Predictive Biomarkers and Personalized Medicine

Prognostic and Predictive Role of Lactate Dehydrogenase 5 Expression in Colorectal Cancer Patients Treated with PTK787/ZK 222584 (Vatalanib) Antiangiogenic Therapy

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Abstract

Purpose: The Colorectal Oral Novel therapy For the Inhibition of angiogenesis and Retarding of Metastases (CONFIRM)-randomized trials, investigating the role of the VEGF-receptor inhibitor PTK787/ZK 222584 (vatalanib) in colorectal cancer (FOLFOX 4 + vatalanib), showed some benefit in patients with high serum lactate dehydrogenase (LDH) levels. Here, we investigated the expression of LDH5 (encoded entirely by the LDHA gene, regulated by the hypoxia inducible factors) in cancer tissues from patients recruited in the CONFIRM trials and relationship to response.

Experimental Design: Paraffin-embedded materials from 179 patients recruited in the CONFIRM trials were analyzed by immunohistochemistry for the expression of the LDH5 protein. Correlations with serum LDH, response, and survival were assessed.

Results: A significant association of tumor burden and of poor performance status (PS) with serum LDH was noted. Poor PS and high tumor LDH5 expression predicted for poor response rates. High tissue LDH5 was related to poor progression-free survival (PFS) only in the placebo group of patients, whereas the addition of vatalanib seemed to improved response and PFS in this subgroup. High serum LDH levels were linked with significantly poorer overall survival, which however was not sustained in multivariate analysis.

Conclusions: Serum LDH and tissue LDH5 levels are complementary features that help to characterize the activity of LDH in colorectal cancer and have a potent value in predicting response to chemotherapy. The addition of vatalanib diminished the impact of LDH expression on the prognosis of patients. Clin Cancer Res; 17(14); 4892–900. ©2011 AACR.

Introduction

Lactate dehydrogenases (LDH) are involved in the reversible transformation of pyruvate, the end product of glycolysis, to lactate (1). The LDH5 isoenzyme composed of 5 M-subunits encoded by the LDHA gene, is the most efficient in catalyzing the conversion of pyruvate to lactate (1). The anaerobic glucose metabolism is intensified in cancer cells, even in presence of oxygen. This phenomenon, first described by Otto Warburg as aerobic glycolysis (2) has been recently elucidated, at least in part, by studies showing the direct control of the hypoxia inducible factors (HIF1α and 2α) on the transcription of a variety of genes involved in angiogenesis, glycolysis, and apoptosis, including VEGF and LDHA (3).

VEGF, one of the most potent angiogenic factors in tumors, has been a major target for the development of antiangiogenic therapies. The anti-VEGF monoclonal antibody bevacizumab, improves progression-free outcome of patients with a variety of human carcinomas (4, 5). The VEGF tyrosine kinase inhibitor PTK787/ZK222584 (PTK/ZK, vatalanib), that blocks all known VEGF receptor tyrosine kinases, and also platelet-derived growth factor receptor, c-kit, and c-fms, after showing promising activity in combination with chemotherapy in phase I/II trials in patients with colorectal cancer (6, 7), entered phase III evaluation in 2 large trials, CONFIRM 1 and 2, recruiting patients with advanced colorectal cancer and treating them with FOLFOX with or without vatalanib (8, 9). Although vatalanib seemed not to offer a survival advantage overall, an analysis according to the prospectively stratified serum LDH levels showed a 40% reduction in progression-free survival.

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doi: 10.1158/1078-0432.CCR-10-2918
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Materials and Methods

LDHA combination with chemotherapy has a biological basis as a marker of response to VEGF receptor (VEGFR)-inhibitor have the worst prognosis (11). As colorectal cancer patients with high serum LDH levels, finding was considered of particular clinical importance (PFS) in patients with high LDH serum levels (10). This finding was considered of particular clinical importance as colorectal cancer patients with high serum LDH levels have the worst prognosis (11).

