

Basic Study

Murine hepatocellular carcinoma derived stem cells reveal epithelial-to-mesenchymal plasticity

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Abstract**AIM**

To establish a model to enrich and characterize stem-like cells from murine normal liver and hepatocellular carcinoma (HCC) cell lines and to further investigate stem-like cell association with epithelial-to-mesenchymal transition (EMT).

METHODS

In this study, we utilized a stem cell conditioned serum-free medium to enrich stem-like cells from mouse HCC and normal liver cell lines, Hepa 1-6 and AML12, respectively. We isolated the 3-dimensional spheres and assessed their stemness characteristics by evaluating the

RNA levels of stemness genes and a cell surface stem cell marker by quantitative reverse transcriptase-PCR (qRT-PCR). Next, we examined the relationship between stem cells and EMT using qRT-PCR.

RESULTS

Three-dimensional spheres were enriched by culturing murine HCC and normal hepatocyte cell lines in stem cell conditioned serum-free medium supplemented with epidermal growth factor, basic fibroblast growth factor and heparin sulfate. The 3-dimensional spheres had enhanced stemness markers such as *Klf4* and *Bmi1* and hepatic cancer stem cell (CSC) marker *Cd44* compared to parental cells grown as adherent cultures. We report that epithelial markers *E-cadherin* and *ZO-1* were downregulated, while mesenchymal markers *Vimentin* and *Fibronectin* were upregulated in 3-dimensional spheres. The 3-dimensional spheres also exhibited changes in expression of *Snai*, *Zeb* and *Twist* family of EMT transcription factors.

CONCLUSION

Our novel method successfully enriched stem-like cells which possessed an EMT phenotype. The isolation and characterization of murine hepatic CSCs could establish a precise target for the development of more effective therapies for HCC.

Key words: Hepatocellular carcinoma; Hepa 1-6; Cancer stem cells; Cancer initiating cells; Epithelial-to-mesenchymal transition; Cellular plasticity; Epithelial-to-mesenchymal transition transcription factors; AML12

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Core tip: Although existing therapies can initially eliminate the bulk population of a tumor, the stem cell properties of cancer stem cells (CSCs) enable them to survive and repopulate the tumor, resulting in disease relapse. Therefore, elimination of CSCs has the potential to improve patient outcomes and survival. Isolation and characterization of liver CSCs is essential for the selective targeting of this crucial population of cells. We report that the sphere culture method is a more precise and reliable tool for the enrichment of murine stem-like cells which relies on their functional property of anchorage-independent growth.

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INTRODUCTION

Hepatocellular carcinoma (HCC) is the fifth most

common cancer worldwide affecting one million individuals annually^[1]. HCC is associated with high mortality rates largely due to the development of resistance to chemotherapy or radiotherapy, recurrence after surgery or intra-hepatic metastases^[2]. While treatments such as surgical liver resection and liver transplantation have had a significant impact in early-stage HCC, these treatments have limited efficacy in most patients with advanced stage HCC^[3]. Moreover, Sorafenib, the only available drug for advanced stage HCC has limited efficacy^[4]. A better understanding of the biology of HCC would have a major impact on the management of this disease.

According to the stem cell model of carcinogenesis cancers are initiated and maintained by a rare fraction of cells called cancer stem cells (CSCs) or cancer initiating cells (CICs)^[5,6]. The presence of CSCs with biological properties such as multipotency and self-renewal, similar to those of normal stem cells, was first reported in leukemia and subsequently in diverse malignancies including breast cancer, glioblastoma, prostate cancer, colon cancer and liver carcinoma^[7-13]. CSCs have proven to play a central role in the development, maintenance, metastasis, and recurrence of HCC^[14-16]. Therefore the prospective identification and isolation of CSCs in HCC could generate a better understanding of hepatocarcinogenesis and facilitate the identification of novel druggable targets for development of more efficient therapeutic strategies.

Recent evidence indicates that CSCs may be generated with the reactivation of the developmental epithelial-to-mesenchymal transition (EMT) program, which impacts tumor metastatic potential^[17-19]. EMT describes a reprogramming of epithelial cells that leads to a phenotype switch from an epithelial to a mesenchymal cellular state. This cellular plasticity occurs during normal development as part of processes such as gastrulation and neural crest cell migration. During cancer progression, this phenotype is associated with metastatic dissemination, acquisition of drug resistance and acquisition of CSC state^[20,21]. Whereas the role of EMT in HCC metastasis is well documented, its role in HCC CSC generation is only just emerging^[22].

Although a number of cell surface markers have been identified for the enrichment of HCC derived CSCs, there is no general consensus on the best CSC markers for HCC^[23,24]. We used an alternate method for the enrichment of HCC CSCs based on functional aspect of CSCs. CSCs exhibit anchorage-independent growth and form spheres that possess the capacity for self-renewal and tumorigenicity, when grown in a stem cell conditioned serum-free medium^[25]. Sphere formation assay thus represent a more precise tool for the enrichment of CSCs. This study therefore aimed to enrich stem-like cells from mouse HCC and normal liver cell lines with the goal to better characterize the 3-dimensional spheres. We also sought to examine the relationship between CSCs and EMT.

