Preclinical Development

A Human Model of Epithelial to Mesenchymal Transition to Monitor Drug Efficacy in Hepatocellular Carcinoma Progression

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Abstract

The epithelial to mesenchymal transition (EMT) of malignant hepatocytes is a crucial event in hepatocellular carcinoma (HCC) progression and recurrence. We aimed to establish a human model of EMT to examine drug efficacy and specificity in HCC progression. Human HCC cell populations were characterized by immunofluorescence analysis, migration and invasion assays, array comparative genomic hybridization, whole-genome expression profiling, and promoter methylation. Therapeutic agents clinically used against HCC were examined for efficacy by determination of IC50 values. We show that liver cancer cell lines exhibited either an epithelial or mesenchymal phenotype of which the latter showed strong migratory and invasive abilities in vitro. The common cellular origin of both cell types indicated that mesenchymal HCC cells have been derived from epithelial hepatocytes through EMT in the HCC patient. Drug exposure of mesenchymal HCC cells showed higher resistance to the targeted therapeutic agents sorafenib and erlotinib as compared to epithelial HCC cells, which were slightly more resistant to cytostatic drugs. Most remarkably, combined treatment with doxorubicin and sorafenib caused increased susceptibility of both HCC cell types resulting in enhanced drug efficacy. Taken together, this EMT model of human HCC allows the identification of molecular mechanisms and the assessment of therapeutic drug efficacy during liver cancer progression in preclinical studies. Mol Cancer Ther; 10(5); 850–60. ©2011 AACR.

Introduction

The epithelial to mesenchymal transition (EMT) enables carcinoma cells to invade into surrounding tissues and to form secondary tumors known as metastases. A particular characteristic of EMT is the downregulation of E-cadherin expression, which causes disruption of cell–cell junctions and dissemination of cells from the primary tumor (1). Dysregulation of E-cadherin is provoked by its transcriptional repressors involving Snail/SNAI1, Slug/SNAI2, ZEB1/AE1F1, ZEB2/SIP1, or Twist (2). Receptor tyrosine kinase/Ras and transforming growth factor (TGF)-β signaling as well as Wnt/β-catenin-, Notch-, Hedgehog-, and NF-κB-dependent pathways can induce and maintain EMT during cancer progression (1, 3).

The pivotal role of EMT in hepatocellular carcinoma (HCC) has been increasingly recognized and various molecular mechanisms of hepatocellular EMT have been identified (4, 5). In human HCC, EMT correlates with invasive tumors, intrahepatic metastasis, and poor survival (6). This is of particular relevance because intrahepatic metastases were observed in more than 30% of HCC cases after liver surgery and in 80% of HCC autopsy cases (7).

Epidemiologically, HCC has a poor prognosis and represents the third most cause of death from cancer worldwide due to diagnosis at advanced stages and lack of effective therapy options (8). Thus, HCC therapy is hampered by the fact that the liver is central for xeno-biotic metabolism resulting in rapid modifications and efflux of drugs. Curative therapies such as resection and liver transplantation are applicable in only 15% of HCC patients (9) and show a high incidence of recurrence (10). Unresectable HCC are treated with locoregional therapies involving transarterial chemoembolization (TACE), percutaneous ethanol injection, or radiofrequency ablation (11). TACE represents an intraarterial administration of therapeutic drugs combined with embolizing agents which leads to a more selective distribution and a higher retention time of therapeutics within HCC. TACE has been established as the standard therapy for patients with intermediate stage cancer (12), although the efficacy of...
TACE is the most frequently used chemotherapeutic for TACE are doxorubicin (Adriamycin RDF), cisplatin (Platinol), and epirubicin (Ellence), either alone or in combination (14), from which doxorubicin and cisplatin showed significant benefits (13). Moreover, targeted therapeutic agents such as the multikinase inhibitor sorafenib (Nexavar) have been shown to have survival benefits especially in patients with advanced stage HCC (15–17). Those studies are the basis to develop treatment modalities to efficiently combat HCC progression that is considered as utmost treatment-resistant. However, suitable human HCC models are required to identify potential molecular targets, to test drug efficacy and to estimate the effective concentration of therapeutic agents.

