Rapid discrimination and quantification of *Theileria orientalis* types using ribosomal DNA internal transcribed spacers

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ABSTRACT

We report the population structure analysis of *Theileria orientalis* types (Ikeda, Buffeli and Chitose), the causative agent of theileriosis in cattle and its cohorts, using ITS1 and ITS2 spacers by fragment genotyping. We utilized primers flanking the two ribosomal RNA internal transcribed spacers (ITS1 and ITS2). Due to varying degrees of sequence polymorphism in the ITS regions found within and between species, we exploited the insertions and or deletions in these regions which resulted in different fragment sizes. On the basis of fragment size polymorphism, we could discriminate the three commonly found types of *T. orientalis*. ITS1 was capable of discriminating all three types (Ikeda-251 bp, Chitose-274 bp and Buffeli-269 bp) in one single reaction by fragment genotyping. In contrast, using ITS2, Ikeda (133-bp) a more pathogenic type was distinguishable from Buffeli/Chitose (139-bp). When compared with previous PCR detection method using, ITS1 and ITS2 genotyping was found to be more sensitive method with high specificity in population analysis and can be deployed in molecular epidemiology studies.

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