MATERIALS AND METHODS

Cell lines and cell culture

Murine HCC cell line Hepa 1-6 and normal liver cell line AML12 were procured from American Type Culture Collection (ATCC) and maintained as per ATCC protocols. The cell lines Hepa 1-6 and AML12 were cultured in Dulbecco's modified Eagle's medium (DMEM) (Lonza, Australia) supplemented with 10% heat-inactivated fetal bovine serum (FBS) (Assay Matrix, Australia) and 1% penicillin/streptomycin (P/S) (ThermoFischer Scientific, Australia) and incubated at 37 °C under a humidified atmosphere with 5% CO₂ in air.

3-dimensional sphere enrichment assay

Cells were cultured as 3-dimensional spheres using a stem cell conditioned serum-free medium which is based on a neural stem cell medium^[25]. Stem cell conditioned serum-free medium was prepared by adding 1:1 mixture of DMEM and HAM's F12 medium (Lonza, Australia) supplemented with 4 µg/mL heparin sulfate (Sigma-Aldrich, United States), 1% penicillin/streptomycin (P/S) (ThermoFischer Scientific, Australia), 2% bovine serum albumin (BSA) (Sigma-Aldrich, United States), 20 ng/mL recombinant human epidermal growth factor (rhEGF) (Lonza, Australia) and 10 ng/mL recombinant human basic fibroblast growth factor (rhbFGF) (Lonza, Australia). Briefly, adherent cells were detached and collected following Trypsin-EDTA (ThermoFisher Scientific, Australia) treatment. Cells were washed three times with 50 mL 1 × PBS to remove serum. Cells were counted and seeded at 5000 cells/ml in a T-25 ultra-low-attachment flask (Corning Incorporated, United States) and cultured with stem cell medium at 37 °C in a humidified atmosphere of 5% CO₂ in air.

Enumeration of spheres

Cells were seeded at 2000 cells/well in a 6-well ultra-low-attachment plates (Corning Incorporated, United States) and cultured with stem cell medium. Diameter of 3-dimensional spheroids and number of spheres per culture well were counted on day 5 using an inverted microscope equipped with a digital camera (Olympus DP21, Japan).

RNA extraction and cDNA synthesis

The parental cells were plated at the same density as the sphere cells and on day 5 total cellular RNA was extracted using the Isolate II Bioline RNA synthesis kit (Bioline, Australia) as per the manufacturer's protocol. We performed on column DNAase digestion using RNase-Free DNase at room temperature (20 °C-30 °C) for 15 min in accordance to Bioline RNA synthesis kit instructions. Spectrophotometric quantification using the Nanodrop 2000 c (ThermoFisher, United States) confirmed purity of RNA and absence of DNA in our samples. One micrograms of the extracted RNA was reverse transcribed using the Bioline SensiFAST cDNA

Table 1 List of primers for quantitative reverse transcriptase-PCR

Primer	Sequence (5'-3')
<i>ActB</i> forward	ATGGAGGGGAATACAGCCC
<i>ActB</i> reverse	TTCTTTGCAGCTCCTTCGTT
<i>Klf4</i> forward	CAGTGGTAAGGTTTCTCGCC
<i>Klf4</i> reverse	GCCACCCACACTTGTGACTA
<i>Bmi1</i> forward	TGGTTGTTCGATGCATTCT
<i>Bmi1</i> reverse	CTTCATTGCTTTTCCGCC
<i>Cd44</i> forward	AGCGGCAGGTTACATTCAAA
<i>Cd44</i> reverse	CAAGTTTTGGTGGCACACAG
<i>E-Cadherin</i> forward	AAAAGAAGGCTGCTTGGC
<i>E-Cadherin</i> reverse	GAGGTCTACACCTTCCCGGT
<i>ZO-1</i> forward	CCTGTGAAGCGTCACTGTGT
<i>ZO-1</i> reverse	CGCGGAGAGAGACAAGATGT
<i>Vimentin</i> forward	AGAGAGAGGAAGCCGAAAGC
<i>Vimentin</i> reverse	TCCATTTCCTTCAAGGTC
<i>Fibronectin</i> forward	ACTGGATGGGGTGGGAAT
<i>Fibronectin</i> reverse	GGAGTGGCACTGTCAACCTC
<i>Snai1</i> forward	AGTGGGAGCAGGAGAATGG
<i>Snai1</i> reverse	CTGTGTCTGCACGACCTGT
<i>Snai2</i> forward	GATGTGCCCTCAGGTTTGT
<i>Snai2</i> reverse	GGCTGCTTCAAGGACACATT
<i>Zeb1</i> forward	TCATCGGAATCTGAATTTGC
<i>Zeb1</i> reverse	CCAGGTGTAAGCGCAGAAAG
<i>Zeb2</i> forward	TGCGTCCACTACGTTGTGAT
<i>Zeb2</i> reverse	TCTTATCAATGAAGCAGCCG
<i>Twist1</i> forward	CATGCCGCTCCCACTA
<i>Twist1</i> reverse	TCCATTTCTCTTCTCTGGA
<i>Twist2</i> forward	GCCTGAGATGTGCAGGTG
<i>Twist2</i> reverse	GTCTCAGCTACGCCCTCTCC

synthesis kit (Bioline, Australia).

