Metabolic Characterization of Hepatocellular Carcinoma Using Nontargeted Tissue Metabolomics

Qiang Huang1, Yexiong Tan2, Peiyuan Yin1, Guozhu Ye1, Peng Gao1, Xin Lu1, Hongyang Wang2, and Guowang Xu1

Abstract

Hepatocellular carcinoma has a poor prognosis due to its rapid development and early metastasis. In this report, we characterized the metabolic features of hepatocellular carcinoma using a nontargeted metabolic profiling strategy based on liquid chromatography-mass spectrometry. Fifty pairs of liver cancer samples and matched normal tissues were collected from patients having hepatocellular carcinoma, including tumor tissues, adjacent noncancerous tissues, and distal noncancerous tissues, and 105 metabolites were filtered and identified from the tissue metabolome. The principal metabolic alternations in HCC tumors included elevated glycolysis, gluconeogenesis, and β-oxidation with reduced tricarboxylic acid cycle and Δ-12 desaturase. Furthermore, increased levels of glutathione and other antioxidative molecules, together with decreased levels of inflammatory-related polyunsaturated fatty acids and phospholipase A2, were observed. Differential metabolite levels in tissues were tested in 298 serum specimens from patients with chronic hepatitis, cirrhosis, and hepatocellular carcinoma. Betaine and propionylcarnitine were confirmed to confer good diagnostic potential to distinguish hepatocellular carcinoma from chronic hepatitis and cirrhosis. External validation of cirrhosis and hepatocellular carcinoma serum specimens further showed that this combination biomarker is useful for diagnosis of hepatocellular carcinoma with a supplementary role to α-fetoprotein. Cancer Res; 73(16); 1–11. ©2013 AACR.

Introduction

Hepatocellular carcinoma is one of the most common malignancies worldwide. In China, chronic hepatitis B virus infection is the primary risk factor for hepatocellular carcinoma (1, 2), and the majority of hepatocellular carcinoma cases develop from hepatitis infections and subsequent cirrhosis. Rapid development and early metastasis are the typical characteristics of hepatocellular carcinoma, which always results in a poor prognosis. The large population infected with hepatitis B virus (HBV) makes the prevention of hepatocellular carcinoma a formidable task. Therefore, investigating the hepatocarcinogenesis mechanism is very important for decreasing the incidence and mortality of hepatocellular carcinoma.

The abnormal metabolism of cancer has been considered an important characteristic of tumors, which could clarify the pathogenesis and provide potential therapeutic targets for clinical treatments (3). According to the Warburg effect, the deregulated energy metabolism of cancer cells may also modify many related metabolic pathways that influence various biological processes, such as cell proliferation and apoptosis. As a common characteristic of cancer cells (4, 5), modified metabolism has been the focus of cancer research.

Metabolomics is a top-down platform in the field of systems biology, which focuses on the dynamic changes of small molecules in response to the disturbance of the organism (6). Nontargeted metabolomic approaches are being widely used for the discovery of new biomarkers and investigation of the carcinogenesis mechanism, and these approaches have also been used to investigate chronic liver diseases (CLD) and hepatocellular carcinoma (7, 8). Some serum or urine metabolites, such as sphingosines (7), bile acids, glycine, trimethylamine-N-oxide, and dipeptides (8, 9), have been reported to be differential metabolites or candidate biomarkers for CLD or HCC. Serum and urine are commonly considered to be a pool of metabolites that reflect systemic metabolic deregulation in patients, and the markers in these biofluids could reflect the characteristics of the system during the course of diseases.
Tissue metabolomics is a useful tool for studying the abnormal metabolisms of diseases, and it can provide information about the metabolic modifications and the upstream regulative mechanism in diseases (10, 11). More importantly, the systemic metabolic characteristics of tissues could provide opportunities for exploring novel diagnostic markers or therapeutic targets for clinical applications (12). Tissue metabolomics is conducted using a pairwise comparison of different parts of tissue from each patient, which can remove individual differences, such as age, sex, region, and so on. The differences between the tumor cells and their surrounding host cells may reflect the interactions of the tumor and the host, which are important clues for studying the invasion and metastasis of tumors (13).

