Relationships between LDH-A, Lactate, and Metastases in 4T1 Breast Tumors

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Abstract

Purpose: To investigate the relationship between lactate dehydrogenase A (LDH-A) expression, lactate concentration, cell metabolism, and metastases in murine 4T1 breast tumors.

Experimental Design: Inhibition of LDH-A expression and protein levels were achieved in a metastatic breast cancer cell line (4T1) using short hairpin RNA (shRNA) technology. The relationship between tumor LDH-A protein levels and lactate concentration (measured by magnetic resonance spectroscopic imaging, MRSI) and metastases was assessed.

Results: LDH-A knockdown cells (KD9) showed a significant reduction in LDH-A protein and LDH activity, less acid production, decreased transwell migration and invasion, lower proliferation, reduced glucose consumption and glycolysis, and increase in oxygen consumption, reactive oxygen species (ROS), and cellular ATP levels, compared with control (NC) cells cultured in 25 mmol/L glucose. In vivo studies showed lower lactate levels in KD9, KD5, and KD317 tumors than in NC or 4T1 wild-type tumors (P < 0.01), and a linear relationship between tumor LDH-A protein expression and lactate concentration. Metastases were delayed and primary tumor growth rate decreased.

Conclusions: We show for the first time that LDH-A knockdown inhibited the formation of metastases, and was accompanied by in vivo changes in tumor cell metabolism. Lactate MRSI can be used as a surrogate to monitor targeted inhibition of LDH-A in a preclinical setting and provides a noninvasive imaging strategy to monitor LDH-A–targeted therapy. This imaging strategy can be translated to the clinic to identify and monitor patients who are at high risk of developing metastatic disease. Clin Cancer Res; 19(18); 5158–69. ©2013 AACR.
LDH-A expression, and to study the effects of LDH-A inhibition on tumor cell metabolism, growth, and the development of metastases. We address several new questions: (i) will shRNA-mediated reduction of LDH-A expression in 4T1 breast cancer cells alter orthotopic 4T1 tumor lactate concentrations?; (ii) does shRNA-mediated reduction of LDH-A expression in 4T1 breast cancer cells alter metabolism and sensitivity to metabolic stress (reactive oxygen species, ROS)?; (iii) does shRNA-mediated reduction of LDH-A expression in 4T1 breast cancer cells alter the development of metastases and tumor growth?; (iv) is there a relationship between tumor LDH-A protein levels and MRSI-measured tumor lactate concentration?

Materials and Methods

Cell culture

4T1 cells were derived from a spontaneous breast tumor in a BALB/c mouse and were provided by Fred Miller (Karmanos Cancer Institute, Detroit, MI; ref. 11). The cell line was not authenticated by the authors as cell authenticity testing can be conducted only on human cell lines. LDH-A knockdown and NC (control) cells, derived from 4T1 murine breast cancer cells, were grown in standard Dulbecco’s modified Eagle medium (DMEM) containing 10% fetal calf serum (FCS) supplemented with either 25 or 5 mmol/L glucose and 6 mmol/L L-glutamine, penicillin/streptomycin, and 4 mg/L of puromycin.

Generation of LDH-A knockdown and control cell lines

4T1 cells were transfected with SureSilencing shRNA plasmids (SABiosciences) to specifically knockdown expression of the mouse LDH-A gene. The vectors contained shRNA under the control of the U1 promoter and included a puromycin resistance gene. Stably transduced clones (knockdown cell lines) were developed along with a control (NC) cell line bearing a scrambled shRNA. LDH-A quantitative real-time PCR (qRT-PCR) RNA and immunoblotting protein assays confirmed successful transduction (see Supplementary Methods).

In vitro assays

In vitro assays were conducted (see Supplementary Data).

Experimental animal model

Cells were orthotopically implanted as described previously (10). Primary tumor volume was determined by caliper measurements and tumor-doubling times were calculated from the tumor volume versus time profiles (12).

In vivo lactate detection

MRSI experiments were carried out on a 7T Bruker Biospec Spectrometer. The lactate signal was acquired using a SEL-MQC editing sequence in combination with chemical shift imaging (CSI; refs. 9, 10, 13) as detailed in the Supplementary Data.

