R1-11-PCFT4 and HepG2 cells, compound **17** is an excellent substrate for PCFT, essentially equivalent to PMX.

4.3.3 Polyglutamylation of Compound 17 in R1-11-PCFT4 and HepG2 Cells.

Polyglutamylation of classic antifolates is a critical factor in drug activity, because these conjugated drug forms are retained within cells and they typically inhibit folate-dependent enzyme targets to a greater extent than their nonpolyglutamyl forms (Goldman and Matherly, 1985; Shane, 1989). To assess the extent of this metabolism for compound 17 in R1-11-PCFT4 and HepG2 cells, cells were treated with 1 μ M [³H]compound **17** for 16 h at pH 6.8 in the presence of adenosine (60 µM). For HepG2 cells, parallel incubations were performed with [³H]PMX [in presence of thymidine (10 µM) and adenosine (60 µM)]. ³H-labeled metabolites were extracted and analyzed by reversed-phase HPLC. Figure 4.4 shows HPLC chromatographs for compound 17 (Panel A) and PMX (Panel B) in HepG2 cells. Up to five polyglutamyl (PG) metabolites of [³H]compound 17 and [³H]PMX (PG₂₋₆) were resolved by HPLC. The identities of the peaks were confirmed by comparing elution times with those for MTX polyglutamyl standards and by treatment with chicken pancreas conjugase which reverted the majority of the polyglutamyl metabolites to the parental drug. The distributions of the individual compound 17 and PMX drug forms in R1-11-PCFT4 and HepG2 cells are summarized in Table 4.2. Although there were differences in the relative amounts of total intracellular compound 17 between the R1-11-PCFT4 and HepG2 sublines (as expected from the transport results in Figure 4.3), in both cases, compound 17 was predominantly polyglutamylated (64 and 84% of the total intracellular drug, respectively). For HepG2 cells, the increased accumulation of [³H]compound **17** over that of R1-11-PCFT4 cells was reflected in the polyglutamate levels. Analogous results were obtained with [³H]PMX in HepG2 cells, although the net extent of drug uptake and metabolism





Figure 4.4 HPLC analysis of polyglutamyl derivatives of compound 17 in HepG2 cells at pH 6.8. HepG2 cells were treated with 1 μ M [³H]compound 17 (*Panel A*) and 1 μ M [³H]PMX (*Panel B*) at pH 6.8 in the presence of adenosine (60 μ M) for 16 h. Polyglutamates were extracted by boiling in 50 mM phosphate buffer (pH 6.0) containing 100 mM 2-mercaptoethanol and separated on a 5 μ m Spherisorb C-18 ODS-2 column (4.6 mm x 250mm) with a Nova-Pak 4 μ m C-18 guard column. Fractions were collected and radioactivity was measured. Percent monoglutamate and polyglutamate (PG₂₋₆) drug forms were determined by chromatographic analysis and the total intracellular radiolabel calculated in units of pmol/mg protein (Table 4.2).



Table 4.2 Distribution of compound 17 and PMX polyglutamates in R1-11-PCFT4 and HepG2 cells. Cells were incubated for 16 h with 1 µM [³H]compound **17** or [³H]PMX. Drug accumulations and HPLC analysis of [³H] polyglutamate metabolites were performed as described in Materials and Methods.

	Comp	ound 17	PMX
Metabolites	R1-11-PCFT4 (pmol/mg)	HepG2 (pmol/mg)	HepG2 (pmol/mg)
Total Drug	5.8	12.8	41.6
PG ₆	0	1.3 (10%)	7.4 (18%)
PG ₅	1.4 (23%)	4.9 (38%)	10.3 (25%)
PG ₄	0.78 (14%)	2.2 (17%)	4.1 (10%)
PG ₃	1.0 (18%)	1.5 (12%)	5.8 (14%)
PG ₂	0.48 (8%)	1.2 (9%)	3.7 (9%)
$\mathbf{PG_1}^{\#}$	2.1 (36%)	2.1 (16%)	8.8 (21%)

Parent (unmetabolized) drug.



of [³H]PMX was elevated over that of [³H]compound **17**. Collectively, these results establish that, like PMX, compound **17** is an excellent substrate for polyglutamylation under conditions (pH 6.8) that favor its membrane transport by PCFT.

4.3.4 Validation of GARFTase and *De novo* Purine Nucleotide Biosynthesis as the Primary Cellular Targets for Compound 17 in R1-11-PCFT4 Cells.

In Chapter 3 the principal intracellular target of compound 17 was established in PCFTexpressing CHO cells as GARFTase, the first folate-dependent enzyme in de novo purine nucleotide biosynthesis (Wang et al., 2010). To confirm this result in R1-11-PCFT4 HeLa cells under acidic conditions (pH 6.8) that favor PCFT transport, we used an in situ metabolic assay that quantifies incorporation of [¹⁴C]glycine into [¹⁴C]formyl GAR as a measure of GARFTase inhibition. Results were compared with those of PMX, an established GARFTase inhibitor, along with its documented effects on TS (Chattopadhyay et al., 2007) and AICARFTase (Racanelli et al., 2009) (Figure 4.5, Panel A). IC₅₀ values for GARFTase inhibition in R1-11-PCFT4 cells by compound 17 and PMX were 43.6 and 69.7 nM, respectively. Although the IC₅₀ for GARFTase inhibition by compound 17 closely approximated the IC₅₀ for growth inhibition of R1-11-PCFT4 cells (Table 3.1), GARFTase inhibition by PMX was incomplete up to 5 µM. Analogous results were described for PMX with PCFT-expressing CHO cells (R2/PCFT4) (Chapter 3) (Kugel Desmoulin et al., 2010b) and with CCRF-CEM cells by Moran and coworkers (Racanelli et al., 2009). To confirm that potent inhibition of GARFTase in R1-11-PCFT4 cells by compound 17 also results in decreased ATP pools, we measured intracellular ATP levels in cells treated with 10 μ M compound **17** for 16, 24 and 48 h under conditions (pH 6.8) analogous to those used for our clonogenicity studies (Figure 4.2, Panel D). Compound 17 caused a time-dependent and concentration-dependent decrease in cellular ATP levels, such that treatment for 48 h led to an





Figure 4.5 *in situ* GARFTase inhibition and intracellular ATP levels in R1-11-PCFT4 cells treated with compound 17 and PMX. *Panel A*, GARFTase activity and inhibition were evaluated *in situ* with R1-11-PCFT4 cells. R1-11-PCFT4 cells were treated with drug for 16 h at pH 6.8 in complete buffered folate-free RPMI 1640 supplemented with 25 nM 5-CHO-THF before incubating in the presence of 4 μ M azaserine for 30 min, followed by [¹⁴C]glycine and L-glutamine treatment. After 8 h, radioactive metabolites were extracted and fractionated on 1 cm columns of AG1x8(Cl-) and the fractions were collected and radioactivity measured. Accumulation of [¹⁴C]formyl GAR was calculated as a percent of vehicle control over a range of antifolate concentrations. *Panel B*, For analysis of ATP levels, cells were treated with 10 μ M compound **17** or left untreated (DMSO) for 48 h at pH 6.8. Nucleotides were extracted and ATP pools were determined by a modification of the HPLC method of Huang et al. (2003a), as previously described (Kugel Desmoulin et al., 2010b). Details are provided in the Materials and Methods.



88% decrease in ATP pools (Figure 4.5, Panel B). These results demonstrate that PCFT-delivery of compound **17** is an efficient mode of drug uptake that effects a potent inhibition of GARFTase and ATP depletion in R1-11-PCFT4 cells.

4.3.5 Effect of Compound 17 on Cell Cycle Progression and Apoptosis Induction in R1-11-PCFT4 Cells.

To determine the impact of GARFTase inhibition and ATP depletion on cell-cycle progression, we treated R1-11-PCFT4 cells with compound 17 (10 µM) for 48 h at pH 6.8, along with a vehicle control. Cells were fixed, stained with PI, and analyzed for cell cycle distribution by flow cytometry. Treatment with 10 μ M compound 17 caused an accumulation of cells in Sphase such that 38.9% of cells were in S-phase, compared with 16.8% of the control (Figure 4.6, Panel A and B). When a range of concentrations (0.5, 1, 5, and 10 μ M) of compound 17 were tested for their abilities to induce S-phase accumulation, we found that maximal arrest was achieved at 1 μ M. Because treatment with compound 17 (10 μ M, 48 h at pH 6.8) causes loss of clonogenicity in R1-11-PCFT4 cells (Figure 4.2, Panel D) and a modest increase in the sub-G1 fraction (Figure 4.6, Panel A and B), we were interested in measuring apoptosis under these same conditions using annexin V/PI staining. Results were compared with those for R1-11-PCFT4 cells treated with etoposide (5 μ M) and with a no-drug control. Whereas etoposide strongly induced apoptosis (12.2% early apoptotic and 22.3% late apoptotic/necrotic) compared with the negative controls (2.9 and 10.3%, respectively), compound 17 was less apoptotic (8.4 and 15.7%, respectively) (Figure 4.6, Panel C). These results are consistent with previous reports that GARFTase inhibitors are distinctly cytotoxic, yet modestly apoptotic (Deng et al., 2008; Smith et al., 1993).