In this study, 50 sets of matched hepatocellular carcinoma tissues, including hepatocellular carcinoma tissue (HCT), adjacent noncancerous tissue (ANT), and distal noncancerous tissue (DNT), were collected. The metabolic characteristics of the tumor tissues and the impact of the tumors on the surrounding host cells were explored through metabolomics strategy based on liquid chromatography-mass spectrometry (LC/MS). On the basis of the defined differential metabolites, metabolic pathways and correlation networks were investigated and their potential for use in clinical diagnostics was investigated.

Materials and Methods

**Chemicals**

Acetonitrile and formic acid [high-performance liquid chromatography (HPLC) grade] were purchased from Merck. Methanol (HPLC grade) was purchased from Tedia. Distilled water was filtered through a Milli-Q system (EMD Millipore Corporation). Glycophosphocholine, betaine, carnitine, homocysteine, S-adenosylhomocysteine, N-acetyl-l-methionine, leucine, phenylalanine, isoleucine, tryptophan, glycococholate, free fatty acid (FFA) C14:0, FFA C18:3, FFA C18:2, and FFA C18:1 were purchased from Sigma-Aldrich. Lysophosphorylcholine (LPC) C18:2, LPC C16:0, and LPC C18:0 were purchased from Avanti Polar Lipids. Ammonium bicarbonate (NH₄HCO₃, HPLC grade) was purchased from Fluka.

**Clinical sample collection and pretreatment**

Written informed consents were obtained from the patients, and the study was approved by the ethics committee of the Eastern Hepatobiliary Surgery Institute. Tissues were collected from 50 patients (male/female, 39/11) having hepatocellular carcinoma who ranged in age from 30 to 70 years. Of these, 38 of the patients were HBsAg-positive, and 1 patient was anti-HCV-positive. In each patient, three types of tissues were resected during the operation, including HCTs, ANTs, and DNTs. The ANTs were collected from less than 2 cm into the solid tumor border. During the operation, DNTs were collected from the distal edge of the resected tissues, which were more than 2 cm from the border of the solid tumor. The lesions were analyzed using histopathology studies. Detailed clinical information about the collected samples is presented in Table 1. The tissue samples were directly placed into liquid nitrogen after surgical resection and stored at −80°C until analysis.

To investigate the diagnostic potentials of the differential metabolites discovered from the tissues, a total of 298 fasting serum samples, including 81 chronic hepatitis, 78 cirrhosis and 139 hepatocellular carcinoma samples, were collected and the detailed clinical characteristics are described in Supplementary Table S1. Another batch of serum samples from

<table>
<thead>
<tr>
<th>Characteristics</th>
<th>Male, n = 39</th>
<th>Female, n = 11</th>
<th>P value</th>
</tr>
</thead>
<tbody>
<tr>
<td>AFP (μg/L) – &lt;20/20</td>
<td>17/22</td>
<td>6/5</td>
<td>0.708</td>
</tr>
<tr>
<td>Age (y)</td>
<td>51.9 (30–70)</td>
<td>51.2 (38–65)</td>
<td>0.845</td>
</tr>
<tr>
<td>ALT (U/L)</td>
<td>116.8 (20.0–417.0)</td>
<td>88.0 (22.0–495.0)</td>
<td>0.437</td>
</tr>
<tr>
<td>AST (U/L)</td>
<td>47.3 (18.4–322.2)</td>
<td>37.6 (16.2–64.1)</td>
<td>0.527</td>
</tr>
<tr>
<td>Cirrhosis/no cirrhosis</td>
<td>23/16</td>
<td>0/11</td>
<td></td>
</tr>
<tr>
<td>HBsAg-positive/negative</td>
<td>30/9</td>
<td>8/3</td>
<td></td>
</tr>
<tr>
<td>Anti-HCV-positive/negative</td>
<td>1/38</td>
<td>0/11</td>
<td></td>
</tr>
<tr>
<td>Tumor diameter (cm)</td>
<td>7.1 (2–18)</td>
<td>7.1 (3.6–11)</td>
<td>0.996</td>
</tr>
<tr>
<td>Edmonson stage</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>II</td>
<td>8</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td>III</td>
<td>21</td>
<td>7</td>
<td></td>
</tr>
<tr>
<td>Edmonson stage</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>II + III</td>
<td>2</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>III + IV</td>
<td>2</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td>Not determined</td>
<td>6</td>
<td>3</td>
<td></td>
</tr>
</tbody>
</table>

