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MINIREVIEWS

Tracing and targeting cancer stem cells: New venture for personalized molecular cancer therapy

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Abstract

Tumors consist of a mixture of heterogeneous cell types. Cancer stem cells (CSCs) are a minor sub-population within the bulk cancer fraction which has been found to reconstitute and propagate the disease and to be frequently resistant to chemotherapy, irradiation, cytotoxic drugs and probably also against immune attack. CSCs are considered as the seeds of tumor recurrence, driving force of tumorigenesis and metastases. This underlines the urgent need for innovative methods to identify and target CSCs. However, the role and existence of CSCs in therapy resistance and cancer recurrence remains a topic of intense debate. The underlying biological properties of the tumor stem cells are extremely dependent on numerous signals, and the targeted inhibition of these stem cell signaling pathways is one of the promising approaches of the new antitumor therapy approaches. This perspective review article summarizes the novel methods of tracing CSCs and discusses the hallmarks of CSC identification influenced by the microenvironment or by having imperfect detection markers. In addition, explains the known molecular mechanisms of therapy resistance in CSCs as reliable and clinically predictive markers that could enable the use of new targeted antitumor therapy in the sense of personalized medicine.

Key words: Cancer stem cells; Cancer recurrence; Cancer therapy; Combination therapy; Chemotherapy; Radiation therapy; Immunotherapy

Core tip: Cancer stem cells (CSCs) are small subpopulation of the tumor that can survive from conventional treatment, scape from the immune system and can cause recurrence of cancer disease. Therefore, any attempt in detection and selective therapeutic targeting of CSCs will ultimately lead to better cancer treatments and can play an important role in reducing the cancer related mortalities. This review highlights the trends and approaches in CSC tracing, isolating, characterizing and targeting, which are key strategies for a novel personalized molecular cancer therapy.

Radpour R. Tracing and targeting cancer stem cells: New venture for personalized molecular cancer therapy. *World J Stem Cells* 2017; 9(10): 169-178 Available from: URL: http://www.wjgnet.com/1948-0210/full/v9/i10/169.htm DOI: http://dx.doi.org/10.4252/wjsc.v9.i10.169

INTRODUCTION

Cancer originates from deregulation of growth and resistance to apoptosis of transformed cells that acquire proliferative and metastatic capacity. While only a few genetic and epigenetic alterations can initiate the malignant transformation of healthy cells, clinically visible tumors are extraordinarily complex structures with cancer cells displaying a large number of mutations and altered gene expression[1]. The hierarchical model of tumor organization represents a similar, albeit distorted, arrangement of the tumor cells, as are their tissues of origin. The stem cell population is positioned at the top of the cell hierarchy and has the ability to self-renew and multilineage differentiate to progenitors or differentiated cell types whose proliferation capacity is restricted[2,3].

The theory of the cancer stem cell (CSC) was postulated in the 1970s and was confirmed experimentally by the isolation of tumor-initiating cells using cellular/molecular biomarkers that allowed the isolation of CSCs in acute myeloid leukemia[4]. Further, CSC has been demonstrated in a variety of solid tumors such as tumors in brain, colorectal, head and neck, liver, lung, mammary glands, pancreatic prostate carcinomas, melanoma and hematopoietic malignancies (*e.g.*, myeloid or lymphoid leukemia)[5-7]. Cell lines derived from these tumors also contain CSCs and tumor precursor cells, which represent a promising model for cancer stem cell research[1]. The functional characterization of CSCs revealed that these cells represent a small subpopulation of the tumor that can survive from conventional treatment, scape from the immune system and therefore can cause recurrence of cancer disease. Therefore, CSCs are driving force of tumorigenesis and metastases (Figure 1). According to the concept of a stem cell, it is assumed that even a few surviving CSCs after tumor therapy, is sufficient to form a new tumor[8].

In each cancer cell clone, which is characterized by harboring different combinations of mutations or genetic alterations, the processes of self-renewal, and differentiation occur differently based on the type of genetic lesions[9]. Nevertheless, significant similarities between normal and tumorigenic, experimentally identified stem cells could be expected. Both stem cell types (normal or cancerous) are rarely active, dependent on a specific microenvironment (so-called "stem cell-niche") and have a number of self-protection mechanisms[2]. This niche enables a dynamic interaction between stem cells and surrounding cells including immune cells ("immune-niche"), cytokines and chemokines that regulates maintenance, quiescence, self-renewal and differentiation of stem cells to provide an optimal stem cell-supporting setting. What contributes to formation of the niche for tumor stem cells is the subject of intensive research[10]. Normal stem cells are more microenvironment dependent in order to get dynamic input to balance between activation and differentiation or self-renewal and quiescence "extrinsic factors"[11,12]. Although CSCs can represent more autonomous regulatory characterization "intrinsic factors", similar concept of stem cell niche support could also hold for them[13]. The majority of studies using the isolated CSCs, shows the dominant effect of intrinsic factors on CSC regulation. While, other studies propose a role for the CSC niche[12]. This model suggests that less malignant tumors may have more demand on the stem cell-niche but upon cancer progress this dynamic interplay might be weaken or even diminished[14].

An inductor of the stem cell phenotype is hypoxia[15-17]. The self-protection mechanisms are due to the expression of numerous proteins, which reduce the effects of genotoxic xenobiotics. These include the members of efflux pumps, such as ABCB1-MDR1, ABCC1-MRP1 and ABCG2-BCRP, other specific detoxification systems, such as aldehyde dehydrogenase and increased DNA repair capacity. The symmetric cell division and asymmetric distribution of the DNA can also be regarded as part of stem cell self-protection mechanisms[9]. For the tumor stem cells, the existence of the same mechanisms is a crucial cause of their therapeutic resistance.

In addition to hypoxia as a triggering factor, growth factors play an important role, leading to epithelial-mesenchymal transition (EMT) in cells. It is shown a high-level regulation of stem cell markers after the induction of EMT in normal epithelial cells of the breast gland tissue and in mammary carcinoma cells[18]. One of the EMT effects can be the induction of the stem cell phenotype[18].

Numerous findings could show that routine tumor therapy approaches (classical chemotherapy or radiation therapy) and even the majority of currently used targeted antitumor drugs, so-called biological therapy, have little effect on the tumor stem cells even in chemo- or radio-sensitive tumors[19]. While, the stationary tumor stem cells largely retain their epithelial character and are therefore responsible for the primary tumor growth or recurrence, the migrating tumor stem cells exhibit ability for invasion and distance metastasis. This highlights the above-mentioned plasticity of the tumor stem cells (Figure 1).

THERAPY RESISTANCE IN CSCs

A small number of immortal cells within the bulk tumor with a character of CSC causes the chemo/radiotherapy resistance. Such cells with stem cell characteristics, seem to grow aggressively and metastasize easily. It is not yet clear how CSCs are formed, whether they develop from tissue stem cells or are formed from differentiated cells by recovering embryonic properties. Chemotherapeutic agents and radiotherapy mainly destroy dividing cells[20].

