

Gene Section

Review

BIRC5 (baculoviral IAP repeat containing 5)

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Abstract

BIRC5, also known as survivin, has been implicated in cell cycle progression and apoptosis avoidance. BIRC5 is highly expressed in embryonic tissues, however very low or absent in adult tissues. BIRC5 overexpression has been frequently associated to cancer development, a poor prognosis and chemoresistance. Besides that, different BIRC5 isoforms has been characterized and related to better or worse chemotherapy responses depending on the isoform and the cancer type. So far, many efforts have been conducted in order to deplete BIRC5 in cancer cells, including gene therapy, pharmacological and nanotechnological approaches. In this review, we will discuss the role of BIRC5 in cancer cell biology and its clinical significance, demonstrating its DNA/RNA and protein aspects, also its relevance for diagnosis and prognosis, and advances as a target for the treatment of different cancer types.

Keywords

BIRC5; Cell cycle progression; Apoptosis; Cancer

Identity

Other names: API4, EPR-1

HGNC (Hugo): BIRC5

DNA/RNA

Description

The entire BIRC5 gene is approximately 11.4 Kb (start: 78214186 and end: 78225636 bp; orientation: Plus strand).

Transcription

There are three transcript variants deposited in the NCBI database (<https://www.ncbi.nlm.nih.gov/gene>).

In general, they present three exons (exon 1, 2 and 3) that are responsible for encoding the BIR domain, which is conserved in all BIRC family members, and the exon 4 that is related to the coiled-coil (CC) domain.

Variant 1 is the predominant transcript (cDNA: 2574 bp), and encodes isoform 1 (142 amino acids [aa]).

Variant 2 lacks an exon in the 3' coding region, which results in a frameshift (cDNA: 2537 bp) and, thus, in a changed protein (143 aa) with a different C-terminus from that of isoform 1 (isoform 2, also known survivin-ΔEx3). Variant 3 exhibits an alternate in-frame segment (cDNA: 2724 bp) and generates a longer (165 aa) and distinct protein (isoform 3, also known survivin-2B), compared to isoform 1.

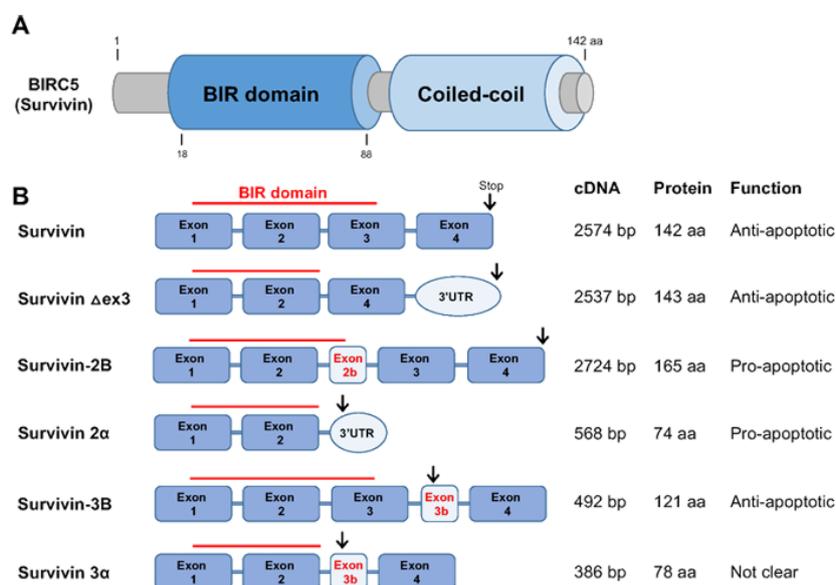


Figure 1. BIRC5 structure and its splice variants. BIRC5 (also known as survivin) presents at least five variants with biological relevance for cancer. A. The protein structure of the most common variant observed presents 142 aa and is composed of a BIR domain that is responsible for its anti-apoptotic activity and a coiled coil. B. The BIRC5 pre-mRNA of the most common expressed variant is composed of 3 exons that codifies the BIR domain and the exon 4 that codifies the coiled coil. This variant presents anti-apoptotic activity. Survivin Ex3 has its exon 3 deleted and an insertion of a 3'UTR, this isoform codes a protein of 143 aa and also exerts anti-apoptotic functions. Survivin-2B presents an insertion of an exon 2b located between exon 2 and exon 3, generates a protein of 165 aa with pro-apoptotic characteristics. Survivin-2 α is characterized by the presence of exon 1 and 2 and the insertion of a 3'UTR, this isoform codifies a protein of 74 aa with pro-apoptotic functions. Survivin-3B presents the insertion of exon 3b between exon 3 and exon 4, which generates a protein of 165 aa with anti-apoptotic properties. Survivin-3 α presents a deletion of exon 3 and generates a protein of 78 aa whose function remains controversial. Arrows indicate the stop codon. UTR- untranslated region. Red line indicates the BIR structure.

Moreover, three additional transcript variants are reported in Ensembl (<http://www.ensembl.org/>): a transcript variant containing 568 bp, which generates a protein of 74 aa (also known as Survivin-2 α); a transcript variant with 492 bp (cDNA) that produces a protein of 121 aa (also known as Survivin-3B); and a transcript variant comprised of 386 bp (cDNA) that gives a protein of 78 aa (also known as Survivin-3 α) (Figure 1).

Protein

Description

The IAPs (Inhibitors of Apoptosis Proteins) are a family of proteins primarily known for inhibiting caspase activity, either directly or indirectly, thus preventing apoptotic cell death (Gyrd-Hansen and Meier, 2010). Still, the IAPs are further implicated in key roles in other processes, such as cell cycle, cell migration, inflammation and, even, in the innate immune response (de Almagro and Vucic, 2012). Structurally, members of the IAPs are characterized by the presence of at least one BIR (Baculovirus IAP repeat) domain, which contains nearly 80 amino acid residues and carries Zn^{2+} in the center. Such domain is a highly conserved sequence that mediates protein-protein interactions, an essential feature for their anti-apoptotic function. Within the eight human IAPs recognized (NAIP [BIRC1], BIRC2 [cIAP1], BIRC3 [cIAP2], XIAP [BIRC4], survivin [BIRC5],

BIRC6 [bruce], BIRC7 [livin] and BIRC8 [ILP-2]) there may be between one and three BIR domains, typically arranged in their N-terminal portion (Budhidarmo and Day, 2015; Lopez and Meier, 2010).

BIRC5 (survivin), the smallest among the IAPs (16.5 kDa), was discovered in 1997 (Ambrosini et al., 1997), is 142 amino acids (aa) long and has a single BIR domain (Peery et al., 2017). This protein is presented as a stable loop-shaped homodimer, formed by interactions of the N-terminal region through a predominantly hydrophobic interface (Chantalat et al., 2000; Verdecia et al., 2000). Furthermore, on the C-terminal portion, survivin carries an alpha-helix CC (coiled coil) domain, its unique structure (Chantalat et al., 2000; Coumar et al., 2013) which conveys the ability to associate to microtubules and a range of other proteins involved, mainly, in the process of mitosis, and further allowing for translocation among the different cellular compartments, such as mitochondria, cytoplasm and nucleus (Rodel et al., 2012) (Figure 1).

