Cancer Usurps Skeletal Muscle as an Energy Repository

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Abstract
Cancer cells produce energy through aerobic glycolysis, but contributions of host tissues to cancer energy metabolism are unclear. In this study, we aimed to elucidate the cancer–host energy production relationship, in particular, between cancer energy production and host muscle. During the development and progression of colorectal cancer, expression of the secreted autophagy-inducing stress protein HMGB1 increased in the muscle of tumor-bearing animals. This effect was associated with decreased expression of pyruvate kinase PKM1 and pyruvate kinase activity in muscle via the HMGB1 receptor for advanced glycation endproducts (RAGE). However, muscle mitochondrial energy production was maintained. In contrast, HMGB1 addition to colorectal cancer cells increased lactate fermentation. In the muscle, HMGB1 addition induced autophagy by decreasing levels of active mTOR and increasing autophagy-associated proteins, plasma glutamate, and 13C-glutamine incorporation into acetyl-CoA. In a mouse model of colon carcinogenesis, a temporal increase in HMGB1 occurred in serum and colonic mucosa with an increase in autophagy associated with altered plasma free amino acid levels, increased glutamine, and decreased PKM1 levels. These differences were abolished by administration of an HMGB1 neutralizing antibody. Similar results were obtained in a mouse xenograft model of human colorectal cancer. Taken together, our findings suggest that HMGB1 released during tumorigenesis recruits muscle to supply glutamine to cancer cells as an energy source. Cancer Res; 74(1); 1–11. ©2013 AACR.

Introduction
Nontransformed mammalian cells produce energy via the tricarboxylic acid (TCA) cycle and the electron transport system in the presence of oxygen. In contrast, transformed cells produce energy through lactate fermentation, mainly in the presence of oxygen, which is called the Warburg effect (1). Recently, the Warburg effect has been shown to result from a switch in the expression of pyruvate kinase (PK) isoforms (2, 3). Activation of cellular myelocytomatosis (c-Myc) changes the alternative splicing pattern from PKM1 to PKM2, and then inactivation of PKM2 via phosphorylation induces anaerobic energy production (4–6). Energy production in cancer-burdened hosts and the relationship between host and cancer remain unclear. Patients with advanced cancer show malnutrition, weight loss, and cachexia, which suggests that cancer affects the energy production pathways of the host. To increase tolerance to anticancer treatments and improve the quality of life for patients with cancer, it is important to elucidate the altered energy production mechanisms in cancer-burdened hosts.

Free amino acids in plasma are supplied by dietary proteins and proteolysis (7, 8); therefore, alterations in the amino acids in plasma reflect changes in metabolism. Proteolysis is driven by ubiquitin-proteosomal degradation and autophagyclysosomal degradation, and the latter is responsible for bulk proteolysis (9). mTOR is a key molecule controlling autophagy (10). Inactivation of the mTOR complex by genotoxic stress, starvation, p53, or AMP-activated protein kinase induces activation of the autophagy machinery, including beclin-1, autophagy-related genes, and the microtubule-associated protein light chain (LC) 3. The plasma free amino acid (PFAA) profile is affected by various pathologic conditions. Japanese patients with metabolic syndrome have altered PFAA profiles; however, reduction of body mass index, blood pressure, and hemoglobin A1c and triglyceride levels was shown to normalize the profile (11). Patients with cancer of the lung, stomach, colorectum, breast, and prostate show altered PFAA profiles (12, 13). The pattern and degree of the changes depend on the type of cancer. Determination of the precise mechanism underlying alterations in the PFAA profile is required to utilize the profile data for disease diagnosis and treatment.