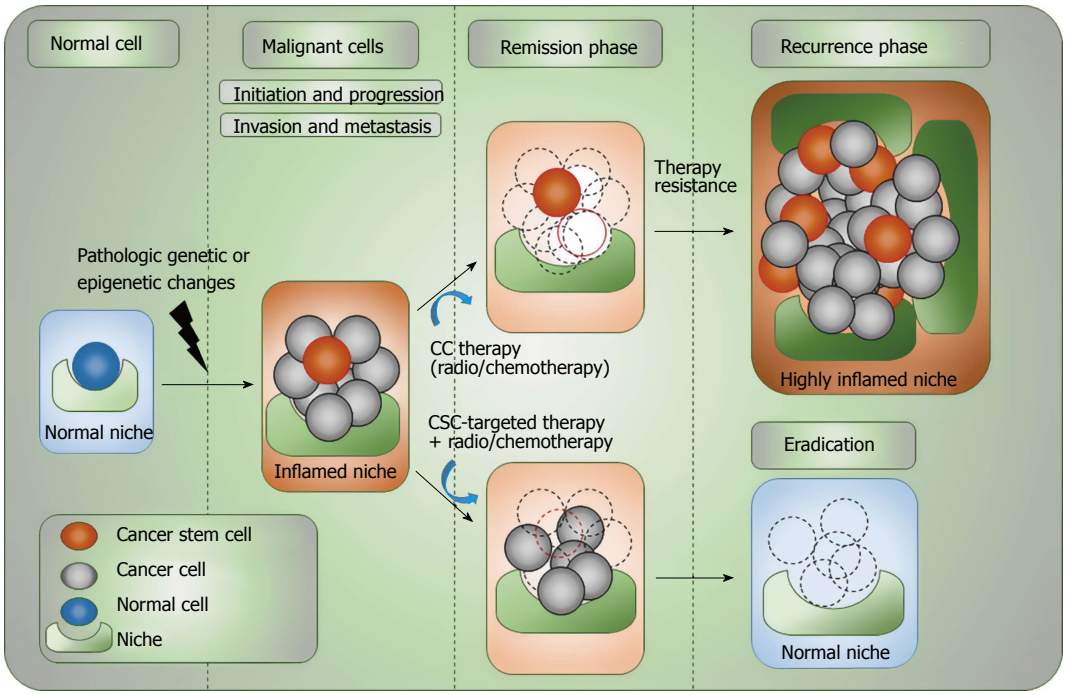

Figure 1 Complex organization of cancer initiation, progress, remission and relapse. CSCs are capable of undergoing extensive cell proliferation after acquiring different pathologic genetic/epigenetic changes while retaining their stemness and giving rise to differentiated progenies. Acquiring further genetic/epigenetic changes during different stages of tumor progression will evolve CSCs, but this may also be advanced through having dynamic interplay with the stem cell-niche. Both CSCs and non-CSCs can be found at the invasive front of primary tumors, which is linked to the process of EMT. However, only CSCs are capable of surviving from immune-surveillance or conventional tumor therapies and are able to give rise to distance metastasis or cause cancer recurrence. The potential eradication of tumor cells and CSCs can be resulted only upon combination targeted therapeutic approaches. Tumor stem cell-targeting drugs should able to prolong the efficacy of cytotoxic tumor therapy and reduce the recurrence risk. CSC: Cancer stem cell; CC: Cancer cell; NC: Normal cell; EMT: Epithelial-mesenchymal transition.

Since CSCs are particularly dormant, in one hand they are not detected by the routine screening measures, and in the other hand, they are positively selected upon the routine therapy approaches.

MOLECULAR MECHANISMS OF THE THERAPY RESISTANCE OF CSCs

Central regulators of the cellular response to DNA damage are checkpoint kinases 1 and 2 (Chk1/2), which are activated after genotoxic stress and stop cell proliferation to allow DNA repair. Activation of Chk1 as a response to DNA damage by ionizing radiation or chemotherapy agents can be detected preferentially in $CD133^+$ glioblastoma precursor cells[21]. By pharmacological inhibition of Chk1, it was possible to increase the sensitivity of $CD133^+$ glioblastoma precursor cells against therapy[21].

An efficient inactivation of reactive oxygen species (ROS) is another feature of CSCs. The excessive production of ROS under chemo/radiotherapy leads to a cell damage because of its interaction with DNA and proteins and triggering the cell death. In some tumors, including mammary carcinoma and gastrointestinal carcinoma, fewer amounts of ROS were detected in CSCs with a simultaneously increased amount of free-radical scavenger compared to the cell populations without CSC phenotype[22]. In addition, the expression of stem cell marker CD44 in tumor cells was associated with an increased expression of the glutathione as a free-radical scavenger[23,24]. Pharmacologically induced reduction in the concentration of free-radical scavenger in tumor cells can significantly increase their sensitivity to the chemo/radiotherapy[25]. It remains unclear whether the increased CD44 expression as a biomarker is suitable for the detection of ROS-resistant CSCs and thus can identify patients who can benefit from therapy with inhibitors of free-radical scavengers in combination with the chemo/radiotherapy.

Another factor contributing to the chemo/radiotherapy resistance of CSCs is hypoxia. Among other factors, hypoxia is the most common cause of therapy-resistance CSCs, which activates the hypoxia inducible factor signaling pathway and triggers cellular processes that can lead to a better survival and expansion of CSCs[26]. The presence of hypoxia in the tumor tissue or its decrease by reoxygenation in the course of chemo/radiotherapy could be correlated with an accelerated repopulation of CSCs with therapy-resistance phenotype[27].

There are several critical proliferation-promoting and survival-inducing pathways triggering the maintenance and survival of CSCs. The canonical Wnt pathway, which is central signaling pathway for stem cell maintenance and development, is constitutively active in breast cancer, colorectal cancer, myeloid leukemia, lung cancer and skin cancer[28,29]. Hedgehog Signaling (HH), which has three different homologues desert Hedgehog, Indian

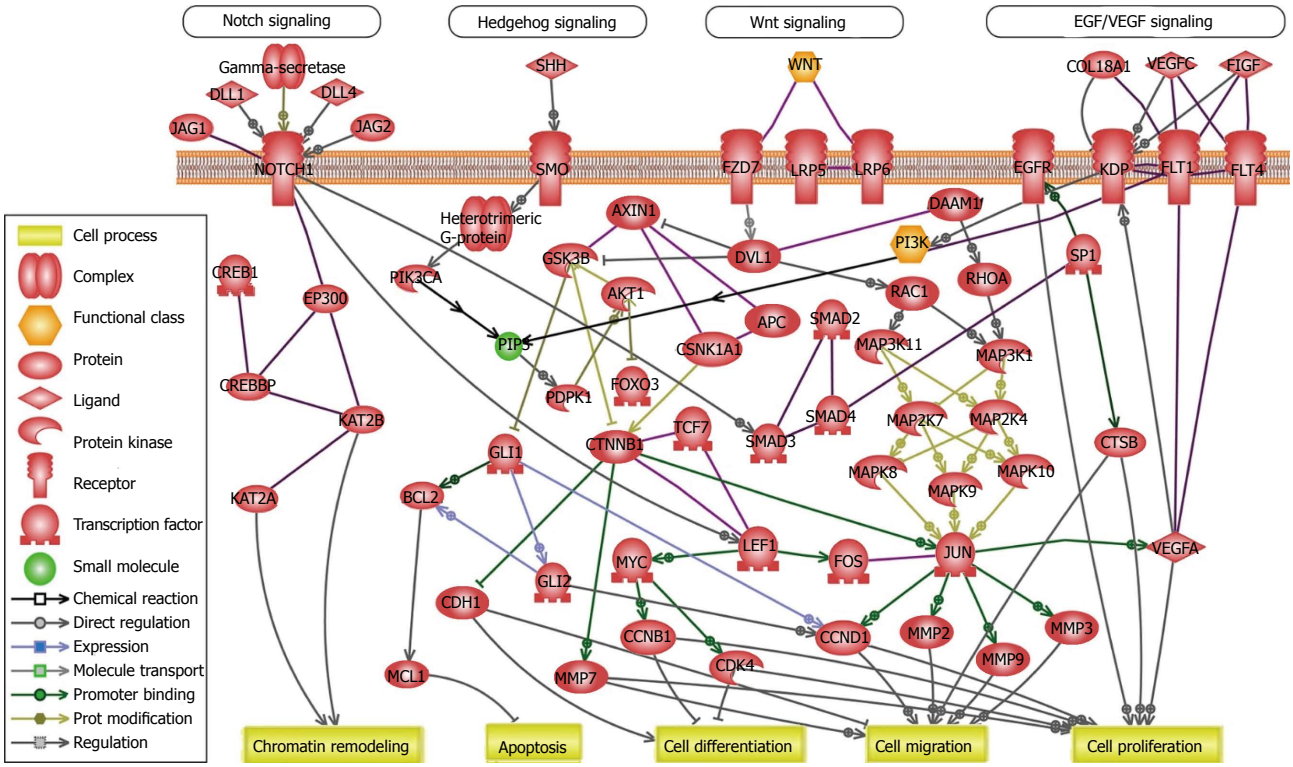

Figure 2 Crosstalk between cancer and cancer stem cell-related pathways. Predicted crosstalk among Wnt signaling, Notch pathway, Hedgehog signaling and other cancer-related pathways like EGF/VEGF signaling in CSCs and cancer. Gene networks and canonical pathways were assessed using the Ariadne Genomics Pathway Studio® program and database (Elsevier). EGF: Epidermal growth factor; VEGF: Vascular endothelial growth factor; WNT: Wnt signaling pathways; PI3K: Phosphoinositide 3-kinase; PIP3: Phosphatidylinositol 3,4,5 trisphosphate; CSC: Cancer stem cell; SHH: Sonic Hedgehog.

Hedgehog and Sonic Hedgehog is essential in a variety of molecular and cellular processes during tissue homeostasis, development or embryogenesis. Aberrant HH activation which regulates the CSC's maintenance and potential proliferation, is reported in different cancers including acute myeloid leukemia (AML), breast cancer, chronic myeloid leukemia (CML), glioblastoma, lung carcinoma, myeloma, pancreatic adenocarcinoma[7,30,31]. Canonical Notch signaling is the other conserved signaling pathway in tissue homeostasis and development. Activation of Notch signaling upon binding of the extracellular ligands, regulates the expression of target genes involving in CSC self-renewal such as Myc, Nanog, Oct-4, and Sox2[32]. Abnormal Notch activation plays a critical role in breast cancer, myeloid leukemia (AML and CML), glioblastoma, lung cancer and pancreatic cancer[7,32,33]. Phosphoinositide-3-kinase/protein kinase B, canonical and non-canonical nuclear factor-κB (NF-κB), stromal-derived factor-1α/CXCR4, ErbB signaling and hedgehog/glioma-associated oncogene are other critical pathways that regulates CSC-related maintenance and proliferation[34-38]. The majority of cancer and CSC-related pathways do not act as isolated units but rather often interact with other pathways as a linked biological network. The predicted crosstalk among Wnt signaling, Notch pathway, Hedgehog signaling and other pathways like EGF/VEGF signaling is illustrated in the Figure 2.

