Complete cDNA sequence coding for the MHC class II RT1.B α chain of the LEWIS rat

Jessica Syha, Wolfgang Henkes and Konrad Reske

Institut für Immunologie, Universität Mainz, Obere Zahlbacher Strasse 67, D-6500 Mainz, FRG
Submitted April 11, 1989 EMBL accession no. X14879

The rat major histocompatibility complex (MHC) encodes three isotypic class II α, β heterodimers referred to as RT1.B, RT1.D and RT1.H. Two serologically discrete α, β heterodimers have previously been identified at the cell surface of LEW rat splenocytes (1). It was suggested that the two polypeptide chain complexes represent stable conformation isomers formed posttranslationally by a rearrangement in association of the RT1.B α and β chains. To examine this notion by means of transfection experiments we decided to establish full length cDNA clones for the two RT1.B ^{I} subunits including the invariant γ chain (2). A cDNA library was prepared in λ gt11 and was probed with a RT1.B ^{u} α cDNA (3) to identify positively hybridizing phages. 22 phage clones were obtained. The nucleotide sequence of the insert derived from the longest cDNA clone pLRα42.1 is presented (Fig.1). Comparison between the sequence of pLRα42.1 and the RT1.B ^{u} α clone revealed sequence identities of 96,3 % at the DNA level while the sequence identity between pLRα42.1 and a number of mouse I-A α and human HLA-DC α cDNA clones ranged from 86,1 to 87,3 % and 70,1 to 78,5 % at the DNA level.

```
                                                Met Pro Leu Ser Arg Ala Leu Ile Leu Gly Val Leu Ala Leu Thr Thr Met Leu Ser
GAAAGCAGCTACAGAGACCACCCAGAGAACAGAG ATG CCG CTC AGC AGA GCT CTG ATT TTG GGG GTC CTC GCC CTG ACC ACC ATG CTC AGC   91
Pro Cys Gly Gly Gln Asp Asp Ile Glu Ala Asp His Val Ala Ala Tyr Gly Ile Asn Met Tyr Gln Tyr Tyr Glu Ser Arg Gly
CCC TGT GGA GGT CAA GAC GAC ATT GAG GCC GAC CAC GTA GCC GCC TAT GGT ATA AAT ATG TAT CAG TAT TAT GAA TCC AGA GGC  175
Gln Phe Thr His Glu Phe Asp Gly Asp Glu Glu Phe Tyr Val Asp Leu Asp Lys Lys Glu Thr Ile Trp Arg Ile Pro Glu Phe
CAG TTC ACA CAT GAA TTT GAT GGT GAC GAG GAA TTC TAT GTG GAC TTG GAT AAG AAG GAG ACC ATC TGG AGG ATC CCC GAG TTT  259
Gly Gln Leu Thr Ser Phe Asp Pro Gln Gly Gly Leu Gln Asn Ile Ala Ile Ile Lys His Asn Leu Glu Ile Leu Met Lys Arg
GGA CAG CTG ACA AGC TTT GAC CCC CAA GGT GGA CTT CAA AAT ATA GCT ATA ATA AAA CAC AAT TTG GAA ATC TTG ATG AAG AGG  343
Ser Asn* Ser Thr Gln Ala Val Asn Lys Val Pro Glu Ala Thr Val Phe Ser Lys Ser Pro Val Leu Leu Gly Gln Pro Asn Thr
TCA AAT TCA ACC CAA GCT GTC AAC AAG GTT CCT GAG GCG ACC GTG TTT TCC AAG TCC CCT GTG CTG CTG GGT CAG CCC AAC ACC  427
Leu Ile Cys Phe Val Asp Asn Ile Phe Pro Pro Val Ile Asn* Ile Thr Leu Val Glu Asn Ser Lys Pro Val Thr Glu Gly Val
CTC ATC TGC TTT GTA GAC AAC ATC TTT CCT CCT GTG ATC AAT ATC ACA TTG GTT GAG AAC AGC AAG CCA GTC ACA GAA GGC GTT  511
Tyr Glu Thr Ser Phe Leu Ser Asn Pro Asp His Ser Phe His Lys Met Ala Tyr Leu Thr Phe Ile Pro Phe Asn Asp Asp Ile
TAT GAG ACC AGC TTC CTT TCC AAC CCT GAC CAT TCC TTC CAC AAG ATG GCT TAC CTC ACC TTC ATC CCT TTC AAC GAC GAC ATT  595
Tyr Asp Cys Lys Val Glu His Trp Gly Leu Asp Glu Pro Val Leu Lys His Trp Glu Pro Glu Val Pro Ala Pro Met Ser Glu
TAT GAC TGC AAG GTG GAG CAC TGG GGC CTG GAC GAG CCG GTT CTA AAA CAC TGG GAA CCT GAG GTT CCA GCC CCC ATG TCA GAG  679
Leu Thr Glu Thr Val Val Cys Ala Leu Gly Leu Ser Val Gly Leu Val Gly Ile Val Val Gly Thr Ile Phe Ile Ile Gln Gly
CTG ACA GAG ACT GTG GTC TGT GCC CTG GGG TTG TCT GTG GGC CTC GTG GGC ATC GTG GTG GGC ACC ATC TTC ATC ATT CAA GGC  763
Leu Arg Ser Asp Gly Pro Ser Arg His Pro Gly Pro Leu
CTG CGA TCA GAT GGC CCC TCC AGA CAC CCA GGG CCC CTT TGA GTCACACCCTGGGAAAGAAGGTGCGTGGCCCTCTACAGGGAAGATGTAGTGTGTG  860
GGGGTGACCTGGCACAGTGTGTTTTCTGCCCCAATTCATCGTGTTCTTTCTCTTCTCCTGGTGTCTCCCATCTTGCTCTTCCCTTGGCCCCCAGGCTGTCCACCTCATGGC  971
TCTCACGCCCTTGGAATTCTCCCCTGACCTGAGTTTCATTTTTGGCATCTTCCAAGTCGAATCTACTATAGATTCCGAGACCCTGATTGATGCTCCACCAAACCAATAAAC 1082
CTCTTATAAGTTG                                                                                                    1095
```

Fig.1: Nucleotide sequence of cDNA clone pLRα42.1 including the deduced amino acid sequence. The stretch of sequence representing the putative transmembrane region is underlined. The two asterisks mark potential N-glycosylation sites.

REFERENCES

(1) Reske, K. and Weitzel, R. (1985) Eur.J.Immunol. 15, 1229-1239.
(2) Henkes, W., Syha, J. and Reske, K. (1988) Nucl.Acids Res. 16, 11822
(3) Wallis, A.E. and McMaster, W.R. (1984) Immunogenetics 19, 53-62