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“DEPHENCE” system—a novel regimen of therapy that is urgently needed in the high-grade serous ovarian cancer—a focus on anti-cancer stem cell and anti-tumor microenvironment targeted therapies

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Ovarian cancer, especially high-grade serous type, is the most lethal gynecological malignancy. The lack of screening programs and the scarcity of symptomatology result in the late diagnosis in about 75% of affected women. Despite very demanding and aggressive surgical treatment, multiple-line chemotherapy regimens and both approved and clinically tested targeted therapies, the overall survival of patients is still unsatisfactory and disappointing. Research studies have recently brought some more understanding of the molecular diversity of the ovarian cancer, its unique intraperitoneal biology, the role of cancer stem cells, and the complexity of tumor microenvironment. There is a growing body of evidence that individualization of the treatment adjusted to the molecular and biochemical signature of the tumor as well as to the medical status of the patient should replace or supplement the foregoing therapy. In this review, we have proposed the principles of the novel regimen of the therapy that we called the “DEPHENCE” system, and we have extensively discussed the results of the studies focused on the ovarian cancer stem cells, other components of cancer metastatic niche, and, finally, clinical trials targeting these two environments. Through this, we have tried to present the evolving landscape of treatment options and put flesh on the experimental approach to attack the high-grade serous ovarian cancer multidirectionally, corresponding to the “DEPHENCE” system postulates.

KEYWORDS

high-grade serous ovarian cancer, ovarian cancer stem cells, metastatic niche, tumor microenvironment, chemo-resistance, experimental therapy, clinical trial

Introduction

Ovarian cancer, especially its type II according to the dualistic model proposed by Kurman and Shih (1), represented mostly by the high-grade serous ovarian cancer (HGSOC) is the most lethal tumor of the female genital tract. The cumulative 5-year survival in the population of patients with all clinical stages does not exceed 48% (2). Despite the fact that some cases of the HGSOC are primarily chemo-refractory, the most of the cancers belonging to this group are chemosensitive to first-line chemotherapy; however, they quickly acquire the secondary chemoresistance that constitutes the main problem in effective management. Moreover, the HGSOC possesses unique behavior that allows spreading of the tumor cells, mostly in the form of cellular spheroids, from the primary tumor into the distant localizations in the peritoneal cavity. Therefore, the HGSOC is a highly malignant, rapidly progressive tumor characterized by poor prognosis and mortality reaching 90% of all ovarian cancer cases (3).

Ovarian cancer stem cells

One of the main problems in the treatment of HGSOC is the existence of ovarian cancer stem cells (OCSCs) that reside inside tumor niches and cooperate with surrounding cells that compose tumor microenvironment (TME). The character of this cooperation shapes tumor behavior and influences several processes including dormancy, proliferation, metastasis, and, most of all, chemoresistance (4). Cancer stem cells are a population of cells capable of self-renewal and reproduction of the original phenotype of the tumor and are enriched especially in the advanced, disseminated, and recurrent tumors (5). There are two functionally distinct populations of CSCs, proliferating and quiescent, which occupy different niches inside the tumor. The proliferative CSCs are chemoresistant but vulnerable to overdoses of the chemotherapeutics; however, quiescent CSCs are in the autophagic state and could survive even high doses of anti-cancer

drugs, thus enabling tumor relapse (6). One of the key phenomena responsible for regulation of stemness is epithelial–mesenchymal transition (EMT) viewed as a continuum of phenotype cellular states from complete epithelial and proliferative state, through several intermediate hybrid states to complete mesenchymal and invasive phenotype. Cancer stem cells could represent any of these steps due to the outstanding plasticity (7). This plasticity of CSCs is highly dependent on the patient’s immunosurveillance as well as on epigenetic and environmental signals from the TME (6). The most recognized stressors that could influence both phenotype and function of CSCs are hypoxia, acidity, mechanical stress, immunological response, epigenetic changes like DNA methylation, histone and non-coding RNA modifications, and, finally, activation of stemness signaling pathways (8–11).

The problem of the stemness is directly connected to the cancer dormancy that is dependent on the presence of circulating tumor cells (CTCs) and disseminated tumor cells (DTCs) that have partially overlapping functions and are enriched by the population of quiescent CSCs (12). CTCs, DTCs, and CSCs are able to produce micrometastases that migrate and home inside the target organs in the pre-metastatic niches composed from tumor cells and recruited local stromal and immune cells from the environment. Quiescent CSCs and dormant DTCs inside pre-metastatic niche show overexpression of signaling pathways, enabling them to survive in stressful conditions, including chemotherapeutics (13–15).

Ovarian CSCs are characterized by cell surface CD44, CD117, CD133, CD24, MyD88, epithelial cell adhesion molecule (EPCAM), leucine-rich repeat containing G protein–coupled receptor-5 (LGR5), and LGR6] and intracellular [aldehyde dehydrogenase (ALDH), sex determining region Y-box 2 (SOX2), octamer-binding transcription factor-4 (OCT4), homeobox protein NANOG transcription factor (NANOG), and forkhead box protein M1 (FOXO1)] markers, as well as by their specific behavior (“side-population” cells). The markers for characterization of OCSCs, their function, and clinical significance are presented in Table 1. The OCSC markers

TABLE 1 The markers for characterization of OCSCs, their function, and clinical significance.

OCSC marker	Function	Clinical significance	Reference
CD44 CD44 spliced variant 6 (CD44v6)	Cell-surface glycoprotein, receptor for the hyaluronic acid receptor Activates EGFR/Ras/ERK and NANOG-dependent signaling pathways Resulting NANOG/STAT3 interaction upregulates multi-drug resistance CD44+ cells possess self-renewal, tumor-initiating and sphere-forming capability	High number of CD44+ cells in early stage HGSOC correlated with shorter PFS Expression correlated with advanced HGSOC, p53 positivity, tumor grade, and chemoresistance CD44+ cells are overrepresented in recurrent compared to primary HGSOC Increased CD44v6+ cell numbers in primary ovarian tumors correlated with shorter OS CD44v6+ cells are overrepresented in metastases Distant metastases-free survival is better in patients with CD44v6-low tumors Population of CD44+CD166+ cells is abundant in platinum-resistant ovarian cancer	(16–24)
CD117	Receptor tyrosine kinase coded by c-kit proto-oncogene Regulates cell proliferation, differentiation, apoptosis, and adhesion	CD117+ cells correlate with chemoresistance shorter OS, and shorter DFI	(25–30)

(Continued)

TABLE 1 Continued

OCSC marker	Function	Clinical significance	Reference
	<p>Binding CD117 to SCF is followed by activation of several pathways, including Ras/ERK, PI3K/AKT, and Src/JAK/STAT</p> <p>SCF produced by TAMs and CAFs is highly expressed in ascites of patients with HGSOE</p> <p>CD117+ cells are abundant in a sphere-forming non-adherent OCSCs and the “side population” OCSCs with increased capacity of self-renewal, tumorigenicity, and chemoresistance, as well as selective expression of ABC transporters</p>	<p>CD117+ expression present in HGSOE and correlated with chemoresistance</p> <p>CD44+/CD117+ cells are abundant in chemoresistant HGSOE and cell lines resistant to paclitaxel-induced apoptosis</p>	
CD133	<p>Prominin-1 is a transmembrane glycoprotein</p> <p>Activates PI3K/AKT pathway</p> <p>Is responsible for tumorigenicity, vascularization and chemoresistance</p> <p>Cooperation between CD133 and ETRA augments sphere-forming capacity and homing to peritoneal surface</p> <p>NF-κB and p38/MAPK-dependent pathways enhance self-renewal of CD133+ cells</p>	<p>CD133+ cells are more abundant in recurrent chemoresistant tumors</p> <p>Expression of CD133+ correlated with the HGSOE type, stage, ascites, and chemoresistance</p> <p>CD133+ cells correlated with shorter PFS and OS</p> <p>CD133+/CXCR4+ cells are more platinum-resistant compared to CD133 negative cells</p>	(31–37)
CD24	<p>Heat-stable antigen CD24, a transmembrane adhesion molecule</p> <p>Activates JAK/STAT3 signaling pathways and NANOG and OCT4 expression</p> <p>Through stimulation of PI3K/AKT/MAPK pathway is able to stimulate EMT</p> <p>Stimulates stemness, tumor growth, and chemoresistance</p> <p>CD24+ cells form spheroid structures</p> <p>Exosomes present in ascites contain CD24 and EpCAM, which regulate signals between OCSCs and TME</p>	<p>CD24+ cells are abundant in peritoneal implants compared to primary tumor</p> <p>Inhibition of JAK/STAT3 pathway reduces OCSC stemness and improves patient’s survival</p> <p>CD24+ expression is a predictor of poor outcome in patients with ovarian cancer</p> <p>Expression of CD24+ correlates with cancer stage and presence of peritoneal implants and metastases</p>	(29, 38–43)
EpCAM	<p>Epithelial cell adhesion molecule is a type I transmembrane glycoprotein regulating intercellular adhesion</p> <p>EpCAM+ cells show greater tumor-initiating potential</p> <p>EpCAM/Bcl-2 pathway prevents platinum-dependent apoptosis of cancer cells</p> <p>EpCAM+CD45+ cells constitute the chemoresistant phenotype in the ascitic fluid of patients with ovarian cancer. These cells overexpress <i>SIRT1</i>, <i>ABCA1</i>, and <i>BCL2</i> genes. EpCAM+CD45+ population is highly invasive with signature mesenchymal gene expression and also consists of CD133+ and CD117+CD44+ OCSCs</p>	<p>EpCAM expression is increased in chemoresistant tumors and correlated with poor outcome</p> <p>EpCAM+ cells are a source of relapse after the chemotherapy</p>	(20, 44, 45)
MyD88	<p>Myeloid differentiation primary response gene 88 is an adaptor protein for signals generated from TLR-4 receptor</p> <p>TLR-4/MyD88 pathway is responsible for chemoresistance and activates inflammatory pathways in carcinogenesis</p>	<p>Expression of MyD88 is an unfavorable prognostic factor in ovarian cancer</p> <p>CD44+/MyD88+ cells show increased tumorigenicity, sphere formation, and chemoresistance</p>	(28, 46)
LGR5 and LGR6	<p>Leucine-rich repeat containing G protein-coupled receptor-5 and receptor-6 are biomarkers of adult stem cells</p> <p>Expression of LGR5 promotes proliferation and metastasis, and EMT in ovarian cancer</p> <p>LGR5- and LGR6-mediated signaling is responsible for activation of Wnt/β-catenin pathway in OCSCs</p>	<p>LGR5 expression is correlated to ovarian tumor stage and histologic grade</p> <p>LGR6 expression and activation of Wnt/β-catenin pathway are observed in tubal fimbria of patients with HGSOE</p>	(47, 48)
ALDH	<p>Aldehyde dehydrogenases are aldehyde-converting enzymes</p> <p>ALDH1 subgroup of enzymes is engaged in protection of cancer cells against chemotherapy and radiation</p> <p>ALDH1A1 and ALDH1A2 are the most popular phenotypes found in OCSCs</p> <p>ALDH1 activates the Wnt/β-catenin pathway and transmembrane transporters</p>	<p>Ovarian cancer cells pre-treated with growing doses of platinum show increased number of ALDH1+ cells</p> <p>HGSOE cells showing ALDH1+/EGFR+ phenotype are correlated with the worse prognosis</p> <p>High expression of ALDH1+ cells correlates with chemoresistance</p> <p>CD44+/CD133+/ALDH1A1+ cells are increased in recurrent tumors</p> <p>Expression of CD133+/ALDH1+ correlates with shorter PFS and OS in HGSOE</p>	(49–52)
NANOG	<p>Homeobox protein NANOG transcription factor</p> <p>Regulates self-renewal and pluripotency of embryonic and CSCs cells, and EMT</p> <p>Through STAT3 signaling pathway upregulates chemoresistance</p>	<p>Expression of NANOG+ cells correlates with clinical stage, histologic grade, and chemoresistance</p>	(17)

(Continued)

TABLE 1 Continued

OCSC marker	Function	Clinical significance	Reference
SOX2	Sex determining region Y-box 2 transcription factor Regulates self-renewal and pluripotency of embryonic and CSCs cells Overexpression of SOX2 enhances stemness by inhibition of PI3K/AKT signaling pathway	Highly SOX2+ cells are present in epithelium of tubal fimbriae in HGSOV and BRCA1/2+ patients	(53, 54)
OCT4	Octamer-binding transcription factor-4 is engaged in self-renewal of undifferentiated embryonic stem cells Stabilizes structure of chromatin in the NANOG locus Cytoplasmic expression of OCT4 regulates EMT Mechanosensory signals in the peritoneum stimulate EMT; enhance stemness by upregulation of OCT4, CD44, and CD117; and increase chemoresistance	Upregulation of OCT4 in ovarian cancer is correlated to chemoresistance Increased expression of OCT4 is observed in CD24+ OCSC cells	(40, 55–57)
FOXM1	Forkhead box protein M1 is a member of the FOX family of transcription factors Regulates cell cycle and controls genomic stability Upregulation of FOXM1 is followed by activation of Wnt/ β -catenin signaling pathway and enhances chemoresistance	Overexpression of FOXM1 is observed in OCSCs exposed to LPA present in ascites FOXM1 deactivation results in restoration of chemosensitivity and loss of ability to spheroid creation in peritoneum	(58–60)
MSH-1/MSH-2	MSH proteins regulate stemness of OCSCs and are aberrantly expressed in tumors. MSH proteins activate the NOTCH signaling	High expression of MSH proteins is correlated to shorter OS and enhances paclitaxel chemoresistance	(61–64)

CD, cluster of differentiation; EGFR, epidermal growth factor receptor; Ras, Ras small GTPase protein; ERK, extracellular signal-regulated kinase; NANOG, homeobox protein NANOG transcription factor; STAT3, signal transducer and activator of transcription 3; PFS, progression-free survival; OS, overall survival; SCF, stem cell factor; PI3K, phosphoinositide-3-kinase; AKT, protein kinase B; Src, non-receptor tyrosine kinase Src; JAK, Janus kinase; TME, tumor microenvironment; TAMs, tumor-associated macrophages; CAFs, cancer-associated fibroblasts; ABC transporters, ATP-binding cassette drug membrane transporters; DFI, disease-free interval; ETRA, endothelia receptor A; NF- κ B, nuclear factor- κ -light chain enhancer of activated B cells; p38/MAPK, p38 mitogen-activated protein kinase; CXCR4, C-X-C chemokine receptor type-4; OCT4, octamer-binding transcription factor-4; EMT, epithelial-mesenchymal transition; Bcl-2, B-cell lymphoma-2 molecule; TLR-4, Toll-like receptor type-4; LGR5, leucine-rich repeat containing G protein-coupled receptor-5; ALDH, aldehyde dehydrogenase; Wnt, wingless and Int-1; SOX2, sex determining region Y-box 2; FOXM1, forkhead box protein M1; LPA, lysophosphatidic acid; SIRT1, sirtuin-1; BCL2, B-cell lymphoma-2; MSH, Musashi protein; NOTCH, neurogenic locus notch homolog.

unfortunately are not cancer stem cell specific, as they are also present on normal stem cells. Another feature of OCSCs is activation of signaling pathways upregulating their stemness, cancer proliferative capability, and chemoresistance. The most important and studied pathways for preservation of OCSC function are Wnt/ β -catenin, Hedgehog, Hippo/yes-associated protein (YAP), neurogenic locus notch homolog (NOTCH), nuclear factor- κ -light chain enhancer of activated B cells (NF- κ B), hypoxia-induced factor-1 α (HIF-1 α), PI3K/protein kinase B (AKT), Janus kinase (JAK)/signal transducer and activator of transcription protein (STAT), transforming growth factor- β (TGF- β), and Rho/Rho-associated protein kinase (Rho/ROCK) pathways. The functional and clinical characterization of these pathways is included in Table 2.

