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## Comparison of mRNA Expression Levels Determined with Taq-Man and Competitive Template RT-PCR

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### ABSTRACT

Two methods for measurement of thymidylate synthase (TS) and dihydropyrimidine dehydrogenase (DPD) mRNA expression were compared. Although the relative mRNA levels compared to  $\beta$ -actin measured with competitive template RT-PCR were different from the data obtained with a TaqMan based PCR, a significant correlation between the two assays was found.

*Key Words:* 5-Fluorouracil; Colorectal carcinoma; Thymidylate synthase; Dihydropyrimidine dehydrogenase; Gene expression; RT-PCR.

### INTRODUCTION

Response to treatment with 5-fluorouracil (5FU) is associated with mRNA expression levels of its target enzyme TS and the rate-limiting catabolic enzyme

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DPD.<sup>[1]</sup> The expression of mRNA can be measured with several methods. Traditionally this was done with Northern blot analysis, but this method is rather insensitive and not quantitative. In the last decade various PCR methods have been developed, which are much more sensitive and (semi)-quantitative. We compared a competitive template RT-PCR method with a real-time PCR (TaqMan PCR) assay to measure the mRNA expression of TS and DPD. Using the TaqMan method, Salonga et al. proposed cut-off levels to determine whether patients would respond to 5-FU based chemotherapy or not.<sup>[1]</sup>

Historical samples from patients with colorectal cancer were used for this comparison. We have previously described that in this group of patients the TS enzyme activity levels and TS immunohistochemistry were related to response to 5FU treatment,<sup>[2–5]</sup> while a relation with survival was also reported.<sup>[6]</sup> TS mRNA levels were also related to enzyme levels.<sup>[7]</sup>

## MATERIALS AND METHODS

Randomly selected tumor samples taken from colorectal cancer patients were evaluated retrospectively for levels of enzyme activity and mRNA expression levels. The samples were taken from both primary tumors and liver metastases as described previously.<sup>[2–5,7,8]</sup> TS levels were measured with standard radiochemical methods, which estimated the number of binding sites for FdUMP, the active metabolite of 5FU.<sup>[3]</sup> TS and DPD-mRNA levels were measured by Oncoscreen (Jena, Germany) using a TaqMan assay as reported by Salonga et al.<sup>[1]</sup> and in our department by using a CT-RT-PCR developed by us<sup>[9]</sup> or in collaboration with H.L. McLeod.<sup>[10]</sup> Evaluation of the data was performed using SPSS with a parametric test (Pearson correlation coefficient) and a non-parametric test (Spearman's rho). Since both the enzyme assay and the TS-mRNA with the TaqMan PCR and CT-RT-PCR were performed in the same tissue samples a one-tailed test was used.

## RESULTS AND DISCUSSION

The mRNA expression of TS and DPD was measured in historical samples collected at our department. In most of these samples we also measured TS enzymatically. The absolute mRNA levels, normalized to  $\beta$ -actin for both TS and DPD, were different when comparing the assays. The TS/ $\beta$ -actin ratio in the TaqMan assay varied from 0.33 to  $9.22 (\times 10^{-3})$  and that for DPD/ $\beta$ -actin from 0.48 to  $6.12 (\times 10^{-3})$ . However, in the CT-RT-PCR assay these values varied from 1.03 to  $68.1 (\times 10^{-3})$  and from 0 (not detectable) to  $668 (\times 10^{-3})$ , respectively. The TaqMan data were in the same range as reported by Salonga et al.,<sup>[1]</sup> who used the same assay. The larger range for the CT-RT-PCR data is possibly related to the use of different primers and differences in amplification efficiency. Despite differences in absolute mRNA expression levels of TS and DPD, both the Pearson and Spearman analysis showed a quite good, significant correlation between the data obtained with TaqMan PCR and CT-RT-PCR (Table 1). Both methods generated reproducible results. Moreover, it has been shown that the CT-RT-PCR method is reproducible among multiple laboratories.<sup>[11]</sup>

**Table 1.** Correlation between mRNA expression levels and enzyme activities.

PCR assay				Pearson correlation		Spearman	
<i>n</i>		<i>n</i>		R	<i>p</i>	Rho	<i>p</i>
TaqMan TS	16	CT-RT-PCR TS	16	0.767	0.0005	0.581	0.009
TaqMan TS	16	TS levels <sup>a</sup>	13	0.600	0.015	0.670	0.006
TaqMan DPD	16	CT-RT-PCR DPD	16	0.798	< 0.0001	0.837	< 0.0001

<sup>a</sup>TS levels were measured with the FdUMP-binding assay.  
(From Ref. [3].)

We also found a significant correlation between TS levels and mRNA expression determined with either the TaqMan or CT-RT-PCR method (Table 1). This correlation is rather satisfactory considering the fact that TS can undergo a number of posttranslational modifications, especially after treatment with 5FU.<sup>[7,12]</sup> The correlation with enzyme levels demonstrates that the PCR assay can also predict levels with a functional assay for which we previously reported a correlation with response.<sup>[3,5]</sup>

These correlations were used to determine cut-off points for the CT-RT-PCR assay. The initial cut-off points were defined by Salonga et al.<sup>[1]</sup> for the TaqMan PCR assay to determine whether patients would respond to 5FU based chemotherapy. The cut-off point for TS in the TaqMan assay was  $3.5 \times 10^{-3}$ , which corresponded to  $5 \times 10^{-3}$  in the CT-RT-PCR assay. For DPD the TaqMan cut-off point was  $2.5 \times 10^{-3}$ , which corresponded to  $45 \times 10^{-3}$  for the CT-RT-PCR assay.

Several retrospective studies have shown that the tumoral levels of TS and DPD might be related to response to treatment with 5-FU.<sup>[1]</sup> Therefore we are currently undertaking a prospective clinical trial in order to determine whether TS and DPD expression can be used to tailor therapy for patients with advanced colorectal cancer. A core biopsy of the metastatic lesion is performed and this tissue is analyzed with the CT-RT-PCR assay. Patients with low mRNA levels of both TS and DPD (based on the above mentioned cut-off levels) are treated with 5-FU and leucovorin, whereas patients with high TS and/or high DPD mRNA expression are given a first-line combination treatment with oxaliplatin and irinotecan. A superior survival of patients in the 5-FU arm would provide support for clinical application of this approach of pretreatment measurement of tumoral TS and DPD levels.

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