

**Four-trait joint estimation of variance components in Nellore cattle**

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The objective of this research was to estimate (co)variance components and genetic parameters jointly for 4 traits in a population of Nellore cattle reared in Brazil, considering management group at weaning as a random effect to increase the size of contemporary groups for post weaning traits. Traits analyzed were weaning weight (WW, kg, N=103,554), post weaning gain (PWG, kg, N=81,908), scrotum circumference (SC, cm, N=39,960) and muscle visual score (MUS, N=72,787). The full animal model had 161,865 animals in  $A^{-1}$  and the models of analysis considered, for each trait, age of dam (linear and quadratic), age at measurement (linear), Julian date (linear and quadratic) and contemporary group, as well random effects of animal (direct and maternal, this not for MUS), permanent environment (PE, not for MUS) and management group at weaning (MGW, not for WW). The program used for the estimation was VCE 6.0 (Groeneveld, 2008). Direct heritability estimates (standard error) were, for WW, 0.22 (0.006), 0.24 (0.006) for PWG, 0.402 (0.007) for SC and 0.236 (0.005) for MUS. Maternal heritability estimates were 0.086 (0.003, WW), 0.036 (0.002, PWG) and 0.090 (0.003, SC). Correlation between direct and maternal genetic effects were low for majority of trait combinations, but around 0.5 between PWG and maternal WW, and MUS and maternal WW and -0.60 (0.026) between direct and maternal PWG and -0.71 (0.024) between maternal WW and PWG. Ratios over phenotypic variance were, for MGW, 0.14 (0.005) for PWG, 0.04 (0.003) for SC and 0.04 (0.002) for MUS. Ratios for PE were 0.12 (0.003), as concerned to WW, 0.04 (0.002), for PWG and 0.012 (0.002) for SC. Genetic correlations between direct effects were all positive and medium, but between PWG and MUS, that correlation was 0.70 (0.018). Estimates of (co)variance components were all within reasonable interval, when compared to two-trait estimates.

**Analysis of inbreeding in the Swedish Gotland pony using pedigree information and microsatellite markers**

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The Swedish indigenous breed Gotland pony is considered endangered by the Swedish Agricultural Board. The breed was near extinction in the beginning of the 20<sup>th</sup> century, but the number of horses has since then increased, and in 2007 there were approximately 600 breeding females and 110 breeding males in Sweden. The ponies are rather small, hardy and long-lived and are used mainly for pleasure riding and pony trotting races. Traditionally, they were bred in a free-range system in the forests on the island of Gotland. Today a herd of about 50 mares are still kept under similar conditions. The majority of Gotland ponies are however bred in the mainland of Sweden. The aim of this study was to describe the population structure and investigate the inbreeding situation using both pedigree data and microsatellite marker information. Pedigree information was available since 1900 and comprised in total 14 941 individuals. Molecular data from microsatellites was available for 343 ponies. The generation interval was on average 10.4 years. Pedigree completeness was generally very high for ponies born after 1940. The average inbreeding coefficient for foals born 2000-2009 was over 11%. The rate of inbreeding was however not alarming, and the effective population size was estimated at about 60 animals. The results from the pedigree data will be compared with results from the molecular data.

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