Combined Functional Genome Survey of Therapeutic Targets for Hepatocellular Carcinoma

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Abstract

Purpose: The outcome of patients with advanced hepatocellular carcinoma (HCC) has remained unsatisfactory. Patients with HCC suffer from chronic hepatitis or liver cirrhosis, and their reserve liver function is often limited.

Experimental Design: To develop new therapeutic agents that act specifically on HCC but interfere only minimally with residual liver function, we searched for genes that were upregulated in 20 cases of HCC [namely, discovery sets 1 (n = 10) and 2 (n = 10)] in comparison with corresponding nontumorous liver and a panel representing normal organs using high-density microarrays capable of detecting all exons in the human genome.

Results: Eleven transcripts whose expression was significantly increased in HCC were subjected to siRNA-based secondary screening of genes required for HCC cell proliferation as well as quantitative reverse transcription-PCR analysis [validation sets 1 (n = 20) and 2 (n = 44)] and immunohistochemistry (n = 19). We finally extracted four genes, AKR1B10, HCAP-G, RRM2, and TPX2, as candidate therapeutic targets for HCC. siRNA-mediated knockdown of these candidate genes inhibited the proliferation of HCC cells and the growth of HCC xenografts transplanted into immunodeficient mice.

Conclusions: The four genes we identified were highly expressed in HCC, and HCC cells are highly dependent on these genes for proliferation. Although many important genes must have been overlooked, the selected genes were biologically relevant. The combination of genome-wide expression and functional screening described here is a rapid and comprehensive approach that could be applied in the identification of therapeutic targets in any type of human malignancy. Clin Cancer Res; 16(9); OF1–11. ©2010 AACR.
Liver cancer is the fifth most common human cancer worldwide and the third most common cause of cancer mortality. Recently, a multikinase inhibitor, sorafenib, has been approved as a systemic chemotherapeutic drug for advanced hepatocellular carcinoma (HCC); however, further improvement seems to be necessary. To identify an “Achilles heel” of HCC cells and develop new therapeutic agents that act specifically on HCC but interfere only minimally with residual liver function, we performed an unbiased survey of the whole genome. We finally identified four genes as candidates. siRNA-mediated knockdown of these candidate genes inhibited the proliferation of HCC cells and the growth of HCC xenografts transplanted into immunodeficient mice, confirming their feasibility as therapy targets.

Materials and Methods

Patients and microarray analysis. Samples of HCC and surrounding nontumorous liver tissue were collected from 84 patients who underwent liver resection for HCC at the National Cancer Center Hospital (Tokyo, Japan) with informed consent. The clinical and histologic data for these patients are summarized in Supplementary Table S1. Total RNA of normal human organs was obtained from a commercial source (FirstChoice Human Total RNA Survey Panel, Ambion).

One microgram of total RNA was converted to end-labeled cRNA using a Whole Transcript Sense Target Labeling kit (Affymetrix). The fluorescent cRNA probes were hybridized to Human Exon 1.0 ST arrays (Affymetrix), as instructed by the supplier. Data analysis was carried out using the ArrayAssist software package (version 5.5.1, Stratagene). A GC content-based background correction followed by quantile normalization was done with an exonRNA algorithm available in the package. Multiple exon expression data were also summarized into a single value using the same algorithm, as instructed by the supplier (http://www.stratagene.com/manuals/ArrayAssist.pdf).

The protocol of this study was reviewed and approved by the ethics committee of the National Cancer Center (Tokyo, Japan).

Cell lines. Three human cell lines derived from HCC were used in this study. KIM-1 was kindly provided by Dr. Masamichi Kojiro (Kurume University, Kurume, Japan). Hep3B was obtained from the Cell Resource Center for Biomedical Research, Tohoku University (Sendai, Japan). HLE was obtained from the Health Science Research Resources Bank (Osaka, Japan). KIM-1 and Hep3B were maintained in RPMI 1640 (Invitrogen) supplemented with 10% fetal bovine serum. HLE was maintained in Dulbecco’s modified Eagle’s medium (Invitrogen) supplemented with 10% fetal bovine serum.

