Hematogenous Dissemination of Hepatocytes and Tumor Cells after Surgical Resection of Hepatocellular Carcinoma: A Quantitative Analysis

Ivy H. N. Wong,1 Wan Y. Lau, Thomas Leung, Winnie Yeo, and Philip J. Johnson

Departments of Anatomical and Cellular Pathology [I. H. N. W.], Surgery [W. Y. L.], and Clinical Oncology [T. L., W. Y., P. J. J.], The Chinese University of Hong Kong, Prince of Wales Hospital, Shatin, New Territories, Hong Kong Special Administrative Region

ABSTRACT

The only hope of long-term survival for patients with hepatocellular carcinoma (HCC) is surgical resection or liver transplantation. However, recurrence or metastasis formation is common after surgery. We aim to assess whether surgical resection leads to hematogenous dissemination of malignant and nontumor hepatocytes and determine the quantity and timing of hepatocyte shedding into the circulation. Using semiquantitative reverse transcription-PCR for α-fetoprotein (afp) and albumin (alb) mRNAs, we measured the mass of malignant and nontumor hepatocytes in 23 peripheral blood samples collected preoperatively, intraoperatively, and postoperatively from 13 HCC patients. We compared these data with those in 54 control samples collected from 24 healthy subjects and patients with chronic hepatitis/cirrhosis and 10 hepatocellular adenoma patients who underwent resection. Clinopathological information of HCC patients was obtained during 3-year follow-up. In 100% (23 of 23) of HCC and adenoma patients, alb mRNA levels increased 10–106-fold intraoperatively and then markedly declined within 8 weeks after operation. Levels of afp mRNA increased 5–7600-fold preoperatively in 8% (1 of 13) and postoperatively in 70% (9 of 13) of HCC patients. All five HCC patients with persistently elevated afp mRNA levels died from intrahepatic/extrahepatic metastasis, liver recurrence, or persistent HCC within 1 year after surgery. The absence/clearance of afp mRNA in 75% (six of eight) of survivors was strongly associated with the absence of metastasis/recurrence (P = 0.02). We present evidence that alb-expressing hepatocytes are released intraoperatively into the circulation, and afp-expressing tumor cells are disseminated mostly postoperatively that many potentially be the source of recurrence or metastasis. Sequential quantification of both alb and afp mRNAs may provide insights for risk assessment and prognostic indication.

INTRODUCTION

The only hope of long-term survival for patients with HCC3 is surgical resection or liver transplantation. However, after apparently curative resection, recurrences are common, and they largely account for poor survival rates of only 68.5% at 1 year and 31.9% at 5 years after resection, and >80% of recurrences are intrahepatic (1–3). Liver recurrences are presumably caused by the incomplete resection of HCC, leaving behind residual tumor at the site of the resected stump, the presence of undetectable regional micrometastasis, and/or the spillage of tumor cells into the bloodstream during surgical manipulation (4, 5). The regenerating liver, after resection, may be a particularly fertile ground for these tumor cells to proliferate.

It has been conceived that one may infer the presence of circulating HCC cells and hence the potential for metastasis if liver-specific alb and afp mRNAs are detected in peripheral blood (6–12). There has been emerging evidence suggesting that afp mRNA detection is strongly associated with the presence of metastasis or liver recurrence, particularly after surgery (8–12). Nonetheless, extremely sensitive nested RT-PCR applied in these studies might possibly give rise to false positivity because nontumor hepatocytes can also express afp mRNA at low levels. In addition, “illegitimate transcription” among normal PBMCs is a potential problem that needs to be addressed (13). To distinguish between the presence of circulating HCC cells/nontumor hepatocytes and normal PBMCs, we have developed a sufficiently sensitive and well-optimized semiquantitative RT-PCR method for measuring levels of afp and alb mRNAs with reference to the equivalent number of HepG2 cells (14).

In the present study, we aimed to assess whether surgical maneuver or resection of HCC could lead to hematogenous dissemination of malignant and nontumor hepatocytes. The quantity and timing of hepatocytes shedding into the circulation of HCC patients were also monitored by semiquantitative RT-PCR before, during, and after surgery. To determine the clinical significance of the findings, we correlated the numbers of circulating HCC cells and nontumor hepatocytes in 23 peripheral blood mononuclear cell.

