

SUMMARY

Tropical theileriosis caused by the tick transmitted protozoa parasite *Theileria annulata* is a major and economically important disease of cattle in many developing countries. Sexual recombination that occurs in parasite has an effective role for genetic diversity in nature. Drug treatments and protective vaccines make selective effect on *T. annulata* populations and in the tick gut, it is therefore important sexual recombination causing genetic and antigenic diversity in parasite populations is investigated.

The completed genome sequence of *Theileria annulata* provided an opportunity to develop genetic markers for population genetic studies and also enabled the identification of new antigens. Sexual recombination that has been occurred in the tick gut, has not been demonstrated in parasite populations either experimentally or using mini and micro satellite markers which provides a reliable method for genotyping. A panel of 23 micro and minisatellite markers selected for population genetic studies in order to identify, characterise and analyse two different clonal and nonclonal *T. annulata* isolates (*T.annulata* Ankara and Akçaova) after recombination. Besides, chromosomal regions where recombinations are intense in new parasite populations and antigenic effect of these determined after genetic crossover.

The analysis using polymorphic mini and mikrosatellit markers showed that new population of two different clonal and nonclonal *Theileria annulata* isolates had many different alleles, genetic variations following crossing over resulting from transmission to tick guts. Chromosomal regions where recombinations are intense ranging chromozom 4>2>1>3 for D7 and chromozom 3>4>2>1 for A10 which is more intense. Analysis is done to determine antigenic effect of recombination showed no effect on 21 different antigenic regions of these parasite isolates.

Keywords: *Theileria annulata*, recombination, population genetics.