siRNA-based functional screening. The day before siRNA transfection, cells were seeded at 5 × 10^3 per well in 96-well plates to obtain 50% to 60% confluency. They were then transfected with siRNA using Lipofectamine 2000 (Invitrogen) at a concentration of 10, 20, or 50 nM in KIM1, Hep3B, or HLE cells, respectively. Three days later, the relative proportion of living cells was assessed using a Premix WST-1 Cell Proliferation Assay System (Takara Bio) in accordance with the manufacturer’s instructions. The siRNA was synthesized by Ambion, and the identification (ID) numbers of siRNAs used in this study are listed in Supplementary Table S5. The amplification reaction was performed with 100 ng of total RNA using SuperScript reverse transcriptase (Invitrogen) at 94°C for 2 minutes, 60°C for 1 minute, followed by 40 cycles of 95°C for 15 seconds, 60°C for 1 minute, and 72°C for 1 minute.

Real-time PCR. First-strand cDNA was synthesized from 1 μg of total RNA using SuperScript reverse transcriptase (Invitrogen). Real-time PCR was done as described previously (14). Primers and probes sets were obtained from Applied Biosystems, and their Assay IDs are provided in Supplementary Table S5. The amplification reaction was done according to the manufacturer’s instructions (95°C for 10 minutes followed by 40 cycles of 95°C for 15 seconds, 50°C for 2 minutes, and 60°C for 1 minute).

Immunohistochemistry and immunoblot analysis. Anti-AKR1B10 (clone 1A6) and anti–HCP-G (clone 4B1) monoclonal antibodies were purchased from Abnova. Anti-RRM2 antibody (E-16) was purchased from Santa Cruz Biotechnology. Anti-TPX2 antibody was purchased from Novus Biologicals. Formalin-fixed and paraffin-embedded liver tissues containing HCC were obtained from the National Cancer Center Hospital, and stained as described previously (15, 16).
Immunoblot analysis of the KIM-1 cell lysate was done as described previously (15).

Animal experiments. Eight million KIM-1 cells suspended in 0.1 mL of PBS were s.c. inoculated into the flanks of 5-week-old female BALB/c nu/nu nude mice (SLC). Eight days later, the tumor-bearing mice were treated with siRNA together with atelocollagen (Koken Co., Ltd.), as described previously (17, 18). The final concentration of siRNA and atelocollagen was 11 μmol/L and 0.5%, respectively, and 200 μL of the siRNA solution were injected directly into each tumor. Tumor volume was determined every 3 days using the formula \( V = \frac{1}{2} (A \times B^2) \), where \( A \) and \( B \) represent the largest and smallest dimensions of the tumor, respectively.

Animal experiments were reviewed by the institutional ethics committee and performed in compliance with the guidelines for Laboratory Animal Research of the National Cancer Center Research Institute (Tokyo, Japan).

Statistical analysis. To extract differentially expressed genes from the array data, a paired \( t \) test with no correction was done (19) with asymptotic distribution to determine the \( P \) value. Correlations between array data and real-time PCR measurements were assessed using the Pearson correlation coefficient. The significance of differential gene expression between HCC and adjacent nontumorous liver tissue was assessed using the permutation paired \( t \) test followed by Bonferroni correction.

The weights and volumes of tumors are given as means (+SE). To evaluate the chronological effect of siRNAs on the growth of xenografts in comparison with control siRNA, a growth of xenografts in comparison with control siRNA, a generalized linear mixed-effects model was used (20). The volume of the xenograft was modeled using \( \gamma \)-error distribution and log link function. This model considers each siRNA treatment as a fixed effect with control siRNA as an intercept and the number of days after implantation as a random effect. Estimates of variance components were obtained using the Laplacian approximation method, and the model fit was assessed using deviances. The significance of effects was estimated from the degree of freedom and \( t \) statistics followed by Bonferroni correction. Analysis was done using the lmer function for fitting generalized linear mixed-effects models, in the R statistical software package (version 2.6.0).

