Abstract

Bacteriophage clones containing ribosomal RNA genes of Theileria parva were isolated from genomic DNA libraries. Physical mapping studies revealed 2 ribosomal DNA units, which were distinguishable by restriction enzyme site polymorphisms in flanking sequences. The cloned ribosomal DNA units were mapped to 2 separate T. parva chromosomes. Analysis of sequences contained in lambda EMBL3 recombinants, together with Southern blot analysis of genomic DNA and data on the copy number of the rRNA genes, suggested that the rDNA units were not tandemly repeated. This organisation of ribosomal transcription units is similar to that described for other genera of apicomplexan protozoa, but 2 rDNA units, each containing single copies of the rRNA coding genes, would be the lowest copy number described for any eukaryote in which amplification of rRNA genes is not known to occur. EcoRI restriction fragment length polymorphisms, which were revealed using rRNA gene probes, separated T. parva stocks into 2 categories. Nucleotide sequence analysis of polymerase chain reaction-amplified internal transcribed spacer DNA revealed 2 different ITS sequences derived from rDNA transcription units within the genome of a cloned T. parva parasite. Polymorphism was also observed between ITS sequences amplified from the DNA of different T. parva stocks. A synthetic oligonucleotide derived from T. parva Uganda ribosomal ITS DNA sequences hybridised to DNA from the T. parva Uganda stock, but not to the DNA of the T. parva Muguga stock. This oligonucleotide is potentially useful as a marker for the T. parva Uganda stock