

F47 POSTER

ESTIMATION OF (CO)VARIANCE COMPONENTS AND GENETIC PARAMETERS FOR TICK RESISTANCE IN BEEF CATTLE MEASURED BY COUNTING IN TWO DIFFERENT BODY REGIONS¹

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The objectives of this study were to estimate (co)variance components and genetic parameters for bovine tick *Rhipicephalus (Boophilus) microplus* resistance in Hereford and Braford cattle measured by counting in two different body regions. The animals belonging to the Delta G Connection genetic improvement consortium were raised in Southern Brazil. The number of ticks at inner hind legs region was counted in 6,622 animals between 2001 and 2008, and was recorded up to three consecutive counts at one side of body in 2,414 bovines between 2009 and 2010. Data consistency and contemporary groups formation were done using SAS, and pedigree file contained 19,063 records. Measurements on the two different body regions were regarded as different traits. Covariance components and genetic parameters were estimated in bivariate analysis using Bayesian inference. The model included the fixed effect of contemporary groups, breed composition, heterozygosity and linear and quadratic coefficients for age of the animal, and random additive genetic effects. The estimated heritabilities were 0.241 ± 0.067 for counting on one side and 0.164 ± 0.038 for counting on inner hinds legs. The genetic correlation between the counting on these two different body regions was 0.737 ± 0.111 . The heritabilities values suggest the possibility of genetic progress with the selection by these criteria. The larger heritability obtained by the multiple counting on one side of body indicates a greater precision in estimates of genetic values by the counting in this region, allowing for greater genetic gains in bovine ticks resistance.