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AF4/FEL, a gene involved in infant leukemia: sequence variations, gene structure, and possible homology with a genomic sequence on 5q31

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Abstract

The most common chromosome abnormality among infants with acute lymphoblastic leukemia is a t(4;11)(q2l;q23) and patients with this 4;11 translocation have a very poor prognosis. This unique genetic rearrangement fuses the MLL/ALL-1/HRX-Htrx gene at 11q23 with the AF4/FEL gene at 4q21. The resulting chimeric mRNAs presumably encode chimeric proteins which contribute to the leukemogenic state. The AF4 gene remains poorly understood with an unknown function. In this report, we describe the cDNA sequence information from human placental tissue where AF4 mRNA is highly expressed. We identified six intron-exon boundaries in the AF4 genomic structure and discussed more than 30 AF4 cDNA sequence variations reported in the literature. In addition, we identified three overlapping genomic sequences in GenBank entitled the "interleukin growth hormone cluster on chromosome 5q31," which, when aligned and translated, had three regions that suggested homology to the predicted AF4 protein sequence (32% amino acid sequence identity over 314 amino acids, 43% over 63 amino acids, and 50% over 40 amino acids). Of interest, this same chromosome 5q31 region has also been implicated in MLL gene rearrangements in human leukemia.

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