

Nucleotide and deduced amino acid sequence for the mouse homologue of the rat T-cell differentiation marker RT6

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The rat T-cell differentiation marker RT6 is expressed as a PI-linked membrane protein (with an Mr of approximately 26 kilodalton) by mature peripheral T cells, but not by thymocytes, recent thymic migrants or other hematopoietic cells (1–3). An inherent defect in RT6 expression has been correlated with lymphopenia and autoimmune diabetes mellitus in diabetes-prone BB rats (4). In the rat, two polymorphic RT6 alleles, $RT6^a$ and $RT6^b$ are known. The corresponding gene locus was mapped to linkage group I between the loci for hemoglobin β and albinism (5), a region of high linkage synteny homology to mouse chromosome 7 and human chromosome 11 (6). We have recently reported the cDNA sequences for $RT6^a$ and $RT6^b$ (7, 8). Remarkably, the coding sequences of $RT6^a$ and $RT6^b$ differ by 18 point mutations, 12 of which result in amino acid substitutions (7, 8, 9).

Using oligonucleotides based on the rat RT6 cDNA sequences in the polymerase chain reaction, we have amplified the homologous cDNA from BALB/c mouse spleen mRNA. The determined nucleotide and deduced amino acid sequences are shown below (note that the underlined nucleotide and deduced amino acid residues at the beginning and end of the sequence are derived from the oligonucleotides used in the pcr reaction). Mouse and rat nucleotide sequences are identical in 79.7% of the residues, the deduced amino acid sequences in 71.6% of the residues. The mouse sequence contains two potential glycosylation sites (amino acid residues 171–173 and 256–258) not present in the rat RT6 and — in addition to four conserved cysteine residues — two extra cysteines (positions 80 and 201). Two insertions of three and nine amino acid residues (dotted underlines) appear in the mouse sequence relative to that of the rat. Homology searches (10) with the deduced mouse RT6 amino acid sequence in the National Biomedical Research Foundation protein sequence data base did not reveal any significant sequence homologies to known T-cell surface proteins or CD markers. The highest homology score obtained was for the human transforming protein (dbl) precursor: initial score 66/optimzed score 76 (19.5% sequence identity in a 113-aa overlap). The data presented here provide the basis for identifying the RT6-homologous gene product of the mouse and for analysis of a possible role of this molecule in mouse models (11) of lymphopenia and autoimmune diabetes. Corresponding experiments are in progress in our laboratory.

REFERENCES

1. Thiele,H.-G., Koch,F., Hamann,A. and Arndt,R. (1986) *Immunol.* **59**, 195–201.
2. Koch,F., Thiele,H.-G. and Low,M. (1986) *J. Exp. Med.* **164**, 1338–1343.
3. Thiele,H.-G., Koch,F. and Kashan,A. (1987) *Transplant. Proc.* **19**, 3157.
4. Greiner,D.L., Mordes,J.P., Handler,E.S., Angelillo,M., Nakamura,N. and Rossini,A. (1987) *J. Exp. Med.* **166**, 461–467.
5. Butcher,G.W., Clarke,S. and Tucker,E.M. (1979) *Transpl. Proc.* **11**, 1629–1630.
6. Lalley,P.A., Davisson,M.T., Graves,J.A.N., O'Brien,S.J., Womack,J.E., Roderick,T.H., Creau-Golgberg,N., Hillyard,A.L., Doolittle,D.P. and Rogers,J.A. (1989) *Cytogenet. Cell Genet.* **51**, 503–532.
7. Koch,F., Haag,F., Kashan,A. and Thiele,H.-G. (1990) *Proc. Natl. Acad. Sci. USA* **87**, 964–967.
8. Haag,F., Koch,F. and Thiele,H.-G. (1990) *Nucl. Acids Res.* **18**, 1047.
9. Haag,F., Koch,F. and Thiele,H.-G. (1990) *Transpl. Proc.* in press.
10. Lipman,D.J. and Pearson,W.R. (1985) *Science* **227**, 1435–1441.
11. Leiter,E.H., Prochazka,M. and Coleman,D.L. (1987) *Am. J. Pathol.* **128**, 380–383.

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M  P  S  N  N  F  K  F  F  L  T  W  W  L  T  Q  Q  V  T  G  L  A  V  P  F  M  L  D  M  A    30
ATGCCATCAAATAATTTCAAGTTCTTCCTAACTTGGTGGCTAACCCAGCAGGTGACTGGCCTTGCAGTGCCTTTCATGCTAGACATGGCT   90
P  N  A  F  D  D  Q  Y  E  G  C  V  E  D  M  E  K  K  A  P  Q  L  L  Q  E  D  F  N  M  N    60
CCAAATGCATTTGATGATCAGTATGAGGGCTGTGTCGAAGACATGGAGAAAAAGGCACCCCAGCTGTTACAAGAAGACTTCAACATGAAT  180
E  E  L  K  L  E  W  E  K  A  E  I  K  W  K  E  I  K  N  C  M  S  Y  P  A  G  F  H  D  F    90
GAGGAATTAAAACTTGAGTGGGAAAAAGCAGAGATAAAATGGAAGGAGATCAAAAATTGTATGAGTTATCCGGCAGGTTTCCATGATTTC  270
H  G  T  A  L  V  A  Y  T  G  N  I  H  R  S  L  N  E  A  T  R  E  F  K  I  N  P  G  N  F    120
CATGGAACAGCTTTAGTTGCCTACACTGGGAACATCCACAGAAGCCTTAATGAGGCTACTAGAGAGTTCAAAATAAATCCTGGTAACTTC  360
H  Y  K  A  F  H  Y  Y  L  T  R  A  L  Q  L  L  S  D  Q  G  C  R  S  V  Y  R  G  T  N  V    150
CACTACAAGGCCTTCCATTACTACTTAACAAGAGCTCTTCAGCTTTTGAGTGACCAGGGTTGTCGTTCAGTTTACCGAGGTACTAATGTC  450
R  F  R  Y  T  G  K  G  S  V  R  F  G  H  F  A  S  S  S  L  N  R  S  V  A  T  S  S  P  F    180
AGGTTTCGTTACACTGGGAAGGGCTCTGTGCGATTTGGGCATTTCGCATCCTCTTCTTTAAACCGGAGTGTAGCTACTTCTAGTCCATTT  540
F  N  G  Q  G  T  L  F  I  I  K  T  C  L  G  A  H  I  K  H  C  S  Y  Y  T  H  E  E  E  V    210
TTCAATGGACAGGGGACATTATTTATCATCAAAACCTGCTTGGGGGCTCACATCAAACATTGTTCCTACTATACTCATGAAGAGGAGGTG  630
L  I  P  G  Y  E  V  F  H  K  V  K  T  Q  S  V  E  R  Y  I  Q  I  S  L  D  S  P  K  R  K    240
TTAATTCCAGGCTATGAAGTATTTCACAAAGTCAAAACACAAAGTGTCGAACGGTATATCCAAATTTCTCTGGACTCCCCAAAAAGGAAG  720
K  S  N  F  N  C  F  Y  S  G  S  T  Q  A  A  N  V  S  S  L  G  S  R  E  S  C  V  P  L  F    270
AAGAGCAACTTTAATTGCTTCTATAGCGGTTCTACTCAAGCAGCCAACGTTAGCAGCTTAGGATCTAGAGAGAGCTGTGTACCCCTGTTC  810
L  V  V  L  L  G  L  L  V  Q  Q  L  T  L  A  E  P                                          287
CTTGTGGTTCTCCTCGGTCTTCTGGTCCAGCAGCTTACTCTTGCTGAGCCGTAG                                      864
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