Since BIRC5 is connected to a diverse network of biochemical processes and therefore has remarkable multifunctionality, its modulation in cancer therapy continues to be extensively explored. Several survivin inhibitors have been identified by in vitro and in silico methods, such as antisense oligonucleotides, siRNA, dominant-negative

mutants, peptidomimetic molecules and other small inhibitory molecules, and even as anticancer vaccine (Fenstermaker et al., 2016; Sarvagalla et al., 2016).

Expression

BIRC5 is normally expressed in embryonic tissues and during fetal development, as well as in fast dividing normal cells (like bone marrow stem cells, basal epithelial cells and thymocytes, even if at lower concentrations), but is virtually undetectable in fully differentiated and healthy adult tissues (Adida et al., 1998; Sah et al., 2006; Stauber et al., 2007). Throughout the cell cycle, BIRC5 is expressed only during mitosis, in a highly regulated manner comprising the chromosomal passenger complex (CPC), as it interacts with tubulin and kinetochores during metaphase, then participates in central spindle organization and cytokinesis, throughout anaphase (Szafer-Glusman et al., 2011).

However, BIRC5 is expressed in cells that undergo malignant transformation, being overexpressed in numerous tumors (Altieri, 2001; LaCasse et al., 2008). Recent studies evidenced that transcriptional activation is not the only cause for BIRC5 overexpression, but also post-transcriptional regulation, specially coordinated by many alternative polyadenylation (APA) sites. For instance, in ovarian cancer, aberrant APA leads to shortening of the 3'-UTR region, enabling escape from negative regulation of miRNAs and causing up-regulation of BIRC5 (He et al., 2016).

Clinically, overexpression of BIRC5 has been correlated with a poor prognosis of cancer, resistance to apoptosis induced by chemotherapy, decreased survival of patients and greater chances of relapse (Islam et al., 2000; Rodel et al., 2012).

Localisation

BIRC5 is located both in the cytoplasm and in the nucleus. Nuclear expression has been associated with a poor prognosis and chemoresistance (Du et al., 2015), which may differ among the different types of cancers (Shintani et al., 2013). BIRC5 splice variants were also related to subcellular localization. This has been shown in samples from acute myeloid leukemia patients, where wild-type survivin and the 2B splice variant were expressed in the nucleus, cytoplasm or both, whereas the Δ Ex3 isoform was only expressed in the nucleus (Serrano-Lopez et al., 2013). However, considering pro-survival factors, localization is not the only relevant feature: it has been recently demonstrated that BIRC5 can be packaged into extracellular vesicles (endosomes) and its delivery may be guided by antiapoptosis stimuli from cancer cells and tumor microenvironment, inducing pro-survival competences in fibroblasts after treatment with paclitaxel. Conversely, knockdown of BIRC5 in

those vesicles promoted increased cell sensitivity to chemotherapeutic agents (Kreger et al., 2016).

Function

Studies have shown that overexpression of BIRC5 inhibits both the intrinsic and extrinsic pathways of apoptosis and the depletion of survivin in human cell culture impairs apoptosis and triggers cell division defects (Li et al., 1998; Roy et al., 2015). The antiapoptotic mechanism of BIRC5 still needs to be better clarified, however, both the direct or indirect binding of BIRC5 to caspases are proposed (Figure 2) (Altieri, 2013; Garg et al., 2016; Li et al., 1998). Evidences also indicate that BIRC5 binds to XIAP, one of the best studied IAPs, forming a complex that protects XIAP against ubiquitination and proteosomal degradation.

This complex then activates multiple signaling pathways, including NF- κ B, inhibits caspases CASP3, CASP7 and CASP9, suppresses apoptosis and accelerates tumor progression. Other cytoprotective mechanisms have been proposed for BIRC5, including the ability of mitochondrial BIRC5 to sequester the pro-apoptotic DIABLO (Smac) protein from its binding to BIRC4 (also known as XIAP), or even preventing its release from mitochondria (Altieri, 2013; Coumar et al., 2013; Song et al., 2003).

Interaction of BIRC5 with CDK4 has been associated with progression of the cell cycle. In mitosis, BIRC5 plays a key role in integrating the transient chromosome complex (CPC), along with INCENP, CDCA8 (borealin) and AURKB, which controls the formation and stabilization of the mitotic spindle (Altieri, 2013; Coumar et al., 2013). Activation of Wnt signaling induces β -catenin (CTNNB1) and BIRC5 nuclear translocation, which contributes in mitotic spindle formation, further regulating CPC, β -catenin, STAT3 and HIF1A (Figure 2). BIRC5 also appears to be involved in the cellular response to stress through the interaction with various chaperones, such as AIP, HSPD1 (HSP60) and HSP90AA1 (HSP90) (Altieri, 2013; Fortugno et al., 2003). Moreover, BIRC5 also partakes in the process of autophagy (Wang et al., 2011) and in DNA repair among several tumor cell lines (Jiang et al., 2009).

BIRC5 has also been shown to induce cell motility, metastasis and increased colonization capacity by AKT-mediated upregulation of the α 5 integrin pathway in a melanoma model (McKenzie et al., 2013).

Additionally, BIRC5 plays an important role in angiogenesis, contributing to endothelial cell proliferation and migration, which was then linked to increased β -catenin protein levels that consequently promotes an elevated expression of BIRC5 and VEGF (Fernandez et al., 2014).

