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A concise review on the current understanding of pancreatic cancer stem cells

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Abstract: Several evidences suggest that a small population of cells known as cancer stem cells (CSCs) or tumor initiating stem-like cells within a tumor is capable of tumor initiation, maintenance and propagation. Recent publications have supported the existence of CSCs in pancreatic tumors. The pancreatic stem/progenitor cells, which express self-renewal markers, are identified to be present in the peribiliary gland. Based on the CSC hypothesis, mutations can lead to the transformation of stem/progenitor cells or differentiated cells into CSCs. The pancreatic CSCs express a wide array of markers such as CD44, CD24, ESA, CD133, c-MET, CXCR4, PD2/Paf1 and ALDH1. The CSCs are isolated based on surface markers or by other methods such as ALDEFLOUR assay or Hoechst 33342 dye exclusion assay. The isolated cells are further characterized by in vitro and in vivo tumorigenic assays. The most important characteristics of CSCs are its ability to self-renew and impart drug resistance towards chemotherapy. Moreover, these distinct cells display alteration of signaling pathways pertaining to CSCs such as Notch, Wnt and Shh to maintain the self-renewal process. Failure of cancer treatment could be attributed to the therapy resistance exhibited by the CSCs. Metastasis and drug resistance in pancreatic cancer is associated with epithelial to mesenchymal transition (EMT). Furthermore, mucins, the high molecular weight proteins are found to be associated with pancreatic CSCs and EMT. Understanding the underlying molecular pathways that aid in the metastatic and drug resistant nature of these distinct cells will aid in targeting these cells. Overall, this review focuses on the various aspects of pancreatic adult/stem progenitors, CSC hypothesis, its markers, pathways, niche, EMT and novel therapeutic drugs used for the elimination of pancreatic CSCs.

Keywords: Cancer stem cells, pancreatic cancer, niche, markers, signaling pathways, drug resistance.

ABBREVIATIONS
ABCB1 - ATP-binding cassette, sub-family B (MDR/TAP), member 1
CXCR4 - Cysteine-x-cysteine chemokine receptor 4
DCLK1 - Doublecortin-like kinase 1
SOX2 - Sex-determining region Y (SRY)-Box2
PDAC - Pancreatic ductal adenocarcinoma
CSC - Cancer stem cell
SP - Side population
NSP - Non side population
EMT - Epithelial to mesenchymal transition

INTRODUCTION
Pancreatic cancer is one of the most lethal cancers among all solid malignancies. According to the National cancer institute, it has been estimated that approximately 46,420 new cases and 39,590 deaths would be reported in the year 2014 [1]. The incidence rates have been increasing for pancreatic cancer over the past several years. Currently, pancreatic cancer has been listed as the fourth leading cause of death due to cancer and by 2020 it is predicted to be ranked as the second leading cause of cancer related deaths [2]. On the positive side, the survival rate has increased from 3% to 6.7% in the past 35 years. There are several risk factors associated with this disease. Primarily, cigarette smoking has been the largest known risk factor for pancreatic cancer development [3, 4]. Other well-known risk factors such as obesity, pancreatitis, diabetes and other forms of tobacco usage are associated with the development of pancreatic cancer. In addition, those individuals who have a strong family history of pancreatic cancer are more prone to an increased risk of developing pancreatic cancer [5]. Approximately,
5–10% of pancreatic ductal adenocarcinoma (PDAC) cases are hereditary with nearly 80% penetrance [6, 7]. Pancreatic cancer is not just a single entity caused by a single mutation; it has various precursors which arise due to multiple mutations.

The three precursors for pancreatic cancer are the highly occurring precursor; such as the pancreatic intraductal papillary mucinous neoplasm (PanINs), and less commonly occurring precursors such as; intraductal papillary mucinous neoplasm (IPMN) and mucinous cystic neoplasm (MCN) [8]. Histologically, normal pancreas undergoes a series of morphological changes giving rise to low grade PanINs which eventually gives rise to high grade PanINs [9]. These PanIN lesions eventually develop into infiltrative adenocarcinoma [10]. Many genetic alterations were defined in pancreatic cancer such as earlier events including K-ras point mutation, EGFR overexpression and gene amplification and HER2/neu overexpression and later events such as inactivation of p16, p53, DPC4 and BRCA. Considering the genetic alterations, currently there are several animal models developed to study the progression of pancreatic cancer [9]. Animal models are developed to recapitulate the genetic alterations of the human pancreatic cancer and also they serve as a tool to understand the mechanisms underlying the disease.