HMGB1 is a multifunctional protein that functions as a growth factor and enhances proliferation, invasion, and metastasis by binding to receptor for advanced glycation endproducts
(RAGE) in cancers (14, 15). HMGB1 is released by necrotic cells and secreted from monocyte-lineage cells, and induces inflammation (16, 17). An excess of HMGB1 induces apoptosis in monocyte-lineage cells, which reduces antitumor immunity and enhances cancer metastasis (15). HMGB1 also plays a pivotal role in the carcinogenesis and progression of colorectal cancer (18–20). In a rat colon carcinogenesis model using azoxymethane, HMGB1 levels continuously increased in the colonic mucosa (20). Several reports have shown that HMGB1 activates autophagy. HMGB1 binds to Toll-like receptor (TLR)-4 to activate innate immunity and immunologic autophagy by activating beclin-1 via dissociation from B-cell leukemia/lymphoma (Bcl-2) (21, 22). Cytosolic HMGB1 also directly interacts with beclin-1 to dissociate it from Bcl-2 (23).

In the present study, we report a new cancer–host energy metabolism relationship. Cancer cell-secreted HMGB1 affects host energy metabolism in colon cancer, resulting in an altered PFAA profile with increased glutamine, which is utilized as an energy source by cancer cells.

Materials and Methods

Clinical cases

Serum samples were obtained from 46 patients with colorectal cancer who were diagnosed in the Department of Molecular Pathology at Nara Medical University (Kashiwara, Nara, Japan).

Cell culture and reagents

A mouse colon cancer cell line, CT26, was kindly provided by Professor I.J. Fidler (MD Anderson Cancer Center, Houston, TX), and a human colon cancer cell line HT29 (Dainihon Pharmcy) was maintained in RPMI-1640 (Sigma) containing 10% FBS (Sigma) in 5% CO2 in air at 37°C. Cell morphology was evaluated daily by microscopic examination. Each cell line was routinely tested for mycoplasma contamination by genomic PCR. Before article submission, each cell line was tested for Trypan blue exclusion viability and hepatitis B virus (HBV) and hepatitis C virus (HCV) infection by genomic PCR. Viability was determined by 12.5% SDS-PAGE, and electrotransferred onto nitrocellulose filters. The incorporated protein was detected using peroxidase-conjugated immunoglobulin G antibodies (MBL). The immune complex was visualized by CSA ECL system (Amersham). Antibodies for mTOR, PKM1 (Epitomics), TLR4, PKM2 (Abnova), phosphorylated mTOR (Thr2448; Assay Biotechnology), RAGE, beclin-1 (Santa Cruz Biotechnology), LC3 (CosmoBio), BCL-2 (DAKO), and tubulin (loading control; Oncogene Research) were used as primary antibodies. For immunoprecipitation, the blots were incubated first with primary antibodies for beclin-1 (Santa Cruz) or BCL-2 (DAKO).

Reverse transcriptase PCR

RAGE mRNA was detected by reverse transcriptase PCR using total RNA (0.5 μg) extracted with RNeasy kit (Qiagen). The
primer sets used to amplify rat HMGB1 (GenBank accession no. NM_012963.20) were forward 5′-GAGCACAAGAAGAGCACCC-3′ and reverse 5′-TAACGAGCCTTGTCAGC-3′ (synthesized by Sigma Genosys).

ELISA
Assay kits were used to measure concentrations of HMGB1 (Shino-test), glutamine (MyBioSource), 1,3-bisphosphoglycerate (Uscn Life Science), pyruvate (IK International), PK (Casabio Biotech), acetyl-CoA (AcCoA; Abnova), lactate, α-ketoglutarate (Biovision), malate (Abcam), and interleukin (IL)-1β (Uscan), and IL-6 (ENZO Life Science). MitoTracker green (MTG; Invitrogen) was used to measure mitochondrial volume and membrane potential (MV; ENZO) according to the manufacturer’s instructions.

Measurement of 13C-labeled metabolites by LC-MS
Thin slices of muscle were placed in 3.5-cm dishes and cultured in regular medium supplemented with 2 mmol/L 13C-glutamine (IsoTech) for 12 hours. Fresh medium was simultaneously incubated without cells as a reference. Cells were then lysed with a solution of 50% methanol/30% acetonitrile in water stored in dry ice/methanol, and then quickly scraped. The lysate was centrifuged at 16,000 × g for 15 minutes at 0°C, and the supernatant was collected for liquid chromatography/mass spectrometry (LC/MS) analysis. The 18,000 cells were lysed in 1 mL of extraction solution. Intermediates were separated using a liquid chromatography system.