NOTE: Age, ALT, AST, and tumor diameter in both male and female were expressed as median (range).
were similar to our previous work (14). The column temperature was maintained at 35°C and the sample manager was set to 4°C. The analysis time for each serum sample was 22 minutes. The resolution of the Orbitrap was set at 60,000 to ensure the mass errors were less than 2 ppm. Both betaine and propionylcarnitine are polar metabolites, and the CE–MS system is appropriate for polar compounds analysis. Thus, the quantitative analysis in the external validation from patients with hepatocellular carcinoma to cirrhosis was carried out by using the CE–MS system, and the detailed method is described in supplementary materials.

To ensure data quality for metabolic profiling, pooled quality control (QC) samples were prepared by mixing all of the samples. Before analyzing the sample sequence, five QC samples were run. During analysis of the sample sequence, one QC sample was run after every 10 injections, which is similar to our previous method (15).

**Data processing and analysis**

First, the raw data were acquired and aligned using the SIEVE software package (V1.2, Thermo Fisher) based on the m/z value and the sample retention time. Before chemometrics analysis, all of the detected ions in each sample from one sample class were normalized to the sum of the peak area defined as 10,000 (16). After the missing values for each sample class were treated using the 80% rule (17), the statistical significance was calculated using the Student t test (P < 0.05) as implemented in the SPSS version 16 for Windows software package.

Ions from both ESI⁺ and ESI⁻ with statistical significance were merged and imported into the SIMCA-P program (version 11.0, Umetrics) for multivariate analysis. Principal component analysis (PCA) and partial least squares discriminate analysis (PLS-DA) were applied with unit variance (UV) scaling (16). The parameters of the models, such as the R²X, R²Y, and Q²Y, and the R²Y-, Q²Y-intercepts, were analyzed to ensure the quality of the multivariate models and to avoid the risk of over-fitting. The normalized amount of each metabolite was plotted in a histogram using the Origin software package (version 8.0). Hierarchical cluster analysis (HCA) was conducted using the MeV software package (version 4.5.1), and the correlation network was constructed using the Cytoscape software package. Receiver operating characteristic curve (ROC) and binary logistic regression were applied to the serum data using SPSS software.

**Results**

A total of 50 patients with hepatocellular carcinoma were enrolled in this study. The diagnosis of hepatocellular carcinoma was confirmed by histopathologic studies after surgery. Twenty-three patients had serum α-fetoprotein (AFP) levels that were less than the cut-off value (20 μg/L). The Edmonson stages of the patients (nine were not determined) ranged from stages II to IV. There was no statistical significance observed between male and female patients (Student t test, P > 0.05) in the clinical tests employed. Steatotic liver tissue was not observed in any of the samples.
Metabolic profiling of liver tissues

In this study, a nontargeted metabolomics strategy was applied. The details of the metabolic profiling method, including sample preparation, metabolite extraction, and LC/MS analysis, were reported in our previous study (18). Supplementary Fig. S1 in supplementary materials presents the typical base peak chromatograms (BPC) of the HCT, ANT, and DNT groups. The metabolic profiles of the ANT and DNT groups were similar, but they were substantially different from that of the HCT group in both ESI+ and ESI− modes.

Validations of method, including linearity, precision, stability, and recovery, were also carried out (18), which indicates that this tissue metabolomics method is reliable. Furthermore, the PCA score plot (Supplementary Fig. S2A) exhibited a clear cluster of the pooled QC samples ($R^2$X, 0.647; $Q^2$, 0.404), indicating that the sample analysis sequence had satisfactory stability and repeatability.

After the peak alignment and the removal of the missing values (17), a total of 880 ions had significantly changed (Student t test, $P < 0.05$) between the HCT and DNT group, 942 ions between the HCT and ANT group, and only 46 ions between the ANT and DNT group were maintained (Supplementary Fig. S2A).

