

LETTER TO THE EDITOR

FLUORESCENCE *IN SITU* HYBRIDIZATION ANALYSIS OF CCND3 GENE AS MARKER OF PROGRESSION IN BLADDER CARCINOMA

A.L. BELTRAN¹, J.L. ORDÓÑEZ², A.P. OTERO², A. BLANCA³, V. SEVILLANO²,
M. SANCHEZ-CARBAYO⁴, Z. KIRKALI⁵, L. CHENG⁶, R. MONTIRONI⁷,
R. PRIETO⁸ and E. DE ALAVA^{2,9}

¹Department of Surgery and Pathology, Cordoba University Medical School, Cordoba, Spain; ²Laboratory of Molecular Pathology, Centro de Investigación del Cáncer-IBMCC, University of Salamanca-CSIC, Salamanca, Spain; ³Biomedical Research Unit, University Hospital, Cordoba, Spain; ⁴Tumor Markers Group, Spanish National Cancer Research Center, Madrid, Spain; ⁵Department of Urology, School of Medicine, Dokuz Eylül University, Izmir, Turkey; ⁶Departments of Pathology and Laboratory Medicine, and Urology, Indiana University School of Medicine, Indianapolis, USA; ⁷Institute of Pathological Anatomy and Histopathology, Polytechnic University of the Marche Region and United Hospitals, Ancona, Italy; ⁸Urology Service Reina Sofia Hospital, Cordoba, Spain. ⁹Department of Pathology, Salamanca University Hospital, Salamanca, Spain

Received December 30, 2012 – Accepted February 11, 2013

The first and second author contributed equally to this paper.

The aim of this study was to assess patterns of *CCND3* gene amplification in bladder cancer and correlate gene status with recurrence-free and progression-free survival. A sequential cohort series of 102 primary bladder tumor samples in which there was enough tissue material to assess *CCND3* gene status by fluorescent in situ hybridization (FISH) was the study group. *CCND3* gene FISH amplification present in 31.4% of bladder carcinomas, was related to tumor progression ($p=0.021$) and lower time to progression (mean \pm SD; 25.75 \pm 15.25 months) as compared to 33.29 \pm 11.0 months in the *CCND3* not amplified group ($p=0.05$). By immunohistochemistry, Cyclin D3 labeling index was higher in the *CCND3* amplified group (mean \pm SD, 76.69 \pm 27.51) than in not amplified (mean \pm SD, 21.57 \pm 7.02) ($p<0.0001$). The univariate survival analysis showed *CCND3* gene amplification to be associated to a shorter progression-free survival ($p=0.020$) together with WHO histological grade ($p=0.001$) and pT stage category ($p<0.0001$). Cox's regression analysis selected *CCND3* amplification as an independent predictor of progression-free survival ($p=0.030$, RR3.561, 95% CI 1.128-11.236) together with pT category ($p<0.0001$, RR5.834, 95% CI 2.364-14.395). Our FISH analysis suggests that *CCND3* gene amplification is a marker of aggressiveness and might be a predictor of tumor progression in bladder urothelial carcinoma.

Nearly 80% of patients who initially present with bladder urothelial carcinoma (BC) have tumors confined to the mucosa or submucosa; so called “non muscle invasive” bladder cancer (NMIBC); the

Key words: bladder cancer, CCND3, Cyclin D3, gene amplification, FISH, Immunohistochemistry

Mailing address: Prof. Dr. Antonio Lopez-Beltran,
Unit of Anatomical Pathology,
Faculty of Medicine,
E-14004 Cordoba, Spain
Tel.: +34 957 218992
Fax: +34 957 218229
e-mail: em1lobea@uco.es

rest initially present as invasive disease or “muscle-invasive”(MIBC) bladder carcinoma (1-5). The natural history of treated bladder cancer is difficult to predict due to biologic heterogeneity; features that characterize NMIBC are disease recurrence and progression (1-9).