siRNA and microRNA
FlexiTube siRNAs for RAGE and TLR4, and AllStars Negative Control siRNA were purchased from Qiagen Genomics. Cells were transfected with 50 nmol/L siRNA using Lipofectamine 2000 (Invitrogen), according to the manufacturer’s instructions. For administration of GLS glutaminase miTarget miRNA (GeneCopoeia), 100 pmol of miRNA was encapsulated in 2 mL of cationic liposome (EL-C-01, DPPC: 26 mmol/L, Nippon Bio Biotech), acetyl-CoA (AcCoA; Abnova), lactate, glutamate (Uscn Life Science), pyruvate (JK International), PK (Cusabio Biotech), glutamine (MyBioSource), 1,3-bisphosphoglycerate, and membrane potential (MV; ENZO) according to the manufacturer’s instructions.

Statistical analysis
Statistical significance was examined by ANOVA, a two-tailed, unpaired Mann–Whitney test, and a Spearman test using InStat software (GraphPad). Statistical significance was defined as a two-sided P < 0.05. Cluster analysis was performed by the Ward method.

Results
Serum concentration of HMGB1 in patients with colorectal cancer
HMGB1 expression has been shown to be closely associated with colorectal cancer progression (15, 18, 30). In the present study, serum HMGB1 concentration was examined in 10 healthy volunteers and 46 patients with colorectal cancer. As shown in Table 1, HMGB1 concentration was significantly associated with colorectal cancer stage (P < 0.0001).

<table>
<thead>
<tr>
<th>Stage</th>
<th>n</th>
<th>Serum HMGB1 concentration (ng/mL)</th>
<th>Serum glutamine concentration (µmol/L)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Control</td>
<td>10</td>
<td>32.4 ± 15.4</td>
<td>512.3 ± 49.5</td>
</tr>
<tr>
<td>I</td>
<td>16</td>
<td>91.8 ± 48.2</td>
<td>520.8 ± 51.9</td>
</tr>
<tr>
<td>II</td>
<td>13</td>
<td>236.4 ± 134.4</td>
<td>543.5 ± 55.2</td>
</tr>
<tr>
<td>III</td>
<td>11</td>
<td>518.4 ± 193.4</td>
<td>577.1 ± 53.8</td>
</tr>
<tr>
<td>IV</td>
<td>6</td>
<td>751.3 ± 196.0</td>
<td>612.7 ± 61.4</td>
</tr>
</tbody>
</table>

Pathology stage was classified according to the TNM classification (46). Stage I, tumor within the mucosal propria or submucosal layers; stage II, tumor invades beyond the muscularis propria without lymph node metastasis; stage III, tumor shows lymph node metastasis; stage IV, lymph node metastases may or may not be observed, distant metastases may be observed.

Effect of HMGB1 on muscle tissues
The effect of HMGB1 on normal tissues was examined in an ex vivo mouse soleus muscle model (Fig. 1). Expression of the HMGB1 receptors TLR4 and RAGE in muscle tissue and colorectal cancer cell was confirmed by Western blotting (Fig. 1A). PK mediates the linker reaction between glycolysis and the TCA cycle, which is followed by oxidative phosphorylation. PKM1 is expressed in mature tissues, whereas PKM2 is expressed in embryonic tissues and cancer cells. In CT26 and HT29 colorectal cancer cells, PKM2 expression was higher than PKM1 expression. After HMGB1 treatment, PKM1 levels in colorectal cancer cells decreased; however, PKM2 levels were not altered (Fig. 1B). HMGB1 treatment decreased PKM1 production, which was only produced in the muscle. Knockdown of RAGE abrogated the HMGB1-induced PKM1 decrease in colorectal cancer cells and muscle (Fig. 1C). In contrast, knockdown of TLR4 did not affect the HMGB1-induced PKM1 decrease. Following HMGB1 treatment, PK activity decreased in the muscle but not in colorectal cancer cells (Fig. 1D).

