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Tumor microenvironment and epithelial mesenchymal transition as targets to overcome tumor multidrug resistance

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Abstract

It is well established that multifactorial drug resistance hinders successful cancer treatment. Tumor cell interactions with the tumor microenvironment (TME) is crucial in epithelial-mesenchymal transition (EMT) and multidrug resistance (MDR). TME-induced factors secreted by cancer cells and cancer-associated fibroblasts (CAFs) create an inflammatory microenvironment by recruiting immune cells. CD11b+/Gr-1+ myeloid-derived suppressor cells (MDSCs) and inflammatory tumor

associated macrophages (TAMs) are main immune cell types which further enhance chronic inflammation. Chronic inflammation nurture tumor-initiating/cancer stem-like cells (CSCs) induce both EMT and MDR leading to tumor relapses. Pro-thrombotic microenvironment created by inflammatory cytokines and chemokines from TAMs, MDSCs and CAFs is also involved in EMT and MDR. MDSCs are the most common mediators of immunosuppression and are also involved in resistance to targeted therapies, e.g. BRAF inhibitors and oncolytic viruses-based therapies. Expansion of both cancer and stroma cells causes hypoxia by hypoxia-inducible transcription factors (e.g. HIF-1 α) resulting in drug resistance. TME factors induce the expression of transcriptional EMT factors, MDR and metabolic adaptation of cancer cells. Promoters of several ATP-binding cassette (ABC) transporter genes contain binding sites for canonical EMT transcription factors, e.g. ZEB, TWIST and SNAIL. Changes in glycolysis, oxidative phosphorylation and autophagy during EMT also promote MDR. Conclusively, EMT signaling simultaneously increases MDR.

Owing to the multifactorial nature of MDR, targeting one mechanism seems to be non-sufficient to overcome resistance. Targeting inflammatory processes by immune modulatory compounds such as mTOR inhibitors, demethylating agents, low-dosed histone deacetylase inhibitors may decrease MDR. Targeting EMT and metabolic adaptation by small molecular inhibitors might also reverse MDR. In this review, we summarize evidence for TME components as causative factors of EMT and anticancer drug resistance.

Abbreviations: 5-FU, 5-fluorouracil; ABC, ATP-binding cassette; ABCA2/3, ABC transporter, subfamily A 2/3; ABCB1, ABC transporter, subfamily B 1 (MDR1, P-gp); ABCC1/4/5/10, ABC transporter, subfamily C 1/4/5/10; AKT, Akt serine/threonine kinase; AMPK, AMP-activated protein kinase; AXIN 2, axin 1-like (or axis inhibition protein 2); BCNU, bis-chlorethyl-nitrosourea (carmustin); BCRP, breast cancer resistance protein; BMP2, bone morphogenetic protein 2; BRAF, B-Raf proto-oncogene, serine/threonine kinase; BSO, buthionine sulfoximine; CAF, cancer-associated fibroblast; Cav-1/2, caveolin-1/2; CCL, chemokine (C-C motif) ligand; CCL1/2/5/11/15, C-C motif chemokine 1/2/5/11/15; CCR1, CC chemokine Receptor 1; CD8, cluster of differentiation 8; cDDP, cisplatin; CHK1, checkpoint kinase 1; CIC, cancer-initiating cell; CNT3, concentrative nucleoside transporter; COX2, cyclooxygenase 2; CRC, colorectal cancer; CSC, cancer stem-like cell; CSF-1R, colony stimulating factor 1 receptor, CXCL1,

chemokine (C-X-C motif) ligand 1; CXCR4/14, C-X-C chemokine receptor type 4/14; DM, double minute; EGF, epidermal growth factor; EGFL7, epidermal growth factor-like domain 7; EGFR, EGF receptor; EMT, epithelial-mesenchymal transition; EMT-TFs, EMT transcription factors; ENT1, equilibrative nucleoside transporter; ERK, extracellular regulated protein kinase; ETC1, MYB-like transcription factor; FGF, fibroblast growth factor; FOXC2/F2/M1, forkhead box transcription factors C2/F2/M1; G-CSF, granulocyte colony-stimulating factor; GLUT1; glucose transporter 1; GPER, G protein-coupled estrogen receptor; Hbx, hepatitis B virus X protein; HDM2/HDMX, aliases for MDM2, mouse double minute 2 homologue; HES1; hairy and enhancer of split 1; HGF, hepatocyte growth factor; HIF-1 α , hypoxia-induced factor 1 alpha; HK2, hexokinase 2; HMBG1, extracellular high mobility group box 1; HNSCC, head and neck squamous cell carcinoma; HPOC, hybrid protein oxygen carrier; HSR, homogeneously stained region; IFN- β , interferon beta; IL-6/10/17A, interleukin 6/10/17A; IGF, insulin-like growth factor; JNK, c-jun N-terminal kinase; KLF5/8, Krüppel-like factor 5/8; KRAS, Kirsten Ras proto-oncogene; MAPK, mitogen-activated protein kinase; MCP1, monocyte chemotactic protein-1; M-CSF, macrophage colony stimulating factor; MDR, multidrug resistance; MDR1, multidrug resistance gene 1; MDSCs, myeloid-derived suppressor cells; MEK, mitogen-activated kinase kinase; MFG-E8, milk fat globule-epidermal growth factor 8 protein; miRNA/miR, microRNA; M-MDSC, monocytic MDSC; MRP1, multidrug resistance-related protein 1; mTOR, mammalian target of rapamycin; MYC; Myc proto-oncogene; basic helix-loop-helix transcription factor; NMSCs, human mesenchymal stem/stromal cells; NF- κ B, nuclear factor kappa B cells; NOTCH, Notch homologue, translocation-associated (*Drosophila*); NOX1, NADPH oxidase 1; NSCLC, non-small cell lung cancer; oxidative phosphorylation (OXPHOS), oxidative phosphorylation protein; PAK1, p21 (RAC1) activated kinase 1; PDAC, pancreatic ductal adenocarcinoma; PDCD4, programmed cell death 4; PDGF, platelet-derived growth factor; PGE2, prostaglandin E2; P-gp, P-glycoprotein; PI3K, phosphatidylinositol-4,5-bisphosphate 3-kinase; PMN-MDSC polymorphonuclear MDSC; pS6, phospho ribosomal protein S6; pSTAT3, phospho-signal transducer and activator of transcription 3; RNAi, RNA interference; RTK, receptor tyrosine kinase; SASP, senescence-associated secretory phenotype; SDF-1 α , stromal cell-derived factor-1 alpha; shRNA, small hairpin RNA; siRNA, small interfering RNA; SIRT1, sirtuin 1; SLUG, Snail 2 zinc finger transcription factor; SMAD, human homology of Mad and Sma; SNAIL1, Snail 1 zinc finger transcription factor; SOX2, Sry-related high mobility group (HMG) box 2;

STAT1/3, signal transducer and activator of transcription 1/3; TAM, tumor-associated macrophages; TGF- β , tumor growth factor β ; TIAM, T-lymphoma invasion and metastasis-inducing protein 1; TKI, tyrosine kinase inhibitor; TME, tumor microenvironment; TNBC, triple negative breast cancer; TNF- α , tumor necrosis factor α ; TRAIL, tumour necrosis factor (TNF)- α -related apoptosis-inducing ligand; TWIST1, class A basic helix-loop-helix transcription factor 1; UCB, urothelial cancer of the bladder; VEGF, vascular endothelial growth factor; VEGFR, VEGF receptor; WNT1, wingless Int-1 signal transducer; ZEB1, zinc finger E-box binding homeobox 1.

Key words: Chemotherapy; Hypoxia; Inflammation; Microenvironment, Multidrug resistance; Small molecules; Targeted therapy,

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1 Introduction

Activation of the epithelial-mesenchymal transition (EMT) program in cancer cells results in increased invasive and metastatic properties as well as multidrug resistance (MDR). Factors provided by the tumor microenvironment (TME) play a major role in EMT, metastasis and MDR phenotype. MDR due to EMT and metastasis could be caused by (1) transmembrane pumps belonging to the ATP-binding cassette (ABC transporter) family (2) mechanisms independent of ABC transporters. Owing to the multifactorial nature of MDR, targeting one mechanism is not sufficient to overcome the resistance (Assaraf et al., 2019; Cui et al., 2018; Gacche and Assaraf, 2018; Gonen and Assaraf, 2012; Li et al., 2016b; Livney and Assaraf, 2013; Milman et al., 2019; Niewerth et al., 2015; Shapira et al., 2011; Vasconcelos et al., 2019; Wijdeven et al., 2016; Zhitomirsky and Assaraf, 2016; Zhong and Virshup, 2020). Although ABC transporters have been extensively reported as a clinically relevant mechanism of MDR (Assaraf, 2006; Gottesman et al., 2002; Li et al., 2016b; Robey et al., 2007), the effectiveness of combination therapy with ABC transporter inhibitors in clinical trials were limited (Linn et al., 1995; Middleton et al., 2013; Werooha et al., 2011). Hence other drug-resistance mechanisms also have to be taken into account to overcome therapeutic failure in cancer patients. There is mounting evidence demonstrating a significant role of factors originating from tumor microenvironment (TME) for both responsiveness or resistance to various structurally and mechanistically unrelated anticancer drugs. The persistent production of inflammatory factors has been reported in TME-mediated EMT, metastasis and chemotherapy resistance (Acharyya et al., 2012; Bunt et al., 2006; Hartmann et al., 2005) (Gao et al., 2020; Krchniakova et al., 2020; Shaked, 2019). This may be due to inflammation-induced expansion and recruitment of macrophages and CD11b⁺/Gr-1⁺ myeloid-derived suppressor cells (MDSCs) (Szebeni et al., 2017; Xu et al., 2017) as well cancer-

associated fibroblasts (CAFs) (Bharti et al., 2016). Specifically, inflammatory cytokines such as tumor growth factor β (TGF- β) and interleukin 6 (IL-6) as well as chemokines that directly or indirectly induce EMT and metastasis are also involved in MDR (Bharti et al., 2016; Ghandadi and Sahebkar, 2016).

In the first part of the review, we therefore discuss the role of tumor-associated macrophages (TAMs), MDSCs and CAFs on MDR. In the second part of the review, we discuss the mechanisms of EMT-related drug resistance at the cellular and transcriptional level. We summarize the findings on the transcriptional factors and cell metabolism changes that are causative of EMT and which sustain the MDR phenotype in cancer cells. Finally, we focus on the indirect mechanisms of hypoxia-induced MDR and the relevance of ABC efflux transporters in this context.

2 Tumor-associated macrophages (Shapira et al., 2011)

2.1 Function of tumor-associated macrophages

TAMs are derived from circulating monocytes recruited within the TME by chemokines such as (C-C motif) ligand-2 (CCL-2), CCL-3, CCL-4, CCL-5, CCL-7, CCL-8, CXCL-12 and cytokines, including vascular endothelial growth factor (VEGF), platelet-derived growth factor (PDGF), macrophage colony-stimulating factor (M-CSF), and interleukin (IL)-10 (Allavena et al., 2008; Cassetta et al., 2019; Chen et al., 2019; Condeelis and Pollard, 2006; Dudas et al., 2020; Li et al., 2020; Li et al., 2019; Lin et al., 2019; Mantovani et al., 2004; Murdoch et al., 2008; Sarode et al., 2020; Yamaguchi and Perkins, 2020; Zhang et al., 2020; Zins and Abraham, 2020). Macrophages are actively recruited to the TME from the bone marrow (Dalton et al., 2017). TAMs are abundant components of the TME and are highly plastic in nature. Macrophage phenotypes present in the TME represent a continuum and cannot be satisfactorily captured with the M1–M2 dichotomy, as previously reviewed in detail (Ginhoux et al., 2016; Hsieh and Wang, 2018). Similarly, the tumor-promoting role of TAMs has been extensively described (De Palma and Lewis, 2013; Li et al., 2020; Lin et al., 2019; Ruffell et al., 2012; Sarode et al., 2020; Zins and Abraham, 2020). Emerging evidence demonstrates that TAMs are also important components of microenvironment-related drug resistance.

Resistance to chemotherapy. Platinum-containing chemotherapy induced differentiation of monocytes into M2-like macrophages by enhancing the secretion of IL-6 and prostaglandin E2 (PGE2) from cervical and ovarian cancer cell lines, thus indirectly inducing chemoresistance

(Dijkgraaf et al., 2013). Accordingly, the prevention of TAM infiltration by an antibody against placental growth factor enhanced the efficacy of chemotherapy (Fischer et al., 2007).

Resistance to targeted therapies and immunotherapy. Receptor tyrosine kinase inhibitor (TKI) sorafenib induces recruitment of TAMs, which leads to drug resistance. Depletion of TAMs by zoledronic acid significantly enhanced the anti-tumor effect of sorafenib (Zhang et al., 2010). The macrophage levels within the tumor tissue increased with the emergence of resistance towards anti-VEGF therapy and depletion of macrophages restored sensitivity of tumors that were initially resistant to anti-VEGF therapy (Dalton et al., 2017). Similarly, TAM depletion restored T cell migration and infiltration into tumor islets. It also improved the efficacy of anti-PD-1 immunotherapy demonstrating that TAMs are responsible for intrinsic resistance to immunotherapy (Peranzoni et al., 2018).

