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Sequence of the right hand terminal palindrome of the human B19 parvovirus genome has the potential to form a 'stem plus arms' structure

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All mammalian parvovirus genomes characterized to date contain imperfect terminal palindromes ranging in size from 115nt to 240nt. There are two classes of genomes, those which have direct terminal repeats (TR) (AAV-2 and B19) and those in which the terminal hairpin sequences are unrelated (MVM, H-1, and BPV). Terminal hairpins for which the complete sequence is known can be arranged into T- or Y-shaped structures, or more generally "stem plus arms" structures (1). Clones of the human B19 parvovirus contain partial terminal repeats due to incomplete synthesis and/or subsequent deletion of the ends when propagated in *E. coli* strains including the *recBCsbcBrecF* strain, JC8111 (2,3) hence sequence data has so far failed to identify a potential "stem plus arms" structure at the ends of the genome (4). We now report the sequence of a ~230bp terminal repeat from the right end of the B19-Wi genome. While we estimate that this TR is missing ~100nt from the full length sequence present in viral DNA, the presence of several internal repeat sequences allows the nucleotide sequence to be arranged into a "stem plus arms" configuration (fig. 1). We have attempted to obtain an intact clone of the viral terminal region, and although we appear to obtain a full length fragment initially (fig.1, inset, "a"), attempts to propagate the clone to obtain sufficient DNA for chemical sequencing have resulted in deletion of the loop end of the terminal palindrome.

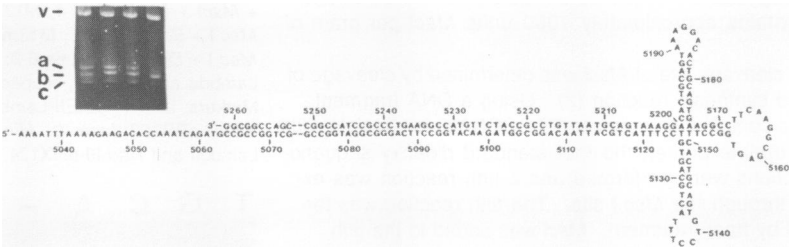

Fig.1 "Stem plus arms structure of the right hand terminal repeat of B19-Wi DNA. DNA from plasmid pYT101(gift of S. Cotmore and P. Tattersall) was sequenced using the chemical method. The sequence of the hairpin reported here corresponds to a fragment of ~230nt, "b" in inset. The smallest band "c" in the inset corresponds to the size of the left hand hairpin of a clone of the B19-Au genome (3). The inset illustrates the different length of inserts observed when annealed B19 (VS isolate) DNA was cloned into a low copy number vector and propagated in *E. coli* strain JC8111. We believe that band "a" is a full length insert, however on amplification, this fragment undergoes deletion. Note that there is a fourth minor band between "b" and "c". The upper band "v" is the vector sequence.

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