

**EXPRESSION OF TRYPANOTOLERANT QUANTITATIVE TRAIT LOCI IN A  
BORAN-BASED BACKCROSS UNDER NATURAL TSETSE CHALLENGE**

A Thesis submitted in fulfilment of requirements for Doctor of Philosophy  
degree of University of Nairobi (Animal physiology)

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## Abstract

African animal trypanosomosis (AAT) or Nagana is a transboundary disease with immense negative impact in Agricultural development across 37 African countries, with 60M livestock at risk. Utilization of trypanotolerant breeds as a form of control may offer a viable and sustainable option following recent identification of nine trypanotolerant quantitative trait loci (QTL) with positive effects in an F<sub>2</sub> cattle population of N'Dama/ Kenyan Boran, under a challenge of 1180 clone of *T.congolence*.

The current study was to confirm whether these identified QTLs would be expressed under natural tsetse and trypanosomosis challenge. To achieve this, a QTL challenge and mapping experiment was designed involving 192 backcross of (N'Dama × Kenyan-Boran) × Kenyan-Boran, BC1, 13 F<sub>1</sub> (N'Dama × Kenyan-Boran) sires and 8 founders of 4 Kenyan-Boran females and 4 N'Dama males. All animals were screened using 35 polymorphic microsatellite markers spanning through BTA2, BTA4, BTA7, BTA16 and BTA17 target chromosomes. Thirty seven F<sub>1</sub>s and 23 Kenyan-Boran were used as controls for the field challenge.

All cattle types were exposed to natural tsetse and trypanosomosis challenge in Narok district, Kenya and monitored for one year against 46 defined traits. Intra-genetic-types (F<sub>1</sub>, BC1, and K-Boran) means and standard deviations of the defined traits were computed and used as a measure of tolerance index for comparison. Overall mean number of N'Dama alleles (ONAS) and specific N'Dama allele score components, inherited by the BC1 from the N'Dama grandsire through the heterozygous F<sub>1</sub> sire were computed. Based on this ONAS

score, BC1 were divided into 30% upper and lower N'Dama alleles inherited and individual traits in each group were ranked in terms of trypanotolerance. In QTL analysis, a single trait QTL model, within the framework of multiple interval mapping (MIM) of MultiQTL software was implemented with 46 trait scores and 35 microsatellite markers span over the five target chromosomes.

Results revealed  $F_1$  as the most trypanotolerant, K-Boran the most susceptible with BC1 intermediate but more towards the K-Boran, an indication of some recessives. The upper 30% N'Dama allele group was more trypanotolerant at individual and overall trypanotolerance trait levels than the lower N'Dama allele group. Despite the expected increased error variance for measurement of traits under field conditions, QTLs were detected in all five chromosomes at false discovery rate of 15%, deriving positive alleles from N'Dama breed. It is concluded that QTLs detected under controlled experiment are expressed under field conditions thus setting a stage for practical application of the results through marker assisted selection and marker assisted introgression programmes. This will benefit farmers in tsetse endemic areas by enhancing disease resistance of the K-Boran susceptible breed while retaining its desired productivity characteristics.