The assumption that serum LDH may serve as a predictive marker of response to VEGF receptor (VEGFR)-inhibitor combination with chemotherapy has a biological basis as both LDHA and VEGF are genes transcriptionally regulated by HIFs (3). Indeed, in previous studies, we confirmed that HIF1α overexpression is directly linked with the expression of LDH5, of VEGF and of the phosphorylated (activated) form of the VEGFR2/kinase insert domain receptor, in primary colorectal cancer, and correlated with metastasis and the postoperative prognosis (12–14).

To further investigate the role of LDH in predicting the efficacy of vatalanib in advanced colorectal cancer, we examined the expression status of LDH5 in cancer tissues obtained from patients recruited in the CONFIRM trials. The relation of tumor LDH5 to response and prognosis of patients is examined in parallel with the serum LDH levels and the performance status of patients.

Translational Relevance

There is major need for biomarkers to assess patients likely to benefit from antiangiogenic therapy. We analyzed a subset of 179 patients from 2 randomized trials (CONFIRM trials) that investigated the combinations of FOLFOX (oxaliplatin and 5-fluorouracil chemotherapy) with or without the VEGF kinase receptor inhibitor, PTK787/ZK222584. High tumor lactate dehydrogenase 5 (LDH5) predicted poor response to chemotherapy, and vatalanib improved the response rate and progression-free survival in the patients. Tumor LDH5 and tissue LDH give complementary information as neither alone fully characterizes the expression of the protein in colorectal cancer, and they have a potential value in predicting a benefit from chemotherapy and antiangiogenic therapy. Justification is provided for further investigation of genes regulated by the hypoxia inducible factors pathway as potential important markers for the effectiveness in subgroups of patients to VEGF kinase inhibitors. Selection of patients on clinical grounds and by appropriate tumor biomarkers would increase cost effectiveness of these therapies.

(PFS) in patients receiving vatalanib and versus controls coincide within the CONFIRM 1 and 2 tissue samples (40 vs. 44 and 44 and 51 vs. 44, respectively). Thus, analysis was conducted in combined CONFIRM 1 and 2 data sets and no separate analysis was attempted because of the relatively low number of tissues collected. A direct comparison of the demographics and survival data of the subset of patients analyzed herein, with the whole CONFIRM trial population is not available, as the clinical data of the studies have not been published, as yet. Nevertheless, the preliminary reports on median PFS in the CONFIRM 1 trial was 7.7 and 7.6 months in patients receiving vatalanib and versus controls coincide at the 7.7 and 7.7 months of the subgroup of patients analyzed in the current study. With regard to the CONFIRM 2 study, the reported median PFS was 5.3 and 4.1 in patients receiving vatalanib and controls, whereas in the current subgroup analysis this was 3.9 and 4.0 months, respectively, implying a slightly reduced median survival in the group of patients receiving vatalanib in the subgroup.
Patient characteristics and response rates according to treatment arm are shown in Table 1. Serum levels of LDH were available from the institutes where patients had been treated and as the normal range depends upon laboratory all values are transformed to the ratio of LDH levels divided by the upper normal limit given by the laboratory. Outcomes and response to treatment data were given by the independent data monitoring board. The follow-up of patients ranges from 1 to 1,418 days (median 610 days). All patients were dead with progression of their disease at the time of analysis.

### Immunohistochemistry

A modified streptavidin technique was used for immunohistochemistry, as previously reported (12, 13). The primary antibody (ab9002 recognizing the LDH5, Abcam) was used. The percentage of cancer cells expressing the proteins under investigation was assessed in all optical fields containing cancer at magnification ×200. The percentage of positive cells per optical field was recorded and the mean value of all fields was used to obtain the final score for each case. LDH5 reactivity is both nuclear and cytoplasmic. The cytoplasmic and the nuclear expression of these proteins was first assessed either separately or combined in a grading system, as previously proposed and tested (15, 16, 17). Briefly, cases with nuclear LDH5 expression in more than 10% of cancer cells and/or strong cytoplasmic expression to 100% reactivity (median 20%), whereas nuclear expression was lower ranging from 0% to 50% (median 0%). Nuclear expression in more than 10% of cancer cells was noted in 25 of 179 cases and for 11 of this pattern was noted in 25 of 179 cases and for 11 of this pattern was decisive for their grouping in the high LDH5 expression group (Fig. 1). Using the established scoring system, 77/179 (43%) of cases had high cancer cell LDH5 reactivity.

