

Accommodating recent contributions under optimal contribution selection

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Summary

Optimal Contributions Selection (OCS) aims to balance genetic gain and genetic diversity when making decisions on the number of matings to allocate to each selection candidate. However, we should also accommodate recent contributions from matings that have produced embryos and juveniles that are too young to be candidates. For example, this will inhibit further use of a sire (and his close relatives) that has recently been widely used. The current paper shows that this is of major importance in species where there are frequent mating rounds throughout the year (e.g. pigs, poultry, dairy) or within a mating season (e.g. salmon, prawns). In these cases there are relatively few matings at each round, with many recent contributions from previous mating rounds. In a simulated pig population, this approach increased genetic gain by 19% while decreasing inbreeding rate by 28%, compared to OCS on prevailing candidates alone.

Keywords: optimal contributions, mate selection, genetic diversity

Introduction

In some species, selection and mating decisions take place on a frequent basis, with a relatively small number of matings being made every few days or weeks throughout the year (typical in pigs and poultry), or even every day throughout a breeding season (typical in salmon and prawns). This contrasts with beef and sheep populations, where the main selection and mating decisions are usually made once per year.

Species with frequent mating sessions are characterised by few matings to be made from a relatively small pool of candidates. This has some impact on progressive breeding programs that use Optimal Contribution Selection (OCS), or Mate Selection that incorporates OCS, described here for the example of a pig population with weekly mating rounds:

Few matings are to be made on each occasion and, yet, there are typically up to 26 weeks of previous mating rounds that constitute a backlog of genetic contributions to the population. These contributions are represented by embryos and juveniles that are not included in the list of candidates that are available for the current mating round. The Mate Selection method used in this paper (Kinghorn, 2011, as implemented in Kinghorn and Kinghorn, 2017) manages these prior contributions through “Committed Matings”, whereby the matings that created these embryos and juveniles are forced to be included in the solution for a mate selection analysis, along with the new matings to be made in the current round.

Method

A pig breeding population was propagated using the simulation program Popsim. Breeding decisions at each cycle were made by the program Matesel (Kinghorn and Kinghorn, 2017). This co-implementation of Popsim and Matesel has recently been used by

Cowling et al. (2017, 2018).

Key population parameters are: Selected boars and sows both produce their first piglets at 52 weeks of age, boars (sows) that do not die and are not culled for merit leave their last piglets at 104 weeks (208 weeks). Mature boars and sows compete with younger stock to remain in the breeding program. Each mating produced a total of 5 progeny to the stage of first selection, with a 50% random allocation of gender. Mortality rate for mature boars (sows) was 0.3% (0.2%) per week. For each treatment, the foundation population was created equally and then bred according to treatment policy for 208 weeks. The selection criterion for genetic gain was a multi-trait index, using traits and parameters typical of pig populations. Fifty replicates were run for each treatment.

The key treatments were Committed Matings (CM) and Control (CT). CM is a method of handling the issue of contributions from juveniles and embryos that are not represented in the current candidates (Kinghorn, 2017). Rather than adding these animals to the list of candidates, the matings that gave rise to them were added to the list of matings to be made. This means that their parents are allocated the status of candidates in the datafile, whether or not they are candidates for the current mating round, and the matings that gave rise to them were made a fixed part of the solution as “Committed Matings”.

This has been implemented in Matesel. In addition to the main data file, the user supplies a list of “Committed Matings” that must be included in the solution. The user can choose to include these previous matings in the declared constraints on usage of candidates at the current mating round – otherwise the program makes appropriate adjustments such that only current constraints need to be declared. These settings and the launching of Matesel are handled at each mating round by the population simulation program Popsim.

The Control treatments did not implement CM and considered only the candidates available at each mating round. For both CM and CT treatments, the policy on balance between genetic gain and genetic diversity was set using Target Degrees, as described in Kinghorn and Kinghorn (2017), where 0 degrees represents full emphasis on genetic gain, and 90 degrees represents full emphasis on genetic diversity. Target Degrees are appended to the treatment name, and the four treatments applied were CT25, CT50, CM15 and CM25.