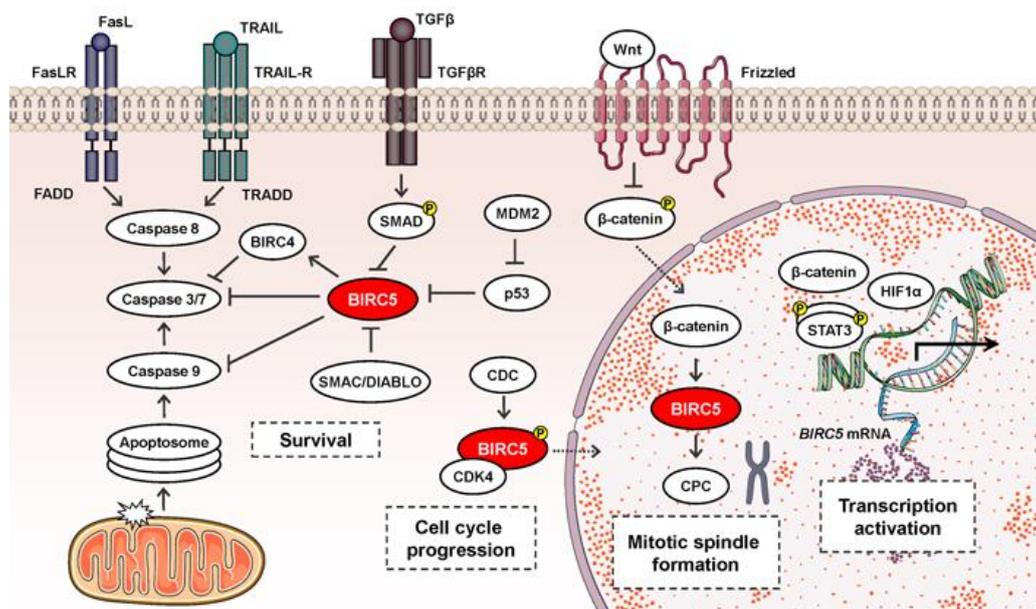


Figure 2. BIRC5: a multitask protein. BIRC5 (survivin) acts on cytoplasm and nucleus and is involved different cellular functions: cell survival, cell cycle progression, mitotic spindle formation and transcription activation. In cytoplasm, BIRC5 modulates apoptosis pathway by binding to and blocking initiator caspase 9 and effectors caspases 3 and 7, demonstrating to be involved in extrinsic and intrinsic apoptosis and contributing to cell survival. BIRC5 may be blocked by SMAC/DIABLO, a factor released by mitochondria. Also BIRC5 potentiates apoptosis inhibition through stabilization of BIRC4 (also known as XIAP). TGF- β signaling negatively regulates BIRC 5 by phosphorylating SMAD protein. p53-mediated signaling also downregulates BIRC5 functions. CDC phosphorylates BIRC5 and promotes its binding to CDK4 that may be translocated to nucleus, and thus promotes cell cycle progression. In nucleus, BIRC5 is involved in the mitotic spindle formation modulated by Wnt pathway through the phosphorylation inhibition and nuclear translocation of β -catenin activating BIRC5 and associated to other proteins (not shown) form the Chromosomal Passenger Complex (CPC). The transcription activation of BIRC5 mRNA is mainly promoted by β -catenin, STAT3 (signal transducer and activator of transcription-3) and HIF 1 α (hypoxia-inducible factor-1 α).

BIRC5 is also directly involved in enhancing anoikis resistance through miR-141/KLF12/Sp1/survivin axis. It is a consensus that anoikis resistance is crucial for establishing a metastatic niche and consequently promoting cancer progression and dissemination (Mak et al., 2017). Dissimilar functions have been attributed to the different isoforms of BIRC5. Survivin-2 α and survivin-2B portray a proapoptotic activity profile, whereas Survivin- Δ Ex3 and Survivin-3B show prominent antiapoptotic activity, with similar activities to those of survivin itself. These distinct variants can predict aggressiveness of cancer phenotype, thus contributing to prognosis (Caldas et al., 2005). BIRC5 can be released from tumor cells in exosomes (Khan et al., 2011). This information provided new insights into biomarkers for determination of early diagnosis and also to predict prognosis. In this context, the splice variant survivin-2B, in breast cancer, was shown to be expressed mostly in primary tumors and exclusively in early stage disease. Conversely, Survivin- Δ Ex3 variant was most commonly expressed in late stages of breast cancer (Khan et al., 2014). Survivin-2B has been further reported to promote cell death in some cancer cells by promoting

autophagy followed by cell death induced by accumulation and stabilization of IKK β (IKKB) in the nucleus (Shi et al., 2014).

Homology

The BIRC5 gene is highly homologous among different species, as shown in Table 1, which demonstrates the comparison of variant 1 among different species.

% Identity for: <i>Homo sapiens</i> BIRC5	Symbol	Protein	DNA
vs. <i>P. troglodytes</i>	<i>BIRC5</i>	98.3	98.8
vs. <i>M. mulatta</i>	<i>BIRC5</i>	97.9	97.9
vs. <i>C. lupus</i>	<i>BIRC5</i>	90.8	90.1
vs. <i>B. taurus</i>	<i>BIRC5</i>	90.1	90.1
vs. <i>M. musculus</i>	<i>Birc5</i>	83.6	82.6
vs. <i>R. norvegicus</i>	<i>Birc5</i>	83.0	81.3
vs. <i>G. gallus</i>	<i>BIRC5</i>	60.6	65.7
vs. <i>X. tropicalis</i>	<i>birc5.2</i>	57.8	64.2
vs. <i>D. rerio</i>	<i>Birc5a</i>	54.3	58.0

Table 1. Comparative identity of human BIRC5 with other species (Source: <http://www.ncbi.nlm.nih.gov/homologene>)

Mutations

Somatic

Recurrent mutations in the BIRC5 gene are rare. Among the 47,119 unique samples reported in COSMIC (Catalogue of Somatic Mutations in Cancer;

<http://cancer.sanger.ac.uk/cancergenome/projects/cosmic>), only 43 presented BIRC5 mutations (29 missense substitutions, 8 synonymous substitutions, 3 nonsense substitutions and 2 frameshift insertions). Similar findings are reported in cBioPortal (<http://www.cbioportal.org>) among the 55,481 cancer samples accessed, that show somatic mutations in BIRC5 occur in merely 0.2% of the tested samples (corresponding to 116 mutations, of which 65 are missense substitutions, 50 truncated genes or 1 other mutation). When mutations, amplifications, deep deletions and multiple alterations were considered, the total of cancer samples with any type of genetic alteration in BIRC5 was 969 (1.7%).

Implicated in

Angiosarcoma

In a cohort including 85 samples from angiosarcoma patients and 88 controls (54 hemangioma and 34 pyogenic granuloma), nuclear BIRC5 expression was observed in all angiosarcoma patients, but in fewer than 7% of the control group. This data indicates that BIRC5 expression may be used as a diagnosis tool in angiosarcoma (Tsuneki et al., 2017). In addition, genetic or pharmacological BIRC5 inhibition reduces cell proliferation in ISO-HAS-B human angiosarcoma cells (Tsuneki et al., 2017).

Brain cancer

Western blot analysis revealed that BIRC5 was expressed in 60.3% of glioma samples, which was associated with a reduced apoptosis ratio and high-grade tumors (Bae et al., 2017). In agreement, samples obtained from gliosarcoma patients presented elevated expression of BIRC5 in the nucleus of tumor cells collected from brain lesions, when compared to normal brain cells (Chen et al., 2010).

BIRC5 expression was also associated to radioresistance: ionization of glioblastoma cell lines promoted BIRC5 upregulation, which mediated dedifferentiation to a stem-like phenotype and, consequently, induced a radioresistant phenotype (Dahan et al., 2014).

Treatment of glioma cells with the survivin inhibitor YM155 overcomes resistance to TRAIL-induced apoptosis, by downregulating MCL1 and BIRC5 (Premkumar et al., 2013). In glioblastoma cell lines,

YM155 treatment reduced BIRC5 expression, and induced apoptosis and DNA fragmentation (Lai et al., 2012). Similar results were reported by Jane and colleagues (Jane et al., 2013), where YM155 downregulated BIRC5 and MCL1 expression and inhibited cell growth in malignant human glioma cells. Interestingly, in resistant glioma cell lines attributed to EGFR activation, YM155 alone did not present any significant effects, however in combination with ABT-373, a BH3-only mimetic that targets the prosurvival members of the BCL2 family, a synergic effect mediated by caspase activation was observed (Jane et al., 2013). Depletion of BIRC5 levels mediated by parthenolide treatment induced apoptosis and cell cycle arrest in glioblastoma cell lines (Tang et al., 2015). Cucurbitacin-I, another natural product, induced cell death in malignant glioma cells, while promoting G₂/M accumulation, depletion of p-STAT3, p-STAT5, p-JAK1 and p-JAK2 levels, and downregulation of AURKA, AURKB and BIRC5 (Premkumar et al., 2015). Medulloblastoma also presents elevated level of BIRC5 expression, as observed for other brain cancers. Similarly, antagonists of BIRC5 impaired proliferation and survival of both murine and human medulloblastoma cells (Brun et al., 2015). High BIRC5 expression was associated to advanced stages and sporadic tumors in patients aged greater than 12 months (Islam et al., 2000), which negatively impacted clinical outcomes (Azuhata et al., 2001). In addition, BIRC5/p53 and BIRC5/FAS ratios have been implicated in neuroblastoma prognosis (Sandler et al., 2002; Tajiri et al., 2001). In neuroblastoma and oligodendroglioma cell lines, BIRC5 silencing reduced cell viability while further inducing mitotic catastrophe and cell death by caspase-dependent and -independent pathways (Shankar et al., 2001).