### Statistical analysis

Statistical analysis was done by using the GraphPad Prism 5.0 and the Instat 3.1 package (GraphPad Software Inc.). A Fisher’s exact test was used for testing relationships between categorical variables (contingency Tables). Linear regression analysis was used to assess correlation with continuous variables. Multinomial regression analysis was used to assess the impact of dichotomous variables on the response rates. PS and OS were estimated by using Kaplan–Meier curves. Curves were compared by using the log-rank test (Mantel–Haenszel). The Gehan–Breslow–Wilcoxon method that gives more weight to events at early time points, a feature that may be important when analyzing progression events following therapy or death events expected to occur at a high rate early in the course of follow-up, was also used. A Cox proportional hazard model including all preoutcome variables was used to further test the independent significance of variables proved of significance at univariate analysis (in at least one of the 2 statistical methods applied). A stepwise selection with backward elimination of subsets was used to determine the final model. A 2-tailed P value of less than 0.05 was used for significance.

### Results

#### Serum LDH versus cancer LDH5 expression and tumor burden

Of 179 patients analyzed in the current study, 98 (54.7%) had serum LDH levels lower than the upper normal limit, 38 (21.3%) had levels 1.01- to 1.49-fold and 43 (24%) had 1.5-fold or more higher value than the upper normal limit. Thus, 3 groups were formed for subsequent analysis (normal, medium, and high serum LDH levels).

Cytoplasmic expression in cancer cells ranged from 0% to 100% reactivity (median 20%), whereas nuclear expression was lower ranging from 0% to 50% (median 0%). Nuclear expression in more than 10% of cancer cells was noted in 25 of 179 cases and for 11 of this pattern was decisive for their grouping in the high LDH5 expression group (Fig. 1). Using the established scoring system, 77/179 (43%) of cases had high cancer cell LDH5 reactivity.

Linear regression analysis of serum LDH levels and of the percentage of cancer cells with cytoplasmic or nuclear expression (separately or combined) of LDH5 did not show any significant correlation. Group analysis of the percentage of cancer cells with high serum LDH5 expression in patients with normal versus abnormal tumor burden showed a significant direct association of cytoplasmic LDH5 expression with serum LDH levels [mean ± standard error (SE): 26 ± 2.8 vs. 33 ± 3.4, P = 0.10; Fig. 2A].

On the contrary, the tumor burden as expressed by the sum of maximum assessable tumor diameters showed a significant direct association with the serum LDH levels but none with the tissue LDH5 expression (Fig. 2B). Linear regression analysis showed a significant association of tumor burden with serum LDH (P < 0.0001, r = 0.52). Analysis in patients with abnormal serum LDH levels showed a significant association of cytoplasmic LDH5 expression with serum LDH levels.

### Table 1. Patient characteristics

<table>
<thead>
<tr>
<th></th>
<th>Placebo</th>
<th>Vatalanib</th>
</tr>
</thead>
<tbody>
<tr>
<td>No.</td>
<td>88</td>
<td>91</td>
</tr>
<tr>
<td>CONFIRM 1/2</td>
<td>44/44</td>
<td>40/51</td>
</tr>
<tr>
<td>PS 0/1,2</td>
<td>51/37</td>
<td>47/44</td>
</tr>
<tr>
<td>Sex M/F</td>
<td>60/28</td>
<td>64/27</td>
</tr>
<tr>
<td>Age (median, range)</td>
<td>62 (38–82)</td>
<td>63 (28–83)</td>
</tr>
<tr>
<td>Size</td>
<td>8.9 (1-35.4)</td>
<td>9.3 (0.5–47.9)</td>
</tr>
<tr>
<td>LDH serum</td>
<td>0.9 (0.3–8.5)</td>
<td>1.0 (0.2–24)</td>
</tr>
<tr>
<td>CR/PR</td>
<td>37/88</td>
<td>39/89</td>
</tr>
<tr>
<td>Median PFS (d)</td>
<td>175</td>
<td>175</td>
</tr>
<tr>
<td>Median OS (d)</td>
<td>600</td>
<td>610</td>
</tr>
<tr>
<td>No. of PFS events</td>
<td>88</td>
<td>91</td>
</tr>
<tr>
<td>No. of deaths</td>
<td>88</td>
<td>91</td>
</tr>
</tbody>
</table>

