

## **Sequencing and analysis of chromosome 1 of *Eimeria tenella* reveals a unique segmental organization.**

### **ABSTRACT**

*Eimeria tenella* is an intracellular protozoan parasite that infects the intestinal tracts of domestic fowl and causes coccidiosis, a serious and sometimes lethal enteritis. *Eimeria* falls in the same phylum (Apicomplexa) as several human and animal parasites such as *Cryptosporidium*, *Toxoplasma*, and the malaria parasite, *Plasmodium*. Here we report the sequencing and analysis of the first chromosome of *E. tenella*, a chromosome believed to carry loci associated with drug resistance and known to differ between virulent and attenuated strains of the parasite. The chromosome - which appears to be representative of the genome - is gene-dense and rich in simple-sequence repeats, many of which appear to give rise to repetitive amino acid tracts in the predicted proteins. Most striking is the segmentation of the chromosome into repeat-rich regions peppered with transposon-like elements and telomere-like repeats, alternating with repeat-free regions. Predicted genes differ in character between the two types of segment, and the repeat-rich regions appear to be associated with strain-to-strain variation.

**Keyword:** Chromosome mapping; Sequencing; Avian parasite.