Tumor microenvironment in ovarian cancer

Ascites is a unique microenvironment for OCSCs and is responsible for exceptional biology of ovarian cancer, shaped by the transcoelomic spread of peritoneal implants. The EMT process enables the tumor cells from primary localization to seed in the form of multiform cellular conglomerates, mostly adopting the form of spheroids enriched in OCSCs. They are transported in fluid into distant places of peritoneal cavity, with the predisposition to home into the adipose tissue collections inside peritoneum, like “milky spots”, omental fat, mesentery, or bowel appendices (125).

Sphere-forming cells express OCSC markers CD44v6, CD117, ALDH1, and NANOG and are resistant to anoikis despite lack of anchorage to the surface (16, 126). The presence of cytokines [interleukin-6 (IL-6), IL-8, IL-10, and vascular endothelial growth factor (VEGF)], osteoprotegerin, and exosomes containing micro RNAs (miRNAs), cytokines, and growth factors further enhances stemness in the spheroids (38, 68, 127–129). Spheroids adhere to and destroy the mesothelium, go through the mesenchymal/epithelial transition, and start to proliferate (130, 131). TGF- β , CD133, and CD44 from spheroids stimulate mesothelium to produce fibronectin for cancer cells adhesion, enhance attachment of floating cells to the epithelial surface, and stimulate secretion of metalloproteinase-9 (MMP-9) that supports mesothelial invasion (108, 132). The initial opinions on random transportation of cellular conglomerates have been replaced by the theory of collective invasion, according to that clusters of cancer cells migrate in a directed and coordinated way (133). Collective invasion is described by some characteristic features, mainly preservation of cell-cell junctions, interaction with surface cells and ECM on their way, cooperative cytoskeleton dynamics enabling migration of clusters as a single unit, and multicellular polarity (120, 133–135). Despite a collective behavior, not all cells in the cluster are invasion-competent, and the population of cells that rule invasion is called “leader cells”. These cells delineate the way, change cellular contractility, and grow invadopodia, as well as respond to environmental signals (120, 136–138). Their presence at the front of the cluster results in its polarization. The coordinated movement requires rearrangement of the cytoskeleton, actinomyosin contraction, and activation of PI3K and Rho/ROCK

TABLE 2 The functional and clinical characterization of ovarian cancer stem cell signaling pathways.

Pathway	Function	Clinical significance	Reference
Wnt/β-catenin signaling	<p>Activation of ABC transmembrane transporter member-2 (ABCG2)</p> <p>Cooperation with LGR5 and LGR6 stemness markers for activation of the pathway in OCSCs</p> <p>Regulation of EMT through increase of the SNAIL/E-cadherin ratio and enhancement of OCSC motility and chemoresistance</p> <p>Promotion of pro-inflammatory and tumor-supporting phenotype of CAFs</p>	<p>Knock-down of β-catenin restores chemosensitivity in ovarian cancer cells</p> <p>Restoration of SFRP5 function inhibits Wnt/β-catenin signaling, EMT and re-establishes chemosensitivity</p> <p>Chemoresistant HGSOc tumors show the upregulation of Wnt/β-catenin-dependent target genes and OCSC markers</p>	(48, 59, 65–67)
Hedgehog signaling	<p>Activation of this pathway in OCSCs stimulates chemoresistance and spheroid formation</p> <p>Proteins GLI1 and SMO are the downward effectors of Hedgehog signaling</p> <p>GLI1 upregulates function of ABCB1 and ABCG2 transporters, thus supporting chemoresistance</p> <p>Hedgehog signaling is important for the interaction between OCSCs and CAFs</p>	<p>Malignant and chemoresistant ovarian tumors show increased expression of GLI1 and SMO compared to benign and chemosensitive tumors</p>	(68–70)
Hippo/YAP signaling	<p>Pathway is activated by stiffness of ECM and shear stress in OCSC environment (mechanosensory signals)</p> <p>Hippo/YAP pathway stimulates proliferation, metastasis, and chemoresistance in ovarian cancer</p> <p>Overexpression of YAP promotes EMT and cancer cell migration while inhibiting cells' anoikis</p> <p>Increase in the OCSC pool results from the activation of the Hippo pathway target genes upon MYPT1 downregulation</p>	<p>YAP expression is an indicator of poor prognosis in ovarian cancer</p> <p>Expression of the key genes related to Hippo/YAP signaling is correlated with PFS</p>	(71–74)
NOTCH signaling	<p>The NOTCH receptors are a membrane receptor proteins responsible for proliferation of cells and angiogenesis of the tumor</p> <p>NOTCH overexpression is observed in ovarian cancer, together with the downstream components of this pathway, like VEGF, VEGFR1, DLL4, and JAG1</p> <p>Tumor hypoxia enhances NOTCH signaling, stemness, and migration of OCSCs</p> <p>NOTCH pathway upregulates NANOG, OCT4, and ABCB1 transporter, thus increasing chemoresistance</p>	<p>High activity of NOTCH pathway is found in paclitaxel-resistant ALDH1+ OCSCs</p> <p>High expression of NOTCH is correlated with poor OS and DFS, and advanced or recurrent cancer</p> <p>Inhibition of NOTCH signaling restores chemosensitivity</p>	(75–77)
NF-κB signaling	<p>NF-κB is a protein complex functioning as a transcription factor responsible for cellular response towards stress, cytokines, reactive oxygen species, antigens, and inflammation</p> <p>Inhibition of NF-κB signaling induces apoptosis, restores chemosensitivity, and decreases the CD44+ OCSC population</p> <p>Cooperation between CAFs and OCSCs results in the upregulation of NF-κB signaling in OCSCs</p> <p>Inflammatory signals from the tumor environment enhance NF-κB pathway and stemness of cancer cells</p> <p>NF-κB over-activity characterizes CD44+MyD88 + OCSCs</p> <p>A matrix protein periostin expressed in highly aggressive ovarian cancer is involved in NF-κB-mediated over-activity of M2 macrophages and CAFs that promote tumor growth</p> <p>The TLR4/NF-κB/HIF-1α signaling loop promotes progression of ovarian cancer</p>	<p>Overexpression of NF-κB is correlated with chemoresistance and poor prognosis in HGSOc</p> <p>Expression of NF-κB is correlated to high stage and grade of ovarian cancer</p> <p>NF-κB mediates the BRCA1-induced chemoresistance</p> <p>Signal transduction pathway activity analysis of HGSOc revealed that the low activity of PI3K together with the high activity of NF-κB pathway has favorable prognosis and indicates more active immune response, whereas the high PI3K and the low NF-κB pathway activity has poor prognosis and indicates high cell proliferation</p>	(78–86)
HIF-1α signaling	<p>Hypoxic environment is followed by increased expression of transcription factor HIF-1α</p> <p>HIF-1α signaling activates EMT and stemness-regulating pathways, like Wnt/β-catenin,</p>	<p>Patients with higher expression of HIF-1α have shorter OS</p> <p>Patients with III stage of platinum-resistant HGSOc has overrepresentation of HIF-1α signaling pathway</p>	(87–90)

(Continued)

TABLE 2 Continued

Pathway	Function	Clinical significance	Reference
	<p>Hedgehog, and NOTCH while downregulating NF-κB pathway</p> <p>HIF-1α signaling upregulates OCSC markers CD133, NANOG, and SOX2</p> <p>SIRT1 is a downstream target gene for the HIF-1α pathway, involved in promotion of OCSCs by hypoxia, and NF-κB signaling cooperates with HIF-1α in SIRT1 upregulation</p>		
PI3K/AKT signaling	<p>CAFs stimulate ovarian cancer invasiveness and chemoresistance through the activation of HGFR/PI3K/AKT signaling</p> <p>Interaction with MSCs leads to activation of PI3K/AKT pathway and MDR proteins in OCSCs</p> <p>Defective function of <i>CTNNB1</i>, <i>PTC</i>, <i>SMO</i>, <i>NOTCH</i>, <i>k-Ras</i>, and <i>MEK</i> genes disturbs between others the function of PI3K/AKT pathway in OCSCs</p> <p>Loss of <i>BRCA</i> expression is also followed by activation of PI3K/AKT pathway in OCSCs</p> <p>PI3K/AKT/mTOR pathway is activated by abundance of nutrients and growth factors in TME that inhibits autophagy in cancer cells</p> <p>Activation of PI3K/AKT/mTOR signaling results in upregulation of CD44v6, CD117, and ALDH1A1 OCSC markers as well as enhancement of EMT in chemo resistant ovarian cancer cell lines</p> <p>Shear stress exerted by ascites together with HGF stimulate stemness and chemoresistance by HGFR/PI3K/AKT-miR-199a-3p pathway</p> <p>Blocking CXCR4/PI3K/AKT/mTOR signaling results in reduction of OCSCs and inhibition of EMT</p> <p>Circular RNA circ_0000745 upregulated by IGF2BP2 stimulates stemness of ovarian cancer cells through a miR-3187-3p/ERBB4/PI3K/AKT pathway</p>	<p>High expression of PI3K or AKT is correlated to shorter OS in ovarian cancer</p> <p>UBE2S is a potential oncogene that, through stimulation of PI3K/AKT/mTOR pathway, enhances proliferation and migration of ovarian cancer. Its high expression is a poor prognostic factor</p> <p>Inhibition of PI3K in wild-type <i>PI3KCA</i> ovarian cancer induces <i>BRCA</i> downregulation and with PARP inhibitors shows synergistic effect against ovarian cancer</p>	(91–103)
JAK/STAT signaling	<p>Inhibition of JAK2/STAT3 signaling results in decrease of stemness and reduced tumor growth</p> <p>Inhibition of JAK/STAT pathway in HGSOC cells and CAFs has anti-tumor activity</p> <p>OCT4 accelerates tumor growth and enhances chemoresistance through activation of JAK/STAT pathway in OCSCs represented by “side population”</p> <p>LIF and IL-6 secreted by MSCs promote OCSC function by STAT3 signaling</p>	<p>Higher expression of STAT3 is correlated to poor prognosis in ovarian cancer</p>	(38, 104–107)
TGF-β signaling	<p>TGF-β is one of the pro inflammatory cytokines secreted by CAFs in the OCSC niche</p> <p>Spheroid cancer cells through secretion of TGF-β force mesothelial epithelium to home cancer implants</p> <p>TGF-β secreted by CAFs and TILs stimulates epigenetic changes that promote EMT</p> <p>Enrichment of OCSC population by MSCs is mediated by TGF-β</p> <p>Upregulation of TGF-β together with VEGF and HIF-1α enhances angiogenesis and stemness</p> <p>OCSCs convert the immature DCs into the TGF-β-secreting cells, which support the expansion of Treg lymphocytes defending the tumor</p> <p>TGF-β induces the population of pro-angiogenic N2-polarized TANs that support tumor growth and vascularization</p> <p>miR-33a-5p through the downregulation of</p>	<p>miR-506 prevents TGF-β-induced EMT. Ovarian tumors showing increased miR-506 expression correlated with better prognosis for the patients</p> <p><i>STMN2</i> and <i>RAD51AP1</i> genes overexpression are correlated with poor prognosis in HGSOC and associated with TGF-β signaling pathway</p> <p>TGF-β-induced stimulation of CAF-derived periostin secretion is correlated with reduced survival in HGSOC</p> <p>Seven unfavorable genotypes associated with regulation of TGF-β-mediated signaling are correlated to shorter OS and PFS in patients with ovarian cancer</p> <p>NR2F1 that reveals a high correlation with poor prognosis and tumor stage regulates EMT and immunosuppressive CAFs infiltration through TGF-β signaling</p>	(84, 108–119)

(Continued)

TABLE 2 Continued

Pathway	Function	Clinical significance	Reference
	CROT and activation of TGF-β signaling promotes tumor growth and paclitaxel resistance		
Rho/ROCK signaling	ECM stiffness and tissue tension exerted by ascites activate Rho/ROCK pathway and regulate EMT Rho/ROCK signaling is an important mediator in tumor angiogenesis Rho/ROCK pathway is used by invading cell clusters and “leader cells”	Pharmacological inhibition of LPA-mediated stimulation of Rho/ROCK pathway decreases tumor aggressiveness Inhibition of Rho/ROCK pathway blocks HIF-1α signaling and restores platinum sensitivity of ovarian cancer cells	(120–124)

