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First genomic sequence of the human T-cell receptor δ2 gene (TRDV2)

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The genomic sequence of the human Vδ2 (TRDV2) gene is reported. One clone, λLY67Vδ2, was isolated from the LY67 library [1] by screening with a 250 bp Hind III-Pvu I fragment containing the 5' region of the cDNA X13 clone [2] and shown to contain the TRDV2 gene. Comparison of the sequence of the genomic TRDV2 gene with those of four V2 cDNAs [2,3] confirms that, in the human TRD locus, like in the TRG one [4], there is no somatic mutation and the variability of the delta chains depends from the combinatorial diversity of the V, D and J gene segments and from the presence of N regions. Hence, the germline V2 sequence, reported here, will allow to assess this N-region diversity in the cells which rearrange functionally and express the TRDV2 gene. Moreover, it will help in defining the contribution of the different D segments.

By southern blot analysis, the genomic TRDV2 probe, clone pDV2SP0.5, a 500 bp Sma I-Pst I fragment isolated from λLY67Vδ2 and subcloned in pUC18, detects a unique band with Eco RI (12.5 kb), Hind III (4.0 kb) and Xba I (3.6 kb) digests showing that the TRDV2 gene is the single member of its subgroup.

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ATG CAG AGG ATC TCC TCC CTC ATC CAT CTC   30
 M   Q   R   I   S   S   L   I   H   L
TCT CTC TTC TGG GCA  GGTAAGGCAGACCCCAGAA  64
 S   L   F   W   A  /
CTTGGGCCAAGCAAGACTCAGCAGCAAAGAAACATCAAGG 104
CTCACAGGACCTTGTACTCATGGACTGTGCTCCTTACTCA 144
ATGACCTAGCCCCCAGCCCTCACTGAGCCCCTCTCTTGTG 184
TCTTTCTCTCAGGA GTC ATG TCA GCC ATT GAG    216
             /G   V   M   S   A   I   E
TTG GTG CCT GAA CAC CAA ACA GTG CCT GTG   246
 L   V   P   E   H   Q   T   V   P   V
TCA ATA GGG GTC CCT GCC ACC CTC AGG TGC   276
 S   I   G   V   P   A   T   L   R   C
TCC ATG AAA GGA GAA GCG ATC GGT AAC TAC   306
 S   M   K   G   E   A   I   G   N   Y
TAT ATC AAC TGG TAC AGG AAG ACC CAA GGT   336
 Y   I   N   W   Y   R   K   T   Q   G
AAC ACA ATC ACT TTC ATA TAC CGA GAA AAG   366
 N   T   I   T   F   I   Y   R   E   K
GAC ATC TAT GGC CCT GGT TTC AAA GAC AAT   396
 D   I   Y   G   P   G   F   K   D   N
TTC CAA GGT GAC ATT GAT ATT GCA AAG AAC   426
 F   Q   G   D   I   D   I   A   K   N
CTG GCT GTA CTT AAG ATA CTT GCA CCA TCA   456
 L   A   V   L   K   I   L   A   P   S
GAG AGA GAT GAA GGG TCT TAC TAC TGT GCC   486
 E   R   D   E   G   S   Y   Y   C   A
TGT GAC ACC  CACCCTGCTGCAGCTCTACTTCTGAGC  522
 C   D   T
AGCTCAAAAACCACTGACCAGGCGCGGTGGCTCACACCTG 562
TAATCCCAGCACTT                           576
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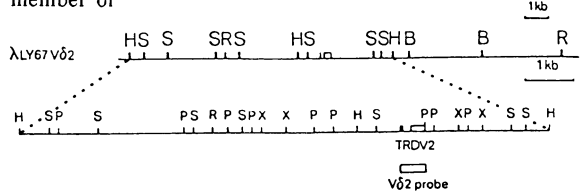

B : Bam HI, H : Hind III,
S : Sac I, R : Eco RI, X : Xba I.

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