Breast cancer

BIRC5 protein expression was found in 78% of high-grade and 21.4% of low-grade patients with ductal carcinoma in situ, indicating that BIRC5 expression is associated with an advanced stage phenotype in breast cancer (Chade et al., 2018). In addition, increased

Estrogen positive breast cancer subtypes have been connected to increased BIRC5 regulation, w levels of BIRC5 mRNA (2.24 fold) were observed in whole blood samples from breast cancer patients when compared to healthy donors (Wang et al., 2016).

Estrogen positive breast cancer subtypes have been connected to increased BIRC5 regulation, which was reverted by treatment with the natural compound myricetin, enhancing apoptosis (Jiao and Zhang, 2016). In triple negative breast cancer, chemoresistance and metastasis were associated to elevated DEPTOR protein expression that, in turn, induced a higher expression of BIRC5, both in vitro

and in vivo (Parvani et al., 2015). Survivin and survivin- Δ Ex3 were overexpressed and associated to chemoresistance in non-responder samples using ex vivo organotypic cultures of primary human breast tumors (Faversani et al., 2014). Using shRNA targeting BIRC5 splice variants isoforms, Zheng and colleagues (Zheng et al., 2011) demonstrated that apoptosis rates were improved considerably by survivin depletion, but survivin-CEx3 isoform silencing only moderately inhibited cell survival and growth in a breast cancer model.

In breast cancer cells, combined therapy using panobinostat with gemcitabine markedly diminished BIRC5 expression (Budman et al., 2012). Similarly, SMAC mimetics (BV6, Birinapant) and BH3-mimetics (ABT-737/263) combined with paclitaxel treatment demonstrated positive results regarding BIRC5 downregulation (Panayotopoulou et al., 2017).

Chemoresistance was also related to the extracellular LGALS1 (galectin-1) expression that, moreover, contributes to cancer progression and doxorubicin resistance in triple negative breast cancer. It must be stated, herein, that galectin-1 expression is mediated by STAT3 activation, which is a transcription factor that culminates in BIRC5 upregulation, corroborating the role of BIRC5 in chemoresistance in breast cancer cells (Nam et al., 2017). The function for STAT3 in BIRC5 upregulation in breast cancer cells was also confirmed by Wang and colleagues (Wang et al., 2015), who demonstrated that MIR204 inhibits STAT3 activation and BIRC5 expression.

BIRC5 also participates on the invasive phenotype by regulating the expression of the vascular endothelial growth factor-C (VEGFC) at both protein and mRNA levels, which culminates in a raised metastasis rate in breast cancer (Cai et al., 2012). In agreement, elevated BIRC5 expression was associated with poor prognostic in stage II/III breast cancer patients (Hamy et al., 2016). The authors proposed that BIRC5 expression might be theranostic, and suggest that high BIRC5-expressing breast cancer patients would be randomized to receive BIRC5 targeting drugs (Hamy et al., 2016). A recent study that evaluate the transcriptome of primary breast cancer patients, demonstrated that, along with NEK2 and TOP2A, BIRC5 gene was amplified in obese breast cancer patients, reinforcing that this gene may be druggable for this population (Nuncia-Cantarero et al., 2018). One factor that may explain such observation is the synthesis of visfatin, an adipokine secreted by adipocytes, macrophages and inflamed endothelial tissue, which was found to be increased in obese and breast cancer patients, while exerting a protective effect on BIRC5, raising its levels and, thus, contributing to tumor progression (Gholinejad et al., 2017).

In breast cancer cell lines, including triple negative phenotype and tamoxifen-resistant cells, YM155, a BIRC5 inhibitor, as previously mentioned, reduces cell viability, with IC₅₀ values in the low nanomolar range, and induced autophagy (Cheng et al., 2015).

In breast cancer cell lines, ABT-263 (navitoclax), a BCL2 family protein inhibitor, promoted a negative modulation of BIRC5 levels in MDA-MB-231, but not in MCF-7, which was associated with a higher sensitivity to the drug (Lee et al., 2018).

Cervical carcinoma

In a recent meta-analysis including eleven studies and a total of 865 cervical carcinoma patients, Cheng and colleagues (Cheng et al., 2016) reported that elevated BIRC5 expression was positively associated with aggressive clinicopathological features, lymph node metastasis and poor survival outcomes.

Colorectal cancer

Immunohistochemical analysis evidenced that patients with colorectal adenocarcinomas exhibited higher BIRC5 levels compared to adjacent non-tumor colorectal mucosa. In the same study, the authors demonstrated that BIRC5 silencing, by siRNA, suppressed survival and cell invasion, and induced cell cycle G0/G1 arrest and apoptosis in colorectal cancer cells (Wang et al., 2017b). BIRC5 splice variants were also evaluated in colorectal cancer, and the distribution of mRNA observed was the following: 48% of wild-type survivin, 38% of survivin-2B isoform and 29% of survivin- Δ Ex3 isoform. The mRNA expression of wild-survivin and survivin- Δ Ex3 was related with tumor size and invasion, respectively (Pavlidou et al., 2011). In contrast, BIRC5 levels were not associated with patients with advanced colorectal adenoma (Choi et al., 2017).

Elevated expression of BIRC5 was also correlated with levels of CD133+, which is associated to chemoresistance to 5-fluorouracil, in colon cancer cells. The elevated expression of BIRC5 induced by activation of the CXCL12/ CXCR4 signaling pathway in cells exposed to radiation may be a crucial factor for the acquisition of chemoresistance in this cancer type (Wang et al., 2017a). However, no association was found between expression of BIRC5 and invasion, lymph node metastasis, nor histologic differentiation (Li et al., 2017). Survivin depletion by the EpCAM-aptamer-guided BIRC5 RNAi enhanced colorectal cancer stem cells sensitivity to 5-FU and oxaliplatin, further inducing apoptosis, reducing tumor growth and improving the overall survival in a colorectal cancer xenograft model (AlShamaileh et al., 2017).

The use of natural products was also implicated in reduction of BIRC5 levels, such as tanshinone I, an active compound from traditional Chinese herbal

medicine (Lu et al., 2016), and the *Pinus roxburghii* essential oil (Sajid et al., 2018). Additionally, treatment with tamoxifen β -estradiol or a combination of these two agents promoted decreased BIRC5 levels and impaired cell migration in colorectal cancer cells (Ou et al., 2017). In colon cancer cells, dimethoxy curcumin inhibited cell growth, increased apoptosis, reduced cell migration, downregulated BIRC5 expression and enhanced CDH1 (E-cadherin) in vitro and in vivo (Chen et al., 2016).