Here, we established a human model of hepatocellular EMT which reflects important aspects of HCC progression and allows studying the underlying molecular mechanisms. The matched pair of epithelial and mesenchymal HCC cells enables us (i) to evaluate the efficacy of currently used therapeutic agents in single or combined treatments and (ii) to assess the effectiveness of novel anticancer agents during HCC progression.

Material and Methods

Cell culture
HCC-1.2 and HCC-1.1 cells, referred to as 3p and 3sp cells, respectively, were established from 1 male patient diagnosed with HCC (grade 2, T2N0M0, hepatitis C virus positive) at the age of 56 years. A fully documented patient’s history and informed consent was obtained. The study protocol conforms to the ethical guidelines of the 1975 Declaration of Helsinki, as reflected by the approval of the Ethic Committee of the Vienna Medical University. Briefly, the primary liver tumor tissue from surgical resection of the HCC patient was cut into pieces of approximately 0.5 mm³ and seeded on collagen I (Sigma) coated tissue culture plates by incubation in RPMI 1640 and 10% FCS. The 3p hepatoma cells were further separately cultivated. The propagation and immortalization of epithelial 3p and fibroblastoid 3sp cells were done by passaging and without particular designation of 3p

and 3sp cells, passage numbers between 40 and 50 were used. All cells were kept at 5% CO₂ and 37°C and routinely screened for the absence of mycoplasma.

Analysis of diploidy
Cells were trypsinized, washed with PBS and 1 × 10⁶ cells were incubated with 1 mL hypotonic DNA staining buffer containing 5 mg/mL propidium iodide (Calbiochem), 0.1% sodium citrate, 0.3% Triton X-100 and 20 μg/mL ribonuclease A (all from Sigma) for 30 minutes on 4°C in the dark. Determination of the DNA content was done by flow cytometry (FACSCalibur, BD Biosciences).

Short tandem repeat analysis
Polymere chain reaction (PCR) of 7 short tandem repeats (Supplementary Table S1) was done to verify the genetic origin of human 3p and 3sp hepatoma cells.

Quantitative real time PCR
PCR reactions were done with Fast SYBR Green Master Mix (Applied Biosystems) in duplicates according to the recommendations of the manufacturer and quantified with the 7500 Fast Real Time PCR System (Applied Biosystems). Arbitrary units were calculated by the dCT method. Forward and reverse primers are described in Supplementary Table S1.

Confocal immunofluorescence microscopy
Cells were seeded onto SuperFrostPlus glass slides (Menzel) and fixed with either 4% paraformaldehyde or methanol/aceton. Collagen gels were fixed in 4% formaldehde/PBS for 10 minutes at room temperature. After blocking for 30 minutes (1% PBS/0.5% Tween 20 or methanol/aceton. Collagen gels were fixed in 4%

After overnight incubation at 4°C the following primary antibodies were applied: anti-p120catenin (p120 ctn; BD Transduction Laboratories), anti-keratin 8 (Progen), Texas Red-X phaloidin (Invitrogen), and anti-vimentin (Sigma). The corresponding secondary antibody (Alexa 488; Invitrogen) was applied after 1 hour. Nuclei were visualized with Topro3 (Invitrogen) at a dilution of 1:10,000. Imaging was done by confocal immunofluorescence microscopy (Zeiss).

Proliferation analysis
The 1.5 × 10⁴ cells were plated and cell numbers were determined after various time points with a multichannel cell analyzer (CASY; Schärfe Systems). Three independent experiments were done in triplicates.

Cell migration and invasion assays
Cell migration and cell invasion was determined by Platypus Technology according to the manufacturer’s protocol (Oris Cell Invasion & Detection Assay). To analyze cell migration, 5 × 10⁵ cells were plated onto 8
not coated wells. To examine cell invasion, same cell numbers were seeded into 8 basal membrane extract (BME; 3.5 mg/mL)-coated wells and overlaid with undiluted BME. Migration and invasion of cells was microscopically analyzed and quantitatively evaluated by measuring the fluorescence after staining with Cell-Tracker (Green CMFDA; Invitrogen).

