Epithelial–Mesenchymal Transitioned Circulating Tumor Cells Capture for Detecting Tumor Progression

Arun Satelli1, Abhisek Mitra1, Zachary Brownlee1, Xueqing Xia1, Seth Bellister2, Michael J. Overman3, Scott Kopetz2, Lee M. Ellis3, Qing H. Meng4, and Shulin Li1,5

Abstract

Purpose: This study aimed to detect cell-surface vimentin (CSV) on the surface of epithelial–mesenchymal transitioned (EMT) circulating tumor cells (CTC) from blood of patients with epithelial cancers.

Experimental Design: In this study, 101 patients undergoing postsurgery adjuvant chemotherapy for metastatic colon cancer were recruited. EMT CTCs were detected from blood of patients using the 84-1 monoclonal antibody against CSV as a marker. EMT CTCs isolated were characterized further using EMT-specific markers, fluorescent in situ hybridization, and single-cell mutational analysis.

Results: Using the 84-1 antibody, we detected CSV exclusively on EMT CTCs from a variety of tumor types but not in the surrounding normal cells in the blood. The antibody exhibited very high specificity and sensitivity toward different epithelial cancer cells. With this antibody, we detected and enumerated EMT CTCs from patients. From our observations, we defined a cutoff of ≤5 or ≥5 EMT CTCs as the optimal threshold with respect to therapeutic response using ROC curves. Using this defined threshold, the presence of ≥5 EMT CTCs was associated with progressive disease, whereas patients with ≤5 EMT CTCs showed therapeutic response.

Conclusion: Taken together, the number of EMT CTCs detected correlated with the therapeutic outcome of the disease. These results establish CSV as a universal marker for EMT CTCs from a wide variety of tumor types and thus provide the foundation for emerging CTC detection technologies and for studying the molecular regulation of these EMT CTCs. Clin Cancer Res; 21(4); 899–906. ©2014 AACR.
Translational Relevance

In the present study, epithelial–mesenchymal transitioned (EMT) circulating tumor cells (CTC) were detected and isolated from patients with colon cancer using cell-surface vimentin (CSV) as a newly developed mesenchymal CTC marker. Patients with progressive disease showed an increasing number of EMT CTC in comparison with patients who are responding/have stable disease. This is of potential clinical importance, as it provides evidence that EMT CTC are critical in detecting patients with tumor progression and are missed using the conventional EpCAM-based CTC isolation technologies. These results help provide more convincing evidence for using EMT CTC detection in future clinical practice.

Materials and Methods

Cell culture

All cell lines used in this study were obtained from the American Type Culture Collection and were grown according to the supplier’s recommendations. All cell lines were cultured within three passages from the time of purchase. Cell lines with no particular culture recommendations were grown in DMEM/F12 medium (Sigma-Aldrich) with 10% fetal bovine serum, 1% L-glutamine, and 0.1% penicillin/streptomycin (Gibco; Invitrogen). NCM-356, normal human colonic cell line was used as control. Primary cultures obtained from human colon (HPC), liver (HLM, primary colon cancer metastasized to liver), and lung (CPm, primary colon cancer metastasized to lung) cancers were obtained after cell dissociation from the primary tumors and cultured in DMEM/F-12 medium with 10% heat-inactivated fetal bovine serum, 1% l-glutamine, 100 μg/mL Primocin (Invitrogen), and 0.1% penicillin/streptomycin. Medium was changed once every 4 days. All cells were maintained at 37°C in an incubator with a 5% CO₂.

Geltrex thin layer method

HPC-1 cells were grown on Geltrex reduced growth factor basement membrane matrix (Invitrogen). This matrix is a soluble form of basement membrane purified from Engelbreth-Holm-Swarm tumor, which gels at 37°C to form a reconstituted basement membrane that provides the matrix for the culture of cells. Major components of Geltrex include various growth factors and laminin, collagen IV, and entactin. According to the manufacturer’s recommendation, Geltrex was thawed on ice and 100 μL was used to coat the Lab-Tek chamber slides (Thermo) 1 hour before the cells were plated. Later, 1,000 HPC-1 cells in 100 μL of cold serum-free DMEM/F-12 medium with 2% Geltrex were plated on the chamber slides with a thin gel coating. The cells were grown at 37°C in a humidified atmosphere of 5% CO₂ in air and observed through a bright-field microscope for the formation of spheres. Sphere-containing chamber slides were then processed for immunofluorescence staining.

