Cloning and characterization of a novel alternatively spliced transcript of the human CHD7 putative helicase.

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Gliomas are the most common brain tumor with grade IV glioblastomas constituting one of the most lethal tumors. To understand the molecular basis of gliomagenesis, our group has been searching for differentially expressed genes both in glioma cell lines and in clinical samples. In previous studies, our group identified the CHD7 gene, which codes for a putative DNA helicase, as being highly expressed in glioblastomas. Herein, we have isolated a novel splice variant (3.5Kbp) of this poorly characterized gene. In view of the importance of alternatively spliced transcripts in several cellular processes and in order to assess the role of CHD7 in glioma tumor progression, we set out to characterize the structure of this novel *CHD7* transcript and to evaluate its expression profile. DNA sequencing enabled us to determine the transcript exon structure. Transcriptomic and genomic data bank analysis confirmed that this transcript is in fact a new alternatively spliced variant of *CHD7*. Its expression profile was evaluated in glioma and other tumor cell lines and in normal human tissues, through RT-PCR analysis using specific primers flanking the splice site regions. In addition to the DU145 prostate carcinoma cell line, from which this new transcript was firstly isolated, it was also detected in normal human liver. The complete characterization of *CHD7* alternative transcripts is a crucial step for future functional studies of the possible role played by this gene in gliomagenesis.
Key words: CHD7, alternative transcripts, gliomas, DNA sequencing and RT-PCR.