3-Dimensional spheroid formation of HCC cells

Spheroid formation and incubation was done as described (18). Briefly, a cell suspension of 3 × 10⁵ 3p cells per 100 µL or a 1:1 mixture of 3p and 3sp cells in RPMI containing 20% methyl cellose (Sigma) was incubated for 3 days at 37°C and 5% CO₂. After harvesting, 96 spheroids were harvested in collagen I (Sigma) and plated into FlexiPERM conA wells (Greiner Bio-One GmbH) to harden at 37°C for 15 minutes. Gels were then transferred into a 24-well plate and incubated with medium at cell culture conditions as outlined. CellTracker (Green CMFDA; Invitrogen) was applied at a concentration of 5 µM before spheroid formation and incubated as outlined by the instructions of the manufacturer (Invitrogen). The fluorescence signal was visualized by microscopy (Nikon, TE 300).

Array comparative genomic hybridization

Genomic DNA was isolated from early and late 3p and 3sp HCC cells using the QiAamp DNA Blood Mini Kit (Qiagen) according to manufacturer’s protocol. Array comparative genomic hybridization (aCGH) analysis was done using human 4 × 44K whole genome oligonucleotide-based arrays (Agilent). Male reference DNA (Promega) and sample DNA were digested with AluI (Promega) and labeled by random priming with radiolabeled Cy3- and Cy5-dUTP (Perkin-Elmer), respectively, labeled by Agilent Bioanalyzer (Agilent Technologies). After purification with Microcon YM-30 filter units (Millipore), the 2 labeled DNA species were hybridized together with human cot-DNA (Roche) onto CGH arrays for 48 hours at 65°C. Slides were scanned with a G2505B Micro Array Scanner (Agilent). Feature extraction and data analysis were done using the Feature Extraction and DNA Analytics software (Agilent), respectively.

Polymerase chain reaction of genomic DNA

Chromosomal DNA was isolated with GenElute Mammalian Genomic DNA Miniprep Kit (Sigma). PCR was done using chromosomal DNA and illustra PuReTaq Ready-To-Go PCR beads (GE Healthcare) and 4 µmol/L primer mix of following primers: human TRPM3: exon 1, forward (for) 5′-CAGGCCAAGGCTGATTTGCT-3′, reverse (rev) 5′-CCAACCTGTGCTTCAGA-3′, exon 3, for 5′-GTTCGAGGAGAAAAGGCA-3′, rev 5′-GGGGGAGGGCACTGAGA-3′; exon 6, for 5′-CTCCTACCTCCCCCCTCA-3′, rev 5′-TGCCAATGTCGGG-3′, exon 8, for 5′-TCAACATGAGGCTGCCA-3′, rev 5′-CTCGGCCACC-CATGCGGAAT-3′; exon 9, for 5′-CTGACTCATAG-CAAGGCCTCTT-3′, rev 5′-GCTGTCAAGGATGACCA-3′, ATCAATTGCC-3′; exon 10, for 5′-ATGCTCTGGCGCC-CAA-3′, rev 5′-AGATGCGGCTGCGAGGA-3′; exon 12, for 5′-TGAACCTGCTCCACCCCA-3′, rev 5′-GATGCTGATCAGGAGGCTC-3′; exon 15, for 5′-AGACAGAGGCTGCTTCGT-3′, rev 5′-CCTGTCGTCATCAGGCTG-3′; exon 18, for 5′-CCGGTGCCTCCCCGCTTCAC-3′, rev 5′-TGGACCTGGCTCTCCCGTTC-3′; exon 21, for 5′-TCCCTCTGTTCCCCACCCTT-3′, rev 5′-TCAACATGCGGCTGCCA-3′, exon 24, for 5′-CTCTGTCACCCCTGCAGCCA-3′, rev 5′-GGCCAGGCACTGGTGATCT-3′. Human AXIN1: exon 1, for 5′-CCCGCTACACGATACTCACAGA-3′, rev 5′-GCTCCA-GGCATCATGGCAGCAA-3′, exon 2, for 5′-CCTCCAGGCTCCGGCAGCA-3′, exon 3, for 5′-CTCCTGTCCTCCCGTCC-3′, exon 4, for 5′-ACAGGACCCAAAGGGAGG-3′, rev 5′-CCCGCTACACGATACTCACAGA-3′, rev 5′-GCTCCA-GGCATCATGGCAGCAA-3′, exon 4, for 5′-ACAGGACCCAAAGGGAGG-3′, rev 5′-CCCGCTACACGATACTCACAGA-3′, rev 5′-GCTCCA-GGCATCATGGCAGCAA-3′, exon 5, for 5′-GCGGCAACAGGAGAAGAGC-3′, rev 5′-CATCAGGACATACGCTTCGCCGC-3′; exon 6, for 5′-CGCGATCCATCTGCAGGAG-3′, rev 5′-GCGGCAACAGGAGAAGAGC-3′, rev 5′-CATCAGGACATACGCTTCGCCGC-3′; exon 7, for 5′-AGGATGAGTTCCTCAGGATCACA-3′; exon 8, for 5′-ACAGGAAAGCCACCACGCA-3′, rev 5′-TGCTCCACGGGCTGCAAGA-3′, rev 5′-TGCTCCACGGGCTGCAAGA-3′; exon 9, for 5′-AGACAGAGGCTGCTTCGT-3′; exon 11, for 5′-GGCCGGACTCCCATCTTCTC-3′, rev 5′-GCTGGCCACCAGGTGCAGTG-3′. Expression profiling using microarrays