Figure 4.6 Compound 17 treatment induces an S-phase accumulation, accompanied by a modest level of apoptosis in R1-11-PCFT4 cells. *Panel A*, Representative cell cycle profiles were determined in R1-11-PCFT4 cells treated with a range of concentrations of compound **17** for 48 h by measuring the cellular DNA content with PI staining and flow cytometry. SubG1 (apoptotic fraction) (white trace), G1 (dark grey trace), S (light grey trace), and G2 (grey trace). *Panel B*, The percentages of cells in each phase of the cell cycle (G1, S, and G2), including those in the subG1 fraction for all concentrations of compound **17**. *Panel C*, Pseudo-color dot plots show the flow cytometric analysis of cells stained with annexin V-FITC and PI. The percentages of viable cells (annexin V-/PI-), early apoptotic cells (annexin V+/PI-), and late apoptotic/necrotic cells (annexin V+/PI+) are noted. As a positive control, cells were treated with 5 μM etoposide for 48 h at pH 6.8 to induce apoptosis.



4.3.6 In vivo Efficacy Study of Compound 17 Against HepG2 Xenografts.

As proof of concept that in vivo antitumor efficacy can result from tumor targeting of compound 17 via its transport by PCFT, an *in vivo* efficacy trial was performed with 8-week-old female ICR SCID mice implanted with subcutaneous HepG2 tumors that express PCFT and RFC but not FRa (Figure 4.1, Panel A). Mice were maintained ad libitum on folate-deficient or standard folate-replete diets. Serum folate concentrations were measured in mice after 14 days on the folate-deficient diet by an L. casei bioassay; the value was 90.2 nM (median) [range, 79.2– 120.7 nM (n = 3)]. This value slightly exceeds serum folate levels (31 and 35 nM, respectively) reported previously in humans (Ganji and Kafai, 2009). With the standard diet, by comparison, serum folate was 715.2 nM (median) [range, 652.8–742.8 nM (n = 3)]. For the trial, control and drug treatment groups were nonselectively randomized (five mice per group); compound 17 was administered intravenously on a schedule of every 4 days for three treatments (180 mg/kg per injection) on days 4, 8, and 12 after implantation (total dose 540 mg/kg). Results were compared with those for paclitaxel (Taxol; every 2 days for six treatments, 7.5 mg/kg per injection). Mice were weighed daily and tumors were measured 2 to 3 times per week. For the mice maintained on the folate-deficient diet, appreciable antitumor activity was recorded with compound 17 (T/Cof 0% on day 21; T - C = 13 days; 1.4 gross log kill) (Table 4.3), exceeding that for paclitaxel (T/C = 16%; 0.8 gross log kill). Antitumor drug efficacy for **17** was completely abolished (99%) T/C) for the standard folate-replete diet. The treatment regimen was well tolerated with doselimiting symptoms manifesting as reversible body weight loss for mice maintained on the folatedeficient diet. Results for the *in vivo* efficacy experiment shown in Figure 4.7 are summarized in Table 4.3. Tumor samples treated with compound 17 and untreated controls were harvested, RNA was extracted and PCFT, RFC and FRα transcripts were measured.





Figure 4.7 *in vivo* efficacy trial of compound 17 in HepG2 xenografts. Female ICR SCID mice were maintained on a folate-deficient diet *ad libitum*. Human HepG2 tumors were implanted bilaterally and mice were non-selectively randomized into 5 mice/group. Compound 17 [dissolved in 5% ethanol (v/v), 1% Tween-80 (v/v), 0.5% NaHCO₃] was administered on a Q4dx3 schedule intravenously on days 4, 8, and 12 (indicated with arrows) at 180 mg/kg/injection. Taxol (dissolved in water) was administered on a Q2dx6 schedule (7.5 mg/kg/injection) beginning on day 4. Mice were observed and weighed daily; tumors were measured twice per week. For the mice maintained on the folate-deficient diet and treated with compound 17, appreciable antitumor activity was recorded (T/C=0%; T-C=13 days; 1.4 gross log kill).



Table 4.3 / SCID mice	Antitume e (under 1	or efficacy e folate defici	valuation (ent and sta	of compo andard fo	und 17 and tax olate replete die	ol again et condit	ist early st ions)	tage huma	ın HepG2	in fema	le
Treatment	Drug Route	Schedule (Start on day 4)	Total Dosage mg/kg	Drug Deaths	Median Tumor Burden in mg on day 21 (range)	T/C mass %	Tumor Free on day 28	Median Time to 500 mg in days (range)	Tumor Growth Delay (days)	Log Kill	Activity Rating
No Rx (Folate deficient)					477 (0-752)	—	5/0	22 (20-41)			
Compound 17	IV	Q4dx3	540	0/5	0 (0-875)	0	0/2	35 (18-38)	13	1.4	‡
Taxol	IV	Q2dx6	45	0/5	75 (0-234)	16	0/5	29 (27-33)	7	0.8	+
Treatment	Drug Route	Schedule (Start on day 4)	Total Dose mg/kg	Drug Deaths	Median Tumor Burden in mg on day 21 (range)	T/C mass %	Tumor Free on day 31	Median Time to 500 mg in days (range)	Tumor Growth Delay (days)	Log Kill	Activity Rating
No Rx (STD diet)					548 (207-740)		0/5	21 (20-31)			
Compound 17	IV	Q4dx3	540	0/5	546 (448-881)	66	0/5	21 (18-22)	NA	None	I
Taxol	IV	Q2dx6	45	0/5	0 (0-88)	0	0/5	31 (30-39)	10	1.1	+
The NCR SC Chemotherap T/C= 0 indica	ID mice y was sta ites very h	were implant rted on day ² iigh antitumo	ted bilateral 4 after tume r activity.	lly subcut or implan The conve	aneously with 3 tation, when the ersion of log tum	0-60 mg number ior cell ki	tumor fra of cells w ill (LK) to	gments by as relative activity rat	a 12-gaug ly small (1 ing is as fo	e trocar $0^7 - 10^8$ ollows: >	on day 0. cells). A 2.8 LK =

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+++ (highly active); 2.0 - 2.8 LK = +++; 1.3 - 1.9 LK = ++; 0.7 - 1.2 LK = +; <0.7 = -- (inactive). + = positive + for LK but negative for T/C. *In vivo* passage of HepG2 cells did not change the expression of RFC (Figure 4.1, Panel B) or FRα (Panel C) transcripts; PCFT (Panel A) on the other hand increased expression in the *in vivo* environment in both treated and untreated tumor samples, suggesting that tumor cells expressing PCFT may be selected for *in* vivo or that the acidic environment may have induced PCFT expression. The results of the *in vivo* efficacy trial demonstrate potent antitumor activity for compound **17** toward subcutaneously engrafted HepG2 tumors associated with significant transport by PCFT and a lack of membrane transport by RFC.

4.4 Discussion.

This chapter significantly expands upon previous results (Chapter 3) (Anderson and Thwaites, 2010; Kugel Desmoulin et al., 2010b; Zhao and Goldman, 2007) suggesting that PCFT may be therapeutically exploitable for treating solid tumors. We further show that the novel 6substituted pyrrolo[2,3-d] pyrimidine thienoyl antifolate compound 17 can be selectively transported by PCFT in a pH- and time-dependent manner. The tumor models employed, R1-11-PCFT4 HeLa and HepG2 cells, express similar levels of PCFT, although they differ in the presence of RFC and FR α . The premise behind our drug discovery efforts, exemplified by compound 17, is that membrane transport of cytotoxic antifolates is a critical determinant of antitumor drug selectivity. Compound 17 is not transported by the ubiquitously expressed RFC (Wang et al., 2010). This is particularly important because drugs such as compound 17 that target FR α and/or PCFT, yet are not substrates for RFC, have the potential to selectively target tumor cells and decrease toxicity to normal tissues. This is a substantial advantage over chemotherapy drugs currently in use; indeed, pursuing the development of these novel antifolates could yield a new class of clinically relevant antitumor agents. Our previous work used engineered CHO models (Chapter 3), as well as KB (nasopharyngeal) and IGROV1 (ovarian) human tumor cells



that express FR α and/or PCFT to deliver cytotoxic antifolates, including compound **17**, that are not substrates for RFC (Deng et al., 2008; Deng et al., 2009; Kugel Desmoulin et al., 2011; Wang et al., 2010).

The present report significantly expands upon this concept by demonstrating exclusive transport of compound **17** by PCFT into human tumor cell lines at pH values characterizing the tumor microenvironment. For R1-11-PCFT4 and HepG2 cells, after its internalization at pH 6.8, compound **17** was extensively polyglutamylated, such that the predominant metabolite was the pentaglutamate form (compound **17** conjugated to 4 glutamate residues). Moreover, compound **17** potently inhibited GARFTase, leading to R1-11-PCFT4 HeLa cell death *in vitro* and HepG2 tumor growth delay *in vivo*.

Expression of PCFT transcripts and protein in normal human tissues is more restrictive than for RFC, high PCFT levels being observed in the liver, kidney, and small intestine and very low levels in the bone marrow and colon (Chapter 2 and Kugel Desmoulin et al. (2010a)). This pattern of PCFT transcripts was also generally observed in mouse tissues (Qiu et al., 2007). Our finding that PCFT transcripts are low in human bone marrow is particularly significant and suggests that PCFT-targeted therapeutics may be less marrow toxic than antifolates presently in clinical use. The microenvironments for most normal tissues probably exhibit a neutral pH (Martin and Jain, 1994), such that even if PCFT is present, the electrochemical proton gradient is reduced, leading to less accumulation of PCFT substrates such as compound **17**. Conversely, RFC would exhibit a far greater activity under these conditions. This, when combined with the greater capacity of RFC to transport reduced folates across the cell membrane compared with PCFT (Zhao et al., 2008), would result in elevated levels of cellular folates in normal tissues. The increased availability of reduced folates would result in competition with internalized



antifolates for polyglutamylation and/or for binding to intracellular drug targets (e.g., GARFTase), thus protecting normal cells from drug cytotoxicity. Likewise, for PCFT-targeted agents in solid tumors, if sufficient RFC were present, enough transport of folates might occur even at slightly acidic pH values to decrease drug efficacy on this basis. This implies that the ratio of PCFT to RFC in tumors is critical to antitumor activities of PCFT-selective cytotoxic antifolates and that MTX-resistant tumors that have substantially lost RFC function may be exquisitely sensitive to the effects of PCFT selective drugs such as compounds **16** and **17** (Chapter 5). Thus, for compound **17** and related agents, tumor selectivity is not only reliant upon differential PCFT levels between normal tissues and solid tumors but is also affected by interstitial pH and activity of RFC.