Therefore, therapies that target CSCs could be more effective than therapies targeting a general reduction in tumor mass. Thus, it can be postulated that the efficacy of the chemo/radiotherapy to eradicate CSCs, can be enhanced by a combination therapy with drugs specifically targeting CSCs (Figure 1).

METHODS FOR SCREENING OF CSCs

Over the past decade, different CSC markers were identified in a wide range of hematopoietic malignancies and solid tumors[39,40]. A widely used method for characterizing CSC-related markers is multiparameter flow cytometry. This method, which is originally developed for the analysis of blood cells and hematopoietic stem cells, offers the possibility to detect CSCs by means of specific surface markers that are stained with fluorescence-coupled antibodies. Frequently, the expression of CD133 or CD44 alone or in combination with further markers such as CD20, CD24, CD90 or α2-β1-integrin is used as a CSC-specific marker (Figure 3). Functional detection of CSC is also possible and is based on the increased expression of detoxification enzyme aldehyde dehydrogenase 1 (*ALDH1*) or the high activity of multidrug resistance transport proteins. These CSC-specific staining methods allow the isolation of single CSCs for further molecular characterization using single cell based molecular approaches (Figure 3). However, identified markers are not always reliable and none of the reported markers solely identify CSCs, therefore need to be used with caution (Table 1).

For example, inter- or intra-tumor heterogeneity

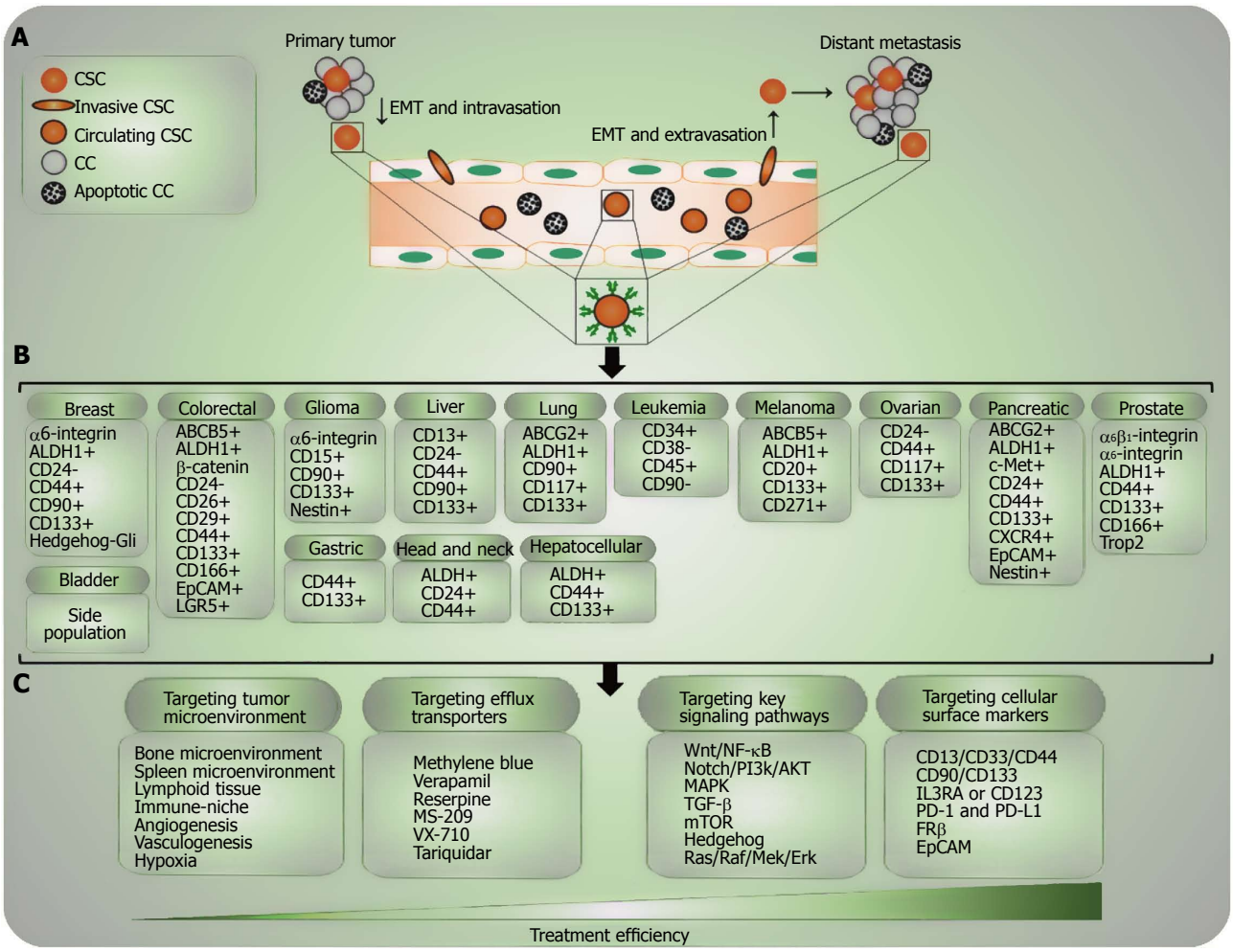

Figure 3 Tracing and targeting cancer stem cells. A: The complex process of distant metastasis including invasion of the tumor microenvironment, EMT, shedding of CSCs into the blood stream (intravasation), MET and invasion of circulating CTCs to the other tissues (extravasation). Only circulating CSCs are able to survive in the circulating blood, escape from immune-surveillance and home to secondary organs; B: The list of known compilation CSC-related molecular markers for different solid tumors and hematopoietic malignancies. The level of specificity of these markers differs per each type of tumor. Markers are ordered alphabetically and not according to their sensitivity or specificity; C: Four important approaches of CSC-targeted therapy. CSC: Cancer stem cell; CC: Cancer cell; NC: Normal cell; EMT: Epithelial-mesenchymal transition; MET: Mesenchymal-epithelial transition; PI3K: Phosphoinositide 3-kinase; MAPK: Mitogen-activated protein kinase; TGF: Transforming growth factor; mTOR: Mechanistic target of rapamycin; RAS: Ras-activated signaling; PD-1: Programmed death 1; PD-L1: Programmed death-ligand 1; EpCAM: Epithelial cell adhesion molecule.

may completely render CSC markers inapt. Such tumor heterogeneity can be the result of different genetically distinct clones within the tumor due to having various genetic lesions or dysregulation of markers *via* pathologic epigenetic regulations[16,37-43]. For example, CD133 marker is frequently inactivated due to the DNA methylation and therefore often inadequate[44]. Inactivation of specific markers due to any scape mechanism in a particular clone may render these CSCs undetectable in the absence of other distinct markers.

While high-throughput genetic screening studies provide essential information about genes which are associated with a particular phenotype, molecular pharmacology can play an important role in development of a specific molecular therapy. Low molecular weight substances ("small molecules") show a higher penetrance in cell-based screening methods. Therefore, small molecules are one of the most frequently used therapeutic agents. The screening of large substance banks has identified many valuable compounds that can be used to modulate biological systems in cancer cells[45]. In order to systematically identify the genes that regulate the death and differentiation of CSCs, high-throughput screenings of RNA interference (RNAi) or chemical substance libraries are carried out using different approaches. The readout of such screen approaches can be survival analysis, reporter assays, luminescence or fluorescence-based analyzes of particular genes or pathways and imaging methods, in which several cellular properties can be examined on a single cell level.

Since CSCs only make up a small fraction in the entire tumor cell pool (Figure 1), appropriate enrichment methods must be applied. Gupta *et al*[46] enriched $CD44^{hi}/CD24^{lo}$ cells within the CSC population of mammary carcinoma cell lines by inducing the EMT. After treatment with inhibitors, the survival of the enriched and

Table 1 Hallmarks of using cancer stem cell-related markers

Problems	Potential solutions
CSC-related markers may not be specific by their own for a certain type of tumor	Combined used of different markers may be the solution
Some of CSC-related markers may be down-regulated or suppressed in a given tumor due to different genetic or epigenetic regulatory mechanisms	Using of distinct markers or a combination them
Splice variants of some CSC-related markers may render detection difficult	The exact splice variant should be considered for the detection
Markers can be detected using one method (*e.g.*, FACS), but not with other methods (*e.g.*, immunohistochemistry)	Stringent selection of related markers might be required
Different tumors have clonal variation and heterogeneous cell population. Less malignant clones may harbor CSCs that express different markers. Therefore, CSC-related markers may be differentially regulated within different clone or be completely missed	Using more specific and sensitive methods, isolate more enriched CSC populations
Many of reported CSC-related markers are not validated, since they derived from cell-line or mouse model studies	Markers should be validated in xenotransplants or primary human materials

CSC: Cancer stem cell; FACS: Fluorescence-activated cell sorting.

the non-selected cell population was investigated using a luminescence-based reporter assay. This study was able to identify salinomycin as a selective inhibitor of the CSC population in breast carcinoma[46].