In the recent past various animal models have been developed using the Cre-Lox technology such as Pdx1-Cre; LSL-KrasG12D, Ptf1/p48-Cre; LSL-KrasG12D and LSL-KrasG12D/+Mist1Cre-ER/ [11–13]. Eventually, animal models harboring additional modifications such as inactivation/mutation of p16, p19, p53, transforming growth factor (TGFβ) and smad4 were developed [14–16]. These in vivo models help in understanding the progression of pancreatic cancer from lower to higher grade lesions which slowly develops to invasive carcinoma and finally to metastasis. Although several aspects of PDAC have been studied so far, the evidences for the emergence of pancreatic cancer from cancer stem cells have been quite limited but intriguing as well.

Cancer stem cells (CSCs) or tumor initiating stem-like cells (TICs) are a small subset of cancer cells which are capable of self-renewal and resist various chemotherapeutic drugs [17]. This sub-population behaves like stem cells by undergoing either asymmetric or symmetric cell division thereby maintaining its population within the cancer. CSCs have been identified in various cancers including brain, breast, ovarian, prostate, pancreatic and colon [18–25]. Simeone et al. [20], demonstrated the presence of CSCs in pancreatic cancer for the first time. Pancreatic CSCs were characterized by CD44+/CD24− and ESA+ markers. Eventually, several pieces of evidence have cropped up to prove the existence of pancreatic CSCs [26–28]. These pieces of evidence emphasize the importance of identifying pancreatic cancer stem cells. Simultaneously, targeting these CSCs in pancreatic cancer has become another challenging area of interest. In this review article, we will summarize the earlier findings of pancreatic cancer stem cells, the potential techniques used to enrich and characterize pancreatic CSCs, pancreatic CSC niche, the various signaling pathways involved in the maintenance of pancreatic CSCs, drug resistance and EMT, mucins in pancreatic CSCs and the current strategies used to target pancreatic CSCs.

**INDENTIFICATION OF PANCREATIC CANCER STEM CELLS**

By the year 2006, many studies reported the existence of CSCs in various cancers [18, 22, 29]. After several years of CSC discovery, the first evidence for the existence of pancreatic CSCs was reported by two groups in the year 2007 [20, 30]. Li et al. [20], demonstrated that the CD44+/CD24−/ESA+ cells isolated from human PDAC could self-renew, had differentiation potential, and had enhanced Shh expression. Subcutaneous injection of 500 cells (positive for CD44, CD24 and ESA) in mice could generate tumors (7/12 mice) whereas implantation of pancreatic cancer cells negative for these markers could not. Equally significant, a second study showed the presence of pancreatic CSCs having the ability to metastasize. Notably, the CD133CXCR4+ CSC subpopulation isolated from pancreatic tumors displayed metastastic activity [30]. Emerging evidence demonstrates that the ZEB1-microRNA200 feedback loop is essential to promote the migratory CSCs in pancreatic cancer [31].

Later in 2011, c-Met was identified as an important CSC marker in pancreatic cancer [28]. Strikingly, the c-Met expressing CSCs (c-Methigh) had the ability to give rise to a larger tumor as opposed to no tumor formation in the c-Met negative cells. A c-Met inhibitor such as XL184 could reduce the CSC population [28]. Subsequently, Van den Broeck et al. [26], used a different method to study the pancreatic CSCs [26]. They have isolated side population (SP) and non-side population (NSP) from PDAC surgical resection specimens using the Hoechst 33342 dye based FACS analysis. Two important genes such as ABCB1, a multidrug resistance transporter as well as CXCR4, a chemokine receptor were found to be upregulated in the SP fraction as opposed to the NSP fraction. They also demonstrated that these two genes have been associated with the worst patient survival. It has been suggested that this subpopulation of cancer cells such as the CSCs should be the prime target for therapy.

A recent study demonstrated that SOX2, a transcription factor which plays a role in the embryonic development has been found to cause de-differentiation thereby imparting stem cell-like characteristics to pancreatic cancer cells. SOX2 is absent in the normal acinar or ductal compartment. However, its expression has been observed in 19.3% of human pancreatic tumors. The study suggested that SOX2 positive cancer cells could serve as an essential therapeutic target; as its expression has significantly increased in the ESA+/CD44+ CSC population, and is
also found to regulate genes controlling EMT and G1/S transition thereby contributing to dedifferentiation and stemness [32]. The latest work by Bailey et al. [27], demonstrated the existence of a distinct population of pancreatic cancer initiating cells in KC\textsubscript{Pdx}, KC\textsubscript{Mist1} and KPC\textsubscript{Pdx} mice expressing DCLK1 which is a microtubule regulator. They have also demonstrated that pancreatic CSCs could be identified at very early stages such as in PanIN 1 (Pancreatic intraepithelial neoplasia-1) in KPC mice. Altogether, these evidences clearly validate the presence of CSC subpopulation in pancreatic cancer.