2.2 Mechanisms of TAM-related drug resistance

Role of IL-6. Several cytokines, chemokines and growth factors secreted by TAMs are likely to mediate MDR. The pro-inflammatory cytokine IL-6 was secreted by TAMs (Xu et al., 2014) and induced signal transducer and activator of transcription 3 (STAT3) activation in cancer cells, leading to therapeutic resistance (Borsellino et al., 1995; Gritsko et al., 2006; Wu et al., 2013) (Diesendruck and Benhar, 2017; Kon and Benhar, 2019; Yin et al., 2019; Yin et al., 2017). IL-6 contributed markedly to poor therapeutic outcome, tumor relapse and aggressive tumor growth (Chang et al., 2013; Ghandadi and Sahebkar, 2016; Grivennikov and Karin, 2008; Kumari et al., 2016; Wu et al., 2013). Specifically, IL-6 induced immunosuppression in patients with advanced cancers (Bromberg and Wang, 2009; Grivennikov et al., 2010) and conferred therapeutic resistance in patients with prostate cancer (Culig and Pühr, 2012; Wu et al., 2013). IL-6-induced resistance was also due to increased cancer stem cell populations, which are mainly responsible for tumor refractoriness (Bharti et al., 2016). IL-6 was a potent inducer of resistance against TKIs directed against epidermal growth factor receptor (EGFR) in non-small cell lung cancer (NSCLC) (Yao et al., 2010) due to STAT3 activation (Yu et al., 2014; Zhong et al., 1994). Similarly, stromal cell-derived factor 1 α (SDF-1 α)-induced IL-6 upregulation mediated chemoresistance and apoptosis in multiple myeloma cells (Liu et al., 2019b). A neutralizing antibody for IL-6 increased the effectiveness of chemotherapy and gefitinib in various tumor models, including trastuzumab-resistant tumors (Zhong et al., 2016).

TAMs and cancer stem cells. Heterogeneous signals from the TME nurture tumor-initiating/cancer stem-like cells (CSCs), which are responsible for therapy resistance and tumor relapses (Chen et al., 2018; Colak and Medema, 2014; Paldino et al., 2014; Rycaj and Tang, 2014; Wang et al., 2014) (Assaraf et al., 2019; Leonetti et al., 2019b). TGF- β is one of the master players of stemness and is highly expressed in TAMs (Chen et al., 2018; Fan et al., 2014). It may also contribute to TAM-induced resistance towards anti-angiogenic treatments (Qin et al., 2015; Rolny et al., 2011). TAMs activated CSC properties in hepatocellular carcinoma by TGF- β 1-induced EMT (Fan et al., 2014), which may led to resistance towards chemo- and targeted therapies (Dal Bo et al., 2020). For instance, TGF- β is primarily involved in erlotinib resistance, EMT and increased activation of the IL-6 axis in drug resistant bronchoalveolar metastatic carcinoma H1650 cells (Yao et al., 2010). Inhibition of the TGF- β activity using shRNA and TGF- β inhibitors increased the efficiency of sorafenib (Kang et al., 2017) in hepatocellular carcinoma. Silencing of TGF- β 1 enhanced sensitivity of A549/DDP cells to cisplatin through the reversal of EMT (Wang et al., 2018). TAMs also provide survival signals to CSCs. Specifically, TAMs release milk fat globule-epidermal growth factor 8 protein (MFG-E8), which protected lung and colon CSCs from the cytotoxic effects of cisplatin. Similar to IL-6, MFG-E8 activated STAT3 in CSCs, enhancing their drug resistance (Jinushi et al., 2011). In accordance, TAM depletion also improved antitumor T cell responses and the efficacy of chemotherapy in a pancreatic cancer model (Mitchem et al., 2013).

Growth factors secreted by TAMs. Growth factors secreted by TAMs may also lead to MDR. Specifically, TAMs are a significant source of the epidermal growth factor (EGF) and insulin-like growth factor (IGF) in tumor tissues (Ireland et al., 2018; Vlaicu et al., 2013). EGF-triggered resistance to sunitinib, vandetanib, and sorafenib by transducing bypass survival signaling through ERK and AKT via activation EGFR in lung cancer cells (Chang et al., 2017) (Leonetti et al., 2019a; Leonetti et al., 2019b). In addition, blocking of IGF increased the efficacy of paclitaxel, a chemotherapeutic agent commonly used for the treatment of invasive breast cancer (Ireland et al., 2018). VEGF, a pro-angiogenic growth factor, is highly expressed in TAMs (Colegio et al., 2014; Qian and Pollard, 2010). Anti-VEGF therapy with bevacizumab (Cohen et al., 2009; Friedman et al., 2009; Lu-Emerson et al., 2015) or multiple RTK inhibitor sunitinib failed to improve survival

in patients with recurrent glioblastoma multiforme (Grisanti et al., 2019). This is likely due to M2-like macrophages, which promoted tumor angiogenesis and vascular abnormalization (Mazzieri et al., 2011; Qin et al., 2015; Rolny et al., 2011). TAMs, resistant to anti-VEGF therapy, showed increased secretion of alternative pro-angiogenic cytokines and chemokines, including platelet-derived growth factor (PDGF) and granulocyte-colony stimulating factor (G-CSF). The expression of VEGFR in macrophages was lower in patients who did not respond to anti-VEGF therapy compared to responders. Hence, VEGFR expression in macrophages may be a predictor of response to anti-angiogenic therapy (Dalton et al., 2017). Hence, increased expression of PDGF and G-CSF in macrophages is likely to be involved in drug resistance.

Other factors involved in drug resistance. TAMs induced gefitinib resistance in head and neck squamous carcinoma cells (HNSCC) by releasing chemokine (C-C motif) ligand 15 (CCL-15), a chemokine mainly expressed in the intestine and liver (Li et al., 2016d). Specifically, chemokine CCL-15 decreased the sensitivity to gefitinib through CC chemokine receptor 1 (CCR1) and NF- κ B pathway signaling. Furthermore, serum CCL-15 levels in HNSCC patients were significantly correlated with patient prognosis (Yin et al., 2019).

TAMs mediated the suppression of T cells *in vitro* and *in vivo* in FVB PyMT mice (DeNardo et al., 2011). In addition, TAMs were responsible for the T cell-excluded tumor phenotype. Specifically, TAMs prevented migration and invasion of tumor nests containing CD8⁺ T cells (Peranzoni et al., 2018), which are required for the efficiency of immunotherapy. Defective T cell migration into and within tumors was a determinant of resistance to cancer immunotherapy (Melero et al., 2014). Melanoma tumors of patients, who responded well to treatment with anti-PD-1 antibodies were characterized by the presence of CD8⁺ T cells in the core of the tumor in contact with malignant cells (Herbst et al., 2014). Conversely, tumors of patients, who did not respond to anti-PD-1 antibodies either were devoid of T cells or contained T cells preferentially located around tumor cell regions (Herbst et al., 2014). Macrophage depletion by PLX3397 in tumor-bearing mice increased the infiltration of tumor nests with CD8⁺ T enhancing anti-tumoral effects of anti-PD-1 treatment (Peranzoni et al., 2018).

In conclusion, TAMs represent an important component of TME-related drug resistance as illustrated in Figure 1. Therefore, strategies to deplete TAMs or block cancer-induced M2-like macrophage programming, bear the potential to increase treatment efficiency and to decrease

resistance to anti-cancer agents (Coussens et al., 2013; Hagemann et al., 2008; Jaiswal et al., 2010). Specifically combination of TAM depletion with dendritic cell immunotherapy generated robust and durable antitumor immunity. Depletion of TAMs using colony stimulating factor 1 receptor (CSF-1R) kinase inhibitor PLX3397 (pexidartinib) alone, however, did not improve survival. These results demonstrated that decreasing local TAM-mediated immune suppression was only effective in the presence of immune activation (Dammeijer et al., 2017). Given the fact that the phenotype of TAMs varied and that under certain conditions TAMs cooperated with T cells to promote tumor regression (Saha et al., 2017; Thoreau et al., 2015), the complete depletion of macrophages may exert unwanted consequences. Several alternative approaches were under evaluation, *e.g.* reprogramming macrophages toward an antitumor phenotypic state (Schultze, 2016). Nevertheless, clinical studies are in progress in several solid tumor types, where macrophages are targeted by CSF-1R inhibitors (Cannarile et al., 2017). It can be expected that these clinical studies will yield better approaches targeting TAMs to reverse MDR and tumor progression.

3 Myeloid-derived suppressor cells in the tumor microenvironment

3.1 Function of myeloid-derived suppressor cells

Tumor-infiltrating myeloid-derived suppressor cells (MDSCs) are the most common mediators of immunosuppression in tumors. They originate from immature myeloid cells that fail to differentiate into granulocytes, macrophages, or dendritic cells. MDSCs co-express Gr-1 and CD11b myeloid lineage differentiation markers in mouse as well as either or both of the common myeloid markers CD33 or CD11b in cancer patients (Gabrilovich et al., 2012; Talmadge and Gabrilovich, 2013) (Hsu et al., 2019; Zhang et al., 2018b). MDSCs consist of two large groups of cells: granulocytic or polymorphonuclear (PMN-MDSCs) and monocytic MDSCs (M-MDSCs). PMN-MDSCs are phenotypically and morphologically similar to neutrophils, whereas M-MDSCs are more similar to monocytes (Gabrilovich et al., 2007; Gabrilovich et al., 2012; Sasidharan Nair et al., 2020). Both the monocytic and the granulocytic subsets display immunosuppressive activity in tumors (Di Mitri et al., 2015). The existence of a third small population of MDSCs represented by cells with colony forming activity was demonstrated in human studies (Dumitru et al., 2012).

Inflammatory cytokines and chemokines mediate the recruitment and expansion of MDSCs. Specifically IL-6, CXCL1, CCL5, CCL2/monocyte chemoattractant protein-1 and CXCL12 caused

accumulation and expansion of MDSCs (Acharyya et al., 2012; Blattner et al., 2018; Gabrilovich et al., 2012; Hartmann et al., 2005; Hawila et al., 2017; Hsu et al., 2015; Huang et al., 2007; Panka et al., 2013; Schlecker et al., 2012; Veglia et al., 2018; Xu et al., 2017; Zhang et al., 2013). Among the other chemokines/receptors, CXCR2 and CX3CR1 (the cognate receptor for CX3CL1) activation mediated granulocytic MDSC trafficking into tumors (Hart et al., 2014). Among the chemokine receptors, CCR5 expressed on MDSCs in melanoma patients played an important role for their recruitment to the TME by CCR5 ligands (CCL3, CCL4 and CCL5) ((Blattner et al., 2018; Hawila et al., 2017). CCR5⁺ MDSCs displayed higher immunosuppressive potential than their CCR5⁻ counterpart (Blattner et al., 2018), pointing to the heterogeneous nature of MDSCs. MDSCs suppressed both innate and adaptive immunity in various cancer types (Kumar et al., 2016; Ostrand-Rosenberg and Fenselau, 2018; Parker et al., 2015; Tcyganov et al., 2018; Umansky and Sevko, 2012). Hence, MDSCs hindered the anti-cancer activity of immunotherapies including immune checkpoint inhibitors (Weber et al., 2018). Growing evidence also demonstrated, however, that MDSCs were involved in resistance to therapeutic approaches other than immunotherapies as explained below. Factors involved in the expansion and recruitment of MDSCs as well as inflammatory factors secreted by MDSCs were likely to mediate chronic inflammation (Meyer et al., 2011) and consequently MDR.

Resistance to anti-angiogenic therapy. The frequent emergence of resistance to anti-angiogenic therapy is a major hindrance towards curative cancer therapy (El Alaoui-Lasmali and Faivre, 2018; Gacche and Assaraf, 2018; Haibe et al., 2020). Inherent anti-VEGF refractoriness was associated with infiltration of the tumor tissue by CD11b⁺Gr1⁺ myeloid cells. Specifically, combining anti-VEGF treatment with a monoclonal antibody that targets myeloid cells inhibited growth of refractory tumors more effectively than anti-VEGF therapy alone (Shojaei et al., 2007a). Similarly, increased MDSCs and related inflammatory chemokines within the TME enhanced angiogenesis and metastasis and were involved in resistance to small molecule inhibitors of VEGFR2 (Ebos et al., 2009; Shojaei et al., 2007b; Yang et al., 2004; Yang et al., 2008). Inhibition of SDF-1 production with the HDM2/HDMX antagonist MI-319 prevented the emergence of resistance to small molecular inhibitors of VEGFR2 in renal cell carcinoma xenograft tumors and inhibited the influx of MDSCs (Panka et al., 2013).

