

Review

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Review of 5-FU resistance mechanisms in colorectal cancer: clinical significance of attenuated on-target effects

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Abstract

The emergence of chemoresistant disease during chemotherapy with 5-Fluorouracil-based (5-FU-based) regimens is an important factor in the mortality of metastatic CRC (mCRC). The causes of 5-FU resistance are multifactorial, and besides DNA mismatch repair deficiency (MMR-D), there are no widely accepted criteria for determining which CRC patients are not likely to be responsive to 5-FU-based therapy. Thus, there is a need to systematically understand the mechanistic basis for 5-FU treatment failure and an urgent need to develop new approaches for circumventing the major causes of 5-FU resistance. In this manuscript, we review mechanisms of 5-FU resistance with an emphasis on: (1) altered anabolic metabolism limiting the formation of the primary active metabolite Fluorodeoxyuridylate (5-Fluoro-2'-deoxyuridine-5'-O-monophosphate; FdUMP); (2) elevated expression or activity of the primary enzymatic target thymidylate synthase (TS); and (3) dysregulated programmed cell death as important causes of 5-FU resistance. Importantly, these causes of 5-FU resistance can potentially be overcome through the use of next-generation fluoropyrimidine (FP) polymers (e.g., CF10) that display reduced dependence on anabolic metabolism and more potent TS inhibitory activity.



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Keywords: Fluoropyrimidine, 5-FU resistance, colorectal cancer, chemotherapy, precision medicine, thymidylate synthase

INTRODUCTION

It is estimated that 1.93 million colorectal cancer (CRC) cases will be newly diagnosed in 2022 worldwide, with 0.94 million CRC-caused deaths. According to the American Cancer Society (ACS), CRC is the 2nd most common cause of cancer-related mortality in the United States, accounting for ~51,000 deaths annually^[1,2]. Surgical approaches are the primary treatment modality for limited-stage CRC when there is no evidence of distant metastasis. However, in elderly patients that constitute most new CRC diagnoses, there is an increased risk of post-operative complications^[3]. Adjuvant chemotherapy with 5-Fluorouracil-based (5-FU-based) combinations reduces the risk of disease recurrence in stage III and high-risk stage II CRC. Chemotherapy with 5-FU-based combinations together with biologics (e.g., bevacizumab or cetuximab) and immunotherapy in some instances are also used to treat metastatic CRC (mCRC)^[4,5], which often occurs in liver and is frequently not amenable to surgical resection.

The chemotherapeutic molecule most widely used for CRC treatment is 5-fluorouracil (5-FU), a synthetic fluorinated pyrimidine (FP) analog of uracil that is used to treat > 2 million cancer patients each year worldwide^[6,7]. In addition to its widespread use for CRC treatment, 5-FU is also widely used to treat pancreatic, stomach, esophageal, breast, and head-and-neck cancer. 5-FU belongs to the antimetabolite class of anti-cancer drugs^[8,9], {Chen, 2019 #42}{Chen, 2019 #42}{Chen, 2019 #42}{Chen, 2019 #42} and its activity results from intracellular conversion into active metabolites that interfere in thymidine biosynthesis and affect DNA- and RNA-mediated processes^[10,11]{Chen, 2019 #42}{Chen, 2019 #43}. The primary molecular target of 5-FU's anti-cancer activity is thymidylate synthase (TS), which is required for *de novo* thymidylate (thymidine 5'-O-monophosphate) biosynthesis^[12]. TS is a well-validated target for cancer chemotherapy^[13] and aggressive malignant cells are relatively more reliant on *de novo* thymidylate biosynthesis than non-malignant cells that utilize the alternative salvage pathway^[14]. The importance of targeting TS for 5-FU's anti-cancer activity is underscored by its invariant clinical use in combination with folinic acid (Leucovorin; LV), a reduced folate co-factor that binds TS in a ternary complex with 5-Fluoro-2'-deoxyuridine-5'-O-monophosphate (FdUMP), the 5-FU metabolite that irreversibly inhibits TS enzymatic activity. TS inhibition depletes cellular stores of thymidylate, resulting in increased misincorporation of 2'-deoxyuridine-5'-triphosphate (dUTP) in DNA. In cells treated with FP drugs, 5-fluoro-2'-deoxyuridine-5'-triphosphate (FdUTP) is also misincorporated into DNA, and this causes Topoisomerase 1 (Top1)-mediated DNA damage^[15]. The Gmeiner lab has developed FP polymers (e.g., CF10) that directly release FdUMP without a requirement for anabolic metabolism. CF10 inhibits TS at 100-1,000-fold lower concentrations than 5-FU in CRC cells^[16-18] and causes extensive Top1-mediated DNA damage to generate increased replication stress, a point of therapeutic vulnerability in CRC cells.