*Tissue samples collected from patients recruited in the CONFIRM 1 or 2 studies.

Abbreviation: CR/PR, complete and partial response.
expression with tumor burden (Fig. 2C). No correlation was found in the group of patients with LDH serum levels lower than the upper normal LDH value.

**Serum and tumor LDH association with patient variables**

High serum LDH values were significantly more frequent in patients with PS 1, 2 (low, median, and high serum LDH levels were noted in 38/81, 15/81, and 28/81 patients with PS 1, 2 vs. 60/98, 23/98, and 15/98 in those with PS 0; \( P = 0.01 \)). Tissue LDH5 was not linked with PS which is explained by the fact that tissue biopsy was conducted at surgery and could not be linked to the PS of patients at diagnosis of metastasis. Female patients also had significantly higher serum LDH levels (low, median, and high serum LDH levels were noted in 76/124, 19/124, and 29/124 male patients vs. 22/55, 19/55, and 14/55 female patients; \( P = 0.007 \)). Age was not related to LDH levels. Tumor burden was strongly associated with the PS of patients. The median tumor dimensions (± SD) were 9.4 ± 6 cm in patients with PS = 0 versus 13.5 ± 9 cm in patients with PS = 1 or 2 (\( P = 0.0008 \)).

**Analysis of response rates**

Response rates (complete and partial) were 42% (37/88) in the placebo group and 82% (39/49) in the group treated with vatalanib (\( P = 0.87 \); for 2 patients response was not available).

Analysis of all patients showed a better response rate in those with good PS (50/98, 51% vs. 26/79, 33%; \( P = 0.02 \)) and low tissue LDH5 score (50/101, 50% vs. 26/76, 34%; \( P = 0.04 \)). Multivariate analysis of all parameters showed

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**Figure 1.** Immunohistochemical LDH5 expression patterns in colorectal cancer tissues: A, strong cytoplasmic and nuclear LDH5 expression (arrows). B, low LDH5 expression in cancer cells (arrows).

**Figure 2.** Analysis of serum and tissue LDH levels: A, serum LDH levels versus tissue cytoplasmic and nuclear expression (bars show the SE). B, serum LDH levels versus size of the measurable lesions (C). Cytoplasmic LDH expression versus size of the measurable lesions in patients with serum LDH levels higher than normal laboratory values (in B and C, boxes show the first and third quartile of values, the horizontal line in the box shows the median value, and the whiskers show the range of values).
that good PS and low tissue LDH5 expression were significantly linked with response to therapy ($P = 0.02$, OR 1.5, and $P = 0.05$, OR 1.4, respectively).

The predictive value of these 2 parameters was maintained in the placebo group, while it was lost in patients receiving vatalanib. In the placebo group, the response rate was 25.8% (8/31) when LDH5 score was high versus 50.8% (29/57) when this was low ($P = 0.02$). In the vatalanib group, the response rate was 40% (18/45) when LDH5 score was high versus 47.7% (21/44) when this was low ($P = 0.52$). In a bivariate model of response to therapy, LDH5 but not PTK/ZK showed an independent predictive value ($P = 0.03$ and $P = 0.57$, respectively).