Treatment failure in colorectal cancer was previously associated to the presence of stem cells bearing a KRAS mutation, which, then, become resistant to chemotherapy. Treatment with Omega-3 fatty acid DHA promoted a reduction of cell viability, with caspase-3 activation mediated by a decrease in transcript and protein levels of BIRC5 and, moreover, an increase in MIR16-1 expression levels, suggesting that BIRC5 and microRNA-16-1 to be promising molecular targets of DHA (Sam et al., 2018).

Endometrial cancer

In endometrial cancer, BIRC5 was identified to be critical for NRF2-driven progestin resistance. The authors also demonstrated that BIRC5 silencing enabled restoration of progestin sensitivity in NRF2-overexpressing RL-95-2 cells (Fan et al., 2017).

Gastric cancer

Gastric adenocarcinoma patients undergoing gastrectomy were evaluated for the expression of markers with relevance for tumor progression and prognosis. Among them, 93.9 % of samples from gastric cancer patients presented nuclear sub-localization of BIRC5, which was associated with a poor prognosis (Lins et al., 2016). It has been demonstrated that BIRC5 upregulation increased VEGF expression in gastric cancer (Zhang et al., 2014). The authors also demonstrated that 51.3% of gastric carcinoma samples presented BIRC5 expression, which was located mainly in the cytoplasm of tumor cells, associated with lymph node metastasis and reduction of overall survival in the univariate analysis (Zhang et al., 2014).

BIRC5 knockdown using shRNA promoted an elevated sensitivity to radiation and chemotherapy using 5-FU, demonstrating that the modulation of BIRC5 levels may be an important adjuvant therapy for gastric cancer patients (Shen et al., 2012). In agreement, BIRC5 silencing mediated by siRNA increased apoptosis rates, inhibited cell proliferation in a cisplatin-resistant cell line (Li et al., 2014) and impaired cell migration in gastric cancer cells (Li et al., 2015).

Head and neck squamous cell carcinoma

High levels of BIRC5 was observed in samples from head and neck squamous cell carcinoma patients, which was associated with poor survival outcomes and chemotherapy resistance (Zhang et al., 2015a). In head and neck squamous cell carcinoma cells, a treatment targeting BIRC5 by using YM155 increased apoptotic and autophagic cell deaths, suppressing pro-survival pathways (Zhang et al., 2015a).

Similarly, treatment with an aliphatic hydroxamate-based compound targeting BIRC5 reduced survivin levels through LKB1/AMPK/p38MAPK signaling, and further enhanced p63 phosphorylation and p21 activation (Yen et al., 2018).

Hepatocellular carcinoma

In SMMC-7721 hepatocellular carcinoma cells, treatment with berbamine, a natural compound from Chinese medicine, promoted upregulation of p53 expression and downregulation of BIRC5, which further triggered mitochondria signaling pathway-mediated apoptosis (Cao et al., 2018).

Kidney cancer

In renal cell carcinoma patients, high BIRC5 expression was associated with increased TNM stage and high Fuhrman grade, which indicates that BIRC5 may be a good prognosis predictor (Ma et al., 2017).

Furthermore, BIRC5 has been associated with tumor progression and chemoresistance to temsirolimus, an mTOR inhibitor. Strategies that abrogate survivin expression, such as shRNA-mediated BIRC5 silencing or pharmacological approach (YM155), reduced chemoresistance of renal cell carcinoma cells in vitro and in vivo (Carew et al., 2015).

Other signaling pathways seem to converge to the induction of BIRC5 expression in renal cell carcinoma.

For instance, combined treatment between the histone deacetylase (HDAC) inhibitor OBP-801 and the phosphatidylinositol 3-kinase (PI3K) inhibitor LY294002 synergistically inhibited cell growth and induced apoptosis in renal cell carcinoma through BIRC5 downregulation (Yamada et al., 2013).

Leukemia

In chronic myeloid leukemia, the oncogenic signaling induced by BCR/ABL1 leads to BIRC5 upregulation by activating the JAK2/STAT3 pathway.

Moreover, BIRC5 silencing promoted pronounced cytotoxic effect in both imatinib-sensitive and -resistant chronic myeloid leukemia cell lines, a similar effect to that observed after treatment with

shepherdin, a cell-permeable peptidomimetic compound that downregulates BIRC5. These findings indicate that survivin may be a target in BIRC5-overexpressing leukemias (Stella et al., 2013). The combined use of C82 (a Wnt/ β -catenin signaling modulator) and nilotinib in chronic myeloid leukemia progenitor cells inhibited the expression of CD44, MYC, BIRC5, p-CRKL and p-STAT5 (Zhou et al., 2017)

In acute myeloid leukemia, BIRC5 overexpression is involved in drug resistance of leukemia stem cells, regulated by the ERK/MSK/Sp1/MYC axis (Zhang et al., 2015b). Interestingly, BIRC5 depletion, by siRNA, reduced cell proliferation, induced apoptosis, and synergistically enhanced cytotoxicity of etoposide in acute myeloid leukemia cells (Karami et al., 2013). Other molecular signaling that has been involved in acute myeloid leukemia resistance is the expression of MUC1 (MUC1-C), an oncoprotein critical for the onset of tumorigenesis, which is overexpressed in acute myeloid leukemia blasts and leukemia stem cells. It has been demonstrated that targeting MUC1-C reduced BIRC5 levels and increased sensitivity to cytarabine, indicating that BIRC5 is involved in multiple signaling pathways required for survival in leukemia cells (Stroopinsky et al., 2018).

Acute lymphoblastic leukemia (ALL) patients also presented elevated levels of BIRC5 and VEGF, especially prior to treatment with an association of idarubicin, cytosine arabinoside and etoposide. Nevertheless, those levels decreased after treatment (Yang et al., 2013). In children diagnosed with acute lymphoblastic leukemia, BIRC5 expression was higher compared to healthy donors. The same group of patients was monitored during the entire treatment period and those who went in to complete remission of the disease presented decreased levels of BIRC5, compared to diagnosis sample. In contrast, BIRC5 protein levels were elevated in non-survived ALL patients (Yahya et al., 2012). In acute lymphoblastic leukemia primary samples and cell lines, treatment with YM155 exhibited elevated cytotoxicity by induction of DNA damage, leading to phosphorylation of CHEK2 and H2AFX and promoting suppression of BIRC5 expression (Chang et al., 2015).

It is well accepted that leukemia stem cells contribute to a reduced treatment efficacy and also to chemoresistance. The natural product curcumin decreased BIRC5 levels in leukemia stem cell-like KG1a in a combined treatment with busulfan, which may overcome such chemoresistant of leukemia stem cells (Weng et al., 2015).

Furthermore, Li and colleagues (Li et al., 2018) observed an association between the presence of C allele of BIRC5 polymorphism rs9904341, but not of rs8073069, and an increased risk of acute leukemia

development in a cohort including 182 childhood acute leukemia patients and 200 controls.

Liver cancer

In samples from hepatocarcinoma patients, 55.4% of tumor tissues were positive for BIRC5 expression, which was higher when compared to non-tumor adjacent tissues (2%). Additionally, BIRC5 expression has been directly correlated with unfavorable clinical staging and tumor score, and the presence of extrahepatic metastasis. The authors also demonstrated a positive correlation between BIRC5 and VEGF expression, implying that besides avoiding apoptosis, BIRC5 may induce angiogenesis contribute to tumor dissemination (Tian et al., 2018).

