Complete nucleotide sequence of the neurotropic murine retrovirus CAS-BR-E

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Neurotropic murine retroviruses were isolated from a population of wild mice by Gardner *et al.* (1). These viruses have an ecotropic host range and cause, after neonatal inoculation, a non-inflammatory neurodegenerative disease characterized by spongiform degeneration primarily localized to motor areas of the brain stem and spinal cord (2). The major determinant of neurovirulence has been mapped to the viral envelope gene (3), but both the U3 region of the LTR (4) and 5′ untranslated region (5) of the viral genome exclusive of U3 affect both the tempo and character of the disease.

The Cas-Br-E clone (15−1) containing the entire viral genome was ligated into the vector pUC 19 at the SalI site within the *pol* gene (base 3698 of the given sequence) (6). Sequence data was obtained on double-stranded plasmid DNA using the dideoxy chain-termination method with *E. coli* DNA polymerase, Klenow fragment, and labeled with α-^{35}S-dATP. Specific primers for sequencing were synthesized on an Applied Biosystems 380B DNA synthesizer.

The sequence of the *env*, 3′ *pol* genes and the LTR was previously published by Rassart *et al.* (7) using a different molecular clone (pBRNE8) of Cas-Br-E. There were only two amino acid differences in *env* and one amino acid difference in 3′ *pol* between the predicted translation products of Cas-Br-E clones 15−1 and pBRNE8. At the nucleic acid level there were 5 discrepancies in the LTR, 5 in *env* and 2 in the 3′ end of *pol*. The level of homology between Cas-Br-E clone 15−1 and two other murine leukemia viruses which have been completely sequenced, is presented in the table below.

Table: Sequence homology between Cas-Br-E clone 15−1 and other MuLV's

	Moloney MuLV[a]		Akv MuLV	
	nt[b]	aa	nt	aa
U3	74.2[c]	–	58.6	–
R	97	–	97	–
U5	93.5	–	89.7	–
5′ Leader[d]	92.6	–	73.2	–
gag	90.1	93.3	78.3	86.4
pol	91.8	96.1	85.2	90.0
env	72.3	76.7	74.5	76.3

[a]The sequence of the complete genomes of Moloney MuLV (8) and Akv MuLV (9) have been reported.
[b]nt = nucleotide; aa = amino acid.
[c]Numbers represent percent identity.
[d]The 5′ leader sequence extends from the 3′ end of U5 to the ATG *gag* start codon.

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