

# Mate Selection

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## Introduction

Selection leads to genetic improvement but also reduces genetic variation in the progeny. When all animals in a population are closely related there is little genetic variation and little scope for further genetic progress. Mate selection procedures are used to help maintain genetic variation, and hence genetic progress, in the future and to avoid the fitness problems related to severe inbreeding.

Animals that are closely related to one another have more genes in common than unrelated animals. Therefore, the close relatives of an animal of high genetic merit are also expected to be of high genetic merit. It follows that selection on estimated breeding value (EBV) tends to result in the selection of related animals, thereby increasing the level of inbreeding in the population. This is true whether your estimate of the genetic merit is a visual appraisal of the animal or the result of a best linear unbiased prediction (BLUP) technique. However, because animal model BLUP gives the most accurate estimates of EBVs, making use of information on all known relatives, selection solely on BLUP EBVs will generate inbreeding faster than less efficient selection methods, while also providing more rapid genetic gain. This tendency is increased when selection is for a trait with low heritability, eg number born alive, where information on family members is relatively more important compared to information on the individual and consequently more members of the same family are selected.

As BLUP has become the dominant method of producing EBVs, interest in mate selection techniques has increased. Mate selection attempts to find a balance between the rate of genetic progress and the degree of relationship among animals in the population, and hence the genetic variation available in later generations.

Mate selection consists of two processes; selection of animals to act as parents and allocation of matings. This is particularly true in the pig industry, where the two steps are carried out at different times, with pigs usually needing time to reach maturity after they have been selected as potential parents but before they can join the breeding herd. Typically, most research has focussed on what might be termed “true mate selection”, in which parents are selected and allocated in a single step.

Various strategies have been proposed for selecting parents and allocating matings, these include strict breeding designs and selection on intentionally biased EBVs (eg Grundy *et al*, 1994). Of most interest to us are the dynamic mate selection procedures (eg Meuwissen, 1997, Kinghorn *et al*, 1999), which include the existing PIGBLUP mate selection procedure.

## Dynamic mate selection procedures

Dynamic mate selection procedures use information on the genetic merit (EBVs) and relationships (eg inbreeding levels) of animals in the population. By solving the selection and mate allocation problems for the specific set of candidate animals, they permit flexibility and adaptability in the breeding program while simultaneously maintaining genetic progress and variation. Dynamic mate selection procedures use a function to assess the overall merit of a mating combination or group of selection candidates. Once a merit function has been chosen, different combinations of mates of selection candidates can be compared in order to find the best mating combination or group of animals to become parents.

The function currently used in PIGBLUP to evaluate mating combinations involves the total genetic merit and inbreeding of the offspring of the matings to be tested. At the time of development this was the state of the art, but not any longer.

Meuwissen (1997) proposed a function that included the genetic merit of offspring and took account of all relationships among the candidate parents. Use of this function has better short and long-term properties than the function used in PIGBLUP – it retains genetic variance better, and has a lower long-term rate of inbreeding.

The function used to assess the merit of mating combinations can contain any relevant information. For example, the variance of offspring breeding values could be included as a way of helping to maintain genetic variation.

## Mate selection as currently implemented in PIGBLUP

Mate selection was introduced into PIGBLUP in version 2 (Long *et al*, 1992). The procedure that is carried out would be more accurately termed mate allocation. The user provides lists of sows requiring a mate and currently active boars and the program suggests the best mate for each sow.

The merit of any given mating is defined as the EBV of the offspring minus the inbreeding of the offspring multiplied by a user-defined weighting factor. The weights applied to inbreeding relate to the “level of inbreeding concern” provided by the user to PIGBLUP. These levels are “No Worries”, “A Little”, “Medium”, “Very Worried” and “Absolutely Concerned” which equate to weights of 0, 0.5, 2, 10 and 25 times the standard deviation of the index EBVs, respectively.

The mate selection module currently in use in PIGBLUP has a number of drawbacks:

- It does not allow you to take account of all relationships when selecting animals.
- Only the currently available prospective parents are considered.
- The alternate boars provided are often the same for most, if not all of the sows to be mated. This results from there being too few limitations on boar usage.

- A lot of user effort is required to identify boars and sows for consideration. This is time-consuming and tedious, making the module unattractive particularly to clients with large herds. *Note: this problem is addressed in version 5.0 of PIGBLUP.*

## **Developments in the new PIGBLUP mate selection module**

### **Separate selection and mate allocation**

Two types of run will be available within the module:

1. Selection of animals after they have finished test to become parents, taking account of the relationships among the selection candidates and with all other animals in the population. If relationships are ignored during the selection of animals to become parents, the use of mate allocation later on is of little value since the pool of available genes has already been reduced.
2. Mate allocation (although some opportunity for selection/culling still exists at this stage too). This will also take account of relationships among the potential mates and of these animals with all other members of the population. Research is on going into other factors for inclusion in the merit function.