**Survival analysis**

All patients had progressive disease and were dead at the time of analysis. Univariate analysis of all patients showed that response to therapy and PS were the most important parameters linked with PFS and with OS ($P < 0.0001$ and $P \leq 0.03$, respectively; Table 2). The addition of vatalanib did not show a significant impact on PFS or OS. High serum LDH levels, age and tumor burden were also linked with poor OS ($P = 0.003$, 0.02, and 0.02, respectively, using the Gehan–Breslow–Wilcoxon method). There was not a significant prognostic relevance of vatalanib administration (PFS: $P = 0.86$ and OS: $P = 0.65$). In multivariate analysis of progression events, the response to therapy was the most significant independent variable–linked progression events ($P < 0.0001$, HR 4.3). Excluding response rate (a postoutcome variable), PS and sex were independent predictors of progression events, whereas PS and age were independent predictors of death events (Table 2).

In the placebo group, univariate analysis showed that response rate was the most significant prognostic factor of PFS and OS ($P < 0.0001$; Table 2). Tissue LDH5 score was significant linked with PFS ($P = 0.005$; Gehan–Breslow–Wilcoxon method), whereas PS and serum LDH1 were linked with OS ($P = 0.005$ and 0.007, respectively; Table 2). Excluding response rates, a multivariate model including parameters significant at univariate (Table 2) showed that

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**Table 2.** Univariate and multivariate analysis of all patients, including preoutcome variables significant at univariate, of those treated with placebo and those treated with vatalanib

<table>
<thead>
<tr>
<th>Variable</th>
<th>PFS</th>
<th>OS</th>
</tr>
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<tbody>
<tr>
<td></td>
<td>Univariate</td>
<td>Multivariate</td>
</tr>
<tr>
<td></td>
<td>HR (95% CI)</td>
<td>P</td>
</tr>
<tr>
<td>All cases</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Response</td>
<td>2.7 (1.9–3.8)</td>
<td>$&lt;0.0001$</td>
</tr>
<tr>
<td>Vatalanib</td>
<td>1.0 (0.7–1.3)</td>
<td>0.99/0.88</td>
</tr>
<tr>
<td>PS</td>
<td>1.4 (1.0–1.9)</td>
<td>0.03/0.001</td>
</tr>
<tr>
<td>LDH5 score</td>
<td>1.1 (0.7–1.4)</td>
<td>0.65/0.38</td>
</tr>
<tr>
<td>LDH serum</td>
<td>1.3 (0.9–1.7)</td>
<td>0.13/0.10</td>
</tr>
<tr>
<td>Age</td>
<td>1.1 (0.8–1.5)</td>
<td>0.43/0.13</td>
</tr>
<tr>
<td>Sex</td>
<td>1.5 (1.1–2.0)</td>
<td>0.05/0.002</td>
</tr>
<tr>
<td>Tumor burden</td>
<td>1.2 (0.9–1.6)</td>
<td>0.19/0.25</td>
</tr>
<tr>
<td>Placebo group</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Response</td>
<td>3.2 (2.0–5.2)</td>
<td>$&lt;0.0001$</td>
</tr>
<tr>
<td>PS</td>
<td>1.1 (0.7–1.8)</td>
<td>0.54/0.12</td>
</tr>
<tr>
<td>LDH5 score</td>
<td>1.5 (0.9–2.5)</td>
<td>0.10/0.009</td>
</tr>
<tr>
<td>LDH serum</td>
<td>1.3 (0.8–2.1)</td>
<td>0.27/0.20</td>
</tr>
<tr>
<td>Age</td>
<td>1.0 (0.6–1.6)</td>
<td>0.89/0.57</td>
</tr>
<tr>
<td>Sex</td>
<td>1.1 (0.7–1.8)</td>
<td>0.58/0.46</td>
</tr>
<tr>
<td>Tumor burden</td>
<td>1.5 (0.9–2.4)</td>
<td>0.08/0.22</td>
</tr>
<tr>
<td>Vatalanib group</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Response</td>
<td>2.4 (1.5–3.8)</td>
<td>0.0002/$&lt;0.0001$</td>
</tr>
<tr>
<td>PS</td>
<td>1.7 (1.1–2.8)</td>
<td>0.01/0.002</td>
</tr>
<tr>
<td>LDH5 score</td>
<td>0.8 (0.5–1.3)</td>
<td>0.52/0.29</td>
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<tr>
<td>LDH serum</td>
<td>1.2 (0.7–1.8)</td>
<td>0.41/0.31</td>
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<tr>
<td>Age</td>
<td>1.3 (0.8–1.9)</td>
<td>0.26/0.18</td>
</tr>
<tr>
<td>Sex</td>
<td>1.9 (1.1–3.3)</td>
<td>0.01/0.003</td>
</tr>
<tr>
<td>Tumor burden</td>
<td>1.0 (0.6–1.5)</td>
<td>0.94/0.71</td>
</tr>
</tbody>
</table>

