An STS in the human T-ALL breakpoint cluster region (T-ALL\textsuperscript{bcr}) located at 11p13

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A region of human chromosome 11p13, designated the T-ALL breakpoint cluster region (T-ALL\textsuperscript{bcr}), is a frequent target site for chromosomal translocations in acute T-cell lymphoblastic leukaemia (T-ALL) (1, 2). It maps, at chromosome 11p13, between the catalase gene and the follicle stimulating hormone \(\beta\) subunit gene (3). Its sequence has been determined (1) and compared to homologous regions in mouse and hamster DNA (4). No gene has yet been found in this region (1, 2, 4). In order to facilitate the study of this region, we have combined our available information in a sequence-tagged site (STS), designated T-ALL\textsuperscript{bcr}.1/11p13. In a previous nomenclature, this region was provisionally named tcl-2 (5). Using the polymerase chain reaction (PCR) described below, a fragment of 401 bp was amplified from human genomic DNA. This can be used as a probe for genomic Southern blots, under conditions previously described (ref.1, equivalent to probe p9RH0.65) or retrieving clones containing this STS from libraries of human (1) or rodent (4) DNAs.

**PCR primers:** forward (300 to 323 in Fig. 6 of ref. 4):
5'GCAGGCAATTAGCCAGAAGGTATCCGTGGGGCAGGCAGCCTAGATCTGATGGGGGAAGC
CACCAGGATTACATCATCTGCTGGTGAGTAGGCTTCATTAATTCTCTGATGAATGGACGA
TTGCAAGGGAACTTTTTTCATCTTCAAGGAGCCAGAAGAAGTGGTGATTAAATTGGTCTT
TTAAATAAAGAGACCTCAAAAGGGTACAAGTCTTCAACTTCACTCTGCTGGCCAGTGAGTCAGGCGCTTGCTGTGTGAGCCGCTGGTTGCTAATGTCTTCGGGAA
CTGCTAATTTACCCATCTAATTTGTTCCTGTACACTGGCCAC

**PCR components:** 100 ng of genomic DNA, 250 ng of each oligonucleotide, 200 \(\mu\)M dNTPs, 2.5 units Taq polymerase (Perkin Elmer Cetus) in 50 \(\mu\)l of 50 mM KCl–10 mM Tris.Cl, pH 8.3 (at 20°C)–1.5 mM MgCl\(_2\)–0.01% (w/v) gelatin.

**PCR reaction:** 30 cycles of 2' at 94°C, 2' at 55°C, 2' at 72°C.

**REFERENCES**

**Fig. 1.** Sequence of PCR product (4) with primers underlined.