It is interesting that under nearly the same conditions, the IC_{50} for GARFTase inhibition in R1-11-PCFT4 cells by the *in situ* GARFTase assay is virtually identical to the IC_{50} for inhibition of cell proliferation. This result differs somewhat from our previous finding with an analogous 6-substituted pyrrolo[2,3 *d*]pyrimidine benozyl antifolate compound **3** in CHO cells for which the IC_{50} for GARFTase inhibition was substantially lower, suggesting that sustained GARFTase inhibition was necessary to manifest as cytotoxicity (Chapter 3 and Kugel Desmoulin et al. (2010b)). This quantitative difference may reflect differences in the size of purine pools between the human and hamster sublines such that R1-11-PCFT4 HeLa cells would be more sensitive to the inhibition of GARFTase. Of course, other factors could also contribute. For instance, differences in drug polyglutamylation and polyglutamate turnover could result in disparate potencies for sustained GARFTase inhibition in different cell lines. Finally, our studies with compound **17** assess the impact of GARFTase inhibition on ATP levels and the mechanism(s) of tumor cell death.



Treatment of R1-11-PCFT4 cells with compound **17** substantially reduced ATP levels and caused S-phase accumulation. Apoptosis resulting from compound **17** was reduced compared with etoposide. This could (at least in part) reflect the requirement of ATP for apoptosis, because ATP levels must be maintained above a minimal level for apoptosis induction (Tsujimoto, 1997).

In conclusion, our *in vitro* studies suggest the feasibility of using PCFT and the acidic tumor microenvironment to selectively deliver a novel PCFT-targeted antifolate to human solid tumors endogenously expressing modest levels of PCFT. Our *in vivo* results with HepG2 tumor cells that express only PCFT and RFC provide compelling proof-of-principle validation and rationale for developing drugs whose transport by PCFT, but not RFC, allows for GARFTase inhibition.



CHAPTER 5

THE IMPACT OF RFC FUNCTION ON THE ACTIVITY OF ANTIFOLATES SELECTIVELY TRANSPORTED BY PCFT

5.1 Introduction.

Classic antifolates such as MTX and PMX, like folate cofactors, have minimal lipid solubility and therefore require specific transport mechanisms to enter tumor cells. There are three primary folate transporters, including RFC, PCFT and FRα (Assaraf, 2007; Goldman et al., 2010). RFC is the predominant transport route for the major circulating folate, 5-methylTHF, and (6S) 5-CHO-THF in mammalian cells and tissues. RFC also mediates cellular uptake of MTX and is essential to MTX antitumor activity (Matherly et al., 2007). Impaired RFC function is a major mechanism of MTX resistance in cultured tumor cells selected *in vitro* (Matherly et al., 2007; Zhao and Goldman, 2003) and in murine leukemia cells *in vivo* (Sirotnak et al., 1981). Loss of RFC function in clinical specimens has also been reported (Gorlick et al., 1997; Guo et al., 1999; Yang et al., 2003). RFC transport of cytotoxic antifolates can also be undesirable since RFC is ubiquitously expressed and exhibits a high level of activity at the physiological pH of most normal tissues (Matherly et al., 2007). Thus, transport of antifolates by RFC could easily preclude tumor selectivity and cause toxicity to normal tissues.

The novel 6-substituted pyrrolo[2,3-*d*]pyrimidine thienoyl antifolates with 3- (compound **16**) or 4- (compound **17**) carbon bridge lengths (Chapters 3 and 4; Figure 3.1, Panel C) represent an entirely new class of antitumor agents that exhibit a lack of significant membrane transport by RFC (Chapters 3 and 4) (Kugel Desmoulin et al., 2011; Wang et al., 2010; Wang et al., 2011). Cellular uptake of compounds **16** and **17** by PCFT and FR α is efficient and offers a promising new strategy for tumor targeting. (Anderson and Thwaites, 2010). Since PCFT functions optimally at acidic pHs (Qiu et al., 2006; Umapathy et al., 2007; Zhao et al., 2008), transport of



16 and **17** by this mechanism may lead to enhanced tumor selectivity owing to the acidic microenvironments of many solid tumors (Anderson and Thwaites, 2010; Helmlinger et al., 1997; Webb et al., 2011). Following internalization, compound **17** is metabolized to polyglutamates (Chapter 4) (Kugel Desmoulin et al., 2011), although this has not been previously confirmed for compound **16**. Both **16** and **17** inhibit *de novo* purine nucleotide synthesis by targeting the first folate-dependent enzyme, GARFTase, causing a dramatic drop in purine nucleotide pools (Chapters 3 and 4) (Kugel Desmoulin et al., 2011; Wang et al., 2010; Wang et al., 2011). In the case of compound **17**, treatment results in S-phase accumulation and cell death, in part by a non-apoptotic mechanism (Kugel Desmoulin et al., 2011). Not surprisingly, compounds **16** and **17** are potent inhibitors of tumor cell proliferation both *in vitro* and *in vivo* (Chapters 3 and 4) (Kugel Desmoulin et al., 2011; Wang et al., 2010).

For agents such as PMX that are excellent substrates for both RFC and PCFT, loss of RFC has limited impact on overall activity, since PMX uptake is maintained by PCFT (Zhao et al., 2004c; Zhao et al., 2008). Paradoxically, RFC loss has been shown to enhance antitumor activity (i.e., collateral sensitivity) of PMX via decreased intracellular THF cofactor pools (Chattopadhyay et al., 2007; Chattopadhyay et al., 2006; Zhao et al., 2004c). This response to RFC loss can be further impacted by the type and amount of extracellular folate (Chattopadhyay et al., 2006; Zhao et al., 2004b; Zhao et al., 2004c).

An analogous effect may exist for PCFT-selective substrates such as compounds **16** and **17** (Kugel Desmoulin et al., 2011), although this has never been systematically tested. In this chapter, the complex interplay between RFC and extracellular reduced folates is examined. Specifically, we investigate the mechanistic ramifications of loss of RFC function toward *in vitro*



and *in vivo* antitumor efficacies of these novel PCFT-targeted antifolates, including the impact on their membrane transport, polyglutamylation, and GARFTase inhibition. The results strongly imply that levels of RFC transport in tumors are a critical determinant of drug efficacy for this novel class of PCFT-selective antitumor agents.

5.2 Materials and Methods.

5.2.1 Chemicals and Reagents.

[3',5',7-³H]MTX (20 Ci/mmol), [³H]PMX (2.5 Ci/mmol), [3',5',7,9-³H(N)](6S)5-formyl tetrahydrofolate (5-CHO-THF) (16.6 Ci/mmol), and custom-radiolabeled [³H]compound **16** (16 Ci/mmol) and [³H]compound **17** (1.3 Ci/mmol) were purchased from Moravek Biochemicals (Brea, CA). Unlabeled MTX and (6R,S) 5-CHO-THF were provided by the Drug Development Branch, National Cancer Institute, Bethesda, MD. Sources of the antifolate drugs were as follows. LMX (5,10-dideaza-5,6,7,8-tetrahydrofolate) and PMX [N-(4-[2-(2-amino-3,4-dihydro-4-oxo-7H-pyrrolo[2,3-d]pyrimidin-5-yl)ethyl] benzoyl)(4)-L-glutamic acid] (Alimta) were from Eli Lilly and Co. (Indianapolis, IN); RTX [N-(5-[N-(3,4-dihydro-2-methyl-4-oxyquinazolin-6ylmethyl)-N-methyl-amino]-2-thenoyl)-L-glutamic acid] was obtained from AstraZeneca Pharmaceuticals (Maccesfield, Cheshire, England); and Nalpha-(4-amino-4-deoxypteroyl)-Ndeltahemiphthaloyl-L-ornithine (PT523) was a gift of Dr. Andre Rosowsky (Boston, MA). Restriction and modifying enzymes were purchased from Promega (Madison, WI). Other chemicals were obtained from commercial sources in the highest available purities. Synthesis and properties of the 6-substituted pyrrolo [2,3-d] pyrimidine thienoyl antifolate compounds 16 and 17 were previously described (Wang et al., 2010; Wang et al., 2011).

5.2.2 Cell Culture.



HeLa cells were purchased from ATCC (Manassas, VA). RFC-null R5 HeLa cells in which RFC is deleted from the genome were selected by high dose MTX and ethylmethanesulfonate treatments (Zhao et al., 2004b). R1-11-mock and R1-11-PCFT4 HeLa cells were derived from RFC- and PCFT-null R1-11 cells by stable transfection with pZeoSV2(+) vector only, or HA-tagged pZeoSV2(+)-PCFT constructs, respectively. Characteristics of the R1-11 HeLa sublines were previously described by Zhao et al. (2008) and Chapter 4). The R5 and R1-11 sublines were gifts from Dr. I. David Goldman (Albert Einstein School of Medicine, Bronx, NY). All cell lines were maintained in regular RPMI 1640 supplemented with 10% fetal bovine serum (Invitrogen, Carlsbad, CA), 100 units/mL penicillin, 100 μ g/mL streptomycin, and 2 mM L-glutamine at 37°C with 5% CO₂. For many experiments, cells were maintained at physiologic folate levels for at least two weeks prior to the experiment. These details are listed in the individual sections.