Recent advances in computer-based image analysis have enabled rapid achievements in the development of image-based high-throughput analysis approaches. The direct visualization of cellular features and biological processes allows a more comprehensive measurement of responses to interferences. Xia *et al*[47] have developed a novel fluorescence imaging method to identify cancer cells with CSC properties through their increased ability to deliver fluorescent dyes *via* dedicated molecular transporters. Based on this method, a library of active substances was examined for their effect in CSCs. It was possible to identify substances that selectively inhibit the molecular transporters[47].

A further high-throughput method has recently been developed to characterize the biochemical and biophysical environmental conditions of CSCs. Microarray glass slides with over 2000 test chambers can be used to cultivate stem cells in different cell densities in a hydrogel of polyethylene glycol, to which different biological molecules have been coupled by robot technology[48]. Using the microscopic imaging, cell proliferation, morphology and differentiation can be monitored at a single cell level. This method as a platform for the investigation of individual stem cells in a microfluid culture system with simultaneous live-cell microscopy, represents an important step towards the miniaturization of the cellular processes as a high-throughput screening approach[49].

TARGETING CSCs

Targeting tumor microenvironment

The heterogeneous tumor microenvironment or cancer cell-niche, provides different self-protection mechanisms which enables a dynamic interaction with surrounding cells including immune cells, cytokines and chemokines to regulate proliferation, maintenance and self-renewal of CSCs. CSCs can represent more autonomous regulatory characterization in an independent manner[13]. Less malignant tumors may have more demand on the stem cell-niche but upon cancer progress this dynamic interplay might be weaken or even diminished[14]. It is known that dormant cancer cells *via* reducing their immunogenicity, can escape the immune surveillance[50]. Therefore, targeting CSC microenvironment may stimulate the host antitumor responses[51]. Strategies to hit the tumor-promoting inflammation are under investigation. Production of prostaglandin E2 (PGE2) by tumor cells in breast cancer, colorectal cancer and melanoma has a key role in the escape phase as it suppresses immunity and induces inflammation[52]. Therefore, the use of antagonists of PGE2 receptor (PTGER4) has proven successful in blocking immuno-suppression and preventing cancer metastases[53].

Targeting efflux transporters

Membrane efflux transporters, which are mainly located in blood-brain barrier, hepatocytes, intestinal cells or kidney proximal tubules, play important roles in drug metabolism, availability, and toxicity of drugs in human body[54]. Several studies indicate that transporter-mediated drug disposition plays an important role in mediating chemo-sensitivity and -resistance of cancer cells and CSCs[55]. The interaction between efflux transporters and chemotherapeutic drugs on cancer cells is significantly linked to the efficacy of cancer therapy. Two major superfamilies of efflux transporters are the ATP-binding cassette (ABC) transporters [ABCB1 (MDR1), ABCC1 (MRP1), ABCC2 (MRP2) and ABCG2 (BCRP)] and the solute carrier (SLC) transporters [SLC19A1 (RFC1) and SLCO1B1 (SLC21A6)]. Therefore, targeting efflux transporters within cancer therapy combined with routine therapies could significantly increase the eradication rate of resistant cancer cells[56].

Targeting key signaling pathways

The CSC phenotype depends on various cellular signals, which are triggered by the underlying genetic lesions and by the support of the stem cell niche. Some of

these signals have already been identified; the most disease cussed signaling pathways are the classic Wnt-β-catenin, Notch and Sonic Hedgehog signaling[57-59]. For these three pathways, pharmacological inhibitors have been developed which are now undergoing clinical trials in many independent studies[60]. However, the clinical effect is largely depending on the tumor type and not all three pathways are equally important in all types of tumors. It has been shown that, although some signaling pathways are highly tumor-promoting in a certain type of cancers (which makes it a suitable therapeutic target), they might react as tumor suppressive in another tumor type; therefore, their inhibition may become dangerous (*e.g.*, Notch-1 has been identified as a tumor suppressor in urinary bladder carcinoma)[61]. High Wnt pathway activity marks colon or leukemia CSCs and is required for stemness signature as a prognostic marker[6,7,62]. In addition, Wnt activity is associated with the CSC markers CD133, CD44 and LGR5 in colon cancer[63] whereas Hedgehog activity is linked to ABC transporter expression in esophageal and prostate cancer[17,64] TGF-β signaling *via* the family members Nodal and Activin is attributed to pancreatic CSCs[65]. The effect of Hedgehog inhibitors is actually the most evident in the basal cell carcinoma. In addition, inhibition of Hedgehog pathway blocks stemness in breast CSCs, whereas its activation enhances self-renewal[66]. It is also necessary to distinguish whether those signaling pathway has been activated within CSCs only because of harbored genetic lesions[67]. If only the CSCs are targeted, it is hardly possible to expect a dramatic tumor shrinkage as in classical successful chemo/radiotherapy; rather, this would be a disease stabilization and a slowing of the progression (Figure 1).

Disulfiram was developed as an inhibitor of aldehyde dehydrogenase for the treatment of alcoholism. This inhibition leads to the accumulation of acetaldehyde after alcohol consumption, resulting in a marked nausea that should reduce the probability of further alcohol consumption[68]. The same enzymatic activity - aldehyde dehydrogenase - is, however, a component of the self-protection of the CSCs, and thus disulfiram was used for the elimination of CSCs. Thioridazine is an inhibitor of dopamine receptors, and is a standard medication for mental disorders such as schizophrenia. Its rational use in tumor therapy is based on the finding that CSCs in several types of tumors (*e.g.*, AML, breast carcinoma, glioblastoma), in contrast to the corresponding normal tissue stem cells, upregulate the expression of dopamine receptors[69].

Niclosamide was identified that specifically targeted Wnt-β-catenin signaling pathways[70]. Interestingly, niclosamide is known as an antiparasitic and inhibitor of oxidative phosphorylation, which has been used in human medicine for almost 50 years[71]. However, what has emerged is that these two antiparasitics are inhibitors of numerous other signaling pathways. Niclosamide inhibits not only the Wnt-β-catenin signaling pathway, but also the Notch, PI3'K-Akt - mTOR, STAT-3 and NFκB signaling pathways, which are essential for tumor stem cells[72]. Salinomycin was similarly described as an inhibitor of ABC efflux pumps and the Wnt-β-catenin signaling pathway[73]. Not enough, analogous effects have been discovered for disulfiram and thioridazine. Disulfiram has not only proved to be an effective inhibitor of aldehyde dehydrogenase, but also polo-like kinase 1 and O6-methylguanine methyltransferase as well as NFκB[74,75].

The advantages of identifying such new indications for old drugs are obvious. These drugs have long been out of patent protection and their use should therefore be much cheaper than for newly developed drugs, which is an important aspect in the current discussion on costs of tumor treatment. In addition, they have already undergone clinical trials, their potential toxicity, side effects, pharmacokinetics, contraindications, and possible drug-drug interactions are known. Therefore, their use in tumor therapy should be relatively easy. Perhaps the best opportunity to see how the effects of tumor stem cell-targeted therapy can be demonstrated is in the area of combination therapy (Figure 1). Tumor stem cell-directed drugs should be able to prolong the efficacy of cytotoxic therapy and reduce recurrence risk[76,77]. On the other hand, combined administration has significantly greater chances of total elimination of all tumor cells. Taken together, there are many possibilities for therapeutic treatment for the elimination of tumor stem cells, both from the group of newly developed inhibitors of some stem cell-specific signaling pathways as well as for some old drugs that can find a new application in tumor therapy.

Targeting cellular surface markers (tumor immunotherapy and cancer vaccination)

Many types of normal cells like immune cells infiltrate tumors. Over the last years, immune infiltration has become a central focus in cancer research[50]. It is increasingly recognized that cancer cells and CSCs need to escape immune recognition. IL-6/JAK/STAT3 signaling an important pathway in many solid tumors. Anti-IL-6 mAb siltux-imab was tested on various cancer types, which was not able to provide promising outcome to improve overall survival of patients with multiple myeloma according to a recent Phase II clinical trial on patients[78]. While, checkpoint blockade antibodies such as cytotoxic T-lymphocyte antigen 4 (CTLA-4) or programmed death-ligand 1 (PD-1/PD-L1) like ipilimumab or nivolumab could provide marked clinical benefits for lung adenocarcinoma, melanoma or Hodgkin lymphomas[79,80]. These agents can boost the immune system and display clinical benefits for a fraction of patients[50].

Many tumors cells including CSCs, alter the expression of their genes or down-modulate of antigen processing and presentation to build an immuno-suppressive microenvironment that creates physical or chemical barriers against immune cells[81]. Indeed, CSCs by low express of MHC-I, and over expressing of IL-4 are escaping from cytotoxic T lymphocytes[82].