**ORIGIN OF PANCREATIC CANCER STEM CELL HYPOTHESIS**

During the embryonic developmental stage, pancreas develops as dorsal and ventral evaginations from the foregut endoderm in the 5\textsuperscript{th} week of gestation [33]. Cells from the dorsal and ventral buds slowly undergo lineage commitment to either of the two compartments such as the endocrine and the exocrine compartments. The endocrine compartment comprises the islets while the exocrine compartment is organized into acinar, ductal and centroacinar cells (Figure 1) [34]. In addition to the above mentioned compartments, a novel gland like mucinous compartment known as the pancreatic ductal gland has been identified to possess a characteristic molecular signature [35]. With different compartments present in the pancreas, the question is from where do the pancreatic progenitors arise?

Pancreas is an essential organ whose size is controlled by the size of the progenitor population that is present in the developing pancreatic bud [36]. On the other hand, the
reduction in the number of progenitor cell population does not control the size of the liver during developmental stages [36]. Results showed the ability of pancreatic progenitors to grow, divide and differentiate after a reduction in the Pdx1 progenitor pool in mice. However, it could not increase the cell division rate in order to make a normal sized organ [36]. Progenitors isolated from mice are found to bear several surface markers. For instance, Samuelson et al. [37], showed that the highly proliferative pancreatic progenitor population isolated from mice has been found to express stem cells antigen 1- (Sca-1). Another study showed the presence of Nestin positive multipotent progenitor cells in the centrilobular ducts of the adult rat pancreas [38]. Interestingly Smukler et al., demonstrated the presence of insulin positive multipotent stem cells which had the ability to divide, thereby contributing to both pancreatic and neural lineages [39].

Recent reports propose that the biliary tree derived cells are the precursors of pancreatic committed progenitors [40]. There is evidence for the presence of pancreatic stem cells and/or progenitors in the peribiliary gland (PBG) which connects to the pancreatic duct glands within the pancreas [40]. The stem cells in the peribiliary gland are highly proliferative and they express pluripotency markers such as NANOG, OCT4, and SALL4 but do not express mature pancreatic markers [40].

Notably, Rovira et al. [41], demonstrated that ALDH1 expressing centroacinar cells behave like adult/stem progenitor cells. Evidences for the origin of CSCs in pancreas are very limited. A recent study demonstrated that the centroacinar cells; which is located at the junction of acini and ducts, has been suggested to be the origin of PanINs and pancreatic ductal adenocarcinoma and since these cells express stem cell markers it could be proposed that CSCs could arise from the centroacinar cells [42]. Recent evidence also demonstrated that DCLK1 expressing cells in the Kras; p53; PdxCre mouse tumors show CSC like progenitor population isolated from mice has been found to express stem cells antigen 1- (Sca-1). Another study showed the presence of Nestin positive multipotent progenitor cells in the centrilobular ducts of the adult rat pancreas [38]. Interestingly Smukler et al., demonstrated the presence of insulin positive multipotent stem cells which had the ability to divide, thereby contributing to both pancreatic and neural lineages [39].

Aldefluor assay
This assay has been developed based on the increased aldehyde dehydrogenase (ALDH) activity in hematopoietic stem cells. ALDH is required for the oxidation of intracellular aldehydes thereby resulting in the oxidation of retinol to retinoic acid [46]. The aldefluor assay employs an ALDH fluorescent substrate called BODIPY-aminoacetalddehyde (BAAA). BAAA passively diffuses into the living cells and gets converted into BODIPY aminoaacetate (BAA-) by the intracellular ALDH. BAA- is retained inside the cells until it is effluxed by ATP binding cassette (ABC) transporters [47]. To determine the background fluorescence an ALDH inhibitor, Diethylaminobenzaldehyde (DEAB) is used. Using this assay, Rasheed et al. [48], claimed that the ALDH+ cells have enhanced tumorigenic potential and they are comparatively more invasive than the CD44+CD24+ pancreatic CSCs. Likewise Kim et al. [49], reported that the ALDHhigh cells are highly tumorigenic compared to the CD133+ and ALDHlow cell population. Gemcitabine treated xenograft tumors showed an enrichment of ALDH1 positive cells suggesting that they can tolerate chemotherapy similar to CSCs [50].