Study cohort

Patients of any age with metastatic colorectal cancer refractory to 5-fluorouracil who were undergoing palliative chemotherapy at The University of Texas MD Anderson Cancer Center were eligible for this study. Patients were at different stages of treatment with different therapeutic regimens as listed in the Supplementary Table S1. Routine diagnostic workup included diagnostic imaging, chest X-rays, bone scan, blood sampling, and clinical examination. Study age matched blood samples from healthy blood donors were obtained from the Gulf Coast Blood Center in Houston, TX. Nine patients had died during the course of this study. For preliminary analysis only, blood samples from patients with breast, bladder, and liver cancer were collected.

Blood collection and processing

Human blood samples for CTC analysis were obtained after informed consent had been obtained from the patient or blood donor, per the Institutional Review Board protocol at the MD Anderson Cancer Center. CTC detection was conducted as and when possible; no attempt made to reach a defined statistical power. At any given blood draw, a maximum of 7.5 mL of blood was obtained using CPT Vacutainer tubes (BD Biosciences). Single nucleated cells were isolated within 48 hours of blood collection, per the manufacturer's recommendation. Cells were then washed in phosphate-buffered saline (PBS) and used for further analysis. Neither patients nor clinicians were informed of the results from the CTC analysis.

84-1⁺ Cell selection

Method of cell isolation, confirmation for positive selection and validation steps were described in (9). Briefly, first CD45⁻ cells were depleted using an EasySep human CD45 depletion kit (StemCell Technologies) according to the manufacturer’s recommendation. To minimize nonspecific binding, antibody against human Fc receptor (Millenyi Biotec) was added to the cocktail. Second, the CD45⁻ cell fraction was subjected to 84-1⁺ selection. Cells were labeled with the 84-1 anti-vimentin antibody, and later mouse IgG-binding microbeads (Millenyi Biotec) were added to the mixture. 84-1⁺ Cells were then extracted using the magnetic column according to the manufacturer’s recommendation (Millenyi Biotec). The cells thus obtained were 84-1⁻ and CD45⁻ and ready for further analysis.

Antibodies

Antibodies against the specific markers EpCAM (D1B3) Rabbit mAb #2626, SLUG (C19G7) Rabbit mAb #9585, E-cadherin (24E10) Rabbit mAb #3193, β-catenin (D10A8) XP Rabbit mAb #8480, and c-myc (D84C12) XP Rabbit mAb #5605 were obtained from Cell Signaling Technology. Antibodies against the specific markers FOXC2 (AF5044), TWIST-1 (AF6230), and SNAIL (AF3639) were obtained from R&D Systems.

Flow cytometry

A total of 5 × 10⁵ cells were detached with a nonenzymatic dissociation buffer, washed, and stained for 20 minutes on ice in the dark. For CSV analysis, cells were stained with the 84-1 monoclonal antibody we developed (1:100); mouse primary
antibody (Invitrogen) was used as an isotype control. Later, cells were rinsed twice in PBS and labeled for secondary antibody using Alexa Fluor–405, –488, or –555 secondary antibody (Invitrogen). Cells were then washed twice in PBS and immediately used for data acquisition using an Attune flow cytometer (Applied Biosystems). Fifty thousand cells were counted for the analysis. The data were analyzed using the FlowJo software (TreeStar).

