Optimizing genetic management within populations with a simulation tool

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ABSTRACT: The optimal contribution method is available to control relatedness within populations, but is less suitable for breeds with little opportunity for central control of breeding decisions. The effectiveness of simpler methods is often unclear. With a newly developed computer simulation program, the effectiveness of methods can be determined for any kind of population. For a pig breed, using an AI-boar on the small Dutch population was simulated. Use of a German boar could help to decrease inbreeding rates. The most effective sire restriction was investigated in a dog population. Surprisingly, restricting matings per life was less effective than per year. Overall managing of population kinship was most effective to reduce inbreeding rates. Simulation can be effective in demonstrating principles and can be used as an educational tool. Genetic management needs to be tailored for specific populations taking both the technical effectiveness and its applicability into account.
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Introduction

Many breeds have low effective population sizes. Genetic management is required to prevent excessive inbreeding rates and associated loss of genetic diversity. To achieve this sophisticated methods, such as optimal contributions (Meuwissen (1997)), are available. However, these methods require full control over all matings in the population plus a reliable pedigree. In practice these methods are seldom applied to local breeds, and breed societies resort to simpler methods such as breeding circles (Windig and Kaal (2008)) or restricting the use of sires (Leroy (2011)). The effectiveness of these methods can be unclear, nor is it known how to best implement them.

Average inbreeding rates can be calculated for simple breeding schemes (e.g. Falconer (1989)). However, in practice situations are often more complicated with overlapping generations, preferential use of relatives of certain sires and subpopulations within breeds. We developed a computer simulation program to accommodate for such complexities so that the effectiveness of different kinds of genetic management can be evaluated in different breeds and species. Simulation has the added advantage that both the average and the variance of inbreeding rates under different management can be estimated.

Methods

Simulation program. The program consists of five steps (Figure 1): 1) Setup of the breeding population, 2) generation of progeny, 3) evaluation of inbreeding of progeny, and age and number of animals alive, 4) culling of old animals and 5) selection of new breeding animals from the progeny of that year. The last four steps are repeated for each year simulated. The user provides input for the simulations such as the number of breeding animals, the number of years and replicates to be simulated, and the measures in operation to restrict inbreeding rates. The program keeps track of each animal, its inbreeding coefficient (0.5 * relatedness of the parents) and its relatedness with all other animals alive. At the start of the program all animals are assumed unrelated and non-inbred. Inbreeding rates between year x1 and x2 of the simulation are determined by $\Delta F=L(1-[(1-F_{x2})/(1-F_{x1})]^{1/x2-x1})$ where F_x is the average inbreeding coefficient of animals born in year x, and L is the average age of parents in that period (= generation interval). This reduces to $\Delta F = L_x[1-(1-F_x)^{1/x}]$ for inbreeding rates since the start of the simulation.

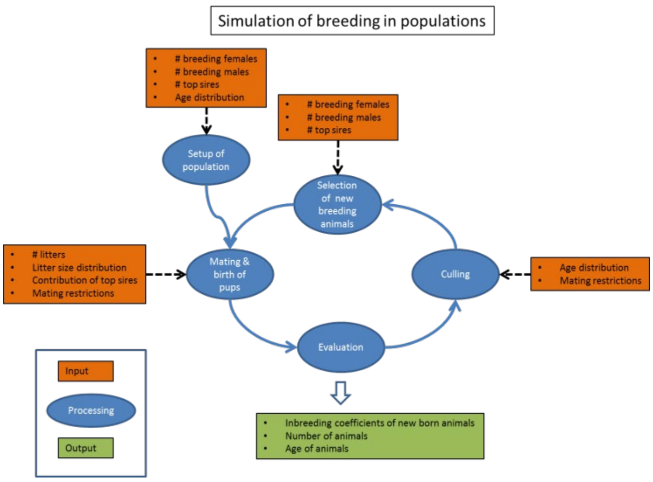

Figure 1. Set up of simulation program to simulate genetic management in populations.

