

Mate selection in pigs: a porcine match.com

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Summary

A key reason to maintain genetic diversity in breeding populations is to facilitate longer-term genetic gains. Therefore most breeding programs need to consider genetic diversity as well as shorter-term genetic gains simultaneously. This paper discusses these issues, and presents developments in methods to integrate genetic gains, genetic diversity and other concerns within breeding programs.

Introduction

Livestock breeders juggle many issues when making breeding decisions. One approach to solving these challenges is to follow sets of rules recommended by geneticists and other practitioners. For example, we might

- Use a particular set of economic weightings in an index, or rank and select boars based on a specific trait estimated breeding value (EBV); or
- Use no more than two boars out of any one sire, not mate full sibs, and(or) mate each boar to the same number of females to minimize inbreeding effects; or
- Choose to cull sows after two mating years no matter what their level of performance might be.

These rules have been derived from generalized concepts and theories, and are often not well integrated with each other. For example, theories and rules about selection, crossbreeding and inbreeding have been developed largely in isolation from each other, such that when we mix them in real applications we are likely to miss the best overall strategy.

There can also be the added advantage in making decisions tactically, rather than following a pre-set strategy. The tactical approach makes use of knowledge of the full range of actual animals available for breeding at the time of decision making, as well as other factors such as facilities availability (e.g., farrowing houses or mating pastures), current costs of semen, current quarantine restrictions on animal migration, current or projected market prices, etc. Tactical implementation of the breeding program provides the opportunity to capitalize on prevailing opportunities – ones that would be often missed when adhering to a set of rules. In other words

“Let the design emerge as a consequence of the actions taken tactically”

In this way, technologies are adopted only where appropriate and there is better balance between technical, logistical and cost issues.

In genetic improvement there is an essentially infinite range of possible actions, but in reality only two critical control points – animal selection and mate allocation. Together these constitute *Mate*

Selection. 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 this mate selection approach, we automatically incorporate decisions on factors such as breeding objectives, selection pressure, crossbreeding, inbreeding avoidance, which animals to take semen and embryos from, migration of sires between herds, and how much to spend on, for example, transport. Moreover, we can also satisfy any logistical constraints we want to impose, such as quarantine restrictions on animal movements.

Balancing gain and diversity

A key task for breeding programs within populations is to balance the relative emphasis on genetic gain and maintenance of diversity (Figure 1). This has now been done quite widely in the context of an objective function that includes measures of genetic merit and coancestry among selected parents (Kinghorn *et al.*, 2008). For example, Wray and Goddard (1994) and Brisbane and Gibson (1994) included a negative weighting on animal relationships in selection indices to help control the rate of inbreeding, and hence genetic diversity. Meuwissen (1997) formalized the optimization of animal contributions, differentiating a function that includes genetic merit and animal coancestries, while handling some constraints, and accommodating individual contribution constraints in an iterative manner. Hinrichs *et al.* (2006) have improved speed in this method considerably, and Pong-Wong and Woolliams (2007) have illustrated a method that handles individual contribution constraints directly, and thus gives a guaranteed optimal solution.

The results from such methods generally give *optimal contributions* as proportions on a continuous scale. The practitioner uses these to help make selections and allocate numbers of matings to each breeding animal. This represents a powerful method of allocating more matings to animals of higher genetic merit in a manner that properly manages genetic diversity.

Progressive breeding programs are motivated by many other issues in addition to genetic gain and diversity, including individual progeny inbreeding, connection between herds, management of genetic marker frequencies and genotypes, multi-stage selection, various types of costs, and various logistical constraints. For such cases, contributions can alternatively be specified in numbers of matings to be allocated or the actual mate allocation set (e.g. Kinghorn 2000). However, the optimal solution must be discovered, rather than derived from a fixed set of rules, due to the complexity of the resulting objective function (Kinghorn and Shepherd, 1999). Such problems can be solved using an Evolutionary Computation (EC) approach, or more specifically adaptations of Differential Evolution (DE; Storn and Price 1997). Evolutionary Computation is a broad field of optimization methods loosely based on the biological evolutionary of mutation, crossing-over and selection. The central idea behind EC is to create populations of candidate solutions of a problem and evolve these populations by selection based on an objective function which emulates natural selection (De Jong 2006). Differential evolution gets its name from the way the algorithm matches the size of mutations to the amount of variability in the current generation of solutions (Mayer *et al.*, 2005). This makes the algorithm more adventurous at early stages, while it is looking for general regions in which a good solution might lie. As it begins to home-in on one or a few promising regions, it takes smaller and more measured steps.