**Spiking assay**

To demonstrate the precision and reproducibility of CTC capture by the 84-1 antibody, cultured cancer cells were spiked into blood collected from healthy donors. For the sensitivity assay, approximately 2, 5, 10, or 25 Calcein AM-labeled (EMD Bioscience) HLM-3 cells were spiked into a sample containing 1 × 10^6 peripheral blood mononuclear cells. To demonstrate specificity, approximately 5 Calcein AM-labeled HLM-3 cells were spiked into samples containing 1 × 10^6, 2 × 10^6, or 2.5 × 10^6 peripheral blood mononuclear cells. All cells used for spiking experiments were subjected to 84-1 selection a day before the spiking analysis to increase the fraction of 84-1+ cells. For cell counting, cells were harvested in culture medium and then serially diluted to achieve the required counts, which were then confirmed in a series of 5-μL spots under a microscope. If lower or higher numbers of cells were observed, we calculated the necessary counts of cells required to be spiked. Spiking experiments were performed in triplicate to ensure the sensitivity and specificity of the method. For negative controls, CSV+ HEK293T and NCM-356 cells were spiked into blood and analyzed for 84-1+ selection. Also, as an additional control mouse IgG was used for the isolation procedure and probed with anti-mouse secondary antibody.

**Statistical analysis**

All statistical analyses were performed using the GraphPad Prism software, where P < 0.05 was considered significant. Differences in baseline characteristics between treatment responders and nonresponders were analyzed using the Fisher exact and t tests. Diagnostic performance of CTC count was assessed by constructing a receiver operating characteristic (ROC) curve, and was further evaluated by calculating the area under each ROC curve (AUC-ROC; ref. 13). An AUC-ROC of value 1 denotes that the test method is able to discriminate perfectly, whereas an AUC-ROC of value 0.5 would denote a worst discrimination of the test. P value was calculated for the difference between each AUC-ROC.
Microscopy image capture and analysis is included in Supplementary Methods.

Results

CSV expression is restricted to cancer cells

Because commercial antibodies against CSV are not available, we generated a CSV-specific monoclonal antibody, called 84-1, using a differential expression screening strategy described in ref. (3). Briefly, to screen for CSV-specific antibodies produced against full-length vimentin, we used the cell line LM7 (human metastatic osteosarcoma cells) to represent CSV-positive cells and the cell lines NCM-356 (human colon epithelial cells) and hFOB (human fetal osteoblasts) to represent CSV-negative cells. The monoclonal antibody had very high affinity for cancer cell CSV and did not bind to normal epithelial or mesenchymal cells. Screening for established cancer [GEO (colonic), MDA-MB-231 (breast), and PANC-1 (pancreatic)] and normal (HEK-293, NCM-356, and MCF-10A) cell lines indicated the presence of vimentin only on the surface of cancer cells (Fig. 1A). It is evident from these results that only a fraction of cells was positive for CSV. This fraction may be strongly associated with metastasis. Furthermore, our 84-1 antibody was specific to cancer cells and did not exhibit binding affinity toward any of the subsets of white blood cells. We have also analyzed several different established cancer cell lines (breast, liver, colon, brain, bladder, and pancreas) for CSV expression using flow cytometry and our results indicate that majority of these cancer cell lines are positive for CSV (Table 1). These results thus prove CSV to be an excellent universal marker for any given tumor type.

To confirm the surface expression of vimentin, we performed immunocytochemical analysis of human liver metastatic cells (HLM-3) and normal human colon cells (NCM-356). The results indicated that vimentin was present on the surface of the cancer cells (Fig. 1B) but not on the surface of the normal cells. In addition, vimentin colocalized with the cell-surface marker wheat germ agglutinin (WGA). Permeabilizing these cells revealed the presence of cytoplasmic vimentin in only the cancer cells and not in the normal cells (Supplementary Fig. S1A). These results confirmed that the surface expression of vimentin was restricted to cancer cells.

To analyze whether CSV-expressing cancer cells are metastatic, we used flow cytometry to analyze CSV expression in primary cancer cells isolated from human colon (HPC), human colon cells metastasized to the liver (HLM), and human colon cells metastasized to the lung (CPM). The results indicated overexpression of CSV in metastatic tumors compared with primary tumors (Fig. 1C), suggesting that CSV expression is mainly associated with metastasis and could serve as a potential biomarker for metastasis. This result also suggested that a subpopulation of primary colon cancer cells that express CSV have an invasive or metastatic phenotype and are shed into the blood circulation for spreading to distant organs. This possibility was supported by the observed presence of CSV+ cells at the periphery of the sphere in a three-dimensional HPC-derived sphere model (Fig. 1D). Cells at the periphery were more aggressive and invasive, which is supported by the increasing nuclear accumulation of β-catenin that denotes the invasive phenotype of these cells (ref. 14; Fig. 1E). From these observations, it was evident that CSV could serve as a specific marker for detecting metastatic cancer cells.