Resistance to targeted therapies. MDSCs also mediated resistance to targeted therapies such as BRAF inhibitors (vemurafenib and dabrafenib) in melanoma (Steinberg et al., 2017). Classically, reactivation of the MAPK pathway is involved in tumor resistance to BRAF inhibitors ((Johnson et al., 2015). However, acquired resistance to BRAF inhibitors still developed in the presence of MEK inhibitors (Long et al., 2014). Resistance to therapy was, in part, due to extrinsic factors present in the TME, including chemokines such as CCL2. This chemokine is also referred to as monocyte chemoattractant protein-1 (MCP-1) ((Knight et al., 2013), which recruits MDSCs (Steinberg et al., 2017). CCL2 was also associated with anti-PD-1 resistance (Hugo et al., 2016; Peng et al., 2016) and was connected to increased tumorigenesis in different tumor types (Yao et al., 2012; Zollo et al., 2012).

Resistance to oncolytic viruses-based therapies. MDSCs are critical determinants of resistance to oncolytic viruses-related therapies (Hou et al., 2016). Oncolytic viruses are vectors designed to selectively replicate in, and destroy cancer cells. Various treatments based on oncolytic viruses are currently undergoing clinical testing (Andtbacka et al., 2016; Heo et al., 2013). TME was also involved in the anti-tumoral effects of oncolytic viruses, since oncolytic virus-mediated immunotherapeutic activity was more important than oncolytic virus-related cytotoxicity (Hou et al., 2016). COX2-mediated production of prostaglandin E2 (PGE2) is one of the key determinant of MDSC tumor infiltration (Fujita et al., 2011; Kalinski, 2012; Obermajer et al., 2011; Rodriguez et al., 2005). In accordance, inhibiting PGE2, the main product of cyclooxygenases in myeloid and stromal cells, reduced MDSC within TME and re-sensitized resistant tumors to therapy with oncolytic viruses (Hou et al., 2016).

Resistance to chemotherapy. Although many studies documented an indirect contribution of MDSCs to drug resistance (see below), a recent study demonstrated the direct contribution of MDSCs to chemoresistance. Specifically, depletion of MDSC by administration of an anti-Gr-1 antibody sensitized 5-fluorouracil-resistant H22 hepatoma to chemotherapy in immunocompetent C57BL/6N mice(Xu et al., 2017) (Xu et al., 2017).

3.2 Mechanisms of MDSC-related drug resistance

Granulocyte colony-stimulating factor (G-CSF), a well-known hematopoietic cytokine regulating granulopoiesis, is required for progenitor cells to differentiate into granulocytic lineage, such as neutrophils, eosinophils and basophils (Natori et al., 2002). G-CSF and its receptor (G-CSFR) were aberrantly expressed in various human tumors including gastric and colon (Morris et al., 2014), bladder (Chakraborty and Guha, 2007), pancreatic (Liongue et al., 2009), ovarian and cervical cancers (Savarese et al., 2001). G-CSF production was associated with poor clinical outcome and MDR (Kawano et al., 2015; Kowanetz et al., 2010; Shojaei et al., 2009). As shown in tumor cell lines, *in vivo* models, and clinical samples of cervical carcinoma, G-CSF expression was significantly associated with increased number of MDSCs, decreased survival, and chemoresistance. The depletion of MDSC by splenectomy or the administration of anti-Gr-1 antibody, sensitized G-CSF-producing cervical cancer cells to cisplatin (Kawano et al., 2015). Similarly, in a colitis-associated cancer, G-CSF promoted MDSCs survival and activation through the STAT3 signaling pathway. Inhibition of G-CSF activity with monoclonal antibody treatment reduced MDSC accumulation and decreased size and number of the tumors (Li et al., 2016c).

Increased coagulation: A pro-thrombotic microenvironment revealed enhanced inflammatory responses (Levi et al., 2004; Vendramini-Costa and Carvalho, 2012) and induced chemoresistance (Nierodzik and Karpatkin, 2006), as observed following cytotoxic treatment by cisplatin and cyclophosphamide (Alexander et al., 2015; Alexander et al., 2016; Swystun et al., 2011). A cross-talk between coagulation system and an inflammatory microenvironment further heightened the inflammatory activity (Danckwardt et al., 2011; Levi et al., 2004). Thrombin increased TGF- β release and activation (Alexander et al., 2015) leading to chronic inflammation, accumulation and expansion of MDSCs (Bunt et al., 2006; Levi and van der Poll, 2010). Accordingly, dabigatran etexilate, a direct thrombin inhibitor and cisplatin co-treatment exhibited significantly greater anti-tumor efficacy than cisplatin alone. In a murine ovarian cancer model, co-treatment decreased MDSCs and pro-tumorigenic cytokines leading to a concomitant increase in CD8⁺ effector T-cell activity (Levi and van der Poll, 2010). Similarly, in breast cancer, dabigatran etexilate and cyclophosphamide co-treatment reduced the accumulation of immunosuppressive MDSCs and TGF- β and induced markedly more potent anti-tumor and anti-metastatic effects (Alexander et al., 2016).

Transforming growth factor β 1 (TGF- β 1). MDSCs are an abundant source of TGF- β 1 production within TME (Bierie and Moses, 2010). TGF- β 1 secreted by MDSCs (Colak and Ten Dijke, 2017; Oshimori et al., 2015) may facilitate resistance to a wide range of anti-cancer agents. TGF- β 1 inhibited antigen-specific CD8⁺ T-cell effector functions as demonstrated in melanoma (Ahmadzadeh and Rosenberg, 2005) and increased the number and immunosuppressive capacity of regulatory T cells (Hu et al., 2018; Huber et al., 2004; Marie et al., 2005; Polanczyk et al., 2019). TGF- β also abolished T cell activation by inhibiting the DC maturation processes (Weber et al., 2005), which thus impeded anti-tumor immune response. In addition, TGF- β -induced EMT and enrichment of CSCs as well as immune suppression were likely to be responsible for drug-resistance and metastasis ((Daroqui et al., 2012; Erin et al., 2018a; Kajiyama et al., 2007; Liu et al., 2017a; Mallini et al., 2014; Singh and Settleman, 2010; Wang et al., 2018). These effects of TGF- β 1 play a significant role in resistance to targeted therapies such as TKI (Huang et al., 2012; Kang et al., 2017; Weber et al., 2018) and to cytotoxic agents (Kajiyama et al., 2007; Mallini et al., 2014; Singh and Settleman, 2010). Hence, MDSCs by secreting TGF- β were involved in MDR. Reciprocally, TGF- β may mediate MDSCs-induced resistance to immune-check point inhibitors (Weber et al., 2018).

Other factors: In a hepatocellular carcinoma model, cancer cell-derived IL-6 activated MDSCs-mediated chemoresistance, which was prevented by an IL-6-neutralizing antibody or by depleting MDSCs (Xu et al., 2017) (Xu et al., 2017). MDSC were also a source for the production of the EF-hand calcium-binding proteins S100A8 and S100A9 (Sade-Feldman et al., 2013; Turovskaya et al., 2008). S100A8 and S100A9 are pro-inflammatory factors, which were associated with chemoresistance (Wang et al., 2013; Yang et al., 2014). Besides certain chemotherapeutic and targeted therapies, commonly used adjuvants (*i.e.* corticosteroids) also induced MDSCs (Varga et al., 2008). These results explained the faster progression of tumors in patients treated with glucocorticoids for prolonged periods (Karagas et al., 2001).

3.3 Therapeutic approaches targeting MDSCs

Therapies targeting MDSCs, and inflammatory factors activating MDSCs or secreted from MDSCs (Weber et al., 2018) are warranted as adjunct therapy to directly treat malignant tumors. Certain cytotoxic agents such as paclitaxel (Sevko et al., 2013) or gemcitabine (Eriksson et al., 2016),

decreased MDSC frequency and increased therapeutic efficiency. Inhibiting STAT3, a main regulator of MDSC immunosuppressive activity (Condamine and Gabrilovich, 2011; Kumar et al., 2016; Vasquez-Dunddel et al., 2013), may also prevent or attenuate the development of drug resistance.

PGE2 is a main product of cyclooxygenases in myeloid and stromal cells and is one of the key mediators of immunopathology in cancer (Kalinski, 2012). PGE2 was shown to be necessary for the development of suppressive TAMs (Heusinkveld et al., 2011; Stolina et al., 2000) and MDSC (Fujita et al., 2011; Obermajer et al., 2011; Sinha et al., 2007). In addition, MDSCs expressed high levels of COX2 and were a major source of PGE2 secretion in human cancer (Obermajer et al., 2011). Hence, inhibition of PGE2 production using non-selective or COX2-selective blockers as well as selective antagonists of PGE2 receptors (Ganesh et al., 2018; Markovic et al., 2017) is likely to prevent MDSC-related MDR.

Lenalidomide, an immune modulatory compound, was included in several current regimens to treat myeloma due to its beneficial efficacy and safety profile (Bartlett et al., 2004; Rollig et al., 2015). Lenalidomide alone decreased the number of systemic MDSCs and regulatory T cell in tumor-bearing but not in naive mice (Sakamaki et al., 2014). Lenalidomide also induced strong anti-inflammatory effects (Yamamoto et al., 2019), which may have been responsible for the suppression of MDSCs, since inhibition of inflammation using CD200 mimetics also decreased MDSCs (Erin et al., 2015; Erin et al., 2018b) and increased the therapeutic potential of doxorubicin (Erin et al., 2020).

Inhibition of mTOR activity with everolimus is a relatively new therapeutic approach for various carcinomas, including breast, prostate, neuroendocrine tumors and renal cell carcinoma (Deniz et al., 2019; George et al., 2019; Huijts et al., 2019; Larouche et al., 2019; Schmid et al., 2019; Wen et al., 2019). Everolimus in combination with metronomic cyclophosphamide led to a reduction in MDSCs and a sustained level of the CD8⁺ T-cell population in patients with prostate cancer. This result further demonstrated that inhibition of MDSC activity also enhanced the efficacy of cytotoxic chemotherapy (Huijts et al., 2019).

Decitabine, a demethylating agent with immunoregulatory effects, depleted MDSCs *in vivo* by inducing apoptosis at relatively low doses (Zhou et al., 2017) and inhibited myeloma growth *in vivo* (Zhou et al., 2019). Histone deacetylase inhibitors are another class of drugs for various carcinomas, including hematological malignancies as well as common solid tumors (lung, breast

and prostate cancer) (Halsall and Turner, 2016). Histone deacetylase inhibitors decreased accumulation of MDSCs in the spleen, blood and tumor bed and increased the proportion of cytotoxic T cells in Balb-c mice with 4T1 mammary tumors (Wang et al., 2017a). This result demonstrated that these group of drugs may also enhance anti-tumor effects of chemotherapeutics in tumors abundantly infiltrated with MDSCs. The role of MDSCs in MDR is illustrated in Figure 2.

4 Cancer-associated fibroblasts

4.1. The functions of cancer-associated fibroblasts

Apart from the tumor itself, the TME is a heterogeneous population of different cells. The tumor recruits endogenous stromal cells in its neighbourhood (Bussard et al., 2016; Cammarota and Laukkanen, 2016). These cells promoted extracellular matrix remodelling, angiogenesis, cellular migration, invasion and drug resistance. Furthermore, these cells generated an environment, which was capable of evading the immunosurveillance through production and secretion of various chemokines, cytokines and growth factors (Liu et al., 2019b). Tumor-associated stromal cells arose from at least six distinct cellular origins: fibroblasts, pericytes, bone marrow-derived mesenchymal stem cells (MSCs), adipocytes, endothelial cells that underwent EMT, or tumor cells that underwent EMT. The transition of these cells occurs by soluble factors, microRNAs (miRNAs) or exosomes, and results in the formation of the different cell subtypes: CAFs, cancer-associated adipocytes, or cancer-associated endothelial cells.

4.2 Correlation of cancer-associated fibroblasts with multidrug resistance and metastasis

There is mounting evidence for the role of CAFs in tumor drug resistance and metastasis (Chen and Song, 2019; Fiori et al., 2019; Kadel et al., 2019; Liu et al., 2019b)The concept of EMT has gained tremendous attention in cancer research. Here, we are discussing the evidence showing the role of CAFs and related events, as well as possible key molecules, which are important for both, drug resistance and metastasis. These molecules are either produced by CAFs directly or secreted from tumor cells influencing further CAFs or other cells in the stroma, which reprogram them to become supporters of tumor growth and progression (Kadel et al., 2019). For example, cell-free medium collected from CAF cultures induced EMT in human head and neck carcinoma cells enhancing their viability as well as decreasing their sensitivity to cisplatin treatment (Steinbichler

et al., 2016). Activated gastric CAFs correlated with poor prognosis of cancer patients and contributed to the malignant phenotype and the development of resistance to 5-fluorouracil by paracrine signalling in gastric cancer (Ma et al., 2018).