Hoechst 33342 dye exclusion assay
This method is one of the most common methods employed to isolate the side population (SP); based on its dye efflux properties in various types of cancer cells. SP cells constitute a subpopulation of cancer cells that can efficiently efflux the fluorescent DNA binding dye, Hoechst 33342, by an ATP binding cassette (ABC) transporter. This assay was initially employed to isolate SP cells from rat C6 glioma cell line [51]. As the SP cells exhibit higher tumorigenicity than non-SP cells it is believed that this method is used to detect CSCs. As a control for sorting the
CSCs, an ABC transporter inhibitor; such as verapamil or reserpine, is used in order to determine the SP gate. These DNA binding dyes inhibit the efflux of the Hoechst dye by SP cells thus serving as an essential control. The main limitation of using Hoechst dye is its toxicity to cells; however, if the concentration and incubation time has been standardized the level of toxicity could be minimized. Small differences in cell densities, dye concentrations and staining timings may affect the phenotype of the SP cells. Despite these limitations, some researchers prefer to use the SP method, or the marker independent method, as it overcomes the barrier of using diverse CSC markers for isolation. By using the hoechst 33342 dye exclusion assay reports clearly show the presence of SP and NSP in various cancers such as brain, lung, prostate and pancreatic [26, 52–54].

**POTENTIAL MARKERS USED FOR THE ISOLATION OF PANCREATIC CSCs**

Pancreatic CSCs can be isolated from cell lines or primary tumors using the markers detailed below.

- c-Met belongs to the receptor tyrosine kinase family and is expressed in both normal and cancer cells [55]. The ligand associated with this receptor is known as hepatocyte growth factor (HGF). It has been reported that pancreatic cancer cells expressing high levels of c-Met (c-Met\textsuperscript{high}) displayed increased self-renewal capacity and tumorigenic potential as opposed to the non-expressing or c-Met\textsuperscript{low} expressing cancer cells [28]. Inhibition of c-MET using either small hairpin RNA or c-Met inhibitor resulted in decreased tumor growth. This work introduces c-Met as an essential CSC marker in pancreatic cancer.

- CD133 and CD44 are cell surface glycoproteins involved in cell-cell interactions and cell adhesion. Epithelial specific antigen (ESA) which is also known as EpCAM is a widely used marker for CSCs isolation in various cancers [56]. Using these three markers, Li et al. [20], has demonstrated the existence of pancreatic CSCs. They have isolated the CD44\textsuperscript{+}/CD24\textsuperscript{-}/ESA\textsuperscript{-} pancreatic CSCs from the pancreatic tumors which accounted for 0.2–0.8\% of pancreatic cancer cells that displayed the CSC features such as the self-renewal property and enhanced tumorigenic potential as opposed to the marker-negative population.

- CD133 also known as Prominin1/AC133 is a surface glycoprotein expressed in the progenitor cell populations and it is a marker of CSCs of various cancer origins. CD133 is found to be expressed in pancreatic CSCs as demonstrated by Hermann et al. [30]. They clearly showed that CD133\textsuperscript{+}CXCR4\textsuperscript{+} CSCs were responsible for the metastatic phenotype of the tumor and on depletion of the CSCs carrying these signature markers; it resulted in the abrogation of metastatic nature of pancreatic tumors [30].

Apart from the aforementioned markers, ALDH1 is one of the widely used markers to isolate pancreatic CSCs. In addition, CXCR4\textsuperscript{+} was used to denote a subset of CD133\textsuperscript{+} pancreatic CSCs which was associated with metastasis as well as drug resistance. Recently, a novel marker pancreatic differentiation 2 (PD2) was identified to maintain the self-renewal and drug resistance properties of pancreatic CSCs [57]. One of the most recent studies explored a novel marker integrin α\textsubscript{6}β\textsubscript{3} as a CSC driver in lung, breast, and pancreatic cancers which are highly resistant to erlotinib; a tyrosine kinase inhibitor [58]. The Kras-RalB-NF-κB pathway and the expression of the integrin were identified to be important for the initiation of tumor, self-renewal, anchorage independence and the resistance developed against erlotinib. Altogether, these markers could solely enrich the CSC population from a heterogeneous cancer cell population (Figure 2). Isolated CSCs are subsequently characterized for its self-renewal and tumorigenic properties.

**CHARACTERIZATION OF PANCREATIC CSCs**

Once the CSCs are isolated using any of the previously mentioned methods these cells are characterized using the following assays:

*In vitro tumorsphere assay*

To demonstrate the self-renewal capacity and the tumorigenic potential of the CSCs an in vitro tumorsphere assay is performed. One way to demonstrate the clonogenicity of the CSCs or the SP fraction is by seeding them in few numbers in a low attachment plate (with appropriate replicates), which are further allowed to grow for approximately 2 weeks. The total number of spheres formed is counted and these primary spheres are then subjected to

![Figure 2. A schematic representation of various pancreatic cancer stem cell markers.](http://cancerstemcellsresearch.com)
serial dilution in order to demonstrate its self-renewal property in the secondary generation. The true CSC population will have the ability to form spheres faster than the primary generation.

