ABSTRACT

Hepatocellular carcinoma (HCC) is the fifth most common cancer, with more than one million fatalities occurring annually worldwide. Multiple risk factors are associated with HCC disease etiology, the highest incidence being in patients with chronic hepatitis B virus and hepatitis C virus, although other factors such as genetic makeup and environmental exposure are involved. Multiple genetic alterations including the activation of oncogenes and inactivation of tumor suppressor genes are required for malignancy in human cancers and are correlated with increased stages of carcinogenesis and further tumor progression. In this study of 21 HCC patients, we analyzed pRb2/p130, vascular endothelial growth factor (VEGF), p27 (KIP1), and proliferating cell nuclear antigen expression (diffuse staining >50% of positive cells in 75% to 100% at 5 years (8–10). Second liver resections from a well-differentiated stage to less-differentiated forms (3).

Received 12/1/03; revised 2/4/04; accepted 2/6/04.

Grant support: From the W. W. Smith Charitable Trust (P. Claudio). NIH and Sbarro Health Research Organization grants (A. Giordano), the Rocco D’Amelio and Family-S.H.R.O. Fellowship, and ex-60% (A. Farina)

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pRb2/p130, Vascular Endothelial Growth Factor, p27 (KIP1), and Proliferating Cell Nuclear Antigen Expression in Hepatocellular Carcinoma: Their Clinical Significance

INTRODUCTION

Hepatocellular carcinoma (HCC) is one of the most prevalent malignancies worldwide, being the third largest cause of cancer deaths. HCC is considered a multistage disease whose occurrence is caused by the interaction between genetic and environmental factors (1). Several studies demonstrated that HCC is more frequent in patients with hepatitis B virus (HBV) and hepatitis C virus (HCV)-related chronic hepatitis and cirrhosis as well as in patients with a history of aflatoxin B1 exposure, chronic alcohol abuse, and cigarette smoking (2). Moreover, a higher incidence of HCC has been shown in certain genetic defects such as porphyria, α-1 antitrypsin deficiency, and Wilson disease (2). Usually, HCC arises from an adenomatous hyperplasia in an already diseased liver and progresses from a well-differentiated stage to less-differentiated forms (3). Ordinary HCCs formed by progression show highly increased cellular proliferation, neovascularization, production of basic fibroblast growth factor, and aneuploidy in some tumors (4). Corresponding to its malignant progression, HCCs show loss of heterozygosity for multiple chromosomes (5).

The long-term prognosis of HCC patients is typically quite poor. In one study involving 245 HCC cases, the median survival from the point of diagnosis was only 8 months (6). In another study of 336 patients, survival was as little as 0.7 months for stage III HCC versus 11.5 months for stage I tumors, with a median survival rate of 2.1 months (7). However, the 5-year survival rate increases with medical treatments. Unfortunately, shortly after curative hepatic resection, HCC tumor recurrence remains the rule, with the recurrence rates ranging from 75% to 100% at 5 years (8–10). Second liver resections
potential HCC Molecular Biomarkers

...proteins, known also as pocket proteins for their unique structure, are phosphorylated in a cell cycle-dependent manner and exhibit growth-suppressive properties in a cell type-dependent manner. Whereas Rb/p105 is found in both cycling and quiescent cells, Rb2/p130 and p107 act exclusively in a cell cycle-dependent fashion to regulate several cellular transcription factors such as E2Fs (19).

p27(KIP1) is a cdk inhibitor that binds to cyclin-CDK complexes and facilitates the inhibition of the catalytic activity of cdk, ultimately inducing G1 cell cycle arrest (20, 21). Inactivation of p27(KIP1) is believed to be a fundamental step in carcinogenesis, and decreased p27(KIP1) protein expression correlates with poor prognosis in many human malignancies (22, 23). Recent studies demonstrated that p27(KIP1) is expressed at lower levels in normal hepatocytes (24). On the other hand, other studies showed that under-expression of p27(KIP1) in HCC was associated with a poor prognosis, high-grade tumors, and early recurrence (25). Furthermore, HCC patients with higher expression levels of the p27(KIP1) protein experienced longer disease-free survival (26). Acquired p27(KIP1) expression is considered to be a favorable independent prognostic parameter for HCC (27).