Magnetic resonance images

Lung metastases were imaged using the Bruker gradient echo fast imaging (GEFI) sequence with TR = 300 milliseconds, TE = 2.5 milliseconds, NA = 4, and matrix = 512 × 256. Gated respiration was used to reduce respiratory artifacts.

Analysis of breast cancer microarray datasets

A compendium of four breast cancer microarray datasets was analyzed using the Bioconductor set of tools (www.bioconductor.org) in R statistical language (www.r-project.org). Data were downloaded from Gene Expression Omnibus (GEO). The four breast cancer datasets that were analyzed included: (i) MSKCC-82 GSE-2603 (14), (ii) EMC-286 GSE-2034 (15), (iii) ECM 192 GSE12276: 204 samples (16), and (iv) EMC-344 [EMC 286 and 58 cases of estrogen receptor-negative (ER-) tumors, GSE 5327; ref. 17]. Data were normalized using the standard gcma procedure (18). Survival analysis was conducted using R package survival. Details are provided in Supplementary Methods.

Statistical analysis

Results are presented as mean ± SD. Statistical significance was determined by a two-tailed Student t test. A P value of less than 0.05 was considered significant.

Results

Selection/characterization of KD9 and NC 4T1 cells

To assess the link between LDH-A expression and the metabolic and metastatic characteristics of an established murine breast cancer model, we transfected 4T1 breast tumor cells with four different SureSilencing shRNAs plasmids specifically targeting mouse LDH-A mRNA (knockdown), and a nonspecific scrambled shRNA (NC), respectively. Several knockdown clones with different levels of
LDH-A protein expression were isolated for further experiments. The shRNA knockdown efficiency was evaluated by analyzing LDH-A mRNA expression using qRT-PCR and protein expression by immunoblotting. Knockdown cells have significantly lower levels of LDH-A mRNA (Fig. 1A) and decreased LDH-A protein expression (Fig. 1B) compared with NC cells. Clone #9 (KD9) transfected with shRNA #2 had the lowest LDH-A mRNA and protein levels, and an unchanged LDH-B level (Fig. 1A and B). Another clone, KD317, was developed from cells bearing the plasmid with shRNA#3 (Fig. 1E).

To validate the correlation between LDH-A expression levels and functional activity of the LDH enzyme complex, we conducted an enzymatic assay on viable KD9 and NC tumor cells in growth medium containing 25 or 5 mmol/L glucose. KD9 cells have 3-fold lower LDH activity than NC cells when cultured in 25 mmol/L glucose-containing media and more than a 4-fold difference in 5 mmol/L glucose (P < 0.01; Fig. 1C). KD9 cells also produce significantly less lactate (P < 0.01; Fig 1D) than NC cells. We also found that LDH-A expression (Western blot analysis) remains high in the control group (NC) and low in the knockdown group (KD9 and KD317) in both high-glucose and low-glucose culture medium (Fig. 1E and F).

**Metabolic properties of KD9 and NC cells**

Glucose usage was significantly less in KD9 cells compared with NC cells, growing in either 25 or 5 mmol/L glucose-containing medium (P < 0.01; Fig. 2A). We used a Seahorse Bioscience XF96 Extracellular Flux Analyzer to measure the extracellular acidification rate (ECAR) and the OCR of these cells. We obtained a baseline measure of ECAR using basic glucose-free XF assay medium, then added glucose to assess glycolysis, and then inhibited the process by adding 2-deoxyglucose (2-DG) to the incubation medium. The injection of glucose (final concentration of 25 mmol/L) caused a significant increase in ECAR in both cell lines, with a higher increase in NC cells compared with KD9 cells (Fig. 2B). The subsequent injection of 2-DG (final concentration of 50 mmol/L) decreased ECAR to basal levels. The effects of these treatments are reflected in the integrated areas under the profile measurements (Fig. 2C); the differences between KD9 and NC cells were significant (P < 0.01) for cells growing under 25 mmol/L of glucose; a similar trend was noted for cells growing in 5 mmol/L glucose, but the difference was not significant (P = 0.147). These results showed a lower glycolytic rate for KD9 cells compared with NC cells (Fig. 2B and C) growing under a high concentration of glucose, and a corresponding lower rate of acidification of the incubation medium over 48 hours (Fig. 2D).