Quantitative reverse transcriptase-PCR

Following reverse transcription, quantitative reverse transcriptase-PCR (qRT-PCR) was performed using Lo-ROX SYBR Green (Bioline, Australia). Reactions were run in 384-well plates on a ViiA7 Applied Biosystems Real-Time PCR system. Amplification was performed according to a three-step cycle procedure consisting of 40 cycles of denaturation at 95 °C for 5 s, annealing at 60 °C for 10 s and extension at 75 °C for 15 s. E-cadherin expression was evaluated using QuantiFast SYBR Green PCR Kit (Qiagen, United States) following the manufacturer's instructions. Amplification was performed according to a two-step cycling procedure consisting of 40 cycles of denaturation at 95 °C for 10 s and combined annealing/extension at 60 °C for 30 s. *Beta-Actin* (*ActB*) was used as an internal control. The primers used are listed in Table 1. Expression levels were normalized to *ActB* and are presented as copies of target gene per 10000 copies of *ActB*, calculated using the formula: $2^{-(CT_{ActB} - CT_{target})} \times 10000$. The copy number values were calculated from a minimum of three independent biological replicates.

Statistical analysis

All experiments were repeated at least three times and representative results are presented. All statistical comparisons of data sets were performed using Student'

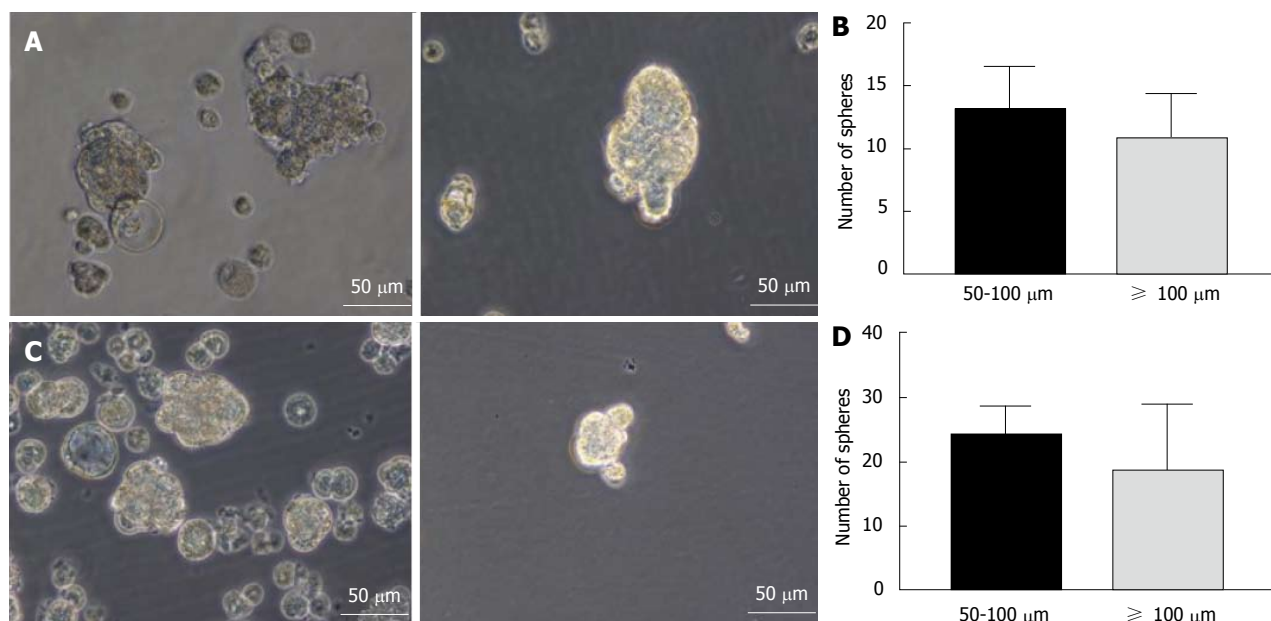


Figure 1 Enrichment of cancer stem cells using the sphere culture method. A: Photomicrographs of Hepa 1-6 3-dimensional spheres on day 5 cultured in stem cell conditioned serum-free medium; B: Hepa 1-6 sphere sizes and numbers were enumerated; C: Photomicrographs of AML12 3-dimensional spheres on day 5; D: AML12 spheres sizes and numbers were enumerated.

s two-tailed *t*-test in GraphPad Prism software version 7.00 (GraphPad Software Inc). Statistical significance was set at ^a*P* < 0.05, ^b*P* < 0.01 and ^e*P* < 0.001.

RESULTS

Mouse HCC and normal liver cells formed anchorage-independent 3-dimensional spheres

Mouse HCC cell line Hepa 1-6 and normal mouse liver cell line AML12 were used for induction of spheres. Both cell lines could form anchorage-independent, non-adherent 3-dimensional spheres when grown in conditioned serum-free culture medium supplemented with rhEGF, rhbFGF and heparin sulfate (Figure 1A and C). Both cell lines formed floating small spheres which eventually form 3-dimensional structures by day 5. No adherent cells were detected. The number of spheres were counted and appeared to be similar in both the cell types (Figure 1B and D).

Embryonic stemness and CSC marker expressions are enhanced in 3-dimensional spheres

With the goal of better characterizing the cells enriched by sphere culture, we examined the expression levels of some stem cell-associated genes important for the proliferation, self-renewal and differentiation of stem cells. As controls, the parental cells were plated as adherent cultures at the same density as the spheres. On day 5 RNA was extracted from 3-dimensional sphere cultures and adherent cultures. qRT-PCR analysis revealed markedly elevated expression of embryonic stem cell-associated genes Kruppel like factor 4 (*Klf4*) and Bmi1 polycomb ring finger oncogene (*Bmi1*) in Hepa 1-6 spheres compared with parental cells (Figure 2A and

B). *Cd44*, a cell surface adhesion molecule which has been used as a CSC marker in HCC showed significantly increased expression in Hepa 1-6 spheres compared with adherent parental cells (Figure 2C). Similarly, AML12 derived 3-dimensional spheres also expressed significantly higher mRNA levels of *Klf4* and *Bmi1* compared with the adherent AML12 population (Figure 2D and E). Higher expression of *Cd44* was detected in spheres from AML12 compared with the parental cells (Figure 2F). These results indicate that the conditioned stem cell serum-free medium is a precise tool for the selective enrichment of hepatic mouse stem-like cells.

