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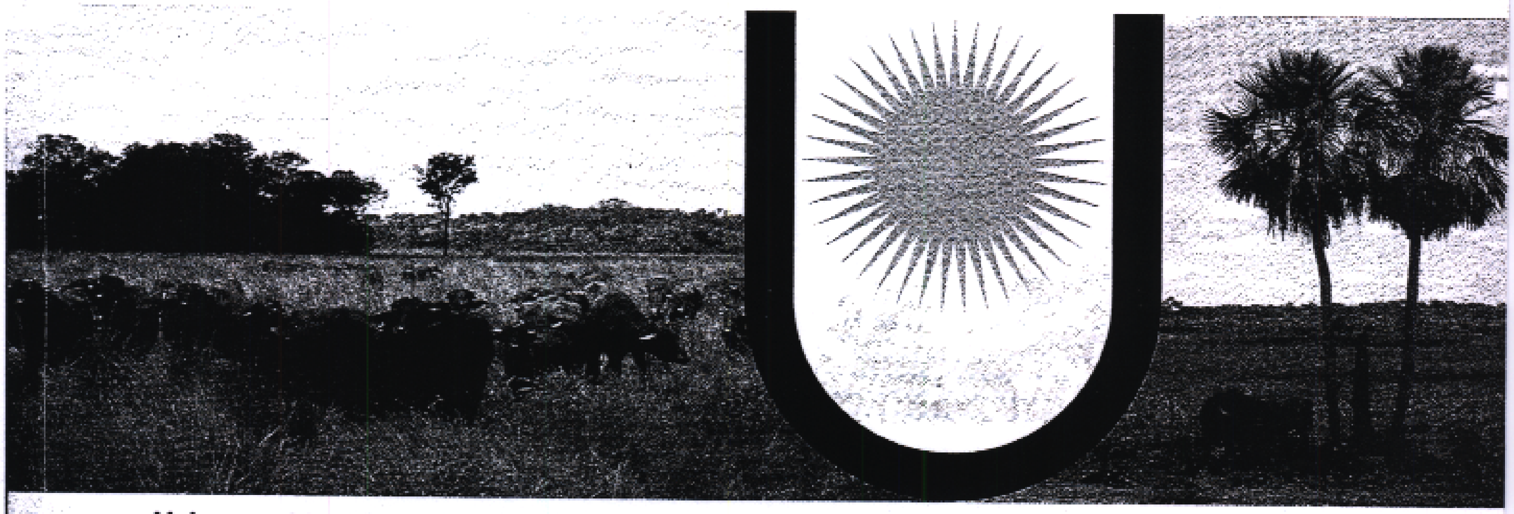

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# Mating Optimization within a Carabao Herd (*Bubalus bubalis kerebao*) Based on *Pedigree* Analysis*[1]

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## ABSTRACS

The Carabao breed is th reatened with extinction and decharacterization in Brazil, and its preservation and population studies are of utmost importance. Information concerning herd composition and the genetic contribution by active breeders may contribute significantly to optimize matings with a view to complementing traits, increasing genetic gains and maintaining or inc reasing genetic variability. This study concerns the simulation of possible matings of active dams, active bulls and young, potential bulls, taking into account the different kinship levels among the bulls. The overall database contained 445 records kinship for Carabao buffalos from the ex situ conservation herd of Embrapa Western Amazon, on the Marajó Island, Pará, Bra zil. The population parameters y ielded by the PEDIG s oftware (2003) were equal to 5.3; 4 .73 and 3.79 animals, respectively for effective number of founders (Nf), effective number of ancestors (Na) and effective number of remaining genomes (Ng). These values point to low genetic variability especially due to a bottleneck effect, possibly because of the small number of individuals mated up until the present. Pairs of reprodu cers were separated that showed kinship levels at 12.5%, 25%, 37.5% or 50%, and there was simulation of their matings with active dams in the herd. The genetic variability resulting from these simulations (represented by new Nf, Na and Ng values, in addition to the genetic contributions by the main ancestors, the average kinship between males and females, and the average coefficient of inbreeding) in the progeny was found to be the higher the smaller the kinship between both bulls. The use of a new mating strategy and the inception of new breeders with no kinship with the present population in the herd will enable a reduction in the loss of genetic variability within the Carabao population in this study.