Results

Figure 1 shows genetic response across traits over time, represented as average true breeding value for the breeding objective. Figure 2 shows mean parental coancestry over time.

There is a distinctive “step-up” pattern, seen particularly for parental coancestry in CT25. This is because the foundation population was generated under no selection, such that 52 weekly cohorts of animals had similar genetic values and identical values for parental coancestry. This is followed by 52 cohorts each having the benefit of one round of selection, etc.

It can be seen from figure 2 that, compared to CT, use of CM has an immediate apparent impact to reduce parental coancestry at the start of the program, following establishment of the foundation population (CM25 vs CT25, week 260). However, this is to be expected, as the Control treatments involved fewer candidates and hence a lower apparent effective population size. The CM results are more correct, as they include essentially a full generation of individuals, from embryo to older parents, whereas the Control treatments exclude consideration of embryos and juveniles that are already generated.

Figure 1. Average true breeding values for the selection objective over 4 years. CT=Control; CM=Committed Matings; 15,25,50=Target Degrees.

Figure 2. Mean parental coancestry over 4 years. CT=Control, CM=Committed Matings, 15,25,50=Target Degrees.

However, what is more important, both here and in real breeding programs, is the *rate of increase* in coancestry (ΔCoan). In particular, CT25 increased at over 4 times the rate for CM25, showing the impact of accommodating the prior contributions involved, under CM25. CT50 was chosen as a treatment as its ΔCoan was only about 28% higher than CM25. And yet CM25 gave about 19% faster rate of genetic gain than CT50 over the period simulated. In addition, ΔCoan for CM15 was less than half that of CT25, but it lagged only by about 5% in short term genetic gain.

Discussion

These simulations reflect only four years of breeding, which is too little to illustrate the longer term benefits in genetic gain to be made from a good approach to conserving diversity. In the longer term, CM15 is likely to overtake CT25 in terms of genetic gain alone. Even if this were not demonstrated, the fast rate of increase in parental coancestry under CT25 would inhibit most breeders from using this policy.

This is the first example known to the author of simulation of a pig population with matings generated at frequent intervals – one week in this case. Such a realistic structure is probably required in order to illustrate the importance and benefit of accommodating contributions that have been made in the past. This is because there are many otherwise unaccommodated contributions “in the pipeline” compared to the number of contributions to be made at the current mating.

In the simulations of beef cattle made by Kinghorn (2017) there are relatively few of these unaccommodated recent contributions, and the benefit of accommodating them through “Committed Matings” was only moderate. Moreover, they could be compensated for by adopting a more conservative approach under optimal contributions selection among current candidates alone. However, with ongoing mating sessions, as in the current simulations, the impact of accommodating recent contributions is considerable.

List of References

- Cowling, W.A., L. Li, K.H.M. Siddique, M. Henryon, P. Berg, R.G. Banks and B.P. Kinghorn, 2017. Evolving gene banks: improving diverse populations of crop and exotic germplasm with optimal contribution selection. *Journal of Experimental Botany* 68, 1927–1939.
- Cowling W.A., L. Li, K. H. M. Siddique, R. G. Banks, and B. P. Kinghorn, 2018. Crop improvement for food security during global warming. Submitted.
- Kinghorn, B.P. 1992. GENUP - a suite of programs to help teach animal breeding theory. *Australian Association of Animal Breeding and Genetics*, 10: 555-559.
- Kinghorn, B.P., 2011. An algorithm for efficient constrained mate selection. *Genetics Selection Evolution*. 43:4. <http://www.gsejournal.org/content/43/1/4>

Kinghorn, B.P., 2017. Committed matings under mate selection. Proc. Assoc. Advmt. Anim. Breeb. Genet., 22: Paper 63.

Kinghorn, B. P. & A.J. Kinghorn, 2017. Instructions for Matesel. <http://matesel.une.edu.au>, accessed 26 September 2017.