

Expression of Human Chorionic Gonadotropin β Subunit Genes in Superficial and Invasive Bladder Carcinomas¹

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Abstract

Increased serum levels of human chorionic gonadotropin β subunit (hCG β) were described previously in patients with bladder cancer. To obtain insight into such production of hCG β , the expression of hCG β 7, 8, 5, and 3 genes in bladder carcinomas and normal urothelia was investigated by reverse transcription PCR. Surprisingly, hCG β mRNAs were detected in both normal urothelial and carcinomatous cells. However, tumor progression was characterized by different patterns of transcription of the hCG β genes; the β 7 gene was the only gene transcribed in normal urothelia and T_a tumors included in this study, whereas in addition to β 7, genes β 5, 8, and 3 were transcribed in T₁ to T₄ tumors. Moreover, transcription levels of the latter three genes increased with the stage of the disease. These observations show that dramatic modifications in the expression of hCG β genes accompany progression of bladder carcinomas.

Introduction

hCG³ is a dimeric hormone produced by the trophoblast during pregnancy (1). It belongs to a glycoprotein hormone family, which includes LH, follitropin, and thyrotropin, and is composed of two noncovalently linked subunits, designated α and β . Whereas the α subunit common to the four hormones is encoded by a single gene located at position 6q14–q21, the hCG β subunit is encoded by a cluster of six genes (β 7, 8, 5, 1, 2, and 3) located at position 19q13.3, adjacent to the β 4 gene coding for the hLH β subunit (2, 3). All six hCG β genes were found to be transcribed in trophoblastic cells (4). However, different levels of mRNA have been detected, with the β 5, 8, and 3 genes being preferentially expressed. Only genes β 7, 8, 5, and 3 present the open reading frame of the hCG β subunit protein. They can be distinguished by variations in the sequence of either the 5' transcribed untranslated regions (4) or the promoters (5). Such variations account for differences observed in the levels of their expression in trophoblastic cells (5).

The dimeric hormone hCG, as well as its free β subunit, are also produced by gestational trophoblastic and gonadal cancers (6–8). Moreover, the presence of the free hCG β subunit has been demonstrated clearly in sera of patients with nontrophoblastic and nongonadal neoplasms (8). In particular, preferential production of the free hCG β subunit in the absence of dimeric hCG was found in the sera of

patients with bladder cancers, and its presence correlated with the stage of the tumor (8, 9).

Bladder cancers are divided into two groups, superficial (T_{is}, T_a, and T₁) and invasive (T₂, T₃, and T₄). Characterization of the molecular genetic pathways involved in the progression of bladder carcinomas is important for the identification of prognostic factors as well as for the development of new therapeutic strategies (10–12). In this study, we investigated the expression of genes hCG β 7, 8, 5, and 3 in both normal bladder and bladder carcinomas at various stages of the disease. Surprisingly, hCG β mRNAs were detected by RT-PCR in both normal and neoplastic tissues, but tumor progression was characterized by dramatic changes in the expression of the different hCG β genes.

Materials and Methods

Tissue RNA Extraction. Four normal urothelia and 34 bladder transitional cell carcinoma fragments were obtained from patients after surgery at the Hôpital Henri Mondor and at the Institut Gustave Roussy, in accordance with protocols approved previously by the human studies committee of each hospital. The proportion of tumor cells in surgical fragments of bladder carcinomas was estimated by visual examination of sections stained with hematoxylin and eosin. Adjacent pathological material sections with a high tumor cell content (>80%) were used for RNA extraction. Three first-trimester placentae were obtained from women undergoing legal abortions. RNA was purified in cesium chloride gradients (13).

Oligonucleotides. Two pairs of primers, β 1- β 2 and β 3- β 4 (DNAgency, Malvern, PA), were designed to commonly amplify the hCG β 7, 8, 5, and 3 mRNA, without amplification of contaminating DNA, hCG β 1, hCG β 2, or hLH β mRNA (Fig. 1A). For this purpose, one primer in each pair was placed at the junction between two exons and contained, therefore, in its 3' end, a mismatch with any contaminating DNA; β 1 was placed upstream of the hLH β transcription start site; β 3 presented, at its 3' end, a 2-bp mismatch with the hLH β sequence (CC versus TG), and oligonucleotide β 1 did not match with the hCG β 1 and 2 mRNA sequences (4). One primer in each pair was fluorescein-labeled at its 5' extremity by adding Fluorprime during oligonucleotide synthesis (Pharmacia, Uppsala, Sweden).

