cDNA Cloning of a Human Brain Finger Protein, BFP/ZNF179, a Member of the RING Finger Protein Family

Naohiko Seki, Atsushi Hattori, Masa-aki Muramatsu, and Toshiyuki Saito

Abstract
The rat bfp/znf179 transcript for a member of the RING finger protein family, is expressed in brain and up-regulated in neural differentiation of P19 embryonic carcinoma cells. Here we report the full-length cDNA structure of human BFP/ZNF179 and its expression profile. The cDNA clone consists of 3082 nucleotides and encodes an open reading frame of a 632-amino acid protein that contains a RING finger domain at its N-terminus, and alanine-rich and glycine-rich domains at its C-terminus. Reverse transcriptase polymerase chain reaction analysis of various human tissues indicated that BFP/ZNF179 is predominantly expressed in brain.

Key words: BFP/ZNF179; RING-finger motif; brain specific; chromosome 17p11.2
poly(A) tail. The putative RING finger motif (C3HC4) is located at the amino-terminal region of the protein (between residues 57 aa and 97 aa) (Fig. 1). A glycine-rich (21/100) and alanine-rich (24/100) domains of unknown function is found at the C-terminus region of the protein (between residues 102 aa to 105 aa (Fig. 1). The nucleotide sequence data reported here will appear in the DDBJ, EMBL, and GenBank nucleotide sequence databases under accession number AB026054.

**Figure 1. Nucleotide sequence and deduced amino acid sequence of BFP/ZNF179 gene.** Asterisk denotes the termination codon. The RING finger motif is underlined. Polyadenylation signal (aataaa) is double underlined. The nucleotide sequence data reported here will appear in the DDBJ, EMBL, and GenBank nucleotide sequence databases under accession number AB026054. A homology search of the cDNA sequence revealed that it significantly matched with mouse bfp/znfl79 (accession number AB130897 and AB013097 and AB026054).
The human BFP/ZNF179 gene is relatively small and spans approximately 6 kb (two times the rule of AG-GT. The human BFP/ZNF179 gene is related to the canonical splicing acceptor and donor sequence, AC004448). All but one splicing sites were determined by aligning the cDNA sequence with the genomic sequence from the cosmid clone (accession number, AC004448). The human BFP/ZNF179 gene is ubiquitously expressed and the transcription does not identity and 92% similarity). The human BFP/ZNF179 gene is one of the most proximal genes in this critical region of Smith-Magenis syndrome, which contains the critical region of SMS has been narrowed down within 5Mb at 17p11.2. The clinical findings of SMS include mental retardation, neuro-behavioral abnormalities, sleep disturbances, short stature, minor craniofacial and skeletal anomalies, congenital heart defect and renal anomalies. At present, the critical region of SMS has been narrowed down within 5Mb at 17p11.2. Human chromosome 17p11-p12 has a high gene density and is genetically unstable. Several candidate genes are mapped within the deleted region. However, the relation of these genes with SMS is still obscure, to date.

Finally, a partial genomic fragment including RING finger domain was isolated and its chromosomal localization was assigned to the SMS critical region of 17p11.2. The subsequent FISH analyses indicated that the genomic DNA including BFP/ZNF179 fragment was deleted in one of the two homologues on 17p11.2. As SMS critical region varies in the proximal break points, and BFP/ZNF179 is one of the most proximal genes in this region, our present data of the full-length cDNA sequence together with the genomic structure of the gene might be a useful tool to detect the deletion or mutation search of BFP/ZNF179 gene in SMS patients.

References
brain finger protein (bfp), a member of the RING finger family, \textit{Genomics}, \textbf{33}, 325–327.