Received 6/21/99; revised 9/15/99; accepted 9/27/99.

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.

1 Supported by the Strategic Grant from the Chinese University of Hong Kong and the Hong Kong Research Grants Council RGC 4263/97M.

2 To whom requests for reprints should be addressed, at Department of Anatomical and Cellular Pathology, Prince of Wales Hospital, Shatin, New Territories, Hong Kong Special Administrative Region. Phone: 852-2632-2344; Fax: 852-2712-2719; E-mail: b730764@mailserv.cuhk.edu.hk.

3 The abbreviations used are: HCC, hepatocellular carcinoma; RT-PCR, reverse transcription-PCR; afp or AFP, α-fetoprotein; alb, albumin; PBMC, peripheral blood mononuclear cell.
cytes detected with the clinical outcomes of the patients studied in 3-year follow-up.

PATIENTS AND METHODS

Patients. With informed consent and ethics approval from the Ethics Committee of the Chinese University of Hong Kong, 83 peripheral blood samples were collected during preoperative, intraoperative, and postoperative periods from 23 patients with HCC or hepatocellular adenoma who underwent surgical resection with curative intent. Preoperative blood samples were collected from the patients studied at least 1 h before surgery. Intraoperative blood samples were collected immediately after tumor resection. Postoperative blood samples were collected at 1–7 months after surgery. The diagnosis of HCC was confirmed histologically on each resected specimen where the tumor size and the mass of hepatectomy were measured. The 10 patients with hepatocellular adenoma served as control subjects undergoing surgical resection. As negative controls for semi-quantitative RT-PCR, 24 peripheral blood samples were collected from healthy subjects and patients with chronic hepatitis or cirrhosis. HCC patients were regularly assessed for tumor recurrence by the measurement of serum AFP, ultrasound examination with computed tomography, and hepatic angiography as appropriate. Clinical and histopathological features of the HCC patients studied were obtained during 3-year follow-up to evaluate the clinical significance of the data (Table 1).

PBMC Isolation and RNA Extraction. PBMCs were isolated by Ficoll-Paque (Pharmacia, Biotech, Uppsala, Sweden) from 20 ml of citrated blood collected from the patients and controls. After washing in 30 ml of PBS and centrifugation at 100 × g for 10 min, the cell pellet was resuspended in 1 ml of PBS, and the number of PBMCs was counted in a hemocytometer. After centrifugation, the cell pellet was resuspended in 0.5 ml of guanidinium thiocyanate solution, and total RNA was extracted by a single-step method (15).

Cell Culture. The hepatoblastoma cell line HepG2 (American Type Culture Collection, Rockville, MD) was used to establish calibration curves for assessing the amounts of albumin and α-fetoprotein mRNAs. The cell line was cultivated in RPMI 1640 added with penicillin, streptomycin, and 10% fetal bovine serum (Life Technologies, Inc., Gaithersburg, MD). The medium was changed every 3 days, and the cells were harvested when the growth was subconfluent. The total number of cells was then counted in a hemocytometer.

Spiking Experiment Using HepG2 Cells. To simulate the presence of HCC cells in the circulation of HCC patients, total RNA was first extracted from 107 PBMCs from a healthy subject and 106 HepG2 cells. Aliquots of total RNA from 106 PBMCs were mixed with HepG2 total RNA, corresponding to 1, 10, 102, 103, 104, 105, and 106 HepG2 cells (based on the calculation of the average amount of HepG2 total RNA extracted per cell). The RNA mixtures were then subject to semi-quantitative RT-PCR for constructing the calibration curves (14).

Semi-quantitative RT-PCR. Total RNA (1–2 μg) was denatured at 65°C for 2 min and annealed with 1 μg of random primers. After reverse transcription, the reactions were amplified by PCR for 30 cycles. Each cycle consisted of denaturation at 95°C for 1 min, annealing at 60°C for 1 min, and extension at 72°C for 1 min. The PCR products were analyzed by electrophoresis on 2% agarose gels and stained with ethidium bromide. The mRNA levels were quantified by densitometry of the autoradiograms and normalized to the levels of GAPDH mRNA afterwards.