Oxygen consumption is an indicator of mitochondrial respiration. A Seahorse Bioscience XF96 Analyzer was used to measure the real-time OCR (pmol/min) in serum-free DMEM with 25 and 5 mmol/L glucose and 6 mmol/L of glutamine (Fig. 2E and F). FCCP (carbonyl cyanide

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**Figure 1.** Selection and characterization of LDH-A knockdown cells. A, qRT-PCR analysis of LDH-A mRNA expression in the 4T1 cell lines transfected with scrambled shRNA (NC, control) and shRNA to mouse LDH-A mRNA (knockdown) n = 3. P-values for KD4, KD5, KD9, KD13, and KD16 cells were P = 0.03; P < 0.0001; P < 0.0001; P < 0.01; and P < 0.01, respectively (*, **, P < 0.01; *, **, P < 0.001; †, ††, P < 0.05). B, Western blot analyses on whole-cell lysates prepared from NC and knockdown clones. C, total LDH enzyme activity in NC and KD9 cells cultured in DMEM with 25 or 5 mmol/L glucose, 6 mmol/L L-glutamine, and 10% FCS (**, P < 0.01). D, lactate production: appearance of lactate in different culture medium between NC and KD9 cells (*, P < 0.01 comparing NC and KD9 cells). E, Western blot analysis of LDH-A expression: cells were grown in DMEM with 5 or 25 mmol/L glucose, and whole-cell lysates were analyzed for LDH-A, and β-actin expression. F, LDH-A/β-actin protein bands ratio were assessed by ImageJ software.
Figure 2. Metabolic properties of NC and KD9 cells in vitro. A, glucose consumption: cell culture media (standard DMEM with 5 or 25 mmol/L glucose) were assayed for glucose following 48 hours of incubation. Fluorescence intensity was normalized to the number of viable cells and background fluorescence (\( * \), \( P < 0.01 \)). B, ECAR: measurements were obtained before and after injection of glucose (initiate glycolysis) and 2-DG (block glycolysis), sequentially. A typical experiment is shown. C, glycolysis assessment calculated from ECAR results (B) for cells previously growing in 25 and 5 mmol/L glucose-containing media; the mean ECAR area under the curve (AUC; mpH/min; \( * \), \( P < 0.01 \) comparing NC and KD9 cells) normalized to total protein (μg/L). D, cell culture medium acidification during NC and KD9 cell growth in standard DMEM with 25 mmol/L glucose (\( * \), \( P < 0.01 \)). E, OCR and the maximal mitochondrial capacity of cells cultured in 25 mmol/L (triangles) and 5 mmol/L (circles) glucose-containing media. FCCP was used as a potent uncoupler of oxidative phosphorylation in mitochondria. F, the uncoupled respiratory capacity was calculated from (E) results: AUC OCR (pmol/min) normalized to total protein. G, ATP levels were measured in cells growing in standard DMEM containing 25 or 5 mmol/L glucose; results were normalized to the number of viable cells, and corrected for background luminescence (\( * \) and \( \dagger \), \( P < 0.01 \)).

p-trifluoromethoxy phenylhydrazone was added to uncouple oxidative phosphorylation from the electron transport chain to measure the maximum respiratory capacity (19). The respiratory rate (OCR) of KD9 cells was significantly higher (2- and 1.5-fold) than that of NC cells cultured in 25 and 5 mmol/L glucose, respectively (\( P < 0.01 \)). OCR increased by a similar level for KD9 and NC cells after FCCP was added (Fig. 2F). Similar results were obtained in separate experiments using trypsinized cells growing in the media with 25 mmol/L of glucose using an Oxylite fiber optic probe; KD9 cells had a 60% higher OCR (\( P < 0.01 \)) than NC cells (Supplementary Fig. S1A).

