

## **IS BREEDING FOR PROFIT STILL THE ANSWER?**

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### **SUMMARY**

This paper addresses changes of attitudes to breeding objectives in various parts of the world, and how arguments for considering more than just farm profit as the primary driver when establishing a breeding goal are becoming more prominent. While genomic selection should in theory lead to levels of genetic progress across a broader range of traits that should satisfy both farmers and other stakeholders within society, it will commonly require investment in phenotyping and genotyping to achieve this in practice. Targeted genotyping and phenotyping investment by industry and governments could lead to reduced green house gas emissions, less disease, improved animal welfare and animal production systems robust to fluctuations in the physical environment and global commodity prices while retaining breeding program focus on improved farm profit.

### **INTRODUCTION**

Farm profit is a key driver of farm decision making but this can lead to conflict between farmers and non-farm stakeholders in the farm production to food value chain. This conflict has been discussed in detail by Nielsen *et al.* (2011) in the context of animal welfare. An additional complication arises through evidence emerging that future breeding goals for reduced greenhouse gas emissions per unit of product may favour improvement of productivity traits that intensify production systems to the detriment of animal welfare (Wall *et al.* 2011). Accounting for greenhouse gas emissions in the breeding goal leads to changes in the economic weights applied to traits (Wall *et al.* 2011, Ludemann *et al.* 2011). Future global changes may lead to instability in weather patterns and more intensive use of marginal grazing lands due to high animal protein prices. Because of inelasticity of food prices, there is a likelihood of increased instability of product prices. Thus, the need to maintain farm profitably from year to year under greater environmental variability may motivate further changes to breeding objectives away from farm profitability at average price levels.

Because of high transaction costs associated with tracing emissions at farm level, and a reluctance by governments around the world to include agriculture into emissions trading schemes, consumer and retailer imperatives are likely to be the main drivers of perceived changes to breeding objectives to incorporate greenhouse gas emissions. They are also likely to be drivers of higher priority placed on traits linked to animal welfare, and to traits linked to product quality, but with market failure in the supply chain failing to incentivise farmers to improve them. In this paper, the artificial evolution concept defined by Gibson (1989) is put forward as providing an opportunity for government, and industry stakeholders to further, and possibly more effectively, manipulate genetic improvement developments to meet objectives beyond farm profitability. The theory is then used to consider how the design of new breeding programs and breeding strategies that incorporate genomic selection (Meuwissen *et al.* 2001) can create further opportunities for off-farm stakeholders to influence the direction of genetic improvement.

### **THEORY**

Gibson (1989) identified the importance of trait recording choices in influencing the direction of genetic change in addition to factors such as trait variances/covariances and economic weights. The argument was that under uncertain economic weights, choice of breeding program design might be influenced by projections of genetic trends that could eventuate; with some technical

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judgement applied as to what might be a preferred outcome. A similar philosophy has been used intrinsically for many years by huge scale breeding programs for intensive livestock species (pigs and poultry) and manifests itself as the use of desired gains indexes when assigning economic weights for traits. In this context, elite breeding lines often service a wide range of multiplier systems for a large number of countries and production environments. A further extension of the Gibson (1989) concept applies to the choice of selection criteria within a breeding scheme design. Because development of new selection criteria often requires outside investment, there is substantial scope for manipulation of the direction of genetic improvement via industry and government investment in research of new selection criteria.

Genomic information as proposed by Meuwissen *et al.* (2001) constitutes a new selection criterion, which is not trait neutral in its impact. With the same number of training animals, selection criteria incorporating high density SNP information in prediction result in greater proportional increases in responses in low heritability traits. Traits where the best phenotypic information on selection candidates and their relatives tends to become available after the primary selection point are also favored. This pattern of trait bias associated with genomic selection is further influenced by the number of phenotypes available for training.

Daetwyler *et al.* (2010) have developed prediction equations for the accuracy of genomic selection strategies for traits with specified heritability and number of training individuals. These equations can be used to predict the types of trait preference bias that might arise with genomic selection, and how steps to increase the number of genotyped and phenotyped training animals become a further instrument of change. Here, a genome of 30 morgans and a group of selection candidates with an effective population size of 120, and a high density marker test tracking 750 independent chromosome segments was assumed. An efficiency ratio of genomic selection relative to mass selection ( $GSeff$ ) for a specific phenotype  $i$  is defined as

$$GSeff(h^2, n)_i = \frac{r_{GS}(h^2, n) \cdot p}{a \cdot \sqrt{h^2}}$$

where  $r_{GS}$  is the accuracy of genomic selection as defined by Daetwyler *et al.* (2010) and which, among other things, is a function of  $h^2$ , the effective heritability of the phenotype of interest and  $n$ , the number of training animals with genotypes. The term  $p$  is the effective proportion of the genome that is covered by markers following Woolliams (2010) and was assumed here to be 0.9. The constant  $a$  accounts for the fact that selection without markers may be inefficient under a breeding scheme designed specifically to exploit genomic information. For example, with high effective heritability, and low numbers of training animals, a breeding program historically relying on progeny testing may not benefit from genomic selection unless more selection is applied to juvenile animals and the generation interval shortened. Both terms  $a$  and  $p$  will tend to be relatively constant across traits within any particular breeding program.