**In vivo tumorigenic assay**

In order to assess the tumorigenic potential of the CSCs, these distinct cells are injected in NOD-SCID mice, nude mice or NSG mice. In various cancers it has been reported that any number between 1 to <1000 CSCs when injected in mice have the ability to form a tumor [22, 59]. In pancreatic cancer, it has been shown that 50% of the mice developed tumor when 100 CD44+CD24+ESA+ cells were injected in mice [20]. The primary tumors are digested with collagenase and trypsin and CSCs isolated from these tumors are injected into the secondary recipients [48]. These mice should have developed the tumors even faster than that of the primary generation. Therefore, these assays are essential to be carried out in order to prove that the isolated CSCs are a true population (Figure 1).

**MUCINS IN CANCER STEM CELLS/PANCREATIC CANCER**

Mucins are heavily glycosylated proteins which form a protective barrier to the cell surface. They are characterized by a heavily O-glycosylated tandem repeat region, rich in proline (P), threonine (T) and serine (S) residues also known as the PTS domain. The slow transition from a healthy to diseased state in pancreatic cancer is accompanied by an altered expression and localization of mucins [60]. There are as many as 21 members in the mucin family which are mainly divided into transmembrane and gel forming proteins. So far, two of the transmembrane mucins such as MUC1 and MUC4 have been found to be associated with cancer stem cells [61, 62].

In pancreatic cancer, it has been demonstrated that the down-regulation of MUC4 results in sensitizing the pancreatic cancer stem/progenitor cells to chemotherapeutic drugs, thus serving as an important therapeutic means in pancreatic cancer treatment [62]. Followed by this finding it was identified that in ovarian cancer, MUC4 was over-expressed in ovarian cancer cell line SKOV3, which led to the increased expression of HER2. This in turn resulted in increased CD133+ population as well as side population [63]. In the recent past, MUC1 was identified to be a potential marker in pancreatic and breast cancer stem cells. Engelmann et al. [64], has identified that around 77% of breast CSCs isolated using the Hoechst 33342 dye method were found to be MUC1bright cells. Similarly in pancreatic cancer, Curry et al. [61], has identified that 80% of the CSCs in patient samples expressed MUC1. Two sets of CSC populations were isolated from pancreatic cancer cell lines such as BXPC3 and Panc-1 using the triple marker such as CD44+CD24+EpCAM+ and the CD133+ cells. CSCs isolated using the triple marker sorting were up to 46.7% and 19.8% in BXPC3 and Panc-1 cell lines respectively. MUC1 expression was found to be detected at higher levels in both the populations [61].

Mucins have gained significant importance in pancreatic cancer research. Therefore, it will be important to explore mucins with respect to CSCs in the near future. Apart from MUC1 and MUC4, other mucins such as MUC5AC, MUC16 and MUC17 are yet to be explored from the cancer stem cell viewpoint.

**SIGNALING PATHWAYS INVOLVED IN THE MAINTENANCE OF PANCREATIC CSCs**

Since self-renewal is a common feature of normal stem cells and CSCs, it is reasonable to believe that these cells share the same signaling pathways. The following signaling pathways such as Notch, Shh and Wnt play an important role in the pancreatic CSCs.

In the normal pancreas, Notch signaling controls the balance between the self-renewal and differentiation processes [65]. Additionally, Notch signaling is important for the pathogenesis of human cancers including pancreatic. Studies showed that the overexpression of Notch-1 resulted in increased clonogenicity, migration, invasion and induction of EMT phenotype in Aspc-1; a pancreatic cancer cell line. Moreover, the overexpression of Notch-1 resulted in a significant increase in the pancreas formation which concomitantly expressed higher levels of the CSC markers, EpCAM and CD44 [66]. Bao et al. [66], has identified that Notch-1 signaling is crucial for the acquisition of EMT phenotype. Likewise, Abel et al. [67], has identified that Notch pathway is essential for the maintenance of pancreatic CSC population. They have observed that knockdown of Hes1 using shRNA and inhibition of the Notch pathway components by gamma secretase resulted in the reduction of the self-renewal capacity of pancreatic CSCs. Altogether, these studies clearly suggest that Notch signaling is important for the pancreatic CSC formation (Figure 3).

Hedgehog signaling pathway is essential for cell differentiation and tissue patterning events during the embryonic development of the pancreas [68]. Among the three hedgehog genes such as Sonic hedgehog (Shh), Indian hedgehog (Ihh) and Desert hedgehog homolog (Dhh), Shh shows the widest range of expression [68]. One of these three ligands binds to the receptor Patched1, which relieves the protein smoothened (Smo) from inhibition. Smo triggers the activation of the downstream target genes such as GLI family of transcription factors and PTCH (Figure 3). It has been reported that a nine fold increase in Shh mRNA levels has been found in the CD44+CD24+ESA+ cells when compared to the unsorted pancreatic cancer cells [20]. Sonic hedgehog- GLI signaling is identified to be essential for the pancreatic CSCs. Sulforhodamine (SFN), an active component in cruciferous vegetables, was found to inhibit the self-renewal capacity of pancreatic CSCs by blocking the hedgehog pathway [69].

