POPULATION STRUCTURE OF GIR LEITEIRO SIRES

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The aim of this study was to analyse the population structure of Gir Leiteiro sires, born from 1987 to 2014, with available semen in artificial insemination centres. Pedigree data from 338 sires were obtained through electronic access and constituted the reference population for this study. The data archive was generated through public access to the Brazilian Association of Zebu Breeders (ABCZ) database. The pedigree was regressed until the absence of ancestor's information, this action generated data from 2,680 animals, 1,065 males and 1,615 females, born between 1924 to 2014 periods. Those imported animals and with unknown parents were considered founders. The archive was investigated using both the statistical package SAS (University Edition v9.2) and the ENDOG v4.8 software. Pedigree completeness in the reference population was 100%, however, in the hole archive it this was only 76%. The generation interval was 14.42 and 7.57 years, in the sire-son and dam-son pathways, respectively. The mean inbreeding coefficient calculated in the reference population was 1.60%. Half of the existing gene pool in the reference population was derived by only 8 ancestors. The effective number of founder and ancestor were estimated at 49 and 21, respectively. A total of five ancestors contributed with 42% of the existing genes in the reference population. The gene origin probability parameters decreased drastically from previous generations to the reference population and indicated the presence of strong bottleneck in the pedigree. The proportion of inbred animals and the addictive relationship between them increased over the generations. The increase in the addictive relationship in this population stratum will certainly lead to further reductions in the gene origin probabilies parameters. Genetic improvement actions may be compromised in the future.

Keywords: bottleneck effect, gene origin probability, generation interval, inbreeding coefficient