SNAIL, zinc-finger transcription factor SNAI1; SFRP5, secreted frizzled-related protein-5; CAFs, cancer-associated fibroblasts; GLI1, zinc-finger protein GLI1; SMO, smoothed class frizzled protein-coupled receptor; YAP, yes-associated protein; ECM, extracellular matrix; EMT, epithelial-mesenchymal transition; MYPT1, myosin phosphatase targeting protein-1; PFS, progression-free survival; VEGF, vascular-endothelial growth factor; VEGFR1, VEGF receptor-1; DLL4, delta-like ligand-4; JAG1, protein Jagged 1; NANOG, homeobox protein NANOG transcription factor; OCT4, octamer-binding transcription factor-4; ABC transporter, ATP-binding cassette drug membrane transporter; OS, overall survival; DFS, disease-free survival; NF-κB, nuclear factor-κ-light chain enhancer of activated B cells; TLR-4, Toll-like receptor type-4; HIF-1α, hypoxia-induced factor-1α; BRCA1, breast cancer type-1 susceptibility protein; SIRT1, sirtuin type-1; HGFR, hepatocyte growth factor receptor; MSCs, mesenchymal stem cells; MDR, multi-drug resistance; CTNNB1, catenin beta-1; PTC, papillary thyroid cancer oncogene; SMO, smoothed protein-coding gene; NOTCH, NOTCH receptor-coding gene; k-RAS, Kirsten rat sarcoma virus gene; MEK, mitogen-activated protein kinase kinase-1 coding gene; TME, tumor microenvironment; HGF, hepatocyte growth factor; mTOR, mammalian target of rapamycin kinase; CXCR4, C-X-C chemokine receptor type-4; UBE2S, ubiquitin-conjugating enzyme E2S; PI3KCA, phosphatidylinositol-3-kinase oncogene; PARP, poly-ADP ribose polymerase; TGF, transforming growth factor; TILs, tumor-infiltrating lymphocytes; DCs, dendritic cells; TANs, tumor-associated neutrophils; STMN2, stathmin-2 gene; CROT, carnitine O-octanoyltransferase; RAD51A1, RAD51-associated protein-1 gene; Rho/ROCK, Rho/Rho-associated protein kinase; LPA, lysophosphatidic acid.

pathways (120, 135, 139). After adhesion to the mesothelial surface, “leader cells” express proteolytic enzymes and penetrate the basement membrane (120, 140). The phenotype of “leader cells” is characterized by the keratin-14 (KRT14) expression. Their functional phenotype resembles the OCSC phenotype but does not correlate to EMT. The KRT14+ cells are able to re-establish the epithelial cells, show clonogenicity, are abundant in metastases, are enriched in response to chemotherapy, and promote the chemoresistance (120, 140–143). Cancer-associated fibroblasts (CAFs) present in TME play important role in collective invasion by regulation of TME remodeling to “pave” the routs for migrating cell clusters (120, 144). After exposition to chemotherapy, the population of apoptosis-resistant “leader cells” increases and shows expression of ALDH1 and CD44v6 stemness markers together with chemoresistance. Functional impairment of the “leader cells” restores chemosensitivity *in vitro* (145). After homing into peritoneal environment, OCSCs reside inside the “metastatic niche” composed of several cell populations, ECM components, lipids, exosomes, regulatory RNAs, and hypoxia that are orchestrated to support the OCSCs. Table 3 presents the function and clinical significance of the main components of the TME inside the “metastatic niche”.

Obstacles in the treatment of the HGSOc

The treatment of ovarian cancer is based on debulking cytoreductive surgery, platinum-taxane-based first line chemotherapy, second-line chemotherapy, and targeted therapy approved by the FDA (Food and Drug Administration) and EMA (European Medicines Agency) using bevacizumab and poly-ADP-ribose polymerase (PARP) inhibitors. Several others drugs are being tested in clinical trials including programmed death-1 (PD-1)/programmed death ligand-1 (PD-L1) inhibitors. HGSOc is initially a chemosensitive tumor, especially in the cases of positive

BRCA germinal or somatic mutations. However, recurrent tumors are mostly chemoresistant due to activation of many mechanisms associated with the exceptional function and proliferative activity of OCSCs or reverse BRCA mutations occurring during the treatment. Moreover, the unique pattern of cancer spread inside peritoneal cavity that utilizes both collective invasion and sanguiferous route is relatively early phenomena in the course of the disease. The important obstacle in the effective treatment of HGSOc is also tumor heterogeneity comprehended as spatial heterogeneity in the different areas of the tumor, the inter-patient heterogeneity, and temporal heterogeneity between primary tumors, metastases, and recurrent disease. Even OCSCs themselves exhibit unexpected phenotypic plasticity and may differ in the same patient or among different patients depending on the cancer molecular type, advancement of the disease, patient health, and treatment scheme. The conclusion from those observations is that the use of the uniform treatment for all patients or for all temporal stages of the tumor is an oversimplification that results in observed unsatisfactory results in the context of both OS and PFS. The complexity of interaction between tumor cells, OCSCs, and TME in metastatic niche is another factor of great importance for supporting tumor growth, enhancing chemoresistance and the immune attack defiance. Therefore, tumor environment with all its components should also be treated as a target for anti-cancer therapy.

Remarks on the targeting of the OCSCs

Taking the abovementioned reflections into consideration, the interesting targets for multidirectional treatment are OCSCs themselves and the components of OCSC microenvironment, particularly metastatic niche. One of the most explored areas of anti-OCSCs therapy is drugs directed against OCSC markers, signaling pathways, and epigenetic regulators. Targeting OCSC

TABLE 3 The function and clinical significance of the main components of the tumor microenvironment inside the “metastatic niche”.

TME component	Function	Clinical significance	Reference
CAFs	<p>CAFs originate from peritoneal fibroblasts or MSCs activated by inflammatory signals, hypoxia, and exosomes produced by cancer cells</p> <p>Activated CAFs secrete TGF-β that stimulates EMT and metastases</p> <p>Increased expression of DKK3 protein enhances Hippo/YAP and Wnt/β-catenin signaling in CAFs thus supporting OCSCs</p> <p>CAFs enhance chemoresistance by activation of HGFR/PI3K/AKT pathway</p> <p>FGF secreted by CAFs stimulates VEGF secretion and OCSC stemness</p> <p>TME remodeling by secretion of ECM components and MMPs</p> <p>Suppression of cytotoxic TILs and enhancement of pro-inflammatory signals</p> <p>The existence of the functional loop between CAFs and ovarian cancer cells is reported, in which CAFs induce angiogenesis by secretion of IL-6, COX-2, and CXCL1, whereas cancer cells induce CAFs to secrete CXCL12, IL-6, and VEGF-A to further enhance angiogenesis</p>	<p>Four genes—<i>AXL</i>, <i>GPRI76</i>, <i>ITGBL1</i>, and <i>TIMP3</i>—identified as ovarian cancer CAF-specific genes allow to construct the prognostic CAF signature. High CAF signature correlates to chemoresistance and activation of signaling pathways regulating tumor progression</p> <p>Molecular CAF signature characterized by the expression of six CAF-related genes (<i>COL16A1</i>, <i>COL5A2</i>, <i>GREM1</i>, <i>LUM</i>, <i>SRPX</i>, and <i>TIMP3</i>) show that high-risk patients have worse prognosis, ineffective immune response, and low tumor mutational burden</p> <p>CAF-score based on molecular characteristics of CAF-related genes and signaling pathways allows classifying patients with ovarian cancer to high- or low-risk population. Higher CAF score is observed in advanced tumors and in patients with worse OS. Patients with low CAF score have better efficacy of immunotherapy</p> <p>CAFs mediate chemoresistance of ovarian cancer to anti-angiogenic therapy</p>	(91, 110, 146–157)
CAAs	<p>Adipocytes are a source of lipids but also secrete adipokines, growth factors, immune mediators, and metabolic agents</p> <p>Omental implants are an example of OCSC niche supporting energetically and proliferatively stem cells</p> <p>Recruitment of OCSCs into the adipose tissue depends on IL-6, IL-8, MCP-1, and TIMP1</p> <p>Interaction between IL-8 secreted by CAAs and CXCR1 on cancer cells activates metastases through p38MAPK/STAT3 pathway</p> <p>Lipid transfer from CAAs to cancer cells depends on FABP4, which is upregulated especially in metastatic tumors</p> <p>ALDH+CD133+ OCSCs show high levels of desaturation of lipids</p> <p>Survival of OCSCs in adipose tissue TME depends on the function of SCD1, and elimination of SCD1 is synonymous with OCSC depletion</p> <p>Fatty acids supply energy for EMT</p>	<p>High levels of fatty acids desaturation and oxidation in FABP4-positive tumors correlate with poor prognosis</p> <p>FASN expression correlates with stage and grade of ovarian cancer, and patients showing high FASN expression have worse prognosis and chemoresistant tumors</p>	(158–164)
ADSCs	<p>ADSCs promote generation of OCSCs with use of Hedgehog/BMP4 signaling. Through secretion of IL-6, IL-8, VEGF, and TNF-α, ADSCs enhance chemoresistance. They are capable to differentiate into CAFs and CAAs</p>		(165–167)
MSCs	<p>MSCs are recruited from bone marrow, adipose tissue, and endometrium and are able to differentiate into CAFs</p> <p>MSCs stimulate proliferation, stemness, angiogenesis, and platinum resistance</p> <p>IL-6 and LIF secreted by MSCs enhance OCSC function in the STAT-dependent way</p> <p>MSC-derived TGF-β and VEGF/HIF-1α signals contribute to OCSC support and angiogenesis</p> <p>Bone marrow MSCs enhance chemoresistance of ovarian cancer by releasing miR-1180 that activates Wnt/β-catenin signaling</p>	<p>Interactions with MSCs activate PI3K/AKT pathway and MDR in OCSCs followed by paclitaxel and platinum resistance</p>	(94, 106, 111, 147, 166, 168–171)
TAMs	<p>Conversion of monocytes into TAMs is triggered by LIF and IL-6 present in ascites</p> <p>TAMs residing inside “metastatic niche” show immunosuppressive M2 phenotype and take part in immune escape of the tumor, regulation of angiogenesis, invasion, and stemness</p> <p>Hypoxia in ovarian cancer TME shifts polarization of TAMs into M2 phenotype through miR-222-3p and miR-940 released from cancer cells and activation of STAT</p>	<p>Patients with higher M1/M2 TAMs ratio have better OS and PFS</p> <p>M2 TAM infiltration is correlated to worse OS</p>	(32, 172–182)

(Continued)

TABLE 3 Continued

TME component	Function	Clinical significance	Reference
	<p>pathway</p> <p>Another signal for M2 differentiation of TAMs are cytokines IL-4, IL-10, and IL-13 secreted from both cancer and MSC cells</p> <p>By secretion of pro-inflammatory IL-17, TAMs stimulate p38MAPK and NF-κB pathways that induce self-renewal of CD133+ OCSCs</p> <p>TAMs secrete VEGF and EGF that induce spheroid formation and peritoneal spread of cancer implants</p> <p>M2-type TAMs create and support tumor tolerance by inhibition of NK and cytotoxic T-cell activity and by stimulation of Tregs</p>		
	<p>UBR5-mediated immunosuppressive TAM infiltration augments tumor growth and metastases and, through activation of p53/β-catenin/CCL2 pathway, stimulates spheroid formation</p> <p>CAPG gene expression is correlated with infiltration of tumors by Tregs, M2 TAMs, and exhausted T cells contributing to immunosuppression in HGSOC</p> <p>TAMs exert pro-tumor and immunosuppressive effects through secretion of IL10, TGFβ, VEGF, and expression of PD-1 and consumption of arginine to inhibit T-cell efficacy</p>		
CD4+CD25+FoxP3+ Tregs	<p>Expression of suppressive molecule IDO by cancer and dendritic cells contributes to recruitment of Tregs into the tumors</p> <p>Tregs from ovarian tumors show upregulation of TGF-β that inhibits secretion of IL-2, IFN-γ and TNF-α followed by impairment of T CD4+ and T CD8+ effector cells</p> <p>Ovarian OCSCs through CCL5–CCR5 interaction recruit Tregs, which, upon culture with CD133+ OCSCs, secrete high levels of IL-10 showing inhibitory immune function and MMP-9 that enables invasion of cancer cells</p> <p>Tregs infiltrating ovarian tumors show highly activated phenotype (PD-1, 4-1BB, and ICOS) responsible for immunosuppression</p>	<p>High numbers of Tregs in tumor immune infiltrates are considered a sign of poor prognosis</p> <p>T CD8+/Tregs and CD4+/Tregs ratio are a good predictors of patient survival</p> <p>Abundance of Tregs and increased VEGF in ascites are observed in patients with poor prognosis</p> <p>However, the prognostic value of Tregs depends on the tumor type and stage, and, in HGSOC tumors, lower Th17/Tregs ratio was correlated with better survival</p>	(183–190)
mDCs and pDCs	<p>Tumor and ascites DCs originate from peripheral blood mDCs express IDO and PD-1 and are associated with immunosuppression of anti-cancer T CD4+ helper and T CD8+ cytotoxic effectors</p> <p>Tumor growth is accompanied by increasing numbers of mDCs, and tumor-derived PGE2 and TGF-β further promote the function of mDCs</p>	<p>The correlation between higher concentration of tumor-associated pDCs and shorter PFS was found</p> <p>The presence of mature DCs correlates with improved prognosis in HGSOC</p>	(191–193)
	<p>Immature mDCs are capable to regulate angiogenesis in the tumor</p> <p>pDCs accumulate preferentially in ascites and their chemoattraction depends on expression of CXCL12</p> <p>pDCs stimulate the generation of IL-10+ T CD8+ suppressor cells and promote angiogenesis through the secretion of IL-8 and TNF-α</p> <p>The population of tumor-associated pDCs differs functionally from ascitic pDCs and secretes lower levels of pro-inflammatory cytokines</p>		(187, 194–197)
MDSCs	<p>MDSC cells possessing CD11b+/Gr-1+ phenotype are a cell population regulating both chronic inflammation and tumor progression</p> <p>MDSCs are able to suppress maturation of DCs and cytotoxic reactions against tumor mediated by T CD8+, NK, and NKT cells</p> <p>Recruitment and functional maturity of MDSCs in the ascites depend on CXCL12/CXCR4 interactions and PGE2 secretion</p> <p>IL-6 and IL10 in ascites increase the number of MDSCs and, through upregulation of STAT3 signaling, promote their suppressive activity by expression of ARG and iNOS</p>	<p>Blockade of a key cytokine for MDSCs function, IL10, restores immunosurveillance and improves survival</p> <p>Peripheral blood ARG/IDO/IL10+ MDSCs are especially abundant in patients with advanced ovarian cancer and their depletion is a good prognostic factor</p> <p>BRCA-mutated patients have less MDSCs and more T CD4+ effectors than patients with wild BRCA copy in early stage HGSOC, what could explain partly the survival benefit in this group of patients</p>	(198–205)