In addition to the above mentioned pathways, there is another pathway which is essential for the signaling in
pancreatic CSCs. During embryonic development the Wnt-β-catenin signaling pathway plays an important role at different stages of pancreatic organogenesis. However, inhibition of this pathway is necessary for pancreatic specification during the early endoderm development [70]. Canonical Wnt signaling is found to be important for the progression of pancreatic cancer [71]. It has been reported that in colorectal cancer Wnt signaling is associated with EMT process and was found to activate a transcription factor snail thereby facilitating EMT. Snail is associated with EMT process and was found to activate a transcription factor activation leads to subsequent upregulation of Shh target genes such as FoxM1, Nanog, OCT4 and Sox2 [91–93]. These genes subsequently lead to activation of downstream GLI (GLI1, 2, 3) family of transcription factors. In pancreatic cancer cells, GLI signaling factor activation leads to subsequent upregulation of Shh target genes such as FoxM1, Nanog, OCT4 and Sox2 [91–93]. These markers play a major role in the self-renewal nature of pancreatic cancer stem cells. C. Notch signaling pathway: In pancreatic cancer stem cells, notch signaling cascade plays a vital role in stem cell maintenance and differentiation process. Notch receptor is composed of an extracellular ligand binding domain, a single transmembrane spanning region and intracellular domain. Activation of notch signaling takes place through binding of delta ligand with notch receptor between neighboring cells. Upon ligand binding to notch receptor, it will undergo a conformational change that allows cleavage at extracellular portion of notch by a metalloprotease TNFα converting enzyme (TACE). Subsequently, the intracellular portion of notch will also be cleaved by γ-secretase, an intramembrane protease thereby releasing intracellular domain containing portion (NICD). In pancreatic cancer cells, NICD will translocate into the nucleus and interacts with its transcription factor activation leads to subsequent upregulation of Shh target genes such as FoxM1, Nanog, OCT4 and Sox2 [91–93].

**Figure 3. Schematic representation of Wnt, Shh and Notch signaling cascades in normal stem cells and pancreatic cancer stem cells. A. Wnt signaling pathway:** Wnt proteins are secreted glycoproteins or ligands that transduce extracellular message to intracellular signaling cascade by binding through frizzled receptors. In the absence of this ligand (off state), β-catenin is sequestered by a complex of molecules such as Axin1, 2/APC/CK1α and GSK-3β, which is commonly known as destruction complex. Phosphorylation of β-catenin within this complex leads to ubiquitin and proteosomal mediated degradation process. In the presence of Wnt ligand (on state), WNT signaling pathway plays an important role during embryonic development for the progression of pancreatic cancer [71]. It has been reported that in colorectal cancer Wnt signaling is associated with EMT process and was found to activate a transcription factor snail thereby facilitating EMT. Snail is found to interact with β-catenin which is required for its activation. Since EMT is a process present in CSCs these findings suggest that β-catenin may play a role in pancreatic CSCs (Figure 3) [72]. However, in the future more studies are required to prove the role of β-catenin in pancreatic CSCs.

Apart from the three important signaling pathways there are other pathways which are involved in the maintenance of pancreatic CSCs. A recent study has reported that the inhibition of mTOR pathway by Rapamycin resulted in decreased viability of CD133 pancreatic cancer cells and reduced the sphere forming ability of pancreatic cancer cells. These results suggest that the mTOR pathway is essential for the self-renewal of pancreatic CSCs [73]. Another study claims that the NF-κB pathway is highly activated in pancreatic CSCs [74]. Altogether, several signaling pathways have been identified to play significant roles in conserving the cancer stem cell phenotype in pancreatic cancer.

