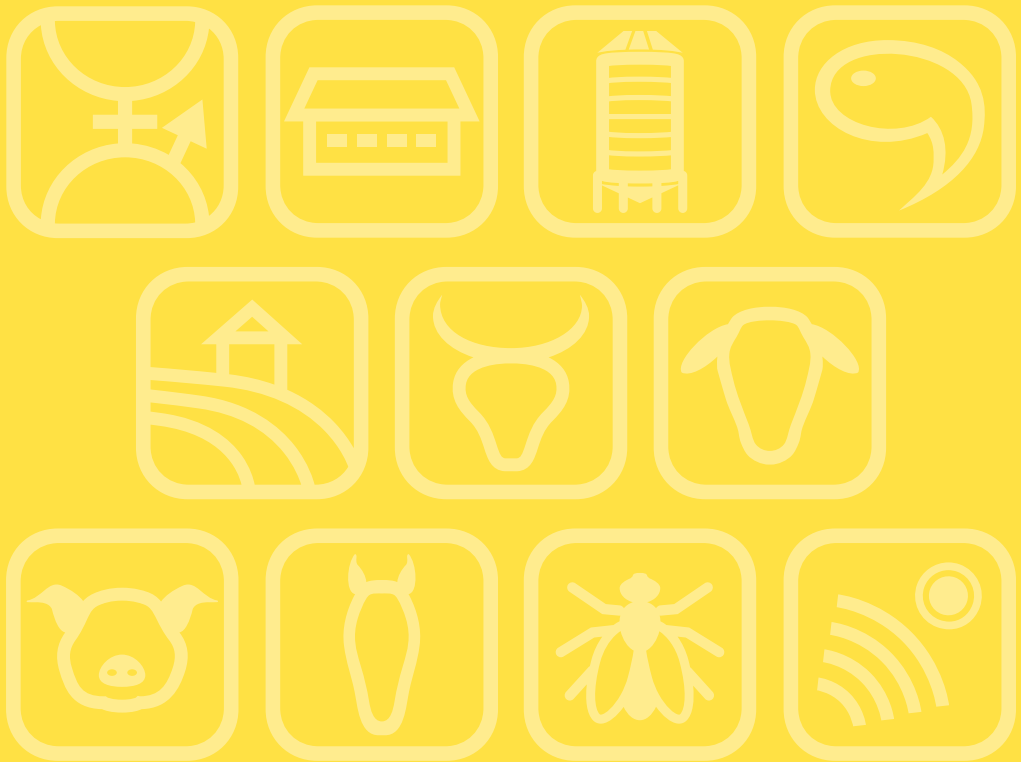


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Genetic parameters for reproductive and longevity traits in Bísaro pigs*G. Paixão¹, A. Martins¹, A. Esteves¹, R. Payan-Carreira^{1,2} and N. Carolino^{2,3}**¹Universidade de Trás-os-Montes e Alto Douro, CECAV, Vila Real, 5000-801, Portugal, ²Universidade de Évora, Departamento de Medicina Veterinária, Évora, 7002-554, Portugal, ³INIAV, Strategic Unit for Biotechnology and Genetic Resources, Vale de Santarém, 2005-048, Portugal; gus.paixao@utad.pt*

The Bísaro pig has gained popularity in recent years reflecting the success of the conservation program. Nevertheless, no data is available for animal genetic evaluation in this breed. Therefore, this study aimed to estimate genetic parameters and trends for reproduction related traits in Bísaro pigs. Through a REML procedure applied to mixed linear models, 27,844 farrowing records, from 1995 to 2017, were used to analyse total number of pigs born per litter (NBT), number of pigs born alive (NBA), number of stillborn (NSB), number of pigs weaned per litter (NBW), age at first farrowing (AFF), farrowing interval (FIT), length of productive life (LPL), lifetime number of litters (LNL), lifetime pig production (LTP) and lifetime efficiency (LTP365). The heritability estimates for litter size traits were low and ranged from 0.007 ± 0.004 to 0.015 ± 0.006 . Differently, the heritabilities for traits related to longevity and lifetime production traits were moderate (0.078 ± 0.026 to 0.121 ± 0.030). AFF registered the highest heritability value (0.345 ± 0.028). NSB and FIT presented high values of additive genetic coefficient of variation (0.177 and 0.271) in contrast with low heritability estimates (0.007 ± 0.004 and 0.002 ± 0.005). Very tight genetic correlations were found between NBT and NBA (0.968), NBW and NBT (0.974), and NBW and NBA (0.945). Weak genetic correlations were found between both NBT and NSB (0.352) and between NBA and NSB (0.107). Longevity and lifetime production traits presented high positive genetic correlations (0.811-0.969) and moderate to high phenotypic correlations (0.266-0.946). No major genetic changes were registered over time for most of the analysed traits, except for AFF and LPL, having registered an overall decreased of mean estimated breeding values (21.3 and 17.5) and negative genetic trends of -0.6 and -0.4 ($P < 0.001$), respectively.