CSC and EMT phenotypes are linked in 3-dimensional spheres

To elucidate whether there were connections between the spheres and EMT phenotype, we assessed the EMT characteristics of the 3-dimensional spheres from Hepa 1-6 and AML12. At the molecular level, EMT is characterized by a series of coordinated changes including down-regulation of the adherens junction molecule *E-cadherin* and tight junction molecule Zonula occludens-1 (*ZO-1*) and upregulation of *Vimentin*, an intermediate filament and *Fibronectin*, a key molecule of extracellular matrix. We observed that the expression of classical epithelial marker genes, *E-cadherin* and *ZO-1* were significantly downregulated in 3-dimensional spheres from both Hepa 1-6 and AML12 compared with parental cells (Figure 3). These 3-dimensional spheres also exhibited the characteristic features of a mesenchymal phenotype with high expression of *Vimentin* and *Fibronectin* (Figure 4). These findings suggest that the stem cell phenotype is closely linked with an EMT phenotype.

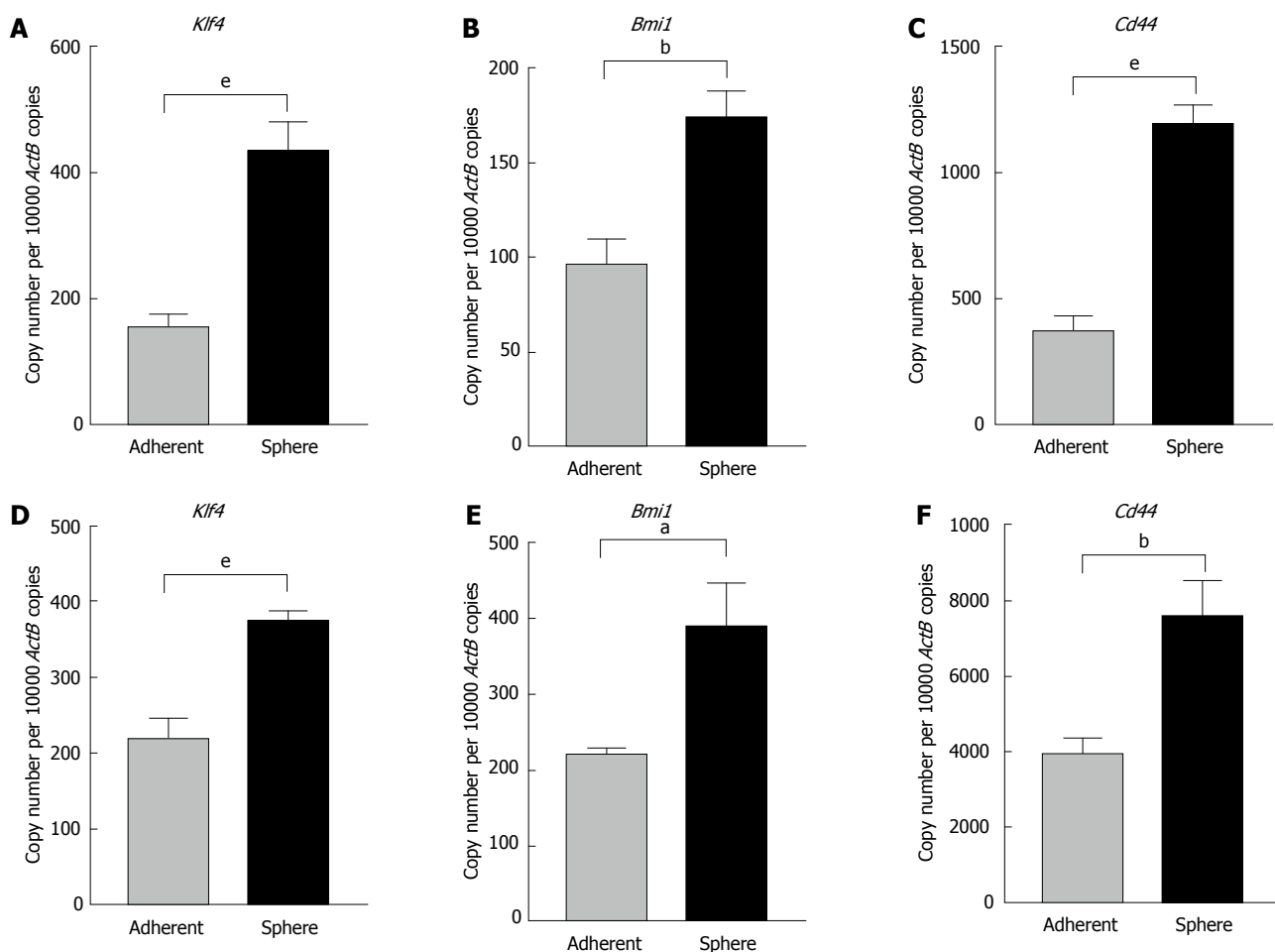


Figure 2 Three-dimensional spheres expressed high stemness and cell surface cancer stem cell markers. qRT-PCR analysis revealed higher expression of A: *Klf4*, B: *Bmi1* and C: *Cd44* in Hepa 1-6 3-dimensional spheres compared with Hepa 1-6 grown as adherent cells. qRT-PCR analysis revealed higher expression of D: *Klf4*, E: *Bmi1* and F: *Cd44* in AML12 3-dimensional spheres compared with AML12 grown as adherent cells. Values are mean \pm SEM of three experiments in triplicate (^a $P < 0.05$, ^b $P < 0.01$, ^e $P < 0.001$). qRT-PCR: Quantitative reverse transcriptase-PCR; ActB: Beta-Actin.

