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SHORT COMMUNICATION

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A novel human gene whose product shares significant homology with the bovine brain-specific protein p25 on chromosome 5p15.3

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Abstract Here, we report on the sequence features and chromosomal location of a novel human gene which shares significant homology with the bovine brain-specific protein p25. Based on polymerase chain reaction analysis with a human/rodent monochromosomal hybrid cell panel and a radiation hybrid panel, the gene was mapped on to p15.3 region of chromosome 5.

Key words Bovine brain-specific protein · Chromosome mapping · Radiation hybrid panel · 5p15.3

A brain-specific protein, p25, was originally isolated as a major protein in the partially purified fraction of bovine τ protein kinases (Takahashi et al. 1991), and its complete sequence was determined with a cDNA from a bovine brain cDNA library (Shiratsuchi et al. 1995). From immunohistochemical studies, p25 was localized in oligodendrocytes and neuropils (Takahashi et al. 1993).

A novel cDNA clone was isolated from a full-length enriched cDNA library constructed from a human neuroblastoma sample using the oligo-capping method described previously (Maruyama and Sugano 1994; Suzuki et al. 1997). A one-pass sequencing and database search revealed that this cDNA clone did not match any human genes. The entire sequence of the clone was determined by a shotgun strategy (Ohara et al. 1997). The isolated cDNA clone was 5019 bp in length, and had an open reading frame of 219 amino acids. The predicted protein had a calculated molecular weight of approximately 24 kDa. A homology search of the conceptual translated amino acid sequence revealed that it is most homologous to bovine brain-specific protein p25, having 90% identity at the amino acid level. The alignment of the amino acid sequence deduced from the human and bovine p25 proteins is shown in Fig. 1. The nucleotide sequence data reported here will appear in the DDBJ, EMBL, and GenBank nucleotide sequence databases with the accession number AB017016.

We examined the distribution of the human p25 transcript in various tissues by reverse transcription-coupled polymerase chain reaction (RT-PCR). Primers corresponding to the separate exons of the messenger were used to differentiate the contaminating genomic DNA-derived PCR products. A clear common signal of the expected size was detected in all the tissues examined (data not shown). In contrast with Takahashi et al. (1991), who reported that bovine p25 was brain-specific, the obtained expression profile indicates that the human p25 gene is constantly transcribed in various tissues. It remains to be investigated if there is another human p25 homolog with a similar expression profile to bovine p25. Considering its ubiquitous expression in a wide variety of tissues, the gene described here seems to be involved in the basic housekeeping functions of cells.

Chromosomal assignment of the human p25 gene was done by PCR analysis of a human/rodent somatic cell hybrid panel and a radiation hybrid panel, as described previously (Seki et al. 1997; Saito et al. 1998). The specific amplified PCR primers were designed in the 3′-untranslated region of the gene (5′-GTTCGCCCGTCCTCACTAGCT-3′, 5′-GGATGGGCCAGGAGAGGTTAG-3′, PCR product size 116 bp). First, a specific amplified product for humans was detected only from the hybrid containing human chromosome 5 (data not shown). Then, we performed further mapping analysis using a PCR-based radiation hybrid panel (Genebridge 4, Research Genetics, Huntsville, AL, USA) with the same primers used in the assay for the human/rodent somatic cell hybrid panel. Statistical analysis of the radiation hybrid data was per-

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Fig. 1 Alignment of the bovine p25 gene (bovp25, accession number X85738) and the human p25 gene (hump25, accession number AB017016). Identities are indicated by a *black background*, and similar residues are *shadowed*. An *asterisk* denotes the termination codon

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bovp25     1  MAD..SRPKPANKTPPKSPGEPAKDKAAKRLSLEAEGAGEGAAAAGAELSALEEAFRKFA
hump25     1  MADKAKPAKAANRTPPKSPGDPSKDRAAKRLSLESEGAGEG.AAASPELSALEEAFRRFA

bovp25    59  VHGDARASGREMHGKNWSKLCRDCQVIDGRSVTVTDVDIVFSKIKGKSCRTITFEQFKEA
hump25    60  VHGDARATGREMHGKNWSKLCKDCQVIDGRNVTVTDVDIVFSKIKGKSCRTITFEQFQEA

bovp25   119  LEELAKKRFKDKSAEEAVREVHKLIEGKAPIISGVTKAISSPTVSRLTDTSKFTGSHKER
hump25   120  LEELAKKRFKDKSSEEAVREVHRLIEGKAPIISGVTKAISSPTVSRLTDTTKFTGSHKER

bovp25   179  FDPSGRGKGRAGRVDLVDESGYVPGYKHAGTYDQKVQGGK*
hump25   180  FDPSGKGKGKAGRVDLVDESGYVSGYKHAGTYDQKVQGGK*
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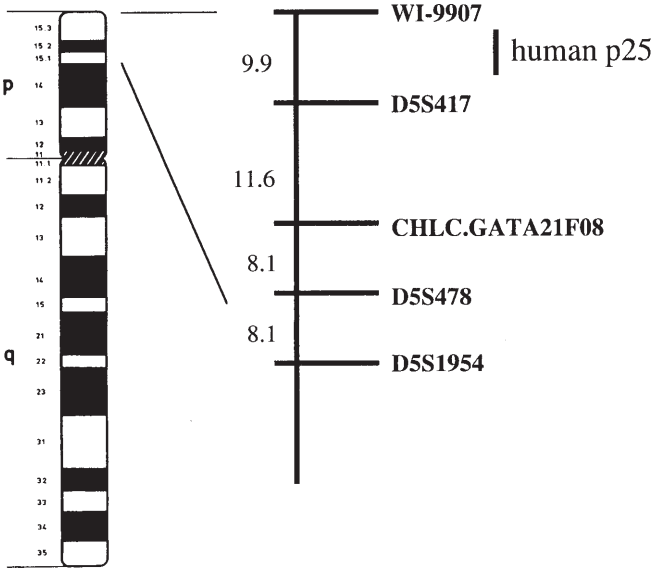

Fig. 2 Chromosomal placement of the human p25 gene at a relative distance to framework markers on the WICGR radiation hybrid map of the human genome. The approximate corresponding cytogenetic location of the gene on the telomeric region of chromosome 5 is indicated. Distances are in centirays

formed using the RHMAPPER software package (http://www-genome.wi.mit.edu/cgi-bin/contig/rhmapper.pl). The data vector for the p25 gene was 0010000101 0011000000 0010100111 1100110000 1110010000 0011000110 0110000010 0101000000 0010011001 000, and the resulting report indicated that the gene was mapped between markers WI-9907 and D5S417, both of which have been cytogenetically mapped to 5p15.3 (Fig. 2). The position of the gene is 4.29 cR proximal to WI-9907.

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