Mitochondrial function of HMGB1-treated tissues
A decrease in the reaction that produces pyruvate could suppress oxidative energy production. In the ex vivo analysis, HMGB1 did not affect mitochondrial density or membrane voltage in the muscle (Fig. 1E and F). The ATP concentration in colorectal cancer cells was not altered by HMGB1. In contrast, following HMGB1 treatment, the ATP level in the muscle decreased by 17% (Fig. 1G). The lactate concentration increased in colorectal cancer cells, whereas in the muscle, lactate was not altered and remained at low levels (Fig. 1H).

Effect of HMGB1 on the amino acid profiles in mice
The effect of HMGB1 on normal mouse tissues was examined. Male BALB/c mice were administered HMGB1 (4.5 mg/kg

Table 1. Concentration of serum HMGB1 and glutamine in patients with colorectal cancer

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body weight) by intraperitoneal injection (Fig. 2A). Physical abnormalities and inhibition of body weight gain were not observed in HMGB1-treated mice. However, HMGB1 treatment decreased PKM1 production and PK activity in the muscle (Fig. 2B and C). HMGB1 treatment also affected the PFAA profile, and glutamate levels increased (Fig. 2C). In the soleus muscle, the levels of all amino acids except aspartate decreased. At autopsy, the serum concentrations of IL-1β and IL-6 were also measured (Fig. 2D). HMGB1-treated mice had higher levels of IL-1β and IL-6 than PBS-injected mice.

**Induction of autophagy in mouse muscle by HMGB1**

We examined the mechanism underlying HMGB1-associated autophagy induction using an ex vivo assay of mouse muscle (Fig. 2E to H). HMGB1 treatment reduced mTOR phosphorylation, which induced autophagy-related beclin-1 and LC3bII expression in the muscle (Fig. 2E). HMGB1 treatment also induced p38 phosphorylation, which is required for activation of the autophagy machinery (Fig. 2F). Treatment with a p38 inhibitor inhibited LC3 upregulation. Knockdown of the HMGB1 receptor RAGE reduced the dephosphorylation of...
mTOR (Fig. 2G). Therefore, mTOR inactivation occurred in response to RAGE activation by HMGB1. In contrast, knockdown of another HMGB1 receptor, TLR4, abrogated the coprecipitation of Bcl-2 with beclin-1 (Fig. 2H). Therefore, HMGB1 activated beclin-1 through TLR4 signaling. HMGB1 treatment decreased the total protein levels in the muscle (Fig. 2I). Because PK links glycolysis to the TCA cycle by supplying AcCoA, the levels of an upstream member of the PK pathway (1,3-bisphosphoglycerate; 1,3BPGA), a downstream product of PK (pyruvate), and AcCoA were examined (Fig. 2J). Treatment of the muscle with HMGB1 increased 1,3BPGA levels and decreased pyruvate and AcCoA levels. Treatment with 3MA inhibited autophagy and significantly increased lactate levels (Fig. 2K). HMGB1 increased glutamine uptake in the muscle (Fig. 2L). The 13C-labeled glutamine was markedly increased in the muscle and was incorporated into α-ketoglutarate (α-KG), malate, and AcCoA, but not into lactate (Fig. 2M).

