Chapter 19

Targeting QTL genotypes using mate selection

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Industry mating structures to exploit QTL

The figure below shows industry mating structures appropriate to QTL with different modes of inheritance and affecting different traits. Each has its own appropriate mating structure. However, when we have access to many QTL affecting the trait(s) of interest, we cannot exploit all QTL optimally within a few generations. We can use mate selection methods to more quickly approach these ideal genotypes while accommodating other issues of importance, such as polygenic effects, inbreeding and costs.

The situation in this figure can be further complicated by interaction between loci, in which case favourable dominance and epistatic interactions need to be accounted for at all stages in development of ideal multi-QTL genotypes. Genetic evaluation of type 4 (as describe in Chapters 17/18) provides the genotype probabilities needed for this.

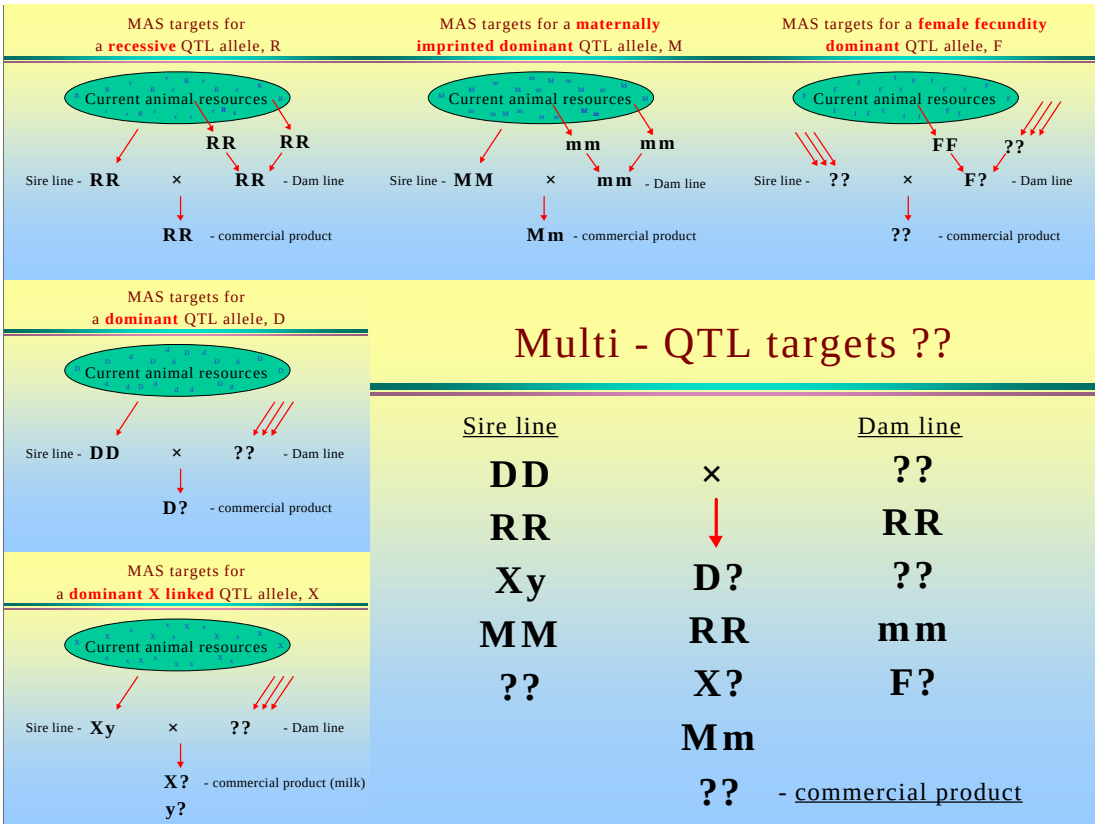

Figure. Mating structures for individual QTL in an industry where maternal effects are important. Also shown are the ideal multi-QTL genotypes that cannot be generated easily.

Non-additive genetic effects and mate selection

[As note previously: Genetic value is the value of an animal's genes to itself. Breeding value is the value of an animal's genes to its progeny. In general, breeding value has

been of much more importance to animal breeders - it reflects the merit that can be transmitted to the next generation. It is the sum of the average effects of alleles carried by the animal, and because of the large number of loci classically assumed, there is no power to capitalize on anything but the average effects of these alleles, as dominance deviations in progeny cannot be predicted under normal circumstances.]

However, when dealing with individual QTL we have the power to set up matings designed to exploit favourable non-additive interaction in the progeny. This means that prediction of breeding value at individual QTL will only be of partial value in many circumstances. Therefore we should consider both prediction of breeding values and prediction of QTL genotypes, and therefore genetic values, at individual QTL.

