Inbreeding effective population size in composite beef cattle breeds

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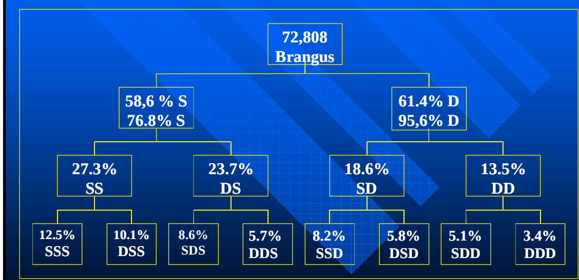
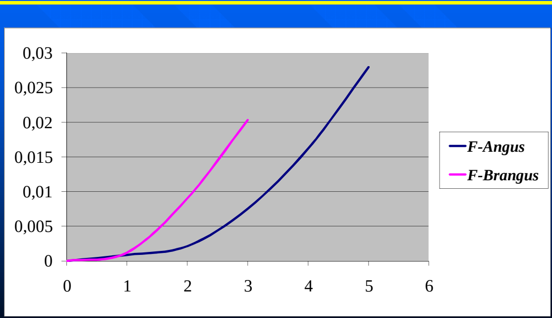
Introduction

- Composites such as Brangus and Braford are the most widespread breeds in subtropical Argentina.
- To retain heterosis in composite breeds, such that the initial advantage of increased heterozygosity is not dissipated by *inbreeding*, a sufficiently large N_e is essential (Gregory et al, 1993).
- An N_e = 250 is required to keep additive variance at its initial value when h^2 is about 0.33 (Hill, 2000).

Percentage of animals with known ancestors



Inbreeding levels in advanced generations of Angus and Brangus

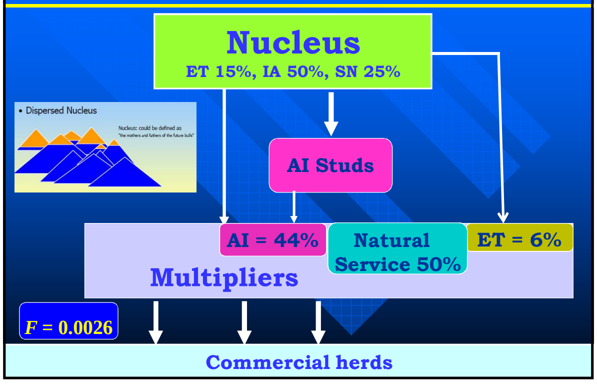


Complex mating structure that can be accurately characterized by demographic parameters.

Objective

To obtain expressions for the inbreeding N_e that depends on demographic parameters. These can be accurately estimated from a data base.

Brangus: breed structure



Inbreeding N_e

- For "metapopulations" under certain mating structures, Chesser (Genetics 1991,1993) derived expressions for the N_e using the inbreeding approach.
- First: produce recursive equations that characterize the mating system and are functions of IBD and demographic parameters: F, and co-ancestries within and between subpopulations.
- Second: build the system and solve for ΔF using, for example, least squares.
- Third: equate ΔF to N_e and solve for the latter.

Equations

1. Average F_t in the nucleus herds.

Average coancestry ***between two individuals*** from:

2. ***a nucleus herd***.

3. ***different nucleus herds***

4. ***nucleus*** (one) and the ***multiplier*** (θ_{NM}).

5. ***multipliers*** herds.

Equation for θ_{NM}

$$\theta_{NM\,(t)} = \tfrac{1}{4}\left[P\left(S_N \equiv S_M\right) + P\left(S_N \equiv D_M\right) + P\left(D_N \equiv S_M\right) + P\left(D_N \equiv D_M\right)\right]$$

Expand, for example, the probability for IBD between sires

$$P\left(S_N \equiv S_M\right) = P\left(S_N \equiv S_M \middle| S_N \to S_M\right) P_N + P\left(S_N \equiv S_M \middle| S_N \not\in S_M\right) \left(1 - P_N\right)$$

P_N = probability that a bull from a multiplied herd is a son of a bull from the nucleus.

$$P_N = \frac{S - \sum_{i=1}^{I} S_{ij}}{S - \sum_{j=1}^{J} S_j^2}$$

S_{ij} = Male progeny of sire i in herd j

S_j = Male progeny in herd j

S = Total male progeny

Conditional on S_N being the sire of S_M we obtain

$$P\left(S_N \equiv S_M \middle| S_N \to S_M\right) = \tfrac{1}{4}\left(1 + F_{t-1}\right)$$

If it is not the sire, then the probability is the relationship in $t - 1$:

$$P\left(S_N \equiv S_M \middle| S_N \not\in S_M\right) = \theta_{NM(t-1)}$$

Then, the probability of genes from the two sires being IBD is

$$P\left(S_N \equiv S_M\right) = \tfrac{1}{4}\left(1 + F_{t-1}\right) P_N + \theta_{NM(t-1)} \left(1 - P_N\right)$$

Using a similar reasoning the probability of genes from D_N being IBD to the genes in S_M we get

$$P\left(D_N \equiv S_M\right) = \tfrac{1}{8}\left(1 + F_{t-1}\right) P_{HE} + \theta_{NM(t-1)} \left(1 - P_N\right)$$

P_{HE} = probability that a cow from a multiplied herd is a paternal half sib of a bull from the nucleus.

On collecting all probabilities, we obtain

$$\theta_{NM(t)} = \frac{3}{16}\left(1 + F_{t-1}\right) P_N + \theta_{NM(t-1)} \left(1 - P_N\right)$$

Las Lilas 3405-E Mauleón 6968 G5 Manuel

Comments

- The system is complex. When solved produced

$$N_e = \frac{1 + C_1^2 + C_3^2 + C_5^2 + C_8^2}{2\left[C_3\left(\alpha_{xy} - C_4\right) + C_8\left(\left(1 - C_9\right)\theta_{ij} - C_8\right) + \gamma\alpha + \left(1-\gamma\right)\theta_{mf} + C_5\left(C_6\,\theta_{NM} - C_7\right) + 16\, C_1 C_2\, \theta_{xy}\right]}$$

- The C’s are function of the *P*’s, and these depend on demographic parameters.
- As the probabilities of IBD are fixed, the value of N_e depends on how much *F* is picked by the *P*’s .
- Currently, the formula is being tested numerically.