While the anti-cancer activities of 5-FU and other FP drugs are considered to primarily result from TS inhibition and DNA damage, only a relatively small percentage of 5-FU administered to humans is converted to FdUMP and DNA-directed metabolites (< 5%^[19]). Most 5-FU (~80%) is either degraded in the liver or excreted intact in the urine^[20]. Among anabolic metabolites, ribonucleotides are produced at approximately 10-fold greater levels than deoxyribonucleotides^[20,21]. The importance of RNA-directed metabolites for 5-FU's anti-cancer activity remains an active area of investigation^[22]; however, the systemic toxicities associated with RNA-directed metabolites are established and include gastrointestinal tract toxicity^[23,24] and immunosuppression^[23,25], both of which are alleviated by uridine administration^[26] to dilute

5-FU's effects on RNA-mediated processes. Patients that are deficient in 5-FU catabolism are highly vulnerable to serious systemic toxicities if treated with 5-FU^[27]. Approximately 5% of the human population display polymorphisms in the gene encoding dihydropyrimidine dehydrogenase (*DPYD*) that catalyzes the initial step in 5-FU degradation and 5-FU use at standard levels is contraindicated in these patients^[28].

5-FU remains a central component of CRC treatment both in the adjuvant setting and in the treatment of mCRC^[4,5], which is the cause of cancer-related lethality. While 5-FU is just one component in combination therapy regimens such as FOLFOX and FOLFIRI that combine folinic acid, 5-FU, and either oxaliplatin (FOLFOX) or irinotecan (FOLFIRI), understanding the mechanistic basis for 5-FU resistance can help guide the development of new and more effective therapeutic approaches. FOLFOX or FOLFIRI are frequently used in frontline treatment of mCRC, often in combination with a biologic, such as bevacizumab^[29]. While current 5-FU-based chemotherapy regimens have contributed to significantly improved survival for mCRC patients (~20 months;^[30]), 5-year survival remains rare, < 14%, indicating a critical need to understand the mechanistic basis of resistance and develop new strategies to more completely eradicate metastatic disease^[31]. Innate or acquired resistance remains a prominent cause of treatment failure for patients with metastatic cancer. 5-FU resistance can result from multiple causes; however, a critical review of the literature indicates cancer cells adapt to 5-FU's cytotoxic effects through: (1) decreasing intracellular FdUMP levels [Figure 1]; (2) elevating activity of the target enzyme, TS; and (3) dysregulating the balance between autophagy and apoptosis to favor cell survival. These endpoints are achieved via multiple mechanisms making overcoming resistance a challenging endeavor. This review focuses on addressing the causes of clinical resistance to 5-FU, considering both clinical data and cellular models of CRC. We review mechanisms by which 5-FU-based therapy fails, intending to provide insight into novel strategies to overcome resistance and improve outcomes beyond the incremental gains achieved in recent years^[32].

CLINICAL DETERMINANTS OF 5-FU RESPONSE IN CRC TREATMENT

The applicability of 5-FU-based chemotherapy for CRC treatment depends upon several factors. For patients with stage III CRC or diagnosed with stage II CRC with risk factors consistent with an elevated likelihood for relapse, 5-FU-based adjuvant chemotherapy is recommended unless tumor biopsy demonstrates high microsatellite instability (MSI-H) or deficiency in DNA mismatch repair (MMR-D). For patients with MSI-High or MMR-D primary CRC tumors, which include familial syndromes such as Lynch syndrome, 5-FU-based regimens are ineffective and testing for MMR-D status prior to treatment is standard care. Testing for MMR-D status is also required for establishing responsiveness to immune checkpoint blockade immunotherapy, which is relatively more effective in CRC patients with high tumor mutational burden associated with MMR-D^[33]. MSI testing by polymerase chain reaction (PCR) and immunohistochemistry (IHC) is used to establish MMR-D^[34]. Two antibody IHC testing for MSH6 and PMS2 is used to identify MMR-proficient CRC patients, and if deficiency is suspected, IHC for mutS homolog 2 (MSH2) and mutL homolog 1 (MLH1) are undertaken to establish MMR-D^[35]. MLH1 promoter methylation testing is done for cases with MLH1-IHC loss.