**NOTES:** All patients had progressed and were dead at the time of analysis. The 2 $P$ values in the univariate analysis correspond to the Mantel–Haenszel and the Gehan–Breslow–Wilcoxon methods, the latter giving more weight to events at early time points.
none of the parameters were independent predictor of death events.

In the group of patients treated with vatalanib, the response rate was once again the most important factor defining the PFS and OS in univariate analysis \( (P < 0.0001; \text{Table 2}) \). PS and gender were significantly linked with PFS \( (P = 0.002 \text{ and } 0.0003, \text{respectively}) \), whereas PS and age were linked with OS \( (0.0003\text{ and }0.03, \text{respectively}) \). Tissue LDH5 did not show a prognostic relevance. Excluding the response rate from a multivariate model and including parameters significant at univariate, PS and gender had an independent prognostic relevance regarding relapse events, whereas PS was the only independent predictor of death events \( \text{Table 2} \).

Figure 3 shows the Kaplan–Meier PFS curves according to tissue LDH5 expression, a parameter suggested to have an impact in defining time to progression following therapy. Figure 4 shows the Kaplan–Meier OS curves according to serum LDH, a parameter suggested to be important in defining time to death.

Discussion

High serum LDH levels are a common finding in human malignancies, including colorectal cancer. In 2 studies from the Memorial Sloan–Kettering Cancer Center, high serum LDH levels were significantly associated with resistance to fluoxuridine \( (15, 16) \). In a meta-analysis by Watine and colleagues, serum LDH was one of the most important prognostic variables in colorectal cancer \( (17) \). Recent studies confirm the adverse predictive role of serum LDH in response of colorectal cancer to chemotherapy \( (18, 19) \). The CONFIRM trials ended in the same conclusion, that serum LDH was one of the most important prognostic factors \( (10) \). Why the addition of the VEGF tyrosine-kinase inhibitor vatalanib offered a PFS advantage in the high serum LDH group of patients remained to be elucidated.

The LDHA gene is directly controlled by the HIF1 transcriptional factor, which at the same time regulates the transcription of the angiogenic factor VEGF \( (3) \). Hypoxia-triggered or oncogene-activated HIF pathways are common events in human malignancy, linked to aggressive clinical behavior and resistance to chemotherapy \( (20) \). This pathway leads to the activation of the LDHA gene, encoding the M-subunit of LDH. We also confirmed the selective upregulation of the LDH5 in colorectal cancer cells compared with the adjacent stroma \( (21) \) and its association with invasion, metastasis, and the expression of HIFs and VEGF \( (12) \). The strong prognostic relevance of tissue LDH5 with the postoperative outcome of patients with colorectal cancer and its close association with the expression of VEGF and VEGF-receptor expression in cancer cells has also been shown \( (13, 22) \).

In this study, we examined the prognostic role of the LDH serum levels and tissue expression in a series of colorectal carcinomas recruited in 2 randomized trials investigating the therapeutic role of the antiangiogenic drug vatalanib. Although this study suffers from the limited
number of cases available for analysis, we had 179 cases assessed in a randomized population analyzed by a blinded technique. This is a retrospective subset analysis but represents a series of steps based on current biological understanding to produce hypotheses for future testing in such trials. This is essential to justify the costs of prospective tissue collection, storage, and analysis.

