Marker Assisted Selection for Disease Resistance in Nucleus Breeding Systems from a Crossbreeding Experiment — a Simulation Study

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Abstract

The aim of the study was to evaluate different breeding strategies for disease resistance in combination with production traits in pastoral systems with experimental data for genetic information and results from questionnaires for socio-economic aspects. Using a stochastic approach, a closed nucleus breeding was simulated. The base population consisted of N = 400 unrelated F2 crossbreed individuals from two breeds with fixed alleles in the desired traits: decrease in packed red blood cell volume (PCVD), decrease in body weight (BWD), natural logarithm of the mean count of parasites (PAR) as indicator of Trypanotolerance, live weight at 12 months of age (LW), milk yield (MY) and calving interval (CI) for production and reproduction traits. There were 10 discrete generations of selection; with selected animals in each generation randomly mated with the assumption of AI and MOET. The genotype of each individual was modeled using 10 unlinked additive quantitative trait loci (QTL) with two flanking markers each and a model with 100 loci without marker information for the polygenic effect. The phenotypic values were sum of genotypic and a residual effect. The input parameters for QTL and marker as well as LW variance and correlations were taken from results of the completed QTL mapping experiments by the International Livestock Research Institute (ILRI) in Kenya; other information for the remaining traits was based on international studies. The economic values came from a socio-economic study in pastoral production systems. Breeding value estimation for selection was based on best linear unbiased prediction (BLUP), BLUP in combination with marker information (MABLUP) and estimation on markers only (MA). Results indicate greater genetic gain via BLUP-evaluation but also reasonable genetic gain via MABLUP with better results for disease resistance. MA-results require more computational time but show the potential genetic gain without infecting the animals for phenotypic observations.

Keywords: Cattle breeding, disease resistance, marker assisted selection, nucleus breeding system, simulation, stochastic approach

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