(Continued)

TABLE 3 Continued

TME component	Function	Clinical significance	Reference
	Inhibition of mTOR activity decreases MDSC infiltration of ovarian tumors and slows progression PGE2 produced by MDSCs enhances expression of PD-L1 through mTOR pathway. PD-L1 expression is particularly high in OCSCs having ALDH1+ phenotype		
ECM	Mechanosensory signals produced by ascites and tumor expansion regulate EMT and interaction with EMC, as well as enhance angiogenesis, stemness, and chemoresistance Shear stress stimulates stemness by increase of CD44, CD117, and OCT4 activity ECM stiffness upregulates expression of stemness CD133 marker Compression changes activity of the Wnt/ β -catenin pathway and regulates EMT Expression of PAX8 links migratory and adhesive properties of Fallopian tube epithelium, STIC, and HGSOE cells. Inhibition of PAX8 reduces ability of cancer cells to migrate and adhere to fibronectin and collagen	Chondroitin sulfate is upregulated in the ECM of more than 90% of HGSOE and linked to poor prognosis Acquisition of mesothelial–mesenchymal phenotype by cancer cells, characterized by expression of CALB2 and PDPN, regulates adhesion to ECM and tumor progression and is correlated to poor outcome	(55, 130, 206–212)
Exosomes	Exosomes loaded with miRNAs miR-409-3p and miR-339-5p are involved in Wnt/ β -catenin signaling pathway and stimulation of metastases in HGSOE Ascites contain exosomes transferring cytokines, growth factors, miRNAs, lipids, and OCSC markers CD44 and EpCAM between tumor environment and OCSCs Exosomes from cancer cells transfer CD44 into mesothelial cells stimulating MMP-9, which supports adhesion and invasion of spheroid cells to the peritoneal surface Tumor cells stimulate conversion of omental fibroblasts into CAFs by production of exosomes containing deregulated miRNAs miR-31, miR-214, and miR-155 Hypoxic environment reprograms TAMs into M2 polarization through exosomes containing miR-222-3p and miR-940 Omental CAFs and CAAs upregulate cancer cells' chemoresistance and activate anti-apoptotic pathways through miR-21–containing exosomes MSCs enhance tumor growth producing exosomes loaded with miR-21, miR-221, and miR-92a	Exosomal miR-146a secreted from MSCs reduces cancer growth and chemoresistance to taxanes Abundance of CD117-containing small extracellular vesicles in ascites correlates with tumor grade, chemoresistance, and recurrence Higher concentration of exosomes containing miR-21, miR-141, miR-200a, miR-200b, miR-200c, miR-203, miR-205, and miR-214 is found in serum of patients with ovarian cancer compared to patients with benign ovarian tumors Expression of <i>LBP</i> , <i>FGG</i> , <i>FGA</i> , and <i>GSN</i> genes in exosomes isolated from plasma is involved in coagulation and apoptosis related pathways and can be a potential diagnostic and prognostic biomarker for OS and PFS <i>CAV1</i> gene, which is the direct target of miR-1246, is involved in the process of exosomal transfer. Patients with high miR-1246 and low Cav1 expression have a significantly worse prognosis Serum exosomal level of lncRNA MALAT1 predicts advanced and metastatic ovarian cancer phenotype and correlates to OS	(43, 172, 173, 213–226)
	Exosomes containing miR-146b-5p produced by TAMs activate TRAF6/NF- κ B/MMP2 pathway that deregulates endothelial cell migration inside tumor Adipose tissue MSC-derived exosomes secreted into ascites promote tumor growth and peritoneal implants by activation of FOXM1 signaling Small extracellular vesicles released from ascites OCSCs upon cisplatin treatment are capable to activate the pro-tumorigenic phenotype in MSCs Exosomes secreted by expanded tumor-derived NK cells containing cisplatin can reverse chemoresistance of cancer cells and augment NK cytotoxic activity CD163+ TAMs secrete exosomes containing miR-221-3p that downregulates <i>ADAMTS6</i> and activate EMT, thus triggering the OCSC phenotype and chemoresistance FasL and TRAIL are components in exosomes secreted by cancer cells, responsible for apoptosis of immune cells of cancer infiltrate Ascite-derived exosomes transfer miR-6780b-5p to cancer cells promoting EMT and metastasizing CD47 is overexpressed in tumors and tumor-derived exosomes and facilitates tumor immune evasion. Inhibition of exosomal CD47 improves anti-cancer macrophage activity and suppresses peritoneal dissemination EXOSC4 is involved in RNA degradation. Knockdown of EXOSC4 inhibits the proliferation, migration, and invasion	Plasma exosomal miR-1260a, miR-7977, and miR-192-5p are significantly decreased in ovarian cancer compared with healthy controls Expression level of miR-205 in plasma exosomes of the ovarian cancer group is significantly higher compared to the benign and control groups and correlates with clinical stage and lymph node metastases	(227–234)

(Continued)

TABLE 3 Continued

TME component	Function	Clinical significance	Reference
	ability of ovarian cancer cells by suppressing the Wnt/ β -catenin pathway		
Hypoxia and acidosis	<p>Hypoxia and HIF-1α activation are capable of sustaining the CD117 expression through Wnt/β-catenin signaling</p> <p>Hypoxia and HIF-1α enhance stemness and EMT via activation of Wnt/β-catenin, Hedgehog, and NOTCH pathways, as well as CD133, SOX2, and NANOG markers</p> <p>Hypoxia/NOTCH/SOX2 signaling is important for maintaining OCSCs, as it enhances spheroid formation, upregulation of ALDH and ABC proteins, and chemoresistance</p> <p>Hypoxia and HIF-1α promote MDSCs to secrete TGF-β, IL-6, and IL-8 that enhance immunosuppressive conditions</p> <p>Hypoxia activates MAPK pathway to induce autophagy in OCSC cells</p> <p>Hypoxia attracts TAMs that support immune tolerance against tumor cells and predisposes mature DC cells to apoptosis</p> <p>Acidosis increases the expression of stemness markers OCT4 and NANOG and secretion of VEGF and IL-8 in OCSC niche</p> <p>Increased aerobic glycolysis in cancer cells is a source of lactate that strongly inhibits T and NK effectors, shifts TAMs into M2 phenotype, and recruits Tregs</p>	<p>The signature of genes associated with regulation of hypoxia and immune response allow to divide patients with ovarian cancer into high- or low-risk groups</p> <p>Higher <i>ALOX5AP</i>, <i>ANXA1</i>, <i>PLK3</i>, and <i>SREBF1</i> mRNA levels are significantly associated with shorter OS, whereas <i>LAG3</i> and <i>IGFBP2</i> lower mRNA levels with better prognosis, respectively</p> <p>Expression of seven hypoxia-related genes—<i>UQCERS1</i>, <i>KRAS</i>, <i>KLF4</i>, <i>HOXA5</i>, <i>GMPR</i>, <i>ISG20</i>, and <i>SNRPD1</i>—divides ovarian cancer into two populations with different prognosis</p> <p>Hypoxia-related miR-23a-3p is overexpressed in HGSOc showing chemoresistance and shorter PFS</p>	(96, 235–247)

TME, tumor microenvironment; CAFs, cancer-associated fibroblasts; MSCs, mesenchymal stem cells; DKK3, dickopf-related protein-3; YAP, yes-associated protein; PI3K, phosphatidylinositol-3-kinase; AKT, protein kinase B; HGFR, hepatocyte growth factor receptor; FGF, fibroblast growth factor; VEGF, vascular endothelial growth factor; ECM, extracellular matrix; MMPs, metalloproteinases; TILs, tumor-infiltrating lymphocytes; AXL, tyrosine-protein kinase receptor UFO coding gene; GPR176, G protein-coupled receptor 176 coding gene; ITGBL1, integrin subunit beta-like 1 coding gene; TIMP3, TIMP metalloproteinase inhibitor-3 coding gene; COL16A1, alpha 1 chain type XVI collagen coding gene; COL5A2, alpha 2 chain type V collagen coding gene; GREM1, Gremlin-1 protein coding gene; LUM, lumina protein coding gene; SRPX, sushi repeat containing protein X-linked coding gene; OS, overall survival; IL-6, interleukin-6; COX-2, cyclooxygenase-2; CXCL1, C-X-C motif chemokine ligand 1; CXCL12, stromal cell-derived factor 1; CAAs, cancer-associated adipocytes; MCP-1, monocyte chemoattractant protein-1; TIMP1, tissue inhibitor of metalloproteinase-1; CXCR1, C-X-C chemokine receptor type-1; FABP4, fatty acid binding protein-4; SCD1, stearyl-CoA desaturase-1; FASN, fatty acid synthase; ADSCs, adipose-derived stem cells; BMP4, bone morphogenetic protein-4; MSCs, mesenchymal stem cells; MDR, multi-drug resistance; LIF, leukemia inhibitory factor; HIF-1 α , hypoxia-induced factor-1 α ; TAMs, tumor-associated macrophages; p38/MAPK, p38 mitogen-activated protein kinase; EGF, epithelial growth factor; NK, natural killer; Tregs, T regulatory lymphocytes; OS, overall survival; PFS, progression-free survival; UBR5, ubiquitin protein ligase E3 component n-recogin-5; CCL2, chemokine ligand-2; CAPG, capping actin protein gelsolin-like gene; PD-1, programmed death-1; IDO, indoleamine 2,3-dioxygenase; TGF- β , transforming growth factor- β ; PGE2, prostaglandin E2; CCL5, C-C motif chemokine ligand-5; CCR5, CCL5 receptor; MMP-9, metalloproteinase-9; 4-1BB, CD137 or TNF factor receptor superfamily T-cell costimulatory receptor; ICOS, CD278 or inducible T-cell costimulator; mDCs, myeloid dendritic cells; pDCs, plasmacytoid dendritic cells; MDSCs, myeloid-derived suppressor cells; NKT, natural killer T cells; ARG, arginine; iNOS, inducible nitric oxide synthase; PAX8, paired box gene 8 protein; CALB, calretinin; PDPN, podoplanin; TRAF6, TNF receptor-associated factor protein-6; FOXM1, Forkhead box protein M1; ADAMTS6, ADAM metalloproteinase With thrombospondin type 1 motif 6; FasL, Fas ligand; TRAIL, TNF-related apoptosis-inducing ligand; LBP, lipopolysaccharide binding protein; FGG, fibrinogen gamma chain; FGA, fibrinogen alpha chain; GSN, gelsolin; CAF1, caveolin-1; lncRNA, long non-coding RNA; MALAT1, metastasis-associated lung adenocarcinoma transcript 1; EXOSC4, exosome component 4; ALOX5AP, arachidonate 5-lipoxygenase-activating protein; ANXA1, annexin-A1; PLK3, Polo-like kinase-3; SREBF1, sterol regulatory element-binding transcription factor 1; LAG3, lymphocyte activation gene-3; IGFBP2, insulin-like growth factor binding protein 2; UQCERS1, ubiquinol-cytochrome C reductase, Rieske iron-sulfur polypeptide 1; KRAS, Kirsten rat sarcoma virus; KLF4, Kruppel-like factor 4; HOXA5, homeobox protein Hox-A5; GMPR, guanosine 5'-monophosphate oxidoreductase; ISG20, interferon-stimulated gene 20-kDa protein; SNRPD1, small nuclear ribonucleoprotein D1 polypeptide.

markers is important as chemotherapy, whereas decreasing tumor burden simultaneously increases the number of OCSCs. After exposition to chemotherapy, increased numbers of ascitic EpCAM+, CD44+, and OCT4+ cells were noted (248). Similarly, recurrent tumors contain more ALDH1+, CD133+, and CD44+ OCSCs than primary tumors (49). These phenomena are observed not only in standard platinum/taxol-based chemotherapy but also in the tumors treated with PARP inhibitors (PARPis), where increased numbers of CD133+ and CD117+ OCSCs precede the acquired PARP resistance (249). However, targeting OCSC markers has to overcome two problems. The first one is that OCSC markers are not able to distinguish cancer stem cells exclusively, as about 75% of known cancer stem cell markers are also present on the surface of embryonic and adult stem cells (250). For instance, CD44 is present on hematopoietic cells, MSCs, and adipose-derived stem cells (251–253). CD117 is positive on 25% of embryonic stem cells (254), whereas CD166 is also found on epithelial cells, MSCs, and intestinal stem cells (255, 256). Intracellular cancer stem cell markers, like NANOG, OCT4, and SOX2, are also present in

normal stem cells (257, 258). The second problem is associated with the fact that there is no universal cancer stem cell marker known. Tumor heterogeneity, differentiation status, and environment are reasons for OCSC different types. Therefore, the more effective strategy of elimination of OCSCs relies on targeting of at least two OCSC markers simultaneously. Targeting the signaling pathways used by OCSCs is also reasoned by the fact that many of them are likewise OCSC markers, activated after exposition to chemotherapy (259). Epigenetic regulation in ovarian cancer is associated with both hypermethylation and hypomethylation of DNA, as well as with histone methylation and acetylation. Hypermethylation of DNA contributes to formation of OCSCs (260). The CpG islands of many onco-suppressor genes were shown to be hypermethylated in ovarian cancer, leading to the loss of DNA-repair function and cell cycle control desynchronization (261). Upon chemotherapy, hypermethylation of genes responsible for cell resistance to apoptosis was detected (262). Gene hypomethylation is frequently observed in advanced HGSOc and correlates with worse survival

(263). Histone methylation is engaged in upregulation of ATP-binding cassette drug membrane (ABC) transporters in chemoresistant OCSCs (264). Disturbed function of histone deacetylases promotes tumor progression (265). Table 4 contains data on both the experimental and clinical trials of targeting OCSCs.

