Mate Selection For Sustained Genetic Improvement In Small Populations

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Introduction

In genetic improvement there is an infinite range of actions, but in reality only two critical control points – animal selection and mate allocation. Because the best animals to select depend on the pattern of mate allocation, and vice versa, these decisions can be made simultaneously as Mate Selection.

When we specify the implementation of the breeding program using a Mate Selection approach, we automatically incorporate decisions on factors such as breeding objectives, selection intensity, crossbreeding, inbreeding avoidance, which animals to take semen and embryos from, migration of sires between herds, and how much to spend on seed stock purchase, transport, etc. Moreover, we can also satisfy any logistical constraints we impose, such as quarantine restrictions on animal movements.

The primary costs associated with genetic improvement are for progeny testing programs and associated facilities. A successful program depends on both the size of the testing facility and the way it is managed. The total number of animals housed is divided into a number of genetic nucleus lines or populations. The use of more lines means more breeding objectives that can be targeted but it also implies a reduction in the size of lines, particularly those considered “minor” or “experimental”. Maintaining many small populations also has applicability in the area of animal genetic resource management (e.g., critical and endangered breeds; Gandini et al., 2004). However, larger lines allow for increased opportunities for improving traits that are expensive to measure and breeding for difficult traits (e.g., sex-linked, low heritability) but imply that fewer lines can be kept within the same testing capacity. Thus, the whole process of allocating resources becomes a population size optimization problem.

The rate of inbreeding quantifies the risk of increased relationships and is an objective criterion used to manage population size. Closer relationships are generated when high genetic gains are targeted, when the breeding populations are small or even when they are large but the traits to be improved force the intense use of family information.

The objective of this study was to assess the effectiveness of Mate Selection to manage genetic improvement and diversity in a set of relatively small simulated pig populations.

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Material and methods

Simulations were based on an expansion of the multi-trait PopSim module of Genup (Kinghorn, 2010), with extensions to run production versions of PIC's genetic evaluation programs, and a simplified version of PIC's Mate Selection program GenMate (Newman et al., 2009).GenMate finds the optimal mating set using evolutionary computation via an adaptation of Differential Evolution (DE, Storn and Price, 1997).

The primary input parameter for Mate Selection is Target Degrees, which defines the amount of restriction to be applied to relationships generated by proposed mating lists while maximizing the average predicted index of resulting progeny. The optimum mating list is chosen among thousands of combinations by iteration. Target degree ranges from 0 to 90, i.e., most restrictive to least restrictive on rate of inbreeding. While 0 target degrees is equivalent to using a minimum number of the highest indexing sires to mate to female candidates, 90 degrees enforces use of most available sires, regardless of their index values. The target degrees used in this study were 5, 25, 45, 65 and 85.

A sire line was simulated. The heritability of the selection index was 0.35 and all weight in the economic scenario was given to the production traits. Population sizes were: 25, 50, 100, 200 and 400 females. Every population had an initial mating ratio of 1 male to 10 females. In subsequent generations number of males was determined by the optimal contributions (Woolliams and Thompson, 1994) proposed by GenMate based on selection index and pedigree relationships.

For each population, 15 years of Mate Selection were simulated, with two reproduction cycles per year. Between 3 and 10 replicates were run; more replicates for smaller populations and fewer for larger ones.

At each parity, targeted average litter size was 10 piglets with a standard deviation of two piglets. Use of sires was constrained to between 10 and 40 matings per reproduction cycle. Weaning rate assumed was 90% and survival rate was 95% for both sexes. Age at first parity was one year for both sires and dams. Sires were kept for up to two years (four reproduction cycles) while dams were kept for up to four years. Animals were born, off-tested, selected and mated twice a year using a single candidate group.

In this study the rate of genetic improvement is presented as the expected percentual change in the average selection index when changing from one population size to another. The index obtained by the population of 100 sows at 45 target degrees (circled 45c) is used as base for calculation. Rate of change in inbreeding was defined as the expected increase in the average inbreeding coefficient year on year, as a percent. Generation interval was considered to be one year.