Results

Exon-based array analysis of HCC. Twenty paired samples of HCC and adjacent nontumorous liver tissue were subjected to genome-wide expression analysis using two different batches of the GeneChip Human Exon 1.0 ST arrays [discovery sets 1 (10 pairs) and 2 (10 pairs)]. Statistical analysis was done separately, and genes expressed differentially in the two sets were selected to eliminate any experimental bias caused by batch-to-batch variations. The exon array can detect mRNAs with low abundance as well as alternatively polyadenylated and spliced mRNA because the probes are designed to hybridize with the entire sequences of the transcripts (21). We identified 124 annotated genes that were differentially expressed between the background (nontumorous) liver tissue and HCC [at least a 3-fold change in transcription signal; \( P < 0.001 \) (paired \( t \) test with no correction)] in discovery set 1 (Supplementary Tables S2 and S3). The genes were clustered according to the similarity of their expression profiles (Fig. 1A), and the differential expression of representative genes was confirmed by real-time PCR (Fig. 1B). It was noteworthy that although 103 genes were found to be significantly downregulated, only 21 were apparently upregulated.

We selected 9 genes (AKR1B10, ANLN, CCNB1, HIST1H3B, HIST1H3C, HIST1H3I, RRM2, TOP2A, and TPX2) whose expression was upregulated in HCC (≥3-fold change in transcription signal; \( P < 0.001 \), \( t \) test) in both discovery sets 1 and 2. Furthermore, two additional genes (HCAP-G and DEPDC1) were selected using a different criterion (>2.5-fold change across all of the 20 cases in discovery sets 1 and 2, and a raw signal of <50 in all 20 of the nontumorous liver tissues; \( P < 0.05 \), \( t \) test).

RNAi-based screening of genes required for HCC cell proliferation. To identify genes that are essential for HCC cell proliferation, siRNA-based screening was done for the 11 genes that were upregulated in HCC. Two or three constructs of siRNA were designed for each gene. Relative cell viability was evaluated by the mitochondrial succinate-tetrazolium reductase activity-based assay 3 days after transfection (Fig. 2A). We selected five genes (TPX2, RRM2, HCAP-G, HIST1H3I, and AKR1B10) based on the criterion that at least two siRNAs per gene reproducibly suppressed cell proliferation by >20% in all of three cell lines (KIM-1, Hep3B, and HLE). Representative data are shown in Fig. 2A and B. The baseline expression of these genes was determined in the three cell lines by real-time reverse transcription-PCR (RT-PCR; Fig. 2C). We confirmed the cell proliferation–inhibitory activity of the siRNA by counting the numbers of cells (Fig. 2D).

Validation of differential gene expression in additional cases of HCC. The increased expression of the five genes selected using the siRNA-based screen was validated in 20 cases of HCC (validation set 1) by real-time PCR (Fig. 3A). The expression of all five genes was confirmed to be increased in HCC. The expression of TPX2, RRM2, HCAP-G, and HIST1H3I was associated with loss of histologic differentiation (Fig. 3A, right). The expression of AKR1B10 was upregulated in HCC regardless of differentiation. We further confirmed the differential expression of these genes between HCC and nontumorous liver tissues in 44 additional independent cases of HCC (validation set 2) by real-time PCR (Fig. 3B).

In the 18 normal organs examined, no significant expression of TPX2, RRM2, or HCAP-G was observed, except for the thymus (Fig. 4, left), which is largely involved in nonjuvenile adults. No organs showed higher expression of AKR1B10 than was the case in HCC. We did not select HIST1H3I, as this gene showed high expression in several vital organs (Fig. 4).

