Genomic sequence of the mouse oncogene tlm

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DNA from the S49 T-lymphoma cell line (BALB/C mouse strain) was found to transform NIH3T3 cells with high efficiencies (0.10−0.15 foci per μg of DNA) in primary and secondary transfection assays (1). Isolation and preliminary characterization of the transforming gene tlm indicated that the transforming region was approximately 3.3 kb in length and that transforming activity could be inactivated by cleavage with EcoRI, but not by cleavage with HindIII, BamHI or EcoR5 (2). The tlm gene is frequently altered in mouse T-cell leukemias and lymphomas by single base mutation or more complex gene rearrangement.

We now report the complete genomic sequence of the tlm transforming gene. The putative start codon is located at 171−173 bases and the polyadenylation signal (AATAAA) is located at nucleotides 3188−3193.

REFERENCES

1. Lane,M.A., Sainten,A. and Cooper,G.M. (1982) Cell 28, 873−880.
2. Lane,M.A., Sainten,A., Doherty,K.M. and Cooper,G.M. (1984) Proc. Natl. Acad. Sci. USA 81, 2227−2231.

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   1 CAGTACTAGG ATTCACTGAA CACTCAGAAC ATATGAGCTA TGAACAGTAG CATACTGAGC
     TATGAACAGG AGTGCCACAA TCCCTGAGAA CCGTCGGGAT TCACTAAAGA TTACAGGGTT
 121 TCATGGAGGA AACTGTGTGG ATATCTACTT CAGAGAGCTG TTCATTCTAC ATGAGAACCC
     ATCTCCTTCT CTCCAGACCT CAGTCATCTA GAGGACCTGC GGCTGGGCAC AGAGGCCTTC
 241 CTCTGGAGTG CTTTTCCCTC ACCTGAGCAG AGAGCGGTAA CAGGAGAAGC CAGATGGCTT
     CTAAGAGAAG GTCACAGTAA GATGTCACAG GAGAGATGGC AACTGCAGGA AGTCTGAGTG
 361 TGACCTGTAT CCTCAAGACT CCTGTGCTTT GAAGACTCAG TTTACTGAGC CAGCTTCCAG
     GGTCCCTGGT CCCTACAGTC ATCTTAGGAT CTGCAGGCCC CTCGCCCCAT TAGGTCACCC
 481 TTGTTTCAGC AAGACACACT GACCTTCTGG TGCTTTTAGA GTCCCCAGCC CCTGTTCTCT
     CCACTGTTAT GATGTGTCTC CTCTGGTGGC CAGCTCCTGC CAAGATCACT TCACACTCTC
 601 TCATCCAATT AACAAATCAA TGCGTTTGCC TTTACTTTGC TCCAGGGCAT ATGTGTGTGT
     GGGTGCTCCC AGGCCATCTA TGGCTCATAT ATGGAGGTGA AAGGAGAATT TGTGTTAAGT
 721 CCATCTTCTT CTTCCATCGT GCCAATCTCA AGGTGGAACT CAGGTCATCA TAATTGGAGG
     AATGTTCTCT TACCATACCC AGATCAATCT CATTCTTATC CATATGACCA GATTTAATGG
 841 GGCCTTAATA GCTCCATCAC TGGGGTCAAT CTATGATAAA GTTGATATAC AAATCTAAAA
     CTAGAAGTTT CAGAATTACA AAGAACCCCG GCAGGATGTA TCAAAGAATG AAGAATCAGG
 961 AGTCCATACC CAGTCCAGCC TGATCCTTGG AGGAAGTGTT GTGGCTATCA GTGTCAGACA
     GCTGTTAGTA CCACTGCAGA TTGACCTTGG CTCCTAATTA TAATTACCAT CATAATTATC
1081 CAAAAAATAA TCCAGAGCCT GCAGTATGGC ACTACAGAGC TTCTTCCTTG TGTCTCTCTG
