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COMMITTED MATINGS UNDER MATE SELECTION

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SUMMARY

As part of implementing a breeding program we aim to manage the numbers of parents selected, and the relationships between them, in order to manage genetic diversity. However, this ignores the fact that some breeding candidates may recently have been widely used, leaving embryos and juveniles in the system that are not yet in the list of candidates, but which are likely to make future breeding contributions. Use of such candidates should be inhibited somewhat to avoid their over-representation in the program as a whole, leading to increased loss of diversity.

A method to account for these prior contributions when implementing the breeding program is introduced, and indeed this makes notable impact to reduce loss of genetic diversity. This is a more correct way to implement the breeding program, however the alternative of using parameters that drive the program in a more conservative (high diversity) direction had similar impact both on the rate of increase in inbreeding coefficient and on genetic response.

Whatever method is used, it is advisable to test policy and parameters using simulation, to more confidently target an appropriate rate of increase in coancestry and inbreeding, in competition with genetic gains and other issues.

INTRODUCTION

Truncation selection on estimated breeding value is predicted to maximise genetic merit in the offspring generation. However, this is generally not the best strategy for maximising genetic gain in the longer term, as lack of attention to genetic diversity will generally lead to reduced opportunity for genetic gains in later generations.

Optimal Contributions Selection (OCS) provides a solution to this (eg. Meuwissen, 1997). We aim to optimise the contribution of each individual to the breeding population, giving rewards not only for high genetic merit, but also for low relationship to the rest of the individuals selected.

For this, we need to consider the relationship between each selection candidate and all other selection candidates of both sexes, in a numerator relationship matrix among candidates (A) or a genomic equivalent, or a hybrid of these. From the selection decisions made we can calculate x, the vector of relative genetic contributions from each candidate, summing to ½ for each sex. The mean parental coancestry is $x'Ax/2$, and this is the measure of the mean relationship that we aim to keep low in order to keep genetic diversity high. For this we want many small contributions in x. However, for high genetic gain ($x'G$, where G is the vector of EBVs or index values) we want to focus genetic contributions on the most meritorious animals, giving relatively few large contributions in x. Overall, we aim to find the vector x that maximises $x'G + \lambda.x'Ax/2$, where λ is a negative weighting that determines the relative emphasis on genetic diversity. Here we focus on mean parental coancestry, $x'Ax/2$.

In scenarios where individuals can only be used as a parent at one mating round, we do not need to consider relationship with ancestors in the pedigree, because the prior contributions of these ancestors are accounted for in the pedigree of the current candidates. In all other scenarios, any prior contributions in previous matings are accommodated if the progeny resulting from these matings are either permanently culled or included in x and A as current candidates. However, if these progeny are not culled and are too young to be candidates – they are juveniles, or even embryos – then their potential future contributions need to be accommodated in some way.

For example, if a bull that is a current candidate has recently been widely used, and has a large number of juvenile and/or embryo progeny in the population, then there should be some inhibition on his further widespread use, and yet these progeny have no impact in $x'Ax/2$ as they are not represented in either x or A. The same argument can be made eg. for a first-use bull whose brother or other relative has juveniles or embryos in the herd.

This issue has been handled in the past by adding these juveniles and embryos in the list of candidates, but restricting their matings to other juveniles and embryos in "virtual matings" that are not of course invoked (Kinghorn et al, 2008). This means that these animals and their relationships with real candidates are accommodated in calculation of parental coancestry. However, somewhat arbitrary decisions have to be made about factors such as the maximum numbers of matings to be allocated to them, and even how many embryos to generate for each pregnant female.

An exception here may be when genomic and/or other information on juveniles is available, whereby these can be included as candidates in the main data file, with juvenile male x juvenile female Grouping set up such that juvenile mating results can be used for selection purposes, but without actual mating, as they are not sexually mature. In this case, Committed Matings for adult selection candidates need only cover matings that have not yet resulted in birth of progeny entered in the main data file as juvenile candidates.

MATERIALS AND METHODS

This paper presents a more appropriate method of handling this issue of contributions from juveniles and embryos that are not represented in the current candidates. Rather than add these animals to the list of candidates, the matings that gave rise to them are 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 are made a fixed part of the solution as "Committed Matings".

This has been implemented in the program Matesel, with detailed instructions at http://matesel.une.edu.au. 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 so that only current constraints need to be declared.