**Alteration of the PFAA profile in mouse colon carcinogenesis**

PFAA profiles were during the development of colon cancer using a DMH-induced C57BL/6 mouse colon cancer model. The PFAA profiles were examined at 25, 35, and 40 weeks after starting DMH administration (Fig. 3A). Adenoma and carcinoma were not observed at week 25, whereas carcinoma was observed in all mice at week 40 (Fig. 3B). In the DMH-induced mouse colon cancer model, HMGB1 was increased, during the colonic carcinogenic process (Fig. 3C to E). Plasma HMGB1 protein levels and mucosal HMGB1 mRNA and protein levels were temporally increased. As
shown in Fig. 3F, the levels of several plasma amino acids were altered. In particular, glutamine levels increased in DMH-treated mice. To examine the role of HMGB1 on the PFAA profile in DMH-treated mice, HMGB1 activity was inhibited with a neutralizing anti-HMGB1 antibody (Fig. 3G). The PFAA profiles in groups of PBS injection, DMH treatment, and DMH treatment with anti-HMGB1 antibody were compared (Fig. 3H). The PFAA profile of the anti-HMGB1 antibody-administered DMH-treated mice with was the same as that of the control mice, but differed from the profile of the DMH-treated mice. In the soleus muscle, AcCoA and PKM1 were lower, whereas p-mTOR and LC3 were higher at weeks 35 and 40 than at week 25 (Fig. 3I and J). Cluster analysis showed that the PFAA profiles of DMH-model mice were compared (Fig. 3H). The PFAA profile of the anti-HMGB1 antibody-administered DMH-treated mice with was the same as that of the control mice, but differed from the profile of the DMH-treated mice. In the soleus muscle, AcCoA and PKM1 were lower, whereas p-mTOR and LC3 were higher at weeks 35 and 40 than at week 25 (Fig. 3I and J). Cluster analysis showed that the PFAA profiles of DMH-model mice
(week 25), DMH-untreated mice, anti-HMGB1 antibody-treated DMH-model mice, and PBS-injected mice belonged to the same cluster. In contrast, DMH-model mice (weeks 35 and 40), control serum-treated DMH-model mice, and HMGB1-injected mice belonged to the other cluster (Fig. 3K and Supplementary Table S1). These findings suggest that the HMGB1 concentration is the most relevant factor distinguishing the different clusters based on PFAA profile. To confirm the importance of HMGB1 on free amino acid metabolism, the serum concentrations of HMGB1 and glutamine were compared (Table 1). The concentrations of HMGB1 and glutamine were significantly correlated (Spearman $r = 0.9824$, $P < 0.01$). The concentration of glutamine was also associated with cancer stage ($P < 0.01$).

Alteration of muscle metabolism in mice with subcutaneous cancer

Plasma HMGB1 levels and metabolism in the muscle were examined in CT26 tumor-burdened BALB/c mice and HT29 tumor-burdened nude mice (Fig. 4). At 4 weeks, the tumors were growing and HMGB1 levels were increased (Fig. 4A). After 4 weeks, the muscle tissues showed decreased PKM1 expression and PK activity; however, no induction of PKM2 was observed (Fig. 4B and C). The ATP levels and mitochondrial voltages did not differ from those in control mice (Fig. 4D). Levels of 1,3BPGA increased, whereas pyruvate and AcCoA decreased (Fig. 4E). The glutamine carbons administered before sacrifice were mainly integrated into AcCoA (Fig. 4F).

![Figure 4.](image-url)
In the CT26 subcutaneous tumor model, a neutralizing anti-HMGB1 antibody was administered intraperitoneally to inactivate HMGB1 (Fig. 4G to I). The antibody treatment decreased the serum HMGB1 concentration secreted by CT26 tumors, which induced gains in both body weight and the protein content of mouse tissues.

**Utilization of muscle glutamine by cancer cells**

Finally, we aimed to elucidate the muscle-tumor glutamine cycle in a mouse tumor model (Fig. 5). A fasting-feeding cycle was repeated five times with 13C-glutamine injection to increase uptake of 13C-glutamine into the muscles of BALB/c mice (Fig. 5A; ref. 24). Then the mice were inoculated subcutaneously with CT26 tumors and were treated with an inhibitory agent of the glutamine cycle, an anti-HMGB1 antibody, an inactive glutamine analog, DON, and knockdown of glutaminase (GLS). Inhibition of the glutamine cycle decreased tumor growth and HMGB1 production from the tumors (Fig. 5B and C). As shown in Fig. 5D to G, the intratumoral distribution of 13C-glutamine from the muscle was examined. In control mice, HMGB1 secreted from cancer cells increased 13C-glutamine integration into AcCoA, and the muscle 13C-glutamine was transferred to cancer cells, which was mainly integrated into lactate (Fig. 5D). In contrast, treatment with the neutralizing
anti-HMGB1 antibody decreased $^{13}$C-glutamine integration into α-ketoglutarate, malate, and pyruvate in the cancer cells and muscle. In particular, it decreased $^{13}$C-glutamine integration into lactate in the cancer cells and into AcCoA in the muscle (Fig. 5E). Treatment with the inactive glutamine analog DON had an effect similar to that in the anti-HMGB1 antibody-treated mice (Fig. 5F). The effect of GLS microRNA injection into the tumor on the tumor $^{13}$C-glutamine integration pattern was similar to that in the DON-treated mice (Fig. 5G). Interestingly, the $^{13}$C-glutamine integration in the muscle was also similar to that in the DON-treated mice, which might be due to the reduced HMGB1 levels.