For further analysis of the metabolic differences between the DNT and HCT group, all of the significant ions from the ESI+ and ESI− modes were merged and imported into the SIMCA-P software package. Subsequently, PLS-DA was applied to the classification of cancer and noncancerous tissues. As illustrated by the PLS-DA score plot (Supplementary Fig. S2B), the noncancerous tissues were clearly separated from the hepatocellular carcinoma tissues. The cumulative $R^2$Y and $Q^2$ were 0.804 and 0.657 respectively, when two components were calculated. No over-fitting was observed according to the results of the chance permutation ($R^2$Y-intercept was 0.420 and $Q^2$-intercept was −0.153). However, there was no obvious separation trend between the ANT and DNT groups.

Differential metabolites between HCT and DNT

PLS-DA S-plot (Supplementary Fig. S2C) can be used to define the differential metabolites for distinguishing the DNT group from the HCT group, 390 ions with a variable importance in the project (VIP) more than one were selected for subsequent chemical structure identification (19). Based on our previously published strategy (20), the following steps were used for the identification of chemical structures in this study. First, the quasimolecular ions were confirmed. Secondly, the exact masses of the monoisotopic molecular weights were used to search the online databases, such as the Human Metabolome Database (http://www.hmdb.ca/), Metlin (http://metlin.scripps.edu/) and the Mass Bank (http://www.massbank.jp/) (21). Then, the MS/MS spectra were also analyzed to verify the structure of the identified metabolites. Subsequently, 44 metabolites in ESI+ mode and 65 in ESI− mode were identified, and some of them were further confirmed using authentic standard samples. The names of the compounds and the related enzymes are presented in Supplementary Table S3.

The relative average normalized quantities of the identified differential metabolites in the HCT and ANT groups compared to those in the DNT group were plotted in a heat map (Fig. 1) using the MeV software package. The metabolites were clustered according to their Pearson correlation coefficients. Overall, the changes in these important metabolites in the HCT samples were quite different from those in the noncancerous tissues.

Based on the knowledge of these differential metabolites and an online database of metabolic pathways (Kyoto Encyclopedia of Genes and Genomes, http://www.genome.jp/kegg/), a map of the hepatocellular carcinoma-related metabolic pathways was constructed (Fig. 2). Several metabolic pathways were modified by the tumor cell, for example, an increase in glycolysis metabolites (6-phosphoglucuron acid) and a decrease in tricarboxylic acid cycle (TCA) metabolites, including succinate, fumarate, malate, and succinic acid semialdehyde, were observed. Most of the amino acids (AA) and their related metabolites significantly increased in the HCT group. The levels of two glucogenic AAs (serine and threonine), which can be transformed into glucose for energy, significantly increased in the HCT group. Glutamine, glutathione, branched-chain amino acids (BCAA), including valine, leucine, and isoleucine, and the aromatic amino acids (ArAA), such as tryptophan, phenylalanine, and tyrosine, were also increased in the HCT group. The increased catabolism may be responsible for the increase in total AAs. These modifications to the host metabolism represented the influence of the cancer cells on energy metabolism, which have also been confirmed in colon and stomach tumor tissues (13).

The change in the free fatty acids was not the same as that of the AAs. The levels of saturated fatty acids (SFA) and monounsaturated fatty acids (MFA) increased, whereas the levels of polyunsaturated fatty acids (PUFA) decreased (Fig. 3A). The ratio of FFA C18:2 to C18:1 also decreased in the HCT group (Fig. 3B), which suggested inhibition of Δ-12 desaturase. Interestingly, the ratio of acetylcarnitine to carnitine (C2/C0) was upregulated in the HCT group, whereas the ratio of propionylcarnitine to carnitine (C3/C0) was downregulated (Fig. 3C). The ratio of C2/C0 indicated that the β-oxidation of even-numbered fatty acids was upregulated in the HCT group. The ratio of C3/C0 conflicted with BCAA (Fig. 3D), which also reflected an increase in lipid oxidation for the production of energy in the tumor tissue (22). A decreased level of LPC was observed in the cancer tissues. However, phosphorylcholine (PC) and phosphoethanolamine (PE) levels were significantly greater in the cancer tissues (Fig. 2).