VEGF is a secreted homodimeric cytokine that positively regulates tumor neovascularization (28). Solid tumors require a constant vascular supply for their survival as do metastasis. Recent studies suggest that angiogenesis, which is a highly orchestrated and multistep process, is essential in tumor growth and progression, including that of HCC, which are typically characterized by a high level of vascularization (29–31). In fact, it has been shown that VEGF expression in HCC tumors is significantly higher than in normal liver tissue (32).

PCNA is a nuclear protein that is synthesized in G1-S-phase of the cell cycle. It is an accessory factor for DNA polymerases α and ε and functions as a DNA sliding clamp. PCNA is required for eukaryotic DNA synthesis, replication, and repair and is expressed at high levels in cycling cells (33). Other PCNA cellular functions include Okazaki fragment joining, DNA methylation, and chromatin assembly (34, 35). Because liver disease progresses from chronic hepatitis infection to HCC, PCNA expression levels increase dramatically (33).

In the present study, we demonstrate that VEGF expression is markedly up-regulated in high-grade HCC tumors and that higher VEGF expression was associated to a poor survival ($P = 0.0257$, log-rank test). Inversely, the negative cell cycle regulator pRb2/p130 was undetectable in advanced HCC. In fact, lower pRb2/p130 expression was associated to a borderline $P$ and to a positive correlation with respect to the time from HCC diagnosis (Spearman coefficient $= 0.568; P < 0.05$). Furthermore, we found that the time from HCC diagnosis is negatively correlated with VEGF expression levels. Additionally, for the first time, we demonstrate that pRb2/p130 is inversely correlated with VEGF expression and tumor aggressiveness ($P < 0.05$) in p27(KIP1)-negative HCC patients. pRb2/p130 and VEGF expression are independent from tumor staging, suggesting their possible role as independent prognostic molecular biomarkers in HCC. Moreover, we have evidence that VEGF together with pRb2/p130 may act as new HCC biomarkers in a p27(KIP1)-independent manner.

MATERIALS AND METHODS

Patient Populations and Clinicopathological Data.

Twenty-one cases of HCC were enrolled in the present study. Sections from paraffin-embedded liver tumors were obtained from patients who underwent hepatic surgical resection as a treatment for hepatocellular carcinoma at the Surgery Department of the Università Cattolica del Sacro Cuore, Roma, Italy.
RESULTS

Expression Levels of pRb2/p130, p27Kip1, VEGF, and PCNA in HCC Specimens. The expression levels of pRb2/p130, p27Kip1, VEGF, and PCNA in hepatocellular carcinoma tumors were determined immunohistochemically (Fig. 1).

The descriptive statistics for the overall series are shown in Table 1. No differences have been observed in variable distributions according to the Mann-Whitney U test.

Survival analysis for the overall series yielded a crude cumulative survival rate of 36 months (70%) with a mean survival time of 28 months as reported in Fig. 2. A stratification of survival rate, based on pRb2/p130, VEGF, and PCNA was performed by using cutoff values able to maximize differences between groups as reported in Table 2 and Figs. 3–5. Lack of pRb2/p130 expression, even if associated with a trend of lower survival, did not reach a statistical P (Table 2; Fig. 3). Higher expression of VEGF was instead associated with a poorer survival (Table 2; Fig. 4). A significant-negative correlation was found, by Spearman coefficient, between VEGF and pRb2/p130 expression levels (P = 0.049), and a positive correlation was found between VEGF and PCNA expression levels (0.472, P = 0.048). Interestingly, grading (well-, moderately, and poorly differentiated), did not statistically correlate (by rank correlation) to the VEGF and pRb2/p130 expression levels. Additionally, we found that VEGF and p27Kip1 expression did not correlate with tumor staging (P > 0.05). VEGF expression showed a borderline correlation with tumor size (P = 0.055). These results open up new prospectives to include markers in a screening model for HCC aggressiveness.

We also found that PCNA expression was significantly increased in poorly differentiated HCC specimens and progressively decreased in moderately and well-differentiated ones, in accordance with previously published literature (35–39). PCNA positively stained cells were <10% in low-grade HCC specimens. In moderately differentiated malignancies, PCNA staining was detected in approximately 30% of the nuclei.
Fig. 1 Immunohistochemical analysis of cell cycle proteins in malignant hepatocellular carcinoma (HCC) liver tissues. All original magnification is ×60 unless noted otherwise. Panel 1, high-grade, undifferentiated HCC. A, H&E. Marked nuclear pleomorphism and anisomoeolosis. Note chromatin clumping, margination, and prominent nucleoli. Malignant hepatocytes are in solid sheets. B, p27Kip1. Note strong and diffuse nuclear positivity. C, pRb2p130. No expression is noted. D, VEGF. 