Protein expression analysis. Expression of the products of four candidate genes, TPX2, HCAP-G, RRM2, and AKR1B10,
Fig. 1. Genes differentially expressed between HCC and nontumorous liver. A, hierarchical clustering of 124 genes whose expression differed significantly (P < 0.001 and >3-fold change) between HCC and adjacent nontumorous liver. Transcriptional signal intensity is shown as a heat map. Red indicates higher signals, whereas blue indicates lower signals. Arrows indicate eight genes selected for validation by real-time PCR (B). B, validation of the microarray data by real-time RT-PCR. The expression levels of eight representative genes whose expression differed significantly between adjacent nontumorous liver (left) and HCC (right) were validated by real-time RT-PCR (shown in arbitrary units). Significant correlation between array (discovery set 1) and real-time RT-PCR data was confirmed by calculating correlation coefficient values in eight randomly selected genes (indicated by arrows in A): C7, 0.96; COLEC10, 0.97; CRHBP, 0.98; HAMP, 0.98; CCNA2, 0.82; RGSS, 0.80; AKR1B10, 0.98; ANLA, 0.92. The significance of differential expression between HCC and adjacent nontumorous liver tissue was assessed using a permutation paired t test, and Bonferroni-corrected P values are provided.
was examined immunohistochemically in 19 independent cases of HCC (Fig. 5). In 84% (16 of 19) of the cases, AKR1B10 protein was detected in the cancer but was hardly evident in the adjacent nontumorous liver tissue. The nuclear staining of HCAP-G and TPX2 was stronger in HCC than in the adjacent nontumorous liver in 42% (8 of 19) and 58% (11 of 19) of cases, respectively. Patchy staining of RRM2 was observed in 84% (16 of 19) of the HCCs.

**Inhibition of tumor growth in vivo.** Finally, we performed an *in vivo* experiment to evaluate the feasibility of the four selected genes as therapeutic targets. siRNA against AKR1B10, HCAP-G, RRM2, and TPX2 mixed with atelocollagen was injected into tumors (31.5 ± 1.9 mm³) established by xenografting KIM-1 cells into the flank of nude mice (Fig. 6). Atelocollagen forms a complex with siRNA, thus enhancing its stability and allowing sustained release of siRNA *in vivo* (17, 18). The silencing of the target genes by each relevant siRNA was confirmed by real-time PCR (Fig. 6A). Treatments with siRNA against AKR1B10, HCAP-G, RRM2, or TPX2 given twice, 1 week apart, significantly suppressed tumor growth (Fig. 6B; Supplementary Fig. 2).
and the growth-inhibitory effects of siRNA were confirmed by weighing the excised tumors (Fig. 6C).

**Discussion**

There is now strong epidemiologic evidence that persistent infection with hepatitis B or C virus is a major cause of HCC. However, the precise molecular mechanism behind the development of HCC is still unclear. Mutation in the tumor suppressor gene TP53 is most frequently observed in HCC associated with aflatoxin B exposure as well as chronic infection with hepatitis B and C viruses (22–24); however, it seems to be a late event during multistep carcinogenesis (22). Deregulation of the Wnt as well as other
signaling pathways has been reported in HCC (22, 25). Therefore, a therapeutic method that can normalize these aberrantly activated oncogenic signals would be clinically valuable. In an attempt to discover therapeutic targets with high specificity for HCC, we searched for genes that are specifically upregulated in HCC in comparison with non-tumorous liver tissue and normal vital organs using high-density microarrays designed to detect all the exons in the human genome (Figs. 1 and 4). This was followed by siRNA-based screening of genes required for HCC cell proliferation (Fig. 2) as well as quantitative RT-PCR analysis and immunohistochemistry of additional cases (Figs. 3 and 5). We finally identified four candidate genes and confirmed their functional involvement in the tumor growth of HCC xenografts (Fig. 6). These genes, AKR1B10, HCAP-G, RRM2, and TPX2, were expressed strongly and specifically in HCC, which is highly dependent on these genes for proliferation, and their feasibility as therapy targets also seems to be supported by the literature.

RRM2 is a subunit of ribonucleotide reductase that catalyzes the conversion of ribonucleoside 5′-diphosphates into their corresponding 2′-deoxyribonucleotides. Because this reaction is the rate-limiting step of DNA synthesis, and inhibition of ribonucleotide reductase stops DNA synthesis and cell proliferation, RRM2 has been considered a promising target for cancer therapy (26).