Total RNA was isolated from duplicates of early and late 3p and 3sp HCC cells using the RNeasy Mini kit (Qiagen). The integrity and quantity of RNA was analyzed by Agilent Bioanalyzer (Agilent Technologies). cDNA labeling and hybridization on Affymetrix GeneChip Human gene 1.0 ST Array (Affymetrix) as well as scanning of signal intensities was done according to the manufacturer’s protocol. The ratio of regulation was calculated and a minimum of 3-fold regulation was considered as significant. Pathway analysis was performed with Gene Set Enrichment Analysis software by comparing the molecular profile data with existing as well as self-defined gene sets. Complete gene expression data have been deposited in National Center for Biotechnology Information’s Gene Expression Omnibus and are accessible by GEO Series accession no. GSE26391.

Analysis of CpG methylation

Genomic DNA was isolated from 3p and 3sp HCC cells grown in quadruplicates and from primary peripheral blood cells using the QiAamp DNA Blood
Mini Kit (Qiagen). The digestion of 600 ng genomic DNA with methylation-sensitive restriction enzymes (MSRE) was done. In total, 327 cancer-specific promoter loci were analyzed by PCR. Six hundred nanograms of genomic DNA of 3p and 3sp HCC cells and from primary peripheral blood cells were digested with MSRE overnight at 37°C by using a mixture of 6 units of each AciI (New England Biolabs), HinfI (Fermentas). and HpaII (Fermentas). Quantitative polymerase chain reaction (qPCR) was done on MSRE-digested DNA covering the CpG rich area at chr5:151,066,289–151,066,501 (human genome annotation: hg; ref. 19), including part of the first gene coding exon. This sequence region contains 9 MSRE sites when using the mixture of 3 enzymes mentioned earlier. Completion of digestion was confirmed using a control PCR covering known differentially methylated regions (DMRs, H19, IGF2, ABL1, PITX2, XIST, and FMR1) as published recently (19). Ten nanograms of MSRE-digested DNA was amplified in 10 µL PCR volume using 0.3 U HotStarTaq polymerase and buffer containing 1.5 mmol/L MgCl2 (Qiagen) using a 384-well format and the LightCycler LC480 (Roche). Cycling was done with 15 minutes of initial denaturation followed by 50 cycles with each 95°C for 10 seconds and 72°C for 10 seconds including a final extension at 72°C for 7 minutes. A melting curve analysis was done for confirming specificity of amplimers with a Tm of 88.4°C ± 0.6°C. Cp values were extracted from qPCR-data using the LightCycler LC480 software. Box plots were generated from quadruplicate 45-Cp values using R statistical software.