Table 1. Cell-surface vimentin expression analysis in different cancer cell lines

<table>
<thead>
<tr>
<th>Cell line</th>
<th>CSV</th>
<th>Cell line</th>
<th>CSV</th>
</tr>
</thead>
<tbody>
<tr>
<td>Breast</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>MCF-7 (H)</td>
<td>+</td>
<td>DLD-1 (H)</td>
<td>++</td>
</tr>
<tr>
<td>SKBR3 (H)</td>
<td>+</td>
<td>GEO (H)</td>
<td>++</td>
</tr>
<tr>
<td>MDA-MB-231 (H)</td>
<td>+</td>
<td>OS-187 (H)</td>
<td>++</td>
</tr>
<tr>
<td>MDA-MB-453 (H)</td>
<td>+</td>
<td>SW620 (H)</td>
<td>+</td>
</tr>
<tr>
<td>MDA-MB-453 (H)</td>
<td>++</td>
<td>SW480 (H)</td>
<td>+</td>
</tr>
<tr>
<td>4T1 (M)</td>
<td>+</td>
<td>HCT-116 (H)</td>
<td>+</td>
</tr>
<tr>
<td></td>
<td></td>
<td>HT-29 (H)</td>
<td>++</td>
</tr>
<tr>
<td>Liver</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>AMLC14 (M)</td>
<td>++</td>
<td>Caco-2 (H)</td>
<td>+</td>
</tr>
<tr>
<td></td>
<td></td>
<td>CT-26 (H)</td>
<td>+</td>
</tr>
<tr>
<td>Brain</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>SKNAS (H)</td>
<td>++</td>
<td>RT4V6 (H)</td>
<td>+</td>
</tr>
<tr>
<td>SKNB2 (H)</td>
<td>+++</td>
<td>T24 (H)</td>
<td>++</td>
</tr>
<tr>
<td>NACH (H)</td>
<td>+</td>
<td></td>
<td></td>
</tr>
<tr>
<td>SH-SYS (H)</td>
<td>++</td>
<td>Pancreas</td>
<td></td>
</tr>
<tr>
<td>LANS (H)</td>
<td>+++</td>
<td>PANC-1 (H)</td>
<td>++</td>
</tr>
<tr>
<td>KCN (H)</td>
<td>+</td>
<td>MiaPACA-2 (H)</td>
<td>+</td>
</tr>
<tr>
<td>DBT (M)</td>
<td>+</td>
<td></td>
<td></td>
</tr>
<tr>
<td>L231 (H)</td>
<td>+</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

NOTE: CSV was scored using flow cytometric analysis by measuring mean fluorescence intensity of CSV.
Abbreviations: H, human; M, mouse.
*+, ++, +++*: <2-, <4-, >4-fold presence compared with isotype control.

84-1 Antibody detects spiked cancer cells with high sensitivity and specificity

On the basis of our detection of CSV in a range of metastatic tumors, we postulated that CSV could serve as a biomarker to detect metastatic CTCs from epithelial cancers. We verified the detection of 84-1 HLM-3 cells, which were labeled with Calcein-AM tracking dye, and spiked different numbers of cells into 7.5 mL of normal human blood. After CD45 depletion and 84-1 detection, the cells were recovered by immunofluorescence staining. From fluorescence microscopy micrographs, it was evident that even a single labeled cell could be isolated from whole blood by using the 84-1 antibody (Fig. 2A). Because the sensitivity (limit of detection) and specificity (no background/unwanted cells) of detection are important parameters for using an antibody for CTC enumeration, we evaluated these parameters in our spiking assay using 84-1 HLM-3 cells. Linear regression of the number of detected tumor cells versus the number of tumor cells spiked yielded a correlation coefficient ($R^2$) of 0.971 ($P < 0.001$; Fig. 2B) with approximately 100% specificity. Normal cells spiked in the blood were undetectable by the 84-1 antibody and tumor cells were undetectable using mouse IgG used as a control. Taken together, these results indicated a very high specificity and sensitivity of the antibody to detect spiked cells at various concentrations.