The risk for both recurrence and tumor progression is related to multiple histopathological factors including tumor grade, depth of invasion, tumor size, multiplicity, tumor growth, vascular invasion, and the presence of CIS (1-9). Although these parameters provide some degree of prognostic information, they fail to clearly evaluate each individual tumor’s malignant potential. These shortcomings with traditional clinical and histopathological features lead to significant efforts to better define a tumor’s true biological potential on a molecular level.

A number of cell cycle aberrations have been studied in an attempt to identify tumors prone to progress (6-16). Tumor proliferation is considered a powerful prognostic indicator of tumor recurrence, and p53 nuclear accumulation is viewed as a marker of progression in bladder tumors; but some studies failed to demonstrate any independent prognostic significance in these patients (6-18). Data concerning other G1-S modulators such as p21Waf1, p27Kip1, and cyclin D1 or apoptotic related markers are limited but of potential interest (6-9).

Alterations of cyclin D3, another upstream regulator of the cell cycle, have been recently reported in bladder cancer (10, 11, 15). Cyclin D3 plays a pivotal role in controlling physiological progression from the G1 to the S phase of the cell cycle (12, 13). Cyclin D3 may be deregulated in a number of human malignant tumors, including lymphoma, breast carcinoma, and melanoma (12, 13). Recent studies suggest that cyclin D3 status might be a marker of response to targeted therapies in neuroblastoma and lung cancer, thus adding interest to studies on cyclin D3 expression in tumors (13, 14, 18).

Cyclin D3 is deregulated in some bladder urothelial carcinomas with data suggesting that cyclin D3 expression could be a marker of aggressiveness (10, 11, 15). *CCND3* gene status has been recently shown to be amplified in urothelial carcinoma *in situ* (CIS) by fluorescence *in situ* hybridization (FISH), a finding that awaits confirmation in other bladder urothelial carcinomas (16).

The aim of this study was to assess patterns of *CCND3* gene amplification in a consecutive series of newly diagnosed bladder urothelial carcinoma by FISH analysis, and to correlate *CCND3* status with patient’s outcome.

MATERIALS AND METHODS

Patients and clinical follow-up

The present study was approved by the committee on ethical standards of the University of Cordoba, (Cordoba, Spain). A sequential cohort series of 102 patients with newly diagnosed bladder cancer was the study group. The patients underwent complete transurethral resection (TURB) and random bladder biopsies and were seen at the University Hospital of Cordoba between the years 2002-2005. Male patients received additional biopsies from the prostatic urethra following standard protocol. A re-TURB was performed when appropriate. Patients showing high grade NMIBC received BCG therapy (Tice strain, $2-5 \times 10^8$ colony forming units weekly for 6 consecutive weeks) followed by maintenance for at least one year. Cystectomy was offered to patients with BCG failure and stage category $\geq pT2$. Patient’s follow-up, calculated as the number of months from the date of the diagnostic procedure to the date of the most recent cystoscopy (or to the date of the last visit or death), was (mean \pm SD) 29.43 ± 13.09 (range, 3-41) months. Tumor recurrence was defined as reappearance of tumor after the initial treatment with at least one tumor-free cystoscopy. Tumor stage progression was defined as shift to any higher stage category (T1, T2-T4) in recurrent tumors or the appearance of metastases. Preoperative excretory urography was performed to exclude cases with evidence of upper urinary tract disease.

All available hematoxylin and eosin stained slides including primary tumors as well as their recurrences were re-evaluated by two dedicated pathologists without knowledge of the clinical status, and were diagnosed and graded in accordance with the most recent World Health Organization grading system. Pathologic staging was determined in accordance with the TNM, 2010 revision.