Table 1. Clinical and histopathological features of HCC patients who underwent surgical resection

<table>
<thead>
<tr>
<th>Patients</th>
<th>Gender/Age</th>
<th>HBsAg</th>
<th>Cirrhosis</th>
<th>Tumor size</th>
<th>Mass of hepatectomy</th>
<th>Resection margin</th>
<th>Metastasis/Recurrence</th>
<th>afp mRNA level</th>
<th>Clinical status</th>
</tr>
</thead>
<tbody>
<tr>
<td>P1</td>
<td>M55</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>P2</td>
<td>M52</td>
<td>+</td>
<td></td>
<td>2.5 × 5.3</td>
<td>195 g</td>
<td>U</td>
<td>&lt;0.3 (T/NC)</td>
<td>3146 A</td>
<td>D of disease (198)</td>
</tr>
<tr>
<td>P3</td>
<td>M53</td>
<td></td>
<td></td>
<td>2.5 × 5.3</td>
<td>195 g</td>
<td>U</td>
<td>&lt;0.3 (T/NC)</td>
<td>3146 A</td>
<td>D of disease (198)</td>
</tr>
<tr>
<td>P4</td>
<td>M46</td>
<td>+</td>
<td></td>
<td>2.5 × 5.3</td>
<td>195 g</td>
<td>U</td>
<td>&lt;0.3 (T/NC)</td>
<td>3146 A</td>
<td>D of disease (198)</td>
</tr>
<tr>
<td>P5</td>
<td>M54</td>
<td>+</td>
<td></td>
<td>2.5 × 5.3</td>
<td>195 g</td>
<td>U</td>
<td>&lt;0.3 (T/NC)</td>
<td>3146 A</td>
<td>D of disease (198)</td>
</tr>
<tr>
<td>P6</td>
<td>M47</td>
<td>+</td>
<td></td>
<td>2.5 × 5.3</td>
<td>195 g</td>
<td>U</td>
<td>&lt;0.3 (T/NC)</td>
<td>3146 A</td>
<td>D of disease (198)</td>
</tr>
<tr>
<td>P7</td>
<td>M48</td>
<td>+</td>
<td></td>
<td>2.5 × 5.3</td>
<td>195 g</td>
<td>U</td>
<td>&lt;0.3 (T/NC)</td>
<td>3146 A</td>
<td>D of disease (198)</td>
</tr>
<tr>
<td>P8</td>
<td>M49</td>
<td>+</td>
<td></td>
<td>2.5 × 5.3</td>
<td>195 g</td>
<td>U</td>
<td>&lt;0.3 (T/NC)</td>
<td>3146 A</td>
<td>D of disease (198)</td>
</tr>
<tr>
<td>P9</td>
<td>M50</td>
<td>+</td>
<td></td>
<td>2.5 × 5.3</td>
<td>195 g</td>
<td>U</td>
<td>&lt;0.3 (T/NC)</td>
<td>3146 A</td>
<td>D of disease (198)</td>
</tr>
<tr>
<td>P10</td>
<td>M51</td>
<td>+</td>
<td></td>
<td>2.5 × 5.3</td>
<td>195 g</td>
<td>U</td>
<td>&lt;0.3 (T/NC)</td>
<td>3146 A</td>
<td>D of disease (198)</td>
</tr>
<tr>
<td>P11</td>
<td>M52</td>
<td>+</td>
<td></td>
<td>2.5 × 5.3</td>
<td>195 g</td>
<td>U</td>
<td>&lt;0.3 (T/NC)</td>
<td>3146 A</td>
<td>D of disease (198)</td>
</tr>
<tr>
<td>P12</td>
<td>M53</td>
<td>+</td>
<td></td>
<td>2.5 × 5.3</td>
<td>195 g</td>
<td>U</td>
<td>&lt;0.3 (T/NC)</td>
<td>3146 A</td>
<td>D of disease (198)</td>
</tr>
<tr>
<td>P13</td>
<td>M54</td>
<td>+</td>
<td></td>
<td>2.5 × 5.3</td>
<td>195 g</td>
<td>U</td>
<td>&lt;0.3 (T/NC)</td>
<td>3146 A</td>
<td>D of disease (198)</td>
</tr>
</tbody>
</table>
primers at 37°C for 10 min (14, 16). Reverse transcriptase reaction was carried out in 1× reverse transcriptase buffer [50 mM Tris-HCl (pH 8.3), 75 mM KCl, and 3 mM MgCl₂] with 10 mM DTT, 0.5 mM deoxynucleotide triphosphates, and 0.5 μl of RNase block (Stratagene, La Jolla, CA). cDNAs were synthesized at 37°C for 1 h using 200 units of Moloney murine leukemia virus reverse transcriptase (Life Technologies, Inc.), and the reaction was stopped at 70°C for 7 min (14, 16).