84-1 Antibody detects EMT CTCs that express EMT-specific markers

Because our spiking assays showed very high specificity for spiked cancer cells, we used the above-described method to detect CTCs from patients with colorectal cancer as well as several methods to confirm the cancerous phenotype of these isolated CTCs. β-Catenin and c-myc proteins are overexpressed in colorectal cancers (15), and in our study we detected and isolated 84-1+ CD45+ CTCs from blood of patients with colorectal cancer and confirmed the overexpression of these proteins in these cells (Fig. 2C). The localization of these proteins in the nucleus indicated that these were active transitioned cells (16). For further
markers (18) revealed increased expression of FOXC2, SNAIL, TWIST-1, SLUG, EpCAM, and E-cadherin with the respective antibodies. Scale bar, 5 μm.

Figure 2.
Spiking assay and detection of CTCs from human colorectal cancer patients. A, detection of HLM-3 cells labeled with tracker dye Calcein-AM (CAM; green) that were spiked into 7.5 mL of blood using fluorescence microscopy. Cells were also stained for nuclei (with DRAQ5; blue) and vimentin (with the 84-1 antibody; red). B, regression analysis of capture efficiency for up to 25 HLM-3 cells spiked in human blood. C, analysis of 84-1⁺ CD45⁻ CTCs from human colon cancer samples that were isolated and stained for nuclei (with DRAQ5; blue), total vimentin (with 84-1; green), β-catenin (red), and c-myc (red). The results indicated complete nuclear localization of β-catenin and c-myc. Scale bar, 10 μm. D, mutational analysis of KIT in colon cancer–derived CTC. E, dual-probe FISH with a centromere probe for chromosome 8 (red) and region-specific probe for KRAS (green). Three chromosome 8 signals and three KRAS signals were detected in the cell at top, whereas two chromosome 8 signals and four KRAS signals were detected in the cell at bottom. Nuclei were counterstained with DAPI (blue). F, analysis of colon cancer–derived 84-1⁺ CD45⁻ CTCs from patient samples for specific molecular EMT markers. CTCs were stained for vimentin (with 84-1 antibody) and for FOXC2, SNAIL, TWIST-1, SLUG, EpCAM, and E-cadherin with the respective antibodies. Scale bar, 5 μm.

validation of 84-1⁺ CD45⁻ CTCs isolated from all cancers, we subjected these cells to cancer-specific mutation analysis. A representative colon cancer sample was positive for mutations in KIT, KRAS, and APC; however, CTCs isolated from this patient harbored a mutation in KIT only (Fig. 2D). Mutational analysis from other patients is listed in Supplementary Table S1. Heterogeneity among CTCs from the same patient have been reported (17), and from our observations it was interesting to note that CTCs harbored only specific mutations.

As a second step for validation, we used fluorescent in situ hybridization (FISH) to detect amplification of the KRAS gene and chromosome 8 signals in EMT CTCs from a representative sample (Fig. 2E). The FISH data indicated a heterogeneous amplification of targets, again highlighting the heterogeneous nature of these CTCs. Taken together, our results indicated that the cells isolated from the blood of patients with cancer were of cancerous origin and were heterogeneous.

Because we were able to detect CSV⁺ CTCs in cancers of epithelial origin and establish vimentin as a marker for EMT, we hypothesized that 84-1⁺ CD45⁻ CTCs had undergone EMT. An analysis of vimentin-positive CTCs with known EMT-specific markers (18) revealed increased expression of FOXC2, SNAIL, TWIST-1, and SLUG and markedly decreased expression of epithelial-specific markers E-cadherin and EpCAM (Fig. 2F), thus confirming the mesenchymal nature of 84-1⁺ CD45⁻ CTCs. Expression of EMT-inducing transcription factors, including the same four proteins, has been associated with tumor invasion and metastasis (18), and TWIST-1 (19) and SLUG (20) overexpression has been shown to be independent prognostic parameters for poor survival in patients with colorectal carcinoma. Thus, “metastatic-like CTCs” might be detected using CSV as a marker.