5.2.3 Preparation of the RFC^{HA}/pZeoSV2 Construct and Generation of Stable RFC Transfectants.

Full length human RFC was subcloned using BamHI and Xho1 restriction enzymes into pZeoSV2(+) (Invitrogen) in-frame with an HA sequence inserted at the C-terminus (hereafter, designated RFC^{HA}/pZeoSV2). The plasmid was transformed into XL10-Gold ultracompetent cells (Agilent) and selected using low salt (<90 mM) LB agar plates containing 25 μ g/mL Zeocin. Plasmids were isolated and the WT RFC construct was confirmed by automated DNA sequencing by Genewiz Corp. (South Plainfield, NJ).

R5 cells were transfected with pZeoSV2 vector control or RFC^{HA}/pZeoSV2 WT with Lipofectamine 2000 and opti-MEM (Invitrogen). After 24 h, the cells were cultured in the presence of zeocin (0.1 mg/mL). Stable clones were selected by plating for individual colonies in



the presence of 0.1 mg/mL zeocin. Colonies were isolated, expanded and screened for expression of RFC^{HA} protein by real-time RT-PCR, Western blotting and transport assays at pH 7.2 (see below). A representative clone (R5-RFC2) was selected for further study. R5 cells transfected with empty pZeoSV2 (R5-mock) were also prepared and used as a negative experimental control. R5-RFC2 and R5-mock cells were cultured in regular RPMI 1640 supplemented with 10% fetal bovine serum (Invitrogen, Carlsbad, CA), 100 units/mL penicillin, 100 μ g/mL streptomycin, and 2 mM L-glutamine with 0.1 mg/mL zeocin.

5.2.4 Gel Electrophoresis and Western Blotting.

To characterize PCFT and RFC protein levels in the assorted solid tumor cell lines and the R5-RFC transfectants, sucrose gradient-enriched plasma membranes were prepared, exactly as described in Chapter 2 (Matherly et al., 1991). Proteins were quantified with Folin-phenol reagent (Lowry et al., 1951). Membrane proteins were electrophoresed on 7.5% polyacrylamide gels in the presence of SDS (Laemmli, 1970) and electroblotted onto PVDF membranes (Pierce, Rockford, IL) (Matsudaira, 1987). For the solid tumor cell lines and RFC clones, immunoreactive human PCFT and human RFC proteins were detected on PVDF membranes with the PCFT or RFC-specific polyclonal antibodies described in Chapter 2. An IRDye800CWconjugated goat anti-rabbit IgG (Rockland, Gilbertsville, PA) secondary antibody was used. For detection of HA-tagged proteins (R5-RFC^{HA}) HA-specific mouse monoclonal antibody (Covance, Emeryville, CA) and an IRDye800CW-conjugated goat anti-mouse IgG (Rockland, Gilbertsville, PA) secondary antibody were used. Membranes were scanned with the Odyssey® Imaging System. PCFT and RFC levels were normalized to Na⁺/K⁺ ATPase protein levels (mouse antibody from Novus Biologicals, Littleton, CO).

5.2.5 Transport Assays.



To measure the pH-dependent uptake of [³H]compound **16**, [³H]compound **17**, [³H]PMX and [³H]MTX (0.5 μ M) in WT and R5 HeLa cells, drug uptake was assayed at 37° C in cell monolayers in 60 mm dishes over 2 min at 37°C in 2 mL "anion-free" HEPES-sucrose-Mg⁺² buffer (20 mM HEPES, 235 mM sucrose, pH adjusted to 7.14 with MgO) (AFB) (Wong et al., 1997) or in MES-buffered saline (20 mM MES, 140 mM NaCl, 5 mM KCl, 2 mM MgCl₂, and 5 mM glucose) at pH 5.5. In either case, transport fluxes were stopped by aspirating the incubation buffer and quenching with excess (>5 mL) ice-cold DPBS, followed by 3 washes with ice-cold DPBS. Cellular proteins were solubilized with 0.5 N NaOH and quantified using Folin-phenol reagent (Lowry et al., 1951). Levels of drug uptake were expressed as pmol/mg protein, calculated from direct measurements of radioactivity with a Beckman Model LS6500 liquid scintillation counter (Beckman-Coulter, Fullerton, CA) and protein contents of the cell homogenates.

5.2.6 Real-time RT-PCR Analysis of RFC, FRa, and PCFT Transcripts.

RNAs were isolated from HeLa, R5 and R5-RFC2 cells using TRIzol reagent (Invitrogen). cDNAs were synthesized using random hexamers, RNase inhibitor, and MuLV reverse transcriptase and purified with the QIAquick PCR Purification Kit (Qiagen). Real-time RT-PCR was performed on a Roche LightCycler 2.1 (Roche, Indianapolis, IN) with gene-specific primers and FastStart DNA Master SYBR Green I enzyme reaction mix (Roche), as described (Ge et al., 2007). Primers are included in Table 2.1. Transcript levels for RFC were normalized to those for GAPDH. External standard curves were constructed for each gene of interest using serial dilutions of linearized templates, prepared by amplification from suitable cDNA templates, subcloning into a TA-cloning vector (PCR-Topo; Invitrogen), and restriction digestions.



5.2.7 Cell Proliferation Assays.

For cell proliferation assays, WT and R5 HeLa sublines were cultured in folate-free RPMI 1640 (pH 7.2), supplemented with 10% dialyzed fetal bovine serum (dFBS), 2 mM Lglutamine and 100 units/mL penicillin 100 μ g/mL streptomycin (hereafter, designated complete folate-free RPMI 1640 medium), containing 25 nM 5-CHO-THF, for at least 2 weeks prior to experiment. For assays of drug inhibitions, the cells were plated in 96 well culture dishes (5000 cells/well; 200 μ L/well) in the above medium with a broad concentration range of drugs (depending on the compound, drug dilutions were in DMSO or water with appropriate vehicle controls); cells were incubated for up to 96 h at 37°C in a CO₂ incubator. Metabolically active cells (a measure of cell viability) were assayed with CellTiter-BlueTM cell viability assays (Promega, Madison, WI) with a fluorescent plate reader (590 nm emission, 560 nm excitation) for determining IC₅₀s, corresponding to drug concentrations that result in 50% loss of cell growth. To test the impact of extracellular folates on the collateral sensitivities of **16** and **17** in R5 and HeLa cells, some growth inhibition experiments included increasing concentrations (25, 100, 1000 nM) of 5-CHO-THF.

5.2.8 Accumulation of [³H]5-CHO-THF.

WT and R5 HeLa sublines were cultured in complete folate-free RMPI 1640 supplemented with 0.06 mM adenosine and 0.01 mM thymidine for five days prior to the experiment. Cells were treated with 0, 25, 100 and 1000 nM [³H]5-CHO-THF (since [³H] (6S)5-CHO-THF was diluted with non-radioactive (6R,S)5-CHO-THF for these experiments, the actual concentration of (6S) stereoisomer was 12.5, 50, 500 nM, respectively) for four days, followed by 3 washes with ice-cold DPBS. 0.06 mM adenosine and 0.01 mM thymidine was added to control dishes that had no [³H]5-CHO-THF to maintain cell viability. Cellular proteins were



solubilized with 0.5 N NaOH and quantified using Folin-phenol reagent (Lowry et al., 1951). Total cellular [³H]5-CHO-THF accumulations were expressed as pmol/mg protein, calculated from direct measurements of radioactivity and protein contents of cell homogenates. Since [³H](6S)5-CHO-THF was diluted with unlabeled (6R,S)5-CHO-THF, as noted above, for purposes of calculating intracellular folate metabolites only the unlabeled (6S) isomer was considered. To measure the impact of the PCFT-targeted therapeutics **16** and **17** on [³H]5-CHO-THF accumulations, some experiments analyzed the uptake of 25 nM [³H]5-CHO-THF in the presence of increasing concentrations (0-1000 nM) of compounds **16** and **17** in complete folate-free RPMI 1640 supplemented with 0.06 mM adenosine.

5.2.9 Measurement of Compound 16 and Compound 17 Polyglutamylation.

Folate-depleted HeLa and R5 cells were plated in complete folate-free RPMI 1640 medium, supplemented with 25 nM 5-CHO-THF, and allowed to adhere overnight. Cells were washed with DPBS and incubated in the same media, supplemented with 25 mM PIPES/25 mM HEPES (pH 6.8), 0.06 mM adenosine and 1 μ M [³H]compound **16** or [³H]compound **17**. After 16 h, cells were washed three times with ice-cold DPBS and scraped mechanically into 5 mL of ice-cold DPBS, pelleted (1500 rpm) and flash frozen. Polyglutamyl and unmetabolized drug forms were extracted and drug levels quantified by HPLC exactly as previously described in Chapter 4 and by Kugel Desmoulin et al. (2011). Cellular proteins were precipitated with ice-cold TCA. The TCA precipitates were solubilized in 0.5 N NaOH before quantifying with Folin-phenol reagent (Lowry et al., 1951).

5.2.10 In vivo Efficacy Study of Compounds 16 and 17 in HeLa and R5 Xenografts.

Cultured WT and R5 HeLa tumor cells were implanted subcutaneously (~ 10^7 cells/flank) to establish a solid tumor xenograft model in female ICR SCID mice (National Institutes of Health



DCT/DTP Animal Production Program, Frederick, MD). The mice were supplied food and water *ad libitum*. Study mice were maintained on a folate-deficient diet (Harlan-Teklad; Product ID: TD.00434) starting 18 days before subcutaneous tumor implant to ensure serum folate levels would approximate those of humans prior to the start of therapy (Kugel Desmoulin et al., 2011; Wang et al., 2010; Wang et al., 2011). This design is analogous to those previously published by others (Alati et al., 1996; Gibbs et al., 2005). Individual mouse body weights for each experiment were within 2 g, and all mice were 19 g (WT) or 19.5 g (R5) HeLa at the start of therapy.

