Emergence of new types of *Theileria orientalis* in Australian cattle and possible cause of theileriosis outbreaks


**Abstract**

*Theileria* parasites cause a benign infection of cattle in parts of Australia where they are endemic, but have, in recent years, been suspected of being responsible for a number of outbreaks of disease in cattle near the coast of New South Wales. The objective of this study was to identify and characterize the species of *Theileria* in cattle on six farms in New South Wales where disease outbreaks have occurred, and compare with *Theileria* from three disease-free farms in Queensland that is endemic for *Theileria*. Special reference was made to sub-typing of *T. orientalis* by type-specific PCR and sequencing of the small subunit (SSU) rRNA gene, and sequence analysis of the gene encoding a polymorphic merozoite/piroplasm surface protein (MSP) that may be under immune selection. Nucleotide sequencing of SSU rRNA and MSP genes revealed the presence of four *Theileria* genotypes: *T. orientalis* (buffel), *T. orientalis* (ikeda), *T. orientalis* (chitoise) and *T. orientalis* type 4 (MSP) or type C (SSU rRNA). The majority of animals showed mixed infections while a few showed single infection. When MSP nucleotide sequences were translated into amino acids, base transition did not change amino acid composition of the protein product, suggesting possible silent polymorphism. The occurrence of ikeda and type 4 (type C) previously not reported to occur and silent mutation is thought to have enhanced parasite evasion of the host immune response causing the outbreak.