Moreover, we detected EMT CTCs from other solid tumors, including those of the breast, bladder, and liver (Fig. 3A), which suggests that CSV has a universal capacity for detecting EMT CTCs. With the use of CSV as a marker, further characterization of transitioned CTCs and better understanding of their contribution to the metastatic spread of a wide variety of cancer types are now possible.

84-1⁺ CTCs isolated from patients with colorectal cancer correlate with disease status

Because we were able to confirm that the CTCs detected with our anti-CSV antibody were cancerous and had transitioned to the mesenchymal phenotype, we next tested human blood samples from 12 healthy blood donors and from 101 patients with metastatic colorectal cancer for 84-1⁺ CD45⁻ CTCs. In this
study, fluorescent images were reviewed independently by researchers blinded to treatment and outcome. No adverse events or complications had been reported during the blood collections. Blood samples from the healthy donors were analyzed under the same conditions. None of the healthy donors had detectable CTCs, indicating a high specificity of the 84-1 antibody. CTCs were detectable in 85 of the 101 (84%) metastatic colorectal cancer patient samples. The number of CTCs isolated from these patients ranged from 0 to 450 per mL (Fig. 3B). We divided the patient population into two groups based on RECIST guidelines: (i) stable or responding disease, (ii) progressive disease. Of these 101 patients, 54 (53%) exhibited progressive disease, whereas 5 patients (5%) with a count of ≥5 per mL had stable disease. This discrepancy might be attributable to the clinical stage of the disease and the treatment type used for each patient. From the analysis, it was observed that CTCs are better prognostic markers for evaluating therapeutic responses.

Sensitivity, specificity, and positive predictive value
From our study data, we determined that enumerating EMT CTCs is highly specific (91%) in identifying the progressive cell population and has a positive predictive value of 87% for the therapeutic outcome of the disease.

Discussion
Many approaches have been implemented to detect CTCs from blood samples, including flow cytometry, size-based separation, and optical imaging-based technology (21). Although these techniques are relatively new, antibody-based separation of CTCs has several advantages that are already making those technologies obsolete. One of the most successful antibody-dependent technologies is the CellSearch (22) method by Veridex, which is the only FDA-approved CTC detection platform available for detecting CTCs from patients. CellSearch technology is dependent on anti-EpCAM antibody for isolating CTCs and on staining with cytokeratins from the blood of patients with epithelial cancers. Although this platform has gained much attention, in recent years, it has been shown that by using EpCAM, cytokeratins, or both as a CTC target, CellSearch and other technologies have overlooked CTCs that have undergone EMT and have lost the ability to express EpCAM (3) and other epithelial markers. EMT CTCs have been shown to correlate with disease progression (4) or relapse and their presence could be a key determinant of metastasis and poor prognosis.

The main goal of our laboratory was to identify EMT CTCs from the blood of patients by using a single, specific marker instead of a multitude of markers and probes. As a first step toward this goal, we analyzed the proteins that are transported to the cell surface of cancer cells during EMT. We previously demonstrated that vimentin is an EMT marker and is localized on the surface of cancer cells during EMT. We previously demonstrated that vimentin is an EMT marker and is localized on the surface of cancer cells during EMT.

CTCs is highly specific (91%) in identifying the progressive cell population and has a positive predictive value of 87% for the therapeutic outcome of the disease.