Boosting T-cell response can be a promising approach to eradicate CSCs. This can be achieved by boosting neo-antigens within CSCs, considered as tumor vaccination. Adoptive transfer of CSC-specific T-cells into tumor-bearing mice could show a success[83]. In addition, genetically modified T cells to express chimeric antigen receptors (CAR T-cells) upon adaptive transfer could provide remarkable benefit for patients suffering from different solid tumors or leukemia[84]. Therefore, the major goal of immunotherapy is to thwart these barriers in order to enhance pre-existing or elicit a new immune response against cancer.

CONCLUSION

Because of the CSCs' ability to therapy resistance and initiate a recurrence after therapy, cancer stem cell is an important therapeutic target. Future research is essential to elucidate how CSCs dictate metastasis, therapy-resistance or immune-scape signature. However, without having reliable markers it will be a challenging pursuit. An exact molecular characterization of this small subpopulation in the tumor tissue requires the development of specific CSC markers and suitable enrichment methods. Particularly from innovative high-throughput screening technologies, we can expect valuable insights regarding suitable CSC-associated biomarkers and new therapeutic approaches to target CSCs. This could be an important step towards individualized cancer therapy.

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ORIGINAL ARTICLE

Basic Study

Aldehyde dehydrogenase activity helps identify a subpopulation of murine adipose-derived stem cells with enhanced adipogenic and osteogenic differentiation potential

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Abstract

AIM

To identify and characterize functionally distinct subpopulation of adipose-derived stem cells (ADSCs).

METHODS

ADSCs cultured from mouse subcutaneous adipose tissue were sorted fluorescence-activated cell sorter based on aldehyde dehydrogenase (ALDH) activity, a widely used stem cell marker. Differentiation potentials were analyzed by utilizing immunocytofluorescece and its quantitative analysis.

RESULTS

Approximately 15% of bulk ADSCs showed high ALDH activity in flow cytometric analysis. Although significant difference was not seen in proliferation capacity, the adipogenic and osteogenic differentiation capacity was higher in ALDH^{Hi} subpopulations than in ALDH^{Lo}. Gene set enrichment analysis revealed that ribosome-related gene sets were enriched in the ALDH^{Hi} subpopulation.

CONCLUSION

High ALDH activity is a useful marker for identifying functionally different subpopulations in murine ADSCs. Additionally, we suggested the importance of ribosome for differentiation of ADSCs by gene set enrichment analysis.

Key words: Adipose-derived stem/stromal cell; Aldehyde dehydrogenase activity; Flow cytometry; Subpopulation; Ribosome

Core tip: Aldehyde dehydrogenase (ALDH) activity is widely used as a stem cell marker in several types of normal or malignant tissues. However, there was no report of ALDH activity in murine adipose-derived stem cells (ADSCs). Here, our study demonstrated a subpopulation defined by high ALDH activity within murine ADSCs. The subpopulation with high ALDH activity (ALDH^{Hi}) showed enhanced differentiation potentials into adipocyte and osteocyte. Furthermore, gene set enrichment analysis revealed that ribosome-related gene sets were enriched in ALDH^{Hi} of murine ADSCs. We showed relationship between ALDH^{Hi} and ribosome biosynthesis, providing a novel insight of mesenchymal stem cell biology.

Itoh H, Nishikawa S, Haraguchi T, Arikawa Y, Eto S, Hiyama M, Iseri T, Itoh Y, Nakaichi M, Sakai Y, Tani K, Taura Y, Itamoto K. Aldehyde dehydrogenase activity helps identify a subpopulation of murine adipose-derived stem cells with enhanced adipogenic and osteogenic differentiation potential. *World J Stem Cells* 2017; 9(10): 179-186 Available from: URL: http://www.wjgnet.com/1948-0210/

INTRODUCTION

Stem cells can self-renew and differentiate into specialized cells of various tissues[1]. Therefore, these cells, for example, embryonic stem cells (ESCs), induced pluripotent stem cells (iPSCs), hematopoietic stem cells, and mesenchymal stem cells (MSCs), have been the object of basic research and clinical applications. Among these types of stem cells, MSCs, as represented by adipose-derived stem/stromal cells (ADSCs) and bone marrow-derived stem/stromal cells (BMSCs), have been recognized as useful material for cell-based therapy[2]. MSCs have been isolated from various tissues, including adipose tissue, the bone marrow, peripheral blood, cord blood, the liver, dental pulp, and fetal tissue; of these, adipose tissue is one of the most abundant source of MSCs[3]. ADSCs possess multipotency and have the potential to differentiate into cell types such as adipocytes, osteocytes, chondrocytes, neurons, vascular endothelial cells, cardiomyocytes, myoblasts, and islet β-cells under appropriate conditions[4].

The researches have suggested that ADSCs are heterogeneous and comprise phenotypically and/or functionally different subpopulations[5-7]. For example, the cluster of differentiation (CD)73^{+} subpopulation of murine ADSCs possesses increased potential for cardiomyocyte differentiation[6]. The CD90^{+} subpopulation of murine ADSCs has higher tube-forming ability than the CD90^{-} subpopulation, which has high adipogenic potential[8]. The CD90^{+} subpopulation also exhibits higher efficiency of iPSC induction than the CD90^{-} subpopulation[5]. Human ADSCs also include the CD105^{Lo} subpopulation, which has high osteogenic potential[7]. Some studies have identified different subpopulations in ADSCs on the basis of surface antigen markers[5-7]. However, it is unclear how these markers (*e.g.*, CD90 and CD105) are functionally related to cell differentiation.

In mice, aldehyde dehydrogenase (ALDH) is a superfamily comprising 20 intracellular enzymes and is responsible for the oxidization of various aldehydes[9]. High ALDH activity has been shown in normal hematopoietic stem cells, neural stem cells, and cancer stem cells in various types of neoplastic diseases[10]. Therefore, high ALDH activity is considered to be a common marker for normal and malignant stem cells. In human ADSCs, however, only one study has been performed on the ALDH^{Hi} subpopulation, whose significance in differentiation potential is unclear[11]. Moreover, to our knowledge, the existence of the ALDH^{Hi} subpopulation within murine ADSCs has not yet been reported.

In the current study, the ALDH^{Hi} and ALDH^{Lo} subpopulations of murine ADSCs were sorted using flow cytometry. The differentiation potential and proliferation of the sorted ALDH^{Hi} and ALDH^{Lo} subpopulations were analyzed. Furthermore, we analyzed the transcriptional profiles of the ALDH^{Hi} and ALDH^{Lo} subpopulations by utilizing gene set enrichment analysis (GSEA).

MATERIALS AND METHODS

Animals and ADSC isolation

C57BL/6J mice were purchased from Kyudo Co., Ltd (Saga, Japan). All animal experiments were carried out in accordance with the National Institutes of Health guide for the care and use of Laboratory animals (NIH Publications No. 8023, revised 1978) and the institutional guidelines of Yamaguchi University. The animal experiments were approved by the institutional animal experiment ethics committee of Yamaguchi University.

Murine ADSCs were isolated from twenty of C57BL/6J female mice of 4- to 6-wk-old, as previously described[8]. Briefly, the subcutaneous adipose tissue was resected, washed with Dulbecco's phosphate-buffered saline (DPBS; Wako, Osaka, Japan), and cut into small pieces. The adipose tissue pieces were digested in high glucose Dulbecco's modified Eagle's medium (DMEM; Wako, Osaka, Japan) containing 1.0 mg/mL collagenase type Ⅰ (Sigma-Aldrich, St. Louis, MO, United States), 10% fetal bovine serum (FBS; Sigma-Aldrich), and antibiotic-antimycotic agents (PSM; penicillin: 100 U/mL, streptomycin: 100 μg/mL, and amphotericin B: 0.25 μg/mL, final concentrations; Nacalai Tesque, Kyoto, Japan), using a shaking incubator at 37.5 ℃ and 250 rpm for 1 h. The digested tissue was filtered through a sterile ø100-μm nylon mesh (EASYstrainer, 100 μm; Greiner Bio-One Japan, Tokyo, Japan), followed by centrifugation at 400 × *g* for 5 min in DPBS supplemented with 1% FBS and 1 mmol/L EDTA·3Na (Wako, Osaka, Japan). The pellet was resuspended in DMEM supplemented with 10% FBS and antibacterial/antimycotic agent and was cultured at 37.0 ℃ in a 5% CO_2 atmosphere, using ø10 cm dish (Corning, NY, United States). When the cultures reached 80%-90% confluence, the ADSCs were dissociated from the dish by using Accutase solution (Innovative Cell Technologies, San Diego, United States), and seeded into new dishes.