Tissue-microarray

One hundred and two bladder carcinoma specimens were collected in a tissue-microarray (TMA) using a precision instrument (Tissue arrayer-Beecher Instruments, Silver Spring, MD). Representative tumor areas were identified and circled on H&E-stained slides from each block. Two 0.6-mm tissue cylinders corresponding to the selected areas were removed from each paraffin donor block and placed side by side in an empty recipient

paraffin block measuring 27 x 20 mm. Hematoxylin and eosin stained slides of the TMA allowed to verify the adequacy of the samples.

Fluorescent In situ Hybridization (FISH)

A specific *CCND3* locus probe (PAC clone RP5-973N23) labeled with Spectrum red-dUTP (red signal) (Vysis, Downers Grove, IL) was made. Briefly, isolated PAC DNA was labeled with Spectrum red-dUTP (Vysis) by nick translation (Vysis) and purified after adding 10 µg of COT-1 (Invitrogen, Carlsbad, CA, USA). A commercially available (CEP 6) probe (Vysis) labeled with spectrum green (green signal) was also used. To check the specificity of the home made probe, co-hybridizations using both commercial CEP6 and *CCND3* specific probes were performed over metaphases of peripheral blood cells.

FISH analysis was done on 2 µm-thick sections obtained from the tissue microarray. Negative controls were samples of unrelated tumors and adjacent normal mucosa or normal tissues of unrelated organs from 20 additional patients. A volume of 10 µl of the diluted probes was applied to the slides. The slide was covered with a glass cover slip and sealed with rubbercement (Royal Talens Apeldoorn, Holland). Using a Hybrite machine (Vysis) denaturation was 75°C for 5 min and hybridization was at 37°C for at least 16 h. After removing the cover slips post-hybridization washing was done at 46°C in 2XSSC, 50% formamide for 5 min and stained with DAPI (6-diamidino-2-phenylindole) and mounted with Vectashield H-1000 medium (Vector). Digital images were obtained using a Zeiss Axioplan2 epifluorescence microscope (Carl Zeiss Oberkochen, Germany) equipped with a digital camera (ORCA-ER-1394, Hamamatsu Photonics KK, Hamamatsu, Japan). In all cases, one hundred nuclei were counted for each punch. The number of red signals (*CCND3*) and green signals (CEP6 centromeric) were counted for each nucleus and the average was recorded. We established a ratio red signal/green signal of 2 or greater as an evidence of *CCND3* gene amplification (16).

Immunohistochemistry

Immunohistochemical analysis was done on 4-µm-thick sections obtained from the tissue microarray. Then, dewaxed sections were rehydrated through phosphate buffered saline. For antigen retrieval, the sections were boiled in 10 mM citrate buffer (pH 6.0). Endogenous peroxidase was blocked by incubating the slides for 30 min with 3% hydrogen peroxide in methanol. Sections were then incubated with anti-Cyclin D3 (clone DCS-22, Dako (Glostrup, Denmark, 1:25 dilution, 60 min) primary antibody at room temperature. Immunohistochemical stains were performed using a sensitive polymer-based system (EnVision system, Dako, Glostrup, Denmark) for

30 min at room temperature. Diaminobenzidine solution served as a chromogen. Sections were counterstained with hematoxylin and mounted using standard procedures. Positive (breast carcinoma) and negative controls (substituting the primary antibody with distilled water) were included.

Cyclin D3 immunohistochemistry was measured by using random fields delineated by a 1 cm² graded ocular grid attached to the eyepiece of the microscope (Nikon Labophot, Tokyo, Japan). The regions were chosen inside high immunoreactive areas examined under high power (×400) view and a mean of 300 cells per case were counted. A labeling index, defined as the percentage of positive nuclei, was established with tumors stratified following the low vs. high expression scheme <25% vs ≥25% (10).