Relevance of MMR-D for CRC chemotherapy is that, in general, MSI-High and MMR-D in early-stage primary colon cancer confer a good prognosis and NCCN does not recommend adjuvant 5-FU for stage II CRC that is MSI-high. However, the FOLFOX regimen is beneficial in MSI-high stage III^[36], and patients with Transforming growth factor- β_{RII} ($TGF-\beta_{RII}$) mutations in particular may be responsive to 5-FU-based therapy^[37]. The $TGF-\beta$ pathway also is implicated in drug resistance in pre-clinical studies and specific inhibition of $TGF-\beta_1$ restored the sensitivity of resistant CRC cells to 5-FU^[38]. Similarly, for patients with mCRC that is MSI-H or MMR-D, alternative frontline therapy to 5-FU-based therapy is implemented,

central and well-established chemotherapy target^[13]. The structural basis for TS inhibition by FPs was shown to result from nucleophilic attack by Cys195 at C6 of FdUMP, resulting in irreversible enzyme inhibition via a ternary complex that also includes a reduced folate co-factor^[49].

The relationship between TS levels and response to 5-FU, other FPs, or TS inhibitors is complex, in part because while elevated TS levels contribute to resistance (since more FdUMP is required for TS inhibition), but very low TS levels slow cell proliferation, which is necessary for replication-dependent DNA damage. Further, establishing elevated TS as a cause of resistance to 5-FU or other TS-targeted therapeutics is challenging because TS is regulated at multiple levels including through gene amplification, polymorphisms in the promoter, and upregulation of transcription factors that regulate its intratumor expression [Figure 2]. TS levels and activity^[52] significantly correlate with response to 5-FU-based treatment and LV enhanced TS inhibition. However, incorporation of 5-FU into either DNA or RNA does not correlate with response to 5-FU^[53].

Transcriptional regulation of TYMS

Transcriptionally, *TYMS* (encoding TS) is regulated by E2F family transcription factors^[54] in an S-phase-dependent manner^[55]. *TYMS* expression is also sensitive to Myc levels and silencing *TYMS* decreases the oncogenic properties of elevated MYC in some cell contexts^[56]. Recently, an analysis from the Cancer Genome Atlas (TCGA) database revealed lower *TYMS* was associated with better response to FOLFOX/FOLFIRI therapy in mCRC patients and MYC was identified as an upstream controller of genes that regulate response to 5-FU+folate therapy^[57]. The forkhead transcription factor forkhead box M1 (FOXO1) is regulated by E2F1 and directly upregulates *TYMS* and is responsive to DNA damage. Elevated FOXO1 is a cause of 5-FU resistance through the upregulation of *TYMS*^[58], and recent studies indicate targeting FOXO1 can overcome 5-FU resistance^[59]. Other signaling pathways may upregulate *TYMS* and cause 5-FU resistance, including HSP90/Src^[60]. Further, *TYMS* is regulated by the MALAT1-miRNA network^[61] and other miRNAs that regulate drug resistance^[62] and can be used as biomarkers^[63].

Gene amplification of TYMS

The importance of TS gene and protein expression for 5-FU resistance was established in CRC tumors. Responsive patients had significantly lower mean TS protein and gene levels relative to non-responsive patients^[64]. Further, CRC cells selected for acquired 5-FU resistance displayed elevated TS, which occurred through gene amplification^[65]. Elevated TS is associated with clinical resistance to 5-FU^[66], consistent with TS being the primary molecular target of FPs. Several studies^[67,68], including a meta-analysis of 13 studies^[69], demonstrated that elevated TS was associated with poor outcomes. However, multiple studies indicate the relationship between TS expression and 5-FU response is complex and may depend on the extent of TS nuclear localization or the expression of other genes, particularly those regulating 5-FU metabolism including dihydropyrimidine dehydrogenase deficiency (DPD) and TP^[66]. TS undergoes reversible SUMOylation^[70] and localizes to the nucleus (nTS) as part of a multi-protein complex that enables efficient *de novo* dDP biosynthesis during S-phase^[71]. Clinical studies indicate that increased intratumor nuclear localization of TS may be a better indicator of disease aggressiveness than overall TS levels^[72]. *TYMS* gene amplification is detected in mCRC from patients pre-treated with 5-FU-based chemotherapy and was associated with shorter median survival for patients treated with chemotherapy following surgical resection^[73]. A summary of studies in which TS gene amplification was implicated with 5-FU resistance is included in Table 1.

TSER and alternative causes of elevated TS

In addition to *TYMS* gene amplification and increased transcription, at least three other processes are potential factors that could increase TS levels and contribute to 5-FU resistance [Figure 2]: i) TS enhancer

Table 1. TS Gene Amplification in 5-FU Resistance

Tissue/cells	Frequency/treatment	Site	Reference
mCRC	18%	Liver metastases	[73]
mCRC	23%	Liver metastases	[74]
CRC	Increased progression	Colon cancer	[75]
CRC cells	FdU treatment	Colon cancer cells	[76]
CRC cells	5-FU treatment	Colon cancer cells	[65]

TS: thymidylate synthase; mCRC: metastatic colorectal cancer; CRC: colorectal cancer.

