

Natural cis-antisense of human tumor suppressor genes

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Motivation

Large-scale bio-informatic analysis of genomes has recently allowed identification of natural antisense transcripts (NATs) in several model organisms. To elucidate a possible functional significance of cis-NATs in gene expression regulation in cancer we computed the incidence of cis-NAT in a dataset of human tumor suppressor genes and determined their expression in cancer cells by experimental approaches.

Results

At least one antisense transcript was present in 20% of the tumor suppressor dataset. Manual annotation showed that potential coding antisenses are prevalent and that 50% of the cases are conserved in mouse (position and/or sequence conservation). Experimental analyses are on-going in order to determinate the expression profiles of a subset of pairs in some matched normal/tumor samples. Our results show that natural cis-antisense could represent important players in the pathogenesis of cancer through expression regulation on cancer related genes, as tumor suppressors, via double strand editing or chromatin modification.

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