hCG β mRNA Pattern. The identification of each hCG β 7, 8, 5, and 3 mRNA was performed by *Hha*I and *Dra*I restriction endonuclease analysis of the β 1- β 2 RT-PCR products (Fig. 1A). One μ g of total RNA was reverse transcribed under 20 μ l using the Gene Amp RNA PCR kit (Perkin-Elmer Cetus, Foster City, CA), according to the manufacturer's instructions. The equivalent of 250 ng cDNA (5 μ l RT product) was amplified under 50 μ l using 2.5 units of Taq DNA polymerase, 50 mM KCl, 10 mM Tris-HCl (pH 8.3), 0.5 mM MgCl₂, and 10 pmol of each of the β 1 and β 2 primers. PCR were processed through 35 cycles of 30 s at 95°C, 30 s at 60°C, and 30 s at 72°C on a 9600 Perkin thermocycler. Restriction endonuclease analysis was performed in a 20- μ l volume reaction using 5 units of *Hha*I and 2.5 units of *Dra*I according to the manufacturer's instructions (Biolabs, Beverly, MA).

hCG β mRNA Steady-State Level. The RT-PCR method was used to quantify hCG β mRNA. To take into account the extent of possible degradation of the RNA preparations, TFIID transcripts were quantified and used as an

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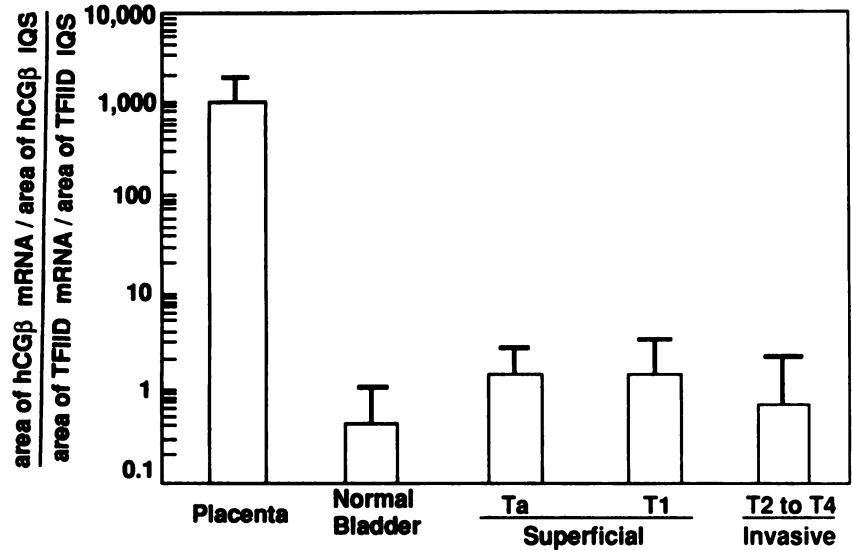
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³ The abbreviations used are: hCG, human chorionic gonadotropin; LH, lutropin; RT, reverse transcription; IQS, internal quantitative standard.

Fig. 3. hCG β mRNA mean steady-state levels in normal and tumoral bladder tissues as compared to first-trimester placenta specimens. For each group, standard deviation is indicated. Quantification was achieved by RT-PCR using IQS DNA. Electrophoresis was performed on an ABI DNA sequencer, and the peak areas were measured. hCG β mRNA levels were normalized, by measuring in a similar manner, the number of transcripts encoding the housekeeping gene TFIID. All experiments were done in duplicate; bars, SD.



and bladders. This result indicated that, whereas the steady-state level of TFIID transcripts was similar in both trophoblastic and bladder tissues, the steady-state level of hCG β mRNAs was dramatically different in these tissues. The steady-state levels of hCG β mRNAs in placental and bladder tissues, normalized with those of TFIID, are presented in Fig. 3. No significant difference was found in the steady-state levels of total hCG β mRNAs between normal bladders and invasive tumors ($U = 15$; $P = 0.79$). The expression of hCG β including $\beta 7$, 5, 8, and 3 genes in superficial tumors was significantly higher than in invasive tumors ($U = 199$; $P = 0.007$).