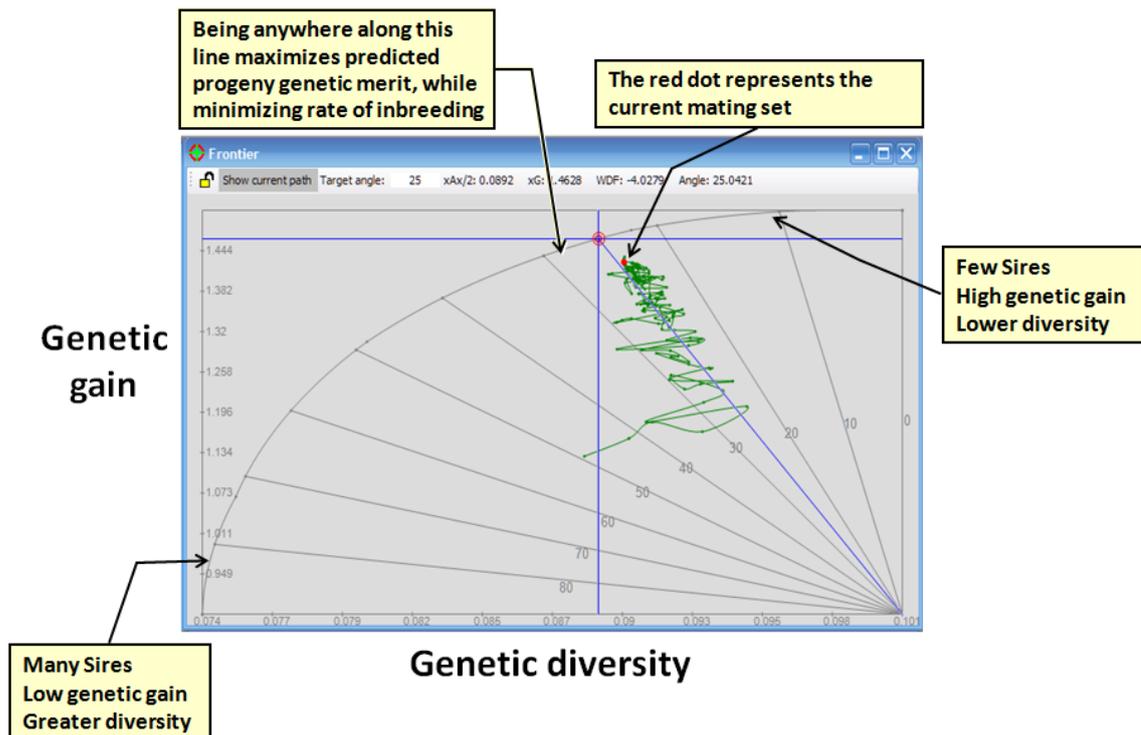


Figure 1. Graphical representation of the relationship between genetic diversity (x-axis) and predicted progeny gain (y-axis). Higher targets along the “genetic frontier” yields higher response and greater loss of diversity. The current mating set is the “target” with a trail behind showing changes as the analysis progresses and as the user changes direction.

The key to making this work relates to how the problem is presented to the solving algorithm. Kinghorn and Shepherd (1999) show how a vector of numbers can be transformed to derive a pattern of animal selection and mate allocation – Mate Selection. This makes the optimization problem simple – the DE algorithm has only to find the vector of numbers that maximizes the objective function.

For each mating set tested, the component outcomes evaluated constitute the overall *Mate Selection Index* (MSI; Figure 2). Each component should ideally be evaluated on the same scale, typically the scale of the breeding objective in units of, for example, dollars profit per breeding female per year. However, in practice it is very difficult to balance disparate issues, and a desired outcomes approach is used whereby the weighting/emphasis for each issue is developed in light of predicted responses that can be achieved, as described in more detail later.

Given a set of weightings, however they have been derived; the MSI is a function of the selections and mate allocations to be made given the available set of candidates in the population (Figure 2). It is used to form a mating set for the specified number of matings in the breeding program.