**DRUG RESISTANCE AND EMT IN PANCREATIC CSCs**

The most important property of CSCs is to acquire the EMT induced stemness phenotype which then leads to
drug resistance to various chemotherapeutic agents. It has been well evidenced that human pancreatic cancer consists of a subset of cells; known as the side population, which is highly resistant to gemcitabine, a very commonly used chemotherapeutic agent in pancreatic cancer therapy [75]. This minor subset of cells displayed an increased expression of genes associated with epithelial-mesenchymal transition (SNAI2, LEF1), apoptotic regulation (FASLG, ETS1) and multi-drug resistance (ABCG2 and ABCA9) [75]. The cancer cells become resistant to drugs partly due to the acquisition of EMT phenotype [17]. It has been identified that the sensitivity of cancer cells is attributed by the EMT process. The epithelial marker such as E-cadherin was found to be strongly expressed in the gemcitabine sensitive pancreatic cancer cells whereas the gemcitabine resistant cells expressed mesenchymal markers such as vimentin and Zeb-1 [76]. Zeb1, a transcriptional suppressor has been identified to be an important player in the process of EMT. On silencing Zeb-1 in the mesenchymal cell lines, the expression of the epithelial markers such as E-cadherin, EVA1 and MAL2 was increased and most importantly the pancreatic cancer cells gained sensitivity to chemotherapeutic drugs [77]. Another report showed that pancreatic cancer cell lines; such as AsPC-1, MIAPaCa-2, PANC-1, Hs766T and MPanc96 cells which were resistant to three different chemotherapy drugs (gemcitabine, cisplatin and 5-fluorouracil), displayed EMT phenotype [77]. The above mentioned reports strongly suggest that drug resistance is associated with EMT phenotype. The migrating cancer progenitor cells play an important role in cancer progression and metastasis [78]. Likewise, another study showed that the gemcitabine resistant pancreatic cancer cells which display EMT characteristics showed down-regulation of single stranded small non coding RNAs namely micro RNAs (miRNA) including miR-200b, miR-200c, let-7 (b-e) when compared to the gemcitabine sensitive pancreatic cancer cells. On re-expression of miR-200 in gemcitabine resistant pancreatic cancer cells, EMT markers such as ZEB1, vimentin and slug were down-regulated [76]. This suggests that miRNAs are important regulators in determining the EMT phenotype. Another study showed that miRNAs such as miR99a, miR100, miR-125b, miR-192 and miR-429 were differentially expressed in pancreatic CSCs. These miRNA clusters were found to be associated with the stem cell associated mRNAs in pancreatic CSCs [79]. Overall, these studies suggest that drug resistance and EMT are inter related and they play an important role in the maintenance of CSCs in pancreatic cancer.

**STRATEGIES EMPLOYED TO TARGET PANCREATIC CSCs**

Pancreatic cancer remains to be one of the most challenging cancers due to its intrinsic and extrinsic drug resistance, thereby leading to invasive carcinoma. Novel drugs are being synthesized to combat this disease. CSCs are a challenging factor for the chemotherapeutic treatments including pancreatic cancer. Metformin is one of the most significant drugs reported to have decreased the CSC population as evidenced by the diminished expression of CSC markers such as CD133, CD44, CXCR4 and SSEA-1 and self-renewal associated genes such as Nanog, Oct-4 and Sox2 [80]. Metformin was able to increase the reactive oxygen species production in CSCs and reduce its mitochondrial transmembrane potential. The *in vitro* tumor-sphere assay revealed a significant decrease in the size and number of metformin treated spheres. Interestingly, they have shown that metformin retarded the formation of secondary and tertiary tumorspheres by hampering the self-renewal capacity of these CSCs. In cancer cells, the mode of action of this drug is by indirect activation of AMP-activated protein kinase (AMPK) signaling followed by inhibition of the mTOR activity thereby resulting in reduced cell proliferation and protein synthesis whereas an AMPK/mTOR independent pathway occurs in CSCs [80].

Another important drug named Salinomycin has been extensively used in the field of CSCs. Salinomycin is identified to target CD133+ pancreatic CSCs. A combinational effect of Salinomycin and gemcitabine has been used to eradicate pancreatic cancer in xenograft mice [81]. The combination of both drugs had an improved effect against CSCs over the individual agents itself. This suggests that administration of Salinomycin could therapeutically improve the efficacy of gemcitabine for the treatment of pancreatic cancer [81].

Sorafenib (SO), a multikinase inhibitor was used for targeting pancreatic CSCs. Studies demonstrated that SO administration led to the decreased spheroid formation, clongenicity, ALDH1 activity, proliferation, angiogenesis and induced apoptosis. On the other hand, it also led to increased survival and regrowth of spheroid due to the SO induced activation of NF-kB. Therefore, in addition to SO, Sulforaphane (SF); a broccoli isothiocyanate, was also used to efficiently target pancreatic CSCs. This combinatorial treatment efficiently abolished SO-induced NF-kB binding which in turn led to abrogated spheroid formation, ALDH1 activity, clongenicity, induction of apoptosis and tumor size reduction [82].

A novel drug namely cabozantinib (XL184) has been identified to inhibit c-MET, a recently established pancreatic CSC marker. Cabozantinib, a FDA approved drug decreased the viability and spheroid formation and also induced apoptosis in cancer cells. It also inhibits self-renewal property and the expression of CSC markers including SOX2, c-Met and CD133. Strikingly, cabozantinib increased the sensitivity of gemcitabine resistant cells. When this drug was administered to 330 medullary thyroid carcinoma patients, several side effects such as diarrhea, weight loss, loss of appetite, oral pain, nausea, hypertension, and hair color changes were reported.
Regardless of these side-effects, this drug inhibited tumor progression and led to reduced tumor size in some patients [83].