Correlation network of differential metabolites in tumor tissue

To investigate the latent relationships of the differential metabolites, a correlation network diagram was constructed using the Cytoscape software (Fig. 4). All of the differential metabolites (880 ions) were included in the diagram to obtain a global view of tumor metabolism. We observed that the metabolites could be divided into two primary groups: upregulated and downregulated. These groups were bridged by lipids.
Fatty acids, including SFA, MFA, and PUFA, were located in the center of the metabolic network. Levels of glycolysis-related metabolites and some AAs were upregulated in the tumor. Lipids, especially phospholipids, were the most correlated metabolites in the downregulated group. There was a decreased amount of bile acids in the tumor tissues. Because the metabolism of phospholipids and bile acids, the deregulation of these metabolites may reflect low differentiation levels of the tumor cells. Unlike long-chain acylcarnitines, the quantity of short-chain acylcarnitines decreased in the cancer tissues. The correlation of the metabolites in the TCA cycle and the short-chain acylcarnitines supported the hypothesis that energy metabolism shows low efficacy in tumor tissues.

Investigation of the diagnostic potential of differential metabolites found in tissues

The tissue metabolome can more directly reflect metabolic deregulation than the body fluid metabolome, but...
the biomarkers for clinical diagnosis should return from the tissue to the biofluids. Therefore, we also investigated the serum diagnostic potentials of these significantly different metabolites. Totally, 298 serum samples, including 81 chronic hepatitis, 78 cirrhosis, and 139 hepatocellular carcinoma, were enrolled.

Considering the complementary role of novel biomarkers to AFP in clinical diagnosis, we focused more on the metabolites that were not related with AFP level. The results of the Pearson correlation analysis (|Cij| < 0.15) indicated that eight important metabolites were irrelevant to serum AFP level, five of them including betaine, propionylcarnitine, proline, methionine, and isoleucyl-L-proline were found to be greatly different (Student t test, \( P < 0.001 \)) between nonmalignant liver diseases and patients having hepatocellular carcinoma (Supplementary Table S5). After the binary logistic regression analysis of the data, betaine and propionylcarnitine were selected as the optimal combination.
for diagnosis of hepatocellular carcinoma. As shown in Fig. 5A, both betaine and propionylcarnitine were markedly decreased in the HCC group. According to the data in patients with hepatocellular carcinoma versus nonmalignant liver diseases, the ROC curve of betaine plus propionylcarnitine yielded an area under the curve (AUC) of 0.982, whereas the AUC of AFP was only 0.697 (Fig. 5B). Two-thirds of the samples (54 hepatitis, 53 cirrhosis, and 93

Figure 3. Metabolic changes of free fatty acids, carnitines, and amino acids in the tumor tissues. A, FFA metabolism. B, ratio of FFA C18:2 to FFA C18:1. C, ratios of carnitines. D, BCAA (leucine, isoleucine, and valine). E, ArAA (phenylalanine and tyrosine). F, activity of phenylalaninehydroxylase (PAH) according to the ratio of tyrosine to phenylalanine. Light and dark chart, relative amount in the DNT and HCT groups, respectively. * , P < 0.05; ** , P < 0.01; *** , P < 0.001.

Figure 4. Metabolic correlation networks of the differential metabolites and related pathways. Highly correlated metabolites (|Cij| > 0.6) are connected with a line. Red, upregulated in tumor tissue; green, downregulated in tumor tissue. PUFA, polyunsaturated fatty acid; MUFA, monounsaturated fatty acid; SFA, saturated fatty acid; SC-AC, short-chain acylcarnitine.
hepatocellular carcinoma) were randomly selected from each group as the training set, and the remaining one-third of the samples (27 hepatitis, 25 cirrhosis, and 46 hepatocellular carcinoma) constituted the test set for validation. In the training set, the diagnostic accuracy of the chronic liver diseases and hepatocellular carcinoma patients achieved 91.6% and 96.8%, respectively. Meanwhile, the accuracy rate of the chronic liver diseases and patients with hepatocellular carcinoma also reached 94.2% and 93.5% in the test set (Fig. 5C). Noticeably, the combination of betaine and propionylcarnitine had a diagnostic accuracy of 92% in the AFP false-negative (AFP < 20 µg/L) patients with hepatocellular carcinoma. More valuably, these two metabolites were also effective for excluding AFP false-positive (AFP > 200 µg/L) patients without malignancy, which attained a diagnostic accuracy of 100% both for hepatitis and cirrhosis (Fig. 5D). These results showed that the capacity of betaine and propionylcarnitine combination as a novel hepatocellular carcinoma serum biomarker, especially its supplementary role to AFP.