The high basal level of OCR is consistent with the 40% higher ATP levels observed in KD9 cells compared with NC cells (\( P < 0.01 \); Fig. 2G), and suggests that ATP production in KD9 cells may be associated with greater proton leak and ROS production than in NC cells. However, this trend occurs only in cells growing in 25 mmol/L glucose. The ATP level was notably higher in NC cells cultured in 5 mmol/L glucose (compared with 25 mmol/L glucose), whereas the difference in ATP levels for KD9 cells growing under 25 and 5 mmol/L of glucose was not significant (Fig. 2G). These differences in ATP levels between NC and KD9 cells at 25 mmol/L glucose can be explained by the higher mitochondrial oxidative phosphorylation of KD9 cells in high glucose-containing media. It is interesting to note the higher OCR and ATP results in NC cells growing in 5 mmol/L glucose compared with 25 mmol/L glucose media (Fig. 2F and G). These data support the concept that some cancer cells, which use aerobic glycolysis, can also switch from glycolysis to oxidative phosphorylation under glucose-limiting conditions (20). This plasticity reflects the interplay between glycolysis and oxidative phosphorylation and the ability to adapt metabolism and energy production to changes in the microenvironment, and to adapt to differences in tumor energy needs or biosynthetic activity (21).

We measured mitochondrial ROS in cells growing under 25 mmol/L of glucose (Supplementary Fig. S1B). Intracellular ROS was significantly higher in KD9 cells compared with NC cells (\( P < 0.01 \)), consistent with prior findings (4). However, the level of mitochondrial mass was similar in these two cell lines (Supplementary Fig. S1C). These
findings are consistent with a higher proton leak and consequent increase in ROS formation in the LDH-A knockdown cells. These results show that LDH-A shRNA knockdown in 4T1 cells leads to an increase in TCA activity and mitochondrial respiration (in KD9 cells compared with NC cells), by switching from aerobic glycolysis (NC cells) to enhanced mitochondrial respiration. However, these cell-response properties are more evident when cells are grown under high concentrations of glucose, and this may reflect their “addiction” to high glucose levels.

In summary, the magnitude of glucose consumption, ECAR and pH changes (Fig. 2A–D) indicate higher aerobic glycolysis in NC compared with KD9 cells under high concentrations of glucose. In contrast, O₂ consumption (Fig. 2E and F and Supplementary Fig. S1A) and ROS (Supplementary Fig. S1B) were greater for KD9 than NC cells, and O₂ consumption was higher at 5 mmol/L glucose than at 25 mmol/L glucose for both cell lines (Fig. 2E and F).

We also studied the effect of excluding either glucose or glutamine from the incubation medium on the two major energy producing pathways of the cell—mitochondrial respiration and glycolysis—using the XF96 Extracellular Flux Analyzer. ECAR in basic glucose-free XF assay medium was low in both cell lines (Figs. 2B and 3A). ECAR (reflecting glycolysis) markedly increased on the addition of 25 mmol/L glucose alone, whereas there was little or no change in glycolysis following the addition of 6 mmol/L glutamine alone (Fig. 3A and C). We intentionally used 25 mmol/L of glucose to saturate the glycolytic pathway and measure the maximal upregulation of ECAR. In contrast, OCR increased markedly in both cell lines following the addition of 6 mmol/L glutamine alone, whereas a smaller increase in OCR was observed following the addition of 25 mmol/L glucose alone (Fig. 3B and D). The ECAR and OCR responses of KD9 and NC cells to the addition of glucose and glutamine indicate that glucose metabolism (not glutamine metabolism) is the primary source of extracellular acidification and aerobic glycolysis in both cell lines and that glutamine metabolism is the significant source of oxidative phosphorylation. The results also suggest that inhibition of LDH-A in 4T1 breast cancer cells leads to enhanced mitochondrial respiration through the glutamine pathway, and is associated with an increase in mitochondrial activity (Supplementary Fig. S1A) and ROS (Supplementary Fig. S1B), but not in mitochondrial number (Supplementary Figs. S1C and S2).
Relationships between LDH-A, Lactate, and Metastases