PCR amplification of alb and afp cDNAs was conducted using gene-specific primers that lie within different exons to give PCR products of 157 and 215 bp, respectively (14). For alb cDNA amplification, sense and antisense primers were 5’-TGC TTG AAT GTG CTG ATG ACA GGG-3’ and 5’-AAG GCA AGT CAG CAG GCA TCT CAT C-3’. For afp cDNA amplification, sense and antisense primers were 5’-TGC AGC CAA AGT GAA GAG GGA AGA-3’ and 5’-CAT AGC GAG CAG CCC AAA GAA GAA-3’. β₂-microglobulin mRNA served as an internal control to ensure that an exact amount of high integrity total RNA was reverse-transcribed to produce cDNAs in each assay (14, 16).

PCR was conducted in 1× PCR buffer [20 mM Tris-HCl (pH 8.4), 50 mM KCl, and 2.5 mM MgCl₂] with 0.2 mM dodeoxynucleotide triphosphates, 30 pmol of sense and antisense primers for alb or afp and β₂-microglobulin cDNAs, 3 μl of cDNAs and 2.5 units of Taq DNA polymerase (Life Technologies, Inc.). The optimized thermal profile was initiated with a 5-min denaturation at 94°C, followed by 30 cycles of 94°C for 1 min, 61°C for 1 min, and 72°C for 1 min, and a final extension at 72°C for 10 min (14). Aerosol-resistant pipette tips and separate areas were used for pre-PCR, PCR, and post-PCR procedures. Each sample was analyzed in duplicate. HepG2 RNA standards and multiple water blanks were analyzed in parallel with blood samples in each set of PCR. PCR products were loaded onto 2% agarose gels and stained with ethidium bromide.

The gene identity of the PCR product was verified by nonradioactive Southern blot analysis using an oligonucleotide labeled at the 3’ end with digoxigenin (14, 16). The alb probe was 5’-CAC AGC ATT CCT TCA GTT TAC TGG AGA TCG-3’. The afp probe was 5’-CAG CAT CGA TCC CAC TTT TCC AAG TTC CAG-3’. Chemiluminescent detection was conducted using CSPD (Boehringer Mannheim, Mannheim, Germany; Refs. 14 and 16). By imaging densitometry (Bio-Rad, Hercules, CA), the PCR signals for blood samples were quantified on the same Southern blots as the PCR products generated for establishing the HepG2 calibration curves (14).

RESULTS

Preoperative, Intraoperative, and Postoperative Levels of alb and afp mRNAs in Control Subjects. Two calibration curves were constructed by measuring levels of alb and afp mRNAs in 1–10⁶ HepG2 cells using semiquantitative RT-PCR (14). According to the HepG2 standard curves, levels of alb and afp mRNAs were quantified in 83 peripheral blood samples collected preoperatively, intraoperatively, and postoperatively from 23 patients with HCC or hepatocellular adenoma who underwent resection (Fig. 1) and 24 blood samples from healthy subjects and patients with chronic hepatitis/cirrhosis. Among all 10 adenoma patients studied, the alb mRNA levels detected before and after surgery were within the “reference range” determined for the 24 negative control subjects. Notably, the alb

![Southern blot analysis and quantification of alb and afp mRNA signals in peripheral blood samples collected preoperatively (Lane A), intraoperatively (Lane B), and 1–7 months postoperatively (Lanes C, D, and E) from HCC patients P1, P2, and P3.](image)
mRNA levels increased 10–10^4-fold during surgery in all of the adenoma patients studied. Conversely, the \( \text{afp} \) mRNA levels were within the reference range before, during, and after surgery in all 10 adenoma patients.