The MSI can include predicted genetic merit in progeny, long-term inbreeding as reflected by parental coancestry, progeny inbreeding, heterosis (if relevant) and various costs and logistical constraints associated with the breeding program (Banks 2000; Kinghorn 2000; Kinghorn *et al.*, 2008). The objective function can be changed (variables added or deleted) to suit the desired outcomes of the breeder if constraints arise.

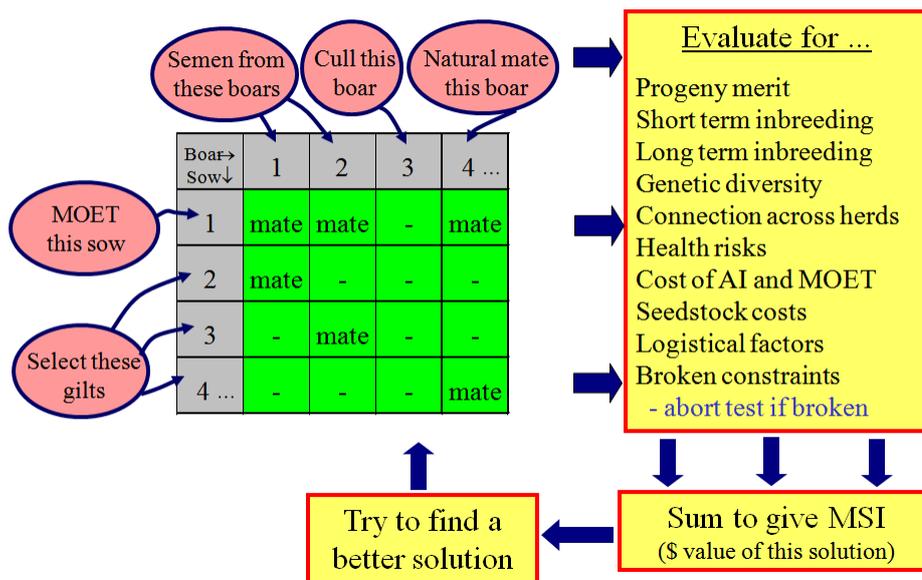


Figure 2. An outline for implementation of a mate selection index (MSI). The set of matings shown is a hypothetical test mating set. The matings specified imply the need for collection of semen, etc., as shown. The mating set is evaluated for all components in the MSI. An efficient algorithm for finding the best mating set is required.

Comprehensive use of a *Mate Selection Tool* (MST) involves decision making at various stages of the life cycle, including selection/culling at various juvenile and adult stages, selections for main round matings and, in some cases, selection of sires for backup matings. Ideally, the MST will accommodate all members of the population, across different groups, including putative embryos *in utero*, immature juveniles, virgin females and pregnant females, as well as candidates for active matings. This helps to accommodate overlapping generations, and to account for contributions already made as reflected by juveniles and embryos in the analysis – sires that have already been used extensively will be inhibited from further use.

Implementing mate selection

The mate selection driver shown in Figure 3 (Kinghorn 2000) was developed to conduct the search across all legal mating sets. The underlined values in Figure 3 drive the three matings noted, and these are the values to be optimised. Number of matings (second column for males, second row for females) is the number of matings for which each animal should be used, and this in turn drives selection, including the extent of use of each animal. An animal is culled if this is set to zero. "Ranking criterion" is simply a real number. It is ranked to give the column "Rank". This in turn drives the mate allocation. The first ranked male mating is the single mating from male 3. He is thus allocated to the first available female mating (the one nearest to the left), i.e., the one mating from female 1. The second ranked male mating is the first mating from male 1. He is thus allocated to the second available female mating (the one second nearest to the left), i.e., the one mating from female 3. The third ranked male mating is the second mating from male 1. He is thus allocated to the third available female mating (female 4).

This process requires the management of constraints on numbers of matings per animal, the number of matings overall, and the management of grouping constraints, as described by Kinghorn (2010). These grouping constraints are required wherever animals can only be allocated to members of the opposite sex that are in an appropriate group, with the two key groups being the male and female active mating groups (although these may be sub-grouped in turn, for example by location).

				Female →	1	2	3	4 ...
Male ↓	No. of matings	Ranking criterion	Rank	<u>1</u>	<u>0</u>	<u>1</u>	<u>1</u>	
1	<u>2</u>	<u>5.32</u> <u>2.16</u>	2 3			Mate	Mate	
2	<u>0</u>	-	-					
3...	<u>1</u>	<u>7.64</u>	1	Mate				

Figure 3. Illustration of the components to be optimized for mate selection. Underlined values (number of matings for males and females and ranking criterion) are to be optimized.