To further externally validate the earlier experimental results, another batch of serum samples was enrolled from 25 patients with cirrhosis and 22 patients with hepatocellular carcinoma. Quantitative analysis of betaine and propionylcarnitine in the external validation serum samples was carried out on the CE–MS system. As shown in Supplementary Fig. S3A, the levels of betaine and propionylcarnitine in the hepatocellular carcinoma group were

![Figure 5. Diagnostic potential for hepatocellular carcinoma by betaine plus propionylcarnitine from serum. A, relative amount in patients who have hepatitis, cirrhosis, and hepatocellular carcinoma. B, ROC curves for distinguishing hepatocellular carcinoma from nonmalignant liver diseases by AFP and the combination of two metabolites, respectively. C, diagnostic accuracy for nonmalignant liver diseases and hepatocellular carcinoma in the training set and test set by using betaine plus propionylcarnitine. D, diagnostic accuracy in different concentrations of AFP serum samples among patients who have hepatitis, cirrhosis, and hepatocellular carcinoma. ***, *P* < 0.001.](image-url)
Discussion

Cancer metabolism has recently become a subject of considerable interest for both the pharmaceutical industry and clinical research. However, a systematic understanding of cancer metabolism remains a challenge. The primary goal in this study is to understand the metabolic features in hepatocellular carcinoma-related tissues by investigating the metabolic differences among the HCT, ANT, and DNT groups using a nontargeted tissue metabolomics method.

Metabolic features of tumor tissue

Based on the current results, we infer that the metabolites of glycolysis in tumor tissues, such as 6-phosphogluconic acid, increased while the metabolites in the TCA cycle decreased (Fig. 2). These data revealed the rapid expenditure of glucose through the glycolytic pathway with a low level of aerobic oxidation through the TCA cycle. Another important feature of the tumor cell can also be observed from the correlation network (Fig. 4), all of the enriched metabolites in tumor tissues are related to energy supply, such as glycolysis-related metabolites and some AA, SFA, and MFA. These results revealed the high energy requirements of the tumor cells for proliferation. Glucose is rapidly consumed in tumor cells through glycolysis. Furthermore, gluconeogenesis and β-oxidation in the tumor cells are upregulated for energy supply. In contrast, the TCA cycle is downregulated, and the short-chain and middle-chain acylcarnitines are also decreased, which shows decreased consumption of carboxylic acids in the mitochondria. This result is consistent with the Warburg effect (23, 24). Moreover, the increased consumption of glucose may upregulate gluconeogenesis from lipids and proteins. Because of the increased catabolism, the quantity of AAs and FFAs consequently increases. Therefore, modified metabolism of FFAs and AAs was observed in the tumor tissues. β-Oxidation of FFA is a multi-step process in which fatty acids are broken down in various tissues to produce energy. As shown in Fig. 4, lipids, including phospholipids and FFA, are the most correlated metabolites. First, the tumor cells modified their lipid metabolism to satisfy the large energy demand during cellular proliferation, which could be observed in the tumor tissue via the increased amounts of SFA and MFA. Furthermore, oxidative stress was increased by the effect of lipid peroxidation (25). Therefore, the suppressed functional enzyme Δ-12 desaturase (Fig. 3A) might be the mechanism through which tumor cells maintain high levels of SFA and MFA. The expression of the desaturase enzyme confirmed that β-oxidation was accelerated in the hepatocellular carcinoma tumor tissues compared with noncancerous tissues.

Because oxidative damage is the primary driver for cell apoptosis, the level of antioxidative metabolites would be accordingly elevated. We observed increased levels of some metabolites that could protect the tumor cells from oxidative damage in the tumor tissue. The striking elevation of 6-phosphogluconic acid suggested an increased flux of metabolic fuels into the pentose–phosphate pathway (PPP), perhaps to create NADPH to manage the perceived increase in oxidative stress in hepatocellular carcinoma (26). Glutamine is a major nitrogen carrier and a carbon substrate for anabolic processes in cancer cells, and it may protect cancer cells from oxidative stress and apoptosis (27, 28). Similarly, glutathione and glutathione disulfide, which are the major redox couple in animal cells (29), were also increased. The increase of glutathione reflected the alteration of the redox state, which is one of the key performance indicators in pathologic conditions, especially in cancer (30).