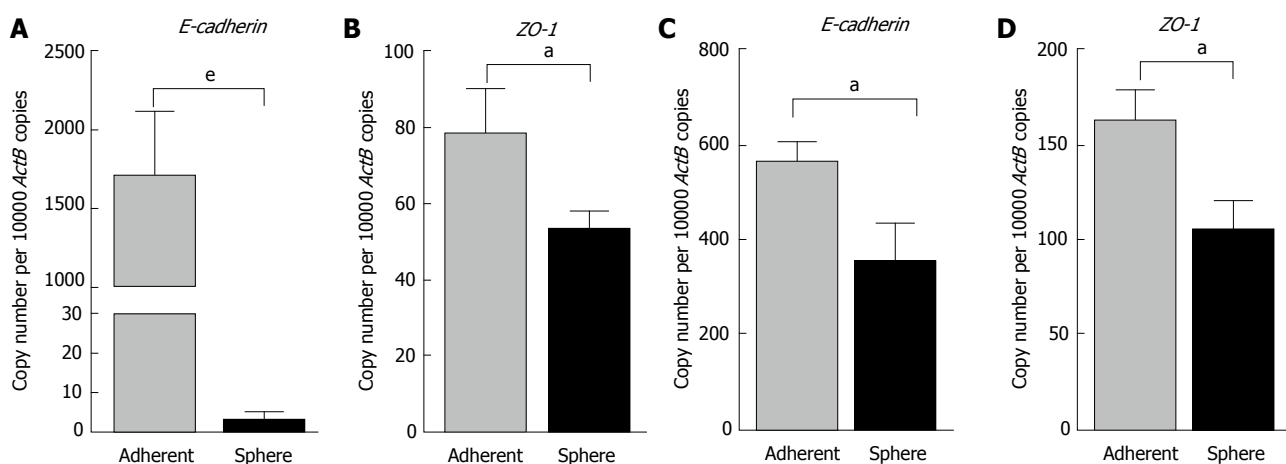


Figure 3 3-dimensional spheres decreased expression of epithelial markers. qRT-PCR analysis revealed downregulation of A: *E-cadherin* and B: *ZO-1* in Hepa 1-6 CSCs compared with Hepa 1-6 grown as adherent cells. qRT-PCR analysis revealed lower expression of C: *E-cadherin* and D: *ZO-1* in AML12 CSCs compared with AML12 grown as adherent cells. Values are mean \pm SEM of three experiments in triplicate (^a $P < 0.05$, ^e $P < 0.001$). qRT-PCR: Quantitative reverse transcriptase-PCR; ActB: Beta-Actin.

Core EMT transcription factors are enhanced in 3-dimensional spheres

To further confirm the occurrence of EMT process in

CSCs we examined the expression levels of core EMT transcription factors that govern cellular plasticity. In Hepa 1-6 spheres we observed significant upregulation

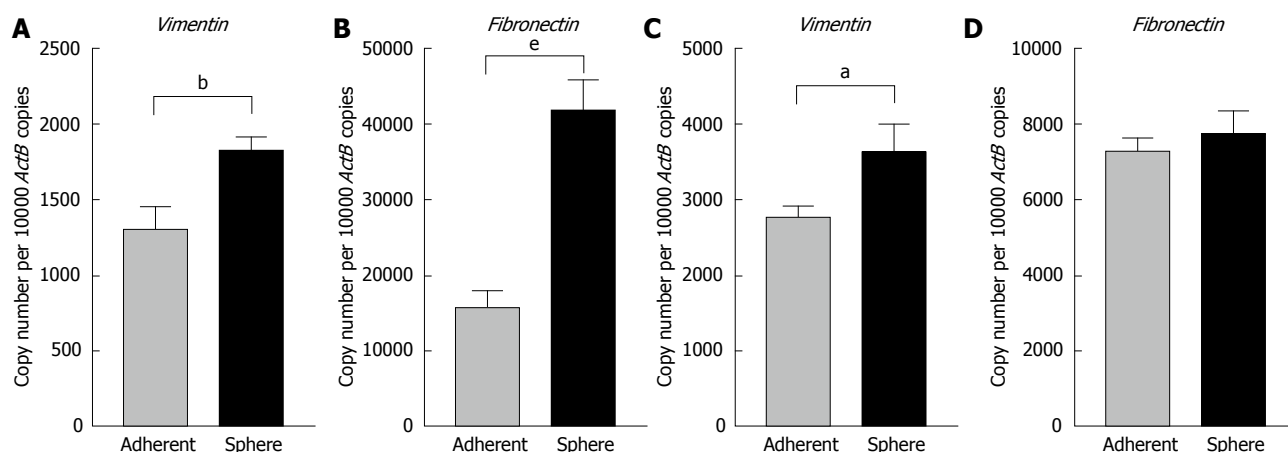


Figure 4 Three-dimensional spheres have higher expression of mesenchymal markers. qRT-PCR analysis revealed upregulation of A: *Vimentin* and B: *Fibronectin* in Hepa 1-6 3-dimensional spheres compared with Hepa 1-6 grown as adherent cells. qRT-PCR analysis revealed higher expression of C: *Vimentin* and D: *Fibronectin* in AML12 3-dimensional spheres compared with AML12 grown as adherent cells. Values are mean \pm SEM of three experiments in triplicate (^a $P < 0.05$, ^b $P < 0.01$, ^c $P < 0.001$). qRT-PCR: Quantitative reverse transcriptase-PCR; ActB: Beta-Actin.