**Therapeutic agents**

Doxorubicin hydrochloride (adriamycin hydrochloride), cis-diammineplatinum (II) dichloride (cisplatin) and epirubicin hydrochloride were purchased from Sigma and dissolved in 0.9% NaCl. Sorafenib ( Nexavar; Bayer HealthCare Pharmaceuticals), erlotinib ( Tarceva; LC Laboratories), and bevacizumab (Avastin; Roche) were dissolved in dimethylsulfoxide (DMSO). Stock solutions were diluted in medium to concentrations indicated in the text.

**Determination of the inhibitory concentration**

Cell viability was determined using the 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT) assay. Briefly, cells were seeded in triplicates at a density of 6 × 10^3 cells per well. After 24 hours, cells were incubated with drug-containing medium for 3 days. Cells were incubated with MTT solution (5 mg/mL; Sigma) and medium was replaced with DMSO after 5 hours. The absorbance was measured at 620 nm by using a microplate reader (Asys HiTech). MTT assays were repeated 3 times for each drug application and untreated cells were used as reference. Determination of the inhibitory concentration (IC_{50}) values were obtained by log-linear interpolation of data points and are depicted by dose–response curves using the software GraphPad Prism 5.01.

**Verification of IC_{50} values by proliferation**

6 × 10^3 cells/well were seeded in duplicates on collagen-coated 12-well plates and incubated with drugs at a concentration of determined IC_{50} values for 3 days. Cells were trypsinized and counted with a cell counter (CASY, Roche). Untreated cells were used as reference to calculate the percentage of proliferation.

**Statistical analysis**

Data were expressed as means ± SD. The statistical significance of differences was evaluated using an unpaired, nonparametric Student’s t test. Significant differences between experimental groups were *P < 0.05, **P < 0.01, or ***P < 0.005.

**Results**

HCC cells show an epithelial phenotype and a mesenchymal one correlating with enhanced cell motility

We analyzed various human hepatoma cell lines for their epithelial and mesenchymal characteristics to establish a model of HCC progression (Supplementary Table S2). Two distinct liver cell lines were of particular interest as these cell types have been isolated from the HCC of one patient (20). Phase contrast analysis suggested an epithelial cell type, termed 3p, and a mesenchymal cell population, designated 3sp (Fig. 1A). Both HCC cells showed diploid DNA content (Supplementary Fig. S1) and short tandem repeat analysis verified their common genomic identity (Supplementary Table S3). qRT-PCR analysis revealed that 3p cells express epithelial markers such as E-cadherin and keratin 8, whereas 3sp cells showed a mesenchymal expression signature by upregulation of the transcription factors LEF1, SNAI1, SNAI2, and ZEB1 (Fig. 1B). Immunolocalization showed intact adherence junctions by expression of E-cadherin, β-catenin, and p<sub>120</sub>catenin at cell borders of 3p cells, whereas 3sp cells failed to show this phenotype (Fig. 1C). In contrast to 3sp, 3p cells displayed cytoplasmic distribution of the epithelial marker keratin 8 by concomitant absence of the mesenchymal interfilament component vimentin. In addition, mesenchymal 3sp cells showed relocalization of actin from the cell membrane to stress fibers suggesting enhanced motility.