Of course prediction of QTL genotype of candidates is only of real value in helping to predict genetic values of their progeny - because the object is to improve performance of descendants. This in turn means that the evaluation system should be intimately associated with the mate allocation process, wherever non-additive effects are to be exploited. The combination of animal selection and mate allocation can be termed *mate selection*. Application of evaluation systems to exploit individual QTL will thus frequently involve mate selection strategies in addition to the simpler ranking processes we are used to with selection.

One extreme example of this is where we manage to use genetic markers to identify QTL and chromosomal regions which can contribute strongly to increased expression of heterosis in crossbred progeny. Recurrent selection of purebreds on the performance of their crossbred progeny has not been of great practical value - however now with extra information from genetic markers and known QTL we have some power to breed for increased heterosis in a systematic manner.

Mate selection

Breeding program design can be pre-determined and implemented through sets of rules, or it can emerge as a consequence of decisions made at the level of individual matings. This latter approach is the tactical approach, with decisions made tactically in the face of prevailing animals and other resources.

Tactical implementation of breeding programs provides a practical means to integrate technical, logistical and cost issues facing animal breeders. Moreover, tactical implementation benefits from opportunistic use of prevailing animals and other resources, resulting in better outcomes.

In any breeding operation, there is an almost infinite range of actions that can be made, involving decisions on issues such as animal selection, semen collection and purchase, and mate allocations. Each set of actions is predicted to have a given utility to the breeder - based on factors such as genetic gains, risk, costs and constraints satisfied. The tactical approach described in this chapter works by searching across all these possible routes ahead, and finding the one that is predicted to best suit the breeder’s needs. This has only recently become possible because of development of

efficient computing algorithms that mimic evolutionary processes to find the best solution.

The key idea here is to integrate Marker Assisted Selection into this mate selection approach. This gives us a basis to exploit multiple interacting genes – whether using direct or indirect markers (or no markers, just segregation analysis) to get a handle on these genes.

The overall approach can be found in one of these:

Kinghorn, B.P. 2000. The tactical approach to implementing breeding programs. Chapter 22 in "Animal Breeding – Use of New Technologies", Kinghorn, B.P., Van der Werf, J.H.J. and Ryan, M. (eds.). The Post Graduate Foundation in Veterinarian Science of the University of Sydney. ISBN 0 646 38713 8. Pages 291-308.

Kinghorn, B.P. 2000. Tactical implementation of beef cattle breeding programs. 3rd National Symposium on Animal Breeding. Belo Horizonte, Brazil. 5-8 June 2000. 8 pages.

… and this will be covered at the presentation of this Chapter.

Objective functions for MAS

The simplest objective function is to maximise trait or index merit in prospective progeny. If we have genotype probabilities to work on, then ideally we should ***not*** predict progeny merit as the mean of parental EBVs, even if these EBVs have been calculated with information from markers using a GRM (Chapter17/18). This is because we will miss out on opportunity to exploit favourable dominance (and maybe also epistasis) as expressed in progeny.

Predicted progeny merit for a single locus can be predicted simply. For example, for a 2-allele locus (A,a), the genotype probabilities for a progeny from a give mating can be found as follows:

Probability of inheriting allele A from sire = $p_s(A) = Prob_{sire}(AA) + ½\ Prob_{sire}(Aa)$

Probability of inheriting allele A from dam = $p_d(A) = Prob_{dam}(AA) + ½\ Prob_{dam}(Aa)$

Progeny genotype probabilities:

$$p(AA) = p_s(A) * p_s(A)$$

$$p(Aa) = p_s(A) * [1-p_d(a)] + p_d(A) * [1 - p_s(A)]$$

$$p(aa) = [1 - p_s(A)] * [1 - p_d(A)]$$

The predicted progeny merit at this locus is then:

$$p(AA) * a + p(Aa) * d + p(AA) * -a$$

where a, d and –a are the estimated effects of the three genotypes. For multiple loci, we can adopt a model such as that in Chapter 10.

To exploit dominance more effectively we can look more than one generation ahead. The same is particularly true for epistasis. In the present context, "look-ahead" idea provides some challenges for optimisation (Shepherd, R.K. and **Kinghorn, B.P.** 1998. A tactical approach to the design of crossbreeding programs. 6th World Congress on Genetics Applied to Livestock Production. Armidale, 11-16 January, 1998. 25: 431-438).

However, as illustrated in the first figure - this is an area that will become important as we get a handle on more and more QTL and directly marked genes.