The gene (PTPN13) encoding the protein tyrosine phosphatase PTP-BL/PTP-BAS is located in mouse chromosome region 5E/F and human chromosome region 4q21


Abstract. Both mouse and human genomic clones were isolated for protein tyrosine phosphatase PTP-BL/PTP-BAS (HGM approved gene symbols Ptpn13 and PTPN13, respectively). Using these clones as a probe, PTPN13 was assigned to human chromosome region 4q21 and mouse chromosome region 5E/F by fluorescence in situ hybridization (FISH).

Protein tyrosine kinases (PTKs) can exert growth stimulatory responses by transient phosphorylation of cellular protein tyrosine residues. Protein tyrosine phosphatases (PTPases) were, therefore, considered negative regulators of cell growth and differentiation. However, evidence is accumulating that PTPases can also stimulate cell proliferation and maturation and can work in concert with PTKs in signal transduction pathways (Brady-Kalnay and Tonks, 1994). Over 30 PTPase family members have been characterized, displaying different structural characteristics (Walton and Dixon, 1993).

Recently, we obtained mouse partial cDNA clones encoding the PTPase PTP-BL (Accession number Z3274Q; Hendriks et al., 1995) which has also been cloned by others and termed RIP (Chida et al., 1995). The deduced amino acid sequence of murine PTP-BL displays 80% overall sequence homology with human PTP-BAS (Maekawa et al., 1994), also known as hPTP1E (Banville et al., 1994) or PTPL1 (Saras et al., 1994). Like its human homolog PTP-BAS, PTP-BL shares intriguing sequence homologies with submembranous tumor suppressors. It contains a band 4.1-like motif also present in the tumor suppressors neurofibromatosis type 2 and expanded (Boedigheimer et al., 1993). At the carboxy-terminal end the single catalytic phosphatase domain is present. In between are five 80 amino acids repeats, a protein motif that is also found in the Drosophila discs-large tumor suppressor. These discs-large homologous regions (DHRs) have now been identified in a large number of intracellular proteins and are thought to act as subcellular routing signals (Ponting and Phillips, 1995). Recently, it was shown that one of the DHRs of PTP-BAS can associate with the regulatory region of Fas, thereby inhibiting Fas-induced apoptosis (Sato et al., 1995). Since tissue homeostasis is dependent upon balanced cell proliferation and cell death, changes in PTP-BL/PTP-BAS expression levels or activities might have pathological consequences.

Knowledge of the exact chromosome location of PTPN13 will facilitate studies that address the possible involvement of PTP-BL/PTP-BAS in tumorigenesis. Recently, PTP-BL and PTP-BAS genes were assigned to mouse chromosome 5 and human chromosome 4, using interspecific backcross mapping (Chida et al., 1995) or PCR on a panel of somatic cell hybrids (Banville et al., 1994), respectively. We used fluorescence in situ hybridization (FISH) to refine the location of the PTP-BL/PTP-BAS genes to mouse chromosome region 5E/F and human chromosome region 4q21, respectively.

Materials and methods

Isolation of mouse PTP-BL genomic clones

Two HindIII fragments of 1.1 kb and 1.3 kb were isolated from the partial 6.5-kb mouse PTP-BL cDNA clone mPTP14-2 (Hendriks et al., 1995). These fragments were labeled radioactively and used to screen a mouse strain 129/SvEv genomic cosmids library. Positive clones were purified by subse-
Results and discussion

To further refine the chromosomal localization of the PTP-BL/PTP-BAS gene we set out to clone mouse and human genomic clones to enable FISH analysis. A human 969-bp PTP-BAS cDNA fragment was generated by reverse transcription PCR using a pair of PTP-BAS specific oligonucleotides.

Using the mouse and human PTP-BL/PTP-BAS cDNA probes three independent but overlapping mouse cosmids clones (mCOSPTPBL/1-mCOSPTPBL/3) and three human PTP-BAS phage clones (hAPTPBAS/1-hAPTPBAS/3) were isolated. To locate the identity of the clones as being PTP-BL and PTP-BAS genomic fragments, appropriate EcoRI subclones were partially sequenced using a primer recognizing both the mouse and human PTPase. Sequences revealed a 100% homology over a 147-bp region between codons 2350 and 2399 of the mouse PTP-BL cDNA sequence or between codons 2384 and 2433 of the human PTP-BAS cDNA sequence, respectively. In addition, a conserved exon-intron boundary was observed in the PTP-BL and PTP-BAS genes after codons 2399 and 2433, respectively.

To determine the regional chromosomal location of the PTP-BL/PTP-BAS gene, FISH analysis was performed using either mouse cosmide clone mCOSPTPBL/2 or human phage clone hAPTPBAS/1 as probes on mouse and human metaphase spreads, respectively. For the mouse PTP-BL gene assignment, 35 metaphase spreads were analyzed. In 31 spreads hybridization signals were found on both homologs in region E/F of chromosome 4. For the human PTP-BAS gene assignment, 35 metaphase spreads were analyzed and in 31 spreads the hybridizing signals were found on both homologs in region 4q21—q32. The FISH results confirm earlier localization data (Banville et al., 1994; Chida et al., 1995) and are in accordance with comparative mapping data of human and mouse genomes that have revealed conservation between human chromosome region 4q21 and mouse chromosome region 5E/F (Searle et al., 1994).

Various cytogenetic abnormalities in human tumors have been reported involving this region of chromosome 4. For instance, loss of region 4q11→q32 has been observed in approximately half of the hepatocellular carcinomas (Seizinger et al., 1991). Also, gain of chromosome 4p16→q35 in acute myeloid leukemia has been reported (Mittelman et al., 1993).
Until now, no obvious candidate disease loci have been identified in mouse in the chromosomal region of PTP-BL.

Further studies on PTP-BL/PTP-BAS are required to elucidate its role in normal or pathological cases of growth, differentiation and apoptosis.

References


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