For the efficacy trial, the experimental animals were pooled and implanted bilaterally subcutaneously with 30-60 mg tumor fragments using a 12-gauge trocar as described in Chapter 4 for the HepG2 *in vivo* tumor model (Figure 4.7) and chemotherapy began on day 3 post tumor implantation, when the number of cells was relatively small (between $10^7 - 10^8$ cells; below the established limit of palpation). An organic solvent (ethanol, 5% v/v), carrier (Tween-80, 1% v/v) and sodium bicarbonate (0.5% v/v) was used to effect water solubilization of compounds 16 and **17.** Injection volumes were 0.2 mL IV, pH adjusted to 7.0. Tumors were measured with a caliper two to three times weekly. Mice were sacrificed when the cumulative tumor burden reached 1500 mg. Tumor weights were estimated as described previously (Chapter 4). Experimental parameters as qualitative and quantitative end points to assess antitumor activities include T/C and T-C (tumor growth delay) [where T is the median time in days required for the treatment group tumors to reach a predetermined size (e.g., 500 mg) and C is the median time in days for the control group tumors to reach the same size; tumor-free survivors are excluded from these calculations], and tumor cell kill $[log_{10} \text{ cell kill total (gross)} = (T - C)/(3.32)(Td)$, where (T - C)is the tumor growth delay, as described above, and Td is the tumor volume doubling time in days, estimated from the best fit straight line from a log-linear growth plot of control group



tumors in exponential growth (100-800 mg range)]. For comparison of antitumor activity with standard agents and comparisons of activity between tumors, the log_{10} kill values were converted to an arbitrary activity rating (Corbett et al., 1998; Corbett et al., 1997; Polin et al., 2011; Polin et al., 1997). For duration of treatment between 5 - 20 days: >2.8 log_{10} kill (Highly active ++++); 2.0-2.8 (+++); 1.3-1.9 (++); 0.7-1.2 (+); <0.7 (Inactive; –). Both tumor studies (WT and R5 HeLa cells) used 4 mice per group. The day of tumor implant was day 0. With the exception of the xenograft model, these methods are essentially identical to those described previously in Chapter 4 (Kugel Desmoulin et al., 2011; Wang et al., 2010).

5.3 Results.

5.3.1 PCFT Transport of [³H]Compound 16 in R1-11-PCFT4 HeLa Cells.

The expression of high levels of PCFT in diverse human tumor cell lines (Chapter 2) gives credence to the notion that folate-based cytotoxins with specificity for PCFT over RFC membrane transport could be used for chemotherapy of human solid tumors. We found that the novel 6-substituted pyrrolo[2,3-*d*]pyrimidine thienoyl antifolates **16** and **17** (Figure 3.1) were potent (nM) inhibitors of cell proliferation in cells engineered to express PCFT in the absence of RFC or FRs (Kugel Desmoulin et al., 2011; Wang et al., 2010; Wang et al., 2011) (Table 3.1), suggesting that **16** and **17** are substrates for PCFT-mediated cellular uptake (Chapter 3). This was extended to human HepG2 human hepatoma cells endogenously expressing PCFT without FRs (Chapter 4) (Kugel Desmoulin et al., 2011). In engineered cell lines, compounds **16** and **17** appeared to be poorly transported by RFC (Chapter 3 and 4) (Kugel Desmoulin et al., 2011; Wang et al., 2010; Wang et al., 2011; Wang et al., 2010; Wang et al., 2011; Wang et al., 2011). The negineered cell lines, compounds **16** and **17** appeared to be poorly transported by RFC (Chapter 3 and 4) (Kugel Desmoulin et al., 2011; Wang et al., 2010; Wang et al., 2011). Both analogs induced current at -90 mV and pH 5.5 in *Xenopus* oocytes microinjected with PCFT cRNAs, and both were competitive inhibitors of [³H]MTX transport in PCFT transfectants from pH 5.5 to pH 6.8 (Chapter 3) (Kugel Desmoulin



et al., 2011; Wang et al., 2011). Transport of [³H]compound **17** by PCFT was directly demonstrated in R1-11-PCFT4 HeLa cells (Chapter 4) (Kugel Desmoulin et al., 2011).

By analogy, to confirm PCFT transport of compound **16**, R1-11-PCFT4 cells were incubated with [³H]compound **16** (0.5 μ M, 5 min, 37 °C) at pH 5.5 and pH 6.8 in the presence and absence of unlabeled compound **17** (10 μ M) as a competitive inhibitor. Transport was detected at a ~4-fold higher level at pH 5.5 than at pH 6.8, and at either pH uptake was substantially abolished in the presence of unlabeled compound **17** (Figure 5.1). These results establish that compound **16**, like its 4-carbon analog, compound **17**, is a *bona fide* substrate for membrane transport by PCFT.

5.3.2 Transport and Membrane Expression of PCFT and RFC in WT and R5 HeLa Sublines.

While compounds **16** and **17** are not RFC transport substrates, levels of RFC could nonetheless markedly impact the anti-proliferative effects of these agents, *via* expansion or contraction of intracellular THF cofactor pools. This could be further impacted by varying concentrations of extracellular THF cofactors. Thus, RFC levels or ratios of PCFT to RFC transport might effectively predict anti-tumor potencies of these prototypical PCFT-targeted antifolates (Figure 2.2, Panel E and Figure 2.5, Panel C).

To explore this concept, we used WT and R5 HeLa cells which express comparable levels of PCFT with or without RFC at the protein (Figure 5.2, Panel A) and transcript levels Figure 5.2, Panel B). R5 cells are resistant to MTX (Figure 5.4, Panel A) because of a genomic deletion that results in loss of RFC (Zhao et al., 2004a). MTX resistance is completely reversible





Figure 5.1 PCFT transport activity of compound 16 in R1-11-PCFT4 HeLa cells. Uptake of [³H]compound 16 (0.5 μ M) was measured at 37°C for 5 min at pH 5.5 (MES-buffered saline) and 6.8 (HEPES-buffered saline) in the presence or absence of unlabeled compound 17 (10 μ M). Internalized [³H]compound 16 was normalized to total protein. Details are provided in Materials and Methods. Results are shown for mean values <u>+</u> SEMs for 3 independent experiments.





Figure 5.2 Characterization of WT and R5 HeLa sublines. *Panel A*, Western blots of sucrose gradient purified membrane fractions (25 μ g) using human polyclonal PCFT and RFC and monoclonal HA antibodies to detect WT and HA-tagged proteins (R5-RFC^{HA}). *Panel B*, RT-PCR was used to measure RFC transcript levels in WT and R5 HeLa sublines, RNA was isolated using TRIzol reagent, cDNA was synthesized using random hexamers and RT-PCR was performed using SYBR green and gene-specific primers (primer sequences are reported in Table 2.1) and transcript levels were normalized to GAPDH. *Panel C*, the uptake of [³H]MTX was measured at 37°C for 2 min in WT and R5 HeLa monolayers at pH 7.2 (Anion-free buffer). Uptake of 0.5 μ M [³H]MTX, [³H]PMX, [³H]compound **17** and [³H]compound **16** was measured at 37°C for 2 min in WT and R5 HeLa cell monolayers at pH 5.5 in MES-buffered saline (*Panel D*) and pH 7.2 (Anion-free buffer) (*Panel E*). Internalized [³H]drug was normalized to total protein. The data in *panels D and E* represent mean values \pm SEMs for 3 independent experiments. While there were slight differences in initial rates of uptake for compounds **16** and **17** in *panel D*, these were not statistically significant (p>0.1).



upon transfection with WT RFC (R5-RFC2 cells), which restores RFC transport (Figure 5.2, Panel C); confirming that loss of RFC transport is causal to the resistant phenotype.

While [3 H]MTX (0.5 µM) transport at pH 5.5 was nearly identical for WT and R5 HeLa cells at pH 5.5 (Figure 5.2, Panel D), MTX uptake in R5 cells in Anion-free buffer at pH 7.2 was decreased ~3-fold compared to WT cells (Figure 5.2, Panel E), consistent with the loss of RFC. pH 5.5 (PCFT) to pH 7.2 (RFC) MTX transport ratios for R5 and HeLa cells were ~11- and ~3-fold, respectively (Figure 2.5, Panel C). Transport was also measured for [3 H]compounds **16** and **17** (both at 0.5 µM; 2 min, 37° C) and for [3 H]PMX at pH 5.5 and pH 7.2. Results were compared to those for [3 H]MTX. For all compounds and both cell lines, transport by PCFT over RFC clearly predominated, as uptake showed a characteristic pH dependence for PCFT with the highest levels at pH 5.5. While there were differences in cellular uptake of the various analogs at pH 5.5 with **16** > **17** > PMX~MTX, there were no obvious differences in net membrane transport of the individual analogs between WT HeLa and R5 cell lines (Figure 5.2, Panels D and E).

5.3.3 Impact of RFC and Extracellular Folate on Antitumor Activities of Compounds 16 and 17.

5-CHO-THF is poorly transported by PCFT at neutral pH and is less effective in supporting proliferation of PCFT-expressing cells (without RFC) than RFC-expressing cells (without PCFT) (Zhao et al., 2008). Thus, the loss of RFC in R5 cells would be predicted to impact THF cofactor requirements for cell proliferation and to contract intracellular pools of reduced folates derived from 5-CHO-THF, compared to those in WT HeLa cells (Chattopadhyay et al., 2006; Zhao et al., 2004b). This response may be exacerbated in the presence of high affinity PCFT-selective substrates which could further restrict the modest levels of THF cofactor uptake via PCFT through direct competition.



