

Abstract

East Coast fever (ECF) is a fatal bovine disease caused by a tick-transmitted protozoan parasite *Theileria parva*. The disease causes high levels of mortality in cattle and results in vast economic losses. The Infection and Treatment Method (ITM) vaccine has been deployed in eastern, central and southern Africa to protect cattle against ECF. The International Livestock Research Institute (ILRI) with the support of the Food and Agriculture Organization (FAO) of the United Nations produced this vaccine stabilate in 1996. This vaccine stabilate named FAO 1 is trivalent containing three live *Theileria parva* stock components namely, Muguga, Serengeti-transformed and Kiambu 5. It is thought that due to sexual recombination in the ticks during cattle-tick passage, there may be a modification in the genotypic composition of the three stock components. This study evaluated the composition of the FAO 1 reference stabilates by generating *T. parva* clones under in vitro conditions and genotyping the clones using a set of five polymorphic mini- and microsatellite markers. Results showed that the FAO 1 vaccine stabilate contains at least nine genotypes. The Muguga reference stabilate was shown to contain eight *T. parva* genotypes of which two of the genotypes were also in the Serengeti-transformed reference stabilate. Kiambu 5 was genotypically homogeneous with only a single genotype identified. The various genotypes identified in the stabilate do not address how functionally relevant they may be in mediating a broad protection. Current studies are under way to address whether or not the observed genotypic diversity affects the antigenic epitopes.