Remarks on the targeting of the tumor microenvironment

One of the most important targets in TME is CAFs. However, the past experience with anti-CAFs therapy has indicated that the aim in this approach should be to revert CAFs functionally back to normal fibroblasts, rather than eradicating them completely from the TME. Eradication of CAFs has proved to change the tumor into more aggressive phenotype, instead of eliminating tumor cells (350). It is even more important taking into consideration that CAF populations of different tumor-promoting abilities and phenotype (CD49e+, fibroblast activation protein FAP-high or FAP-low) have been identified (351). The reprogramming of M2 tumor-associated macrophages (TAMs), another key population of tumor-supporting cells, into M1 phenotype could be similarly to CAFs, which is a better option than eliminating them completely (352). Another, recently identified population of cells in TME is cancer-associated mesothelial cells (CAMs) that originate from peritoneal normal mesothelial cells activated by cancer-derived promoting factors that induce mesothelial-mesenchymal transition and secretion of factors, enhancing peritoneal metastases and chemoresistance (353). Hepatocyte growth factor (HGF) released from ovarian cancer cells in hypoxic conditions induces the senescence of mesothelial cells and downregulates the expression of junctional proteins that results in disintegration of mesothelial integrity and enables cancer invasion through the mesothelial barrier (354, 355). Phenotypic changes of mesothelial cells to CAMs are mediated by TGF- β and CD44 and annexin A2 secreted inside exosomes from cancer cells (356–358). In response to those changes, CAMs secrete VEGF and upregulate fibronectin expression in ECM, thus promoting tumor vascularization and binding of tumor cells' integrins to ECM to support metastases (108, 359). Moreover, CAMs increase secretion of IL-8 and CCL2 that stimulate pyruvate dehydrogenase kinase-1 in cancer cells followed by increased expression of integrins to enhance adhesion and migration (360, 361). Interaction between intelectin-1 on CAMs and lipoprotein receptor-related protein-1 on cancer cells also contributes to invasion by upregulation of MMP-1 (362). CAMs pre-stimulated by cancer cell-derived TGF- β secrete osteopontin, which, in turn, activates CD44/PI3K/AKT pathway in OCSCs, leading to ABC transporters' overexpression and chemoresistance (363). M2-shifted TAMs also support CAMs activity by macrophage inflammatory protein-1 β that activates P-selectin secretion by CAMs, followed by stimulation of CD24 on the cancer cells' surface and increased adhesion (364). CAMs are, in turn, able to polarize the TAM phenotype into M2 type (365). CAMs are also capable to regulate the expression of glucose transporter type 4, resulting in increased glucose intake by cancer cells and growth promotion (362). Because of all above functions, CAMs are an interesting target for anti-TME therapy in ovarian cancer.

The next promising target for the therapy is metabolism of cancer cells. Cancer cells use both aerobic glycolysis (the Warburg effect) and oxidative phosphorylation (OXPHOS). Aerobic glycolysis protects cells from oxidative stress and fuels proliferation. However, OXPHOS and resistance to glucose deprivation in tumor environment are a metabolic adaptation enabling chemoresistance. Both ways of glucose metabolism are therefore used by cancer cells, including OCSCs and are another sign of their plasticity (366–368). The metabolic interactions between omental adipocytes and OCSCs are another reason for cancer progression and chemoresistance. Fatty acids could be very efficient source of energy that fuels the spread and growth of peritoneal implants (369). Adipocytes are stimulated by cancer cells to release fatty acids into metastatic niche, and, in turn, adipocytes induce expression of fatty acid receptor CD36 on cancer cells, thus enhancing uptake of fatty acids by cancer (370). Colonization of omental tissue depends on expression of salt-inducible kinase 2 (SIK2) in cancer cells. SIK2 kinase stimulates cell proliferation in PI3K/AKT-mediated manner and enhances paclitaxel resistance in HGSOc cells (371). Moreover, fatty acid oxidase and fatty acid synthase (FASN) have been shown to sustain survival of cancer cells in TME and increase resistance to anoikis and chemotherapy and spheroid formation in HGSOc lines (347, 372). Ovarian cancer CSCs indicate increased concentration of unsaturated lipids and what enhances cell membrane fluidity and facilitates OCSC plasticity and self-renewal. Inhibition of desaturases inhibits spheroid formation and abrogates tumor growth and metastases (373).

Another potential target for anti-TME therapy in HGSOc is exosomes. The identification of their origin inside TME and the recognition of their cargo have the key role in exosome-directed therapy. Exosomes could be also used as potential vehicles for the transportation of drugs into the tumor. It was also found that exosomes secreted from untreated tumors have a significant influence on the expression of many genes involved in functional change of fibroblasts into CAFs and in stimulation of tumor metastases. Such ability was less evident in exosomes secreted by pre-treated tumors (374). The situation is, therefore, complicated, as it seems that exosomes differ depending not only on the type of secreting cell but also on its functional status and temporal changes during therapy. Exosomes are able to influence several mechanisms of tumor growth. Their cargo, including proteins, neoantigens, cytokines, growth factors, and miRNAs, is responsible for cancer progression, metastases, and chemoresistance. Exosomes contain also modulators of immune response capable of inhibition of macrophages: natural killer (NK) cells, dendritic cells (DCs), and B and T lymphocytes (375, 376). Exosomes negatively regulate immunosurveillance of the host against tumor, through inhibition of T lymphocytes, NK cells, DCs, and monocytes in tumor environment and ascites (227, 377–379). Exosomes stimulate tumor angiogenesis affecting the VEGF and HIF-1 α expression and by activation of Wnt/ β -catenin and NF- κ B signaling pathways (380, 381). Exosomes influence also stroma remodeling by cooperation with CAFs and adipocyte-derived stem cells (165). Recently, tumor-derived exosomal miR-141 was identified as a regulator of stromal-tumor interactions and inducer of tumor-promoting stromal niche by activation of YAP/chemokine (C-X-C motif) ligand 1 (GRO α)/CXCR signaling pathway (382). One of the most interesting vectors

TABLE 4 Data on both the experimental and clinical trials devoted to targeting the OCSCs.

Target	Drug	Mechanism of action	Trial	Reference
CD44	ALM201	ALM201 is a residue peptide of FKBP1, which targets angiogenesis and CD44+ OCSCs by affecting the CD44/STAT3 pathway ALM201 is safe and well-tolerated, with stabilization of the disease in 22% of patients	Experimental Phase I dose-escalation human trial EudraCT	(266) (267)
	Imatinib mesylate monotherapy	Inhibition of CD117/PDGF signaling pathway. Treatment was well-tolerated, but no complete or partial responses were documented during a median follow-up of 6.6 months. However, 33% of patients had stable disease lasting from 4 to 8+ months. There was no relationship between best response (stable disease) and target expression Treatment showed low toxicity but also unsatisfactory anti-tumor activity. There were no objective responders. Median PFS was 2 months, and median OS was 10 months. Higher pre-treatment plasma concentrations of PDGF and VEGF were associated with shorter PFS and survival	Phase II NCT00510653 Gynecologic Oncology Group study Southwest Oncology Group Protocol S0211	(268) (269) (270)
CD117	Imatinib mesylate + docetaxel	Patients with heavily pre-treated recurrent ovarian cancer expressing CD117 or PDGFR α showed ORR of 22%, which included one complete and four partial responses, and additional three patients had stable disease for more than 4 months	Hoosier Oncology Group trial	(271)
	Salinomycin monotherapy	Salinomycin is the mono carboxylic polyether antibiotic inhibiting ABC-transporter system and promoting OCSC apoptosis. Encapsulated salinomycin in the form of salinomycin-loaded high-density lipoprotein showed effective cellular uptake and reduced the EMT, stemness, and angiogenesis mediated by OCSCs	Experimental	(272) (273) (274)
CD44/ CD117	Salinomycin + paclitaxel	Combined treatment reduced stemness and spheroid forming capability and enhanced apoptosis of ascitic OCSCs	Experimental	
	Metformin + bevacizumab + cisplatin	Combination of drugs reduced a significant number of CD44+CD117+ OCSCs and inhibited tumor growth	Experimental	
CD44/ MyD88	NV128	Isoflavone derivative causing depression of mitochondrial function and cellular starvation of OCSCs	Experimental	(275)
ALDH	673A	The result of ALDH1A inhibition is an accumulation of toxic aldehyde metabolites in OCSCs. The effects are stronger in combination with ATR inhibitors	Experimental	(276)
	CM37	ALDH1A inhibitor that disturbed spheroid production by the OCT4 and SOX2 downregulation	Experimental	(277)
	ATRA + carboplatin	A vitamin A derivative, in combination with carboplatin, suppresses ALDH1 expression and downregulates functionality of OCSCs	Experimental	(278)
	673A	The pan-ALDH1A inhibitor that preferentially kills CD133+ OCSCs through initiation of necroptosis and sensitizes tumor to platinum-based chemotherapy	Experimental	(279)
	Disulfiram	The anti-alcoholic medication, ALDH inhibitor, in combination with cisplatin, induced apoptosis and necrosis in ALDH+ cisplatin-resistant OCSCs	Experimental	(280)
	Selumetinib + Saracatinib	Both Src and MEK signaling kinases are co-activated in 31% of HGSOE. Combined treatment with Src inhibitor saracatinib and MEK inhibitor selumetinib decreased ALDH1+ cell sphere formation and loss of ALDH1+ OCSCs	Experimental	(281)
	PNA3 + guadecitabine	LncRNA HOTAIR is upregulated in HGSOE and especially in ALDH1+ OCSCs. Peptide nucleic acid PNA3 inhibits HOTAIR, and enhancer of zeste homolog 2 (EZH2) interaction and when combined with DNMT inhibitor guadecitabine abrogates ALDH1+ spheroid formation and decreases their number and tumor-promoting ability	Experimental	(282)
ALDH/ CD133	Salinomycin monotherapy	Graphene oxide–silver nanocomposite combined with salinomycin showed high toxicity against ALDH+CD133+ OCSCs	Experimental	(283)
	Licofelone	COX/5-LOX inhibitor that reversed stem-like properties in spheroids and augmented paclitaxel activity resulting in prolongation of mice survival	Experimental	(284)
	Metformin	Ovarian cancer II-IV FIGO. Metformin in combination with standard chemotherapy in neoadjuvant and adjuvant setting. Median PFS of 18 months, and median OS of 58 months. Tumors treated with metformin had a 2.4-fold decrease in ALDH+CD133+ CSCs and showed increased sensitivity to cisplatin	Phase II NCT01579812	(285)
CD133	Salinomycin monotherapy	Conjugates of salinomycin with anti-CD133 antibody and nanoparticles are effective in transportation of the antibiotic into CD133+ OCSCs	Experimental	(286)
	dCD133KDEL	Deimmunized <i>Pseudomonas</i> endotoxin conjugated to anti-CD133 antibody inhibits tumor growth	Experimental	(287)
	anti-CD133 CAR-NK cells + cisplatin	Sequential treatment using CAR-NK cells and cisplatin eradicated CD133+ OCSCs from cell lines and cell cultures obtained from ascites samples	Experimental	(288)

(Continued)