We next assessed the migratory and invasive potential of 3p and 3sp cells. First, we did proliferation kinetics to exclude an influence of differential cell doubling rates on migration and invasion assays. No significant difference in proliferation of 3p and 3sp cells could be detected (Fig. 2A). Yet, a 4-fold increased migratory potential of mesenchymal 3sp cells was determined when compared to 3p cells (Fig. 2B and 2C). To analyze invasion, HCC cells were embedded into matrigel. Although epithelial...
3p cells showed no invasive potential, mesenchymal 3sp cells displayed a more than 5-fold stronger ability to invade into the matrix (Fig. 2D and E). The invasive potential of mesenchymal 3sp cells was further analyzed by 3-dimensional spheroid formation in collagen gels (18). Epithelial 3p cells formed compact and round spheroids without cell invasion into the surrounding gel (Supplementary Fig. S2A), even though proliferation was not impaired (data not shown). On the contrary, mesenchymal 3sp cells failed to form spheroids on their own, however, these cells attached onto the surface of epithelial 3p spheroids after cocultivation, and showed strong invasion into the surrounding matrix (Supplementary Fig. S2A and B). Immunofluorescence analysis of E-cadherin and β-catenin indicated epithelial characteristics of 3p-derived spheroids, whereas these markers could not be detected in invading 3sp cells due to disassembly of epithelial junctions (Supplementary Fig. S2C).
together, 3p and 3sp cells showed a distinct epithelial and mesenchymal phenotype correlating with poor and strong migratory and invasive abilities, respectively.

**Mesenchymal HCC cells developed through undergoing EMT in the patient**

We further investigated whether 3sp cells have been derived from epithelial 3p cells through EMT in the HCC patient. aCGH analysis showed that changes in the genomic DNA of these HCC cell lines were widely identical (Supplementary Fig. S3), which were exemplified by the loss of genomic DNA in the TRPM3 and AXIN1 loci of both cell types (Fig. 3A and B). PCR analysis of multiple exons could identify the exact chromosomal breaks, which are located between exons 12 and 15 and between exons 2 and 3 in TRPM3 and AXIN1, respectively (Supplementary Fig. S4). This homozygous loss of chromosomal regions indicates an identical cellular origin of 3p and 3sp hepatoma cells, and thus shows that 3sp cells have been developed from 3p cells via EMT in the patient.

To verify EMT, we analyzed the 3p/3sp HCC cell lines by whole-genome expression profiling (Fig. 4A and B). Remarkably, a large cluster of liver-specific genes were down-regulated in 3sp cells compared to 3p cells (Supplementary Fig. S5), including CYP450 phase I enzymes, *alcoholdehydrogenase (ADH)* and *aldehydedehydrogenase* (ALDH) and phase II enzymes such as *UDP-glucuronosyl-transferases (UGT)* and *glutathione-S-transferase (GST).*

![Figure 2](image-url)
Importantly, a cluster of epithelial markers involving components of tight junctions (claudins), desmosomes (desmoplakin), and adherence junctions (E-cadherin) were found to be strongly down-regulated in mesenchymal 3sp cells (Fig. 4A). Moreover, EMT-specific genes such as vimentin, LEF1, and SNAI2 were highly up-regulated in 3sp cells (Fig. 4B), as shown in Fig. 1B and C. In addition, expression profiling revealed (i) upregulation of growth factors and matrix metalloproteinases (MMP) such as connective tissue growth factor (CTGF), TGF-β2, and MMP2; (ii) upregulation of receptors associated with EMT such as platelet-derived growth factor (PDGF)-Rβ and discoidin domain receptor tyrosine kinase (DDR2); and (iii) increase of EMT-associated proteins such as fibroblast activation protein (FAP), lysyl oxidase, tenascin C and SPARC (secreted protein, acidic and rich in cysteine). qPCR further confirmed the upregulation of PDGF-Rβ, TGF-β2, DDR2, and FAP in 3sp cells as detected by microarrays analysis (Supplementary Fig. S6). From these data we conclude that mesenchymal 3sp HCC cells derived from epithelial 3p cells via EMT in the HCC patient.

**SPARC activation by CpG demethylation**

We next addressed the differences in the methylation status of gene promoters in 3p and 3sp cells. To exclude cell culture effects, genomic DNA of 3p/3sp cells from early as well as late passages was analyzed. Most notably, SPARC was identified to be epigenetically regulated, in line with a 128-fold upregulation of the transcript level (Fig. 4B). Methylation-specific PCR of the SPARC promoter revealed a lowered methylation status in both early and late passaged mesenchymal 3sp cells (Fig. 4C), which was verified by qRT-PCR analysis showing a >30-fold increase of SPARC mRNA in 3sp cells (Fig. 4D). Because the aCGH profile of the SPARC locus was unaffected, these data provide first evidence that the upregulation of SPARC is caused by demethylation during HCC progression.