There are different types of molecules that are involved in chemoresistance and promotion of metastasis including chemokines, cytokines, membrane proteins, and chromatin proteins (Figure 3). Caveolin-1 (Cav-1) plays a role in tumorigenesis via its various functions in lipid transport, membrane trafficking, gene regulation, and signal transduction (Koleske et al., 1995) (Ketteler and Klein, 2018; Lamaze and Torrino, 2015). It is down-regulated in CAFs from human breast cancer compared to normal fibroblasts isolated from the same patient (Mercier et al., 2008). Breast cancer patients lacking stromal Cav-1 benefit from tamoxifen therapy, since Cav-1 acts as a tumor suppressor in the stromal environment. More specifically, loss of Cav-1 in CAFs predicted early tumor recurrence, lymph node metastasis, and tamoxifen-resistance (Witkiewicz et al., 2009). In addition, Cav-1-deficient stromal fibroblasts contribute to tumor growth and angiogenesis by providing energy-rich metabolites in a paracrine fashion. This phenomenon has been termed *reverse Warburg effect* (Pavlides et al., 2009) (Martinez-Outschoorn et al., 2014; Wilde et al., 2017). A two-component human tumor xenograft model system, was established in nude mice, in which the animals were co-injected with human MDA-MB-231 breast cancer cells and wild-type versus Cav-1^(-/-) deficient stromal fibroblasts. These mice were treated with glycolysis inhibitors, which were functionally blocking the positive effects of Cav-1-deficient stromal fibroblasts on breast cancer growth. Thus, pharmacologically induced metabolic restriction (by treatment with glycolysis inhibitors) may be a promising new therapeutic strategy for breast cancers that lack stromal Cav-1 expression (Bonuccelli et al., 2010). Furthermore, CAFs of MCF-7 breast cancer lacking caveolin-2 (Cav-2) better induced EMT, indicating that CAFs contributed to a more malignant phenotype. Their role in therapy resistance should therefore be considered for breast cancer treatment (Soon et al., 2013). A possible role of another membrane located protein, β 1-integrin, in anti-hormone therapy response in breast cancer patients was suggested too. G protein-coupled estrogen receptor (GPER) and epidermal growth factor receptor/extracellular regulated protein kinase (EGFR/ERK) signalling upregulated β 1-integrin expression and activated downstream kinases, which contributed to CAF-induced cell migration and EMT in tamoxifen-resistant MCF-7R cells. GPER contributed to tamoxifen resistance by interaction with the TME in a β 1-integrin-dependent pattern ((Yuan et al., 2015).

Conditioned media collected from CAFs isolated from human breast cancer tissues significantly induced migration of MDA-MB-231 breast cancer cells and protected them from doxorubicin-induced cell death probably by extracellular high mobility group box 1 (HMBG1) protein released from dying cancer cells (Amornsupak et al., 2014). Furthermore, lung fibroblasts reduced melanoma sensitivity to the BRAF inhibitor vemurafenib. In the presence of fibroblasts, the melanoma cells acquired a de-differentiated mesenchymal-like phenotype. Upon drug treatment, melanoma cells maintained high levels of phosphorylated ribosomal protein S6 (pS6), *i.e.* active mammalian target of rapamycin (mTOR) signalling, which was suppressed in vemurafenib-sensitive cells without stromal contacts (Seip et al., 2016).

Tumors recruited human MSCs and induced their conversion into CAFs (Jung et al., 2013; Mishra et al., 2008). The cross-talk between stromal cells and TRAIL-sensitive cancer cells reduced metastatic features of triple-negative MDA-MB-231 breast cancer cells (Yoon et al., 2016). T-lymphoma invasion and metastasis-inducing protein 1 (TIAM1) mediated resistance to chemotherapeutic agents via enhancement of stemness. Clinical data supported the importance of TIAM1 in colorectal cancer drug resistance. Furthermore, CAFs induced TIAM1 overexpression in colorectal cancer cells and enhanced drug resistance (Izumi et al., 2019).

miRNAs are involved in the regulation of gene expression at the posttranscriptional level by degrading their target mRNAs and/or inhibiting their translation. They are important molecules affecting tumor drug resistance and metastasis (Brozovic, 2017; Si et al., 2019)(Leonetti et al., 2019a; Naser Al Deen et al., 2019). Oncogenic miR-21 was overexpressed in most solid tumors (Feng and Tsao, 2016). This miRNA protected colorectal cancer cells from oxaliplatin-induced cell death. Ectopic stromal miR-21 expression increased cell invasiveness (Bullock et al., 2013). Gemcitabine-resistant pancreatic ductal adenocarcinoma (PDAC) patients displayed higher miR-21 levels and more activated CAFs. CAFs with high miR-21 expression had elevated MMP-3, MMP-9, PDGF, and CCL7 expression and promoted the invasiveness of PDAC tumor cell lines. MiR-21 overexpression also contributed to the activation of CAFs by regulating the programmed cell death 4 (*PDCD4*) gene (Zhang et al., 2018a). By secreting stromal cell-derived factor-1/chemokine (C-X-C motif) ligand 12 (SDF-1/CXCL12), which was regulated by miR-1, CAFs enhanced cell proliferation and cisplatin resistance in lung cancer A549 and 95D cells by the C-X-C chemokine receptor type 4 (CXCR4)-mediated signalling pathway (Li et al., 2016a). CXCL1 was expressed in human urothelial bladder cancer, especially in high-grade and late-stage tumors

and was secreted into the stromal area or bloodstream. The disruption of signalling of this chemokine may represent a promising therapeutic approach for bladder cancer (Miyake et al., 2016). Down-regulation of miR-29b in CAFs promoted cell growth and metastasis of SK-BR-3 and MCF-7 breast cancer cells by activating p38-STAT1 (signal transducer and activator of transcription 1), which regulated CXCL11 and CXCL14 (Liu et al., 2017b). The importance of chemokines was further confirmed by results showing that CAFs-derived CXCL12 activated CXCR4 in MDA-MB-231 cells and, thereby, significantly enhanced cell proliferation (Ham et al., 2018).

Interestingly, chemotherapy itself activated CAFs, which further promoted self-renewal of colorectal cancer-initiating cells (CIC; characterized by intrinsic drug resistance). Moreover, chemotherapy induced cancer growth *in vivo* associated with the secretion of different chemokines and cytokines such as interleukin-17A (IL-17A). As CICs contributed to tumor invasion and metastasis, the exogenous IL-17A nearly doubled the CIC migration rate (Lotti et al., 2013). IL-6 as an upstream regulator played an important role in increasing CXCR7 expression as a major inducer of tumor cell proliferation and drug resistance (Qiao et al., 2018). After docetaxel therapy, MDA-MB-231 cells co-cultured with primary CAFs displayed increased adhesive, invasive and proliferative properties as compared with MDA-MB-231 cells without CAFs co-culture. Additionally, 35 differentially expressed genes were identified among CAFs before and after chemotherapy (Rong et al., 2013). Gemcitabine-resistant CAFs expressed a pro-inflammatory senescence-associated secretory phenotype with enhanced migration capacity, viability and drug resistance of human MiaPaCa-2 and PANC-1 pancreatic ductal adenocarcinoma cells. Signalling pathways controlling senescence-associated secretory phenotype induction after chemotherapy, including stress-associated MAPK activation, represent potential therapeutic targets to enhance the efficacy of chemotherapeutic regimens (Toste et al., 2016). A recent review paper reported a detailed analysis about the interplay between tumor cells and CAFs (Fiori et al., 2019). In conclusion, CAFs and other TME factors represent important regulators of tumor behavior and additional *in vivo* studies should be performed to explore possibilities for therapeutic intervention that could be translated to clinical practice.

5 Role of the EMT transcription factors and EMT-related metabolic adaptations in MDR

5.1 Micronenvironmental signals involved in activation of EMT

EMT is the differentiation program necessary for tissue morphogenesis during embryonic development, in which cells lose some of their epithelial characteristics and acquire mesenchymal migratory properties. Activation of EMT in cancer cells results in increased invasive and metastatic potential as well as drug resistance. EMT is regulated by a limited number of transcription factors, mainly from the SNAIL, TWIST and ZEB family (De Craene and Berx, 2013; Dongre and Weinberg, 2019; Ribatti et al., 2020; Wilson et al., 2020; Yang and Weinberg, 2008). Various molecules in the extracellular microenvironment derived from CAFs, tumor-infiltrating immune cells and vessels – TGF- β , FGF, EGF, HGF, IGF-1 as well as members of the Hedgehog, Notch and Wnt signaling pathway – can induce EMT. Here, we briefly mention environmental signals directly inducing the expression of EMT transcription factors (EMT-TFs) that contribute to MDR to set the stage for reviewing the role of EMT-TFs in multidrug resistance.

Transforming growth factor β 1 (TGF- β 1).

Induction of EMT by TGF- β is regulated through SMAD-dependent and SMAD-independent transcriptional regulation of transcription factors of the SNAIL, TWIST and ZEB family as well as miRNAs (*e.g.* miR-34, miR200) (Moustakas and Heldin, 2012; Xu et al., 2009). TGF- β and FGF cooperated in the induction of SNAIL expression (Peinado et al., 2003), and TGF- β induced SNAIL in both cancer cells and CAFs, which led to EMT and fibroblast activation, respectively (Lambies et al., 2019). Adult fibroblasts did not express SNAIL, but SNAIL was found in fibroblasts of malignant tumors. In colorectal cancer, SNAIL overexpressing CAFs induced chemoresistance of colon cancer cells to 5-FU and paclitaxel *in vitro* and *in vivo*. This resistance was mediated by CAF-derived CCL1 and TGF- β (Li et al., 2018a). Perivascular TGF- β could also promote the survival of carcinoma progenitor cells, by reprogramming glutathione metabolism, thus increasing progenitor cell drug resistance and cancer recurrence (Oshimori et al., 2015). In gastric cancer, the TGF- β /ZEB axis played a role in trastuzumab resistance (Zhou et al., 2018).

Additional factors.

Various receptor tyrosine kinases (RTKs) promoted EMT through ERK, JNK and MAPK signaling pathway induction of EMT transcription factors (Gonzalez and Medici, 2014). Hepatocyte growth factor (HGF) induced EMT by induction of SNAIL and SLUG (Grotegut et al., 2006; Savagner et

al., 1997), insulin-like growth factor 1 (IGF-1) by induction of SNAIL and ZEB1 (Graham et al., 2008; Kim et al., 2007) and epidermal growth factor (EGF) by induction of TWIST (Lo et al., 2007).

WNT ligands and WNT/ β catenin signaling pathway promoted EMT on several levels (Gonzalez and Medici, 2014). In terms of induction of EMT transcription factors, the WNT/GSK-3 β /AXIN 2 axis stabilized *SNAIL* (Yook et al., 2006; Zhou et al., 2004), and WNT1 upregulated TWIST expression (Howe et al., 2003). SLUG and SNAIL were also induced by NOTCH (Leong et al., 2007) and Hedgehog signaling (Li et al., 2005), respectively.

5.2 Role of EMT transcription factors in multidrug resistance

It has long been postulated that EMT-TFs contribute to phenotypic acquired resistance (Goossens et al., 2017). Most recently, it has been shown by single cell sequencing that a subpopulation with the upregulated EMT and stemness genes with a predisposition to drug resistance was also present in the parental drug-naive cancer cell population (Prieto-Vila et al., 2019). The promoters of many ABC transporter genes contain binding sites for EMT-TFs, hence, EMT program activation simultaneously increased drug resistance (Saxena et al., 2011; Xin et al., 2013). EMT-TFs also induced drug resistance independently of ABC transporters by increasing cellular resistance to drug-induced apoptosis (Li et al., 2018a; Tomono et al., 2017). It has even been suggested that the expression of EMT-TFs in tumor biopsies may serve as predictive marker for therapy-sensitive or -resistant subgroups (Goossens et al., 2017). Here, we focus on the major EMT-TFs implicated in the MDR phenotype.

SNAIL (SNAIL1) and SLUG (SNAIL2) are zinc-finger transcriptional repressors, which induce EMT by epithelial gene repression (i.e. repressing the E-cadherin, occludin, and claudin genes). SNAIL induced both expression of P-glycoprotein/MDR1 (Li et al., 2011) and BCRP (Chen et al., 2010) as well as P-glycoprotein (P-gp) drug efflux activity (Tomono et al., 2017). SNAIL and SLUG also induced chemoresistance independently of ABC transporters. SNAIL repressed cyclin D2 transcription, thus impairing cell cycle progression and conferring resistance to both intrinsic and extrinsic apoptotic pathways (Vega et al., 2004). In cancer, this contributed to drug resistance by repression of apoptosis mediated by the DNA-damage response pathway (Haslehurst et al., 2012; Kajita et al., 2004), antagonism of p53-induced apoptosis and promotion of the CSC

phenotype (Kurrey et al., 2009). Concomitantly with EMT, SNAIL overexpression also induced metabolic reprogramming in cancer cells, *i.e.* increased glucose uptake and lactate production as well as reduced mitochondrial respiration (Kim et al., 2017; Lee et al., 2012; Liu et al., 2019a; Thoreau et al., 2015), thus enhancing chemoresistance (see the section on the metabolic rewiring in EMT).