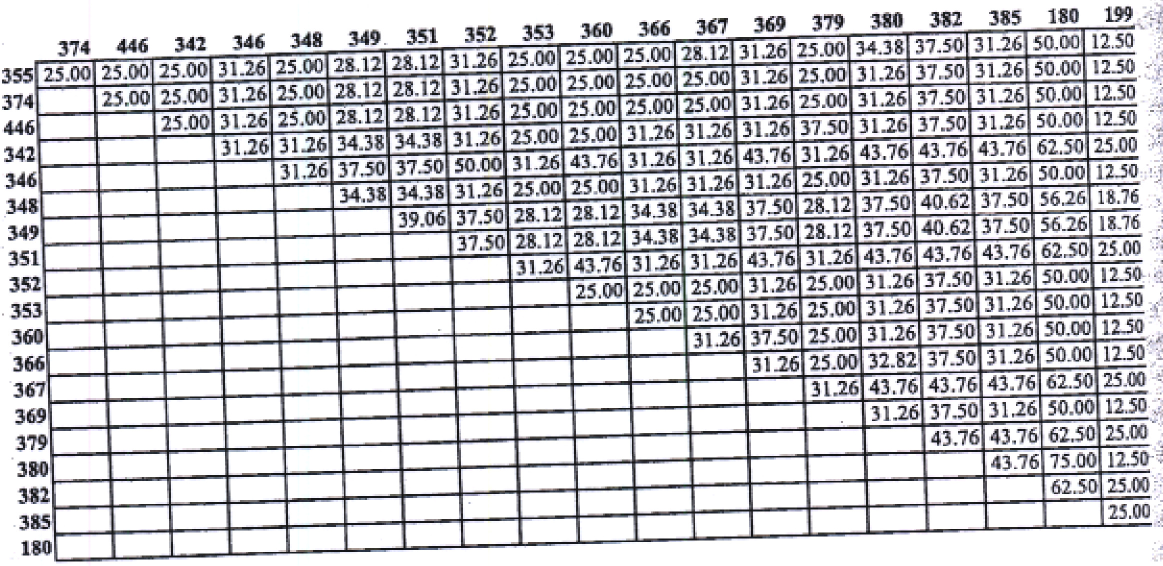
**Key words:** marginal contribution, preservation, swam buffaloes, the Amazon.

## INTRODUCTION

The Carabao breed is threatened with extinction and decharacterization in Brazil, and its preservation and population studies are of utmost importance[1]. A study with a conservation herd of Embrapa Western Amazon, in Salvaterra, Marajó Island, Pará, Brazil, has made evident both the bottleneck effect to which the population has been subjected and the need to optimize matings following pedigree analysis[2]. Additional information concerning herd composition and the genetic contribution by active reproducer may contribute significantly to optimize matings with a view to complementing traits, increasing genetic gains and maintaining or increasing genetic variability[3]. This study concerns the simulation of possible matings of active dams, active bulls and young, potential bulls, taking into account the differen kinship levels among the bulls.

## MATERIAL AND METHODS

The overall database contained 445 records kinship for Carabao buffaloes from the ex situ conservation herd of Embrap Western Amazon, on the Marajó Island, Pará, Brazil. The population parameters yielded by the PEDIG software4 were equa to 5.3; 4.73 and 3.79 animals, respectively for effective number of founders (Nf), effective number of ancestors (Na) an effective number of remaining genomes (Ng). These values point to low genetic variability especially due to a bottlenec effect, possibly because of the small number of individuals mated up until the present. Details provided elsewhere Figure 1 shows the genetic kinship between reproducers (males), ranging between 12.5% and 75%.