To test this method, Matesel was used to make all selection decisions in a 20-year breeding program simulated using the program PopSim, developed from the version available within Genup (http://bkinghor.une.edu.au/genup.htm). PopSim has recently been used in a similar manner by Cowling et al (2016), who give some detailed description.

A breeding population typical of *Bos Indicus* cattle was simulated, the key features being 100 females mated each year, bulls and cows first mated to drop progeny at 3 years of age, culling for age at 6 and 10 years for bulls and cows, mating group sizes constrained between 20 and 40 females, random mate allocation, and BLUP EBVs leading to a multi-trait index. Bulls and cows can be culled by Matesel at intermediate ages for reasons related to genetic merit and impact on diversity.

In the **Control** treatments, no account was taken of the matings made by candidates in previous years, whereas in the **CM** (Committed Matings) treatments, previous matings that had not yet resulted in progeny of breeding age were accommodated as described above.

The Target Degree mode of balancing genetic gain and genetic diversity was used in Matesel, with 0 degrees relating to full emphasis on genetic gain and 90 degrees relating to full emphasis on genetic diversity. Treatment Control25 used 25 target degrees for a moderate outcome, and Control32.5 used 32.5 degrees for a more conservative outcome (more diversity at the cost of lower short-term genetic gain). Treatments CM25 and CM17.5 used the Committed Matings approach with lower target degrees, for reasons that become apparent.