In this paper we will give two examples where the simulation program was used to solve practical questions in genetic management, and then use the program to compare different types of genetic management for both breeds of the examples.

Use of AI boar in the pig breed "Bonte Bentheimer". The Bonte Bentheimer (Sundag et al. (2006)) is a transboundary pig breed having a relatively small Dutch population. The Dutch registered population consists of about 12 breeding boars and 50 breeding sows that produce about 40 litters each year. To facilitate breeding a boar could be placed at an AI station, so that all Dutch breeders have access to semen of a superior boar. The disadvantage, however, is that use of a single boar on a large part of the population will cause high inbreeding rates.

To quantify the effect of using an AI-boar on the inbreeding rate we simulated 7 scenarios. The first scenario was the current situation with all twelve boars having the same chance to sire a litter. In the other 6 scenarios an AI-boar sired 50% of the litters each year. In four of these scenarios, the AI-boar was recruited from the Dutch population and used for 1, 2, 3 or 4 years. In the last 2 scenarios the AI-boar was recruited from the large German population and used for either 2 or 4 years.

Sire restrictions in the Golden retriever. Small effective population sizes, high inbreeding rates and associated genetic defects are a common phenomenon in pedigreed dog breeds (Calboli et al. (2008)) A common cause is the use of popular dogs (show champions for example) to sire a large part of the population. One category of measures to enlarge the effective population size is to restrict the use of sires. Such measures can, however, result in substantial loss of income for the breeders of those dogs and often face strong opposition of individual breeders. Therefore, the effectiveness of sire restrictions should be determined and compared, before breeding societies implement the restrictions so that they may convince their members to adopt these.

The Dutch Golden Retriever population consists of about 150 breeding males and 600 breeding females that produce around 300 litters with in total 1800 pups each year. The 5 most popular dogs sire around 25% (75 litters) each year. Such a population was simulated in the computer, where each year the first 75 litters were assigned at random to the 5 ‘top dogs’, and the remaining 225 litters assigned at random to the other 145 dogs. Sire restrictions from 2 to 20 litters per dog were simulated either per year or per life. As soon as a dog had sired the maximum number of litters allowed, it was removed from the breeding pool that year, or from the population altogether in the case of a restriction per life.

Comparing different types of genetic management. There are basically two types of genetic management. The first category is to put restrictions on individual animals such as a restriction on the number of litters per sire, or the number of offspring that may be used for breeding. The second category is to control inbreeding or relatedness itself. In practice, a common measure is to mate each dam to the sire in the population that is least related (minimum coancestry mating). Another example is to exclude animals from breeding that have a higher than average relatedness to the rest of the population (restricting population relatedness). For the two populations described above we compared sire restriction, minimum coancestry mating and restricting population relatedness.

Table 1. Expected inbreeding rate in the “Bonte Bentheimer” pig breed, with or without use of an AI boar. Results of 20 computer runs, simulating 20 years.

Use of boars	Inbreeding rate / generation		
	Mean	minimum	maximum
Natural boar			
Evenly used	1.9%	1.7%	2.0%
AI boar from Dutch population siring 50% of the litters			
1 year	2.3%	1.9%	2.9%
2 years	3.0%	2.8%	3.3%
3 years	3.9%	2.9%	5.4%
No restrictions	5.1%	3.9%	5.8%
Unrelated AI boar from German population			
2 years	0.5%	0.3%	0.7%
4 years	1.0%	0.5%	1.3%

Table 2. Effect of restricting use of sires in the Golden Retriever on inbreeding rates and age of breeding animals. Results of 20 computer runs, simulating 20 years.