Growth profiles of KD9 and NC cells

The proliferation of KD9 and NC cells was studied in DMEM medium with different concentrations of glucose (0, 5, and 25 mmol/L) and 1-glutamine (0 and 6 mmol/L). KD9 cells have a considerably slower growth rate compared with NC cells (Fig. 3E and F; Table 1). The doubling times were calculated and showed no differences between cells growing under high (25 mmol/L) and a more physiologic concentration of glucose (5 mmol/L) in the media (Table 1). The growth of the cells in 5 mmol/L glucose are similar to their growth in 25 mmol/L glucose medium for the first 48 hours, but slows after day 2, compared with their growth in 25 mmol/L glucose ($P < 0.01$), as glucose is consumed from the medium. Both cell lines have markedly reduced growth in the absence of glucose or glutamine, and the effect was greater in KD9 cells (Fig. 3E and F).

Growth and metabolic profiles of KD9 and NC tumors

Downregulation of LDH-A expression leads to slower growth, reduced glycolytic flux, and increased mitochondrial respiration in vitro. We asked whether enhanced mitochondrial respiration and dependence on glutamine could affect in vivo tumor growth, lactate production, and the potential for developing distant metastases. We injected cells into the mammary fat pad and evaluated the effect of LDH-A suppression on the tumorigenicity of the 4T1 breast cancer cell clones. We compared the growth profiles of KD9, KD5, and KD317 with NC and wild-type 4T1 tumors (Fig. 4A). By 2 weeks after injection, a significant tumor volume difference had developed, and LDH-A knockdown KD9, KD5, and KD317 tumors had significantly longer doubling times compared with NC and wild-type 4T1 tumors (Fig. 5C). The mean lung weight for animals bearing orthotopic NC tumors was 0.03 g ($P < 0.01$), whereas the mean lung weight for animals bearing orthotopic KD9 tumors was 0.03 g ($P < 0.01$; Supplementary Fig. S3). In another cohort of animals, MRI-identified lung metastases and survival were monitored. A 2- to 3-week delay in the

Migration potential of KD9 and NC cells

Migration and invasiveness of tumor cells are important aspects of metastasis formation. In transwell migration assays at 25 and 5 mmol/L glucose, fewer KD9 cells migrate through the 8-μm pores of a transwell chamber compared with NC cells (Fig. 5A). Invasion through a Matrigel environment (3-mm thick) also showed a significantly smaller number of invading KD9 cells compared with NC cells. These differences were more profound in 5 mmol/L glucose ($P < 0.01$; Fig. 5A), but were significant in both glucose environments. In the in vitro scratch assay (Fig. 5B), KD9 cell migration (wound closure) was significantly slower compared with NC cell migration over 6 hours in both 25 and 5 mmol/L glucose ($P < 0.01$). In the absence of glucose or glutamine, wound closure was similar for both cell lines and the reduction in closure was marked in the absence of glucose (Fig. 5B).

Metastatic potential of KD9 and NC tumors

We tested the effects of LDH-A knockdown on the development of metastases by comparing orthotopic KD9 and NC primary tumors. All animals bearing orthotopic NC tumors developed lung metastases 1 to 3 weeks after tumor inoculation, whereas no animals bearing orthotopic KD9 tumors developed visible metastases over the first 3 weeks. This MRI observation was confirmed by India ink injection and histology in one set (5 animals/group) of animals that were sacrificed and examined after 21 days of primary tumor growth (Fig. 5C). The mean lung weight for animals bearing primary KD9 tumors was 0.16 ± 0.03 g, whereas the corresponding lung weight of NC tumor-bearing animals was 0.27 ± 0.03 g ($P < 0.01$; Supplementary Fig. S3). In another cohort of animals, MRI-identified lung metastases and survival were monitored. A 2- to 3-week delay in the

Table 1. In vitro cell doubling time

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<tr>
<th>Medium glucose concentration</th>
<th>Cell line doubling time, h*</th>
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<tr>
<td>5 mmol/L</td>
<td>19.6 ± 0.5</td>
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<tr>
<td>25 mmol/L</td>
<td>20.5 ± 0.6</td>
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*Estimated over 2 days following cell plating and media change.
development of lung metastases and survival were observed between KD9 and NC tumor-bearing mice (Fig. 5D).