To examine these possibilities, folate-depleted WT, R5 and R5-RFC2 cells were cultured in 25, 100, or 1000 nM [3 H]5-CHO-THF [corresponding to 12.5, 50, or 500 nM of the active (6S) stereoisomer] for 96 h in order to determine cellular accumulation of [3 H]THF metabolites. During sustained culture, the media pH decreases to ~6.8 (Kugel Desmoulin et al., 2010b) and was accompanied by a dose-dependent accumulations of [3 H]5-CHO-THF (Figure 5.3, Panel A). At 25 nM extracellular [3 H]5-CHO-THF, R5 HeLa cells experienced a 31.6% decreased net accumulation of [3 H]5-CHO-THF compared to WT cells (p<0.05), and a 49.6% decrease compared to R5-RFC2 cells (p<0.005).

We measured proliferation for WT HeLa and R5 cells grown in 25 nM 5-CHO-THF in the presence of antifolates (over a range of concentrations up to 1000 nM), including PCFTselective compounds 16 and 17, for comparison with MTX, LMX, RTX and PMX, classic antifolates which are transported by both RFC and PCFT (Goldman et al., 2010; Kugel Desmoulin et al., 2011; Kugel Desmoulin et al., 2010b), and with PT523, which is transported by RFC but not PCFT (Kugel Desmoulin et al., 2011; Kugel Desmoulin et al., 2010b; Zhao and Goldman, 2007). Cytotoxicity and transport inhibition experiments have demonstrated that MTX, PDX, RTX, and LMX can be transported by PCFT, albeit to a lower extent than RFC. Similar to published results (Zhao et al., 2004c), R5 (and R5 mock-transfectant) cells were substantially resistant to PT523 compared to WT (>213-fold) and R5-RFC2 (>303-fold) cells (Figure 5.4, Panel A and Table 5.1). Further, compared to WT HeLa cells, R5 cells were 1.4-, 4.6-, 6.5-, 13.28- and >213-fold resistant to PMX, MTX, LMX, RTX and PT523, respectively. Thus, the greater the affinity of the antifolate for RFC, the more its cytotoxicity is reduced by RFC loss, especially if the drug has a lower selectivity for PCFT over RFC. For PMX, WT and R5 cells showed similar sensitivities (IC₅₀s of 48.3 and 66.1 nM, respectively). Notably, RFC-





Figure 5.3 [³**H**]**5-CHO-THF accumulation in WT and R5 HeLa sublines.** Folate depleted R5 HeLa sublines were treated with increasing concentrations of [³H]5-CHO-THF (0-1000nM) for 96 h in the absence (*Panel A*) or presence (0-1000nM) of unlabeled compound **17** (*Panel B*) or compound **16** (*Panel C*). Internalized [³H]5-CHO-THF was normalized to total protein. The data in *panel A* summarize the results as mean values \pm SEMs for 3 independent experiments. For each 5-CHO-THF concentration, statistically significant differences were calculated between WT HeLa or R5-RFC2 cells and R5 cells and are noted with * (p<0.05) and ** (p<0.005). For *panels B and C*, both R5 and HeLa cells showed decreased total folate metabolites derived from [³H]5-CHO-THF, accompanying treatment with increased concentrations of compounds **17** or **16** (results as mean values \pm SEMs for 3-5 independent experiments). This difference was somewhat greater for R5 cells over WT HeLa cells (52.9% versus 72.9% and 52.7% versus 71.1%, respectively). Statistical analyses were performed and for compound **16**, the difference between the two sublines was statistically significant (p=0.006), although statistical significance was not quite reached for compound **17** (p=0.078).





Figure 5.4 Growth inhibition by antifolate drugs toward WT and R5 HeLa sublines. (*Panel A*) Growth inhibitions were measured by a fluorescence (CellTiter-BlueTM)-based assay after 96 h of exposure of folate-depleted WT and R5 HeLa sublines to a range of inhibitor concentrations. Results are presented as 50% inhibitory concentrations (IC₅₀s) as mean IC₅₀ values \pm SEMs from 5-12 independent experiments. IC₅₀ values are summarized in Table 5.1. Statistically significant differences between results for WT HeLa or R5-RFC2 cells and those for R5 cells are noted with a * (p<0.01). For compound **17** (*Panel B*) and compound **16** (*Panel C*), growth inhibition experiments were performed in the presence of increasing concentrations (25-1000 nM) of extracellular 5-CHO-THF. Results are summarized as mean IC₅₀ values \pm SEMs from 3-11 independent experiments. Statistically significant differences between results for WT HeLa and those for R5 cells are noted with a * (p<0.005).



Table 5.1 Growth inhibition by antifolate drugs toward WT and R5 HeLa sublines.
Growth inhibition was measured by a fluorescence (CellTiter-Blue TM)-based assay after 96 h
of exposure of folate depleted WT and R5 HeLa sublines to a range of inhibitor
concentrations. Results are presented as 50% inhibitory concentrations (IC ₅₀ s) \pm standard
error means (SEM) from more than six experiments.

Antifolate	R5	R5-mock	HeLa	R5-RFC2
MTX	229.5 (22.5)	220.8 (21.0)	49.4 (4.8)	30.3 (1.38)
LMX	114.4 (22.5)	82.3 (28.5)	17.5 (5.5)	22.1 (3.8)
RTX	138.8 (13.0)	143.9 (33.3)	10.5 (1.0)	8.5 (1.7)
РМХ	66.1 (3.6)	77.1 (7.4)	48.3 (3.3)	43.9 (7.4)
PT523	>1000	>1000	4.7 (0.45)	3.3 (0.48)
Compound 17	80.1 (6.1)	63.9 (8.8)	290.6 (37.1)	292.3 (19.2)
Compound 16	17.4 (1.7)	9.3 (2.1)	55.8 (12.2)	144.7 (34.0)



deficient R5 cells were *more sensitive* to the PCFT-specific antifolates **16** and **17** than were WT HeLa cells (3.6- and 3.2-fold, respectively) and the R5-RFC2 transfected cells (3.6- and 8.3-fold, respectively). While differences in growth inhibitions between R5 and WT HeLa cells for **16** and **17** were preserved at 100 nM 5-CHO-THF (4.3- and 15-fold, respectively), the effects of both drugs were abolished when the concentration of 5-CHO-THF was increased to 1000 nM (Figure 5.4, Panels B and C).

Since compounds **16** and **17** are high affinity substrates for PCFT (Kugel Desmoulin et al., 2011; Wang et al., 2010; Wang et al., 2011), we hypothesized that these drugs compete with [³H]5-CHO-THF for PCFT-mediated uptake, leading to a more severe contraction of the cellular folate pool in R5 cells compared to WT cells than in their absence. Indeed, both compounds **16** and **17** affected a striking dose-dependent decrease in net accumulation of [³H]5-CHO-THF which were greater in RFC-null R5 cells than in WT HeLa cells. At 1000 nM compound **17**, levels of [³H]5-CHO-THF accumulation in R5 and WT HeLa cells were 52.9% and 72.9%, respectively, of levels without drug; for compound **16**, the corresponding values were 52.7% and 71.1%, respectively (Figure 5.3, Panels B and C).

Collectively, these results establish that loss of RFC contributes to a contraction of cellular folate pools, which is exacerbated in the presence of the PCFT-selective analogs compounds **16** and **17**. Importantly, decreased intracellular folates were accompanied by markedly increased antiproliferative effects of compounds **16** and **17**.

5.3.4 Polyglutamylation of Compounds 16 and 17 in WT and R5 HeLa Cells.

Analogous to physiologic folates and other classic antifolate drugs such as MTX (Goldman and Matherly, 1985; Shane, 1989), compound **17** is metabolized to polyglutamates (Chapter 4 and Kugel Desmoulin et al. (2011)), catalyzed by FPGS. Polyglutamylation of


compound **16** has not been previously assessed. For classic antifolates, polyglutamylation is critical to drug activity since polyglutamates are retained in cells and typically inhibit folatedependent enzyme targets more than their non-polyglutamyl forms (Stokstad, 1990). As polyglutamylation of antifolate drugs by FPGS can be regulated by elevated extra- and intracellular folates (Shane, 1989), it seemed possible that the impact of RFC and cellular THF cofactors on the anti-proliferative effects of compounds **16** and **17** (Figure 5.4, Panel A and Table 5.1) may be partly explained in this manner.

To assess this possibility, HeLa and R5 cells were incubated with 1 μ M [³H]compound 16 or [³H]compound 17 for 16 h at pH 6.8 in the presence of 25 nM 5-CHO-THF and 0.06 mM adenosine. Total cellular radiolabeled drug levels were quantitated and tritiated parent drug and PGs were extracted and analyzed by reverse-phase HPLC as described in Chapter 4. At least four polyglutamyl metabolites (PG₂₋₅) of [³H]compound 17 and five metabolites for [³H]compound 16 (PG₂₋₆) were resolved by HPLC. Migrations were compared to those for non-polyglutamyl 16 or 17, and to MTX and MTX polyglutamate standards. Further, samples were treated in parallel with conjugase (Kugel Desmoulin et al., 2011), which reverted the majority of the polyglutamyl metabolites to the parental drug (data not shown). Results are summarized in Figure 5.5 (Panels A and B). HPLC chromatograms for the compound 16 in WT HeLa and R5 cells are shown in Figure 5.5 (Panels C and D). For R5 and WT cells, there was a 7-8-fold greater accumulation of total and polyglutamyl [³H]compound **16** than [³H]compound **17**. WT and R5 cells accumulated similar levels of total 16 and 17 drug forms, although there were slight differences in relative accumulations of individual PGs between the cell lines. This difference was most obvious for the longest chain-length PGs (PG_5 and PG_6) and appears to be somewhat greater for 17 than 16.