Max # litter/sire/year	No[1]	20	10	4	2
ΔF mean	0.41%	0.43%	0.27%	0.18%	0.16%
ΔF min	0.34%	0.31%	0.22%	0.16%	0.12%
ΔF max	0.56%	0.68%	0.33%	0.24%	0.27%
Gen. int.[2]	3.6	3.6	3.8	3.7	3.8

Max # litter/sire/life	No	20	10	5	2
ΔF mean	0.41%	0.49%	0.42%	0.26%	0.13%
ΔF min	0.34%	0.38%	0.39%	0.24%	0.11%
ΔF max	0.56%	0.63%	0.51%	0.30%	0.17%
Gen. int.[2]	3.6	3.5	3.5	2.6	2.4

[1]Without restrictions the 5 most popular sires produce on average 15 litters per year

[2]Generation interval calculated as average age of parents

Results

Use of AI boar in the pig breed "Bonte Bentheimer". The simulations indicated a high inbreeding rate in the current population of 1.9% per generation (Table 1). Use of an AI boar recruited from the Dutch population increased the inbreeding rates up to 5.1% when used for its whole life span. Importing the AI-boar from the large German population, decreased the inbreeding rates. Consequently the breeding organisation was advised to use an AI-boar only when relatively unrelated animals are available and preferably replace the AI boar every two years.

Sire restrictions in the Golden retriever. Restricting the use of sires decreased the inbreeding rates if the restriction was to a maximum of 10 litters or less per year, or 5 litters or less per life (Table 3).

Restrictions on litters per life had as a side effect that the generation interval decreased. Since the inbreeding level and average relationship increases with each generation, decreasing the generation interval leads to higher inbreeding rates. This explains why sire restrictions per life are less effective than sire restrictions per year, and why moderate restrictions per life increase the inbreeding rates instead of decreasing them.

Table 3. Inbreeding rates per generation (average and min. – max.) compared for several methods in two generations.

Genetic management	Bunte Bentheimer	Golden Retriever
None	2.51%	0.41%
	2.01%-3.05%	0.34%-0.56%
Sire restriction		
4 per year	1.89%	0.18%
	1.54%-2.47%	0.16%-0.24%
Minimising coancestry mating		
Year 0-20	1.53%	0.04%
	1.25%-1.81%	0.02%-0.05%
Year 20-70	2.21%	0.39%
	2.16%-2.39%	0.37%-0.42%
Restricting population relatedness		
Year 0-20	1.26%	0.12%
	0.97%-1.58%	0.09%-0.15%
Year 20-70	1.46%	0.14%
	1.44-1.45%	0.12%-0.17%

Comparing different types of genetic management. Results are similar for the two populations. Sire restriction is more effective in the Golden Retriever than in the Bunte Bentheimer population, but in both breeds less effective than restricting population relatedness. In the short run minimising coancestry mating is most effective, but in the long run restricting population relatedness is more effective.

Discussion

Genetic management of populations can be complex. Theoretically, the most optimal solution can be found, but in practice simpler methods may be needed. We have shown here that simulations can be used to determine the best way to apply such measures. For the sire restriction it was somewhat surprising that restrictions per life were less effective than the less severe restrictions per year, since we had not realized that the generation interval may change if sires are excluded from breeding. In practice, the effect may be less clear if breeders decide to wait longer before using the last allowed mating of a sire, but nevertheless breeding organisations should be aware that sire restrictions per life may decrease generation intervals.

Simulations can also serve as an educational tool. The effect that managing relatedness at the population level is in the long run more effective than managing single matings is, for example, well known theoretically (Falconer (1989); Montgomery et al. (1997)), and nicely illustrated here (Table 3). Another example is that minimising coancestry has as the main effect that the variance of inbreeding rates decreases (Falconer (1989)), as can be seen from the smaller range of inbreeding rates between simulations (Table 3).

Genetic management should be tailored to the animal population at hand. As a consequence, it is not always possible to use the theoretically best method. Which methods can be realised in practice should be determined in close collaboration with the breeders themselves. Simulations can help to decide which methods are suitable and how they can be applied. The software used here also provides possibilities to simulate sub-populations with limited exchange of individuals between them, and to simulate selection against genetic defects. The software is available on request to the first author.

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