Flow cytometry analysis

Adherent ADSCs from passage 4 were dissociated using Accutase solution; 1 × 10^6 cells were resuspended and incubated for 5 min on ice with 2 μL of anti-mouse CD16/32 rat monoclonal antibody (BioLegend, San Diego, CA, United States). Cells were stained with 1 μL viability probe (Zombie NIR, Biolegend) for 20 min at room temperature to stain dead cells. ALDH activity was assessed by utilizing the ALDEFLUOR kit (Stemcell Technologies, Vancouver, Canada) according to the manufacturer's instructions. Briefly, 1 × 10^6 cells were resuspended in 1 mL assay buffer and 5 μL ALDEFLUOR reagent was added after thorough mixing; then, 0.5 mL of the cell suspension was transferred to a new tube with 5 μL diethylaminobenzaldehyde (DEAB) reagent (ALDH inhibitor) for negative control of ALDH activity. Flow cytometric analysis and cell sorting were performed using Accuri C6 (BD Bioscience, San Jose, CA, United States) and the SH800 cell sorter (Sony, Tokyo, Japan). Flow cytometric data were analyzed with the FlowJo (Tree Star, Ashland, OR, United States) software.

Measurement of proliferation potential

To assess the viability of the ADSC subpopulations, we used a cell WST-8 assay (Cell Counting Kit-8; Dojindo Laboratories, Kumamoto, Japan) according to the manufacturer's instructions. Briefly, sorted $ALDH^{Hi}$ or $ALDH^{Lo}$ murine ADSCs were seeded in 96-well plates at a density of 3 × 10^3 cells/well. After 12, 24, 48, and 72 h, 100 μL fresh medium containing 10 μL CCK-8 solution was added to each well, followed by incubation at 37 ℃ for 1 h. The absorbance of each well at 450 nm was measured using an Epoch microplate spectrophotometer (BioTek Instruments, Winooski, VT, United States). Six replicates were prepared for each group.

Cell differentiation and immunofluorescence staining

The adipogenic and osteogenic differentiations of ADSCs were characterized using a Mouse Mesenchymal Stem Cell Functional Identification Kit (R and D Systems, Minneapolis, MN, United States) according to the manufacturer's instructions. Briefly, for adipogenic differentiation, cells (3 × 10^3/well) were cultured at 37 ℃ in a 5% CO_2 atmosphere in a 96-well plate in 100 μL adipogenic differentiation medium composed of α-minimal essential medium (αMEM) supplemented with 10% FBS, 1% PSM, L-glutamine, and 50 μL adipogenic supplement containing hydrocortisone, isobutylmethylxanthine, and indomethacin for 15 d in 37 ℃ and a 5% CO_2 atmosphere.

For osteogenic differentiation, cells were cultured in osteogenic differentiation medium composed of 5 mL α-MEM basal medium and 250 μL osteogenic supplement containing ascorbate-phosphate, β-glycerolphosphate, and recombinant human bone morphogenetic protein-2 for 15 d in 37 ℃ and a 5% CO_2 atmosphere. The medium was replaced every 2-3 d.

To assess adipogenic and osteogenic differentiation by immunocytochemistry, cultured cells were fixed in 4% paraformaldehyde phosphate buffer solution (Wako, Osaka, Japan) for 20 min. After the cells were washed with DPBS, they were permeabilized and blocked with DPBS supplemented with 0.3% Triton X-100 (Sigma-Aldrich), and 10% FBS for 45 min. The cells were subsequently incubated for 1 h in DPBS containing 10 μg/mL goat anti-mouse fatty acid binding protein (FABP) 4 polyclonal antibody to label adipocytes or were incubated with 10 μg/mL goat anti-mouse osteopontin polyclonal antibody to label osteocytes. They were then washed with DPBS and incubated for 1 h in DPBS containing phycoerythrin (PE)-conjugated rabbit anti-goat IgG antibody [rabbit F(ab')2 anti-goat IgG-H and L (PE), pre-adsorbed, Abcam, Cambridge, United Kingdom]. Nuclei were stained with 5 μg/mL Hoechst 33342 (Dojindo Laboratories, Kumamoto, Japan). Photographs were obtained and analyzed using a fluorescence microscope (BZ-9000; Keyence, Osaka, Japan) and its analysis software.

Gene expression array analysis and GSEA

Gene expression array analysis and GSEA were performed

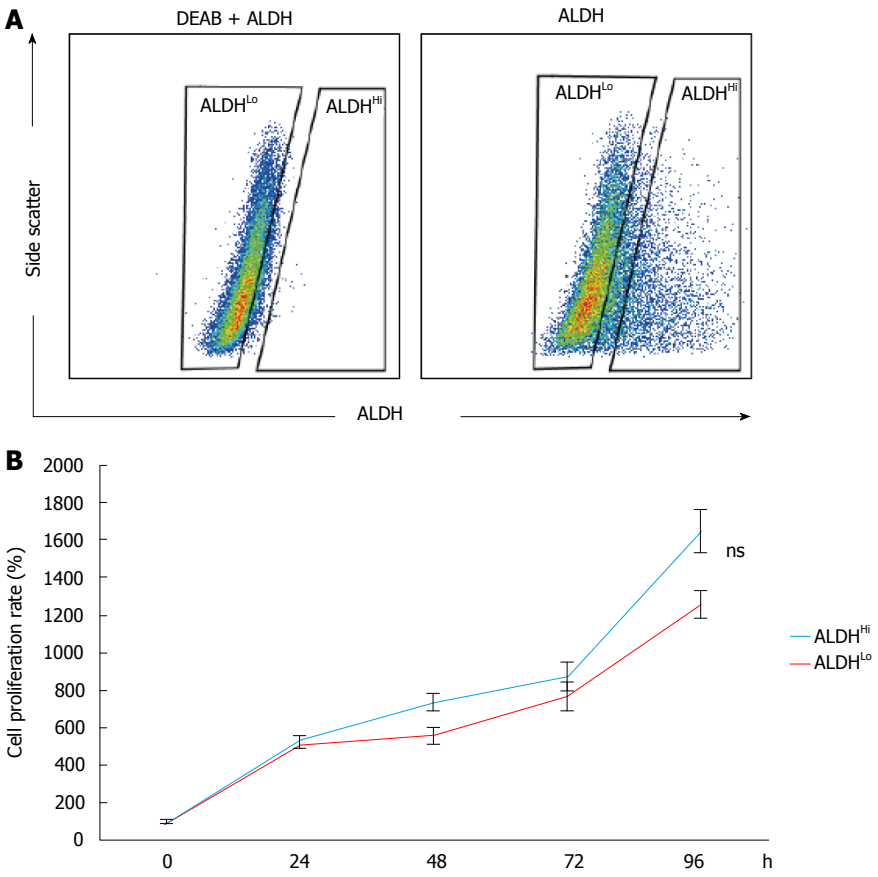

Figure 1 Detection of aldehyde dehydrogenase-positive subpopulations of murine adipose-derived stem cells and evaluation of proliferation rates. A: Flow cytometric analysis of murine ADSCs. Baseline fluorescence was established by adding the ALDH inhibitor diethylaminobenzaldehyde; B: Cell proliferation rates were not significantly different between the ALDH^{Hi} and ALDH^{Lo} subpopulations. Values have been expressed in terms of mean ± SE (n = 5). ns: Not significant; ALDH: Aldehyde dehydrogenase; ADSCs: Adipose-derived stem cells; DEAB: Diethylaminobenzaldehyde.

on the published gene expression profile of C57BL/6 mice divided by ALDH^{hi} and ALDH^{lo} subpopulations of ADSCs. About 3 × 10^6 cells from each subpopulation were lysed and total RNA was isolated using the RNeasy Mini Kit (Qiagen, Hilden, Germany). Cyanine-3 (Cy3)-labeled cRNA was prepared from 0.1 μg total RNA by using the Low Input Quick Amp Labeling Kit (Agilent Technologies, Santa Clara, CA, United States) according to the manufacturer's instructions; this was followed by RNeasy column purification (Qiagen). Dye incorporation and cRNA yield were checked with the NanoDrop ND-2000 Spectrophotometer (Thermo Fisher Scientific, Waltham, MA, United States). Cy3-labelled cRNA (0.6 μg) was fragmented at 60 ℃ for 30 min in a reaction volume of 25 μL containing 1 × Agilent fragmentation buffer and 2 × Agilent blocking agent following the manufacturer's instructions. On completion of the fragmentation reaction, 25 μL of 2 × Agilent hybridization buffer was added to the fragmentation mixture and hybridized to SurePrint G3 Mouse GE 8 × 60 K Ver1.0 (Agilent Technologies) for 17 h at 65 ℃ in a rotating Agilent hybridization oven. After hybridization, the microarrays were washed for 1 min at room temperature with GE Wash Buffer 1 (Agilent Technologies) and 1 min with 37 ℃ GE Wash buffer 2 (Agilent Technologies). The slides were scanned immediately after washing on the Agilent SureScan Microarray Scanner (G2600D), using one color scan setting for 8 × 60 k array slides (scan area, 61 × 21.6 mm; scan resolution, 3 μm; dye channel set for Green PMT was set to 100%). The scanned images were analyzed with Feature Extraction Software 11.5.1.1 (Agilent Technologies), using default parameters to obtain the subtracted background and spatially detrended Processed Signal intensities.