The growth of primary NC and 4T1 tumors were significantly more rapid than that of primary KD9, KD5, and KD317 tumors (Fig. 4A and Table 2). NC and KD9 cells cultured for 2 weeks in DMEM with 5 mmol/L glucose were also injected orthotopically into the mammary fat pad. These tumor growth profiles and calculated tumor-doubling times were similar to that obtained when the glucose concentration in the culture medium was 25 mmol/L (Table 2).

To control for the effect of differing tumor volumes and growth rates, and to more closely simulate the clinical situation where the primary tumor is removed, we studied a separate group of animals (10 per group) and surgically removed the primary mammary tumor (tumor volume, $\leq 100 \text{ mm}^3$). The NC tumor-resected animals began to die 4 weeks after tumor inoculation, whereas the KD9 tumor-resected animals began to die 6 weeks after tumor inoculation (Fig. 5E). A 2-week increase was observed in the survival of the KD9 tumor-resected animals, compared with NC tumor-resected animals (Fig. 5E). The mean survival time for tumor-resected animals was 33.5 ± 6 days for NC and 44 ± 7 days for the KD9 ($P < 0.01$).

<table>
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<th>Table 2. Tumor volume doubling time</th>
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<tr>
<td><strong>Glucose concentration</strong></td>
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<tr>
<td><strong>Tumor cell line</strong></td>
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<td>KD9</td>
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<td>NC</td>
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<td>4T1</td>
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*Estimated over first 2 weeks following implantation.

bGlucose concentration in preimplantation culture medium.
LDH-A expression in NC and KD9 tumors and metastases

LDH-A protein (immunoblotting) levels in small (~100 mm³) KD9 tumors were approximately 4-fold less than in comparable, small-size NC tumors (P < 0.01; Figs. 4D and F). However, there was a reappearance of LDH-A protein expression in KD9 tumors as they enlarged (from ~100 to 250–300 mm³), and LDH-A protein levels in the larger KD9 and NC tumors were similar (Fig. 5F). Metastases to lymph nodes and lungs, as well as recurrent tumor at the primary site (KD9 and NC) had similar high expression of LDH-A (Fig. 5F and G). Thus, the larger KD9 and NC tumors, and metastatic nodules from both tumors, had similar LDH-A protein expression levels.

Discussion

Tumors with high tissue lactate concentrations and high LDH-A expression have been linked to poor prognosis (22–25), and are associated with greater metastatic potential (24, 25). Shifts in metabolism have been shown to have a
significant impact on the tumor microenvironment, disease evolution, progression, and development of metastases (1, 3–6, 26–28). In our analysis of 4 clinical datasets (622 patients with breast cancer; refs. 14–17), we show that patients with high levels of LDH-A expression have a significantly higher probability ($P < 10^{-16}$) of developing metastases compared with women with low levels of LDH-A (Fig. 6).

We also focused on LDH-A, because it is a bridge between several metabolic pathways, and because the product of LDH-A activity (lactate) can be assessed noninvasively and quantitatively using MRSI. Although it has been shown that the inhibition of LDH-A has an antiproliferative effect on primary breast tumors (5), in human alveolar adenocarcinoma A549 xenografts (29), and human hepatocellular carcinoma HCCLM3 xenografts (30), there have been no studies investigating the effect of LDH-A inhibition on the development and growth of metastases. This is an important clinical issue, as the cause of death in patients with breast cancer is almost always due to metastases.

The inhibition of LDH-A by a small-molecule inhibitor, FX-11, reduces progression of human lymphoma P493 xenografts (4). The inhibition of pyruvate conversion to lactate by oxamate (pyruvate analog) also resensitizes taxol-resistant human MDA-MB-435 breast tumor xenografts (31). The inhibition of LDH-A may enhance oxidative stress, and is linked to tumor cell death (4, 5, 29, 30). We previously measured greater amounts of LDH-A protein and lactate production in 4T1 cells and tumors (metastatic phenotype) compared with isogenic 67NR cells and tumors (nonmetastatic phenotype; ref. 10). We selected the murine 4T1 breast cancer metastatic model to test whether LDH-A silencing, using shRNA-knockdown technology, has a significant effect on the development of metastases, as well as on cell/tumor metabolism and cell/tumor growth, and can we measure these changes noninvasively by MRSI using lactate as a surrogate marker of LDH-A.