The computing challenge is to find the mating set that gives to best MSI. Part of the need for high speed in such MSTs relates to the need to explore the solution space to find a result that gives a satisfactory balance among the wide range of issues that can be represented in the objective function. It is difficult to be economically rational across issues such as level and cost of migration, pattern of trait distributions, and marker genotype frequencies. Experience shows that iterations of quickly finding an apparently optimal solution for the prevailing objective function followed by adjustments to weighting factors and/or thresholds set in the objective function gives the practitioner a good feel for the trade-offs involved in putting differential emphasis on component objectives. In decision-making theory these solutions are sometimes referred to as *satisficing* – they are optimal given all of the information at hand. This leads to some understanding of what can be achieved, and acceptance of a final mate selection solution. In practice, there is a trade-off between what rigorous scientific effort might determine to be the “best” overall direction, and the direction that is chosen by the practitioner. The latter has the advantage that it is in fact implemented, and not left hanging as a mere recommendation. In addition, of course, the scientific method gets well implemented ‘around’ the constraints and weightings applied by the practitioner - for example, the theory of optimal contributions (Meuwissen, 1997) is invoked, given the prevailing constraints.

Breeding decisions are made on a frequent basis in the pig and poultry industries and so this discovery process needs to be captured in a manner permitting essentially automatic running of the MST with little or no user intervention. This can be achieved using algorithms to maintain certain key outcomes, such as keeping the relationship between parental coancestry and predicted progeny merit within a narrow trajectory, so that other issues cannot displace the final solution from that path. We term this “*Desired Outcomes*” and is analogous to a desired gains selection index (e.g. Brascamp 1984), but where the ratio of gains between two traits (*issues* in the MST case) is softly constrained within certain bounds. Overall response surfaces can be very flat – giving good opportunity to move one issue in a favourable direction, with little compromise in other key issues.

There are a number of operational tools available for the management of genetic diversity. For example, PIGBLUP contains a module PBSAMA (PIGBLUP Selection and Mate Allocation; Crump *et al.*, 2009; Hermesch and Crump, 2006,). Other tools and services include (1) Total Genetic Resource Management, or TGRM, offered by X'Prime (www.xprime.com.au); (2) GENCONT (Meuwissen, 2002; Hinrichs *et al.* 2006); (3) EVA (Berg *et al.*, 2006) (www.nordgen.org/index.php/en/content/view/full/63/); (4) Ani-Mate, a service provided by AbacusBio (www.abacusbio.co.nz/products.html); and (5) MateSel in Pedigree Viewer (www-personal.une.edu.au/~bkinghor/pedigree.htm). Tools such as these are now being used in breeding programs for sheep, beef and dairy cattle, pigs, poultry and other species.

The Implementation level of these tools ranges from providing target numbers of matings for each candidate animal, with the aim of maximizing genetic gain at a defined rate of inbreeding, through to dictation of all stages of selection, culling, semen collection, mate allocation and backup matings, with comprehensive attention to the full prevailing range of technical and operational constraint issues. More complete implementations take a considerable amount of setting-up. However, once established they provide for routine optimal implementation of progressive breeding programs. They also constitute an appropriately competitive framework for implementation of new technical opportunities, such as reproductive boosting, targeting pools of opposing homozygotes for nominated genetic markers, or engineering extra genetic variation in key traits well before the physical splitting or merging of breeding lines.

Look ahead mating strategies (Hayes *et al.* 2002, Shepherd and Woolliams, 2004) have been proposed, aiming to exploit non-additive components some generations ahead. This includes the setting up of “investment matings” (such as F₁ crosses) to capitalize on “realization matings” (such as a 3-breed cross using F₁ females; Shepherd and Kinghorn, 1998). This constitutes short-term management of genetic variation for longer term gains. A simulated example has been given by Li *et al.* (2006) where an MST operating on cohorts rather than individuals was implemented for simultaneous decision making over generations, resulting in the setting up of divergent lines to exploit dominance at known loci. This approach has the potential to give tactical targeting of a suitable route through genotypic changes across multiple interacting loci, should we ever have sufficient understanding of the genotypic effects involved.

Acknowledgements

Portions of this paper were presented at the 58th National Breeders Roundtable; St. Louis, Missouri, 7 to 8 May 2009.

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