

Antigenic Diversity of *Theileria parva* Isolates from Cattle and Buffalo at the Wildlife-Livestock Interface in Southern and Eastern Africa

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Abstract : Theileriosis is a tick-borne disease of cattle caused by an apicomplexan protozoan parasite of the genus *Theileria*. In eastern and southern Africa, *Theileria* infections in cattle are caused by the species *Theileria parva* whose natural reservoir is the African buffalo (*Syncerus caffer*). Currently, East Coast Fever (ECF) caused by the cattle-derived *Theileria parva* is still a major problem in eastern Africa and some parts of southern Africa but not in South Africa following its eradication in the 1950s. However, Corridor disease (CD) caused by the buffalo-derived *Theileria parva* still remains a concern in South Africa. The diversity of *Theileria parva* in South Africa in comparison to other affected countries is poorly defined yet its known to be the survival strategy of this parasite. We assessed the antigenic diversity of *Theileria parva* isolates from Buffalo and cattle at the wildlife-livestock interface comparing samples from South Africa, Zimbabwe, Kenya, Tanzania, and Uganda. Antigenic epitopes of eight schizont antigen genes (Tp1, Tp3, Tp4, Tp5, Tp6, Tp7, Tp8 and Tp10) were amplified by PCR from genomic DNA extracted from blood samples collected from cattle and buffalo at the wildlife-livestock interface. Amplicons were purified and then sequenced on NGS platform. Full length open reading frames (ORFs) of two schizont antigen genes (Tp2 and Tp9) and one sporozoite antigen gene, p67 were also amplified from genomic DNA. Amplicons were then purified and cloned for sequencing. Analysis was based on sequence differences in the genes. Preliminary results show an extensively diverse population of *Theileria parva* circulating in buffalo and cattle populations at the wildlife-livestock interface. Diversity of the antigen genes contributes to the evasion of the immune system of the host by *Theileria parva*. This possess a concern in that, some of the *Theileria parva* populations may re-assort and become adapted to cattle to cause a form of theileriosis that is as fatal as ECF in areas where ECF was eradicated or is absent

Keywords : *Theileria parva*, east coast fever, corridor diseases, antigen genes, diversity

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