**Preoperative, Intraoperative, and Postoperative Levels of \( \text{alb} \) mRNA in HCC Patients.** In all 13 HCC patients studied, the \( \text{alb} \) mRNA levels detected preoperatively were within the reference range that might be attributed to "illegitimate transcription" (14) equivalent to 0–727 HepG2 cells per 20 ml of blood (Fig. 2). Levels of \( \text{alb} \) mRNA were then elevated 50–10^6-fold intraoperatively in all of the HCC patients studied (Fig. 2), which were significantly higher than the reference range (\( P < 0.00001 \), Mann-Whitney test). The number of \( \text{alb} \)-expressing cells detected ranged from 870 to 6.1 × 10^5 HepG2 cell equivalents per 20 ml of blood. The intraoperative \( \text{alb} \) mRNA level positively correlated with the mass of hepatectomy, regardless of tumor capsule formation (\( r = 0.50; \ P = 0.06 \)) but did not correlate with the tumor size (\( r = 0.01; \ P = 0.96 \)) or the resection margin (\( r = -0.02; \ P = 0.95 \); Spearman’s correlation; Table 1). Within 8 weeks after operation, the \( \text{alb} \) mRNA levels declined to the reference range in all of the HCC patients studied (Fig. 2).

**Preoperative, Intraoperative, and Postoperative Levels of \( \text{afp} \) mRNA in HCC Patients.** In all preoperative blood samples (except patient P7’s) and all intraoperative samples analyzed, \( \text{afp} \) mRNA levels were found to be indistinguishable from the reference range (\( P = 0.44 \) and 0.14 for preoperative and intraoperative samples, respectively, Mann-Whitney test; Fig. 3). In P7, the preoperative \( \text{afp} \) mRNA level was nearly 50-fold higher than the reference range (275 HepG2 cell equivalents per 20 ml of blood) but fell to the reference range during surgery (Fig. 3A). In postoperative blood samples from 9 of the 13 HCC patients studied (P1, P2, P3, P4, P7, P9, P11, P12, and P13), \( \text{afp} \) mRNA levels were significantly higher (5–7600-fold) than the reference range (\( P < 0.00001 \), Mann-Whitney test; Fig. 3). Four of these nine patients (P1, P7, P11, and P12) harbored large HCCs >5 cm in diameter (Table 1). The number of \( \text{afp} \)-expressing cells detected ranged from 32 to 46,000 HepG2 cell equivalents per 20 ml of blood. The \( \text{afp} \) mRNA levels were persistently elevated in five patients (P1, P2, P7, P11, and P12; Fig. 3A) but fell to the reference range 2–4 weeks later in P3 and P4 (Fig. 3B). In four patients (P5, P6, P8, and P10), levels of \( \text{afp} \) mRNA detected postoperatively were all within the reference range (Fig. 3B). Among the HCC patients studied, the maximal \( \text{afp} \) mRNA level detected over the times did not correlate directly with the tumor size (\( r = 0.35; \ P = 0.23 \)) or the resection margin (\( r = -0.14; \ P = 0.64 \); Spearman’s correlation; Table 1).

**Correlation between Levels of \( \text{afp} \) mRNA and \( \text{alb} \) mRNA/Serum AFP.** Consistent with our previous findings (14), levels of \( \text{afp} \) mRNA did not correlate with levels of \( \text{alb} \) mRNA in 53 peripheral blood samples from the HCC patients studied during the preoperative, intraoperative, and postoperative periods (\( r = 0.08; \ P = 0.55; \ n = 53 \); Spearman’s correlation). In addition, levels of \( \text{afp} \) mRNA detected at different times did not correlate directly with serum AFP levels in the same HCC patients (\( r = 0.25; \ P = 0.08; \ n = 53 \); Spearman’s correlation). Instead, the maximal \( \text{afp} \) mRNA levels detected over the times (postoperatively in 11 of the 13 HCC patients; Table 1) strongly correlated with the amounts of serum AFP monitored at the same times (\( r = 0.77; \ P = 0.002; \ n = 13 \); Spearman’s correlation).
Clinical Relevance of Raised afp mRNA Levels. All of the four patients (P5, P6, P8, and P10) who showed afp mRNA levels within the reference range during the periods monitored remain alive and well with no evidence of tumor recurrence at 3 years (Table 1). Two additional patients (P3 and P4) had evidence of circulating malignant hepatocytes within the first 2 postoperative months, but these cells were cleared within 2–4 weeks. They also remain alive and well with no evidence of recurrence at 3 years (Table 1). Of the other seven patients with postoperatively raised afp mRNA levels, five patients with persistently elevated levels (including P11 and P12 with the highest recorded levels) developed lung metastasis (P11), liver recurrence (P2, P7, and P12), or had persistent HCC with intrahepatic metastasis (P1; P = 0.02, Fisher’s exact test). They all died from the recurrences or metastases (Table 1). The other two patients with raised afp mRNA levels, P9 and P13, were
unfortunately lost to follow-up to obtain further blood samples afterward. They remain alive and well with no evidence of recurrence or metastasis at 3 years (Table 1).