Statistical analysis

Statistical analysis was performed using GraphPad Prism version 6.01 for Windows (GraphPad Software, La Jolla, CA, United States). The results have been expressed in terms of mean ± SE. Comparisons of two groups were performed with the independent t-test. Multiple comparisons were performed with one-way analysis of variance. Data were considered statistically significant when the P value was ⩽ 0.05.

RESULTS

ALDH activity of murine ADSCs

To identify the subpopulation defined by ALDH activity in murine ADSCs, single-cell suspensions of cultured murine ADSCs were stained using the ALDEFLUOR kit and analyzed with flow cytometry. A small subpopulation

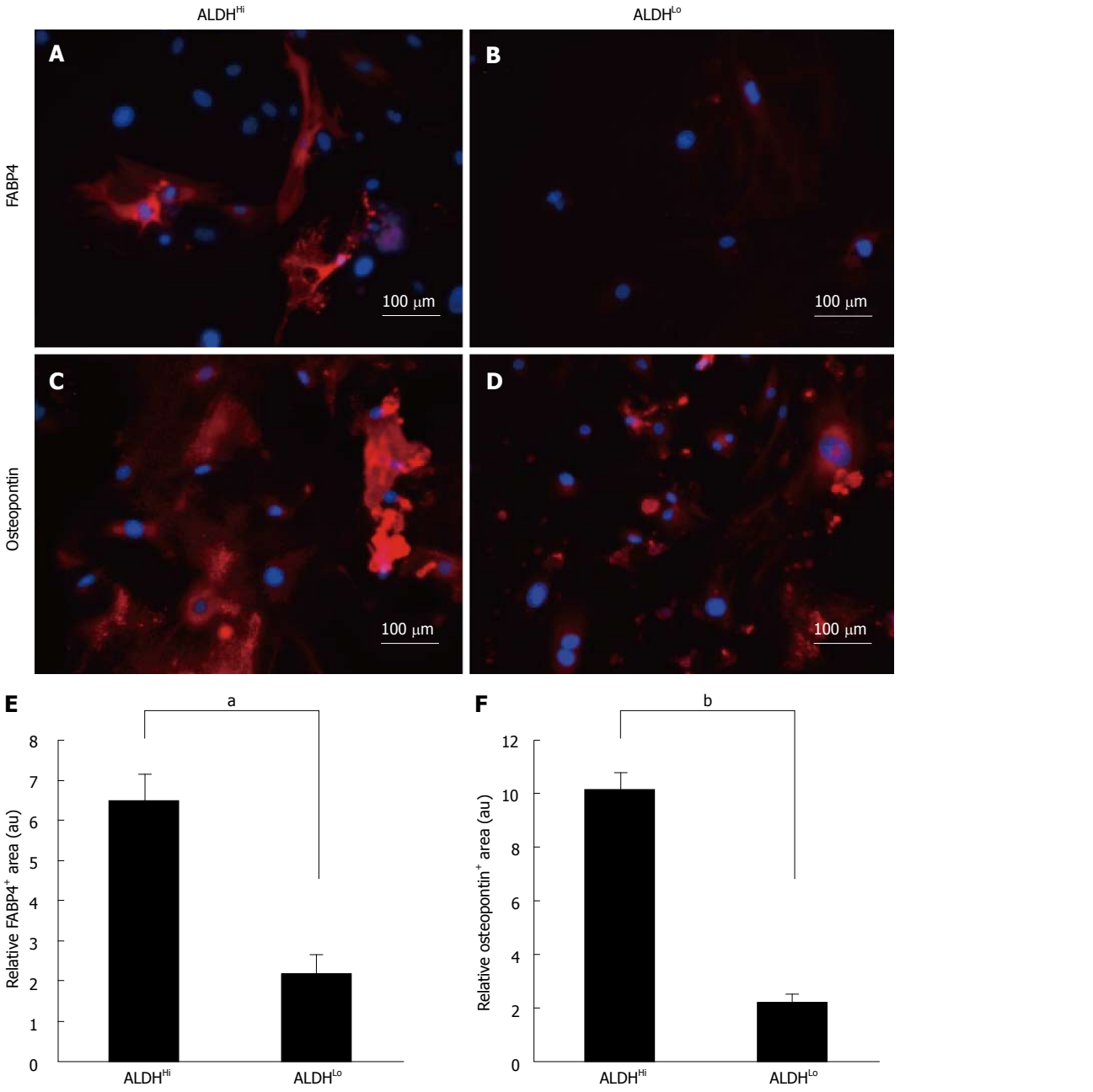

Figure 2 Marker analysis of differentiation potentials. Differentiation potential of ALDHHi (A, C) and ALDHLo (B, D) subpopulations of ADSCs. FABP4 (A, B) and osteopontin (C, D) expression in ADSCs (red) following adipogenic (A, B) and osteogenic (C, D) differentiation of ALDH^{Hi} and ALDH^{Lo} subpopulations, as determined by immunocytochemistry. The nuclei were stained with Hoechst 33342 (blue). Quantitative analysis of differentiation-marker-positive areas in differentiated ADSCs. FABP4-positive (E) and osteopontin-positive (F) area ratios relative to respective areas of nuclear staining for ALDH^{Hi} and ALDH^{Lo} subpopulations of ADSCs after adipogenic (E) and osteogenic (F) induction. Values have been expressed in terms of mean ± SE (n = 5). $^{a}P < 0.05$, $^{b}P < 0.0001$, au: Arbitrary unit. ALDH: Aldehyde dehydrogenase; ADSCs: Adipose-derived stem cells; FABP: Fatty acid binding protein.

with distinctively high ALDH activity (ALDH^{Hi} cells) was detected within the bulk populations of ADSCs (Figure 1A). The percentage of ALDH^{Hi} cells was approximately 15% of the bulk murine ADSC population (Figure 1A). However, on adding the ALDH inhibitor N,N-diethylaminobenzaldehyde (DEAB), a distinct ALDH^{Hi} subpopulation was not detected (Figure 1A). To assess the difference in the proliferation potentials of the ALDH^{Hi} and ALDH^{Lo} subpopulations, we measured the proliferation rate of each subpopulation by using the WST assay. The proliferation potential of the ALDH^{Hi} subpopulation of ADSCs was not significantly different compared to the ALDH^{Lo} subpopulation (Figure 1B).

Cell differentiation to adipocytes and osteocytes

To assess the adipogenic and osteogenic differentiation potential of the two subpopulations, sorted ALDH^{Hi} and ALDH^{Lo} cells were cultured under adipogenic or osteogenic differentiation conditions. After *in vitro* differentiation, immunofluorescence staining for FABP4 (marker of adipocytes) and immunofluorescence staining for osteopontin (marker of osteocytes) were performed