TWIST1 and TWIST2 are basic helix-loop-helix TFs that are major regulators of the mesenchymal phenotype during embryonic development. They are highly upregulated in multiple cancers and are associated with poor prognosis and invasive potential. TWIST1 conferred increased resistance to both P-gp and non-P-gp substrate drugs (Li et al., 2009). It regulated P-gp (MDR1/ABCB1) expression and drug efflux activity (Deng et al., 2016; Li et al., 2018a; Zhu et al., 2012), as well as expression of other ABC transporters: MRP1 (ABCC1) (Liu et al., 2017c), ABCA2, ABCA3, ABCC5 and ABCC10 (Saxena et al., 2011). TWIST and SNAIL both suppressed the expression of nucleoside transporters, thus inducing chemoresistance to nucleoside analogues (Zheng et al., 2015). In a PDAC mouse model with genetic deletion of TWIST1 or SNAIL1, equilibrative nucleoside transporter 1 (ENT1) and concentrative nucleoside transporter 3 (CNT3) were significantly upregulated. This contributed to response to gemcitabine (Zheng et al., 2015). TWIST/*TWIST* and SNAIL/*SNAIL* were frequently co-expressed in human cancers. In breast cancer, SNAIL2 (SLUG) expression was directly dependent on TWIST1. TWIST1 also increased the expression of the proto-oncogene AKT serine/threonine kinase 2 (AKT2), and decreased chemosensitivity to paclitaxel by increased cell survival signaling (Cheng et al., 2007). Given the role of SLUG in conferring resistance to programmed cell death (Kajita et al., 2004), the TWIST/SLUG/SNAIL axis strongly contributes to MDR (Shen et al., 2017; Tomono et al., 2017). **ZEB1** is a zinc-finger E-box binding homeobox 1 transcription factor that induces EMT mostly by transcriptional upregulation. ZEB1 induced resistance to conventional chemotherapeutic drugs with divergent mechanisms of action (Arumugam et al., 2009; Lazarova and Bordonaro, 2017; Siebzehnrubl et al., 2013). ZEB1 increased the expression of multiple ABC transporters (MRP1, BCRP, ABCC4 and ABCC5) in several breast cancer cell lines *in vitro* (Saxena et al., 2011). ZEB1 also protected cells from genotoxic stress caused by chemotherapy by checkpoint kinase 1 (CHK1) and promotion of recombinant-dependent DNA repair (Zhang et al., 2014) in radioresistant human

breast cancer cells. In non-small lung cancer model, ZEB1 contributed to acquired resistance to EGFR inhibitors (*e.g.* erlotinib) as well (Yoshida et al., 2016).

Other TFs.

There is ample evidence that other EMT-related transcription factors also promote chemoresistance. Several members of the FOX transcription factor superfamily promoted drug resistance through induction of EMT: FOXC2 (Zhou et al., 2015), FOXM1 (Chiu et al., 2015; Hou et al., 2017) and FOXF2 (Cai et al., 2015). SOX2, a transcription factor important for the maintenance of embryonic stem cell characteristics and represents a cancer stem cell marker (Chen et al., 2012; Leis et al., 2012). It regulated the expression of BCRP and SNAIL, thus contributing to chemoresistance (Lee et al., 2014). Overexpression of hairy and enhancer of split 1 (HES1), a transcription factor that triggers EMT (Wang et al., 2015), increased the expression of P-gp, MRP1 and BCRP (Sun et al., 2017). Colon cancer cells with HES1 overexpression were resistant to 5-FU. Whole-genome cDNA microarray analyses showed that pathways related to drug metabolism were up-regulated (including ABC transporters), whereas pathways associated with adherens junctions, focal adhesions and actin cytoskeleton, were down-regulated (Sun et al., 2017).

5.3 Targeting of EMT-TFs as a potential therapeutic approach

The correlation between EMT, CSCs, and drug resistance provides a rationale for therapeutic targeting of EMT in combination with chemotherapy in solid tumors. Targeting TFs themselves might be technically challenging, although a number of small molecule inhibitors of EMT have been proposed to target drug resistance: curcumin, mocetinostat, palbociclib, icaritin, zerumbone etc. (reviewed in (Du and Shim, 2016). Mocetinostat is an HDAC inhibitor that interferes with ZEB1 function and restores sensitivity to chemotherapy by epigenetic regulation; this has been shown for gemcitabine in highly resistant PANC1 cell line and freshly-established patient-derived PDAC cells, as well as for docetaxel in docetaxel-resistant DU145-DR prostate cancer cells (Meidhof et al., 2015). The anti-diabetic drug metformin also modulated EMT; it caused transcriptional reprogramming and decreased ZEB1, TWIST1 and SLUG, thus decreasing EMT, stemness and drug resistance in four genetically different breast cancer models (Hirsch et al., 2009; Vazquez-Martin et al., 2010). Metformin down-regulated the expression of P-gp and MRP1, as well as HIF1 α through the AMPK/mTOR pathway and sensitized cells to 5-FU in 5-FU-resistant

hepatocellular carcinoma cells *in vitro* (Ling et al., 2014). Metformin reversed acquired resistance to 5-FU in 5-FU resistant MCF7-FU breast cancer cells (Qu et al., 2014), to doxorubicin in MCF7-ADR cells (Kim et al., 2011) and increased the sensitivity of radiation- and 5-FU-resistant rectal cancer cells via attenuation of anti-apoptotic gene expression and inhibition of EMT (Park et al., 2019). Small chemical inhibitors of SNAIL-p53 interaction (Lee et al., 2010) or of the zinc finger-binding domain have been similarly proposed as anti-EMT agents and chemosensitizers. For example, screening of a small molecule library of over 500 compounds yielded specific inhibitors of the SNAIL-p53 interaction, which activated p53 in a KRAS-dependent manner and induced apoptosis in both p53-wt and p53-mutated (one allele) pancreatic and breast cancer cell lines (Lee et al., 2010). This makes these inhibitors of potential interest for the overcoming of MDR. On the other hand, oligonucleotide-conjugated Co (III) complexes prevented SLUG and SNAIL from binding to their DNA targets (Harney et al., 2009). Thus, inactivation of their transcriptional activity may be used in combating MDR.

5.4 Effects of metabolic rewiring in EMT on MDR

Metabolic rewiring towards increased anaerobic glycolysis (Warburg effect) and mitochondrial dysfunction have a seminal role in tumor progression (Kang et al., 2019). During EMT, cancer cells acquire an enhanced glycolytic phenotype, maintained by increased glucose uptake and lactate secretion, which drive an undifferentiated cellular state (Li and Li, 2015; Liu et al., 2016). Increased extracellular lactate levels activated SNAIL and maintained the EMT phenotype (Li et al., 2018b). SNAIL caused a range of metabolic adaptations during EMT depending on the cellular context: mitochondrial repression (Lee et al., 2012; Liu et al., 2019a), concomitant elevation of intracellular ATP levels and oxygen consumption (Jiang et al., 2015) as well as a switch in glucose flux towards the pentose phosphate pathway (Kim and Lee, 2017). Nevertheless, all these adaptations that maintain EMT can at the same time sustain the MDR phenotype.

Increased intracellular ATP production represents an extraordinary determinant of chemoresistance (Zhou et al., 2012). In oxaliplatin-resistant colon cancer cells with increased glycolytic capacity and increased expression of glucose transporter (GLUT1) and hexokinase (HK2), depletion of intracellular ATP resulted in partial reversal of MDR and increased sensitivity to oxaliplatin and 5-FU (Zhou et al., 2012). In addition to increased production, cancer cells also took up ATP by macropinocytosis (Qian et al., 2014), which led to resistance to both standard chemotherapy and

targeted kinase inhibitors. Elevated extracellular ATP levels increased resistance to sunitinib, sorafenib, gefitinib, erlotinib, imatinib, paclitaxel, doxorubicin and cisplatin in lung, liver, breast, colon and pancreatic cancer cell lines (Wang et al., 2017b). In a model system with sunitinib (which binds to the ATP-binding site of receptor tyrosine kinases) in mice xenografted with A549 tumors, macropinocytosis of ATP enhanced resistance. The macropinocytosis inhibitor IPA3 and siRNA against serine/threonine-protein kinase PAK1, an enzyme involved in macropinocytosis, both mitigated this effect (Wang et al., 2017b). In another study, inhibition of macropinocytosis with EIPA (Author: Spell out EIPA) reduced intracellular ATP in A549 cells and reduced the efficacy of sunitinib and pazopanib (Qian et al., 2014). Extracellular ATP also increased ABC transporter drug efflux and increased the transcript levels of P-gp and MRP1 (Wang et al., 2017b). Taken together, increased ATP levels fuel ABC efflux transporters, increase their expression, compete with TKI inhibitors for binding sites and increase phosphorylation of growth factor receptors (Wang et al., 2017b), thus contributing to MDR towards both conventional and targeted therapeutics.

EMT, metabolic reprogramming, and MDR are molecularly intertwined and are summarized in Figure 4. Consequently, biochemical overexpression of ABC transporters in cancer cells influences cellular metabolism: MDR efflux transporters increased the glycolytic rate and glutathione consumption and decreased the pentose phosphate pathway and the oxidative phosphorylation rate (Lopes-Rodrigues et al., 2017). One should keep in mind that the genetic landscape of the cancer cell and the TME (*e.g.* mutational status of proto-oncogenes such as KRAS, BRAF or p53, hypoxia, and stromal cells) strongly influence the outcome of metabolic alterations on the MDR phenotype. For example, increased OXPHOS in metastasis contributed to reduced expression of ABCB1, ABCC1, ABCC5 and ABCG2 in wild-type p53-expressing cells and to increased expression of the same transporters in mutated or null p53-expressing cells (Belkahlia et al., 2017). The interplay between EMT, MDR and autophagy, another cellular process hijacked during the metabolic adaptation in cancer cells, is also two-sided. Autophagy protected cells from nutrient deprivation and recycled damaged cellular components. Early during tumor progression, autophagy restricted EMT by selective degradation of specific EMT proteins. However, during the metastatic dissemination, EMT induced autophagy to enable cell survival under conditions of low oxygen and nutrient deprivation (reviewed in (Gugnoni et al., 2016)). Autophagy acted in a pro-survival manner in the context of MDR (Ajabnoor et al., 2012; Bao et

al., 2015; Liang et al., 2016; Sui et al., 2013; Sun et al., 2011). By contrast, it also enhanced the anti-cancer efficacy of drugs by inducing autophagic cell death (Li et al., 2017; Sotelo et al., 2006; Sui et al., 2013) depending on the underlying cellular conditions. For example, in cisplatin- or vincristine-resistant ovarian cancer cells autophagy had cytoprotective role, and its inhibition by chloroquine or 3-methyladenine re-sensitized cells and potentiated apoptosis (Bao et al., 2015; Liang et al., 2016). Furthermore, autophagy was also cytoprotective and induced resistance to epirubicin and paclitaxel in MCF7 cells (Ajabnoor et al., 2012; Sun et al., 2011). Inhibition of autophagy in triple-negative breast cancer (TNBC) *in vitro* and *in vivo* significantly improved drug response of both anthracycline-sensitive and -resistant TNBC (Chittaranjan et al., 2014). Adding the autophagy inhibitor chloroquine to standard chemotherapy in glioblastoma multiforme patients increased mid-term survival (Sotelo et al., 2006). On the other hand, induction of autophagy led to autophagic cell death in cells with altered apoptotic pathways. For example, in cisplatin-resistant urothelial cancer cells the activation of autophagic flux with dual PI3K and mTOR inhibitor induced cytotoxicity (Li et al., 2013). Plant alkaloids that potentiated autophagy induced autophagic cell death in drug-resistant cells (Donadelli et al., 2011; Meschini et al., 2008).