**DISCUSSION**

We analyzed the quantity and timing of shedding of both *alb*-expressing hepatocytes and *afp*-expressing HCC cells into the circulation of patients with HCC or hepatocellular adenoma undergoing surgical resection. Our present data clearly demonstrate that hepatocytes are released into the bloodstream during surgery, as reflected by the significantly elevated *alb* mRNA levels detected in 100% (23 of 23) of HCC and hepatocellular adenoma patients. The intraoperative *alb* mRNA level was not proportional to the tumor size but positively associated with the mass of hepatectomy, regardless of tumor capsule formation. The presence of such a large number of *alb*-expressing hepatocytes, which expressed *afp* mRNA at low levels, implicated the mechanical spillage of predominantly nontumor hepatocytes into the circulation during surgery. These cells most likely originated from nontumor liver tissues surrounding the HCCs. Virtually all of these *alb*-expressing cells were removed from the circulation within 8 weeks after operation.

It has been noted that the frequency of tissue-specific cell detection far exceeded the expected rate of tumor recurrence in patients with prostate, colon, and lung cancers (5, 17–19). The removal of intraoperatively detected tissue-specific cells from the circulation has also been reported in patients with prostate cancer after surgery (5). This could possibly be related to the fact that some of these cells detected were not malignant cells (20, 21). The fate of the *alb*-expressing hepatocytes detected in our HCC patients appears to be similar to that of those circulating tissue-specific cells described in patients who underwent resection of prostate cancer (5). Thus, the presence of tissue-specific mRNAs in peripheral blood does not necessarily reflect the existence of malignant cells nor the clinical status of patients, suggesting that cancer-specific mRNAs should be applied for the detection of micrometastases. The RT-PCR approach is generally considered as a more sensitive and efficient method than the detection of genetic alterations, such as the *p53* mutations, in that not all HCC tumors have the same aberration reserved for the test.

By applying both *afp* and *alb* mRNAs as markers, we may distinguish between the presence of malignant HCC cells and nontumor hepatocytes based on differential *afp* expression between these two cell populations. Our findings clearly showed significantly raised *afp* mRNA levels in postoperative peripheral blood from 9 of 13 HCC patients (70%), among which P3 and P4 showed the clearance of *afp* mRNA afterward. As a result, seven patients were identified to be at high risk for recurrence or metastasis. Indeed, five of these seven patients (72%) showed persistently elevated *afp* mRNA levels and died from lung metastasis, liver recurrence, or persistent HCC with intrahepatic metastasis within 1 year after surgery. The significantly raised *afp* mRNA levels presumably originated from malignant circulating HCC cells. The absence of *afp* mRNA-expressing circulating cells in all of the patients who underwent adrenalectomy resection further supported that the elevated *afp* mRNA levels reflected the genuine existence of malignant HCC cells. The maximal *afp* mRNA levels detected, mostly postoperatively, strongly correlated with the serum AFP levels monitored, which might primarily arise from the circulating HCC cells. On the contrary, only two of the patients studied had postoperative serum AFP of >500 ng/ml, suggesting that the serum AFP level alone could not accurately indicate the presence of circulating HCC cells nor the potential for metastasis.

A small proportion of the circulating tumor mass could potentially be responsible for the formation of a secondary deposit (22). By lodgment and extravasation, some of the circulating HCC cells detected were possibly arrested by target organs from which they could be released into the circulation again (23), as shown in the five patients who developed metastases or recurrences. It is noteworthy that 80% (four of five) of relapse took place in the liver, a particularly fertile ground for HCC cells to proliferate. In accordance with Paget’s “seed and soil” hypothesis, the disseminating capacity of tumor cells rather than the local outgrowth is controlled by the “soil” characteristic (24). In P3 and P4, who showed no evidence of recurrence or metastasis, almost all *afp*-expressing circulating cells detected were cleared within 2–4 weeks. The selective growth of highly metastatic tumor cells is definitely required, which are endowed with properties allowing them to complete the metastatic cascade successfully.