Statistical analysis

Bivariate and multivariate analysis using contingency tables were tested for significance using *Chi*-square analysis and comparison of the means was carried out using the Student *t*-test. The end point of the study was recurrence-free and progression-free survival. Univariate survival analysis was conducted using the Kaplan-Meier method, and differences among groups were tested for significance using the Log-rank test. Significant parameters in the univariate analysis entered a multivariate analysis of independent prognostic factors using Cox proportional hazard regression analysis, and the relative risk with 95% confidence interval was calculated. All the statistical analyses were performed using the SPSS 15.0 for Windows Software (SPSS Inc, Chicago, IL). A *p* value of less than or equal to 0.05 was considered indicative of a statistically significant difference.

RESULTS

Table I shows patients' characteristics. A total of 102 patients (92 men) with bladder carcinoma were the study cohort. Their mean age was 71.08 (±SD, 11.17) years.

Most patients had high grade tumors (58.8%) with size < than 3 cm (66.7), and were multiple (58.8%). Pathologic stage was pTa (49%), pT1 (29.4%) or ≥pT2 (21.6), and 7.8% of patients had concurrent CIS. On follow up 47.5% of tumors recurred (mean±SD, 27.30±12.52, range 4-41 months and 23.5% progressed in stage (mean±SD, 30.92±12.83, range 1-41 months). *CCND3* gene amplification seen by FISH as multiple scattered or grouped red signals was present in 31.4% of cases and was

Table I. Clinico-pathologic features of bladder cancer according to *CCND3* gene status.

Variable	Overall N=102 (%)	CCND3 amplified N=32 (%)	CCND3 not amplified N=70 (%)	*P-value
Gender				0.662
Male	92 (90.2)	28 (87.5)	64 (91.4)	
Female	10 (9.8)	4 (12.5)	6 (8.6)	
§Age (y)	71.08±11.17 (45-92)	71.31±10.70 (54-85)	70.97±11.54 (45-92)	**0.921
Grade				0.330
LG	42 (41.2)	10 (31.3)	32 (45.7)	
HG	60 (58.8)	22 (68.8)	38 (54.3)	
pTcategory				0.171
Ta	50 (49)	12(37.5)	38 (54.3)	
T1	30 (29.4)	8 (25)	22 (31.4)	
≥T2	22 (21.6)	12 (37.5)	10 (14.3)	
CIS				0.775
Present	8 (7.8)	2 (6.3)	6(8.6)	
Absent	94 (92.2)	30 (93.8)	64 (91.4)	
Tumor size				0.670
≤ 3 cm	68 (66.7)	20 (62.5)	48 (68.6)	
> 3 cm	34 (33.3)	12 (37.5)	22 (31.4)	
Tumor number				0.718
Single	42 (41.2)	12 (37.5)	30 (42.9)	
Multiple	60 (58.8)	20 (62.5)	40 (57.1)	
¥Tumor recurrence				0.361
Yes	38(47.5)	12 (60)	26 (43.3)	
No	42(52.5)	8 (40)	34 (56.7)	
§Time to recurrence (months)	27.30±12.52 (4-41)	27.20±12.14 (5-41)	27.33±12.86 (4-41)	**0.977
Tumor progression				0.021
Yes	24 (23.5)	14(43.8)	10 (14.3)	
No	78 (76.5)	18 (56.3)	60 (85.7)	
§Time to progression (months)	30.92±12.83 (1-41)	25.75±15.25 (1-41)	33.29±11.00 (4-41)	** 0.050
§Cyclin D3 IHC status	38.86±30.46 (6-120)	76.69±27.51 (29-120)	21.57±7.02 (6-32)	**< 0.0001

* Chi-square analysis; ** Student *t* test; SD: standard deviation of the mean; LG: low grade; HG: high grade; IHC: immunohistochemistry: (y) age in years; §: mean±SD, range; ¥ tumor recurrence based on pTa/pT1 cases, N=80.

associated to tumor progression ($p=0.021$), lower time to progression ($p=0.050$) and higher Cyclin D3 labeling index by immunohistochemistry ($p<0.0001$) (Table I, Fig. 1).