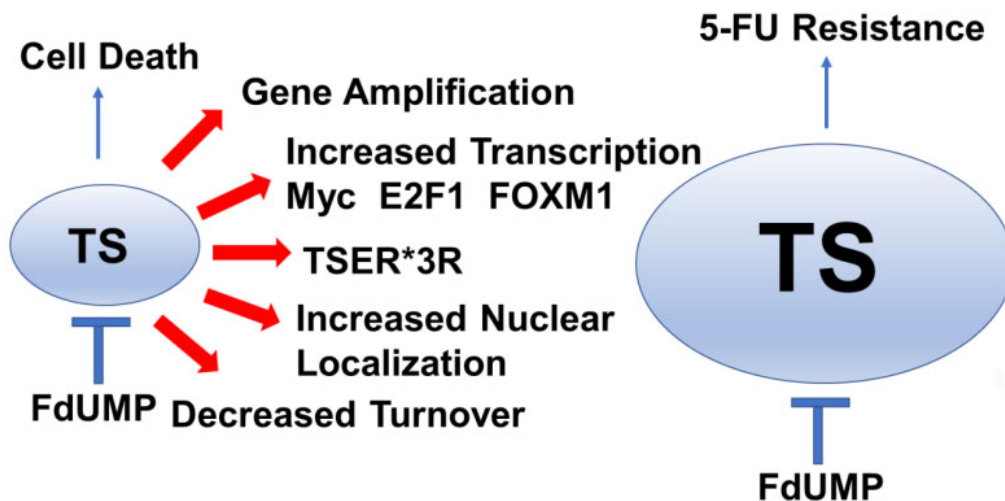


Figure 2. 5-FU Resistance develops from processes that increase thymidylate synthase (TS) activity in cancer cells. Increased TS activity can result from multiple processes including gene amplification, increased transcription, TSER*3R polymorphism, increased TS nuclear localization, and decreased TS protein degradation, which are indicated by red arrows. Increased TS activity renders cells 5-FU-resistant because FdUMP levels are insufficient to inhibit all the TS available. 5-FU: 5-Fluorouracil; FdUMP: 5-Fluoro-2'-deoxyuridine-5'-O-monophosphate; FOXM1: forkhead box M1.

region (TSER) polymorphisms; ii) TS translational autoregulation; iii) TS proteasomal degradation. Polymorphisms in the 5'-UTR of *TYMS* contribute to elevated *TYMS* expression in some contexts^[77,78]. A triple tandem repeat (TSER*3)^[79] in the 5'-UTR of the TS gene^[80] resulted in elevated *TYMS* expression and 5-FU resistance^[81]. The clinical significance of TSER genotypes remains largely unproven in CRC; however, prospective selection of patients with gastric cancer have at least one TSER*2 allele favoring lower *TYMS* expression therapy resulted in an encouraging disease control rate for treatment with FOLFOX^[82]. Further, *TYMS* polymorphisms, together with *KRAS* and *BRAF* mutation status, retrospectively, were associated with reduced relapse in CRC^[83]. TS also poses a negative autoregulatory function at the translational level by binding to its own mRNA; thus, it prevents the synthesis of functional TS enzyme^[73]. Autoinhibition of TS protein expression is countered by FdUMP binding and ternary complex formation. At present, there is no evidence that autoregulation of TS by this mechanism contributes to 5-FU resistance. However, another aspect of translation is affected by 5-FU, which is the efficiency and selection of proteins translated by the ribosome^[84]. TS also undergoes proteasomal degradation and TS levels reflect a dynamic balance of new protein synthesis, dependent upon gene expression and translational efficiency, that is countered by the rate of degradation for expressed protein. A recent study showed that decreased O-GlcNAc transferase (OGT), an enzyme responsible for post-translational modification of multiple proteins including TS, affected TS proteasomal degradation in 5-FU-resistant cells^[85].

Increased TS and intrinsic 5-FU resistance

The elevated expression of TS is commonly accepted as a primary molecular mechanism for acquired 5-FU resistance^[86], but it also is important for intrinsic resistance. The stability of the ternary complex is highly dependent on 5,10-methylenetetrahydrofolate (CH₂THF) levels^[78], and lack of CH₂THF creates an unstable TS: FdUMP binary complex resulting in poor inhibition^[81,86,87]. Increased TS level prior to 5-FU-based treatments is associated with perturbed folate pools, which cause intrinsic resistance compared to acquired resistance associated with upregulated *TYMS* expression and gene amplification^[73,86]. These findings suggest that patients with tumors showing TS amplification prior to treatment should not be treated with 5-FU to avoid systemic toxicity without the likelihood of clinical benefit^[73,74].