Lung cancer

A meta-analysis study including 3,206 non-small cells lung cancer (NSCLC) patients and 816 normal controls, BIRC5 was found to be overexpressed in tumor samples and strongly correlated with histological differentiation, tumor-node-metastasis stage and lymph node metastasis, which indicates that BIRC5 may be a tumor progression marker for such cancer type (Duan et al., 2016). Another study indicated that BIRC5 may be involved in chemoresistance of NSCLC cells (Hu et al., 2016). Additionally, it was demonstrated that the GC+CC genotypes in the promoter region (-31) of the BIRC5 gene (polymorphism rs9904341) were significantly associated with EGFR mutations in a cohort of 360 lung cancer patients (Liu et al., 2016).

Recently, BIRC5 was identified as a target of MIR195, a microRNA that induced apoptosis and senescence in NSCLC cells (Yu et al., 2018). A combined therapy using the natural product resveratrol and the epidermal growth factor receptor (EGFR) inhibitor erlotinib promoted an increase in cell death mediated by BIRC5 depletion in NSCLC cells (Nie et al., 2015). Similarly, depletion of BIRC5 induced by treatment with YM155 increased the sensitivity of such cells to radiation (Hu et al., 2015).

Treatment with the natural product fisetin also increased sensitivity to cisplatin in cisplatin-resistant NSCLC cells by modulation of MAPK/BIRC5/Caspase axis (Zhuo et al., 2015).

Lung cancer stem cells were more sensitive to FL118, a BIRC5 inhibitor, than cisplatin. Additionally, FL118 downregulated cancer stem cell related markers, which may improve drug-sensitivity in this kind of tumor cells (Wang et al., 2017c).

Lymphoma

In non-Hodgkin lymphoma, specifically the aggressive subtype extranodal natural killer/T-cell lymphoma, which is frequently associated with resistance to anthracyclines, presence of BIRC5

serum levels were detected in approximately 25% of patients, which is associated with advanced stages of the disease. In addition, the percentage of lymphoma cells that demonstrated BIRC5 nuclear localization was significantly associated with BIRC5 serum concentration (Kim et al., 2015).

BIRC5 expression was positive in 40% of lymph node biopsy of diffuse large B-cell lymphoma patients. Such observation correlated with unfavorable factors for therapy response and predicted shorter survival outcomes (Markovic et al., 2012). A meta-analysis, including 17 studies and 1,352 diffuse large B-cell lymphoma patients, found positive BIRC5 expression to be associated with advanced clinical stages and reduced overall survival (Zhang et al., 2015c).

The combinatory use of bendamustine and rituximab associated with BIRC5 inhibitor, YM155, presented potentiating effects on induction of cell death by triggering DNA damage and cell cycle arrest in lymphoma cells, and, moreover, reduced tumor size and metastatic capacity in diffuse large B-cell lymphoma xenograft murine models (Kaneko et al., 2014). A combined treatment of rituximab and YM155 was shown to reduce tumor growth more effectively than monotherapy (Kita et al., 2012). In B and T cell lymphoma cells, BIRC5 abrogation using the non-toxic tellurium compound, AS101, has overcome chemoresistance, sensitizing these cells to paclitaxel (Danoch et al., 2015). BIRC5 expression presented anti-apoptotic functions and is regulated by NF- κ B and PI3K/AKT signaling pathways in nasal NK/T-cell lymphoma cells (Sun et al., 2015).

Malignant pleural mesothelioma

In two independent cohorts of malignant pleural mesothelioma patients, nuclear BIRC5 expression in both, pre- and post-chemotherapy tissues, was associated with shorter freedom from recurrence and overall survival, indicating that BIRC5 expression may be a prognostic factor for poor clinical outcomes in this cancer type (Meerang et al., 2016).

Melanoma

BIRC5 expression was previously demonstrated in melanoma and melanocytic nevus, which demonstrated all nevi, regardless of histologic type, expressed detectable levels of BIRC5 (Yan et al., 2006). Additionally, a cytoplasmic staining of BIRC5 was evidenced in dysplastic nevi (Florell et al., 2005). In normal melanocytes, it was demonstrated that p53 and RB1 are required to repress BIRC5 expression. A role for E2F2 in the negative regulation of BIRC5 expression was also pointed out (Raj et al., 2008). Increased BIRC5 expression was observed in vivo in melanocytes that were more resistant to UV-induced apoptosis, which was further associated to lower rates of spontaneous apoptosis, earlier melanocytic tumor development

and increased tendency for lymph node and lung metastasis (Thomas et al., 2007). Furthermore, BIRC5 overexpression in melanocytes activated the AKT and MAPK signaling pathways, acquiring a more invasive phenotype, and demonstrating the involvement of BIRC5 on the onset and progression of melanoma (McKenzie et al., 2013).

In melanoma cells, BIRC5 was associated to enhanced AKT and MAPK signaling dependent migration and invasion, as well as to the upregulation of ITGA5 (α 5 integrin) (McKenzie et al., 2010). BIRC5 silencing through RNA interference promoted cell cycle arrest and reduced cell proliferation and metastasis in vivo and in vitro in melanoma models. Moreover, as observed for other tumor types, BIRC5 inhibition led to increased sensitivity to chemotherapy in melanoma cells (Kedinger et al., 2013). In another study, a proposed strategy to overcome chemoresistance and to promote melanoma cell death was the combination of vemurafenib and Nutlin-3, whose synergism was responsible for BIRC5 depletion and apoptosis induction (Ji et al., 2013).

Pharmacological suppression of BIRC5 expression, using YM155, increased apoptosis induction and tumor regression in melanoma xenograft models. In the same study, combined treatment of YM155 and docetaxel presented potentiating effects in induction of apoptosis compared to monotherapy, corroborating the notion that targeting BIRC5 may be an interesting approach in melanoma management (Yamanaka et al., 2011). Similar results were obtained using natural compounds extracted from plants that target BIRC5 through β -catenin and STAT3 suppression (Habibie et al., 2014).

Another alternative approach for targeting BIRC5 was the generation of recombinant fusion proteins containing the TAT protein transduction domain and either wild-type survivin (TAT-Surv-WT) or a dominant-negative mutant (TAT-Surv-T34A). The mutant promoted in vitro cell death through apoptosis and DNA fragmentation in melanoma cells. In vivo injections of such mutant in melanoma xenograft mice increased apoptosis, induced aberrant nuclei formation and impaired tumor growth (Yan et al., 2006).

BIRC5 mRNA was detected in 98% of samples from metastatic melanoma patients. High BIRC5 mRNA levels were significantly associated with poor overall survival (Takeuchi et al., 2005).

Multiple myeloma

BIRC5 expression was positive in 35% of samples from newly diagnosed multiple myeloma patients, but no association with clinical and laboratorial characteristics, treatment response and survival outcomes was found (Zeng et al., 2014). On the other hand, Yang and colleagues (Yang et al., 2016b), in a

study that evaluated the efficacy of a combination treatment with fludarabine, vincristine, epirubicin, dexamethasone and thalidomide (FVADT) chemotherapy regimen for refractory multiple myeloma patients, reported that complete remission and efficacy rates were significantly lower in the BIRC5-positive group, when compared with the BIRC5-negative group.