The univariate survival analysis showed that *CCND3* gene amplification was related to progression-free ($p=0.020$) but not to recurrence-free survival ($p=0.558$) (Tables II, III and Fig. 2). Cox's regression analysis selected concurrent CIS as independent predictor of recurrence-free survival

($p=0.015$, RR 7.108, CI1.458-34.653); and *CCND3* amplification ($p=0.030$, RR3.561, CI1.128-11.236), and pT stage ($p<0.0001$, RR 5.834, CI 2.364-14.395) as independent predictors of progression-free survival (Table IV).

DISCUSSION

Urothelial carcinoma of the urinary bladder is a distinct entity which frequently shows an unpredictable

Table II. Univariate survival analysis according to recurrence-free survival (*pTa-pT1* cases).

Variable	Overall N=80	Recurrence-free (%)	Log-rank	P-value
Gender			0.989	0.320
Male	72	40 (55.6)		
Female	8	2 (25)		
Grade			0.000	0.998
LG	42	22 (52.4)		
HG	38	20 (52.6)		
pTstage			0.008	0.931
Ta	50	26 (52)		
T1	30	16 (53.3)		
CIS			8.093	0.004
Present	4	0 (0)		
Absent	76	42 (55.3)		
Tumor size			1.535	0.215
≤ 3 cm	56	34 (60.7)		
> 3 cm	24	8 (33.3)		
Tumor			1.366	0.243
Single	34	20 (58.8)		
Multiple	46	22 (47.8)		
CCND3 gene status			0.342	0.558
amplified	20	8 (40)		
not amplified	60	34 (56.7)		

CIS: Associated Urothelial Carcinoma In situ; LG: low grade; HG: high grade.

course (1-5). The untreated natural history indicates 30-50% stage progression rate and an even higher recurrence rate (1-5). Current BCG protocols in high grade tumors have improved substantially the prognosis of these patients, but in non-responding patients the risk of tumor progression is high.

Clinical factors are of limited help as predictors of aggressiveness in selected cases (1-5). Some recent reports, however, clearly indicate the value of p53, and Shariat et al (19) showed that a combined p53/p21Waf1 expression was associated with progression and cancer-specific survival. Hopman et al (20) also found an association between *TP53* mutation, loss of chromosome 9 and 9p21, and invasive bladder cancer in CIS patients. Loss of E-cadherin expression was reported as another risk factor for progression and disease-specific survival in patients with high grade

urothelial carcinoma (21). Likewise, other molecular markers do not seem powerful enough to predict response to therapy or progression in daily practice (6, 7). Therefore, studies on newer molecular markers to define patterns of aggressiveness in bladder cancer are needed.

Cyclin D family, mainly Cyclin D1 and Cyclin D3, form complexes with cyclin dependent kinases 4 and 6 and thus promote phosphorylation and inactivation of the retinoblastoma protein releasing the promoter factor E2F-1 (13). This, in turns activates genes involved in DNA synthesis, thereby mediating the progression of cells from G1-to-S phase of cell cycle. Cyclin D3 expression in urothelial bladder cancer has received recent interest with some reports showing high cyclin D3 expression by immunohistochemistry to be an independent predictor of patients' survival

Table III. Univariate survival analysis according to progression-free survival.

Variable	Overall N=102	Progression-free (%)	Log-rank	P-value
Gender			0.001	0.973
Male	92	70 (76.1)		
Female	10	8 (80)		
Grade			10.261	0.001
LG	42	42 (100)		
HG	60	36 (60)		
pTcategory			23.679	<0.0001
Ta	50	50 (100)		
T1	30	20 (66.7)		
≥T2	22	8 (36.8)		
CIS			2.070	0.150
Yes	8	4 (50)		
No	94	74 (78.7)		
Tumor size			0.000	1.000
≤ 3 cm	68	52 (76.5)		
> 3 cm	34	26 (76.5)		
Tumor number			0.337	0.561
Single	42	34 (81)		
Multiple	60	44 (73.3)		
CCND3 gene status			5.414	0.020
Amplified	32	18 (56.3)		
Not amplified	70	60 (85.7)		

CIS: Associated Urothelial Carcinoma In situ; LG: low grade; HG: high grade.