GENES MODULATING 5-FU METABOLISM

Acquired drug resistance is a principal cause of treatment failure and significantly contributes to cancer-related mortality. In the case of 5-FU, elevated TS is clinically established as a significant cause of drug resistance^[69]. Still, other reasons have been identified, and prominent among them are alterations in genes that modulate 5-FU metabolism, affecting both its degradation and its conversion to FdUMP, the TS inhibitory metabolite^[88] [Figure 1]. A key aspect of 5-FU activity, toxicity, and resistance is mediated by *DPYD*, the gene encoding DPD, the first and rate-limiting step in 5-FU degradation. Atypical 5-FU degradation in liver is associated with serious systemic toxicities^[89]. In many countries, genetic screening is used to identify CRC patients with *DPYD* polymorphisms associated with decreased DPD activity that result in serious 5-FU toxicities unless the administered dose is reduced from standard dosing^[90]. Since DPD is not the only potential cause of altered 5-FU toxicity or sub-optimal therapeutic response, alternative procedures such as therapeutic drug monitoring^[91] are used to quantify patient response on an individualized basis and to customize 5-FU treatment to account for individual variations in drug metabolism.

Intratumor 5-FU catabolism

In addition to the role of *DPYD* polymorphisms in modulating 5-FU toxicity and therapeutic response by affecting systemic drug degradation, intra-tumoral *DPYD* expression is an important factor in modulating therapeutic response. For example, elevated intra-tumoral *DPYD* expression, together with elevated *TYMS*, is associated with poor outcomes in CRC patients treated with 5-FU-based chemotherapy^[66]. A third gene, thymidine phosphorylase (TP; encoded by *TYMP*), was implicated together with *DPYD* and *TYMS* in this study. TP catalyzes a reversible reaction that may produce thymidine or 2'-deoxyuridine, or analogs such as 5-fluoro-2'-deoxyuridine (FdU), from their respective nucleobases (e.g., 5-FU), together with 2'-deoxyribose 1-phosphate. Alternatively, TP degrades thymidine analogs such as FdU to the nucleobase after dephosphorylation by ecto-5'-nucleotidase (NT5E)^[92]. The directionality of TP catalysis depends on intra-tumor substrate/product ratios; however, levels of 2'-deoxyribose 1-phosphate in plasma were also found to be predictive of chemotherapy sensitivity in gastric cancer that included a fluoropyrimidine^[93]. Findings from this study^[66] that elevated *TYMP* levels together with *TYMS* and *DPYD* are associated with decreased response to 5-FU are consistent with TP primarily catalyzing FdU degradation in CRC tumors and resistance to 5-FU is associated with elevated *TYMP* expression. Further, TP-mediated degradation of trifluorothymidine (TFT), the FP component of TAS-102, limits activity resulting in the inclusion of a TP inhibitor, Tipiracil^[94]. TP is also known as platelet-derived endothelial cell growth factor (PDEC GF), a growth factor promoting angiogenesis, and increased PDEC GF/TP is a prognostic factor for poor survival in CRC^[95] that acts through the production of 2'-deoxyribose 1-phosphate from thymidine to promote chemotaxis of vascular endothelial cells^[96].

Anabolic 5-FU metabolism and resistance

The anabolic biosynthesis of FdUMP from 5-FU can occur via either of two major pathways: (1) TP/thymidine kinase (TK) in which FdUMP is produced by 5-FU in two steps; or (2) via a multi-step biosynthetic pathway (UMPS/RNR) that involves UMP synthase (UMPS), uridine kinase (UK), and UMP kinase (UMPK) to produce FUDP. FUDP is a substrate for ribonucleotide reductase (RNR) to produce FdUDP, which can be converted to 5-fluoro-2'-deoxyuridine-5'-diphosphate (FdUDP) through conversion to FdUTP followed by dUTPase cleavage. Enzymes important for the *de novo* biosynthesis of pyrimidines are upregulated in CRC relative to non-malignant tissue^[97], and reduced activities of these enzymes which may occur via altered splicing^[88,98] are associated with 5-FU resistance^[99]. The importance of FdUMP biosynthesis via the UMPS/RNR pathway is demonstrated by studies that identify reduced expression and activity of enzymes in this pathway in 5-FU-resistant cells. Studies in KM12C xenograft tumors showed resistance to 5-FU was associated with decreased RNR activity^[100], while analysis of clinical samples indicated 5-FU resistance was associated with high TS mRNA and low RNR activity^[101].

