

IMPRINTING AND TRANSCRIPTIONAL REGULATION MECHANISM OF THE SLC22A18 GENE FROM HUMAN CHROMOSOME SEGMENT 11p15.5.

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Aim: To understand the regulation of *SLC22A18* expression and its imprinting mechanism. **Methodology:** In order to understand the regulation of *SLC22A18* expression, we have characterized its promoter. We have used PCR methodology to isolate 5' flanking region of *SLC22A18* gene and cloned in pGL3 basic promoter less vector and carried out luciferase assay in HepG2, HEK293 and BeWo cell lines. **Results:** The isolated sequence has directed a high level of expression of luciferase activity in three human cell lines HepG2, HEK293 and BeWo. Successive 5' and 3' deletion analysis has suggested that a ~198 bp region, from position +78 to -120 from the transcription start site (TSS), contains the core promoter. Interestingly, this region contains no consensus TATA box. However, a 414-bp fragment surrounding the TSS exhibits the characteristics of a CpG island which overlaps with the promoter region. **Concluding remarks:** Human chromosome 11p15.5 contains several maternally and paternally imprinted genes. *SLC22A18* is a paternally imprinted gene belonging to the 11p15.5 region that has been shown to carry mutations in some human neoplasms. Reduced expression of *SLC22A18* has been found in hepatoblastomas (HB) and it was proposed that the reduced expression may contribute to HB development. The mechanism of *SLC22A18* imprinting is not known. The identification of *SLC22A18* promoter will not only help to understand its role in tumorigenesis but it will also help to understand the mechanism of imprinting of this gene. We are in the process of studying the nature and mechanism of genomic imprinting using sodium bisulfite genomic sequencing and chromatin immunoprecipitation techniques.