**Discussion**

In the present study, we examined the effects of HMGB1 on PK status and autophagy-proteolysis in muscle. HMGB1 decreased production of the PKM1 isoform in the muscles, which did not produce PKM2. In contrast, treatment of CT26 and HT29 colorectal cancer cells, which produce both PKM1 and PKM2, with HMGB1 decreased only PKM1. It has been shown that c-Myc is responsible for switching the expression from PKM1 to PKM2 (4); however, c-Myc is not expressed in the muscle. Therefore, PKM1-PKM2 switching did not occur, and PK activity decreased. This PK inactivation decreased the supply of pyruvate and AcCoA (downstream of pyruvate); however, mitochondrial energy production was maintained without increasing lactate production. To compensate for the decreased production of AcCoA from pyruvate, glutamine was used to supply α-ketoglutarate to the TCA cycle. The results of the carbon chase experiments indicated that glutamine was metabolized to produce primarily AcCoA so that the TCA cycle could continue to produce energy. We also examined the effect of HMGB1 on the liver (data not shown). The liver expresses the liver form of PK (PKLR) instead of PKM1 and PKM2. Because PKLR was not affected by HMGB1, the liver maintained aerobic energy production without glutamine usage. These results suggest that HMGB1-affected muscle might utilize amino acids as substrates for the TCA cycle.

To use amino acids as an energy source, free amino acids need to be generated from proteins. Our data suggest that in the presence of HMGB1, proteolysis associated with autophagy was induced. Autophagy involves the selective degradation of cellular components, including aged proteins, protein debris, and damaged organelles, which results in nutrient recycling and energy generation (10, 31). Autophagy is coupled with ubiquitination and subsequent proteasomal degradation in the protein quality control system (9, 32). Therefore, we examined autophagy signals in the tissues of HMGB1-treated mice. HMGB1 induced the dephosphorylation of mTOR, which upregulated the autophagy-associated proteins beclin-1 and LC3II through RAGE-associated p38 phosphorylation. RAGE has been shown to induce sustained autophagy and suppress apoptosis (33).

Moreover, HMGB1 activates TLR4 to release beclin-1 from the complex with Bcl-2. TLR4-induced autophagy is associated with defense against microbes, inflammation, and tumorigenesis (21, 22). Therefore, HMGB1 induces proteolysis through autophagy, which might supply free amino acids. An autophagy-induced glutamine supply might be important for maintaining mitochondrial energy production in the muscle. Bluemlein and colleagues stated that PK maintains amino acid homeostasis, whereas low PK increases cellular glutamine (34).

AcCoA generation from glutamine is thought to be an adaptation for retaining aerobic energy production in cancer-burdened hosts. Indeed, inhibition of autophagy by 3MA decreased AcCoA levels and induced lactate production in the muscle.

In contrast, cancer cells utilize glucose and glutamine as a carbon skeleton and produce energy through lactate fermentation (35, 36). HMGB1 treatment increased lactate fermentation in colorectal cancer cells in culture. Moreover, cancer cells consumed the plasma glutamine released from the muscle. The mouse model of muscle-integrated $^{13}$C-glutamine showed that it was used for lactate fermentation in the cancer cells. These findings suggest a cancer–host relationship in energy production. DeBerardinis and Cheng have advocated a cancer–muscle relationship through glutamine (37). They showed that glutamine is utilized to deliver carbon to the TCA cycle in cancer cells. c-Myc activation switches mitochondrial metabolism from glucose dependent to glutamine dependent (38, 39). The glutamine dependency of cancer cells is diverse. However, the possibility of this cancer–muscle relationship should be considered when treating patients with cancer (40). The wasting of muscle protein due to cancer–muscle interaction is an important mechanism that causes cachexia (37). Some “aberrant” energy production systems have been reported in cancer cells. For adapting hypoxic-hypoglycemic condition, some cancer uses fumarate as an energy source, which is known to occur in parasites (41).

