Evaluation of the Expression of S-100A2 mRNA in Human Bladder Cancer

Introduction and Objective: The human S100 proteins are a calcium-binding protein comprising around 20 sorts, at least 16 of these genes included pseudogenes are clustering to chromosome 1q21, known as the epidermal differentiation complex. We have reported that S100A1 and A10 are expressed in human renal cell carcinoma (RCC) (Teratani T et al; Cancer Lett 2002, Teratani T, et al; BBRC 2002, Domoto, et al Cancer Sci. 2007) and we also show the diminished expression of S100A2mRNA in human clear cell RCC, but not in non-clear cell RCC (ASCO-GU 2012 abstruct#457). We planned to evaluate the S100A2 mRNA expression in human bladder cancer.
Materials and Methods: Thirty patients, who performed TUR-Bt (transurethral resection of the bladder tumor), were used in this study. Genomic DNA and RNA were extracted from tumor samples in each patient. First-strand cDNA was synthesized from 2 micrograms RNA, and reverse transcription polymerase chain reaction (RT-PCR) were performed using specific primers for S100A2, and we conducted real-time PCR using TaqMan Assay. The methylation of the CpG islands in the promoter lesion of the S100A2 gene using COBRA assay (combined bisulfite restriction analysis).
Results: In contrast to clear cell RCC, all cases had the expression of S100A2mRNA. Hypomethylation of S100A2 showed much frequent in non-invasive cases (7/14 vs. 2/9 cases). In pTa cases (N=17), high S100A2mRNA level cases were 4/13 cases, but tested 7 cases with COBRA assay were no methylated cases.
Conclusions: Methylation status of S100A2 might not contribute to the expression level of S100A2 in bladder cancer samples. This series has few advanced cases and further experiments using larger samples should be needed for confirmation. Overexpression of S100A2 seems to frequently show in the non-advanced bladder cancer.