Discussion
Many approaches have been implemented to detect CTCs from blood samples, including flow cytometry, size-based separation, and optical imaging-based technology (21). Although these techniques are relatively new, antibody-based separation of CTCs has several advantages that are already making those technologies obsolete. One of the most successful antibody-dependent technologies is the CellSearch (22) method by Veridex, which is the only FDA-approved CTC detection platform available for detecting CTCs from patients. CellSearch technology is dependent on anti-EpCAM antibody for isolating CTCs and on staining with cytokeratins from the blood of patients with epithelial cancers. Although this platform has gained much attention, in recent years, it has been shown that by using EpCAM, cytokeratins, or both as a CTC target, CellSearch and other technologies have overlooked CTCs that have undergone EMT and have lost the ability to express EpCAM (3) and other epithelial markers. EMT CTCs have been shown to correlate with disease progression (4) or relapse and their presence could be a key determinant of metastasis and poor prognosis.

The main goal of our laboratory was to identify EMT CTCs from the blood of patients by using a single, specific marker instead of a multitude of markers and probes. As a first step toward this goal, we analyzed the proteins that are transported to the cell surface of cancer cells during EMT. We previously demonstrated that vimentin is an EMT marker and is localized on the surface of cancer cells during EMT.
transported to the surface); we were unable to detect this antigen on the cell surface of cancer cells. Therefore, we created the specific monoclonal antibody 84-1 to fill this gap in technology. This antibody showed very high specificity toward cancer cells and had very high sensitivity as assessed from spiking assays (see Fig. 2B). These characteristics thus fulfilled the basic requirements for establishing a CTC marker: sensitivity, specificity, and reproducibility. Moreover, this technique of isolating CTCs provides an opportunity to study the morphologic and other characteristics of these CTCs and to further use a wide variety of markers, including protein markers and FISH probes (Fig. 2E and F).

EMT involves a functional transition of epithelial cells into mobile mesenchymal cells (23). The common mesenchymal cell markers used to identify EMT cells include FOXC2 (24), TWIST1 (19), SNAIL (25), SLUG (20), and vimentin (5). Although negative staining results for epithelial markers suggest EMT, researchers mainly rely on mesenchymal EMT markers. In this study, we showed that EMT CTCs are in fact associated with multiple EMT markers. However, it remains unclear whether the expression of multiple EMT markers in different CTCs is heterogeneous. Also, colocalization of epithelial and EMT-specific markers may define an intermediate phenotype of EMT cells (4), i.e., cells that are in transition. In our study, we observed that most EMT CTCs had lost the ability to express EpCAM and just a few of the EMT CTCs still retained the epithelial phenotype. Not much is known about the function or role of intermediate EMT cells.

Cytoplasmic vimentin is overexpressed during EMT and is associated with metastasis, invasion, and proliferation (5). It is still unclear what the role of vimentin transported to the cell surface is. In this study, we observed a positive correlation between CSV EMT CTCs and disease progression, which suggests a role for CSV in promoting disease progression. Because vimentin is an intermediate filament protein and is known to form vimentin adhesion networks (5), CSV could be involved in routing CTCs to the metastatic site and assisting in the invasion process to reseed the metastatic niche, thus promoting tumor progression. Also, CSV EMT CTCs might represent a unique subset of CTCs that are chemoresistant and thus do not respond to chemotherapeutic regimens. In addition, CSV could be associated with cancer stem-like cells, which have the propensity to form stable colonies. These possibilities need to be tested to confirm the role of CSV in cancer.

CTCs have been used in several studies to monitor response to chemotherapy (26). However, an exclusive correlation between EMT CTC count and disease progression has never been reported. To our knowledge, we are the first to report a correlation between therapeutic outcome in metastatic patients with colorectal cancer and EMT CTC count. Because our cohort consisted of only patients undergoing chemotherapy for metastatic colorectal cancer, the results suggested that the CTCs detected in the bloodstream were released mainly from the metastatic sites. Also, from our study, it is evident that these CTCs were heterogeneous, so these cells should be assessed in regard to their propensity to successfully form metastases or reseed the primary tumor. Capturing and culturing these CTCs and determining their propensities would allow characterization their phenotypes using in vitro and in vivo modeling, studies of which are currently in progress.