In our experiments, the PFAA profile was altered because of autophagy, proteolysis, and utilization of amino acid as an energy source. From the present study and our previous reports, HMGB1 levels were increased beginning in the early stage of colon carcinogenesis (20). The PFAA profile was also altered during DMH-induced colon cancer development, and this alteration, including the increased glutamine, occurred before and after the neoplasm developed. These alterations in the PFAA profile resulted from the effects of HMGB1 on catabolism and energy production in the muscle, which altered amino acid metabolism. Cluster analysis clearly showed that the PFAA profiles were primarily distinguished by the level of HMGB1 (Fig. 3K). In addition to the mouse model results, human data for HMGB1 and glutamine showed evidence for this relationship at every stage of human colorectal cancer. Therefore, the PFAA profile might reflect a carcinogenic change, and could provide an opportunity to detect carcinogenic processes at the preclinical and precancerous phases (12). The PFAA profile in patients with several human cancers has been reported to be altered from that in healthy volunteers (12, 42). These findings suggest that the PFAA profile might be a sensitive probe of altered host metabolism due to cancer development.

Cancer possesses a chronic inflammation aspect, which could also alter the amino acid metabolism of the host. HMGB1

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is a key factor in innate immunity as a ligand of TLR4. The HMGB1-injected mouse model (Fig. 2) showed increased serum IL-1β and IL-6. These inflammatory cytokines are also candidates for catabolic factors in patients with cancer (43). Excessively high concentrations of HMGB1 induce apoptosis of macrophages and macrophage-lineage dendritic cells (15), and modest levels of HMGB1 induce inflammatory cytokines and might concurrently alter muscle metabolism. In the present study, neutralization of HMGB1 abrogated the changes in the PFAA profile in the carcinogenesis model. Therefore, HMGB1 might alter muscle metabolism both directly and through inflammatory cytokines.

Cancer cells consume both glucose and glutamine as energy sources, targeting just one of them, glutamine, is sufficient to suppress cancer growth, because glutamine is essential in DNA synthesis (24). Glutamine targeting using the inactive analog DON or GLS knockdown has been reported to be effective in suppressing cancer metastasis in an animal model (25). Our data also showed that glutamine targeting with an anti-HMGB1 antibody, DON, or GLS knockdown inhibited the growth of subcutaneous tumors. Inhibition of tumor growth decreased HMGB1 secretion, which abrogated the cancer–muscle relationship. Despite the difference in the PFAA of human and mouse, patients with colorectal cancer also show increased plasma glutamine (12). This suggests that glutamine targeting should be attempted in human patients with colorectal cancer.

Glutamine targeting is a way to correct the abnormal PFAA profile. For example, autophagy-induced malnutrition leads to compromised immunity and cancer progression; thus, tolerance to anticancer treatment might be diminished (44). To avoid extreme catabolic changes in cancer-burdened hosts with altered energy production, an adequate amino acid supply could be important. The necessity of supplying branched side chain amino acids to cancer-burdened hosts has been proposed (44). The observed PFAA profile suggests altered energy production in the host. A suitable amino acid supply could be necessary to improve energy production in a case-specific manner. This concept might be applicable to other diseases in addition to cancer.

HMGB1 is released in bulk from necrotic cancer cells, and activates living cancer cells to regrow (45). Adding these findings to the present observations, HMGB1 released from necrotic cancer cells might induce the degradation of host muscle tissues by autophagy to provide glutamine to the remnant cancer cells. Particularly in this situation, targeting HMGB1 and/or glutamine should be emphasized.

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

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Writing, review, and/or revision of the manuscript: Y. Luo, H. Kuniyasu
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Study supervision: H. Kuniyasu

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