Tumor cells have a deregulated oxidative mitochondrial machinery that supplies ATP (via OXPHOS), but still enables catabolism of glucose and glutamine (DeBerardinis and Chandel, 2016) for the supply of precursors for DNA, protein and lipid synthesis (Ahn and Metallo, 2015). Down-regulation of mitochondrial genes was strongly correlated with EMT across 20 different cancer types (Gaude and Frezza, 2016). The depletion of mitochondrial DNA provided survival advantages through AKT2 signaling and anoikis resistance (Moro et al., 2009), thus decreasing chemosensitivity. On the other hand, disseminating cancer cells displayed increased OXPHOS (LeBleu et al., 2014), and one of the emerging mechanisms of chemotherapy-induced drug resistance induced a switch from glycolysis to OXPHOS (Vellinga et al., 2015). For example, in samples from liver metastases of colon cancer patients that were exposed to chemotherapy before surgery, genes that are involved in oxidative phosphorylation were upregulated compared to the samples from untreated patients. 5-FU and oxaliplatin caused an upregulation of sirtuin-1 (SIRT1) (Vellinga et al., 2015). SIRT1 is a protein deacetylase, known to regulate multiple physiological functions by deacetylating different protein substrates. Cumulative studies revealed key roles of SIRT1 in different aspects of cancers including genomic instability, metabolism, cell proliferation, and drug resistance (Farcas et al., 2019). SIRT1 was activated in response to DNA damage and

initiated mitochondrial biogenesis (Knight and Milner, 2012). Therefore, mitochondria acted as a hub between metabolism and cell signaling, with temporally defined metabolic adaptations along EMT route, where increased mitochondrial metabolism promoted resistance to apoptosis, whereas mitochondrial dysfunction favored metastasis (reviewed in (Porporato et al., 2016).

EMT-related changes in protein glycosylation patterns also influenced the MDR phenotype. Incomplete glycosylation of ABC transporters prevented their proper membrane localization and, thus, decreased their efficacy as drug efflux pumps ((da Fonseca et al., 2016; Wojtowicz et al., 2015). EMT was also accompanied with a change in lipid metabolism providing alternative energy sources(Sanchez-Martinez et al., 2015) (Sánchez-Martínez et al., 2015) and reorganization of lipid rafts and increased migration ((Babina et al., 2014; Luo et al., 2017). Composition of the membrane lipids and membrane recycling contributed to resistance in MDR cells: altered lipid composition limited drug entry across the plasma membrane and altered kinetics of internalization preventing drug accumulation (Omran et al., 2017).

5.5 Targeting metabolic adaptations in EMT as a potential therapeutic approach

Control over the metabolic adaptation may be an effective modality to overcome drug resistance. It remains to be explored, whether targeting glycolysis, autophagy or OXPHOS may serve as promising therapeutic strategies against MDR tumors. For example, inhibition of glycolysis in MDR cells with activated AKT/mTOR/MYC pathway restored sensitivity to doxorubicin (Zhang et al., 2017). The glycolysis inhibitor, 3-bromopyruvate, sensitized MDR cells (Zhou et al., 2012). The specific lactate dehydrogenase-A inhibitor, oxamate, sensitized paclitaxel-resistant cells (Zhou et al., 2010). The antidiabetic drug metformin, a dual AMPK activator and mitochondrial electron transport chain complex I inhibitor (Wheaton et al., 2014), decreased glucose oxidation (Fendt et al., 2013), modulated autophagy (Kim and You, 2017) and eradicated CSCs when combined with chemotherapy (Hirsch et al., 2009).

6 Role of hypoxia in metastasis and drug resistance

6.1 Hypoxia in tumor progression

During tumor progression, the velocity of proliferation exceeds the tumor's capacity to supply enough oxygen and nutrients by passive diffusion from the surrounding normal tissues. This situation results in hypoxia, a hallmark of most solid tumors. The role of the TME, which consists

not only of the tumor cells themselves, but also of immune cells, CAFs, endothelial cells, adipocytes etc., cannot be underestimated for invasion, metastasis and development of drug resistance (Almeida et al., 2019). Tumors have the capacity to adapt to hypoxic stress by several mechanisms such as the induction of neoangiogenesis, the metabolic shift and apoptosis resistance (Kim and Lee, 2017). These mechanisms are orchestrated by hypoxia-inducible factors (HIF), which act as transcription factors for a plethora of genes involved in tumor progression and metastasis (Bhattarai et al., 2018; Tong et al., 2018). EMT also contributes to chemoresistance (Sui et al., 2014). Stem-like cancer cells are not only crucial for EMT, but are also drug- and radiation-resistant at the same time. Hypoxia can mediate resistance either directly or indirectly. Direct resistance due to hypoxia occurs to radiation and some anticancer drugs (Raz et al., 2014), which need oxygen for full activity, while indirect modes of hypoxia-mediated resistance represent alterations of cellular signaling or increased genetic instability (Teicher, 1994; Kim and Lee, 2017; Salem et al., 2018). Here, we focus on indirect mechanisms of hypoxia-induced MDR and the relevance of ABC transporters in this context.

6.2 Coexpression of HIF-1 α and P-glycoprotein in clinical tumor biopsies

Hints that hypoxia may be relevant for the development of resistance to chemotherapy response emerged from investigations with clinical tumor biopsies. Interestingly, in diverse tumor types statistically significant correlations have been observed between the expression of HIF-1 α and P-gp, including common epithelial tumors (carcinomas of the breast, lung, larynx or colon) and hematological malignancies (multiple myeloma) as well as rare tumors (such as chordoma) (**Table 1**). This was not only true for primary tumors but also for lymph node metastases (Badowska-Kozakiewicz et al., 2017; Lu et al., 2016). In chordoma, HIF-1 α expression did, however, not correlate with MRP1 expression – a result that deserves verification in other tumor types. There is also a clue from advanced colon carcinoma that the simultaneous expression of HIF-1 α and P-gp has clinical impact, since tumors with co-expression of these two proteins poorly responded to chemotherapy when compared to those devoid of co-expression (Chen et al., 2014).

Table 1: Expression of HIF-1 α and P-glycoprotein in clinical tumor samples.

Tumor type	Biomarker expression	Reference
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Breast cancer and lymph node metastases	Significant correlation between HIF-1 α and P-gp expression	Badowska-Kozakiewicz et al., 2017
Multiple myeloma	Significant correlation between HIF-1 α and P-gp expression	Muz et al., 2017
Lymph node metastases of non-small cell lung cancer	Significant correlation between HIF-1 α and P-gp expression	Lu et al., 2016
Advanced colon carcinoma patients	Patients with HIF-1 α and P-gp co-expression were more resistant to chemotherapy than those lacking expression	Chen et al., 2014
Laryngeal squamous cell carcinoma	Significant correlation between HIF-1 α and P-gp expression	Xie et al., 2013
Chordoma	Significant correlation between HIF-1 α and P-gp expression, but not MRP1 expression	Ji et al., 2010
Colon carcinoma	Significant correlation between HIF-1 α and P-gp expression	Ding et al., 2010

6.3 Molecular modes of action of hypoxia-induced MDR

The statistically significant co-expression of HIF-1 α and P-gp supported the hypothesis that HIF-1 α may regulate the expression of ABC transporter genes and thereby induce resistance to anticancer drugs. Numerous authors investigated this hypothesis, and it turned out that hypoxia seems to induce drug resistance by both ABC-transporter dependent and -independent mechanisms in cancer and also in normal tissues (**Table 2**).

A considerable portion of papers reported on the hypoxia-induced activation of HIF-1 α leading to transcriptional activation of the *ABCB1* promoter and expression of *ABCB1* mRNA and P-gp, which in turn caused resistance to typical drug substrates of P-gp such as doxorubicin (**Table 2**). While the majority of papers focused on P-gp, a few authors also analyzed other ABC transporters such as MRP1, BCRP, and ABCB5. A similar trend as with P-gp was found, *i.e.* hypoxia caused overexpression of these drug efflux pumps. In addition to HIF-1 α , the tightly related HIF-2 α seems to play a role for these ABC transporters.

While the vast majority of authors found HIF-1 α -mediated ABC transporter overexpression, some papers reported on P-gp overexpression as a consequence of amplification of the gene encoding for the murine, rodent and human P-gp (Assaraf and Borgnia, 1994; Assaraf et al., 1989; Genovese et al., 2017; Luk et al., 1990; Sharma et al., 1991). Hypoxia was shown to induce fragile sites in the genome, which favor genomic rearrangements. Breaks at these fragile sites initiate DNA amplifications and the generation of intrachromosomally localized gene amplifications

(cytogenetically visible as homogenously stained regions, HSR) or extrachromosomally organized elements (double minutes, DMs) (Coquelle et al., 1998).

In some cases, resistance to anticancer drugs which are known to be non-ABC transporter substrates was also observed, *e.g.* BCNU, ifosfamide and methotrexate (Takeshita et al., 1996; Harrison and Schwartz, 2017; Nikolova et al., 2017). This result is a clue that ABC transporters may be overexpressed under hypoxic conditions, but that resistance to these non-MDR drugs may occur via additional P-gp-independent mechanisms. Indeed, a number of investigations came to the conclusion that hypoxia-mediated drug resistance can occur in an ABC transporter-independent manner (**Table 2**). These authors searched for alternative mechanisms and suggested cell cycle related effects (up-regulation of cell cycle inhibitors and down-regulation of cyclins) or regulation of genes that affect drug response by their modes of actions (*e.g.* KLF8, KFL8, NOX1, EGFL7 etc.).

Hypoxia-mediated resistance is not restricted to cancer cells, but has also been observed in normal tissues and cells (**Table 2**). Here, hypoxia also induced HIF-1 α activation followed by P-gp or BCRP overexpression or other mechanisms. This may have important implications for healthy organisms, which have to cope with a plethora of xenobiotic and partwise harmful compounds from the environment. Tissue hypoxia may support the detoxification of xenobiotics taken up with food or breathing air. While hypoxia-induced resistance can cause chemotherapy failure with fatal outcome in cancer patients, it may contribute to salutogenesis in healthy subjects by keeping them off from the detrimental effects of harmful exogenous compounds.

Table 2: Role of hypoxia and hypoxia-inducible factors (HIF-1 α , HIF-2 α) for the expression of ABC transporters (P-gp, MRP1, BCRP, ABCB5) in tumor cells and normal cells and tissues.

Model	Mechanism	Reference
ABC-transporter-dependent drug resistance by hypoxia:		
OVCAR-3 S and CAOV-3 S ovarina cancer cells	Hypoxia induced HIF-1 α , HIF-2 α expression and doxorubicin resistance. HIF-1 α knockdown sensitized to and HIF-1 α overexpression induced resistance to doxorubicin. HIF-2 α directly promoted transcription/expression of BCRP	He et al., 2019
SKOV3 ovarian cancer cells	Hypoxia induced P-gp and MRP1 expression	Cai et al., 2018
	Hypoxia induced HIF-1 α and P-gp expression and P-gp internalization, lysosomal doxorubicin accumulation, and doxorubicin resistance	Al-Akra et al., 2018
Multiple myeloma	Hypoxia induced P-gp expression and resistance to carfilzomib and bortezomib	Muz et al., 2017

HT-29 colon cancer cells	Hypoxia induced HIF-1 α , P-gp and BCRP expression	Pinzón-Daza et al., 2017
A549/DDP non-small lung cancer cells	Hypoxia induced P-gp and EGFL7 expression and drug resistance	Shen et al., 2017
CH27, CH27/DOX, A549, H1299, H460 lung cancer cell lines	Hypoxia-induced inhibition of MRP1 and P-gp expression in a HIF-1 α -dependent manner and DOX resistance	Chen et al., 2016
Laryngeal cancer cells	Hypoxia-induced P-gp expression was downregulated by <i>ABCB1</i> RNAi leading to chemosensitization and increased drug accumulation	Li et al., 2016
LoVo colon cancer cells	Chemical hypoxia by cobalt chloride induced HIF-1 α , P-gp and MRP1 expression and decreased intracellular doxorubicin retention	Yang et al., 2016
Colon cancer cells	Chemical hypoxia by cobalt chloride induced HIF-1 α , P-gp and MRP1 expression. HIF-1 α bound to <i>ABCC1</i> promoter	Lv et al., 2015
Melanoma cells	Hypoxia-mediated downregulation of miR-340-5p induced upregulation of ABCB5 regulation	Wozniak et al., 2015
Gastric cancer cells	Hypoxia-induced KLF8 and HIF-1 α expression, KLF8-mediated <i>ABCB1</i> promoter activation and P-gp expression	Zhang et al., 2014
LoVo colon cancer cells	Hypoxia-induced HIF-1 α and P-gp expression, HIF-1 α silencing reduced P-gp expression and sensitized cell to four drugs, HIF-1 α bound to the <i>ABCB1</i> promoter	Chen et al., 2014
Osteosarcoma cells	HIF-1 α induced P-gp expression and doxorubicin efflux	Roncuzzi et al., 2014
Hep-2 laryngeal squamous carcinoma cells	Hypoxia induced HIF-1 α and P-gp expression, HIF-1 α downregulation also inhibited P-gp expression in hypoxic cells	Xie et al., 2013
HT-29 colon cancer cells	Digoxin increased intracellular [Ca ²⁺] and activated calmodulin kinase II, which activated HIF-1 α and P-gp expression	Riganti et al., 2009
SGC7901/VCR gastric cancer cells	Hypoxia induced doxorubicin efflux, <i>HIF1A</i> siRNA reversed this effect, HIF-1 α overexpression induced P-gp and MRP1 expression	Liu et al., 2008
Colon cancer cells	Hepatitis-B-virus X protein (HBx) increased <i>ABCB1</i> activity through transcriptional activation by HIF-1 α activation	Han et al., 2007
Colon cancer cells	Hypoxia alone had no effect, but together with acidosis the P-gp expression increased	Lotz et al., 2007
Oral squamous cell carcinoma cells	HIF-1 α knockdown decreased P-gp expression and increased intracellular drug concentrations	Sasabe et al., 2007
A549 lung cancer cells	HIF-1 α transfection increased P-gp expression and 5-fluorouracil expression	Zhang et al., 2006
A549 lung cancer cells	Hypoxia induced HIF-1 α and P-gp expression and doxorubicin resistance	Xia et al., 2005
DU-145 prostate tumor spheroids	NOX-1-induced ROS generation reduced HIF-1 α and P-gp expression and increased intracellular doxorubicin retention. Free radical scavengers (vitamin C and E) reversed this effect on the protein but not mRNA level	Wartenberg et al., 2005
DU-145 prostate cancer spheroids, Hepa1 hepatoma spheroids	Hypoxia activated JNK activity and P-gp protein and <i>ABCB1</i> mRNA expression. JNK inhibition reversed this effect. Hypoxia-induced HIF-1 α signaling depended on JNK activation	Comerford et al., 2004
DU-145 prostate cancer spheroids, Hepa1 hepatoma spheroids	Hypoxia and chemical hypoxia (by cobalt chloride or desferrioxamine) induced HIF-1 α and P-gp expression. Prooxidants	Wartenberg et al., 2003