Collectively, the preponderance of evidence indicates that altered *de novo* thymidine biosynthesis, either by affecting TS expression [Figure 2] or modulating genes important for 5-FU anabolic metabolism to FdUMP [Figure 1], is central to 5-FU resistance. In a few instances, 5-FU resistance is mediated by changes affecting RNA-directed processes including tRNA modifications^[102,103] and rRNA^[22]. However, the clinical significance of RNA-directed activities for 5-FU anti-tumor activity is not yet proven. Further evidence for anabolic metabolism of 5-FU to FdUMP being important for 5-FU resistance comes from studies demonstrating elevated expression of ABCC10^[104] and ABCC5^[105], two ATP binding cassette proteins^[106] that mediate FdUMP efflux from 5-FU-treated cells, cause of 5-FU resistance as does elevated FOXM1, a major transcriptional regulator of ABCC10^[104] [Figure 1].

CELL DEATH SIGNALING IN 5-FU RESISTANCE

The cytotoxicity of multiple anti-cancer drugs, including 5-FU, depends on the activation of programmed cell death that irreversibly commits drug-treated cells to destruction^[107,108]. p53 is considered to be the most highly mutated gene in cancer and it plays a central role in determining if drug-treated cells undergo cell cycle arrest mediated by p53's downstream effector p21, or initiate apoptosis mediated by Bax and other p53-dependent pro-apoptotic genes^[109] [Figure 3]. In the case of established DNA-damaging drugs such as Adriamycin, either p53 or p21 deficiency leads to loss of the G1/S checkpoint and efficient apoptosis^[110]. However, 5-FU deletion of p53 in HCT-116 cells resulted in resistance to apoptosis and 5-FU was less effective towards p53^{-/-} HCT-116 xenografts relative to isogenic tumors that were p53^{+/-}. Furthermore, 5-FU-induced apoptosis both required p53 and was inhibited by exogenous uridine, but not thymidine, consistent with apoptosis induction in response to an RNA-directed process under these treatment conditions^[110]. Studies from our laboratory confirm that p53 deletion causes 5-FU resistance in HCT-116 cells with expression of the R248W gain of function p53 mutation causing greater resistance, while the DNA-directed FP polymer CF10 showed reduced resistance indices relative to 5-FU^[1].

However, even in cell models of CRC, there is variability in the extent that p53 is required for 5-FU-induced apoptosis. Studies report that 5-FU-induced apoptosis occurs in both wild-type and mutant p53 CRC cells with increased expression of the pro-apoptotic Bcl-2 family proteins Bax and Bak identified as being particularly important for 5-FU-induced apoptosis^[111] [Figure 3]. The importance of p53 for regulating 5-FU-induced apoptosis has also been shown to occur via altered chromatin accessibility upon 5-FU treatment that affects the transcription of genes important for apoptosis^[112]. The clinical significance of p53 mutations for 5-FU resistance is not established, although some clinical data indicate *TP53* mutations confer a worse prognosis^[113], while p53 together with Rb and the anti-apoptotic bcl-family member Mcl-1