Figure 5.5 HPLC analysis of polyglutamyl derivatives of compound 17 and 16 in WT and R5 HeLa cells at pH 6.8. Folate depleted WT and R5 HeLa cells were treated with 1 μ M [3H]compound 17 (*Panel A*) and 16 (*Panel B*) at pH 6.8 in the presence of adenosine (0.06 mM) and 25 nM 5-CHO-THF for 16 h. Polyglutamate drug forms were extracted and analyzed as described in Materials and Methods. Percent monoglutamate and polyglutamate drug forms were determined by chromatographic analysis and the total intracellular radiolabel calculated in units of pmol/mg protein. Results are presented as average values plus/minus ranges for two independent experiments. *Panels C and D*, show representative HPLC chromatograms for R5 and HeLa cells treated with compound 16.



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These results establish that: (i) compounds **16** and **17** are both excellent substrates for polyglutamylation under conditions (pH 6.8) that favor their membrane transport by PCFT; (ii) net drug accumulation and polyglutamylation of compound **16** far exceeds that for compound **17**; and (iii) expression of functional RFC exerts only a modest effect on net polyglutamate synthesis of compounds **16** and **17**.

5.3.5 In vivo Efficacy Study of Compounds 16 and 17 Against HeLa and R5 Xenografts.

To extend our *in vitro* cell proliferation studies *in vivo*, we performed *in vivo* antitumor efficacy studies with 8 week old female ICR SCID mice implanted with subcutaneous R5 or WT HeLa cells.

Mice were maintained *ad libitum* on a folate-deficient diet which decreases serum folates to levels approximating those seen in humans (Kugel Desmoulin et al., 2011; Wang et al., 2010; Wang et al., 2011). For the drug trial, control and drug treatment groups were non-selectively randomized (four mice/group); compounds **17** or **16** were administered intravenously (180 and 32 mg/kg per injection, respectively) on days 3, 7, 14 and 18 post-implantation. Mice were weighed daily and tumors were measured 2-3 times per week. As reported for other tumor models (Kugel Desmoulin et al., 2011; Wang et al., 2011), compounds **17** and **16** showed substantial efficacy toward R5 and WT HeLa xenografts (Table 5.2). Both compound **17** and compound **16** showed greater efficacy toward R5 cells (0% T/C, (T-C (tumor growth delay) = 23 days, 3.3 gross log kill, ++++ activity for compound **17**; 3% T/C, T-C = 17.5 days, 2.5 gross log kill, +++ activity for compound **17**; 7% T/C, T-C=13 days, 1.9 gross log kill, ++ activity for compound **17**; 7% T/C, T-C=13 days, 1.9 gross log kill, ++ activity for compound **16**. The treatment regimens with compounds **16** and **17** were well tolerated with



Table 5. SCID mi	2 Antitumor efficies (under folgte	cacy evaluation deficient cond	n of comp(itions)	ound 17 and 16 against ea	rly stage	human R5	and HeLa	a in female
Tumor	Agent	Total dose (mg/kg)	Drug Deaths	Median tumor mass in mg (range) on day 21	T/C (%)	T-C (days)	Gross Log ₁₀ kill	Activity rating
	No Rx	Ι	NA	1054 (916 – 1272)	Ι	I	I	I
R5	Compound 17	720	0/4	0 (all zeroes)	0	23	3.3	++++
	Compound 16	128	0/4	32 (0 – 75)	3	17.5	2.5	+++
	No Rx	Ι	NA	1009 (847 – 1701)	I	I	I	I
HeLa	Compound 17	720	0/4	63 (0 – 247)	9	13	1.9	+
	Compound 16	128	0/4	69 (0 - 189)	L	13	1.9	+
The 8-week trocar on da	c old female NCR in 0. Chemotherap	SCID mice were	e implanted 1 day 3 afte	l bilaterally subcutaneously we set tumor implantation, when t	vith 30-6(the numb) mg tumor er of cells w	fragments b as relatively	y a 12-gauge r small $(10^7 -$

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 10^8 cells). A *T/C* = 0 indicates very high antitumor activity. The conversion of log10 tumor cell kill to activity rating is as follows: >2.8 log10 kill (highly active ++++); 2.0 - 2.8 (+++); 1.3 - 1.9 (++); 0.7 - 1.2 (+); <0.7 (Inactive -). Day 0 = day of implant

dose-limiting symptoms manifesting as reversible body weight loss (nadirs sustained for body weight loss.

The results of the *in vivo* efficacy trial provide proof-of-principal confirmation of our *in vitro* findings that the antitumor effects of both compounds **16** and **17** are greater in RFC-deficient R5 cells than in WT HeLa cells. Interestingly, the impact of loss of RFC is greater with compound **17** than compound **16** *in vivo*.

5.4 Discussion.

In this chapter, we significantly expanded upon previous reports (Kugel Desmoulin et al., 2011; Kugel Desmoulin et al., 2010b; Wang et al., 2010; Wang et al., 2011; Zhao and Goldman, 2007) that PCFT may be therapeutically exploitable for treating solid tumors, reflecting unique patterns of PCFT expression and transport activity at pHs approximating the tumor microenvironment (Chapters 2-4).

We demonstrated that functional loss of RFC in R5 cells caused a contraction of total cellular THF cofactor pools derived from 5-CHO-THF which enhanced the antitumor activities of both compounds **16** and **17** compared to WT cells. Importantly, reduction of total cellular folate pools in R5 cells was exacerbated in the presence of compounds **16** and **17**, through direct competition at PCFT, which further restricted cellular uptake of exogenous 5-CHO-THF. Efficacies of compounds **16** and **17** were also increased toward R5 tumors compared to WT tumors transplanted into SCID mice with serum folate concentrations approximating those achieved in humans.

There is ample precedent for an impact of extra- and intracellular folate pools on antifolate drug efficacy. Indeed, this is the premise of leucovorin rescue from MTX toxicity (Matherly et al., 1987a) or of low-dose folic acid protection from LMX *in vivo* toxicity (Roberts et al., 2000a),



whereby elevated extra- and intracellular folates compete at multiple levels to reverse drug activity (Zhao et al., 2001a). *In vitro* studies in assorted cell line models have extended these findings to both classic (PMX, LMX) and non-classic (trimetrexate) antifolates, which inhibit a range of cellular targets (DHFR, TS, and GARFTase) (Goldman et al., 2010; Tse and Moran, 1998; Zhao et al., 2001a). Further, effects on antifolate drug activities are enhanced by decreased intracellular folates resulting from a RFC genomic deletion (Chattopadhyay et al., 2006; Zhao et al., 2004b; Zhao et al., 2004c) or RFC mutations (Zhao et al., 2000a). Similarly antifolate activities are reduced by increased intracellular folates resulting from a RFC mutations (Zhao et al., 2000a). Similarly antifolate activities are reduced by increased intracellular folates resulting from the activities are reduced by increased intracellular folates resulting from the activities are reduced by increased intracellular folates resulting from the activities are reduced by increased intracellular folates resulting from the activities are reduced by increased intracellular folates resulting from the activities are reduced by increased intracellular folates resulting from the activities are reduced by increased intracellular folates resulting from the activities are reduced by increased intracellular folates resulting from the activities are reduced by increased intracellular folates resulting from the activities are reduced by increased intracellular folates resulting from the activities are reduced by increased intracellular folates resulting from the activities are reduced by increased intracellular folates resulting from the activities are reduced by a mutant RFC (Tse et al., 1998; Tse and Moran, 1998).

Regardless of the underlying mechanism and intracellular drug target involved, markedly decreased total intracellular THF pools can result in collateral sensitivities to antifolates, often in the face of substantially decreased levels of drug uptake (Chattopadhyay et al., 2006; Zhao et al., 2000b; Zhao et al., 2004c). This could reflect inhibitory effects on antifolate polyglutamylation (with consequent impact on drug retention and inhibition of folate-dependent enzyme targets) due to competitive feedback inhibition at FPGS by high levels of THF cofactor PGs (Shane, 1989). Additionally, FPGS activity has been found to increase in response to decreased extraand intracellular folates (Gates et al., 1996). There can also be direct competitive interactions between polyglutamyl folates and antifolates that interfere with drug binding and inhibition at their enzyme targets, as documented for MTX and other classic antifolates (Matherly et al., 1983). Changes in drug efflux are also possible, as ABC transporter (ABCG2, ABCC1) levels and/or intracellular distributions have been described in response to folate deprivation (Ifergan et al., 2005).



In the present study, we found that transport of compounds **16** and **17** by PCFT was virtually identical between the RFC-deficient R5 and WT HeLa cell lines. By analogy with other classical antifolates (Mendelsohn et al., 1999; Shih and Thornton, 1999), the increased accumulation of long chain polyglutamyl forms of compounds **16** and **17** observed in the R5 subline might be expected to result in increased inhibition of intracellular GARFTase and *de novo* purine nucleotide biosynthesis (Kugel Desmoulin et al., 2011; Wang et al., 2010; Wang et al., 2011). However, even though total and polyglutamyl accumulations of compounds **16** and **17** during sustained drug exposures were similar between WT and R5 cells; there were slight differences in distributions of compounds **16** and **17** polyglutamates between the lines. This difference was greatest for the longest chain length PGs (PG₅ and PG₆) and appeared to be somewhat greater for compound **17** than **16**.