(H₂O₂, BSO) upregulated and antioxidants (N-acetylcysteine, vitamin E) upregulated HIF-1 α and P-gp

Murine KHT-LP1 cells	Hypoxia induced <i>mdr1a</i> gene amplification in the presence of doxorubicin	Luk et al., 1990
ABC-transporter-independent drug resistance by hypoxia:		
Non-small cell lung cancer cells	Hypoxia induced KLF5 expression. KLF5 knockdown suppressed hypoxia-induced cisplatin resistance and HIF-1 α -dependent glycolysis	Gong et al., 2018
A549/DDP non-small lung cancer cells	Hypoxia induced P-gp and EGFL7 expression and drug resistance	Shen et al., 2017
Gallbladder cancer cells	NOX1-induced ROS generation and HIF-1 α /P-gp pathway activation	Zhan et al., 2015
Oal suamous cell carcinoma cells	Hypoxia induced resistance to 5-fluorouracil by G1/S transition through upregulation of cell cycle inhibitors (p21, p27) and downregulation of cyclin D	Yoshiba et al., 2009
MIA PaCa-2, PANC-1, BxPC-3 pancreas cancer cells	Hypoxia did not induce ABCB1 expression	Lo et al., 2009
R3327-AT1 prostate cancer cells	Hypoxia mildly increased P-gp expression, but decreased MRP1 expression	Thews et al., 2008
MCF-7 and SW1573 breast cancer cells	Hypoxia induced resistance to mitoxantrone, but not doxorubicin. No changes in P-gp, MRP1 or BCRP expression under hypoxia	Greijer et al., 2005
Neuroblastoma cells	Hypoxia induced <i>ABCB1</i> downregulation	Jögi et al., 2004
Testicular germ cell tumors	Hypoxia induced resistance to cisplatin, etoposide, bleomycin, 4-OOH-ifosfamide, carboplatin, paclitaxel, gemcitabine, oxaliplatin, irinotecan, and mitomycin C	Koch et al., 2003
MCF-7 and MCF-7/VP breast cancer cells	Hypoxia reduced 99mTc-sestamibi and 99mTc-tetrofosmin radiotracer uptake independent of MRP1 function	Kinuya et al., 2003
U373 MG and PFAT-MT glioma cells	Hypoxia induced resistance to BCNU and cisplatin without change in drug resistance genes	Liang et al., 1996
MDA-468 and MCF-7/Adr	Hypoxia did not induce doxorubicin resistance and doxorubicin response was not increased by the P-gp inhibitor verapamil	Kalra et al., 1993
Murine EMT6/Ro cells	Hypoxia induced resistance to doxorubicin, 5-fluorouracil and actinomycin D, but not to colchicine, vincristine or cisplatin. Hypoxia did not induce <i>ABCB1</i> mRNA expression	Sakata et al., 1991
Hypoxia effects in normal tissues and cells:		
Human placenta	Hypoxia increased P-gp and <i>ABCB1</i> mRNA expression, but not BCRP expression	Javam et al., 2014
Rats	Hypoxia increased P-gp protein expression but not <i>ABCB1</i> mRNA expression	Fradette et al., 2007
Murine stem progenitor cells	Hypoxia induced HIF-1 α -mediated BCRP expression	Krishnamurthy et al., 2004
Nontransformed, primary human microvascular endothelial cells	Hypoxia induced HIF-1 α -mediated P-gp protein and <i>ABCB1</i> mRNA expression	Comerford et al., 2002
Chinese hamster lung fibroblasts	Hypoxia induced doxorubicin resistance, which was not reversible with verapamil	Kalra et al., 1993

6.4 Approaches to overcome hypoxia-induced MDR

Given that many (though not all) forms of hypoxia-induced drug resistance are based on the HIF-1 α mediated induction of P-gp overexpression, it is worthwhile to search for strategies to overcome resistance by targeting the HIF-1 α /P-gp axis (**Table 3**). This has been attempted by the application of ribonucleotide drugs (siRNA, shRNA or RNAi against *HIF1A*) with or without encapsulation in nanoparticles. Remarkably, this approach led not only to down-regulation of HIF-1 α , but also of P-gp, which can be taken as further evidence that P-gp overexpression is driven by HIF-1 α under hypoxic conditions. Furthermore, nanoparticles have been used to encapsulate the anticancer drug doxorubicin with other drugs (*i.e.* metformin, chlorin E6) resulting in down-regulation of HIF-1 α and P-gp as well as in increased doxorubicin concentrations in tumor cells. HIF-1 α inhibitors (YC-1, 3-(5'-hydroxymethyl-2'-furyl)-1-benzylindazole) and other synthetic compounds (Buthionine sulfoximine and thiosemicarbazones) exhibited comparable effects in overcoming hypoxia-mediated drug resistance. Interestingly, hypoxia-induced and P-glycoprotein-mediated MDR has not only been reversed by synthetic compounds and nanoparticles, but also by natural products such as the dipeptide L-carnosin and phytochemicals. Epigallocatechin-3-gallate is a polyphenolic catechin and a major constituent of green tea (*Camelia sinensis*), and hispulidin is a flavone found in plants of the genus *Artemisia* and *Salvia* and others.

Table 3: Strategies to overcome hypoxia-induced multidrug resistance by nanoparticles, synthetic compounds and phytochemicals.

Model	Compound	Mode of action	Reference
Ribonucleotide drugs with or without nanoparticle encapsulation:			
	<i>HIF1A</i> siRNA nanoparticle	Expression of HIF-1 α and P-gp \downarrow , drug efflux \downarrow	Huang et al., 2019
PC3 prostate cancer cells	<i>HIF1A</i> siRNA nanoparticle	<i>ABCB1</i> expression \downarrow , sensitization to doxorubicin	Liu et al., 2012
HT-29 colon cancer cells	<i>HIF1A</i> shRNA	Expression of HIF-1 α and P-gp expression <i>in vitro</i> and <i>in vivo</i> \downarrow	Zhang et al., 2017
MCF-7 breast cancer spheroids	<i>HIF1A</i> siRNA	P-gp expression \downarrow , intracellular doxorubicin accumulation \uparrow	Doublier et al., 2015
MCF-7 breast cancer cells	<i>HIF1A</i> siRNA		Li et al., 2006
SPCA1 and A549 non-small lung cancer cells	<i>HIF1A</i> RNAi	Expression of HIF-1 α \downarrow , doxorubicin and cisplatin resistance \downarrow , but P-gp was not increased under hypoxia	Song et al., 2006
Chemical drug-containing nanoparticles:			

MCF-7/Adr breast cancer cells	Doxorubicin-metformin cationic liposomes	Hypoxic stress↓, expression of HIF-1 α and P-gp↓	Li et al., 2019
	Encapsulated doxorubicin and chlorin e6 in tumor-targeted hybrid protein oxygen carriers	Expression of HIF-1 α and P-gp↓, drug efflux↓	Luo et al., 2018
Synthetic compounds:			
Glioblastoma xenograft tumors	YC-1 (HIF-1 α inhibitor)	<i>ABCB1</i> expression↓, survival rate to BCNU therapy↑	Chou et al., 2012
HepG2 liver cancer spheroids	YC-1 (HIF-1 α inhibitor)	Doxorubicin accumulation↑	Liu et al., 2017
MCF-7 breast cancer spheroids	3-(5'-hydroxymethyl-2'-furyl)-1-benzylindazole (HIF-1 α inhibitor)	P-gp expression↓, intracellular doxorubicin accumulation↑	Doublier et al., 2015
	Lysosomal targeted thiosemicarbazones	Hypoxia-induced doxorubicin resistance↓	Al-Akra et al., 2018
HepG2 liver cancer cells	BSO	HIF-1 α and P-gp expression↓	Jin et al., 2011
Natural products:			
HT-29 colon cancer cells	L-carnosine	Cell viability↓, HIF-1 α and P-gp expression↓	Iovine et al., 2016
Gallbladder cancer cells	Hispidulin	HIF-1 α protein expression, but not mRNA↓, AMPK signaling↑, HIF-1 α /P-gp signaling↓, sensitization to gemcitabine and 5-fluorouracil	Gao et al., 2015
PANC-1 pancreas cancer cells	Epigallocatechin-3-gallate	HIF-1 α expression↓, P-gp protein and <i>ABCB1</i> mRNA↓, cell proliferation↓	Zhu et al., 2012

7 Conclusions and perspectives

It is known that tumor drug resistance is frequently multifactorial (Kadioglu et al., 2016). However, nowadays it becomes evident that drug resistance is much more complex than initially thought some decades ago. A plethora of distinct yet intertwined mechanisms contribute to drug resistance. Many cancer patients succumb to the metastatic disease that is typically non-responsive to therapeutic interventions. Hence, the metastatic process and the development of drug resistance are seemingly interconnected by common molecular modes of action.

This situation may explain, at least in part, why drug resistance phenomena dogged oncology during the past 7 decades. This situation underscores, how complex drug resistance really is in the clinical context. The more we understand the individual factors contributing to the entire phenomenon of therapy failure, the more we have tools to develop sophisticated individualized

strategies to surmount drug resistance, which ultimately would improve the survival rates of cancer patients.

The emerging questions that arise are: how should we cope with the complexity of drug resistance and would it be ever possible to develop efficient strategies to overcome and reverse chemoresistance? With the expansion of the integrative research fields of genomics, transcriptomics, proteomics, interactomics, and metabolomics of tumors in the past decade, a large amount of information was generated. We are yet to grasp and consolidate the impact of these new findings in the context of MDR. The future of cancer therapy will be revolutionized by cutting-edge technologies to handle big data such as artificial intelligence. The future of drug resistance research lies in the bioinformatic handling of big data from experimental and clinical settings, in order to develop personalized, patient-tailored protocols that will hopefully overcome drug resistance in each individual tumor (Efferth et al., 2017; Efferth and Volm, 2005; Volm and Efferth, 2015).

To come closer to this final goal, a first step is to develop a hierarchy of mechanisms of drug resistance. This is still non-sufficiently understood, i.e. which mechanisms contribute more to drug resistance than others in well defined tumors. Based on experimental results *in vitro* and *in vivo*, the clinical relevance of the prioritized mechanisms should be verified in translational settings. While the entire field of drug resistance becomes increasingly complex, the chances and opportunities to fight tumor refractoriness also increase, which presents a hope for novel treatment strategies for cancer patients worldwide.

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Conflicts of interest

NE, JG, AB and TE have no conflict of interest to disclosure.