Chronic inflammation is an important factor of hepatocarcinogenesis (4), and it could influence tumor lipid metabolism. The metabolism of cholesterol and phospholipids is a primary function of normal liver cells, and the down-regulated synthesis of bile acids may lead to the malabsorption of lipids. The significant increases in taurine and 4-hydroxythreonine and decreases in urorbilinogen and glycine-conjugated bile compounds in hepatocellular carcinoma suggested that the co-metabolism of gut microbes was altered in hepatocellular carcinoma, and potential changes in the enterohepatic circulation may also have occurred (31). Moreover, bile acids are closely correlated with lipids, which may cause potential regulatory effects on nuclear receptors (32). The abnormal metabolism of phospholipids may influence many biological processes, for example, inflammation. PUFA, especially arachidonic acid, is the precursor for diverse inflammatory molecules (33). Phospholipids from the plasma membrane are the primary source of arachidonic acid. A decreased level of LPC was observed in the cancer tissues. However, the levels of PC and PE were significantly greater in the cancer tissues (Fig. 2). PC could be converted into LPC and arachidonic acid by the catalysis of phospholipase A2 (PLA2). To escape possible damage from the immune system, the tumor cell may reduce the generation of endogenic inflammation molecules by downregulating the related enzymes, such as PLA2 (34). According to the current results, it can be hypothesized that levels of PLAs or Δ-12 desaturase are altered in tumor cells in an attempt to modify the metabolism of lipids, thereby supporting the proliferation of tumor cells as well as their escape from immune attack and apoptotic cell death.

In addition to energy metabolism, AAs also serve a variety of biological functions. For example, several N-acetyl AAs (Ala, Met, and Trp) consistent with the observed increase of acetylcarnitine were elevated in hepatocellular carcinoma (Fig. 3C). These observations may suggest elevated acetyl coenzyme A concentrations in hepatocellular carcinoma (35). Furthermore, increased levels of BCAAs and ArAAs were observed in the tumor tissues (Fig. 3D and E). The increase of BCAAs occurred in concert with increases in
ArAAs (Trp, Tyr, and Phe), which implied that the enhancement of large neutral amino acids (LNAA) was facilitated by the t-type AA transporter-1 (LAT1; ref. 36).

The ratio between Phe and Tyr can be used as an indicator of phenylalanine hydroxylase (PAH; ref. 37). The decrease of the Tyr/Phe ratio in the HCT group (Fig. 3F) suggests the inhibition of PAH in tumor tissues. There were also some other metabolic features of hepatocellular carcinoma that reflected the upregulation of cellular proliferation. For example, the level of hypoxanthine increased in the HCT group, whereas that of xanthine declined sharply, which may suggest decreased activity of xanthine dehydrogenase/oxidase (38) and active cellular proliferation.

As indicated by the current results, the rapid expenditure of energy causes the cancer cells to modify the metabolic pathway to provide a sufficient amount of energy. Moreover, the cancer cells also try to avoid oxidative damage and chronic inflammation, which may reduce the occurrence of cellular apoptosis.

Diagnostic potentials of differential metabolites

The metabolic changes observed in biofluids might be caused by differences among individuals, including diet, sex, age, and so on. In this study, the significant changes in metabolites were defined by a pairwise comparison of different parts of the liver tissue from individuals, and the differences of other non-disease factors were removed. The relationship of differential metabolites with the clinical information of samples, including HBsAg, tumor diameter, as well as AFP, ALT, and AST levels, was investigated carefully (Supplementary Table S4). Thirty-eight patients with hepatocellular carcinoma were HBsAg-positive, and 12 patients were HBsAg-negative (Table 1). Citralacetic acid in tumor tissue was significantly decreased in patients who were HBsAg positive compared with those who were HBsAg negative (Supplementary Fig. S4). This finding may explain the suppression of TCA cycle under inflammatory status.