We show a close association between LDH-A gene and protein expression, LDH enzyme activity, cell proliferation, and transwell migration assays between KD9 and NC cells. In vitro experiments also show a reduction in the rate of glucose usage and glycolysis (ECAR), and a compensatory increase in OCR, maximum respiratory capacity, ROS, and cellular ATP levels (reflecting increased oxidative phosphorylation) following stable LDH-A shRNA knockdown in 4T1 cells. Glucose and glutamine dependence studies were also conducted, and they showed that glucose metabolism (not glutamine metabolism) is the primary source of extracellular acidification and aerobic glycolysis. Glutamine is essential for cell proliferation and wound-healing (scratch) assay, and may have a significant impact on mitochondrial activity of LDH-A knockdown cells.

4T1 cells and variants reported here (NC, KD9, etc.) were grown in DMEM with high and normal concentrations of glucose (25 and 5 mmol/L, respectively) and glutamine (6 mmol/L). Many tumor cell lines are routinely cultured in media containing high amounts of glucose and glutamine (32–34), ensuring the survival of most cells over longer periods of cell culture, without the need to monitor glucose or glutamine concentration. However, most healthy, non-diabetic adults maintain fasting glucose levels at about 5 mmol/L and glutamine levels at 1 mmol/L (35–38), considerably less than that in most cell culture media. Therefore, we conducted comparison studies of cells growing in 25 and 5 mmol/L glucose, as it is known that “hyperglycemic” conditions may lead to changes in cellular functions, such as carbohydrate and fatty acid metabolism, proliferation, and cell motility (39). In addition, glucose concentrations in tumors can vary considerably in different tumor regions during tumor progression, and can be significantly lower than that in normal tissues (40). Thus, the tumor microenvironment can be variable and characterized as being “glucose starved” to “glucose addicted” in comparison with other tissues, reflecting an imbalance between poor supply and high consumption rate. Despite the differences in glucose and glutamine concentrations between our in vitro and in vivo experiments, we found no significant differences in the tumor growth and metastatic ability when we used cells that had been adapted to 5 mmol/L glucose over 2 weeks. These 5 mmol/L glucose-adapted NC and KD9 cells had similar in vitro and in vivo growth (doubling times) and similar metastatic patterns compared with cells grown in 25 mmol/L glucose. A close relationship between LDH-A gene and protein expression, tissue lactate levels, and tumor metastatic potential was shown. Significant in vivo biologic effects of LDH-A silencing were shown, which included, decreased lactate production in vivo, the slowing of tumor growth and a reduction and delay in the development of metastases of several knockdown clones (KD9, KD5, and KD317).

![Figure 6. Metastatic-free breast cancer survival: LDH-A gene expression. Kaplan–Meier estimators for metastasis-free survival from a compendium of four breast cancer patient datasets (14–17). Survival data were separated into low-medium and high groups according to the expression level of LDH-A: 2 of 3 of data points are in the low group (dashed line) and 1 of 3 are in the high group (solid line). Patients with high levels of LDH-A expression have a significantly higher ($P < 10^{-16}$) probability of developing metastases compared with women with low levels of LDH-A.](clincancerres.aacrjournals.org)
Therefore, we explored the evolution of LDH-A protein expression in primary orthotopic KD9 and NC tumors, and conducted immunoblots on enlarging tumors (from ∼100 to 250–300 mm³), and on metastases in the same animals. Most notable were the similar high LDH-A protein levels that were measured in the larger primary KD9 and NC tumors, and in the metastatic lesions as well. These data, along with our previous studies (10), suggest that small (∼100 mm³) wild-type 4T1 and NC tumors (with high LDH-A expression and high lactate levels) are already seeding metastatic cells into the circulation. Nevertheless, small KD9 tumors (with lower LDH-A expression and only moderate lactate levels) are capable of forming metastases, but at a delayed rate.