of *Snai* family of transcription factors (*Snai1* and 2), Zinc-finger E-box-binding homeobox family of transcription factors (*Zeb1* and 2) and helix-loop-helix *Twist* family of transcription factors (*Twist1* and 2) compared with adherent parental cells (Figure 5). We observed a significant increase in the *Zeb* family of transcription factors in AML12 3-dimensional spheres compared with parental cells. AML12 3-dimensional spheres showed downregulation of *Snai2*, *Twist1* and *Twist2* RNA levels (Figure 6). This raises the possibility that distinct family of transcription factor may enable maintenance of CSC cellular plasticity in different cell types. Together, these features of EMT strongly suggest a possible relationship of EMT with the hepatic stem-like cell phenotype.

DISCUSSION

Worldwide, HCC, a primary liver cancer is one of the most common malignancies with a poor outcome^[2]. Non-resectable advanced stage HCC remains an incurable disease for which novel therapies are urgently needed. Accumulating evidence suggests that CSCs play an important role in HCC tumorigenicity and the reactivation of EMT process has been implicated in the generation of CSCs^[22]. The CSC field has experienced rapid advances in the past decade and a number of strategies have been applied to identify and harvest them^[12-14,26-28]. Several markers have been proposed for the identification of CSCs in HCC, but not all are uniformly expressed in all CSC populations and single markers have been deemed insufficient to represent the real CSC phenotype^[24]. Alternately, the sphere culture method, which is not dependent on markers, has been increasingly utilized in various tumors, including HCC for isolating, enriching, maintaining or expanding the potential CSC subpopulations^[25,29-32]. To our knowledge, this is the first time that murine HCC and normal hepatocyte cell lines have been examined for sphere

forming capacity, enrichment of stem-like cells and occurrence of epithelial-mesenchymal plasticity.

Enrichment and characterization of murine derived CSCs provides a better understanding of how these CSCs interact with the CSC niche environment and host immune system in order to form a tumor and are indispensable for the development of new therapies for the elimination of CSCs. In HCC, the majority of studies of CSCs have utilized patient-derived material or established human tumor cell lines inoculated into immunocompromised mice^[29,31,32]. The immunocompromised mouse microenvironments do not recapitulate the microenvironment in a human patient with naturally occurring cancer and have limited value in assessing therapies targeting CSCs. Moreover, the ability of cells to grow in immunocompromised mice does not distinguish CSCs from non-CSCs, as it demonstrates selection for cells that can best adapt to growth in murine tissue, and therefore might not represent a true approximation of CSCs^[25]. We have previously demonstrated that immunocompetent syngeneic models allow for interactions of the recipient mouse host immune system with CSCs, a situation that more closely models cancer in humans^[25]. Future studies are needed to address whether mouse HCC derived CSCs are able to initiate tumors in syngeneic immunocompetent mice compared with the parental counterparts.

Our stem cell enrichment medium comprised of serum free media supplemented with rhEGF, rhbFGF and heparin sulfate, while others have previously used media supplements such as B27, leukemia inhibitory factor, N-acetyl-L-cysteine and neural survival factor for enriching human HCC CSCs^[29,30]. Our finding that murine 3-dimensional spheres had enhanced expression of stem cell markers namely, *Klf4*, *Bmi1* and *Cd44* lends credence to the use of the sphere culture model for CSC enrichment. Positive expression of *KLF4* was correlated with tumor relapse and a poor prognosis in patients with HCC^[33]. *CD44* expression was highly correlated with

