Population structure of Girolando cattle using pedigree analysis

Maíza S. da Rosa[1], Lucas R. Lopes*[2], Elisandra L. Kern[2], Lethissia A. da Silva Coelho[2], Marcos V. G. B. da Silva[3], Jaime A. Cobuci[1]
[1]Universidade Federal do Rio Grande do Sul, Porto Alegre/RS; [2]Universidade Federal Rural do Rio de Janeiro, Seropédica/RJ; [3]Empresa Brasileira de Pesquisa Agropecuária, Juiz de Fora/MG
*Undergraduate student; - elisandra.kern@ufrrj.br

The population genetic structure knowledge of animal production breeds is essential for promoting genetic improvement and the genetic diversity of these populations. The aim of this study was to estimate and evaluate different population genetic parameters using pedigree information from Girolando animals. This data refers to 988,124 animals, from all genetic groups of the breed, born between 1955 to 2020. RelaX2 software was used to estimate the average coefficient of relatedness (AR), effective population size (Ne), generation interval (L), equivalent complete generations (ECG) and the effective number of founders (fe), ancestors (fa) and founder animals (Nf), while the integrity of the pedigree (INP) was obtained using PopRep software. The INP of the Girolando population has increased every year, with the greatest variation being observed from 1955 to 1978, which may be due to the lower number of animals born, or even the low use of artificial insemination at the time. It should be noted that for the animals born in 2020, the INP was 95.4, 79.2, 61, 47.5, 38.2 and 31.9% from the first to the sixth generation, respectively. The average ECG value was 6.04 and 4.21 for the reference population (animals born from 2012 to 2020) and the total population, respectively. The AR found for the reference population was 4.03%, indicating that there was intensive use of few bulls in mating between 2012 and 2020. When the AR was evaluated annually, a gradual increase was seen, starting at 2.32% in 2012 and reaching 5.65% in 2020, which shows a gradual increase in the average genetic similarity between the animals in this most recent period. The estimated Ne was 382.5 animals for the reference population, and 326.71 animals for the total population, which is above 100, the minimum value recommended to avoid drastic losses in genetic diversity. The L value was 7.03 years. It was observed that L varied between the selection routes, being higher in the bull selection routes compared to the cow selection routes, with 3.70 years more in the bull-daughter route when compared to the cow-daughter route. This can be explained by the long time required to obtain the results of the progeny test (approximately six years) and also by the low replacement of bulls in the herds. The values of fe and fa, in the reference population were low, with values of the 144.26 and 56.64 animals, respectively. The evaluation of the genetic contribution of the ancestors showed that only 20 of the 106,565 ancestors that contribute to the reference population are responsible for 50% of the genetic variability in the Girolando population. The fe/fa ratio (2.54) indicated the existence of population bottlenecks throughout. Although the genetic diversity of the breed has been preserved to a certain extent, population bottlenecks and the genetic contribution of a few individuals were observed, which suggests caution when increasing the intensity of selection. Strategies to increase genetic variability and reduce the risk of inbreeding are necessary to ensure long-term sustainability in the breed.

Keywords: inbreeding, genetic variability, generation interval, effective population size, population parameters.