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Genetic contribution of the main ancestors of the Mangalarga breed

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In breeding programs, the monitoring of the genetic variability of a population is essential for an adequate management of matings and the development of selection strategies. One of the tools used for this monitoring is the analysis of probabilities of gene origin. In this context, this study aimed to evaluate the genetic contribution of the ancestors of the Mangalarga breed. Genealogic information from Brazilian Association of Mangalarga Horse Breeders (ABCCRM) was used, considering animals born between 1919 and 2018 (n= 206,426) as the total population (TP) and those born between 2009 and 2018 (n= 20,539) as the reference population (RP). The *software* ENDOG 4.8 was used in evaluation of genetic variability, based on the probability of gene origin. It was observed that ancestors who individually contributed with at least 1% of the genetic *pool* of the TP are: Gigante JO (5.18%), Turbante JO (3.65%), Paladino (3.46%), Chapéu JO (2.03%), Maxixe (1.86%), Rigoni (1.77%), Dança JO (1.36%), Feitiço (1,17%) and Congada (1.11%). In the TP, nine animals, only two of which female (Dança JO and Congada), accounted for 21.58% of the breed variability. The ancestors that individually contributed with at least 1% of the genetic *pool* of the RP are: Turbante JO (6.64%), Gigante JO (3.95%), Chapéu JO (3,76%), Dança JO (3,10%), Birmânia do Cedro Alto (2.88%), Nairobi Mangalarga (1.94%), Jacira DL (1.70%), Premiada RN (1.64%), Rigoni (1.53%), Jorael do Jaó (1.06%) and Feitiço (1.01%). In the RP, eleven animals, four of which female (Dança JO, Birmânia do Cedro Alto, Jacira DL and Premiada RN), accounted for 29.21% of the breed variability. Between 1944 and 1969, the animals that most contributed genetics to the Mangalarga breed were born. Among them, stallion Turbante JO, leaving a total of 1,686 offspring. Due to the enormous success of that animal, its father (Gigante JO) and siblings were widely used in reproduction, making stallion Gigante JO (114 offspring) the ancestor with the greatest influence on the TP and the second animal with the largest genetic contribution to the RP. It was observed that in the Mangalarga breed, founders and ancestors, followed a paternal line, attributing to the stallion the condition of main influencer of the genetic variability of the herd. This is due to the females having physiological limitations that allow them to generate only a single foal per year, whereas males, are able to cover tens of mares within a single mounting season. In addition, with the use of reproductive techniques, especially artificial insemination, the number of descendants left by males became even higher. The embryo transfer technique, started being used in the late 1990s in the Mangalarga herd, increases the participation of the maternal side in variability. Embryo transfer allowed the RP to have twice as many female ancestors with greater contribution than the TP. It is concluded that, in the Mangalarga breed, there is the preferential use of breeders, which has been intensified by the use of reproductive techniques. This practice can lead to genetic erosion, compromising the genetic variability of the breed.

Keywords: equine, *pedigree*, reproduction.