TABLE 4 Continued

Target	Drug	Mechanism of action	Trial	Reference
EpCAM	EpCAM-specific CAR-T cells Catumaxomab	Infusion of CAR-T cells delayed tumor progression in xenograft mice model of peritoneal carcinomatosis	Experimental	(289)
		Hybrid moAb against EpCAM/CD3. Intraperitoneal use of this moAb resulted in prolongation of puncture-free interval (two-fold from 12 to 27.5 days) and time to first therapeutic puncture (four-fold from 12 to 52 days) in heavily pre-treated patients with EpCAM+ recurrent tumors complicated with malignant ascites. The median puncture-free survival and overall survival were 29.5 and 111 days, respectively	NCT00326885 Phase II European Medicines Agency approved	(290)
		Deterioration of quality of life appeared earlier in control than in catumaxomab-treated group of patients with ascites (19–26 days vs. 47–49 days)	Phase II/III NCT00836654	(291)
		In patients with malignant ascites, peritoneal catumaxomab infusion enhanced the expression of the CD69 and CD38 activation molecules in T CD4+ and T CD8+, NK cells, and macrophages and enhanced T CD8+ accumulation into the peritoneal cavity	CASIMAS Phase IIIb NCT00822809	(292)
ATR	Ceralasertib (AZD6738) + olaparib M6620 (VX-970) + carboplatin	ATR is a protein kinase involved in recognition of DNA damage and activation of DNA damage checkpoint. Inhibitors of ATR combined with PARP inhibitors (PARPi) were able to overcome PARPi and platinum resistance in <i>BRCA</i> and <i>CCNE1</i> wild and mutated cell lines	Experimental	(293)
		Well-tolerated therapy with reduction in tumor burden, especially in <i>BRCA</i> -mutated patients (median PFS was 4.2 months overall and 8.2 months for patients with <i>BRCA1</i> mutations)	CAPRI phase II	(294)
		Partial response in platinum-resistant patients with <i>BRCA1</i> mutation. A patient with advanced germline <i>BRCA1</i> ovarian cancer achieved RECIST partial response despite being platinum-refractory and PARP inhibitor-resistant	Phase I	(295)
FAK	Defactinib (VS-6063) + paclitaxel VS-4718 + platinum APG-2449	FAK is a tyrosine kinase activated by matrix and integrin receptors controlling cell motility. FAK inhibitor VS-6063 enhances chemosensitivity and decreases CD44 OCSC marker. Combination with paclitaxel reduces >90% tumor weight. Modest activity in advanced platinum-resistant ovarian cancer	Experimental	(296)
		FAK inhibitor combined with platinum triggered ovarian cancer cell apoptosis and restored chemosensitivity	NCT01778803 Phase I Experimental	(297) (298)
		A multikinase inhibitor of FAK, ROS proto-oncogene 1 receptor tyrosine kinase (ROS1), and anaplastic lymphoma kinase (ALK). Combination of APG-2449 and osimertinib (EGFR tyrosine kinase inhibitor) and mitogen-activated extracellular signal-regulated kinase inhibitor trametinib overcomes osimertinib resistance	Experimental	(299)
Calcium channels	Manidipine Lacidipine Benidipine Lomerizine Manidipine + paziotinib	Calcium channel blockers were found to target the OCSC function by decreasing steroid formation, proliferation, and induction of apoptosis. Use of these drugs downregulated expression of stemness markers OCT4, NANOG, SOX2, ALDH1, and CD133.	Experimental	(300)
		Combination of calcium channel blocker with pan-HER inhibitor paziotinib showed synergism in reduction of OCSC spheroid formation, expression of stemness markers, and enhancement of apoptosis	Experimental	(301)
MSH-1/ MSH-2	siRNA	Dual knockdown of MSH-1 and MSH-2 downregulated OCSC ALDH4A1 and Myc and improved chemosensitivity	Experimental	(302)
ERβ receptor	LY5000307 (Erteberel) monotherapy	Selective agonist of estrogen receptor ERβ. Treatment with the agonist reduced the viability, sphere formation capacity, self-renewal, and invasion of OCSCs while augmenting their apoptosis	Experimental	(303)
NAMPT	FK866 + cisplatin	NAMPT is an enzyme for the NAD+ biosynthetic salvage pathway and is overexpressed in cancers. Combination of NAMPT inhibitor and cisplatin inhibited expression of ALDH1 and CD133 OCSCs and improved survival in the mouse model	Experimental	(304)
Survivin	AS602801	Inhibitor of c-Jun N-terminal kinase downregulates survivin. Chemo-sensitization of OCSCs to carboplatin and paclitaxel	Experimental	(305)
	CEP-1347	A small-molecule kinase inhibitor downregulates survivin and sensitizes OCSCs to standard chemotherapy	Experimental	(306)
Wnt signaling pathway	Ipafricept (OMP54F28) + carboplatin + docetaxel WNT974 + carboplatin Vantictumab (OMP-18R5)	Inhibitor of Fc-Frizzled-8 receptor antagonizing Wnt signaling. Sequential combined treatment is well-tolerated but has limited efficacy. The ORR was 76%. Median PFS was 10.3 months and OS was 33 months	NCT02050178 Phase I	(307)
		Inhibitor of PORCN that lowers secretion and binding of Wnt to its receptor. Combined therapy caused cell cycle arrest and cytotoxicity of cells isolated from ascites of patients with HGSOc	Experimental	(308)
		moAb that inhibits Wnt pathway by targeting the Frizzled receptors on cancer cells. Treatment with vantictumab before paclitaxel therapy sensitizes cancer cells to death	Experimental	(309)

(Continued)

TABLE 4 Continued

Target	Drug	Mechanism of action	Trial	Reference
Hedgehog signaling pathway	Cyclopamine	Steroidal alkaloid isolated from poisonous plant <i>Veratrum californicum</i> that inhibits Hedgehog signaling. Inhibition of spheroid-forming cells in the cell culture was observed upon treatment with cyclopamine	Experimental	(69)
	Vismodegib (GDC-0449) monotherapy	The SMO receptor antagonist. Therapy was well-tolerated; however, the anticipated increase in PFS was not achieved. Median PFS was 7.5 months in the treated group and 5.8 months in the placebo group. Hedgehog expression was detected only in 13.5% of tissues	NCT00739661 phase II	(310)
	Sonidegib (LDE225) + paclitaxel	The SMO receptor antagonist. Combination of drugs was well-tolerated and showed partial responses or stabilization of the disease in ovarian cancer	Phase I	(311)
NOTCH signaling pathway	LY900009 monotherapy	Inhibitor of γ -secretase protein. Therapy was well-tolerated, and five patients with solid tumors including ovarian cancer had stabilization of the disease	Phase I	(312)
	MK-0752 + cisplatin	Inhibitor of γ -secretase protein. Combination effectively stimulated cancer cells apoptosis and reduced growth of ovarian cancer xenografts in mice	Experimental	(313)
	RO4929097 monotherapy	Inhibitor of γ -secretase protein. Monotherapy in recurrent ovarian cancer was well-tolerated but had insufficient activity. Fifteen of the 40 patients had stabilization of the disease lasting with median of 3 months. The results were better in HGSOC with high expression of intracellular NOTCH protein	Princess Margaret, Chicago and California consortium Phase II	(314)
	Enoticumab (REGN421) monotherapy	moAb against DLL4–NOTCH ligand involved in angiogenesis. Therapy had acceptable toxicity. In the group of patients with solid tumors including ovarian cancer, two partial responses and 15 stabilizations of the disease were observed	Phase I	(315)
	Enoticumab + aflibercept	Combination of anti-DLL4 and anti-VEGF therapy showed greater anti-tumor effects compared to either monotherapy in murine model of ovarian cancer	Experimental	(316)
	Demcizumab (OMP-21M18) + paclitaxel	moAb against DLL4. Combination showed ORR of 21% with manageable toxicity in the group of patients with highly pre-treated HGSOC with platinum-resistant tumors	SIERRA Phase Ib	(317)
	Navicixizumab (OMP-305B83) monotherapy	Combined dual moAb anti-DLL4/anti-VEGF. Showed acceptable toxicity profile and reduced the tumors in seven of the 11 of patients with pre-treated ovarian cancer	Phase Ia	(318)
PI3K/AKT/mTOR signaling pathway	Navicixizumab (OMP-305B83) + paclitaxel	Combination demonstrated manageable toxicity and ORR of 33% in bevacizumab pre-treated patients, 64% in bevacizumab naive patients, and 62% in the biomarker (high angiogenesis and suppressed immune response)-positive group	Phase Ib	(319)
	Metformin monotherapy	Activation of AMPK followed by inhibition of signaling and reduction of energy consumption by OCSCs. Metformin inhibited cell viability, invasion, and autophagy while promoting apoptosis in paclitaxel-resistant ovarian cancer cell lines via downregulation of lncRNA SNHG—a regulator of PI3K/AKT/mTOR pathway	Experimental	(320)
	Metformin + cisplatin/paclitaxel	Combination of Metformin with chemotherapy significantly reduced cell proliferation and migration and increased chemosensitivity by reducing the OCSCs in treated cell lines	Experimental	(321)
	LY294002 + carboplatin	Addition of metformin to standard adjuvant or neo-adjuvant chemotherapy reduced two-fold concentration of ALDH+CD133+ OCSCs and increased cisplatin sensitivity of tumors, resulting in median OS of 58%	NCT01579812 Phase II	(285)
NF-κB signaling pathway	Atorvastatin	PI3K antagonist combined with carboplatin enhances its anti-cancer effect in mouse xenograft model	Experimental	(322)
	Metformin + cisplatin/paclitaxel	Statin that, through inhibition of AKT/mTOR pathway, stimulates apoptosis of ovarian cancer cells and inhibits cell invasion	Experimental	(323)
NF-κB signaling pathway	MK-5108 monotherapy	Metformin through inhibition of NF- κ B signaling pathway enhanced sensitivity to standard chemotherapeutics in both sensitive and resistant cell lines	Experimental	(324)
	Aurora-A kinase inhibitor	Aurora-A kinase inhibitor. Its use in ovarian cancer cell lines caused cell cycle arrest, inhibition of NF- κ B signaling, and cytokine secretion	Experimental	(325)
Hippo/YAP signaling	Verteporfin	Photosensitizer releases a singlet oxygen and ROS toxic to cancer cells upon exposure to light of particular wavelength. Verteporfin-loaded lipid nanoparticles inhibited tumor xenografts in mice upon laser light exposure	Experimental	(326)
	Verteporfin + carboplatin/taxol	Combination was efficient in reducing proliferation, invasion, and clonogenic capacity of ovarian cancer cell lines	Experimental	(327)
JAK/STAT signaling	Ruxolitinib + paclitaxel	Inhibitor of JAK, thus inhibiting the JAK/STAT pathway. Synergic effects of combined therapy on tumor growth in mouse model of advanced/ascites+ ovarian cancer	Experimental	(328)
	TG101209	JAK2 inhibitor that induced cytotoxicity in spire-forming CD24+ cells, thus inhibiting migration and metastasis of ovarian cancer in murine model	Experimental	(329)
	CYT387 + paclitaxel	Combination of JAK2 inhibitor with chemotherapy inhibited paclitaxel-mediated OCSC enrichment and reduced tumor burden in mouse xenografts	Experimental	(38)
	JQ1	Selective small-molecule bromodomain inhibitor that inhibits JAK/STAT pathway. JQ1 resensitized ovarian cancer cells to platinum	Experimental	(330)

(Continued)

TABLE 4 Continued

Target	Drug	Mechanism of action	Trial	Reference
TGF-β signaling	SB525334	TGF-β1 receptor inhibitor blocked ALDH1+ OCSCs self-renewal, invasion, and spheroid formation	Experimental	(331)
Src and MAPK signaling kinases	Selumetinib + Saracatinib	MAPK and Src inhibitors showed synergistic induction of apoptosis and tumor inhibition in ovarian cancer mouse model. Treatment decreased spheroid formation and ALDH1 expression	Experimental	(281)
DNA methylation	Decitabine + carboplatin	Decitabine is a DNMT1 inhibitor, a hypomethylating agent. In the group of pre-treated patients with solid tumors, containing two ovarian HGSOc tumors, a partial response to combined therapy was observed	NCT01799083 Phase II	(332)
	Decitabine + carboplatin/ paclitaxel + cytokine-induced killer cells (CIK)	The population of patients with chemoresistant recurrent ovarian cancer treated with combined regimen showed ORR of 87.5% and prolongation of PFS to 8 months and OS to 19 months	Phase II	(333)
	Guadecitabine + carboplatin	This regimen combining DNMT1 inhibitor with chemotherapy, compared to second-line chemotherapy alone, resulted in increased rate of patients having 6-months PFS (37% vs. 11%)	Phase II	(334)
	Guadecitabine + PNA3	PNA3 is HOTAIR inhibitor. Combined with DNMT1 inhibitor showed reduction of spheroids and ALDH1+ OCSCs	Experimental	(282)
	Azacitidine + carboplatin	Combination of DNMT1 inhibitor with carboplatin caused stabilization of the disease > 4 months in three patients with refractory or resistant ovarian cancer	Phase II	(335)
		Sequential combined treatment significantly slowed platinum-resistant HGSOc growth and activated immune-related pathways priming tumor for checkpoint inhibitor immunotherapy	Experimental	(336)
Histone deacetylation	Vorinostat monotherapy	HDAC inhibitor that induces accumulation of acetylated histones and transcription factors that arrest cell cycle. Monotherapy of platinum-resistant progressive HGSOc was well-tolerated; however, clinical efficacy was minimal (two women had PFS over 6 months, with one having a partial response)	Gynecologic Oncology Group Phase II	(337) (338)
	Vorinostat + carboplatin + gemcytabine	Combination was effective (partial response in six of the 15 patients) in recurrent platinum-sensitive ovarian cancer but was accompanied with hematological toxicity	Phase I	
	Belinostat (PXD-101) + carboplatin + paclitaxel	HDAC inhibitor that induces apoptosis and sensitizes tumor for chemotherapy. Combination had acceptable toxicity; in three of the 35 patients, complete response was obtained, and, in 12 of the 35 patients, partial response was obtained. ORR was 44% in platinum-resistant and 63% in platinum-sensitive patients.	Phase II	(339)
	Belinostat (PXD-101) + carboplatin	Combination was effective in 14 of the 27 patients with platinum-resistant ovarian cancer (one complete and one partial response; 12 patients had disease stabilization)	Gynecologic Oncology Group Phase II	(340)
	Entinostat (MS-275) monotherapy	Benzamide derivative of HDAC that inhibits selectively class I and IV HDAC. Entinostat was effective in therapy of intraperitoneal tumors in mouse model; however, its activity depended on immunocompetence represented by upregulation of MHCII and infiltration of T CD8+ cytotoxic cells in the tumors	Experimental	(341)
	Entinostat (MS-275) + olaparib	Combination potentiates the effect of olaparib in HR-proficient ovarian cancer and enhances olaparib-induced DNA damage	Experimental	(342)
Metabolism	2-deoxy-D-glucose (2DG)	Glycolysis inhibitor. In HGSOc tumors with reduced beta-F1-ATPase/oxidative phosphorylation, it sensitized cancer cells for platinum	Experimental	(343)
	Devimistat (CPI-613)	Mitochondrial metabolism inhibitor. Preferentially targets OCSCs and prevents acquired chemoresistance into olaparib or carboplatin/paclitaxel therapy	Experimental	(344)
	TVB-3166	Fatty acid synthase (FASN) inhibitor. Induced apoptosis in HGSOc model	Experimental	(345)
	USP13 knockdown	Inhibits ATP citrate synthase (ACLY) followed by inhibition of ovarian HGSOc tumors in the mouse xenograft model	Experimental	(346)
	Etomoxir	An irreversible inhibitor of carnitine palmitoyltransferase-1 (CPT-1) in mitochondria. Targets OCSCs and induces their apoptosis, and inhibits growth of tumor xenografts	Experimental	(347)
	Perhexiline	Inhibitor of carnitine palmitoyltransferase-1 (CPT-1) in mitochondria. Sensitized NKX2-8-deleted HGSOc lines to cisplatin	Experimental	(348)
	CAY-10566	Selective inhibitor of stearoyl-CoA-desaturase-1 (SCD1). Induced apoptosis and ferroptosis in HGSOc lines and eliminated OCSCs and spheroid formation	Experimental	(162, 349)