Results and discussion

Results presented in Figure 1 summarise genetic gain and rate of inbreeding for animals born in the 15th and final year of simulated selection. Trend lines depict the effect of changing number of sows. Labels (target degrees, ranging from 5 to 85 out of 90) show the amount of restriction applied while trying to restrict the buildup of relationships while maximizing genetic improvement.

It is generally accepted that a 1% rate of change in inbreeding (ΔF) is a safe target for most livestock populations, i.e., an effective population size of 50 (i.e., $N_e = 1/(2*\Delta F) = 1/0.02 = 50$; Falconer and Mackay, 1996). It may be argued that for multiparous species and under a riskier or short-term policy a level of 2% might be acceptable (N_e=25). The “comfort zone” between 1% and 2% rate of inbreeding is highlighted in the figure by two vertical reference lines.

Number of sows was chosen so that it doubles every time a new population size is considered. Thus, in Figure 1 when moving from one trend line to the next the costs associated either doubles (when going to the left) or halves (when going to the right). The same magnitude of change is not observed in the associated genetic gain, especially as we consider the area in the top half of the figure with the higher rates of improvement.

Figure 1 shows that little or no response will be generated by applying less restriction on inbreeding using lower target degrees in the sire line scenario. Trend lines in this figure reach an asymptote at around 30 target degrees.

Results show that Mate Selection can find solutions within the “comfort zone” of 1 to 2% inbreeding rate for all population sizes included in the study, with the exception of the smallest population (25 females).

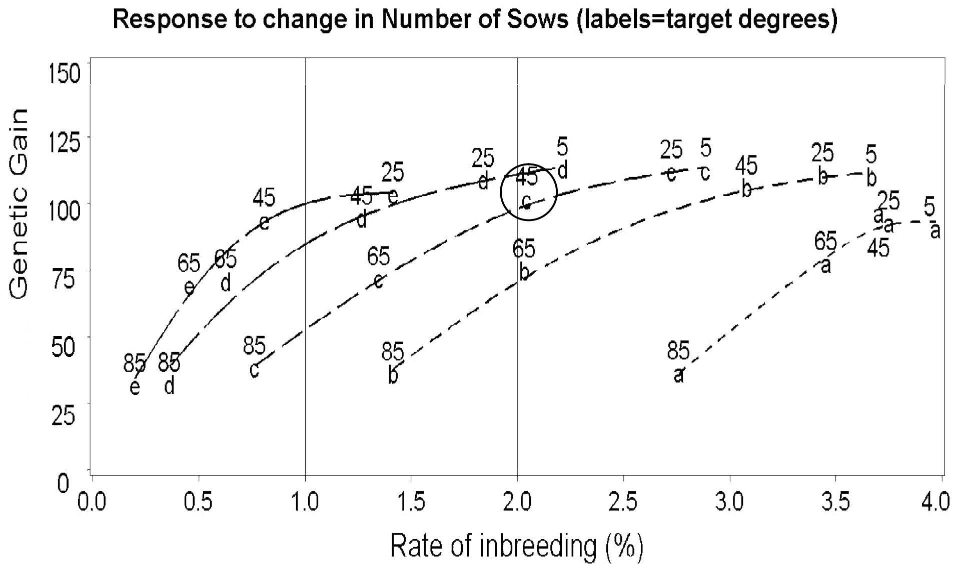

Figure 1: Genetic gain and rate of inbreeding after 15 years of simulated Mate Selection in a sire line. Selection index h^2=0.35, full economic weight on production traits, number of sows: a=25, b=50, c=100, d=200, e=400, buildup of relationships restricted via target degrees: 5, 25, 45, 65 and 85 (out of 90).

Conclusions

Mate Selection is an extremely efficient and flexible tool for managing inbreeding rate while maximizing genetic gain in any size of breeding population.

At a given rate of inbreeding for a given breeding scenario, fine-tuned Mate Selection allows for significant genetic gain to be obtained by increasing population size. However, in practice this must be carefully balanced against associated changes in resource allocation.

In animal genetic resource management, Mate Selection could be used very effectively to minimize rate of inbreeding in conservation programs of critical and endangered breeds.

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