
Short gene inversion involving two adjacent heavy chain joining minigenes and one heavy chain diversity minigene in the nonsecretor Sp2/0-Ag14 myeloma cell line

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We report here the nucleotide sequence in the region involving the heavy chain joining (J_H) minigenes in a BALB/c mouse nonsecretor Sp2/0-Ag14 myeloma cell line which is one of the commonly used fusion partners in hybridoma technology. It is contained in a 5.4 kb EcoRI fragment (1) isolated by a probe consisting of 700 bp between the XbaI and EcoRI sites 3' to the J_H4 minigene. Based on restriction mapping data, it is generally accepted that a diversity (D) minigene was rearranged with the J_H2 minigene in that region. Nucleotide sequencing, however, suggests that the same D minigene was also joined to the J_H3 minigene, giving rise to a short gene inversion of 398 bp marked by the two vertical arrows in the figure. Nonamers and heptamers in the signal regions are denoted by 9 and 7 respectively. The J_H2 and D minigenes are inverted and are indicated by arrows to the left. The J_H3 minigene is marked by an arrow to the right. This configuration was most likely derived by a similar mechanism used in several other gene inversions (2-4). In the present case, the gene segment inverted is shorter than all others, and can only be detected by nucleotide sequencing.

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          9                               7
ATGTTCTCCTGCAGAACCTGTACCTTACTTGGCAGG GATTTTTGT CAAGGGATCTAC TACTGTG CACC
↓ 7
CACATTG TGACAACAATGATTAGACCCCTG ACAATAAAT GATCCTTGCTAGGGCTCCAGGATTATCTC
AGATGGAGGCCAGTGAAGGACAAAGCAAAGCATAGAAGAGAGGGACCTAGCGGCAATGCTGGCCAGGATCCCT
ATAAATCTCTGGCCATGAAGTCTGGGAGCTGAGGATGTCTGTCTGCATCAGCCAGGGTCCCAATGACCCTT
TCTGACTCCCAAGGTGTCCCTAGTCTTCATGACCTGAAATTCAGATACACACATTTCCCCCAACAAATG
CAGTAAAATCTATCTAAGCTGAATAGAAGAGAGGTTTAAAGGACTCAC C TGA GGA GAC TGT GAG
----- JH2 ----- D -----
AGT GGT GCC TTG GCC CCA GTA GTC AAA GTA G TCGTACCTATAGTAGA ↓ AGGGA C TGG
----- JH3 -----
TTT GCT TAC TGG GGC CAA GGG ACT CTG GTC ACT GTC TCT GCA G

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