| | 374 | 446 | 342 | 346 | 348 | 349 | 351 | 352 | 353 | 360 | 366 | 367 | 369 | 379 | 380 | 382 | 385 | 180 | 199 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 355 | 25.00 | 25.00 | 25.00 | 31.26 | 25.00 | 28.12 | 28.12 | 31.26 | 25.00 | 25.00 | 25.00 | 28.12 | 31.26 | 25.00 | 34.38 | 37.50 | 31.26 | 50.00 | 12.50 |
| 374 | | 25.00 | 25.00 | 31.26 | 25.00 | 28.12 | 28.12 | 31.26 | 25.00 | 25.00 | 25.00 | 25.00 | 31.26 | 25.00 | 31.26 | 37.50 | 31.26 | 50.00 | 12.50 |
| 446 | | | 25.00 | 31.26 | 25.00 | 28.12 | 28.12 | 31.26 | 25.00 | 25.00 | 25.00 | 25.00 | 31.26 | 25.00 | 31.26 | 37.50 | 31.26 | 50.00 | 12.50 |
| 342 | | | | 31.26 | 31.26 | 34.38 | 34.38 | 31.26 | 25.00 | 25.00 | 31.26 | 31.26 | 31.26 | 37.50 | 31.26 | 37.50 | 31.26 | 50.00 | 12.50 |
| 346 | | | | | 31.26 | 37.50 | 37.50 | 50.00 | 31.26 | 43.76 | 31.26 | 31.26 | 43.76 | 31.26 | 43.76 | 43.76 | 43.76 | 62.50 | 25.00 |
| 348 | | | | | | 34.38 | 34.38 | 31.26 | 25.00 | 25.00 | 31.26 | 31.26 | 31.26 | 25.00 | 31.26 | 37.50 | 31.26 | 50.00 | 12.50 |
| 349 | | | | | | | 39.06 | 37.50 | 28.12 | 28.12 | 34.38 | 34.38 | 37.50 | 28.12 | 37.50 | 40.62 | 37.50 | 56.26 | 18.76 |
| 351 | | | | | | | | 37.50 | 28.12 | 28.12 | 34.38 | 34.38 | 37.50 | 28.12 | 37.50 | 40.62 | 37.50 | 56.26 | 18.76 |
| 352 | | | | | | | | | 31.26 | 43.76 | 31.26 | 31.26 | 43.76 | 31.26 | 43.76 | 43.76 | 43.76 | 62.50 | 25.00 |
| 353 | | | | | | | | | | 25.00 | 25.00 | 25.00 | 31.26 | 25.00 | 31.26 | 37.50 | 31.26 | 50.00 | 12.50 |
| 360 | | | | | | | | | | | 25.00 | 25.00 | 31.26 | 25.00 | 31.26 | 37.50 | 31.26 | 50.00 | 12.50 |
| 366 | | | | | | | | | | | | 31.26 | 37.50 | 25.00 | 31.26 | 37.50 | 31.26 | 50.00 | 12.50 |
| 367 | | | | | | | | | | | | | 31.26 | 25.00 | 32.82 | 37.50 | 31.26 | 50.00 | 12.50 |
| 369 | | | | | | | | | | | | | | 31.26 | 43.76 | 43.76 | 43.76 | 62.50 | 25.00 |
| 379 | | | | | | | | | | | | | | | 31.26 | 37.50 | 31.26 | 50.00 | 12.50 |
| 380 | | | | | | | | | | | | | | | | 43.76 | 43.76 | 62.50 | 25.00 |
| 382 | | | | | | | | | | | | | | | | | 43.76 | 75.00 | 12.50 |
| 385 | | | | | | | | | | | | | | | | | | 62.50 | 25.00 |
| 180 | | | | | | | | | | | | | | | | | | | 25.00 |

**Figure 1.** Kinship between Carabao active (180 and 199), reserve (355, 374 and 446) and potential (342 a reproducers.

Pairs of reproducers were separated that presented kinship levels at 12.5%, 25%, 37.5% or 50%, and there was sim tion of their matings with active dams (N=78) in the herd to compare them with matings based on two active reprod (numbers 180 and 199). New Nf, Na and Ng values were estimated by the PEDIG software.

## RESULT AND DISCUSSION

The mean endogamy that resulted from the matings of active females with two active males was 11%, in which case 14 referred to reproducer 180 and 6.8% to reproducer 199. The Nf, Na and Ng values for pairs of reproducers (rang between 12.5% and 50%) are shown in Table 1.

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1 Part of the master's research by the second author. Related to FAPESPA Project n. 035/2008 and Embrapa MP1 Proj 01.06.01.06.04.00

**Table 1.** Values (initial and new) for effective number of founders (Nf), effective number of ancestors (Na), effective number of remaining genomes (Ng), genetic contributions by the main ancestors (a), genetic contributions by ten principal ancestors (b), average kinship between males and females (R) and average coefficient of inbreeding in the progeny (F) in Carabao herd, as a result of simulation.

| Kinship level (males) | Nf | Na | Ng | a | b | R | F |
|---|---|---|---|---|---|---|---|
| 12.5 % | 6.70 | 6.15 | 4.01 | 31.09 | 84.78 | 14.80 | 7.40 |
| 25.00 % | 6.70 | 5.31 | 3.34 | 37.18 | 83.01 | 17.60 | 8.80 |
| 37.50 % | 5.60 | 5.28 | 3.00 | 36.64 | 84.79 | 22.20 | 11.10 |
| 50.00 % | 5.00 | 4.90 | 2.79 | 37.37 | 85.90 | 22.40 | 11.20 |

The genetic variability resulting from these simulations (represented by new Nf, Na and Ng values), in addition to the genetic contributions by the main ancestors, the average kinship between males and females, and the average coefficient of inbreeding) in the progeny was found to be the higher the smaller the kinship between both bulls.

## CONCLUSION

The use of a new mating strategy and the inception of new reproducers with no kinship with the present population in the herd will enable a reduction in the loss of genetic variability within the Carabao population in this study.

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