Discussion

The aim of this study was to characterize the hCG β mRNA pattern in a series of normal and tumoral bladder tissues at various stages of disease and to compare the pattern observed in urothelial cells to that displayed by normal trophoblastic cells. To investigate the steady-state level of each of the hCG β 7, 5, 8, and 3 mRNAs, we developed an original strategy based on the RT-PCR method, combined with restriction endonuclease analysis and competitive PCR quantitation.

Similar levels of hCG β mRNA were detected in both normal and tumoral bladder tissues, but the overall steady-state level of hCG β mRNAs in bladder tissues was found to be a thousand-fold lower than that detected in first-trimester placental tissues. In contrast to trophoblastic cells from normal placenta, which preferentially express hCG β 5, 8, and 3 genes (4), only $\beta 7$ mRNA was detected in four normal urothelia. Indeed, the transcription of hCG β genes had been observed already in normal tissues other than the trophoblast; hCG β mRNAs were detected by RT-PCR in normal testis (15), and there is evidence for hCG production by human pituitary cells (16). Although the limited number of normal urothelia included in our study does not enable extrapolation to all bladder controls, it is striking that distinct β genes were transcribed by different normal tissues. The present observation in normal bladder, when compared with previous data observed in normal trophoblast, suggests that regulation of $\beta 7$ gene transcription within the hCG β cluster varies with the differentiation of the tissue. At least two mechanisms might account for such distinct regulation: differences in the sequence of the distal promoter of the $\beta 7$ and $\beta 5$, 8, and 3 genes (5); and variability in the degree of methylation of the hCG β cluster, depending on the origin of the cells (17). Finally, it is noteworthy that both the hCG and free hCG β subunit are detected at very low levels in serum and urine of men and nonpregnant women (8, 18). Until now, such production was thought to

originate from the pituitary (16), but other normal tissue, such as the bladder urothelium, might also be responsible for the presence of the free hCG β subunit in biological fluids.

Whereas only hCG β 7 mRNA was detected in normal urothelia and T_a tumors, simultaneous expression of the $\beta 7$ and $\beta 5$, 8, or 3 genes was detected in 45% of T_1 and 95% of invasive (T_2 to T_4) tumors. In fine, hCG β 5, 8, or 3 gene expression was detected in 61% of bladder carcinomas. Qualitative ($\beta_{5,8,3}:\beta_{7,5,8,3}$ hCG β mRNAs ratio) as well as quantitative (steady-state mRNA levels) analyses of $\beta 7$, 5, 8, and 3 mRNA patterns indicated that the level of expression of the $\beta 5$, 8, and 3 genes is correlated with the tumor stage. Interestingly, the simultaneous presence of hCG β 5, 8, or 3 and hCG α mRNAs was detected in two superficial tumors (11%) and seven invasive tumors (41%; data not shown). This molecular pattern is close to that observed in trophoblastic cells. This observation is in agreement with the hypothesis that the origin of hCG β productive bladder cancer cells involves metaplasia of the carcinomatous tissue into a tissue similar to trophoblast tissue (7, 8, 19). Nevertheless, the secretion of hCG-related proteins is quantitatively and qualitatively different in productive bladder tumors and in placenta; while dimeric hCG is preferentially produced by normal trophoblastic cells in pregnant women, bladder carcinomas preferentially produce the free hCG β subunit (8, 9, 20).

It is tempting to speculate that the acquired expression of the $\beta 5$, 8, and 3 mRNAs in invasive bladder carcinomas is responsible for the increase in hCG β serum levels (≥ 100 pg/ml) detected in 47% of patients with bladder carcinomas (8). Indeed, we observed that both the expression of the hCG β 5, 8, or 3 genes and the presence of the hCG β subunit in the sera of patients with bladder carcinomas (8, 9) correlate with the stage of the disease. However, the use of highly sensitive fluoroimmunoassays (2 pg/ml) shows that low serum hCG β levels (< 100 pg/ml) are detected in normal individuals (8, 18). The interest of determining the pattern of hCG β mRNAs might be to enable the distinction between expression of hCG β genes by normal tissues and expression by invasive bladder carcinomas, as well as to determine whether combined ultrasensitive serological assays (15, 18) and analysis of the pattern of hCG β gene expression in surgical fragments optimizes the management of patients with bladder carcinomas.

Taken together, the present results demonstrate that the pattern of expression of various hCG β genes differs in normal urothelium and bladder carcinomas and that progression of the disease is characterized by increased levels of expression of $\beta 5$, 8 and 3 genes.

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