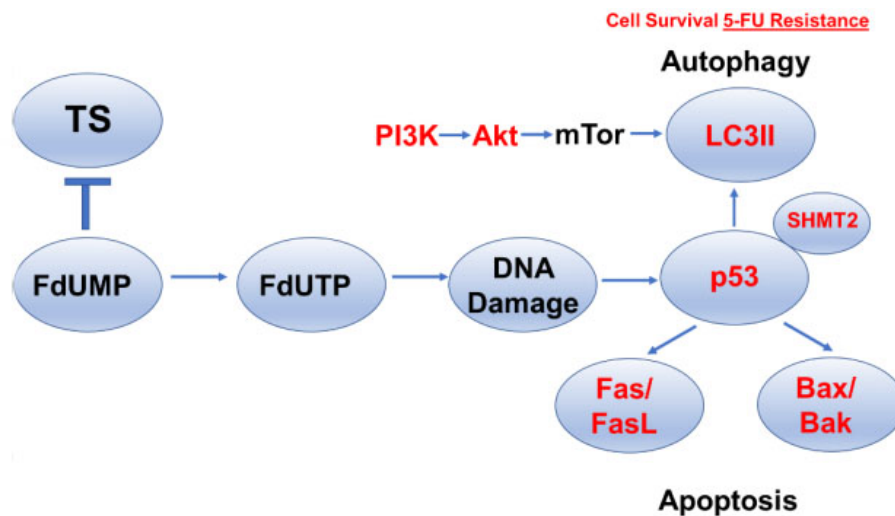


Figure 3. 5-FU Resistance develops from an altered balance between autophagy, which favors cell survival and apoptosis in 5-FU-treated cells. p53 is a key regulator of autophagy/apoptosis balance in 5-FU-treated cells and is modulated by SHMT2. Increased signaling through the PI3K/Akt/mTOR pathway stimulates LC3II and upregulates autophagy to promote cell survival and 5-FU resistance. Induction of apoptosis involves upregulation of the death receptor pathway or mitochondrial pathway for programmed cell death, and downregulation of Fas/FasL or Bax/Bak decreases 5-FU-induced apoptosis and promotes cell survival and 5-FU resistance. 5-FU: 5-Fluorouracil; TS: thymidylate synthase; FdUMP: 5-Fluoro-2'-deoxyuridine-5'-O-monophosphate; FdUTP: 5-fluoro-2'-deoxyuridine-5'-triphosphate; SHMT2: serine hydroxymethyl transferase.

correlated with clinical outcomes in patients with colorectal liver metastases^[114]. Factors other than p53 that are important for activating apoptosis in response to 5-FU treatment include Fas, which was shown to be induced in response to 5-FU treatment in a p53-dependent manner and to regulate apoptosis^[115] [Figure 3]. Houghton and co-workers showed that different CRC cell lines varied in the efficiency of Fas upregulation in response to 5-FU/LV treatment and this correlated with the efficiency of thymidine reversal, indicating 5-FU's DNA-directed effects were cell line dependent and correlated with Fas upregulation and activation of extrinsic apoptosis^[116]. Resistance to 5-FU-induced Fas upregulation and apoptosis can occur via methylation of the Fas promoter, silencing its expression, which can be reversed by 5-Aza deoxycytidine^[117]. Clinical significance for Fas upregulation in 5-FU response was shown by increased Fas expression in biopsy specimens following 5-FU treatment^[118].

AUTOPHAGY IN 5-FU RESISTANCE

Autophagy plays an important role in tumorigenesis and modulating drug response and can either be complementary to apoptosis by promoting drug lethality or protective of the cytotoxic effects of drug treatment^[119]. Activation of the PI3K/Akt/mTOR signaling pathway upregulates autophagosome formation and inhibitors of this pathway modulate drug response, in part, through downregulating autophagy. Treatment of CRC cells with 5-FU was shown to increase LC3-II levels consistent with autophagy activation and co-treatment with 3-methyl adenine (3-MA), a PI3K inhibitor, blocked autophagosome formation and promoted 5-FU-induced apoptosis implicating a protective role for autophagy in 5-FU treatment^[120] [Figure 3]. However, reduced autophagy has also been reported in 5-FU-resistant CRC cells^[121]. Overactivation of the Akt pathway is also associated with 5-FU resistance and Akt inhibition may overcome resistance in some CRC cells^[122], in part by modulating autophagy, while miRNA regulation of Akt deactivation by the PP2A phosphatase complex also regulates 5-FU resistance^[123]. The autophagy inhibitor chloroquine also enhanced the lethality of 5-FU to CRC cells, and in these studies, a serine hydroxymethyl transferase (SHMT2) was shown to regulate 5-FU resistance by binding p53 and inhibiting its degradation [Figure 3]. Overall, SHMT2 was upregulated in CRC tissue compared to non-malignant tissue; however,

patients with low SHMT2 had worse outcomes and this correlated with elevated LC3-II and p62 consistent with autophagy activation in SHMT2-low, 5-FU-resistant CRC^[124]. Interestingly, trifluorothymidine (TFT), the FP used in TAS-102, differed from 5-FU in the extent of activating autophagic survival^[125]. Activation of the p38MAPK pathway is also a determinant in autophagy activation and modulates cellular responses to 5-FU. Inhibition of the p38MAPK pathway correlated with attenuation in 5-FU-mediated apoptosis and promoted CRC cell resistance^[126]. Thus, the p38MAPK signaling pathway modulates 5-FU resistance by regulating the pivot between autophagy and apoptosis^[126]. The autophagy-regulated gene HSPB8 was found to be key in regulating interactions with the tumor microenvironment that regulate 5-FU resistance^[127]. Autophagosome formation is also regulated by Rho kinases^[128], which are implicated in 5-FU resistance^[129]. Curcumin has been studied to inhibit AMPK/ULK1-dependent autophagy with the potential to overcome 5-FU resistance through autophagy activation^[130], and studies from our laboratory indicate curcumin enhances the cytotoxicity of DNA-directed polymeric fluoropyrimidines^[131,132].