### **Improved merit functions**

The merit functions used in the new PIGBLUP model will include information on relationships with all animals in the population. On going research is investigating other elements for possible inclusion.

### **Increased automation**

This will be primarily achieved through obtaining additional data in a revised format PIGBLUP file. This will allow the program to determine more accurately which animals are due for consideration in the current run. The final format has not been determined, but will be circulated to PIGBLUP users and herd-management software developers soon. The information that will be requested relates to identifying the current status of an animal (eg pregnant, on test).

## **An example**

We will consider a simple mate allocation problem in order to illustrate some of the principles involved and to highlight the benefits of the development work. Although mate allocation is considered here, the selection procedure is very similar in structure.

The problem under consideration is to allocate mates for two sows from a pool of three available boars. In Table 1, you see the relationships among these five animals and their EBVs. To interpret the values in the relationship matrix in Table 1, the relationship between any two different animals is the proportion of genes that they are expected to have in common. In our example none of the five animals are inbred, that is none of the parents of these animals were related to one another. If they were then the diagonal elements would be  $1+F$ , where  $F$  is the inbreeding coefficient of the animal, rather than 1.

**Table 1** Relationships among candidates and estimated breeding values.

		Relationships				EBV	
		Boar			Sow		
		A	B	C	1		2
Boar	A	1.0	0.5	0.0625	0.0625	0.25	11
	B	0.5	1.0	0.0625	0.0625	0.25	10
	C	0.0625	0.0625	1.0	0.5	0.0625	8
Sow	1	0.0625	0.0625	0.5	1.0	0.0625	8
	2	0.25	0.25	0.0625	0.0625	1.0	9

### The present PIGBLUP mate selection tool

As previously mentioned, mate selection in PIGBLUP considers the genetic merit (EBVs) and the inbreeding of the offspring that would be generated. The EBVs for offspring are equal to half the sum of the EBVs of the sire and dam, while the inbreeding coefficient of the offspring is half the relationship between the two parents. Table 2 contains these values for the six possible matings. To keep the example simple, we assume that both sows are to be mated and that there is no limitation on the use of boars. There are therefore nine possible outcomes of the mate allocation procedure ([boar A × sow 1 and boar A × sow 2], [A×1 and B×2], [A×1 and C×2], [B×1 and A×2], [B×1 and B×2], [B×1 and C×2], [C×1 and A×2], [C×1 and B×2], and finally [C×1 and C×2]). Table 3 contains the value of the sum of the mating merit function for each possible outcome and each level of inbreeding concern, assuming a standard deviation of 10 for the EBVs. For each level of concern about inbreeding, shading of cells Table 3 highlights the best mating combination.

**Table 2** Inbreeding coefficients (F) and estimated breeding values of offspring from all possible matings

		Sow			
		1		2	
		F	EBV	F	EBV
Boar	A	0.03125	9.5	0.125	10
	B	0.03125	9	0.125	9.5
	C	0.25	8	0.03125	8.5

When there is no concern about inbreeding, Table 3 shows that the best strategy is to mate boar A to both sows (function value is 19.5), this is still the best strategy at a low level of concern (value is 18.7 = total genetic merit of the offspring – inbreeding concern weight × combined inbreeding coefficient of the offspring = 9.5+10-5×(0.03125+0.125)). At medium and higher levels of inbreeding concern the preferred mating combination is boar A with sow 1 and boar C with sow 2. The combined genetic merit of the offspring of mating boar 1 with both sows is 19.5, while that of from the mating of boar A with sow 1 and boar C with sow 2 is 18. However, the combined inbreeding from these same two mating combinations are 0.28 and 0.094, respectively. We can see that in order to avoid inbreeding we would compromise on the genetic merit of the offspring (and hence genetic progress in subsequent generations).

**Table 3** Sum of PIGBLUP mating merit function values

Matings	Weight applied to inbreeding				
	0	5	20	100	250
A×1 and A×2	19.5	18.7	16.4	3.9	-19.6
A×1 and B×2	19.0	18.2	15.9	3.4	-20.1
A×1 and C×2	18.0	17.7	16.8	11.8	2.4
B×1 and A×2	19.0	18.2	15.9	3.4	-20.1
B×1 and B×2	18.5	17.7	15.4	2.9	-20.6
B×1 and C×2	17.5	17.2	16.3	11.3	1.9
C×1 and A×2	18.0	16.1	10.5	-19.5	-75.8
C×1 and B×2	17.5	15.6	10.0	-20.0	-76.3
C×1 and C×2	16.5	15.1	10.9	-11.6	-53.8

**Applying the methods of Meuwissen (1997)**

In Table 4 we present the results of applying the method of Meuwissen (1997) to the same mate allocation problem. Again, for each level of concern about inbreeding shading of cells in Table 4 highlights the mating combinations of highest merit. The function used to assess the merit of any mating combination is, in matrix notation,  $x'u - wx'Ax$ , where  $x$  contains the contribution of each mate to the next offspring,  $x'u$  is the total genetic merit of offspring,  $x'Ax$  is a summation of the relationship information and  $w$  is the weight applied to the relationship information based on the user's level of concern about inbreeding. We applied the same weights as currently specified in PIGBLUP, as in the first part of this example, but note that the weights are being given consideration during the development of the new mate selection module.