Recent work by Zeng et al. [84], have demonstrated the synergistic activities of MET/RON inhibitor BMS-777607 and mTOR inhibitor AZD8055 on pancreatic cancer and pancreatic CSCs. Together, these drugs target the chemoresistant cancer cells and CSCs. Therefore, novel drugs causing minimal side effects and maximal targeting of CSCs is the current need in the field of pancreatic CSCs. Moreover, there is a significant need in the area of developing small molecular inhibitors and nanoparticles targeted against CSCs to reduce the expression of the overexpressed proteins solely in CSCs. It is extremely important to design and improve the combinatorial therapies which could target the bulk of the tumor cells, CSCs and the residual dormant cells. It is well evident by now that CSC markers such as CD44, CD133 and CD24 are upregulated in pancreatic CSCs (Figure 2). Thus, raising antibody against CSC surface markers would be a major tool to target pancreatic CSCs. For example, antibody raised against CD44 led to the inhibition of pancreatic tumor initiation and postradiation recurrence in mice [85].

Wang et al. [86], reported that successful targeting of pancreatic CSCs could be achieved by targeting Notch using natural agents such as genistein, curcumin, quercetin and sulphorapane. It has been identified that chloroquine targets pancreatic CSCs by inhibiting CXCR4 and hedgehog signaling [87]. Thus, based on the above mentioned reports it could be suggested that novel strategies encompassing combinatorial therapies could be used to achieve improved treatment outcome for pancreatic cancer patients.

CONCLUSION AND PERSPECTIVES

The uncontrolled expansion of self-renewing CSCs results in cancer. Extensive studies over the past several years revealed the importance of this small subset of cells that could sustain the tumor. Although there are several methods employed to isolate CSCs, there are limitations with each of the currently used methods. Therefore, there is a need to identify improved methods for isolating purely the CSC population. Markers such as CD44, CD133 and ESA have been well established in pancreatic cancer but they serve as markers for other cancers as well. It is of utmost importance to identify specific markers which aid in the maintenance of pancreatic CSCs. As every organ has a specific gene expression pattern, it would be ideal to identify the specifics of pancreatic cancer. In the past, the identification of circulating tumor cells opened a new chapter in the field of cancer. The methods employed for the detection of tumor cells circulating in the blood stream are crucial. The most current methods used are based on the surface marker expression such as EpCAM. Similarly, if the CSCs have a sequence of signature markers expressed on its surface specific for each type of cancer, it enables the identification of CSCs, thereby facilitating easy targeting of these cells.

Given that very few CSCs when injected in mice can give rise to tumor much faster than the cancer cells, successful targeting of CSCs with a combination of chemotherapeutic agents could likely yield dramatic results. Besides CSCs, the players of the tumor microenvironment facilitate the pathogenesis of pancreatic cancer. As a result, it can be suggested that tumor microenvironment be considered as a crucial site for drug delivery. The most effective way of targeting pancreatic cancer is by destroying the CSC niche or by altering the expression of the important players which support the survival of CSCs. In the future, in vivo animal studies which explore the biology of pancreatic CSCs are required.

The signaling pathways such as Notch, Wnt and Shh are altered in CSCs. Therefore, clinical trials should focus on novel therapeutic agents that target CSCs and the important molecules in the signaling pathways in order to control the aggressiveness of pancreatic cancer. Reversal of EMT phenotype will aid in the treatment of pancreatic cancer. Different clonogenic CSCs have been identified in many other cancers in the recent past. It is also important to identify the clonogenicity of aggressive CSCs in pancreatic cancer. Origin of CSCs is one of the emerging fields; hence it is also important to identify the specific origin of pancreatic CSCs in order to target the CSCs.

The major problem with pancreatic cancer is tumor recurrence. Once the drug is withdrawn or due to the development of resistance towards drugs, the cancer reappears. Therefore, there is a need to elucidate the mechanisms of treatment resistance in patients. This could be possible with the advancements in animal models which are further administered with drugs; as the cure for pancreatic cancer partly relies on the elimination of pancreatic CSCs. Since, the genomic make up of each individual is different; individualized or personalized treatment is required to win the battle against cancer. In vitro engineering of mesenchymal stem cells (derived from pancreatic cancer patients) with anti-tumor genes could yield in targeting the cancer cells [88]. Due to the tumor homing capacity of the engineered mesenchymal stem cells, this strategy holds promise towards pancreatic cancer therapy. This strategy could be further expanded to target cancer stem cells which may result in specific treatment options for pancreatic cancer patients.

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