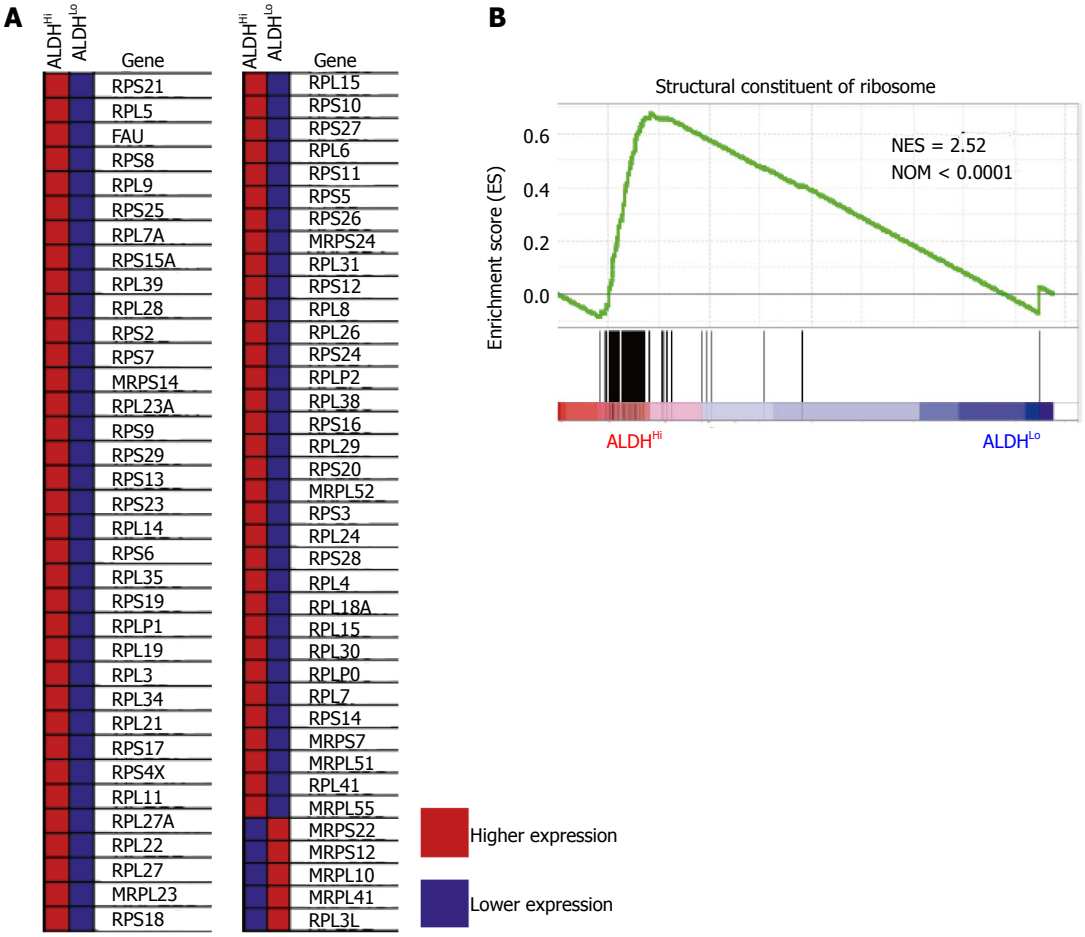

Figure 3 Gene set enrichment analysis of each ALDH^{Hi} and ALDH^{Lo} subpopulation. A: Heat map of enrichment profile of ribosomal protein mRNAs for ALDH^{Hi} and ALDH^{Lo} subpopulations; B: Gene set enrichment analysis of transcription data related to structural constituents of ribosomes for the ALDH^{Hi} and ALDH^{Lo} subpopulations. Normalized enrichment score and nominal *P* values are shown. ALDH: Aldehyde dehydrogenase.

(Figure 2A-D). ADSCs that differentiated into adipocytes appeared as accumulated lipid droplets in the cytosol in each ALDH^{Hi} and ALDH^{Lo} subpopulation (Figure 2A and B). Furthermore, immunofluorescence staining for osteopontin revealed that ADSCs that differentiated into osteocytes appeared as accumulated granules in the cytosol in each ALDH^{Hi} and ALDH^{Lo} subpopulation (Figure 2C and D).

Evaluation of differentiation

Adipogenic and osteogenic differentiation of each ALDH^{Hi} and ALDH^{Lo} subpopulation was quantitatively assessed using the BZ-9000 microscope and its analysis software. Ten visual fields were taken randomly for every 3 wells, and the immunofluorescence-staining positive-areas in 30 visual fields were analyzed. Subsequently, the immunofluorescence-staining-positive area was divided by the Hoechst 33342-positive area for each of the 30 visual fields. The ALDH^{Hi} subpopulation was found to have significantly more adipogenic and osteogenic relative-differentiation-marker-positive areas than the ALDH^{Lo} subpopulation (Figure 2E and F).

GSEA

To identify the sets of gene that were up- or down-regulated in the ALDH^{Hi} subpopulations, we performed GSEA for the published gene expression profile of C57BL/6 mice divided by the ALDH^{Hi} and ALDH^{Lo} subpopulations of ADSCs. Intriguingly, high gene set enrichment scores were obtained for the structural constituents of ribosomes (Figure 3).

DISCUSSION

MSCs are reported to commonly express CD29, CD73, CD90, and CD105 and to be negative for markers such as CD45 and CD56[12,13]. There have been many studies on cell surface antigen markers of ADSCs, such as CD34 and CD44[12,14,15]. Recently, however, studies have shown that some markers such as CD90 or CD105 are not expressed homogenously in bulk ADSC populations but are expressed in small ADSC subpopulations, suggesting that ADSCs are phenotypically heterogeneous[5,7,8]. In our current study, we detected ALDH activity as a stem cell marker in murine ADSCs. High ALDH activity has been reported as a marker for cells such as hematopoietic stem cells and cancer stem cells[10]. However, not many studies have been performed on ALDH activity and cell differentiation potential in MSCs. In one of these studies, Estes *et al*[11] showed the presence of a subpopulation

with high ALDH activity in human ADSCs; however, no difference was found in terms of differentiation potential. In our present study, the cultured murine bulk ADSC population contained approximately 15% of the ALDH^{Hi} subpopulation. Additionally, in the induction experiment for adipogenic and osteogenic differentiation for each sorted ALDH^{Hi} and ALDH ^{Lo} subpopulation, significantly higher adipogenic and osteogenic potentials were found in the ALDH^{Hi} subpopulation. The ALDH^{Hi} subpopulation had higher cell differentiation potential than the ALDH^{Lo} subpopulation. To the best of our knowledge, this is the first report on the functionally distinguishable subpopulation defined by ALDH activity within murine ADSCs.

Relationships between ribosome biogenesis and stem cells have been described only recently. For example, it was reported that the transition from self-renewal to differentiation depends on the enhancement of ribosome biogenesis accompanied by increased protein synthesis in female Drosophila germline stem cells[16]. Slow growth, low biosynthesis and markedly reduced ribosome biogenesis were observed in hematopoietic stem cells that lacked RUNX1, which is known to promote the transcription of essential ribosome-related proteins[17]. We have few reports about relationship between ribosome biogenesis and MSCs. One of these reports presented one of core proteins of 60S ribosome is necessary for differentiation of osteocyte from MSCs[18]. In our current study, GSEA revealed the significant enrichment of ribosome-related genes in the ALDH^{Hi} subpopulation compared to that in the ALDH^{Lo} subpopulation, suggesting that ribosome biogenesis is part of the mechanism underlying the higher differentiation potential of the ALDH^{Hi} subpopulation.

ADSCs can be obtained in a less invasive manner from adipose tissue. Therefore, ADSCs are considered to be a promising source of cell-based therapy in the clinical setting. ADSCs have already been used in clinical studies for cardiovascular disease, breast reconstruction after mastectomy, spinal cord injury, cirrhosis, renal insufficiency, skin fistula after surgery, and skin fistula with Crohn's disease[4,19,20]. Some of those trials reported the therapy to be safe and effective; however, there is obvious room for improvement. For instance, in a phase 3 trial for therapy with allogeneic expanded ADSCs for treatment-refractory complex perianal fistulas in patients with Crohn's disease (ADMIRE-CD trial), approximately 50% of patients who received ADSC-therapy experienced remissions[21]. Although this is a significant achievement, further research and development are required in relation to the patients who did not respond to this trial.

Purification of specific subpopulations and engineering of ADSCs into cells that are highly efficient in differentiating into specific tissues might help obtain basic knowledge for cell-based therapy, which is more specific to individual disease conditions of each organ for which ADSCs are used. Further investigation is required to identify the underlying mechanisms that regulate ribosome biogenesis and differentiation in ALDH^{Hi} ADSCs.

In conclusion, we demonstrated that murine ADSCs have a distinct subpopulation defined by ALDH activity. Furthermore, the ALDH^{Hi} subpopulation had higher osteogenic and adipogenic differentiation potential than the ALDH^{Lo} subpopulation. Ribosome biosynthesis is suggested to be a remarkable difference between ALDH^{Hi} and ALDH^{Lo} subpopulations.

COMMENTS

Background

Adipose-derived stem cells (ADSCs) are recognized as useful materials for regenerative therapy. Recent study revealed the existence of subpopulations in ADSCs by surface antigen markers. However, functions of these markers remain elusive. Aldehyde dehydrogenase (ALDH) activity is commonly used as functional marker to identify human and mouse hematopoietic stem cell, though there has been no report about identification of a subpopulation(s) in murine ADSCs using ALDH.

Research frontiers

Several surface antigen markers are reported to be capable of prospectively identifying distinct ADSCs subpopulations in human and murine. However, the function(s) of those reported markers are poorly understood. ALDH has its known function, such as a protective effect to hematopoietic stem cells through acetaldehyde detoxification, although it is not known in ADSCs.

Innovations and breakthroughs

The authors suggest a novel area of research consisted of ALDH, stem cell, and ribosome biosynthesis, by reporting here ALDH^{Hi} murine ADSCs are highly capable of differentiation, and have enriched ribosome-related gene sets.

Applications

The authors current findings of ALDH^{Hi} subpopulation of ADSCs might provide future application for enrichment of more useful cells which is applicable to an efficient cell-based therapy. Moreover, by elucidating mechanisms of the higher differentiation potentials shown in ALDH^{Hi} subpopulation of ADSCs might provide knowledge of a key regulator(s) of differentiation, and links between ribosome biosynthesis.

Terminology

ADSCs: Adipose-derived stem cells can be obtained from adipose tissues and induced to differentiate into adipocytes, osteocytes and chondrocytes; ALDH: ALDH is a superfamily comprising 20 intracellular enzymes and is responsible for the oxidization of various aldehydes. Some reports identified ALDH is a marker that detect hematopoietic stem cells and cancer stem cells; GSEA: Gene set enrichment analysis is a comprehensive analysis of gene expression by a computational method.

Peer-review

This is a very interesting and well executed piece of work, with suitable controls.

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