     GCTACTTCCC TGGCAAAACC CAGCACGGTT TTTCCTTCCT TCTCTAATCA ACAGAGGATT
1201 CTTTGATTCA ATGTCACCCC TCCAATGCAC TCTTGTTCTG TCTGTGGTCC TAGCCTCTCT
     TGGTAGCTGT TCTCTTTACA CCATGTTCCC TGACCAAAGA ATTGCTAGAC CATGAAAGCT
1321 GGGAAGTTCC CAGATCCTCC AATCTCAGGA TGGAGTAACC AGATCCCAAT GGTACTGGGC
     ATCACTGTGC TTTTTTTTTA AATTAATTTA TTTTTTAATT GGATATTTTC TTTATCTACA
1441 TTTCAAATGT TATCCCCTTT CCTGCCCCCT GGAAATTCCC TATCCCATCC TCCCTCCCCC
     TGCCTCCACC CACCCACCTA CCTACTCCTA CCTCTCTTCC CTCAGTTCCC CTACACTGGG
1561 GCATCTATAG AGCCTTCATA GGACCAAGGA ATCTTTTCCC ATTGATGCAT GACAAGGCCA
     TCCTCTGCAA TGTATGCAGC TGGAGCCATG TGTACTCCTT TGTTGATGGC TTAGTCCCTG
1681 GAAGCTCTGG GGGTCTGGTT AGTTGATGTT GTTCTTCCTA TGGGGCTGCA AACCCCTTCA
     AATCCTTCAG TCCTTTCTCT AACTCTTCTA TTGGGGACCC CACACTCAGT TCAATGGTTG
1801 GCTGTGAGCA TCCATCTCTG TATTTGTAAG GCTCTGTCAG GGCCTCTCAG GAGACAGCCA
     TATCAGGCTC CTTTCAGCAT GTACTTCTTG GTATCCACAA TAGTGTCTGG GTTTGGTAAC
1921 TGTATATGGG ATGAATCTCC AGGTGGCACA GTGAGTGGTC TTTCCTTTAG TATCTCTTCT
     ACACTTTTAT CTCCATATTT GCTCATGTAT TTTGTTCTTC TTCTAAGAAG GCACGGACCA
2041 CCCACACTTT AGTCTTCTTC TTGAGCTTCA TGTGGTCTGT GAGTTGTATC TTGGTTATTT
     GGAGCTTTTG GGCTAATATC TACTTATCAG CGAGGGCATT TGATGTGTGT TCTTTTGTGA
2161 CTGGGTTACC TCACTCAGGA TGATATTTTC TAGTTCTATT CATTTGCCTA AGAATTTCAT
     GAATTCATCA TTTTTAATAG CTGAATAGTA CTCCATTGTG TAAATATACC ACATTTTCTG
2281 TATCCATTCC TCTGTTGAAG GACATCAGGG CTCTTTCTAG CTCCTGGTTA TTATAAATAA
     GGCTGCTATG AACACGGTGG AGCATGTGTC CTTATTACAT GTTGTAACAT CTTCTGGGTA
2401 TATGCCCAGG TGTGGTATAG TTGGGTTCTC AGGTAGTACT ATGCCCAATT TTCTGAGGAA
     CTGTCAAACT GATTTCCAGA GTGGTTGTAC TAGCTTGCAA TCTCACCAGC AATGGAGGAG
2521 TGTCCTTCTT TCTCCACATC CTCGTCAGCA TCTGTTGCCA TCTGAATTTT TGATTTTAGC
     CATTTTGACT GGTGTGAGAT GGAATCTCAG GGTTGTTTTG ATTTGCATTT CCCTGATGAC
2641 TAAGGATGTC TTTAACTGCT TCTCAGCCAT TCGAGATTCC TCAGTTGATA ATCCTTTGTT
     TAGCTCTGTA CCCCATTTTT AAATAGGGTT ATTTGGTTCT CTGGAGGCAA CCTTCTTGAC
2761 TTCTTTTTTT TTTTCCATTT TTTATTAGGT ATTTAACTCA TTTACATTTC CAATGCTATA
     CCAAAAGTCC CCCATATCCA CCCACCCCCA CTCCCCTGCC CACCCACTCC CCCTTTTTGG
2881 CCCTGGTGTT CCCCTGTACT GGGGCATATA AAGTTTGCAA GTCCAATGGG CCTCTCTTTC
     CAGTGATGGC CGACTAGGCC ATCTTTTGAT ATATATGCAG CTAGAGTCAA GAGCTCCGGG
3001 GTACTGGTTA GTTCATAATG TTGTTCCACC TATAGGGTTG CAGATCCCTT TAGCTCCTTG
     GCTACTTTCT CTAGCTCCTC CATTGGGAGC CCTATGATCC ATCCATTAGC TGACTGTGAG
3121 CATCCCACTTC TGTGTTTGCT AGGCCCCGGC ATAGTCTCAC AAGAGACAGC TACATCTGGG
     TCCTTTCAAT AAAATCTTGC TAGTGTATGC AATGGTGTCA GCGTTTGGAT GCTGATTATG
3241 GGGTGGATCC
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