Most tumor cells show strong cytoplasmic expression. This aspect is present throughout the entire tumor. Original magnification ×40. E, proliferating cell nuclear antigen (PCNA). Approximately 70% of nuclei show strong nuclear positivity. 

Panel 2, moderately differentiated HCC. F, H&E. Moderate nuclear pleomorphism and anisomoeolosis; clearing of chromatin and prominent eosinophilic nucleoli are noted. The malignant hepatocytes tend to aggregate in disorganized laminae. G, p27Kip1. No expression is noted. H, Rb2p130. No nuclear expression is noted. I, vascular endothelial growth factor (VEGF). Some groups of tumor cells show strong and coarse cytoplasmic expression whereas the remaining cells show faint expression. Original magnification ×40. J, PCNA. Approximately 30% of nuclei show nuclear positivity. 

Panel 3, low-grade, well-differentiated HCC with tubular features. K, H&E. Nuclei are round to oval with centrally placed eosinophilic nucleoli. There is mild pleomorphism and anisomoeolosis. The malignant hepatocytes are arranged in tubular structures surrounded by well-defined sinusoidal spaces lined by histiocytic and endothelial cells. L, p27Kip1. No expression is noted. M, Rb2p130. Most of the nuclei show positivity with variable intensity. Note the clearing of the chromatin that may give a false-negative aspect of nuclear staining if not carefully examined. N, VEGF. Some diffuse but weak cytoplasmic expression is present. In other areas, there is no VEGF expression. Original magnification ×40. O, PCNA. Approximately 10% of the nuclei are positive.
High-grade malignancies showed >70% of tumor cells positive to PCNA.

PCNA staining was also scored as the total percentage of tumor cells stained. PCNA staining as a percentage of total tumor cells that were positive was scored using the exact Pearson χ² test analysis with a significant P of 0.007.

Again, we found pRb2/p130 expressed in low-grade, highly differentiated HCC tumor specimens. pRb2/p130 expres-
von der Léon observe in the nuclei and shows variable degrees of staining intensity. Furthermore, it is important to point out that chromatin clearing may cause a false-negative staining aspect unless one carefully examines the nuclei. Although tumor malignancy increases and the tumor cells become less differentiated, pRb2/p130 expression levels decrease. In high-grade undifferentiated HCC tumor samples, pRb2/p130 expression is not detectable. It has been reported previously that in normal liver cells, the level and intensity of VEGF is not detectable (4, 18, 30, 32). We found that VEGF was undetectable in the low-grade HCC tumors that we assayed. However, we discovered that VEGF expression increases in advanced tumor malignancy, and it is found in the cytoplasm of HCC cells, being highly up-regulated in high-grade, undifferentiated HCC specimens. We found an inverse statistically significant correlation between VEGF and pRb2/p130 expression (P < 0.05). In fact, high-grade tumors having low expression levels of pRb2/p130 show intense staining for VEGF and vice versa (P = 0.048).

The statistical and clinical findings of our study reside in the fact that VEGF and pRb2/p130 expressions are both associated with different survival rates. Multivariate techniques as well as Cox regression would be useful in a wider series of data, to quantify the marker-associated risk and to calculate a predictive value for the mortality associated with the marker

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**Table 2**  
Stratified survival analysis

<table>
<thead>
<tr>
<th>Variable</th>
<th>Cut-off</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td>pRb2/p130</td>
<td>+, +, +, +</td>
<td>Negative</td>
</tr>
<tr>
<td>Survival rate</td>
<td>85%</td>
<td>60%</td>
</tr>
<tr>
<td>Median survival time (months)</td>
<td>32</td>
<td>25</td>
</tr>
<tr>
<td>VEGF a</td>
<td>Negative</td>
<td>+, +, +, +</td>
</tr>
<tr>
<td>Survival rate</td>
<td>90%</td>
<td>33%</td>
</tr>
<tr>
<td>Median survival time (months)</td>
<td>34</td>
<td>18</td>
</tr>
<tr>
<td>PCNA</td>
<td>P and &lt;50%</td>
<td>P and ≥50%</td>
</tr>
<tr>
<td>Survival rate</td>
<td>84%</td>
<td>25%</td>
</tr>
<tr>
<td>Median survival time (months)</td>
<td>32</td>
<td>15</td>
</tr>
<tr>
<td>Grading</td>
<td>3</td>
<td>&lt;3</td>
</tr>
<tr>
<td>Survival rate</td>
<td>50%</td>
<td>23%</td>
</tr>
<tr>
<td>Median survival time (months)</td>
<td>61</td>
<td>34</td>
</tr>
</tbody>
</table>

a VEGF, vascular endothelial growth factor; PCNA, proliferating cell nuclear antigen.