The differential metabolites found in tissues can be used as candidates biomarkers to investigate their diagnostic potential using serum as the sample. According to the results from Pearson correlation analysis, betaine and propionylcarnitine were found to be irrelevant to serum AFP level; they were defined to investigate the potential for distinguishing hepatocellular carcinoma (Fig. 5). The result indicated that betaine plus propionylcarnitine was efficient for distinguishing hepatocellular carcinoma from nonmalignant liver diseases with a 0.982 AUC value of the ROC curve, which was much better than that of AFP (0.697; Fig. 5B). The changes of betaine and propionylcarnitine in the external validation had the same change trend as the first batch of serum samples. In addition, good validation results further confirmed that the combination of these two metabolites was effective for hepatocellular carcinoma diagnosis.

Conclusions

In summary, the metabolic profiling analysis of liver tissues provided a holistic view of the metabolic features of hepatocellular carcinoma. The differential metabolites in the tumor tissues were filtered and identified, and the results showed that the metabolism in the tumor was modified to promote cellular proliferation or escape from apoptosis. The rapid consumption of energy by the tumor cells upregulated glycolysis and downregulated the TCA cycle, both of which are consistent with the Warburg effect. Gluconeogenesis and β-oxidation are also upregulated for energy supply, which could be observed from the enriched quantities of AAs and fatty acids. Based on the correlation network, modified metabolism of lipids is the most important feature of the hepatocellular carcinoma tumor, which may be important to protect the tumor cell from oxidative damage. This protective effect included increased levels of antioxidative metabolites and decreased levels of inflammation-related metabolites of PUFA, which is supposed to be related to the upstream enzymes, such as PLA2. This mechanism may be important for the tumor cell to break the balance of proliferation and apoptosis.

The diagnostic potential of the differential metabolites found in tissues, further studied in serum samples, and validated in another group of serum samples showed that the combination of betaine and propionylcarnitine has a better ROC curve than AFP; it is useful for both AFP false-positive and false-negative patients in distinguishing hepatocellular carcinoma from hepatitis and cirrhosis. These two metabolites have potential as hepatocellular carcinoma biomarkers in clinical diagnosis.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

Authors’ Contributions

Conception and design: Q. Huang, Y-X. Tan, P. Yin, G. Xu

Acquisition of data (provided animals, acquired and managed patients, provided facilities, etc.): Y-X. Tan

Analysis and interpretation of data (e.g., statistical analysis, biostatistics, computational analysis): Q. Huang, P. Yin, P. Gao, X. Lu, G. Xu

Writing, review, and/or revision of the manuscript: Q. Huang, Y-X. Tan, P. Yin, X. Lu, G. Xu

Administrative, technical, or material support (i.e., reporting or organizing data, constructing databases): Y-X. Tan, G. Ye

Study supervision: Y-X. Tan, G. Xu

Other (sample treatment): G. Ye

Other: H-Y. Wang

Acknowledgments

The authors thank Jun Zeng for the measurement of metabolites by using CE-MS.

Grant Support

The study has been financially supported by the State Key Science & Technology Project for Infectious Diseases (grant nos. 2012ZX10002-009 and 2008ZX10002-019), the key foundation (grant no. 21175132), and the creative research group project (grant nos. 81221061 and 21021004) from the National Natural Science Foundation of China.

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 January 31, 2013; revised May 27, 2013; accepted June 7, 2013; published OnlineFirst July 1, 2013.
Metabolic Modifications of HCC Based on Tissue Metabolomics

References


Published OnlineFirst July 1, 2013; DOI: 10.1158/0008-5472.CAN-13-0308
Metabolic Characterization of Hepatocellular Carcinoma Using Nontargeted Tissue Metabolomics

Qiang Huang, Yexiong Tan, Peiyuan Yin, et al.

Cancer Res  Published OnlineFirst July 1, 2013.

Updated version
Access the most recent version of this article at:
doi:10.1158/0008-5472.CAN-13-0308

Supplementary Material
Access the most recent supplemental material at:
http://cancerres.aacrjournals.org/content/suppl/2013/07/09/0008-5472.CAN-13-0308.DC1

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.