FKBP1, FK506-binding protein-like; PDGF, platelet-derived growth factor; PDGFR, platelet-derived growth factor receptor; ALDH, aldehyde dehydrogenase; ATRA, all-trans retinoid acid; COX, cyclooxygenase; 5-LOX, Arachidonate 5-lipoxygenase; NK, natural killer cells; CAR, chimeric antigen receptor; EpCAM, epithelial cell adhesion molecule; ATR, ataxia telangiectasia and Rad3-related protein; OCT4, Octamer-binding transcription factor 4; SOX2, sex determining region Y-box 2; NANOG, homeobox protein NANOG; FAK, focal adhesion kinase; CCNE1, cyclin E1; MSH, Musashi protein; siRNA, small interfering RNA; NAMPT, nicotinamide phosphoribosyltransferase; PORCN, porcupine acetyltransferase; SMO, smoothened receptor; moAb, monoclonal antibody; DLL4, delta-like ligand-4; VEGF, vascular endothelial growth factor; ORR, overall response rate; AMPK, AMP-activated protein kinase; lncRNA, long non-coding RNA; SNHG, small nucleolar RNA host gene 1; OS, overall survival; Src, Src non-receptor tyrosine kinase; MAPK, mitogen-activated protein kinase; JAK, Janus kinase; STAT, signal transducer and activator of transcription protein; DNMT1, DNA-(cytosine-5)-methyltransferase-1; ORR, overall response rate; PNA, peptide nucleic acid; HOTAIR, lac RNA HOX antisense intergenic RNA; PFS, progression-free survival; HDAC, histone deacetylase; MHC, major histocompatibility complex; HR, homologous recombination; USP13, ubiquitin specific peptidase 13; NKX2-8, NK2 Homeobox 8 protein.

of information between cancer cells and TME is non-coding miRNAs and long non-coding RNAs (lncRNAs). They were found in the serum and ascites of patients with ovarian cancer (227, 228); however, their presence in tumor-derived exosomes ensures safe and undisturbed transportation to the target cells. Non-coding RNAs play extremely important functions. Exosomes loaded with miR-1246 are able to enhance pro-tumorigenic effects of M2-shifted TAMs and to facilitate paclitaxel resistance (383). Cancer cell-derived miR-21-3p, miR-222, miR-125b-5p, miR-181d-5p, and miR-940 target TAMs and polarize them into M2 phenotype (172, 384). miR-99a-5p affects human peritoneal mesothelial cells and enhances cancer cell invasion (385). The Let-7a and miR-200a regulate tumor invasiveness (386). Exosomes containing lncRNAs ENST00000444164 and ENST0000043768 are responsible for activation of NF- κ B signaling in cancer cells (387). Table 5 presents data on targeting the components of TME and OCSC niche.

A novel regimen of therapy

The urgent need for improvement of efficacy in the HGSOc treatment is obvious, and many researchers have called attention to the novel approaches in diagnosis, monitoring, and management of patients with ovarian cancer. We have learned from the experience from therapy of hematologic cancers and several solid tumors that the individual approach to the treatment based on genetic, molecular, or metabolic signatures of the patients and the cancer itself usually results in better treatment efficacy and improved outcome. However, such individualization of therapy is much more difficult to be used in solid tumors, compared to hematologic malignancies, and ovarian cancer due to its unique biology is even more demanding and challenging target.

In the recent article devoted to OCSCs and OCSC-targeted treatment (470), we proposed that the novel complex standard of ovarian cancer therapy called the “DEPHENCE” system (“Dynamic PHarmacologic survEillaNCE”) should be worked out. In our opinion, it ought to be based on the following rules:

- 1) avoidance of monotherapy, as usually combination of several drugs directed against different targets, is more efficient and, if properly orchestrated, could be less toxic;
- 2) identification of the markers for pharmacologic compliance or resistance of the tumor and stratification of the patients according to the prognosis of treatment efficacy;
- 3) performing the sampling of the tumor (primary, metastatic, and recurrent) repetitively for characterization of genetic signature and TME features, which could change in the course of the disease and in the response to the treatment;
- 4) using the repeated biopsy of the tumor, but preferentially liquid biopsy, which enables to obtain more complex picture of growing tumor, as compared to standard biopsy the results of liquid biopsy do not depend on the site of the harvest of the sample;
- 5) such approach and individualization of the therapy could enable to restore the pharmacologic surveillance over the

tumor that fits the actual status of both tumor and the patient;

- 6) every line of treatment should simultaneously target cancer cells, OCSCs, and elements of TME, as well as should generate potentialization of the patient’s immune status;
- 7) HGSOc molecular types and different phases of the disease need different approach to the therapy;
- 8) at the beginning, such therapy could allow for stabilization of the disease, hopefully enabling prolongation of PFS and OS; however, in a distant future the goal of this approach should be complete curative.

We think that the necessary components incorporated into the DEPHENCE system should also be

- 1) identification of the high-risk population of women (gene mutations, single-nucleotide polymorphisms, metabolic syndromes, and environmental factors);
- 2) searching for the techniques of early detection or even for the screening tools both in the high-risk and general populations;
- 3) searching for the infection factors responsible potentially for ovarian cancer origin (viruses, microbiome disturbances);
- 4) looking for prognosis biomarkers of ovarian cancer.

The practical implementation of the “DEPHENCE” system in the diagnosis and therapy of ovarian cancer is still awaiting, although the first signs of its use can be seen in the attempts to classify the molecular signatures of the tumors and TME components (158, 458, 471–476), to personalize therapy according to the tumor origin, histology, and most of all to genomic and epigenomic disturbances. The first such studies grouped HGSOc tumors T into four subtypes: C1, high stromal response; C2, high immune signature; C4, low stromal response; and C5, mesenchymal, with low immune signature. These subtypes differed in the extent of immune infiltration, desmoplasia, and EMT predisposition, and what could suggest different approach to the treatment, including immunotherapy, and patients from the C1 and C5 subtypes showed poor survival compared with other subtypes (3). Another genomic classification was proposed by The Cancer Genome Atlas Research Network, which, based on the genomic pattern, divided the ovarian cancer into four subtypes: mesenchymal, immunoreactive, proliferative, and differentiated. Mesenchymal and proliferative subtypes showed profound desmoplasia and invasive gene expression pattern, with limited immune infiltration and activation of stemness markers. Both were characterized by unfavorable prognosis. Immunoreactive subtype showed extensive immune infiltration and, similar to differentiated more mature tumors, had better prognosis (477–479). The next analysis of tumor genome identified three novel ovarian cancer subtypes named tumor-enriched, immune-enriched, and mixed. The meaning of these subtypes for therapy implies that tumor-enriched tumors should be treated with tumor killing therapy, whereas immune-enriched tumors with immunotherapy or mixture of both approaches (480). Molecular

TABLE 5 Data on the experimental and clinical trials of drugs targeting the tumor microenvironment and OCSC metastatic niche.

Target	Drug	Mechanism of action	Trial	Reference
MSCs	Metformin	Prevention of reprogramming of MSCs into active cancer-associated cells and decrease of tumor Tregs. Clinical utility in early ovarian cancer and pre-treatment in immunotherapy regimens	Experimental	(388)
	Letrozole + Ruxolitinib	Combined therapy of anti-estrogen drug with inhibitor of JAK enables inhibition of LIF/IL-6-mediated signals from cancer-associated MSCs, which is followed by sensitization of ovarian cancer to anti-estrogen therapy	Experimental	(389)
MDSCs	Alemtuzumab	moAb targeting CD52 expressed by vascular leukocytes and Tie2+ monocytes, thus disturbing interactions with SIGLEC10. This moAb induces complement-dependent lysis of CD52-positive cells in ascites and restricts angiogenesis	Experimental	(390)
CAMs	Rilotumumab (AMG102)	Anti-HGF moAb. Although well-tolerated, the treatment showed very limited efficacy	Phase II	(391)
	Oregovomab monotherapy	Anti-MUC16 moAb. While used in monotherapy, oregovomab did not show any benefit to patients with persistent advanced ovarian cancer	Phase II	(392)
	Oregovomab + carboplatin + paclitaxel	moAb combined with first line standard chemotherapy in patients with advanced ovarian cancer showed prolongation of both PFS and OS	Phase II	(393)
		In patients with optimally resected advanced ovarian cancer, combination of drugs resulted in more than three times longer PFS compared to chemotherapy alone	Phase II	(394)
	REGN4018 monotherapy	Bispecific anti-MUC16/CD3 moAb inhibited the growth of murine peritoneal tumors	Experimental	(395)
	Anetumab ravtansine + pegylated liposomal doxorubicin	Conjugate of anti-MUC16 moAb with cytotoxic maytansinoid tubulin inhibitor DM4. In recurrent ovarian cancer, this combination showed 28% response rate, mostly in the form of partial response	Phase Ib	(396)
	Intetumumab (CNTO-95) monotherapy	moAb targeting $\alpha\gamma\beta 3$ and $\alpha\gamma\beta 5$ integrins. In patients with solid tumors including ovarian carcinosarcoma, it showed stabilization of the disease	Phase I	(397)
	Volociximab monotherapy	moAb against $\alpha 5\beta 1$ integrin. In advanced platinum-resistant ovarian cancer, it failed to demonstrate efficacy	Phase II	(398)
TAMs	Anti-CD24 moAb	CD24 is a “do not eat me” signal for macrophages. Disrupting the signal between CD24 on cancer cells and SIGLEC-10 on TAMs enhanced phagocytosis of cancer cells and could be a novel target for therapy	Experimental	(399)
	Hu5F9-G4 moAb	moAb blocking phagocytosis mediated by CD47.	NCT02216409	
	Celecoxib + cyclophosphamide	Partial remission in two patients	Phase I	(400)
	Celecoxib + carboplatin	COX-2 inhibitor that blocks M2 shift of TAMs mediated by OCSC-derived COX-2 activity.	Phase II	(401)
	Celecoxib + carboplatin + docetaxel	Combination therapy did not show therapeutic benefit in recurrent ovarian cancer	Phase II	(402)
	G5-MTX	The response rate to this combination in recurrent platinum-resistant ovarian cancer was 29%	DoCaCel study	(402)
		In the group of Ic-IV stage ovarian cancer, addition of celecoxib to first-line standard chemotherapy did not show any benefit	Phase II	(403)
		G5-methotrexate nanoparticles depleted TAMs in models of ovarian cancer and ascites and were able to reverse anti-angiogenic therapy resistance	Experimental	(404)
	Clodronate liposomes (biphosphonate)	Reduced metastases and ascites formation in HGSOC xenografts	Experimental	(405)
	Trabectedin	Extract from the sea squirt <i>Ecteinascidia turbinata</i> selectively cytotoxic to macrophages and reducing angiogenesis in mouse model of ovarian cancer	Experimental	(406)
	Trabectedin monotherapy	Sensitizes platinum-resistant tumors for the consecutive platinum treatment	Phase II	(407)
	Trabectedin + pegylated liposomal doxorubicin	Combination showed ORR of 28% in advanced recurrent ovarian cancer	Phase I	(408)
	Trabectedin + durvalumab	Patients with germline BRCA1/2 mutations and platinum-free interval of 6–12 months had survival benefit from this treatment	Phase III	(409)
	Trabectedin + bevacizumab	Combination with PD-1/PD-L1 inhibitor resulted in tumor shrinkage and 6-month PFS in 43% of patients with advanced ovarian cancer	TRAMUNE Study	(410)
		Combination showed benefit; 75% of patients had PFS of 6 months	Phase Ib	(411)
			Phase II	(411)
	GW2580	CSF1R inhibitor inhibits CSF1/CSF1R pathway responsible for TAMs survival. Reduction of ascites in the mouse model of ovarian cancer	Experimental	(412)
	ARRY-382 + pembrolizumab	Combination with PD-1/PD-L1 inhibitor. One patient with ovarian cancer had partial response	NCT02880371	(413)
	AC708 + anti-VEGF + paclitaxel	Partial restoration of sensitivity to anti-VEGF therapy in mouse xenograft model	Phase Ib/II	(414)
	Mannose receptor (CD206)-targeted nanocarrier of IRF5 and IKK β mRNA	Reversing TAM phenotype into M1. Reduces tumor growth in mouse model of ovarian cancer	Experimental	(415)
CAAs	Metformin	Inhibits adipocyte-mediated cancer cell proliferation, migration, and bio-energetic changes	Experimental	(416)
CAFs	A-83-01	CAF-derived TGF- β promotes tumor supporting environment. Inhibitor of TGF- β signaling pathway decreased peritoneal metastases and improved survival in mouse model of ovarian cancer	Experimental	(417)
	LY2109761 + cisplatin			

(Continued)