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**Fig. 2**  
Crude survival probability of the overall hepatocellular carcinoma series.

**Fig. 3**  
Survival probability stratified according to the pRb2/p130 staining (negative versus positive).

**Fig. 4**  
Survival probability stratified according to the vascular endothelial growth factor (VEGF) staining (positive versus negative).
expression. Furthermore, confirming our previously published studies demonstrating that pRb2/p130 expression down-regulates VEGF expression in vitro and in vivo (40), we have established, for the first time, the clinical possibility of a mutual exclusivity of pRb2/p130 and VEGF expression in HCC specimens (P = 0.049).

DISCUSSION

The prognosis of HCC-suffering patients still remains poor, although by studying them in the clinical setting, many advances have been made (41). With new emerging technologies in cancer biology, the pathological and biological prognostic factors of HCC have been studied quite extensively. It is universally accepted that biomarkers can be measured and evaluated as indicators of normal biological or pathological processes or as pharmacological response to a therapeutic intervention. Prognostic molecular biomarkers are invaluable for the clinician to evaluate patients and to aid in tumor control. Molecular indicators for the HCC malignancy phenotype include alterations in DNA ploidy, nuclear morphology, and the expression levels of proteins involved in cellular proliferation such as tumor suppressors and cell cycle regulators, apoptotic factors, telomerase activity, adhesion molecules, extracellular matrix proteinases, and angiogenic factors (17, 18, 24, 25, 27, 30, 37, 39, 42). Molecular surveillance of at-risk patients, those who are chronically infected with HBV or HCV or those who have cirrhosis, can result in earlier detection and more favorable treatment outcomes including increased survival. Cases with advanced tumors, impaired liver function, and generally poor health do not respond positively to treatments and typically receive palliative treatments only, whereas those with more favorable prognostic indicators receive an aggressive treatment regimen including surgical resection, trans-arterial chemo-embolization with various chemotherapeutic agents, and chemo-lipiodol treatments (43–46).

Liver transplant is a potentially curative HCC treatment. Although liver transplants do offer a safe and potentially effective treatment for patients in stage I, II, and III HCC, unfortunately, the availability of usable organs remains an issue (13). In modern medicine, biomarkers are critical key elements for optimizing clinical treatment and drug discovery. Previous studies clearly demonstrated that PCNA expression is a reliable molecular biomarker for HCC. In fact, a progressive increase in the PCNA-labeling index from regenerative to dysplastic nodules to HCC has been observed (39). Additionally, an increase in the DNA index was correlated with an increase in PCNA labeling, and both were correlated with pathological changes in HCC tumors (47). PCNA staining in low-grade HCC tumors is typically <10%. However, in moderately differentiated malignancies, PCNA staining is observed in approximately 30% of the nuclei. Staining increases to ≥70% of tumor cells in high-grade malignancies (33, 39, 47). In our study, we scored PCNA staining according to its intensity from 0 to 4 and also scored the total percentage of PCNA-positive tumor cells. Exact Pearson χ²-test analysis yielded a significant P of 0.007 for PCNA staining as a percentage of total tumor cells stained. Cumulative survival curves (Fig. 5) generated from these data showed that when a diffuse intensity and 50% of tumor cells were positively stained for PCNA, the cumulative survival rate decreased over time. These data served us as an internal quality control because PCNA expression has been shown to be a significant HCC prognostic biomarker.