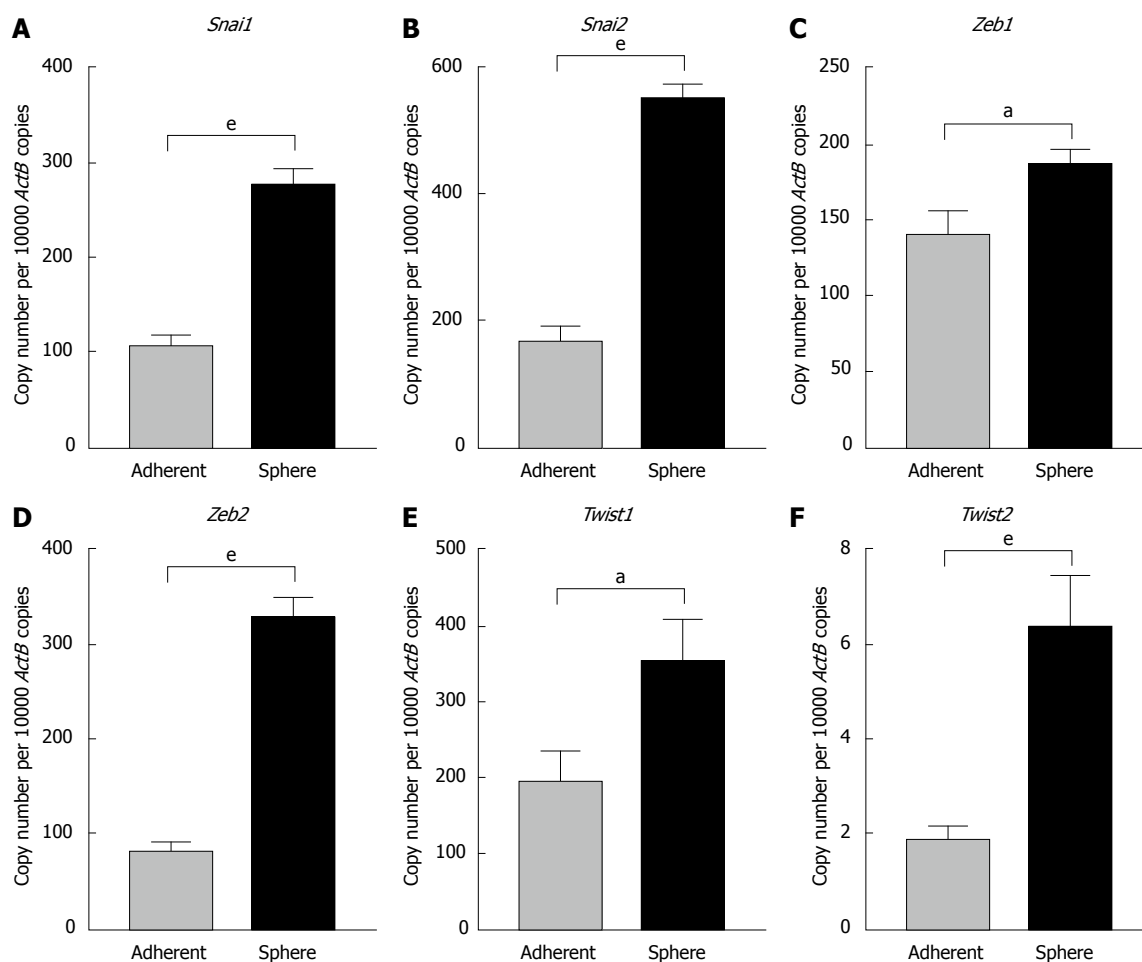


Figure 5 Expression of putative epithelial-to-mesenchymal transition transcription factors in Hepa 1-6 3-dimensional spheres. qRT-PCR analysis revealed upregulation of A: *Snai1*, B: *Snai2*, C: *Zeb1*, D: *Zeb2*, E: *Twist1*, and F: *Twist2* in Hepa 1-6 3-dimensional spheres compared with Hepa 1-6 grown as adherent cells. Values are mean \pm SEM of three experiments in triplicate ($^{\circ}P < 0.05$, $^{\circ}P < 0.001$). qRT-PCR: Quantitative reverse transcriptase-PCR; ActB: Beta-Actin.

decreased overall survival in HCC patients^[34] while high *BMI1* expression was associated with a poor prognosis in HCC patients^[35].

Finally we demonstrate a striking association between the expression of CSC and EMT markers. The biologic link between EMT phenotypes and CSCs has recently been evidenced in many types of cancer, including HCC^[3,22]. *E-cadherin* functions as a key gatekeeper of the epithelial state. Loss or downregulation of *E-cadherin* has been considered to be a hallmark of EMT^[20,21]. In our study, 3-dimensional spheres demonstrated downregulation of *E-cadherin* and *ZO-1*. We also found that the 3-dimensional spheres exhibited high *Vimentin* and *Fibronectin*, the phenotypes of mesenchymal cells that have more aggressive biological behaviour. Most notably, we found elevation of core EMT transcription factors in 3-dimensional spheres. Downregulation of *E-cadherin* is often mediated by core EMT-controlling transcription factors of *Snai*, *Zeb* and *Twist* families which have recently been molecularly linked to self-renewal programs^[36]. AML12 have yielded mixed results for EMT transcription factors in spheres with downregulation of *Twists* and *Snai2*. This indicates apparent cell type-

specific differences and the cause for this variance in transcription factor expression remains elusive and warrants further investigation. Taken together, our findings indicate that EMT transcription factors such as *Snai1*, *Zeb1* and 2 may provide opportunities for therapeutic targeting of CSC *via* blocking EMT. An in-depth investigation of crosstalk of stemness with EMT is essential for a better understanding of tumor progression in HCC. It is clear that further studies of CSC characterization will be critical to better understand plasticity and the mediators of phenotype switching as contributors to HCC initiation, progression, treatment failure and disease relapse. As a central player in these processes, EMT transcription factors may well serve as druggable targets in strategies to better treat HCC.