Now consider a breeding program with two traits of interest; a primary trait has a higher effective heritability, and a large number of recorded animals, while a secondary trait has a lower effective heritability and less recorded animals. The degree of emphasis shift towards genetic progress away from the primary trait and towards the secondary trait that might be expected with genomic selection can be measured using a ratio defined as follows:

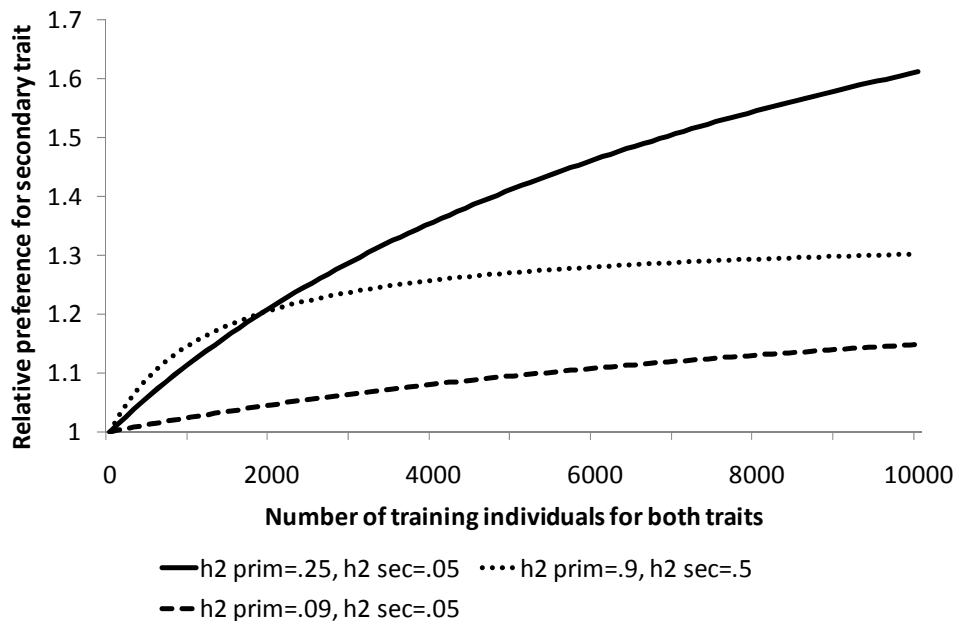
$$ratio_{2:1} = \frac{GSeff(h_{secondary}^2, n_{secondary})_i}{GSeff(h_{primary}^2, n_{primary})_i}$$

A value of  $ratio_{2:1}$  greater than one indicates that genomic selection would lead to the secondary trait contributing a greater proportion of response, relative to a breeding program without genomic

selection. Note that this occurs without any change in economic weights in line with the Gibson (1989) concept of artificial evolution.

**RESULTS**

Figure 1 shows how genomic selection favours genetic progress in secondary traits under the assumption of equal numbers of training animals for both the primary and secondary trait. This secondary trait preference rises quite quickly with lower numbers of training animals when the primary and secondary traits have high heritability, but the greatest secondary trait preference occurs when there is a large difference in heritability between the primary and secondary trait.



**Figure 1. Relative change in selection responses in the secondary versus the primary trait with the introduction of genomic selection.**

In practice, secondary traits are commonly less well recorded than primary traits and so the assumption of equal numbers of training animals will often not hold. For example, in the situation where the primary and secondary traits have low heritabilities of .05 and .09 respectively and there are less than 5000 training individuals, then the secondary trait must have at least 80% of the number of training individuals of the high heritability trait or genomic selection favours genetic progress in the primary trait. This pattern is less severe for the other heritability combinations shown in Figure 1, and further declines as the number of training individuals increases.

**DISCUSSION**

Over the past decade, the selection emphasis applied to secondary traits in livestock breeding programs has increased due to efforts to expand selection criteria and broadening of breeding goals such that more traits have estimated breeding values and economic weights. However, there are many stakeholders who feel that unfavourable effects on animal welfare traits and loss of robustness of animals to fluctuations in production environments are still too high. These stakeholders would like to see more selection emphasis placed on secondary traits that are not

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directly associated with productive output such as milk yield, growth rate and meat yield, including traits that could lead to reduced livestock greenhouse gas emissions. Vertically integrated supply structures and increased demands placed on farm suppliers by retailers will drive this trend further, but such drivers are blunted by lack of market signals as many livestock products are sold into commodity markets.

In theory, genomic selection offers opportunities to improve the relative rate of genetic progress in secondary traits. It is a major advantage that this can occur without switching selection emphasis away from farm profit, and will likely lead to faster rates of genetic improvement in farm profitability. However, results shown here indicate that considerable investment in both genotyping and phenotyping will be required to realise the full potential of this opportunity. This strengthens the case for government and industry investment in genomic selection initiatives.

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