The results provide proof-of-principal evidence that RFC levels and function are critical determinants of *in vitro* antitumor activities and *in vivo* efficacies of PCFT-targeted antifolates that are not themselves substrates for RFC. It is this lack of RFC transport which should confer tumor selectivity and decreased toxicity to normal tissues for this novel class of agents. Tumor selectivity would be enhanced by substantial levels of PCFT protein in solid tumors and by acidic pHs characterizing the tumor microenvironment which favor PCFT over RFC transport (Kugel Desmoulin et al., 2011). Conversely, at neutral pHs characterizing most normal tissues, RFC transport of reduced folates would be increased, resulting in elevated levels of THF cofactors within cells which further protect from untoward drug effects. Of course, in tumors with sufficiently high RFC levels, uptake of THF cofactors by this process may still occur even at somewhat acidic pHs. Accordingly, any decrease in RFC function would serve to augment the inherent antitumor selectivity and increase sensitivities to PCFT-selective antifolates.



CONCLUSIONS

The goal of this dissertation research was to determine the therapeutic potential of using PCFT-mediated membrane transport to selectively deliver novel cytotoxic antifolates into tumor cells. To establish the feasibility of this approach the expression and function of PCFT in normal and tumor tissues was determined and compared to RFC levels (Chapter 2). Additionally, novel antifolates with selective uptake by PCFT were identified and characterized *in vitro* and *in vivo* to evaluate their preclinical antitumor efficacies (Chapters 3 and 4). Finally, the influence of RFC-mediated folate uptake on drug efficacy was determined for these novel PCFT-selective antifolates (Chapter 5).

The comprehensive analysis of PCFT expression and function in human normal and tumor tissue established for the first time that PCFT is present in tumor tissue and is functional at the acidic pH surrounding most solid tumors. There were significant levels of PCFT transcripts in the majority of human solid tumor tissues and cell lines of different origins (e.g., breast, prostate, ovarian, etc.), and uniformly low PCFT transcript levels in human leukemias, including both ALL and AML. PCFT levels were highest in Caco-2 (colorectal) SKOV3 (ovarian), HepG2 (hepatoma), HeLa (cervical), and T47D (breast) cancer cells. In human normal tissues, PCFT expression was detected in the small intestine, kidney, liver, and the adrenal gland. When compared to the ubiquitously expressed RFC, the presence of PCFT was more limited. This suggests, based on PCFT expression patterns, antifolates preferentially using PCFT and not RFC as a means of drug entry into tumor cells may be less toxic compared to antifolates presently used in cancer therapy.

The rational drug design and screening of novel 6-substituted pyrrolo[2,3-*d*]pyrimidine benzoyl (compound **3**) or thienoyl (compounds **16** and **17**) analogs identified the first antifolates



that are selective for PCFT-mediated uptake and have no appreciable transport by RFC. The novel antifolates were identified and characterized in multiple engineered cell lines that express PCFT alone (R2/PCFT4 CHO and R1-11-PCFT4 HeLa sublines), or RFC alone (PC43-10 CHO and R1-11-RFC6 HeLa sublines), to determine selectivity, as well as solid tumor cell lines such as HeLa and HepG2 that express both PCFT and RFC to determine therapeutic potential. The PCFT-mediated uptake of the novel antifolates was very efficient and led to growth inhibition in all cells tested expressing PCFT.

When further characterized these analogs were found to be directly transported by PCFT in a pH- and time-dependent manner, where uptake was enhanced at acidic pHs that are relevant to the solid tumor microenvironment. Once internalized the novel antifolate compounds were polyglutamylated and up to five or six polyglutamyl metabolites were identified. The principle intracellular folate-dependent enzyme target for compounds **3**, **16** and **17** was GARFTase, a key *de novo* purine nucleotide biosynthesis enzyme. This was determined by both nucleoside protection and an *in situ* GARFTase assay. Inhibition of GARFTase led to a dose- and time-dependent decrease in ATP and GTP levels, which caused an S-phase accumulation and irreversible cell death as measured by discontinuous colony formation. The mechanism of cell death was partially through apoptosis and partially through an unidentified process that remains to be elucidated.

RFC function had a large impact on the cytotoxicity of analogs selective for PCFTmediated uptake. While the novel compounds are not RFC transport substrates, levels of RFC nonetheless markedly impacted the anti-proliferative effects of these agents, via expansion or contraction of intracellular THF cofactor pools. Loss of RFC, which occurs in clinical cases of *de novo* and acquired resistance to the classic antifolates, leads to enhanced sensitivity to



antifolates selective for PCFT-mediated uptake. This was due to contraction of reduced folate pools and enhanced polyglutamylation of the novel drugs presumably leading to better GARFTase inhibition.

The *in vitro* cytotoxicity of compounds **16** and **17** has been recapitulated *in vivo* in subcutaneous HepG2 and HeLa xenografts in which PCFT was the predominant mode of drug uptake. Treatment with compound **16** led to potent tumor growth delay of HepG2 tumors, providing compelling proof-of-principle validation that PCFT is an efficient mechanism of drug delivery. Additionally, subcutaneous HeLa tumors that lacked RFC function were exquisitely more sensitive to PCFT-targeted drugs compared to wild-type HeLa tumors that expressed functional RFC. These data suggests that drugs selective for PCFT may be useful in tumors with antifolate resistance due to lack of RFC function. Importantly, RFC levels or ratios of PCFT to RFC transport might effectively predict anti-tumor potencies of these novel PCFT-selective antifolates.

The evidence in this dissertation of widespread PCFT expression in human solid tumors paired with the discovery of novel antifolates selective for PCFT-mediated uptake offers exciting new therapeutic possibilities to selectively deliver novel antifolate drugs to tumors by exploiting the acidic tumor microenvironment. Data presented here suggests that PCFT is a surprisingly efficient means of delivering antifolates into a tumor cell both *in vitro* and *in vivo* and there is a strong rationale for developing drugs whose transport by PCFT, but not RFC, allows for GARFTase inhibition.



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ABSTRACT

THE PROTON-COUPLED FOLATE TRANSPORTER: BIOLOGY AND THERAPEUTIC APPLICATIONS TO CANCER

by

SITA KUGEL DESMOULIN

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Advisor: Larry H. Matherly, Ph.D.

Major: Cancer Biology (Pharmacology)

Degree: Doctor of Philosophy

Folates are essential cofactors of tumor cell proliferation and survival required for nucleotide biosynthesis and amino acid metabolism. In cancer therapy, inhibition of folatedependent metabolic pathways has been achieved through the use of antifolates. Unfortunately, the efficacy of many clinically approved antifolates is limited by a lack of tumor selectivity. Facilitative transport of folates into mammalian cells is achieved by the reduced folate carrier (RFC) and proton-coupled folate transporter (PCFT). As PCFT is a folate-proton symporter with an acidic pH optimum, PCFT may provide a mechanism for targeting cytotoxic antifolates to tumors, based on their acidic microenvironments. To establish the feasibility of this approach, we systematically determined the expression profiles for PCFT and RFC. In various human malignant cell lines and tissues PCFT was highly expressed and functional, while its expression in normal tissue was more limited compared to RFC.

Screening and characterization of multiple series of novel antifolates led to the identification of 6-substituted pyrrolo[2,3-*d*]pyrimidine benzoyl and thienoyl antifolates, which were selective for PCFT-mediated uptake, but not RFC. Upon internalization, these novel


antifolates were extensively polyglutamylated, as detected by high performance liquid chromatography (HPLC). Growth inhibition assay paired with nucleoside protection identified glycinamide ribonucleotide (GAR) formyltransferase (GARFTase) in the *de novo* purine biosynthesis pathway as the principle drug target. This was confirmed by *in situ* measurement of [¹⁴C]glycine incorporation into [¹⁴C]formylGAR in treated cells. Furthermore, contraction of intracellular purine nucleotide triphosphate pools occurred in a dose- and time-dependent manner, as demonstrated by quantitative HPLC analysis. Further, drug treatment induced S-phase accumulation eventually leading to irreversible cell death. Drug treatment caused a significant delay in tumor growth in an *in vivo* efficacy trial of SCID mice implanted with subcutaneous human tumors where PCFT was the sole mechanism of drug uptake.

Although these compounds are not substrates for RFC, its expression does impact drug efficacy by influencing intracellular tetrahydrofolate (THF) cofactor pools. Loss of functional RFC leads to increased polyglutamylation of these analogs within the cell causing enhanced cytotoxicity. Similarly, these novel PCFT-selective antifolates displayed increased *in vivo* efficacy in subcutaneously implanted human tumors lacking RFC.

Our finding of widespread PCFT expression in human solid tumors paired with our discovery of novel antifolates internalized via PCFT offers exciting new therapeutic possibilities for selectively targeting tumors based on their acidic microenvironments. These compounds display immense therapeutic potential, especially in tumors with *de novo* or acquired resistance to classic antifolates caused by lack of RFC function.



AUTOBIOGRAPHICAL STATEMENT

EDUCATION	
Wayne State University Detroit, MI	2007 - 2012
Doctor of Philosophy: Cancer Biology (Minor in Pharmacology)	
Simon Fraser University Burnaby, British Columbia, CANADA	2001 - 2006
Bachelor of Science: Kinesiology (Minor in Anatomy and Physiology)	
GRANTS	
Pre-doctoral Training Grant - Canadian Institutes of Health Research (CIHR)	2009 - 2012

SELECTED PUBLICATIONS

- **Kugel Desmoulin, S.** & Matherly, L.H. The Human Proton-coupled Folate Transporter: Biology and Therapeutic Applications to Cancer. *Cancer Biology & Therapy*. Invited Review. **2012**.
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