

1987

Nucleotide Sequence of an Anti-Fluorescyl Hapten Antibody Heavy Chain Variable Region Gene from a BALB/c Mouse Hybridoma Cell Line

Zhen-qian Liu

Northwestern University, Evanston, IL

Charles Wood

University of Nebraska - Lincoln, cwood1@unl.edu

Tai Te Wu

Northwestern University, Evanston, IL

Follow this and additional works at: <http://digitalcommons.unl.edu/virologypub>

 Part of the [Virology Commons](#)

Liu, Zhen-qian; Wood, Charles; and Wu, Tai Te, "Nucleotide Sequence of an Anti-Fluorescyl Hapten Antibody Heavy Chain Variable Region Gene from a BALB/c Mouse Hybridoma Cell Line" (1987). *Virology Papers*. 179.
<http://digitalcommons.unl.edu/virologypub/179>

This Article is brought to you for free and open access by the Virology, Nebraska Center for at DigitalCommons@University of Nebraska - Lincoln. It has been accepted for inclusion in Virology Papers by an authorized administrator of DigitalCommons@University of Nebraska - Lincoln.

Nucleotide sequence of an anti-fluorescyl hapten antibody heavy chain variable region gene from a BALB/c mouse hybridoma cell line

Zhen-qian Liu, Charles Wood¹ and Tai Te WuNorthwestern University, Evanston, IL 60201 and ¹University of Kansas, Lawrence, KS 66045, USA

Submitted June 30, 1987

Accession no. Y00393

We report here the nucleotide sequence of an anti-fluorescyl hapten antibody heavy chain variable region gene from a BALB/c mouse hybridoma cell line 3-13 (1). This gene segment was contained in a 5.0 kb EcoRI fragment isolated by a 700 bp probe 3' to the mouse heavy chain joining minigene region between the XbaI and EcoRI sites. Mature protein starts at *. The first 21 amino acid residues have also been confirmed by direct amino acid sequencing and they are identical to those of immunoglobulin MOPC104E heavy chain (2). Complementarity determining regions (CDRs) are underlined. The third CDR is unusually long and does not match any of the mouse heavy chain diversity minigene sequences (3). However, GGCTAC is found in the D_{FL16.2}-minigene, and GTAA in the D_{Sp2.5}-minigene, suggesting that ten of the 30 nucleotides in CDR3, GGCTACGTAA, may be derived from a D-D joining.

```
GCTGCTGTCTTGTGAGTCCCCTGCTCTCATTATGGCAAATTACCTGAGTCTATGGTCATTA AACAGGATGT
CCACACCCTTAAATCAACCGAGCATGAGTGTCTCTCCAAAGTCCCTGAACACACTGACTCTAACCC ATG G
AA TGG AGT TGG ATA TTT CTC TTT CTC CTG TCA GGA ACT GCA G GTAAGGGGCTCACCA
GCTTCAAAATCTGAAGTGGAGACAGGACCTGAGGTGACAATGACATCTACTCTGACATTCTCTCCTCAG GT
GTC CAC TCT*GAG GTC CAG CTG CAG CAG TCT GGA CCT GAG CTG GTA AAG CCT GGG
GCT TCA GTG AAG ATG TCC TGC AAG GCT TCT GGA TAC ACA TTC TCT AGC TAT GTT
CTA TAC TGG GTG AAA CAG AAG CCC TGG GCA GGG CTT GAG TGG ATT GGC TTT ATT
TTT CCT TAC AAT GAT GGT ACT AAG TAC AAT GAG AAG TTC AAA CGG CGA GGC ACA
CTG ACT TCA GAC AAA TCC TCA AGC ACA GCC TAC ATG GAA CTC AGC AGC CTG ACC
TCT GAG GAC TCT GCG GTC TAT TAC TGT GCA CGA ACG GGC GCA GAC AGC TCG GGC
TAC GTA AGG GCT ATG GAC TAC TGG GGT CAA GGA ACC TCA GTC ACC GTC TCC TCA
G GTAAGAATGGCCTCTCCAGGCTTTATTTTAACTT
```

ACKNOWLEDGEMENTS Supported by a grant from the Leukemia Research Foundation of Chicago to TTW, and a grant from the University of Kansas General Research Fund to CW.

REFERENCES

- (1) Reinitz, D. M. and Voss, E. W., Jr. (1984) Fed. Proc. 43: 1680.
- (2) Kehry, M., Sibley, C., Fuhrman, J., Schilling, J. and Hood, L. (1979) Proc. Natl. Acad. Sci. USA 76: 2932-2936.
- (3) Kurosawa, Y. and Tonegawa, S. (1982) J. Exp. Med. 155: 201-208.