Myxoid liposarcoma

Using high-throughput drug screen and myxoid liposarcoma cell lines, BIRC5 has been identified as a relevant protein important for cell survival (de Graaff et al., 2017).

Oral squamous cell carcinoma

Elevated BIRC5 mRNA expression was observed in samples from oral squamous cell carcinoma patients compared to peritumoral or normal tissues (Li et al., 2012). Still, such increase was shown to be insufficient to drive tumor progression in oral squamous cell carcinoma, however nuclear expression of BIRC5 was correlated with tumor stage and differentiation grade (Liu et al., 2017). Additionally, the authors suggested that nuclear localization of BIRC5 has been due to the acetylation at K129 in the protein C-terminal region (Liu et al., 2017). In oral squamous cell carcinoma cells, treatment with YM155 reduced BIRC5 levels and increased apoptosis rates (Yan and Su, 2017).

Ovarian cancer

High BIRC5 levels correlate with advanced stage, metastasis and poor disease-free survival in ovarian cancer (Aune et al., 2011; No et al., 2011). Moreover, BIRC5 serum levels were significantly higher, while DIABLO (Smac) levels were significantly lower in patients with serous ovarian carcinoma when compared to healthy controls (Dobrzycka et al., 2015).

The association of nuclear and cytoplasmic BIRC5 expression and prognosis remains controversial in ovarian cancer. The evaluation of BIRC5 expression in patients treated with taxane and platinum agents concluded that, in this treatment regimen, higher nuclear BIRC5 expression was associated with reduced risk of disease recurrence and death (Felisiak-Golabek et al., 2011). By contrast, another study reported that nuclear BIRC5 was significantly associated with chemoresistance to taxane-based chemotherapy, predicting poor progression-free survival (Du et al., 2015). Immunohistochemistry analysis revealed that BIRC5 expression presented a positive correlation with FIGO stage in epithelial ovarian cancer, benign epithelial ovarian tumor tissue and borderline ovarian tumor tissues (Ju et al., 2016).

BIRC5 splices variants were also correlated to the development of ovarian cancer and resistance to chemotherapy. Taxane-resistant ovarian cancer cells

expressed higher BIRC5 mRNA levels than their taxane-sensitive counterparts. Survivin-2B expression was significantly higher in taxane-resistant cells, when compared to sensitive cells (Vivas-Mejia et al., 2011).

YM155 treatment induced BIRC5 downregulation, cell growth inhibition, cell cycle arrest, reactive oxygen species formation and apoptosis, and enhanced docetaxel efficacy in ovarian cancer cell lines (Hou et al., 2018). In agreement, in ovarian cancer cells, BIRC5 knockdown enhanced cisplatin sensitivity in resistant cancer cells, inducing apoptosis and inhibiting the invasive process through downregulation of MMP2 (Jiang et al., 2013).

Pancreatic cancer

In a cohort of 51 pancreatic adenocarcinoma patients, BIRC5 expression was found in 49% of samples and was associated with poor survival outcomes (Contis et al., 2018). Similar results were reported by Zhou and colleagues (Zhou et al., 2018), who described that nuclear BIRC5 was higher in tumor compared to non-tumor pancreatic tissues, and a high nuclear BIRC5 expression was an independent predictor of disease-specific survival in ductal pancreatic adenocarcinoma patients. In pancreatic cancer models, FL118, a BIRC5 inhibitor, reduced cell viability, including for stem cell like and cisplatin-resistant cells, and decreased xenograft tumor growth and metastasis (Ling et al., 2018).

Prostate cancer

BIRC5 levels was not detected in normal tissues, slightly detected in benign prostate hyperplasia tissues and considerably higher in prostate adenocarcinoma, which was positively correlated with higher tumor stage (Eslami et al., 2016). In agreement, increased BIRC5 levels were also associated with poor survival outcomes in prostate cancer patients (Xu et al., 2015).

In a cohort including 157 prostate cancer patients and 145 controls, genetic polymorphisms c.-31G>C (rs9904341), c.454G>A (rs2071214), and c.*148T>C (rs1042489) of BIRC5 were associated with risk for prostate cancer development (Karimian et al., 2018).

Treatment with BIRC5 inhibitor (YM155) inhibited cell growth, cell migration and invasion in prostate cancer cells (Xu et al., 2015). Overexpression of miR-494 (a microRNA targeting BIRC5) and/or BIRC5 silencing using shRNA attenuated cell growth in vitro and in vivo (Zhu et al., 2016). Moreover, treatment of prostate cancer cells with a selective inhibitor of nuclear export, KPT-330, inhibited proliferation and promoted apoptosis of tumor cells, by increasing protein degradation of exportin XPO1, BIRC5 and CCND1, further leading to cell cycle arrest and apoptosis (Gravina et al., 2015). Natural products, such as the triterpenoid

pristimerin, demonstrated that BIRC5 levels may modulate therapeutic responses, once BIRC5-overexpressing prostate cancer cells became resistant to pristimerin (Liu et al., 2014).

Salivary adenoid cystic carcinoma

In SACC-83 salivary adenoid cystic carcinoma cells, treatment with simvastatin reduced cell viability and induced apoptosis by decreasing BIRC5 levels (Cai et al., 2018).

Thyroid cancer

Nicotinamide phosphorybosyltransferase (NAMPT), a marker for thyroid cancer that is positively associated with tumor stage and metastasis, presented a positive correlation with BIRC5 (survivin) and survivin splice variant $\Delta Ex3$, but not with survivin-2B, expressions, reinforcing that survivin and its variant $\Delta Ex3$ are associated with poor prognosis and advanced stage cancer (Sawicka-Gutaj et al., 2015).

Urinary tract cancer

In SK-NEP-1 Wilms tumor cells, YM155 treatment reduced cell proliferation, induced apoptosis and inhibited growth of xenograft tumors. Interestingly, YM155 treatment promoted an elevation in levels of other BIRC-related genes, such as BIRC3 and BIRC8, suggesting that the regulation of cell death induced by BIRC5 suppression is highly orchestrated with other members of the IAP family (Tao et al., 2012).

To be noted

Pharmacological Advances for BIRC5 inhibition

YM155, a small-molecule BIRC5 inhibitor, was developed in 2007 and tested in multiple cancer models. YM155 caused a concentration-dependent cytotoxic effect with IC_{50} values reaching nanomolar concentrations (Nakahara et al., 2007; Rauch et al., 2014). The mechanism of action for YM155 involves a selective inhibition of BIRC5 promoter activity by disrupting Sp1 interaction in a specific region of the BIRC5 core promoter. Such repression occurs in a cell cycle-independent manner (Cheng et al., 2012).

A novel survivin inhibitor developed in 2012, FL118, presents structural similarities to irinotecan. Such molecule selectively inhibits survivin promoter activity and gene expression in a TP53 status-independent manner.

Additionally, it promotes the inhibition of three additional cancer-associated survival genes (MCL1,

BIRC4 and BIRC3) (Ling et al., 2012). FL118 was able to suppress BIRC5 expression in cancer stem cells in a lung cancer model (Wang et al., 2017c), which are known to be a cell population that presents chemoresistance and are responsible for disease recurrence in multiple type of cancer (Zhao, 2016).