**Table 4** Merit of matings using the approach of Meuwissen (1997)

Matings	x'u	x'Ax	Weight applied to relationships				
			0	5	20	100	250
A×1 and A×2	19.5	1.8	19.5	10.3	-17.4	-164.9	-441.4
A×1 and B×2	19.0	1.6	19.0	11.0	-12.9	-140.4	-379.4
A×1 and C×2	18.0	1.5	18.0	10.5	-12.0	-132.0	-357.0
B×1 and A×2	19.0	1.6	19.0	11.0	-12.9	-140.4	-379.4
B×1 and B×2	18.5	1.8	18.5	9.3	-18.4	-165.9	-442.4
B×1 and C×2	17.5	1.5	17.5	10.0	-12.5	-132.5	-357.5
C×1 and A×2	18.0	1.5	18.0	10.5	-12.0	-132.0	-357.0
C×1 and B×2	17.5	1.5	17.5	10.0	-12.5	-132.5	-357.5
C×1 and C×2	16.5	2.1	16.5	6.0	-25.4	-192.9	-506.9

When there is no concern about inbreeding at all, the mate allocation is carried out on genetic merit alone, and boar A should be mated to both sows as before. However, at low levels of concern about inbreeding we now have two alternative matings of equal merit, boar A with sow 1 and boar B with sow 2 or boar A with sow 2 and boar B with sow 1.

*Why are these two combinations of equal merit?* Whichever way we combine boars A and B with sows 1 and 2, we are only rearranging the same genes and so the value of these matings must be equal. At higher levels of concern about inbreeding, there are

again two equal top-ranked mating combinations, boar A with sow 1 and boar C with sow 2 or boar A with sow 2 and boar C with sow 1.

*Why are these two matings now ranked above the mating of boar A to both sows?* Table 5 includes the total genetic merit of the offspring from the two mating combinations and only using boar A results in a higher total genetic merit, by 0.5 units. The calculation of  $x'Ax$  can be split up into the parts due to relationships between the two boars, between the two sows and between boars and sows. Table 4 contains the relationships between the five candidate animals, and the weights applied in the calculation of  $x'Ax$ . The weights given relate to the mating combinations where boar A is mated to both sows (light grey cells) and boar A is mated to sow 1 while boar B is mated to sow 2 (dark grey cells). The same sows are involved in both matings, so the contribution of their relationships with each other is the same in either combination. The two boars are full-sibs, so their relationships with the two females are the same, and the contribution of this part is therefore the same for each combination. Using the two full-sib boars, which have 50% of their genes in common, contributes 0.25 less to  $x'Ax$  than using the same boar for each mating ( $\frac{1}{4} + \frac{1}{4} \times \frac{1}{2} + \frac{1}{4} \times \frac{1}{2} + \frac{1}{4} = 0.75$ , rather than 1). When multiplied by the weighting applied to relationships this is sufficient to make the use of boars A and B better than using boar A alone.

**Table 5** Relationships among the potential mates, and weights applied to them in constructing  $x'Ax$  for two specific mating combinations (shaded boxes).

		Boar			Sow	
		A	B	C	1	2
Boar	A	1	$\frac{1}{2}$	$\frac{1}{16}$	$\frac{1}{16}$	$\frac{1}{4}$
	B	$\frac{1}{2}$	1	$\frac{1}{16}$	$\frac{1}{16}$	$\frac{1}{4}$
	C	$\frac{1}{16}$	$\frac{1}{16}$	1	$\frac{1}{2}$	$\frac{1}{16}$
Sow	1	$\frac{1}{16}$	$\frac{1}{16}$	$\frac{1}{2}$	1	$\frac{1}{16}$
	2	$\frac{1}{4}$	$\frac{1}{4}$	$\frac{1}{16}$	$\frac{1}{16}$	1

So, for our small example, when we have concern about levels of relatedness we get some combinations of equal merit. It is then a random choice as to which mating combination you would use. However, the function that we use to compare different mating combinations can contain anything that we want. For example, if we included a term specific to the inbreeding coefficients of offspring (ie the term used by the current PIGBLUP module) as well as the measure of relationships used by Meuwissen (1997), then the result in Table 4 would differ. The mating combination of boar A with sow 1 and boar C with sow 2 generates offspring with a combined inbreeding coefficient of 0.06, whereas offspring from the mating combination boar C with sow 1 and boar A with sow 2 have a combined inbreeding coefficient of 0.38, so these combinations would no longer be equivalent. We can also include information on the relationships of our candidate parents with other animals – not current candidates – in the population.