Another established HCC biomarker is the cdk inhibitor p27(KIP1). p27(KIP1) has been emerging as a predictor of survival and tumor behavior. It has been suggested that p27(KIP1) loss occurs early in the carcinogenesis process (24). The more aggressive, metastasizing cancers tend to lack p27(KIP1) expression as well (18, 24). High p27(KIP1) expression, correlated with prolonged survival, is a favorable independent prognostic parameter for HCC (24, 27). Furthermore, it is known that HCC is formed by a heterogeneous cell population, and hence, protein expression may vary within the same tumor. Recently, it has been demonstrated that p27(KIP1) protein was frequently overexpressed in primary HCC and that longer disease-free survival rates were seen in patients whose tumors had higher p27(KIP1) expression (26). On the other hand, in a recent study it was shown that p27(KIP1) expression is reduced at relatively early evolutionary stages of HCC, and it was not associated with tumor stage (25). In our study, lack of p27 expression was observed in >90% of our cases (17 of our HCC samples), and it was independent from tumor stage, in accordance with Armenogel et al. (25).

Those samples that stained positively for p27(KIP1) were not considered statistically significant (P > 0.05); therefore, we deduced that p27(KIP1) expression was not correlated in this cohort. It is possible that in our study group, hepatocarcinoma is independent from p27(KIP1) expression levels, suggesting another possible molecular scenario in which other protein products could be involved, leaving the following question open: are there any other biomarkers involved in HCC etiology? Recently, in our laboratory we were able for the first time to identify new
target genes, the expression of which is modulated by pRb2/p130 (48). Moreover, we have demonstrated previously that RB2/p130 inhibits angiogenesis in vitro and in vivo by down-regulating VEGF expression at the transcriptional and translational levels (40). Our findings that higher VEGF and lower pRB2/p130 expressions correlated with survival are in agreement with our previous results (40). In fact we have shown, for the first time, a mutual exclusivity of pRB2/p130 and VEGF expressions.

Multiple risk factors are associated with HCC disease etiology, the highest incidence being in patients with chronic HBV and HCV, although other factors such as genetic makeup and environmental exposure such as aflatoxins are involved. Although it is conceivable to hypothesize that some of these agents could induce, either directly or indirectly, pRB2/p130 or VEGF expression, it is important to point out that to date, the relationship between HBV/HCV infection and VEGF expression is still unclear. In fact, in the last 4 years, different studies have highlighted some interesting but conflicting scenarios. One of these studies suggested that the presence of HCV infection increased de facto the expression of VEGF (49, 50). The second scenario suggested that in HCC samples infected by HCV, VEGF is down-regulated (51). A further complication is presented by the study of Shimoda et al. (52), which demonstrated that VEGF mRNA expression is not related at all to HBV and HCV infection in HCC patients.

Furthermore in HCC tissues, the mechanisms of HBV infection involved in VEGF modulation remain unknown. In fact, a study by Lee et al. (53) demonstrated that HBV-X protein can stimulate VEGF transcription. Nevertheless, Iizuka et al. (51) reported a minimal up-regulation of VEGF in HBV-positive samples by using a high-density microarray analysis of 45 HCC samples.

Moreover, to our knowledge, no in vivo study has been published showing the presence of HBV and HCV infection in HCC tissues and pRB2/p130 regulation. In light of this conflicting or absent evidence, there are no definitive data that HBV and HCV infections induce directly and/or indirectly VEGF and/or pRB2/p130 expression at this time. Additionally, very recently another paper reported that expression of the entire HCV genome in the primary liver cancer cell line HepG2 up-regulates the CDK-Rb-E2F pathway, causing pRB/p105 hyperphosphorylation and its subsequent protein degradation via the ubiquitin pathway (54). Our study demonstrating low expression of the retinoblastoma family member pRB2/p130 in either HBV- and/or HCV-positive HCC patients could be in part explained by a change in the phosphorylation status in Rb2/p130 similar to that which occurs in vitro with pRB/p105. More studies regarding pRB2/p130 phosphorylation status both in vitro and in vivo are needed to fully comprehend the potential prognostic power of the Rb family members together with VEGF expression in HCC.

To our knowledge, this is the first investigation in which VEGF and pRB2/p130 are suggested to be independent novel prognostic markers in HCC. More studies are needed to confirm the clinical significance of the inverse correlation between VEGF and pRB2/p130 expression patterns that together could be “de facto” new biomarkers in hepatocarcinoma and to confirm the role of HBV and HCV infection and VEGF/pRB2 gene regulation in hepatocarcinogenesis.

ACKNOWLEDGMENTS

G. Russo thanks the Diagnostic, Quantitative, and Molecular Pathology PhD program of the University of Siena, Italy. We thank Dr. Massimo Di Mugno for technical help in collecting the specimens.

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