Table IV. Cox multivariate analysis showing independent variables related to recurrence and progression-free survival in patients with bladder cancer.

Variable	RR	CI 95%	P-value
Recurrence-free survival			
CIS	7.108	1.458-34.653	0.015
Progresión-free survival			
pT category	5.834	2.364-14.395	<0.0001
CCND3 gene status	3.561	1.128-11.236	0.030

CIS: Associated Urothelial Carcinoma In situ. CI: Confidence interval. RR: Risk ratio.

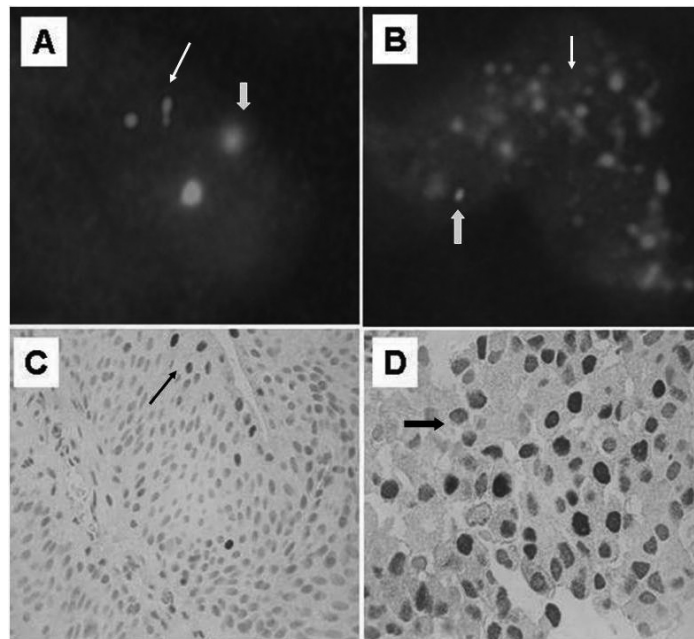


Fig. 1. *CCND3* gene normal expression (not amplified) showing two red signals (thin arrow) and two centromeric green signals (thick arrow) on chromosome 6 (normal expression) in bladder cancer (case 15) (A) as compared with *CCND3* gene amplification characterized by multiple red signals (thin arrow) in contrast to two centromeric green signals (thick arrow) on chromosome 6 (normal expression) in bladder cancer (case 26) (B) (A and B, FISH: fluorescence in situ hybridization). Low Cyclin D3 labeling index in case 15 showed not amplified (thin arrow) *CCND3* gene by FISH (C) and high Cyclin D3 labeling index (thick arrow) in case 26 that showed amplified *CCND3* gene by FISH (D) (C and D, anti-Cyclin D3 Immunohistochemistry).

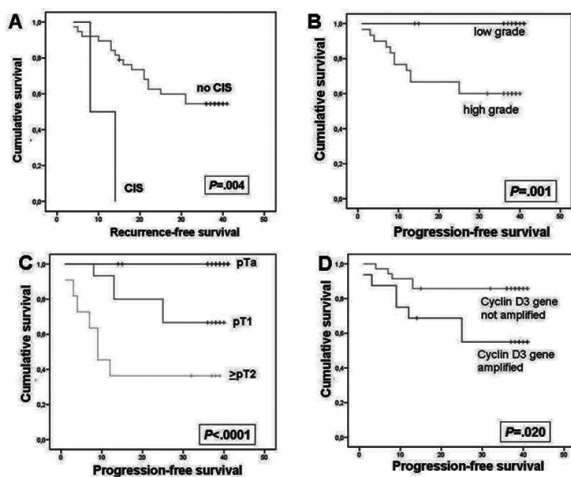


Fig. 2. Kaplan–Meier plots illustrating the association between urothelial carcinoma in situ (CIS) and recurrence-free survival (months) (A), and histological grade (B), pT stage (C) and *CCND3* gene status by FISH (D) associated to progression-free survival (months) in bladder cancer.