Our study had a few limitations. For example, we retrospectively analyzed information on patients with colorectal cancer treated with different chemotherapeutic protocols. Because this was a pilot study to assess the therapeutic outcome based on EMT CTC counts, we recruited postsurgery patients who were undergoing chemotherapy. It would be interesting to follow up with a large group of patients at different stages of treatment (before surgery, preneoadjuvant chemotherapy, postneoadjuvant chemotherapy, and after surgery). Also, long-term follow-up would be essential to understanding how EMT CTCs could be used to predict relapse. Technical limitations of the study included the optimization of assays, positive selection of cancer cells a day before spiking experiments, timing of blood collection, and preservation of the integrity of the CTCs in blood. In addition, because several types of host cells in the blood are mesenchymal and express vimentin, the CTCs isolated must be tested for EMT-specific markers that are absent in host cells. The protein Plastin3 (11) has been used to identify EMT CTCs from blood samples of patients with colon cancer, but it has not been tested with other types of solid tumors. We presented here, for the first time, evidence that EMT CTCs can be detected in multiple solid tumor types by using a single, specific marker.

In conclusion, we demonstrated that CSV is a marker for EMT CTCs and that by using the 84-1 anti-vimentin antibody we developed, these CTCs can be isolated from the blood of cancer patients with metastatic colorectal cancer. A key protein that is overexpressed during EMT, vimentin has been shown to be overexpressed in other types of cancers that undergo EMT, thereby making it a universal EMT CTC marker. Also, by using this antibody, we can not only isolate or detect EMT CTCs but also characterize the nature of these cells by using other specific markers. Therefore, isolating CSV EMT CTCs will help us understand the metastatic precursor cell subpopulation and will help in developing novel diagnostic, treatment, and prognostic options based on therapeutic monitoring.

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

Authors’ Contributions
Conception and design: A. Satelli, S. Kopetz, L.M. Ellis, S. Li
Development of methodology: A. Satelli, A. Mitra, X. Xia, Q.H. Meng
Acquisition of data (provided animals, acquired and managed patients, provided facilities, etc.): A. Satelli, A. Mitra, Z. Brownlee, S. Bellister, M.J. Overman, S. Kopetz, Q.H. Meng
Analysis and interpretation of data (e.g., statistical analysis, biostatistics, computational analysis): A. Satelli, Z. Brownlee, S. Kopetz, Q.H. Meng, S. Li
Writing, review, and/or revision of the manuscript: A. Satelli, Z. Brownlee, M.J. Overman, S. Kopetz, S. Li
Administrative, technical, or material support (i.e., reporting or organizing data, constructing databases): A. Satelli
Study supervision: A. Satelli, Q.H. Meng

Grant Support
The work in the authors’ laboratory was supported by a grant from the NIH to S. Li (NIH RO1CA120895). The authors thank the Cancer Center Support Grant (CCSG), Hybridoma, Flow Cytometry, and DNA Analysis Core facilities at MD Anderson Cancer Center (MDACC) for their assistance. The costs of publication of this article were defrayed in part by the payment of page charges. This article must therefore be hereby marked advertisement in accordance with 18 U.S.C. Section 1734 solely to indicate this fact.

Received April 11, 2014; revised November 14, 2014; accepted December 1, 2014; published OnlineFirst December 16, 2014.
References

Epithelial–Mesenchymal Transitioned Circulating Tumor Cells Capture for Detecting Tumor Progression


Updated version
Access the most recent version of this article at:
doi:10.1158/1078-0432.CCR-14-0894

Supplementary Material
Access the most recent supplemental material at:
http://clincancerres.aacrjournals.org/content/suppl/2014/12/17/1078-0432.CCR-14-0894.DC1

Cited articles
This article cites 26 articles, 10 of which you can access for free at:
http://clincancerres.aacrjournals.org/content/21/4/899.full.html#ref-list-1

Citing articles
This article has been cited by 3 HighWire-hosted articles. Access the articles at:
/content/21/4/899.full.html#related-urls

E-mail alerts
Sign up to receive free email-alerts related to this article or journal.

Reprints and Subscriptions
To order reprints of this article or to subscribe to the journal, contact the AACR Publications Department at pubs@aacr.org.

Permissions
To request permission to re-use all or part of this article, contact the AACR Publications Department at permissions@aacr.org.