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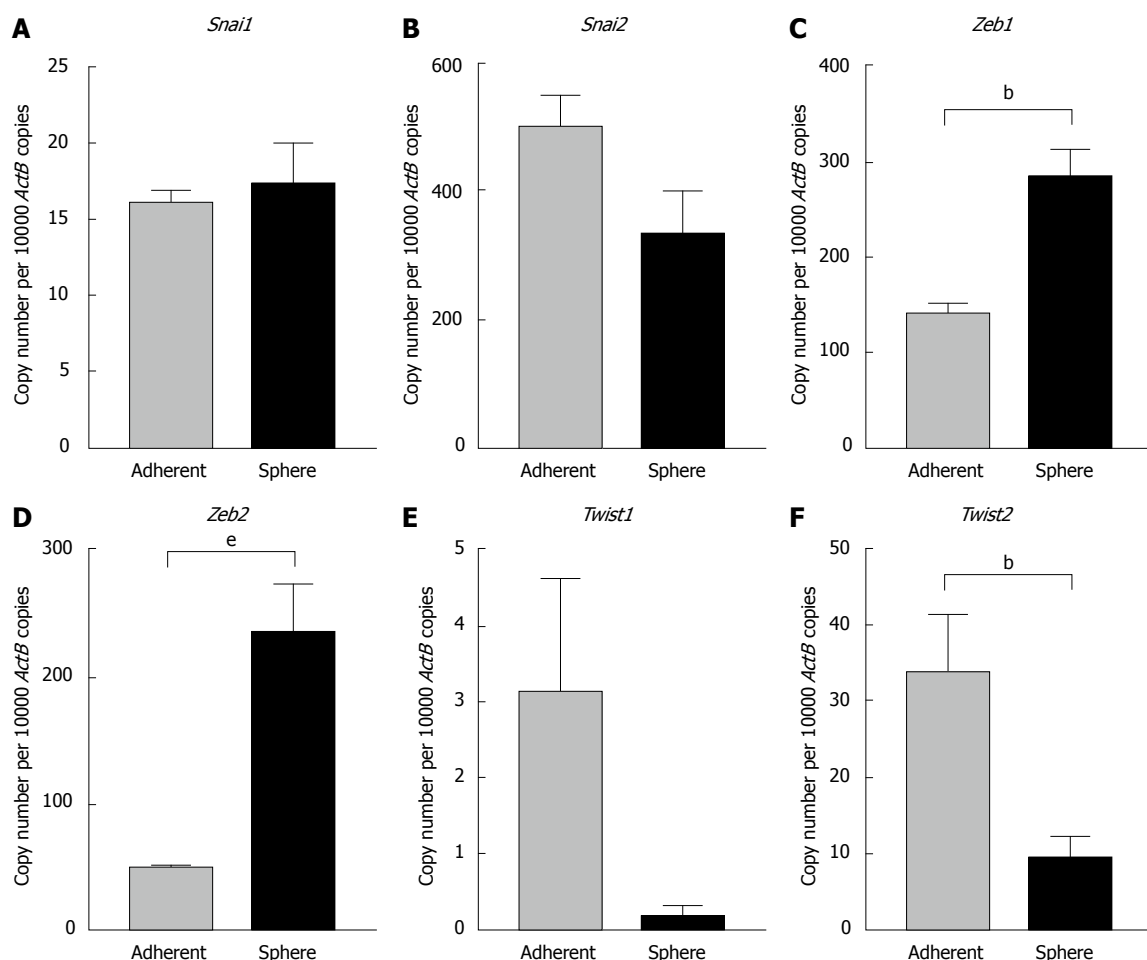


Figure 6 Expression of putative epithelial-to-mesenchymal transition transcription factors in AML12 3-dimensional spheres. qRT-PCR analysis revealed upregulation of A: *Snai1*, C: *Zeb1*, D: *Zeb2* and downregulation of B: *Snai2*, E: *Twist1*, and F: *Twist2* in AML12 3-dimensional spheres compared with AML12 grown as adherent cells. Values are mean \pm SEM of three experiments in triplicate (^b*P* < 0.01, ^e*P* < 0.001). qRT-PCR: Quantitative reverse transcriptase-PCR; ActB: Beta-Actin.

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COMMENTS

Background

Cancer stem cells (CSCs) have proven to play a central role in the development, maintenance, metastasis, and recurrence of hepatocellular carcinoma (HCC). Therefore the prospective identification and isolation of CSCs in HCC could generate a better understanding of hepatocarcinogenesis and facilitate the identification of novel druggable targets for development of more efficient therapeutic strategies.

Research frontiers

Although a number of cell surface markers have been identified for the enrichment of HCC derived CSCs, there is no general consensus on the best CSC markers for HCC. The authors used an alternate method for the enrichment of HCC CSCs based on functional aspect of CSCs.

Innovations and breakthroughs

To the knowledge, this is the first time that murine HCC and normal hepatocyte cell lines have been examined for sphere forming capacity, enrichment of stem-like cells and occurrence of epithelial-mesenchymal plasticity.

Applications

The authors' findings indicate that EMT transcription factors such as *Snai1*, *Zeb1* and 2 may provide opportunities for therapeutic targeting of CSC *via*

blocking EMT. An in-depth investigation of crosstalk of stemness with EMT is essential for a better understanding of tumor progression in HCC. It is clear that further studies of CSC characterization will be critical to better understand plasticity and the mediators of phenotype switching as contributors to HCC initiation, progression, treatment failure and disease relapse.

Terminology

CSC is cancer stem cells which have biological properties such as multipotency and self-renewal, similar to those of normal stem cells. EMT describes epithelial-to-mesenchymal transition, a reprogramming of epithelial cells that leads to a phenotype switch from an epithelial to a mesenchymal cellular state.

Peer-review

This manuscript is interesting, presenting a feasible method for concentrating a stem-like population from hepatic cancer cells by extending their previously reported technique for enriching a cancer-initiating population from lung cancer cell lines.

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