The first step we examined was the relation between serum and tissue LDH. We concluded that the serum levels are defined mainly by the tumor burden. The fact that the LDH5 cancer cell expression was assessed on primary tumor tissues, whereas the serum LDH levels were measured at documentation of metastasis does not allow a reliable comparison of these 2 parameters, which in any case did not show a significant association.

It is also stressed that, as the serum levels of LDH before the development of the carcinoma are unknown, patients with serum LDH levels falling into the normal LDH range of the general population may in fact be elevated above the normal level for the patient and this cannot be discriminated on the basis of postdiagnosis serum LDH assessment. Thus, "normal" serum LDH may not have low cancer cell LDH activity. On the other hand, low tumor burden may result in low serum LDH levels even in tumors with intense LDHA activity. Thus, serum LDH and tissue LDH5 expression are complementary and their combined use better delineates the LDH tumor activity profile. The factors causing release of LDHA are also unknown.

Analysis of response rates to chemotherapy showed that poor PS and cancer cell LDH5 content were linked with a 2-fold reduced response probability to chemotherapy. In addition, however, of vatalanib to chemotherapy diminished the adverse effect of tissue LDH5 on tumor responsiveness. In fact, tumors with high LDH5 content seemed to have better response to chemotherapy/vatalanib combination compared with tumors with low LDH5 expression. It is notable that although the tissue LDH5 was measured in the primary tumor, there was a relationship to response of metastases years later, indicating that this hypoxia-regulated pathway may persist in secondary deposits.

Analysis of the PFS showed that the response to chemotherapy was the most significant predictor of the progression-free interval. Taking into preoutcome parameters only, LDH5 was a significant predictor only in cases who did not receive vatalanib, as addition of this angiogenesis inhibitor reversed the adverse effect of high LDH5 on the efficacy of chemotherapy. In OS analysis, serum LDH and PS were significantly related to OS but no effect of vatalanib on OS was noted.

It is stressed that the current study has several limitations as this is a retrospective attempt to evaluate a role of a tumor molecular variable, namely, LDH, following a previous confirmation of its prognostic role when assessed in the serum of patients (a secondary end point of CONFIRM trial 2). Retrospective collection of tissues is not always feasible and the random collection of tissue blocks from less than 10% of the total number of patients recruited in

Figure 4. Kaplan–Meier overall (disease specific) survival according to the serum LDH (sLDH) levels in all patients (A), in patients receiving placebo (B) and in patients receiving vatalanib (C). The 2 P values correspond to the Mantel–Haenszel and the Gehan–Breslow–Wilcoxon methods, the latter giving more weight to events at early time points.
the CONFIRM trials may have bias. This is further aggravated by the fact that the 2 CONFIRM trials were not addressed to the same patient population and also because the LDH5 expression in metastatic tumors may not be reliably reflect the results we obtained from primary tumors. The relatively low number of samples and the multiple variable analysis also have a risk of bias from multiple comparisons. Despite the above limitations, this study provides evidence that serum LDH and tissue LDH5 levels are complementary markers of LDH activity in colorectal cancer. Clinical studies have already established serum and tissue LDH levels as strong prognostic indicators in colorectal cancer (12, 13, 15–19). The new information from the current study is that tissue LDH5 is also associated with resistance to standard chemotherapy and worse PFS in patients with advanced colorectal cancer. Addition of the antiangiogenic agent, vatalanib seemed to reduce the adverse predictive and prognostic relevance of LDH5, at least in the current series of patients. This retrospective analysis is the first to provide evidence that a specific marker may be of value in future-randomized trials investigating low molecular weight VEGF kinase inhibitors. Our pilot data suggest combined selection of patients on clinical grounds and by appropriate tumor biomarkers would increase cost effectiveness of these therapies. Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed. Grant Support

This study was financially supported by the Tumor and Angiogenesis Research Group and the Bayer–Schering Pharma. Additional support was from the Oxford NIHR Comprehensive Biomedical Research Centre (A.L. Harris). 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 November 5, 2010; revised May 14, 2011; accepted May 16, 2011; published OnlineFirst June 1, 2011.

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Clin Cancer Res 2011;17:4892-4900. Published OnlineFirst June 1, 2011.

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