The eventual appearance of delayed metastases in knockdown tumor-bearing mice may be explained in several ways, including the fact that LDH-A silencing was incomplete. We have seen reexpression of LDH-A protein in knockdown cells, when cells were cultured without antibiotic selection ( Supplementary Fig. S4). We show an outgrowth of non-LDH-A–silenced KD9 cells in enlarging primary KD9 tumors (250–300 mm³) that lead to higher lactate levels, and the presence of high LDH-A protein levels in distant KD9 metastases, similar to that measured in distant NC metastases.

Reappearance of LDH-A in vivo could also explain the moderate levels of lactate in small (100 mm³) primary KD9 tumors, resulting in failure to more effectively suppress tumor growth and development of metastases. Other explanations for the growth and metastatic profile of KD9 tumors include the fact that the KD9 cells use oxidative metabolism more than NC or wild-type 4T1 cells to produce metabolic intermediates, and they are less dependent on glycolysis (greater use of the TCA cycle and oxidative phosphorylation). In addition, enhanced mitochondrial oxidative activity and elevated ROS can induce a more aggressive tumor phenotype through hypoxia-inducible factor 1 (HIF-1; refs. 41, 42), as well as increased oxidative stress and cell death (41).

Other possible factors include the use of other metabolic fuels, such as glutamine, which could feed in through the TCA cycle and provide metabolic intermediates (43). Stromal tissue surrounding the tumor cells can also play an important role in tumor progression and metastasis (44). This mechanism could account for KD9 tumor growth and metastases, where the production of either lactate or pyruvate by the tumor stroma could be used to ‘feed’ the malignant tumor cells and to alter the microenvironment (45). The production of lactate by tumor stromal cells (requiring LDH-A) would not be affected by LDH-A silencing in tumor KD9 cells, as the stromal cells originate from the host animal. Thus, several possible explanations exist that could account for the modest and increasing levels of LDH-A expression and lactate concentration in small and larger KD9 tumors. Such changes would be consistent with the slower growth profile of primary orthotopic KD9 breast tumors and their delayed ability to form metastases.

Imaging paradigms developed in this study can be translated to the clinic for selecting patients at high risk for developing subsequent metastases and who need closer surveillance, or patients appropriate for treatment with metabolic inhibitors. The noninvasive monitoring of LDH-A–targeted therapy using lactate MRSI is novel, even though lactate 1H MRSI has been conducted in a limited number of oncology studies previously (9, 10, 13, 46, 47). In contrast to hyperpolarized 13C NMR studies, lactate 1H MRSI measurements do not require special instrumentation and injection of hyperpolarized molecules. Pulse sequences for lactate detection have been implemented on clinical scanners (46–49). Therefore, the barrier to translation is modest and these studies can be implemented with currently available technology. These preclinical studies support the wider clinical application of lactate 1H MRSI, including the identification and monitoring of women with breast cancer who are at high risk of developing metastatic disease, and to specifically monitor LDH-A–targeted drug treatment.

Conclusions

Because elevated LDH-A is a component of many aggressive tumors (4–6, 22, 28), it is a potential drug target for cancer therapy (4, 31). Our results show for the first time that LDH-A inhibition reduces and delays the development of metastases, affects tumor cell metabolism, and confirms the reduction of primary tumor growth in an established murine model of breast cancer (4T1). Our LDH-A shRNA silencing experiments show a strong association between LDH-A gene and protein expression, tumor lactate levels, and development of metastases. LDH-A–targeted drug therapy may avoid the loss of shRNA-based LDH-A silencing, that we observed, and it will also affect both tumor and stromal components.

These results suggest that LDH-A drug-targeted therapy is likely to be effective in aggressive breast cancer, and that lactate MRSI could serve as a surrogate for measuring LDH-A expression and target inhibition in the development of LDH-A–targeted therapies. Inhibition of LDH-A in patients is expected to be tolerable and associated with low toxicity. LDH-A deficiency is a rare, but well-characterized human disease that can lead to exercise intolerance, cramps, myoglobinuria, but is not associated with severe dysfunction of major organs (50, 51).

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

Authors’ Contributions

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