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Cyclin D1 gene G870A polymorphism predicts response to neoadjuvant radiotherapy and prognosis in rectal cancer.

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► To cite this version:

Alexandre Ho-Pun-Cheung, Eric Assénat, Simon Thezenas, Frédéric Bibeau, Rouanet Philippe, et al.. Cyclin D1 gene G870A polymorphism predicts response to neoadjuvant radiotherapy and prognosis in rectal cancer.. International Journal of Radiation Oncology, Biology, Physics, Elsevier, 2007, 68 (4), pp.1094-101. 10.1016/j.ijrobp.2007.01.022 . inserm-00150983

HAL Id: inserm-00150983

<https://www.hal.inserm.fr/inserm-00150983>

Submitted on 4 Jun 2007

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Table 1. Characteristics of the patients

Parameter	Number of patients (%)
Total patients	70 (100)
Gender	
Male	44 (62.9)
Female	26 (37.1)
Tumor grade	
Well differentiated	36 (51.4)
Moderately differentiated	28 (40.0)
Poorly differentiated	6 (8.6)
Pretherapeutic UICC TNM stage	
Stage I	11 (15.7)
Stage II	22 (31.4)
Stage III	25 (35.7)
Stage IV	12 (17.2)
Radiotherapy (Gy)	
45	41 (59.0)
60	29 (41.0)
TRG (grouped)	
Nonresponder group (TRG 0 and 1)	30 (42.9)
Responder group (TRG 2, 3, and 4)	35 (50.0)
Non-evaluable*	5 (7.1)
pT	
T0	4 (5.7)
T1	6 (8.5)
T2	26 (37.1)
T3	34 (48.7)
pN	

N-	48 (68.6)
N+	22 (31.4)
Local Recurrence	
L-	62 (88.6)
L+	8 (11.4)
Distant Recurrence [†]	
D-	46 (79.3)
D+	12 (20.7)

Abbreviations: UICC = International Union Against Cancer; TRG = tumor regression grade; pT and pN = pathologic tumor stages.

*The number of available tumor paraffin-embedded sections was not sufficient for TRG evaluation.

[†]Patients with synchronous metastases were excluded.

Table 2. Association between patient characteristics and response to radiotherapy

Characteristics	Major response	Poor response	<i>p</i> -value
	<i>n</i> (%)	<i>n</i> (%)	
Gender			NS
Male	24 (57.1)	18 (42.9)	
Female	11 (47.8)	12 (52.2)	
Age			NS
≥ 65	18 (52.9)	16 (47.1)	
< 65	17 (54.8)	14 (45.2)	
Tumor grade			NS
Well differentiated	19 (55.9)	15 (44.1)	
Moderately differentiated	11 (44.0)	14 (56.0)	
Poorly differentiated	5 (83.3)	1 (16.7)	
Pretherapeutic UICC TNM stage			NS
Stage I	7 (63.6)	4 (36.4)	
Stage II	7 (35.0)	13 (65.0)	
Stage III	13 (59.1)	9 (40.9)	
Stage IV	8 (66.7)	4 (33.3)	
Synchronous metastases			NS
S+	8 (66.7)	4 (33.3)	
S−	27 (50.9)	26 (49.1)	
Radiotherapy (Gy)			NS
45	19 (50.0)	19 (50.0)	
60	16 (59.3)	11 (40.7)	
CCND1 G870A polymorphism			0.022
A/A genotype	9 (90)	1 (10)	
A/G genotype	17 (42.5)	23 (57.5)	
G/G genotype	9 (60.0)	6 (40.0)	

Table 3. Multivariate analysis of risk factors related to local recurrence

Characteristics	Hazard ratio	95% Confidence interval	<i>p</i> -value
CCND1 G870A polymorphism			
A/A + A/G genotypes	1		
G/G genotype	5.6	1.3–23.5	0.020
pN			
N-	1		
N+	5.5	1.5–21.3	0.011