The high-risk patients P11 and P12, who showed the largest circulating tumor mass, demonstrated evidence of lung metastasis or liver recurrence after the elevation of *afp* mRNA levels. A proportion of the HCC cells detected appeared to implant and form clinically detectable metastasis or recurrence in the fertile “soil.” The frequency of relapse/death seems to correlate with the circulating tumor mass, as has been shown by immunohistochemistry in lung cancer patients undergoing surgery (18). Sequential quantification of *afp* mRNA in peripheral blood would thus shed light on the persistent existence or removal of circulating HCC cells. Conversely, P7, who developed liver recurrence, showed a larger circulating tumor mass preoperatively as compared with that detected postoperatively. It is possible that micrometastasis could be established while still in an intravascular stage, at which some preexisting circulating HCC cells were sequestered and hence undetected postoperatively (25).

It is well documented that gene expression in tumor cells is heterogeneous. Levels of *alb* mRNA did not correlate directly with levels of *afp* mRNA in the 53 peripheral blood samples analyzed. The circulating HCC cells detected postoperatively in all of the nine patients expressed the *afp* gene more strongly than the *alb* gene. This is in concordance with the considerable heterogeneity in cellular distribution and expression of *alb* and *afp* mRNAs in moderately and poorly differentiated HCCs (26). These circulating tumor cells disseminated postoperatively, regardless of the tumor size or the resection margin, and were possibly released from undetectable micrometastases or minimal residual tumor in the liver as a consequence of surgical maneuver. Apparently, they were not liberated from primary HCCs into the circulation during surgical intervention, as implicated by the negligible *afp* mRNA levels detected intraoperatively in all of the HCC patients studied. It is likely that they were biologically triggered to disseminate postoperatively by cytokines and growth factors released from the regenerating liver (27–30).

A disease-free survival rate of 62% (8 of 13) at 3 years was observed among our patients. Four survivors showed *afp* mRNA
levels within the reference range during the periods monitored. The other two showed the clearance of the αf p mRNA signal from peripheral blood after its initial detection after resection. Overall, the absence or clearance of αf p mRNA in peripheral blood was strongly associated with the absence of local recurrence or distant metastasis in 75% (six of eight) of survivors. In striking contrast, all of the patients who died from intrahepatic/extrahepatic metastasis, liver recurrence, or persistent HCC had shown persistently raised αf p mRNA levels in the peripheral blood. Our findings could potentially open up prognostic implications that would be consolidated by our current quantitative analysis of a larger cohort of patients together with long-term follow-up.

We present evidence that alb-expressing hepatocytes are released intraoperatively into the circulation, and αf p-expressing HCC cells are disseminated mostly postoperatively that may implicitly be the source of recurrence or metastasis in HCC patients undergoing surgical resection. In the near future, this quantitative information may provide an additional guideline for selection of patients for the most appropriate treatments. Sequential quantification of circulating HCC cells by our rapid and reliable method may prove valuable for assessing the potential for metastasis and monitoring patients’ response to therapies.

ACKNOWLEDGMENTS

We thank Dr. Y. M. D. Lo for review of the manuscript and Eric Wong, our statistician, for helpful advice on statistical analysis of data.

REFERENCES


Hematogenous Dissemination of Hepatocytes and Tumor Cells after Surgical Resection of Hepatocellular Carcinoma: A Quantitative Analysis


Updated version
Access the most recent version of this article at:
http://clincancerres.aacrjournals.org/content/5/12/4021

Cited articles
This article cites 30 articles, 2 of which you can access for free at:
http://clincancerres.aacrjournals.org/content/5/12/4021.full#ref-list-1

Citing articles
This article has been cited by 9 HighWire-hosted articles. Access the articles at:
http://clincancerres.aacrjournals.org/content/5/12/4021.full#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, use this link
http://clincancerres.aacrjournals.org/content/5/12/4021.
Click on "Request Permissions" which will take you to the Copyright Clearance Center's (CCC) Rightslink site.