**The 3p/3sp EMT model is suitable for drug testing**

We next used this human HCC model to assess the efficacy of clinically used anti-cancer agents. Dose–response relationships and corresponding half maximal inhibitory concentrations (IC₅₀) of drugs were determined (Supplementary Table S4) and verified by viability assays (Supplementary Fig. S7A). Chemotherapeutics such as doxorubicin, cisplatin, and epirubicin currently used for TACE were compared to targeted therapeutic drugs such as the multikinase inhibitor sorafenib, the EGFR-inhibitor erlotinib, and the VEGF-inhibitor bevacizumab. 3sp cells showed a slightly increased susceptibility against chemotherapeutics when compared to 3p cells (Fig. 5A–C; Supplementary Table S4), which is explained by downregulation of multiple drug resistance genes in 3sp cells (Supplementary Fig. S8A). Interestingly, 3sp cells were more resistant to targeted therapies including sorafenib and erlotinib (Fig. 5D and E; Supplementary Table S4). Bevacizumab did not show an effect on neither of the cells (Fig. 5F; Supplementary Table S4). These data provide first evidence that the upregulation of SPARC is caused by demethylation during HCC progression.
we investigated the effect of the combined treatment of these anticancer drugs in our model of HCC progression. We therefore treated cells with one drug in increasing concentrations, whereas the second drug was kept constant at its IC50. First, variable amounts of doxorubicin were applied in combination with the IC50 of sorafenib on 3p and 3sp cells (Fig. 6A). Compared to doxorubicin monotherapy, cells showed a drastic susceptibility for the combined treatment, leading to a reduction of the IC50 for doxorubicin of 60% and 39% in 3p and 3sp cells, respectively (Fig. 6B; Supplementary Table S4). The vice versa treatment, applying variable amounts of sorafenib in combination with the IC50 of doxorubicin (Fig. 6C) showed a similar result, leading to a reduction of the IC50 for sorafenib of 18% and 50% in 3p and 3sp cells, respectively (Fig. 6D; Supplementary Table S4). Most interestingly, we observed a normalization of the IC50 values between 3p and 3sp cells after combined treatment in both approaches (Fig. 6B and 6D; Supplementary Table S4). Taken together, these results indicate that the monotherapy shows considerable differences in the susceptibility between HCC cells undergoing EMT. Our data provide evidence that the combined use of doxorubicin and sorafenib is highly efficient to target both epithelial and mesenchymal HCC cells.

Discussion

EMT has been increasingly recognized to play a crucial role in HCC progression by the acquisition of invasive properties. In line with the transdifferentiation of neoplastic hepatocytes to motile mesenchymal derivatives,
HCC is described as a heterogenous tumor at advanced stages showing clonal expansion of genetically distinct malignant cell populations. Therefore, efficient anticancer therapy depends on targeting cancer cells at all stages of differentiation.

EMT has been suggested as the critical step in tumor cell dissemination and particularly associates with resistance towards chemotherapy and immunotherapy (1). Here we established and characterized the first human cellular model of EMT in HCC progression which correlates with the recently established molecular expression pattern of early and late TGF-β signatures (22). The late TGF-β signature of HCC was shown to associate with tissue invasion, EMT and metastasis, vascular transmigration and angiogenesis, earlier recurrence and shortened survival time as well as downregulation of glycolysis-regulating and acute-phase response genes. Aligning the gene expression sets of 3p and 3sp cells revealed a correlation with early and late TGF-β signature of more than 70 percent, respectively (data not shown). Moreover, we observed upregulation of TGF-β1 in mesenchymal 3sp cells and a resistance against TGF-β treatment suggesting an autocrine regulatory TGF-β loop. Thus, this model is a reliable tool to determine novel key players and to test drug efficacy of new and currently approved anticancer agents within HCC progression.