(10, 11, 15, 17).

In the present study, *CCND3* gene status has been found to be independent predictor of progression-free survival. This is an original finding not previously reported. We found amplification and up-regulation of *CCND3* gene to be present in about one third of urothelial bladder cancer cases and in about two thirds of high grade carcinomas. This, is in agreement with our previous work showing cyclin D3 protein up-regulation in bladder carcinoma mainly in high grade cancers, (10, 11) an observation recently confirmed by Levidou et al. (15), and, also agrees with the finding of *CCND3* gene amplification by FISH in secondary urothelial carcinoma in situ but not in primary CIS cases; CIS is considered a high grade urothelial disease (16). Moreover, a recent study based on quantitative gene expression profiles showed that *CCND3* gene was a significant predictor or recurrence and progression in high grade bladder

cancer, thus supporting our findings on *CCND3* gene amplification by FISH in bladder cancer (22). Our observation of a strong association of *CCND3* gene amplification with progression-free survival could indicate that there is an important deregulation of *CCND3* gene along with protein overexpression in high grade bladder cancer. Moreover, it seems that cyclin D3 alteration is a potentially relevant finding since the use of cell cycle regulatory proteins as therapeutic targets of their modulators, represents an active field of research (6, 13-16, 23-25). Available modulators of Cyclin D3 expression such Interferon- α and flavopiridol, that can induce cell cycle arrest by directly inhibiting cyclin dependent kinases and by down-regulation of Cyclin D3, might represent a future alternative to other conventional therapeutic approaches in a subset of bladder cancer patients at higher risk of aggressive behavior. In fact, recent studies show that cyclin D3 might be a potential biomarker of response to targeted therapy in neuroblastoma and lung cancer; a finding that awaits confirmation in bladder cancer patients (6, 13-16, 23-25). Recent reports support the role of cyclin D3 in different pathways known to be altered in bladder cancer, i.e. cyclin D3 is also a downstream STAT3 target such as Mcl-1, Bcl-2, and Bcl-xL, all of which are implicated in apoptosis and the cell cycle. (6, 13-16, 23-25) There was greater expression of the PI3K-AKT-cyclin D3 molecular pathway downstream to the activation of pPDGF- β R in neoplastic compared with normal tissue in bovine bladder cancer (17). Cyclin D3 might be a microRNA (MiR-138) target in hepatocellular carcinoma (26). This new information suggests a role of cyclin D3 in bladder cancer biology and pathology.

Our study also highlights that *CCND3* gene amplification is associated to higher cyclin D3 protein labeling index, suggesting that overexpression of Cyclin D3 protein, as detected by immunohistochemistry, is mediated by gene amplification. Observed differences between *CCND3* gene and Cyclin D3 protein expression concerning significance in predicting bladder cancer progression, might be related to the quantification method of the immunohistochemistry, which is far to be as precise as the quantification of FISH color signals.

In conclusion, we have shown the apparent role of *CCND3* gene amplification and up-regulation

as a biomarker which helps to select a subset of tumors at higher risk of developing invasive disease. This warrants further prospective studies on the expression of this cell cycle regulatory gene and protein in bladder cancer patients.

ACKNOWLEDGEMENTS

Supported by the grants SAF2007-64942 (Ministry of Education and Research, Madrid, Spain), P07-CVI-02974 and PI0003/2007 (Junta de Andalucia, Seville, Spain). Work at CIC is also funded by Instituto de Salud Carlos III III-FEDER (PI081828, PI110018, RD06/020/0059). JLO is supported by CSIC (Contratos Postdoctorales JAEDOC).

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