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

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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