## Considering relationships with other groups of animals

The animals we are allocating to matings will be related to a greater or lesser degree with other groups of animals in the population. We can include this in the function to assess the merit of any particular mating combination. In this way, we can penalise matings that generate higher degrees of relationship in the population at large, as well as those that generate relationships within the specific group of offspring to be produced. We can take account of relationships with other groups of animals in the breeding herd (eg pregnant sows, nursing sows) and growing pigs that will potentially join the breeding herd (right through from foetuses to already-selected, maturing young boars and gilts). We can incorporate this relationship information into our mate allocation by using the following function to assess the merit of any mating combination:  $\mathbf{x}'\mathbf{u} - w\mathbf{x}'\mathbf{Ax} + \mathbf{x}'\sum_i g_i \mathbf{a}_i^*$ , where  $g_i$  is the weight applied to relationships with the  $i^{\text{th}}$  group of animals,  $\mathbf{a}_i^*$  is a vector containing the accumulated relationship of each animal with all animals in the  $i^{\text{th}}$  group and other symbols are as previously defined.

For our example, we will only consider relationships with offspring of candidate parents, and assume that they are all equally likely to reach the breeding herd (so that we can group them all together). We assume that boars A, B and C have sired 7, 5 and 3 litters, respectively, and that sows 1 and 2 are in fact gilts. Assuming that the litters are of equal size, that the boars were mated to an unrelated group of females to produce them and using a weighting ( $g$ ) equal to the weighting applied to the information on relationships among the candidate parents ( $w$ ) then we get the mate allocation results given in Table 6.

Table 6 gives values of  $\mathbf{x}'\mathbf{a}_i^*$  for each mating, the other components of the mating combination merit function are as presented in Table 4. As soon as there is any concern about the level of relationships, boar A is penalised for having more related animals in our population, leaving the two reciprocal combinations of boars B and C with sows 1 and 2 as the best alternatives. Again, if we included an additional term involving the inbreeding of offspring then the value of these two mating combinations would be different.

This part of the example illustrates how to include information on relationships with other animals in the population and also demonstrates how the system might be used to generate culling suggestions, or indeed to “auto-cull”, the active animals.

**Table 6** Merit of matings when including relationships with offspring

Matings	$\mathbf{x}'\mathbf{a}_i^*$	Weight applied to relationships				
		0	5	20	100	250
A×1 and A×2	3.5	19.5	-7.2	-87.4	-514.9	-1316.4
A×1 and B×2	3	19.0	-4.0	-72.9	-440.4	-1129.4
A×1 and C×2	2.5	18.0	-2.0	-62.0	-382.0	-982.0
B×1 and A×2	3	19.0	-4.0	-72.9	-440.4	-1129.4
B×1 and B×2	2.5	18.5	-3.2	-68.4	-415.9	-1067.4
B×1 and C×2	2	17.5	0.0	-52.5	-332.5	-857.5
C×1 and A×2	2.5	18.0	-2.0	-62.0	-382.0	-982.0
C×1 and B×2	2	17.5	0.0	-52.5	-332.5	-857.5
C×1 and C×2	1.5	16.5	-1.5	-55.4	-342.9	-881.9

## Summary

In this paper we have tried to demonstrate some of the differences between the existing PIGBLUP mate selection module and the system that is under development. In particular, we have shown the difference between accounting for all relationships among candidates rather than inbreeding of the offspring, and the usefulness of including information on relationships with all animals in the population.

If we ignore relationships when selecting the animals that will become parents, taking account of them during mate allocation is of little value, as the pool of genes available to form the next generation has already have been reduced. The provision of a tool to aid in the selection of parents using information on relationships as well as EBVs will therefore have a big impact on the effectiveness of a breeding program.

The development program is well underway:

- The basic components of the system are in place – code for construction and optimisation of the merit function has been written.
- Research is being carried out, via simulation of pig populations, to ascertain:
  - The benefit of using other components in the merit function and the appropriate range of weights to be allowed for each element in the function.
  - How far it is worth going with grouping of non-candidate animals. Animals can be grouped to reflect their current status in the herd, and it may be appropriate to give different weights to information on different groups. This may reflect, for example, the different probabilities of animals joining the breeding herd
- A test dataset has been constructed from information provided by Bunge Meat Industries that will allow the preparation and testing of the interface to be completed.

## References

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