CONCLUSION

5-FU remains central to the management of colorectal cancer and it is widely used both in the adjuvant setting to treat CRC patients with limited-stage disease and in combination with chemotherapy regimens to treat mCRC^[4]. The evasion of 5-FU cytotoxicity through intrinsic or acquired resistance in patient tumors contributes to poor outcomes manifest either as a high rate of relapse despite adjuvant chemotherapy or limited survival in the metastatic setting despite multiple lines of chemotherapy that include 5-FU or other FP drugs^[5]. Lack of response to 5-FU chemotherapy is predictable in patients with deficiencies in DNA MMR, or high microsatellite instability, and therapy with 5-FU is contra-indicated in these patients. 5-FU therapy is also predictably toxic in patients with polymorphisms in *DPYD* that limit 5-FU degradation in the liver^[89], and these patients require special management^[90]. Beyond these limited exclusions, there are currently no defined criteria for determining which CRC patients are not likely to be responsive to 5-FU-based therapy. Thus, there is a need to systematically understand the mechanistic basis for 5-FU treatment failure, and an urgent need to develop new approaches for circumventing major causes of 5-FU resistance.

In this review, we have summarized major mechanisms that contribute to 5-FU resistance with an emphasis on those for which available data support clinical significance and that affect the on-target activity of 5-FU (TS inhibition). The causes of colorectal cancer are multi-factorial and involve both lifestyle choice and personalized genetic susceptibility^[133]. Further, response to treatment also depends on multiple factors^[134]. Collectively, the reviewed literature consistently implicates resistance as developing from processes that limit the anabolic metabolism of 5-FU to FdUMP, the TS inhibitory metabolite [Figure 1], and from mechanisms that result in elevated TS activity that results from gene amplification, polymorphisms in the TS promoter, elevated levels of transcription factors that regulate *TYMS* expression, and/or altered nuclear localization of TS [Figure 2]. Dysregulation in the balance between cell survival and programmed cell death is also important in the development of 5-FU resistance [Figure 3]. We have not attempted to review miRNA regulation of *TYMS* ^[61] or other epigenetic causes of 5-FU resistance^[135], and these have recently been reviewed^[136-138]. We also have not directed the reader to literature focused on cellular changes that promote quiescence and stemness to escape the cytotoxic effects of 5-FU^[139,140], although these are likely to be of clinical significance. Further, it is clear that the tumor microenvironment modulates therapy response by processes independent of on-target effects on cancer cells and these processes are not reviewed in this manuscript.

The focus of this review is on acquired resistance to 5-FU with decreased anabolic metabolism and elevated TS activity^[49] as clinically relevant causes. In principle, these causes of 5-FU can be addressed through the translation of next-generation FP drugs that retain the anti-tumor activity associated with targeting TS in

CRC, but that do not require multiple steps of anabolic metabolism required by 5-FU. TAS-102, a combination of the FP trifluorothymidine and a TP inhibitor Tiperacil, shows efficacy in 5-FU-resistant models and activity in refractory metastatic CRC^[141]. TAS-102 activation requires thymidine kinase and it is not a substrate for DPD^[94]. Our laboratory has pioneered the development of DNA-based FP polymers to deliver Fluorodeoxyuridylate, the TS-inhibitory metabolite of 5-FU, without a requirement for metabolic activation. We showed that the prototype FP polymer F10 was, on average, 338-fold more potent than 5-FU across the NCI60 cell line screen^[15,135], but it was still very well tolerated *in vivo*^[142], indicating 5-FU toxicities do not necessarily arise predominantly from on-target effects. The 2nd generation FP polymer CF10 is even more potent and shows promising activity in pre-clinical models of CRC and pancreatic cancer^[16,17]. Further, the cytotoxic mechanism of CF10 results from both inhibiting TS and poisoning of DNA topoisomerase 1 (Top1)^[41,143], which results from a distinct mechanism distinct from current Top1 poisons in clinical use^[144]. In summary, the next generation of FPs has the potential to overcome the established mechanism of resistance for 5-FU reviewed herein that has limited clinical response to FPs to date.

DECLARATIONS

Authors' contributions

Conceptualization: Gmeiner WH, Okechkwu CC

Original draft preparation: Okechkwu CC, Gmeiner WH

Writing, review, editing, visualization, supervision, and funding acquisition: Gmeiner WH

Both authors have read and agreed to the published version of the manuscript.

Availability of data and material

Not applicable.

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Conflicts of interest

Gmeiner WH is an inventor on a pending patent application on CF10 for the treatment of colorectal cancer.

Ethical approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

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