TABLE 5 Continued

Target	Drug	Mechanism of action	Trial	Reference
	Sorafenib monotherapy Sorafenib + bevacizumab	Combination of TGF-β type I/type II inhibitor with cisplatin increased significantly cytotoxic activity of chemotherapeutic in chemoresistant cell line In recurrent ovarian cancer and peritoneal carcinomatosis, therapy was effective in two of the 59 patients with partial response and 20 of the 59 patients with disease stabilization but showed substantial toxicity CAFs secrete growth factors stimulating cancer proliferation. Combination of multi-kinase inhibitor against PDGFR, VEGFR, Raf, and CD117 with anti-angiogenic therapy resulted in partial response in 9 of the 35 patients and stabilization in 18 of the 35 of patients	Experimental Gynecologic Oncology Group Phase II Phase II	(418) (419) (420)
	Sorafenib + topotecan Sorafenib + gemcitabine Sorafenib + paclitaxel + carboplatin	In recurrent ovarian cancer, therapy was effective in five of the 30 patients with partial response, and 14 of the 30 patients with disease stabilization but showed substantial toxicity Oral sorafenib in combination with topotecan and continued as maintenance monotherapy showed significant prolongation of PFS compared to placebo in recurrent ovarian cancer, with acceptable toxicity The combination was associated with encouraging rates of stable disease and CA-125 response, with manageable toxicity The combination of sorafenib and standard therapy in the first-line treatment of advanced ovarian cancer did not improve efficacy and substantially increased toxicity	Hoosier Oncology Group Phase II NCT01047891 Phase II Princess Margaret Hospital Phase II Sarah Cannon Research Institute Phase II	(421) (422) (423) (402, 424)
	Aflibercept monotherapy Cediranib (AZD2171) monotherapy	This recombinant fusion VEGFR1/2 protein extracellular domain is a decoy receptor that inhibits pro-angiogenic signaling from CAFs. Aflibercept was effective in controlling of malignant ascites in advanced ovarian cancer Receptor tyrosine kinase inhibitor that inhibits VEGFR1/2/3 and PDGFR-α/-β and CD117, thus blocking signals from CAFs; 17% of patients and 13% of patients had partial response and stable disease, respectively In platinum-sensitive group, there was partial response in 26% and stable disease in 51% of patients. In the group of platinum-resistant patients, only stabilization of the disease in 66% was observed	Phase II Phase II Princess Margaret, Chicago and California consortium Phase II	(425) (426) (427)
	Cediranib + olaparib	Combination of two drugs used in the group of patients with progressive HGSOC pre-treated with platinum (both resistant and sensitive) and with acquired PARP inhibitors resistance. Sixteen-week PFS varied from 39% to 55% and was dependent on genomic alterations, being the shortest in the group with reverse <i>BRCA1</i> , <i>BRCA2</i> , and <i>RAD51B</i> mutations and <i>ABCB1</i> upregulation In platinum-sensitive recurrent ovarian cancer, combination of drugs did not improve PFS, compared to platinum-based chemotherapy. However, in patients with germinal <i>BRCA</i> mutation, it was significantly effective In patients with platinum-resistant recurrent <i>BRCA</i> germline mutation-negative ovarian cancer pre-treated with a median of 4 lines of chemotherapy and bevacizumab, the ORR with this drug combination was 15%, PFS was 5 months, and OS was 13 months	EVOLVE Phase II NRG-GY004 Phase III CONCERTO Phase III	(428) (429) (430)
	Nintedanib (BIBF1120) monotherapy Nintedanib (BIBF1120) + carboplatin + paclitaxel Pazopanib (GW786034) + paclitaxel	Receptor tyrosine kinase inhibitor that inhibits VEGFR1/2/3 and FGFR1/2/3 and PDGFR-α/-β. Maintenance therapy after completed chemotherapy for relapsed ovarian cancer showed improvement of PFS (16% vs. 5%) Combination of drugs compared to standard chemotherapy alone showed modest efficacy (improved PFS) in the group of patients with advanced HGSOC and upfront debulking surgery Receptor tyrosine kinase inhibitor that inhibits VEGFR1/2/3, PDGFR-α/-β, and CD117. Combination of drugs compared to paclitaxel alone showed improvement in PFS (6.3 vs. 3.5 months) and OS (18.7 vs. 14.8 months) in advanced platinum-resistant or platinum-refractory ovarian cancer	Phase II AGO-OVAR12 Phase III MITO-11 Phase II	(431) (432) (433)
	Pazopanib (GW786034) + paclitaxel Pazopanib (GW786034) + cyclophosphamide Pazopanib (GW786034) + chemotherapy	In ovarian cancer relapse during maintenance therapy with bevacizumab, combination of drugs compared to paclitaxel alone did not improve efficacy but increased toxicity In the group of recurrent, platinum-resistant and pre-treated ovarian cancer combination of drugs showed promising results (PFS of 8 months and OS of 25 months) Meta-analysis of five studies indicated that pazopanib combined with chemotherapy improved ORR, but without improvement in OS and with increase of toxicity	TAPAZ Phase II PACOVAR Phase I Experimental	(434) (435) (436) (437)

(Continued)

TABLE 5 Continued

Target	Drug	Mechanism of action	Trial	Reference
	Tumor suppressor miRNA	MiR-199a-3p loaded to exosomes inhibited ovarian cancer proliferation and invasion and, in xenograft mouse model, inhibited peritoneal dissemination of cancer	Experimental	(459)
	Exosomes with Triptolide	Diterpenoid epoxide packed into exosomes showed anti-proliferative effect on ovarian cancer cell lines and xenografted tumors, however with considerable hepatic and splenic toxicity	Experimental	(460)
	Exosome-liposome hybrid nanoparticle delivery system	Hybrid transport system packed with Triptolide and miR-497 showed apoptotic effects and enabled to overcome platinum resistance	Experimental	(461)
	α -Mangostin + cisplatin	Combination of natural plant derivative with cisplatin changed the number and activity of CAF-derived exosomes	Experimental	(374)
RNAs-targeted therapy	Circ_EXOC6B RNA	Circ_EXOC6B RNA suppressed the progression and paclitaxel resistance of ovarian cancer cells through sequestering miR-376c-3p	Experimental	(462)
	miR-671-5p	miR-671-5p reduces tumorigenicity of ovarian cancer through suppressing histone deacetylase 5 (HDAC5) and HIF-1 α expression	Experimental	(463)
	Icariside II	Herbal component from <i>Epimedium brevicornum</i> . Suppresses the tumorigenesis of ovarian cancer by promoting autophagy by miR-144-3p/IGF2R axis	Experimental	(464)
	Circ_TYMP1 RNA	Downregulation of circ_TYMP1 decreased ovarian cell proliferation and invasion by miR-182A-3p/TGF- β pathway	Experimental	(465)
	circ_0026123 RNA	Downregulation of this circRNA inhibited proliferation and metastases of ovarian cancer through miR-124-3p/enhancer of zeste homolog 2 (EZH2) pathway	Experimental	(466)
	miR-146a	MiR-146a secreted by MSCs increased the chemosensitivity of ovarian cancer resistant cell lines to docetaxel	Experimental	(220)
	Follistatin mRNA	Lipid nanoparticles containing mRNA for follistatin injected intraperitoneally inhibited cancer dissemination and prevented the onset of cachexia in the mouse model of ovarian cancer	Experimental	(467)
	anti-PLXDC1 siRNA	Chitosan nanoparticles containing anti-PLXDC1 siRNA decreased tumor proliferation and microvessel density and increased apoptosis in murine model of ovarian cancer	Experimental	(468)
	miR-20c	MiR-200c was used as an inhibitor of NRP1 transmembrane receptor highly expressed by ovarian cancer and connected to multi-drug resistance. Combination of miRNA with olaparib enhanced its cytotoxicity	Experimental	(469)

MSCs, mesenchymal stem cells; MDSCs, myeloid-derived stem cells; HGF, hepatocyte growth factor; MUC16, mesothelin; CD52, CAMPATH-1 antigen; SIGLEC-10, silica acid binding Ig-like lectin-10; Tregs, T regulatory cells; CAAs, cancer-associated adipocytes; DNMT1, DNA-(cytosine-5)-methyltransferase-1; TAMs, tumor-associated macrophages; COX-2, cyclooxygenase-2; ORR, overall response rate; CSF1, colony-stimulating factor-1; CSF1R, colony-stimulating factor-1 receptor; IFR5, Interferon regulatory factor; IKK β , I κ B kinase beta; PDGFR, platelet-derived growth factor receptor; VEGFR, vascular endothelial growth factor receptor; Raf, RAF proto-oncogene serine/threonine-protein kinase; PFS, progression-free survival; BRCA, breast cancer type 1 susceptibility protein; RAD51B, RAD51 paralog B; ABCB1, ATP-binding cassette sub-family B member 1; FGFR, fibroblast growth factor receptor; ORR, overall response rate; PARP, poly-(ADP-ribose) polymerase; CTLA-4, cytotoxic T-cell antigen 4; IGF2R, insulin-like growth factor-2 receptor; mRNA, messenger RNA; siRNA, small interfering RNA; PLXDC1, plexin domain containing 1; NRP1, neuropilin-1.

characterization of platinum-refractory and platinum-resistant ovarian tumors identified three tumor clusters: cluster 1 with overrepresentation of growth factor signaling pathways, cluster 2 with pathways regulating cell survival in hypoxic conditions and senescence, and cluster 3 related to cellular senescence. A possible treatment of choice for cluster 1 could be tyrosine kinase or angiokinase inhibitors, cluster 2 could theoretically respond to mTOR inhibitors, whereas cluster 3 could be treated with the deacetylase inhibitors (87, 481, 482). Another single-cell transcriptome study revealed the heterogeneity of HGSOC, which was found to be composed of several cell clusters. The first one called EC1 showed gene enrichment for glycolysis/gluconeogenesis and ECM-receptor interactions. The EC2 subtype expressed genes, suggesting their origin from tube epithelium. The EC3 subtype showed overexpression of genes associated with function of ABC transporters, suggesting a potential to be a drug-resistant subtype. EC4 subtype was characterized by the immune response-related pathways indicating the activity of EC4 cells in immune response. The chemoresistance responsible genes were strongly represented in EC5 cell population (483).

Epigenomic analysis of immune-related lncRNAs revealed RNAs having the potential to divide the population of patients with ovarian cancer into high-risk and low-risk groups characterized by a shorter

or longer overall survival (OS), respectively. High-risk score tumors were positively correlated with abundant representation of checkpoint and immunosuppressive molecules, indicating the group of patients with compromised anti-tumor immune response (484). The DNA methylation signatures represent another epigenetic point of interest in ovarian tumors. The hypomethylated upregulated tumor necrosis factor (*TNF*), estrogen receptor 1 (*ESR1*), mucin 1 (*MUC1*) genes, and hypermethylated downregulated forkhead box O1 (*FOXO1*) gene could serve as targets for epigenetic therapy and were correlated with patients' prognosis (485).

According to the TME components, the four different CAF subsets (S1 to S4) were identified in ovarian tumors. The HGSOC of mesenchymal subtype, defined by stromal gene signatures and poor survival, had high numbers of CAF-S1 cells, which attracted and sustained immunosuppressive infiltration of Treg CD25+FoxP3+ T lymphocytes (475). The study of immunological profile of HGSOC showed the presence of activated-immune and CAF-immune subtypes. Activated-immune subtype showed anti-tumor features exemplified by active immune response and better prognosis. The CAF-immune subtype was characterized by tumor-promoting signals like, activated stroma, M2 macrophages, and a poor prognosis. The activated-immune subtype was more likely than the CAF-immune subtype to respond to checkpoint blockade immunotherapy (486).

The most painful problem in ovarian cancer therapy is the acquired chemoresistance following the initial good response to the first-line chemotherapy. Therefore, identification of the biomarkers of chemoresistance is one of the most important activities in ovarian cancer surveillance. The classic biomarkers of platinum and PARP chemosensitivity are the germinal and somatic mutations of *BRCA1/2* genes (487). However, the reversion mutations in *BRCA* genes and in other homologous recombination repair (HR) genes were found to be responsible for secondary resistance to platinum- and PARPi-based therapy (488, 489). On the basis of the homologous recombination deficiency, insertions and deletions, copy number changes, and mutational signatures, a combined predictor of platinum resistance, named DRDscore, was established, and, when validated in a cohort of patients with HGSOC, it reached sensitivity of 91% (490). Four miRNA biomarkers (miR-454-3p, miR-98-5p, miR-183-5p, and miR-22-3p) identified in ovarian cancer tissues were able to discriminate between platinum-sensitive and platinum-resistant patients with HGSOC (491). Treatment using PARPis results in acquired PARPi resistance. The reason for this is a promotion of STAT3 activity both in tumor cells and populations of immune and CAF cells, followed by creation of an immunosuppressive environment. Treatment of olaparib-resistant ovarian cancer cell line with napabucasin, the STAT3 inhibitor, improved PARPi sensitivity (492). Hypoxia and therapy-induced senescence are the key drivers of primary chemo-refractoriness and secondary chemoresistance of HGSOC (493). Hypoxic TME induces the M2-phenotype in TAMs, which, in turn, secrete exosomes containing miR-223 that, when transported into ovarian cancer cells, makes them chemoresistant (494). To overcome chemoresistance, there are plenty of different drug combinations tested in both experimental and clinical settings (Tables 4, 5). Simultaneously, identification of potentially resistant tumors is of the utmost importance for successful therapy. Identification of ovarian cancer cells with high-stress signature and disturbed drug responsiveness could optimize the subsequent therapy to attenuate their function or eliminate them from the tumor (493, 495, 496). Moreover, as HGSOC tumors are characterized by temporal heterogeneity, the repetitive circulating tumor DNA (ctDNA)/CTCs testing should be performed to have the most actual picture of the disease.

The exploration of the infection factors in the origin or predisposition to ovarian cancer is also being realized in the

analysis of microbiome and viral infections (497–499). Another field of intensive investigation is searching for prognostic biomarkers (500–503). It is a lot of work to do to safely and effectively combine different drugs, but the practical use of the “DEPHENCE” system philosophy could, in our opinion, lead doctors and researchers in proper direction.

Author contributions

All authors contributed to the conception of the review. Data collection and analysis were performed by JW, MW, and EP. The first version of manuscript was written by JW and MW, and all authors commented on previous versions of the paper. EP and MW read and approved the final version of the manuscript, made linguistic corrections, and revised the text. All authors contributed to the article and approved the submitted version.

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Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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