Vaccines against BIRC5

Survivin-2B80-88 (AYACNTSTL) is an antigenic peptide that can be recognized by CD8+ cells and demonstrated promising results as a potent immunogenic cancer vaccine (Idenoue et al., 2005). By using an HLA-A24/survivin-2B80-88 tetramer, the number of cytotoxic T-lymphocytes precursors in peripheral blood mononuclear cells of HLA-A24+ cancer patients was increased. Interestingly, cytotoxic cells positive for this peptide were found among peripheral blood mononuclear cells obtained from 100% of patients with breast cancers (n=7), 83% with colorectal cancers (n=7) and 57% with gastric cancers (n=7) (Idenoue et al., 2005).

Dendritic cells vaccines using recombinant BIRC5 were tested in hormone refractory prostate cancer patients and results revealed cellular response, disease stabilization, partial tumor remission and no adverse events (Xi et al., 2015).

Using the DepoVax platform, a BIRC5 vaccine was developed (DPX-Survivac) and produced antigen-specific immune responses in ovarian cancer patients. Of note, 12 out of 18 ovarian patients remained without clinical progression after a 6-month treatment (Berinstein et al., 2015).

A study using vaccination with a long BIRC5 peptide demonstrated a BIRC5-specific CD8-mediated tumor cell lysis and, more importantly, the presence of circulating anti-BIRC5 antibodies was found in both, murine glioblastoma models and human glioblastoma patients following vaccination. The same vaccine showed promising results in GL261 glioma and B16 melanoma murine models (Fenstermaker et al., 2018).

Gene Therapy targeting BIRC5

Gene therapy has already been used as an approach for inhibiting the expression of BIRC5 and to improve cell death induction in cancer. A combined gene therapy using BIRC5 siRNA and the fusion suicide gene γ CDglyTK system displayed a relevant antitumor effect, inducing apoptosis more efficiently and eradicating colon cancer cells. Furthermore, this therapeutic system was able to inhibit the migration of colon cancer cells in vitro (Ye et al., 2017).

Pharmacological approaches			
Drug	Clade	Cancer type	References
YM155	Small-molecule survivin inhibitor	Multiple cancer types	Cheng et al., 2014; Jane et al., 2013; Kita et al., 2012; Lai et al., 2012

FL118	Small-molecule survivin inhibitor	Cancer Stem Cell	Wang et al., 2017
<u>Vaccines</u>			
Vaccine	Clade	Cancer Type	References
Survivin-2B80-88	Antigenic peptide	Breast cancer; Gastric cancer; Colorectal cancer	Idonoue et al., 2005
Dendritic Vaccines	Cell Dendritic cells vaccines using recombinant BIRC5	Hormone refractory prostate cancer patients	Xi et al., 2015
DPX-Survivac	BIRC 5 vaccine developed based on DepoVax platform	Ovarian cancer	Berinstein et al., 2015
SurVaxM	Long BIRC5 peptide	Glioblastoma	Fernstermarker et al., 2018
<u>Gene Therapy</u>			
Strategy		Cancer Type	References
Suicide gene yCDglyTK combined with BIRC5 siRNA		Colon cancer cells	Ye et al., 2017
Heparin-polyethyleneimine (HPEI) nanoparticles to deliver a dominant-negative human BIRC5 T34A (hs-T34A)		Ovarian carcinoma	Luo et al., 2016
Packaging RNA (pRNA) of bacteriophage phi29 DNA-packaging motor to carry BIRC 5 and methallothionein siRNA		Ovarian carcinoma	Tarapore et al., 2011
Adeno-associated virus (aaV)-mediated the dominant-negative human BIRC5 T34A (raaV-Sur- Mut(T34a))		Gastric cancer	Dang et al., 2015
<u>Nanotechnology</u>			
Strategy of use	Nanoparticle	Cancer Type	References
	Fe3O4 core covered respectively by polyacrylate (PA) and polyethyleneimine (PEI) layer (Fe3O4-PA-PEI)	Breast cancer	Arami et al., 2016
Nanoparticles for siRNA delivery	Magnetic nanoparticles containing polyethyleneglycol-lactate polymer (PEG-LAC), chitosan, and polyethyleneimine (PEI)	Breast cancer and Leukemia	Arami et al., 2017
	Poly(ethylene glycol)-modified chitosan (PEG-CS)	Murine breast cancer	Sun et al., 2016
	NDCONH(CH2)2NH-VDGR/survivin	Breast cancer	Bi et al., 2016
Nanoparticles for shRNA delivery	Monomethoxypolyethylene glycol-chitosan (mPEG-CS)	Prostate cancer	Yang et al., 2015
Nanoparticles for combinatory treatment	Nanoparticles were also developed for co-delivery of siRNA targeting BIRC5 and paclitaxel	Murine cancer models	Jin et al., 2018; Salzano et al., 2015

Table 2. Summary of BIRC5 targeting strategies in cancer.

Gene therapy using degradable heparin-polyethyleneimine (HPEI) nanoparticles to deliver a dominant-negative human BIRC5 T34A (hs-T34A) gene was also used in ovarian cancer with promising results. HPEI nanoparticles effectively delivered the hs-T34A into ovarian carcinoma cells with low systemic cytotoxicity. Additionally, intraperitoneal administration of HPEI/hs-T34A complexes inhibited tumor growth in ovarian cancer xenograft murine model (Luo et al., 2016). The use of

packaging RNA (pRNA) of bacteriophage phi29 DNA-packaging motor to carry siRNA for combined BIRC5 and metallothionein silencing presented a stronger effect on reducing cell proliferation and aggressiveness in ovarian tumor cell lines than either one applied alone (Tarapore et al., 2011). Adeno-associated virus (aaV)-mediated the dominant-negative human BIRC5 T34A (raaV-Sur-Mut(T34a)) delivery inhibited cell proliferation, induced apoptosis and sensitized gastric cancer cells

to 5-FU in vitro and impaired tumor growth in vivo (Dang et al., 2015).

Nanotechnology for BIRC5 depletion

Several nanotechnology-based systems were developed to improve the delivery of siRNA or shRNA targeting BIRC5 in cancer cells, including a Fe₃O₄ core covered respectively by a polyacrylate (PA) or polyethyleneimine (PEI) layer (Fe₃O₄-PA-PEI) (Arami et al., 2016). Moreover, magnetic nanoparticles containing polyethyleneglycol-lactate polymer (PEG-LAC) have also been used for such means, as well as other systems, like chitosan and polyethyleneimine (PEI) (Arami et al., 2017), poly(ethylene glycol)-modified chitosan (PEG-CS) (Sun et al., 2016), NDCONH(CH₂)₂NH-VDGR/survivin (Bi et al., 2016) and monomethoxypolyethylene glycol-chitosan (mPEG-CS) (Yang et al., 2016a). These systems have been shown to inhibit expression of BIRC5, increase apoptosis, reduce cell proliferation and metastasis, and to shrink tumor size in multiple cancer models. Nanoparticles were also developed for co-delivery of siRNA targeting BIRC5 and paclitaxel, which constrained tumor growth, prolonged survival and augmented anticancer properties of paclitaxel in murine cancer models (Jin et al., 2018; Salzano et al., 2015).

A summary of approaches to BIRC5 targeting in cancer is described in Table 2.

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