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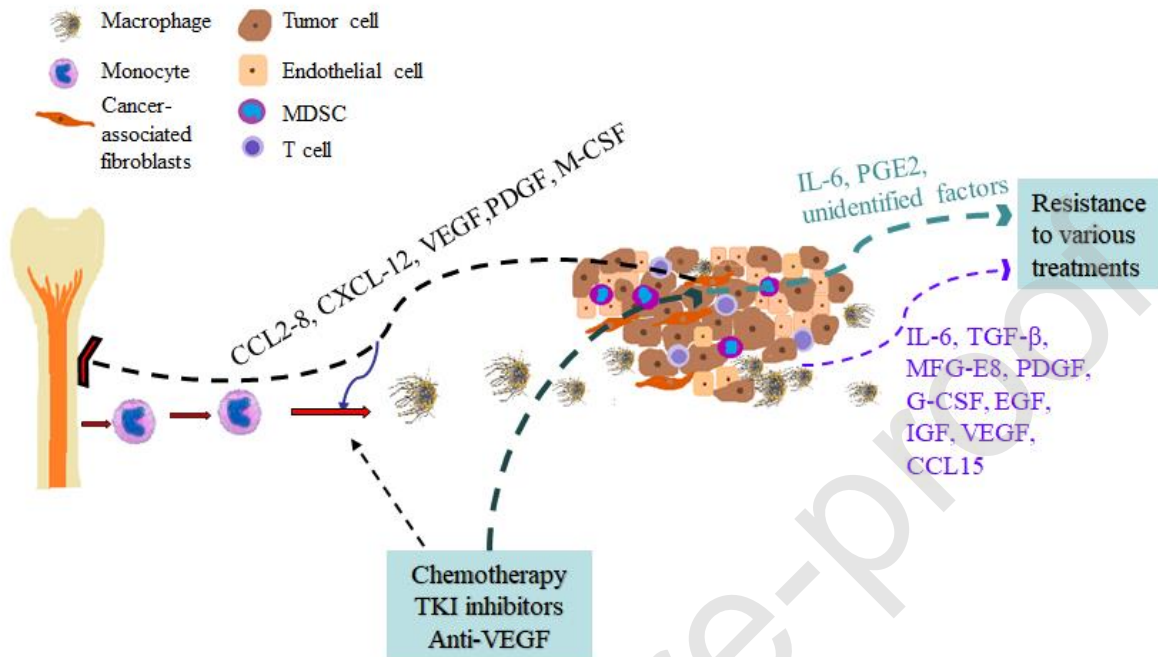


Figure 1. Factors involved in MDR due to TAMs. Factors originating from cancer cell and TME such as CCL-2 to 8, CXCL-12, VEGF, PDGF and M-CSF induce the formation of macrophages from monocytes. Factors secreted from TAMs (IL-6, TGF- β , MFG-E8, PDGF, G-CSF, EGF, IGF, VEGF, and CCL15) or from cancer cells (*e.g.* IL-6 and PGE2) that were exposed to chemotherapy are involved in MDR as described in detail in the text.

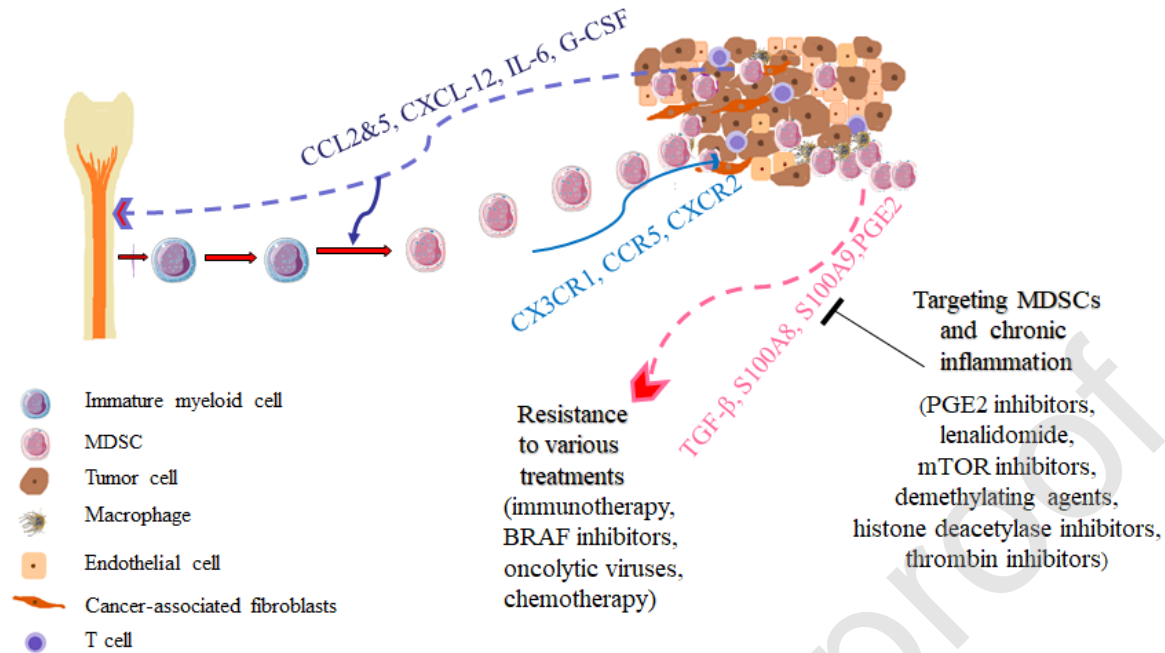


Figure 2. Factors involved in MDR due to MDSCs. Factors originating from cancer cell and TME such as CCL-2 and 5, CXCL-12, IL-6 and G-CSF induce the formation of MDSCs from immature myeloid cells. MDSCs expressing certain chemokine receptors (CX3CR1, CCR5 and CXCR2) are effectively recruited to TME and involved in MDR partly by secreting TGF- β , S100A8, S100A9 and PGE2. Targeting MDSCs and chronic inflammation with various therapeutic approaches may overcome MDR, as described in detail in the text.

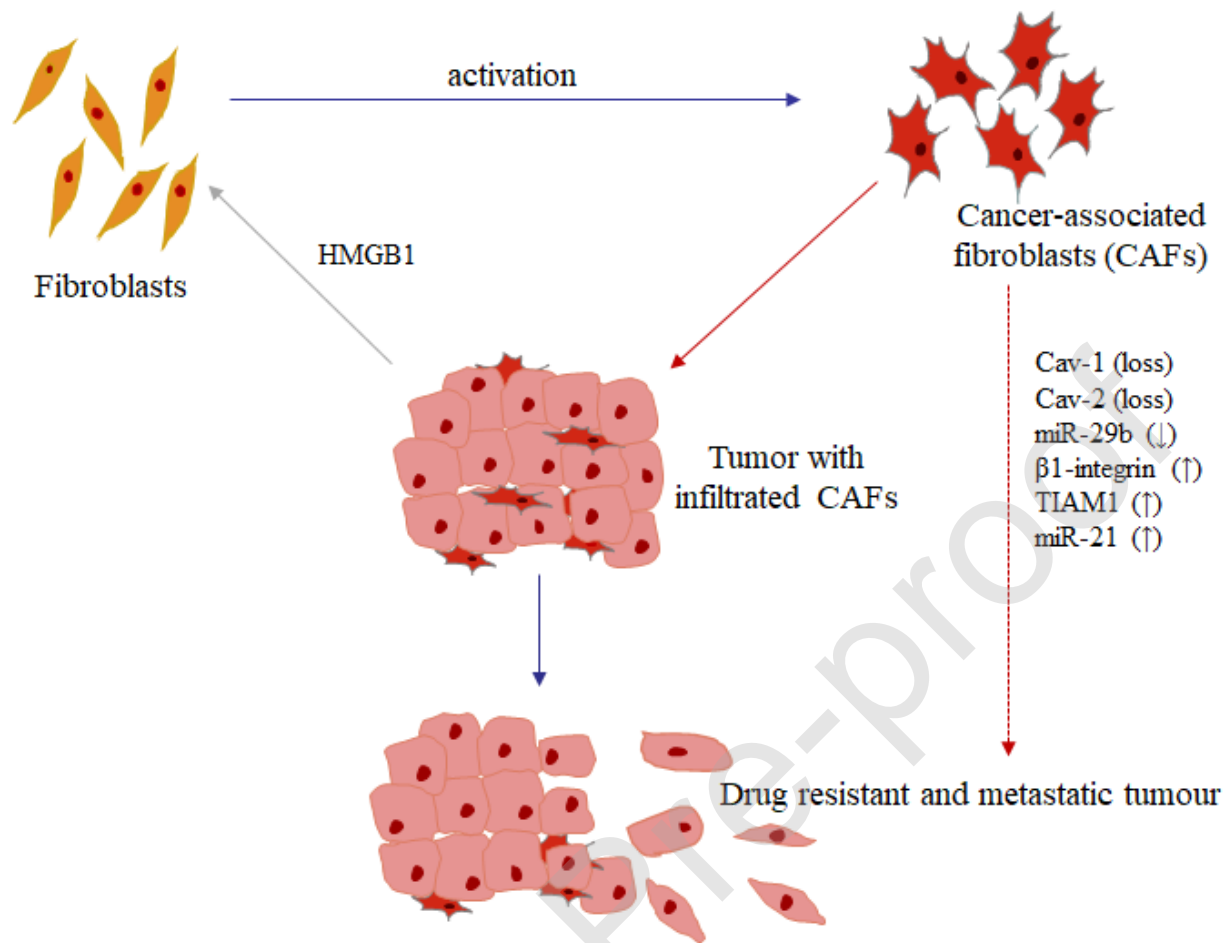


Figure 3. A mutual play between fibroblasts, CAFs and tumor cells resulting in metastatic drug-resistant tumors. Loss of Cav-1 or Cav-2, downregulation of miR-29b, upregulation of β 1-integrin, TIAM1 or miR-21 in CAFs are involved in the formation of metastatic drug-resistant tumors. Dying tumor cells release HMGB1, which activates stromal fibroblasts and further development of metastatic drug-resistant tumors.

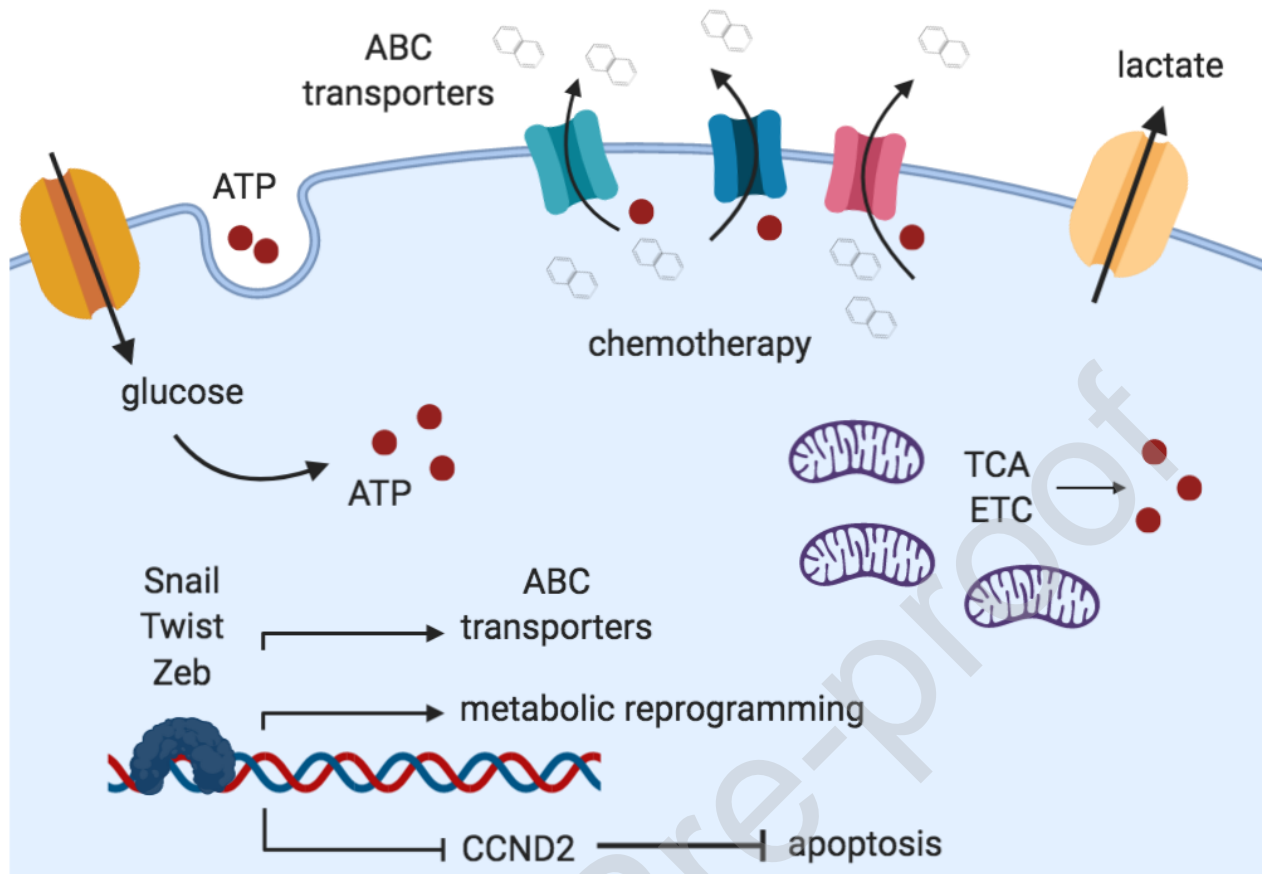


Figure 4. EMT transcription factors contribute to the MDR phenotype through ABC transporter-dependent and -independent mechanisms; among the latter is the metabolic rewiring in cancer cells.