Figure 5. Increased resistance of mesenchymal HCC cells against targeted anticancer drugs. Cytotoxicity of cytostatic agents (A) and targeted therapeutic drugs (B) was analyzed by MTT assays and IC₅₀ values were calculated. Dose–response relationships of 3p and 3sp cells were compared. Dotted lines indicate IC₅₀.
using this model we show that epithelial cells are more sensitive to the targeted therapeutic agents such as sorafenib and erlotinib, whereas mesenchymal cells show a slightly more efficient susceptibility to chemotherapeutic drugs such as doxorubicin, cisplatin, and epirubicin. This might be caused by the downregulation of various multiple drug resistance proteins in the 3sp cells (Supplementary Fig. S8A). In the same line, the high sensitivity towards erlotinib might be explained by the higher phosphorylation status of $\text{EGFR}$ found in 3p cells (Supplementary Fig. S8B).

We propose that the molecular changes on EMT are crucial for differential drug efficacy. In this regard, we could show for the first time in vitro that the combined application of sorafenib and doxorubicin shows 2 advantages. First, combined therapy is capable of targeting both, epithelial and mesenchymal cells, which might have the potential to reduce the risk of HCC recurrence. Second, the effective concentrations of drugs could be reduced and thus side effects can be minimized. Yet, both cell lines showed no response against bevacizumab, referring to the limitation of the HCC model to study angiogenic mechanisms in vitro.

The efficacy of combining sorafenib and doxorubicin was shown in a phase II trial, resulting in increased overall and progression free survival in patients with advanced HCC compared to those who received monotherapy with doxorubicin (23). Furthermore, a phase III randomized study which compares sorafenib together with or without doxorubicin treatment in advanced or metastatic liver cancer is currently recruiting HCC patients. Clinical trial information of the U.S. National Institutes of Health is available under the identifier NCT01015833.

Remarkably, our data obtained by using 3p/3sp HCC cells confirm these observations and thus underline the synergistic effects of sorafenib and doxorubicin in interfering with HCC progression. Other ongoing clinical trials investigate the combination of sorafenib and doxorubicin or other chemotherapeutics using TACE. Clinical trial information of the U.S. National Institutes of Health is available under the identifiers NCT01011010, NCT00478374 and NCT0085528. Interestingly, treatment of the 3p/3sp HCC model with both sorafenib and erlotinib (currently used in a phase III study) also revealed to be effective at reduced concentrations while targeting both epithelial and mesenchymal HCC cells (data not shown).

Our data revealed a significant upregulation of $\text{SPARC}$ in mesenchymal 3p cells which has been reported in patient samples at advanced stages of disease (24). The role of this protein in hepatocarcinogenesis, however, is rather ambiguous by acting either as a tumor promoter (25) or tumor suppressor (24). Notably, we could show for the first time that $\text{SPARC}$ is epigenetically up-regulated in human HCC progression by demethylation. Further studies will reveal the consequences of $\text{SPARC}$ overexpression in hepatocarcinogenesis. In the same line, aCGH analysis revealed homozygous loss of the Wnt
signaling component AXIN1 as well as of the cation-selective channel TRPM3. Although deletion of TRPM3 has not been reported in cancer progression, AXIN1 was found to be mutated in 5% to 25% of HCC patients and associated with poor differentiation (26). These findings show that our EMT model is genetically well defined and thus particularly valid to study human HCC progression without unknown genetic variations in widely used human hepatoma cell lines.

Human models of hepatocellular EMT which reliably reflect HCC progression are invaluable tools in preclinical studies for (i) the identification of molecular mechanisms underlying HCC progression, (ii) the pharmacological determination of dose-effect relationships and thus the efficacy of single and combined treatments with novel and currently used anti-cancer drugs, and (iii) the (re)-evaluation of drug target specificity and pleiotropic effects after drug application.

Disclosure of Potential Conflicts of Interest
No potential conflicts of interest were disclosed.

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