TPX2 (C20ORF1) is a microtubule-associated protein whose expression is restricted to the S, G2, and M phases of the cell cycle. Suppression of TPX2 expression by RNAi causes defects in microtubule organization during mitosis, leading to the formation of two microtubule asters that do not form a spindle (27). TPX2 is necessary for maintaining aurora A kinase in an active conformation (28, 29). Aurora kinases are essential for the regulation of chromosome segregation and cytokinesis during mitosis and have been reported to be overexpressed in a wide range of human tumors. Several aurora kinase inhibitors, such as VX-680/MK-0457, have been showed to have anticancer effects.

**Fig. 3. Continued.** B, expression levels of mRNAs for selected genes in 44 independent pairs of HCC (41-84T) and adjacent nontumorous liver tissue (41-84N; validation set 2) determined by real-time PCR.
in vitro and in vivo (30, 31). The binding of TPX2 modulates the conformation of aurora A and reduces its affinity for VX-680 (32). Inhibition of TPX2 may increase the efficacy of this class of aurora kinase inhibitors.

HCAP-G is a component of the condensin complex that organizes the coiling topology of individual chromatids. Condensin also contributes to mitosis-specific chromosome compaction and is required for proper chromosome

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**Fig. 4.** Expression in normal organs. Expression levels of mRNAs for selected genes in 10 pairs of HCC (1-10T) and adjacent nontumorous liver tissue (1-10N; discovery set 1) and 18 normal organs determined by Human Exon 1.0 ST arrays (shown in arbitrary units). The significance of differential expression between HCC and adjacent nontumorous liver tissue was assessed using permutation paired t test, and Bonferroni-corrected P values are provided. S. muscle, skeletal muscle; S. intestine, small intestine.
segregation, although the functional significance of HCAP-G in the condensing complex is largely unknown (33, 34).

AKR1B10 (ARL1, aldose reductase-like 1) was originally isolated as a new member of the aldo-keto reductase superfamily overexpressed in HCC and is reportedly related to the histologic differentiation of HCC (35, 36). AKR1B10 was also overexpressed in squamous cell carcinoma of the lung and its precursor conditions (37). Because the expression of AKR1B10 was highly specific to HCC and its inhibition suppressed tumor growth (Fig. 6), chemicals that specifically inhibit AKR1B10 activity may be useful anticancer drugs with minimal side effects.

It cannot be denied that many important genes were probably overlooked at every step of the present screen, although the four selected genes seem to be highly relevant from a biological viewpoint. HCC has been recognized as a single category of disease; however, the overall gene expression patterns seem to differ markedly

Fig. 5. Protein expression in HCC. Hematoxylin and eosin (HE) staining (original magnification, × 100) and immunoperoxidase staining (original magnifications, × 100 and × 400) of AKR1B10, HCAP-G, RRM2, and TPX2 proteins in HCC and adjacent nontumorous liver tissue. The specificity of antibodies was determined by immunoblotting of the KIM-1 cell lysate (left). N, nontumorous liver.
among individual cases. A search for the genes responsible for the different clinical outcomes of HCC will be the subject of a future study. We used the cell proliferation assay for siRNA-based functional screening. However, the use of other assays capable of evaluating cell motility, migration, drug sensitivity, or cell death may help to identify genes differing in their biological significance. The combination of genome-wide expression and functional screening described here provides a rapid and comprehensive approach that could be applicable for studies of various aspects of human cancer.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

Fig. 6. Suppression of tumor growth by siRNA. A, KIM-1 cells were s.c. inoculated into the flanks of nude mice. Eight days later, control siRNA or siRNA against AKR1B10, HCAP-G, RRM2, or TPX2 was injected into the developed tumors. The tumors were excised 2 days after the injection, and the expression levels of the indicated genes were determined by real-time PCR. Values of control siRNA were set at 1. B, chronological changes in tumor volume after two injections of the indicated siRNA. Volume of tumors was determined every 3 days as described in Materials and Methods. **, significantly different with a Bonferroni-corrected P value of <0.001. *, significantly different with a Bonferroni-corrected P value of 0.012. C, weight (mean + SE in mg) of xenografts measured 18 days after the second injection of the indicated siRNA and controls. D, macroscopic appearance of xenografts injected with control siRNA (top) and siRNA against TPX2 (bottom).
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