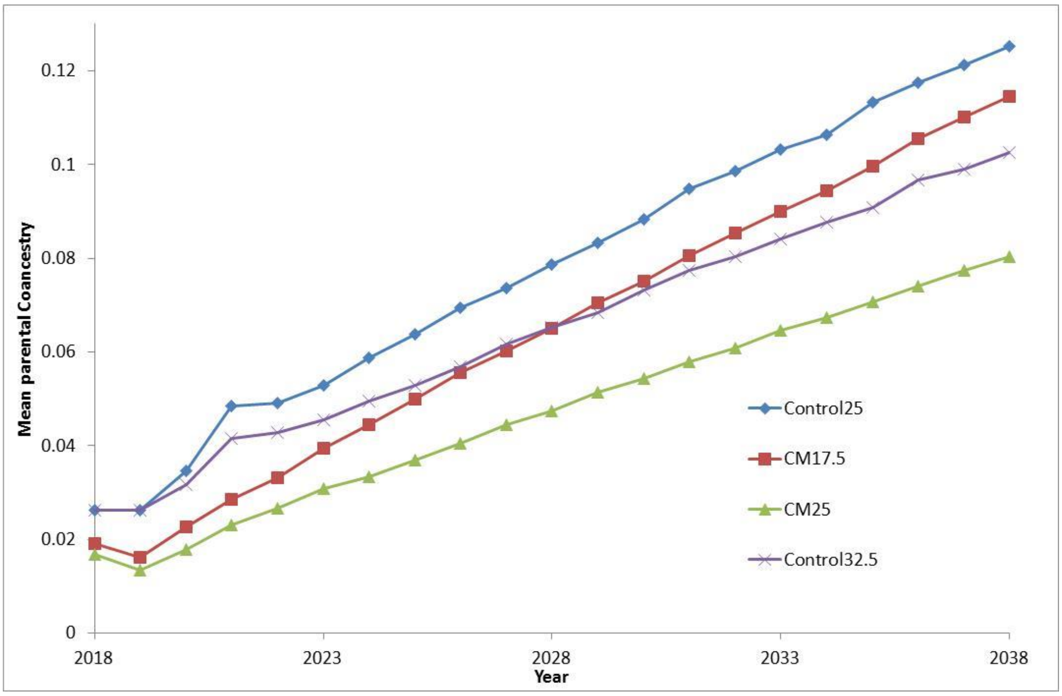

Figure 1. Mean parental coancestry by year over the four treatments

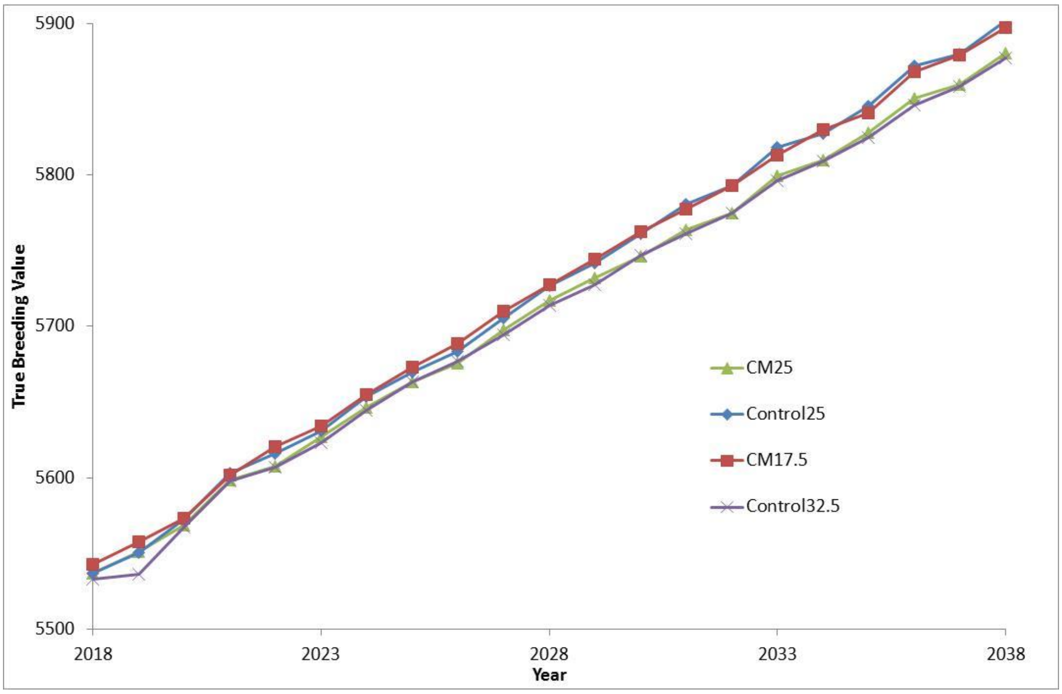

Figure 2. Progeny mean true breeding value for the objective in dollars by year for the four treatments.

RESULTS AND DISCUSSION

Figure 1 shows mean parental coancestry and figure 2 shows true breeding value in progeny for the breeding objective, over the 20 years of breeding. All results are averages over 50 replicates.

Notice that the Control programs immediately show a higher level of coancestry at the start of the programs. This is to be expected, as these treatments involve 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.

However, what is more important, both here and in real breeding programs, is the *rate of change* in coancestry. In particular, CM25 increases nearly 30% more slowly than Control25, showing the impact of accommodating the prior contributions involved.

Figure 1 shows that this slower rate of increase in coancestry in CM25 is approximately matched by a more conservation control policy of 32.5 Target Degrees. Moreover, the faster rate of increase in coancestry for Control25 is approximately matched by a more aggressive CM policy of 17.5 Target Degrees.

Figure 2 shows that the genetic responses are higher and approximately equal for the treatments with higher rates of increase in coancestry (Control25 and CM17.5), and likewise, responses are lower and approximately equal for the treatments with lower rates of increase in coancestry (Control32.5 and CM25). In the longer term we can expect genetic progress in the more conservative programs to benefit from increased conservation of genetic diversity.

A simple conclusion is that, despite the use of the Committed Matings method being the correct thing to do, it is possible to not do this, but to compensate by adopting an appropriately more conservative policy, with a higher value for Target Degrees (or constraint to a lower mean parental coancestry if using that approach to manage coancestry). This is perhaps understandable, as a more conservative policy operates not only on current matings, but also on all previous matings, and it seems that the impact on overall optimal contributions is appropriately balanced.

What is "an appropriately more conservative policy"? The actual level of coancestry is probably not so important – this depends critically on the amount and quality of pedigree and/or genomic information available, as well as on prior breeding policies. We should ***predict*** the rate of change in coancestry over time, and yet this is very difficult to do for a real (multi-faceted) breeding program. However, we can ***discover*** the rate of change in coancestry using simulation, as in this paper.

The recommendation here is to discover what the rate of change in coancestry is as a function of parameters/policy chosen, and to choose parameters accordingly. Under random mating, the rate of change in inbreeding coefficient is expected to be equal to the rate of change in coancestry, so choose a rate of change that fits your attitude to ΔF, in competition with genetic gain and other issues.

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